Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of Toxoplasma gondii

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Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of *Toxoplasma gondii*

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Short title

Aspartyl protease 5 and its substrates during *Toxoplasma* encystation

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Abstract

Virulence and persistence of the obligate intracellular parasite *Toxoplasma gondii* involve the secretion of effector proteins belonging to the family of dense granule proteins (GRAs) that act notably as modulators of the host defense mechanisms and participate in cyst wall formation. Subset of GRAs residing in the parasitophorous vacuole (PV) or exported into the host cell, undergo proteolytic cleavage in the Golgi upon the action of the aspartyl protease 5 (ASP5). In tachyzoites, ASP5 substrates play central roles in the morphology of the PV and in the export of effectors across the translocon complex MYR1/2/3. Here, we used N-terminal amine isotopic labelling of substrates to identify novel ASP5 cleavage products by comparing the N-terminome of wild-type and Δ*asp5* lines in tachyzoites and in bradyzoites. Validated substrates reside within the PV or PVM in an ASP5-dependent manner. Remarkably, Δ*asp5* bradyzoites are impaired in the formation of the cyst wall *in vitro* and exhibit a considerably reduced cyst burden in chronically infected animals. More specifically two-photons serial tomography of infected mouse brains revealed a comparatively reduced number and size of the cysts throughout establishment of persistence in the absence of ASP5.

Author summary

The obligate intracellular parasite *Toxoplasma gondii* replicates within a parasitophorous vacuole (PV) and co-opts host cellular functions including defense mechanisms via the secretion of effector proteins (GRAs) from the dense granules. During their intracellular traffic, a subset of GRAs residing in the PV or exported into the host cell are subjected to a proteolytic cleavage catalyzed by the Golgi aspartyl protease 5 (ASP5). In fast replicating tachyzoites, ASP5 substrates play central roles in the morphology of the PV and in the translocation of effector GRAs via the complex MYR1/2/3 across the PV membrane. In slowly dividing bradyzoites, ASP5 plays a key role in cyst wall formation and hence is an important virulence factor critical for establishment of chronic infection. Our results indicate that ASP5 substrates are not translocated across the mature cyst wall, suggesting that ASP5 might play a structural role for maintenance of the cyst wall.

Introduction

Together with *Eimeria spp*, *Sarcocystis spp*, *Besnoitia*, *Cystoisospora*, *Frenkelia*, *Neospora* and *Hammondia*, *Toxoplasma gondii* belongs to the tissue-cysts forming clade of enteric coccidians that constitute a considerable threat for human and animal health. *T. gondii* relies on felids as definitive hosts for sexual reproduction and on a broad range of warm-blooded animals to persist and ensure transmission. Most developmental stages of *T. gondii* possess a unique ability to invade almost any nucleated cell and replicate inside a parasitophorous vacuole (PV), which facilitates rapid systemic distribution of tachyzoites during the acute phase of infection. Subsequently, a potent host immune response induces differentiation of tachyzoites into bradyzoites, a slowly-replicating developmental stage enclosed within tissue cysts. Cysts are established in long-lived cells, predominantly in neurons and skeletal/smooth muscle cells. They represent a transmissible form between intermediate and definitive hosts during predation, but also between intermediate hosts, which greatly contributes to the high prevalence of *T. gondii* in animals and humans. A thick cyst wall (CW) limits detection by the immune system and protects the parasites within. The CW is elaborated from the PV membrane (PVM) and is decorated with dense granule proteins (GRAs) (1), including markers exclusively expressed during bradyzoite development (2). The CW is typically covered by highly glycosylated proteins, binding to lectins (3). While intravacuolar GRAs were shown to participate in the maturation of the cyst matrix and CW (4), the dynamic of CW formation as well as the precise molecular composition of this structure remain poorly understood.

Distinct classes of GRAs have been previously described and are associated to various functions linked to parasite-host communication and nutrient acquisition (5, 6). In the tachyzoite stage, many GRAs are restricted to the PV and participate in the elaboration of an intravacuolar network (IVN) embedding parasites and shaping the vacuole (6). In addition, several GRAs localize to the PVM, at the interface with the host cell cytosol, where they modulate host cell signaling pathways (GRA6 (7); GRA7 (8); GRA12 (9); GRA15 (10, 11); GRA60 (12)) or mediate the recruitment of host organelles to the vicinity of the PVM notably via MAF1 (13). Finally, a category of GRAs containing intrinsically disordered domains are exported beyond the PVM and reside in the host cytosol such as GRA18 (14) or are imported into the host cell nucleus i.e. GRA16 (15), GRA24 (16), GRA28 (17), IST (18, 19) and TEEGR (20, 21) to remodel the host transcriptome in favor of parasite long-term persistence. Intriguingly, GRAs are often polymorphic proteins that are associated to virulence phenotypes depending on the type of *T. gondii* strain (5). While kinases and pseudokinases discharged into the host cells by the rhoptries during invasion tend to be crucial for the virulence of type I strains (22), GRA effectors play a pivotal role in establishing persistence of type II strains (5). In the mouse model, animals infected with type I strains cannot control the acute infection and rapidly succumb to toxoplasmosis, whereas type II strains produce a chronic infection. Consequently, mice infected with type II strains are a useful model to study tissue cyst formation and chronic toxoplasmosis.

Several GRAs are proteolytically processed by the Golgi-resident aspartyl protease 5 (ASP5) that typically cleaves after an arginine-arginine-leucine (RRL) motif termed TEXEL (Toxoplasma export element) (23-25). A subset of GRAs harboring a TEXEL motif i.e. GRA19, GRA20 (25), and ROP21 (previously incorrectly assigned to rhoptries but localizing to the PV space, thus possibly originating from the dense granules (26)) are directly cleaved by ASP5 and localize to the PVM. The ASP5 substrates GRA16 (23, 24) and IST (18, 19) belong to the class of GRAs that are exported across the PVM into the host cell in a ASP5-dependent fashion. ASP5 indirectly affects the export of GRA24 and TEEGR, that do not contain a recognition motif, by processing MYR1 (20, 27). Mature MYR1 forms a complex with MYR2 and MYR3 to facilitate protein translocation across the PVM into the host cytosol (27, 28).

Recently, a proteomics method to selectively enrich N-terminally derived peptides termed Terminal Amine Isotopic Labeling of Substrates (TAILS) was used to uncover additional ASP5 substrates, all residing in the PV, i.e. LCAT, WNG1 (formerly ROP35), WNG2 (formerly ROP34), GRA44, GRA45 and GRA46 (29). Although the repertoire of ASP5 and MYR1-dependent exported effector proteins is to some extent redundant, the overlap is not complete. Indeed, a comparative analysis of the transcriptome of human foreskin fibroblasts (HFF) infected with type I Δ*asp5* or Δ*myr1* tachyzoites revealed that, in addition to a large core of genes showing similar differential regulation in both cases, ASP5 and MYR1-dependent exported effectors modulate independently the expression of a subset of genes in the infected host cell (30-32). The impact of ASP5 and MYR1 on the host transcriptome translates *in vivo* into a decreased virulence of type II tachyzoites individually deleted for these genes (25, 27, 30). However, there is little information about the contribution of ASP5 and MYR1 to protein export in bradyzoites and to persistence during the chronic stage of infection.

Here, we compared ASP5 substrates repertoires of tachyzoites and stage-converted bradyzoites *in vitro*. We used a TAILS approach for a comparative proteomic profiling of wild-type (WT) and Δ*asp5* in both developmental stages. This revealed novel PV-targeted GRAs and allowed refinement of the ASP5 cleavage signature motifs. We carried out a global analysis of GRA-related functions in tachyzoite and bradyzoite stages, by examining the translocation of GRAs across the CW upon maturation and through phenotyping of ASP5 and MYR1 mutants, including the impact on PV morphology and CW formation *in vitro*. Further, we evaluated the contribution of ASP5 on cyst formation and dissemination in brains of chronically infected mice by performing full brain imaging. This study broadens our understanding of the roles of ASP5 and MYR1 in the formation of the parasite-induced subcellular membrane bounded compartments during acute and chronic stages and outlines the dynamics of parasite dissemination in the brain.

Results

N-terminome analysis uncovered novel ASP5 substrates

In an effort to determine the repertoire of ASP5 substrates in tachyzoites and bradyzoites, we applied the Terminal Amine Isotopic Labelling of Substrates (TAILS) analysis that was successfully employed to uncover ASP3 substrates and to establish its role as broad maturase for microneme and rhoptry proteins in the endosomal-like compartment (ELC) (33). We conducted a quantitative comparison between the N-terminomes of wild-type (WT) and Δ*asp5* tachyzoites and bradyzoites. Candidate proteins identified from these datasets are presented in Table 1 with a comprehensive output in S1 and S2 Tables. 2299 and 616 N-terminal peptides were identified in the tachyzoite and *in vitro* differentiated bradyzoite samples, respectively. Normalized log2 abundance ratios (WT/Δ*asp5*) were calculated for each peptide group. Arbitrary upper and lower thresholds of <0.5 and >2 ratios were applied to identify proteins with ASP5-dependent processing. Among the labelled peptide groups, we found 133 and 225 peptides in tachyzoites and bradyzoites, respectively, with either <0.5 or >2 ratios in the absence of ASP5. The candidate list was further refined by filtering for structural features i.e. the presence of a predicted signal peptide (SP) or N-terminal transmembrane (TM) domain. This yielded 84 and 104 peptide groups, respectively, corresponding to 49 and 74 proteins, in the tachyzoite and bradyzoite lists, respectively. Previously identified and validated ASP5 substrates served as positive control to validate the results (25, 29). In addition, all protein sequences were interrogated for the presence of intrinsically disordered regions (IDR), as a potential signature for exported effector GRAs (34) (S1 Fig). Consistent with the role of ASP5 as a maturase for GRA proteins, we found several previously characterized GRAs in the list (GRA1, GRA2, GRA3, GRA4, GRA6, GRA7, GRA12, GRA17, and GRA23). Some of these GRA proteins were recently reported as ASP5 substrates (29), while others were not known to be processed by ASP5 (Table 1 and S2 Table). Importantly, the TAILS analysis also uncovered several hypothetical and uncharacterized proteins as well as proteins of the cyst wall proteome (35).

Identification of novel PV and PVM proteins processed by ASP5 in tachyzoites

We selected eight candidates from the filtered TAILS tachyzoite dataset for further investigation of ASP5-dependent cleavage and localization (Table 1). Candidate genes were epitope-tagged at the endogenous locus in WT parasites and Δ*asp5* lines (S2 and S3 Fig). To this end, we designed Cas9-targeting guides against the gene of interest for co-transfection with the PCR product of 3Ty tags linked to a DHFR selection cassette and flanked by 25-bp homology regions (S2 and S3 Fig).

Five out of the eight candidates were confirmed as ASP5 substrates: TGME49_241240 (GRA65), TGME49_320490 (GRA66), TGME49_247440 (GRA33), TGME49_279100 (GRA67) and TGME49_240090 (WNG2). GRA65 has no known domain and possesses a predicted SP and two TEXEL motifs at positions 68 (RLLAE) and 83 (RELVD) amino acids (aa), with the peptide at the RRLAE motif enriched in the TAILS tachyzoites dataset. GRA65 is detected as two products around a molecular weight (MW) of 110 kDa by Western blot (WB) (Fig 1A). In the absence of ASP5, only the upper band was detected. Immunofluorescence assays (IFA) shows weak expression in tachyzoites as a faint vesicular signal in the cytoplasm of tachyzoites and in the PV (Fig 1B). GRA65 accumulates in the region of the tachyzoite Golgi in Δ*asp5* parasites. GRA66 is a novel GRA with a MW of 126 kDa predicted to contain an N-terminal TM domain that might serve as SP and a beta lactamase superfamily domain. A tryptic peptide containing a non-canonical TEXEL motif at position 361 (RHLLT) was enriched in the TAILS bradyzoite dataset. GRA66 migrates as a major product around 120 kDa by WB, and at a lower apparent MW in Δ*asp5* (Fig 1C). Its PVM localization in WT parasites is disrupted in Δ*asp5*, where it localizes inside the PV (Fig 1D). GRA67 belongs to the *MAF1a* family (36) and is also a novel GRA. It has a predicted MW of 48 kDa and contains a SP and an internal TM domain. It migrates as multiple products from 40 to 55 kDa in SDS-PAGE and intermediate bands are detected by WB in Δ*asp5* (Fig 1E). GRA67 is detected in the PV in WT but accumulates in the parasite Golgi and endosome-like compartment (ELC) in Δ*asp5* parasites, as shown by partial co-localization with GRASP and ASP3 markers (Fig 1F).

Among all candidate genes, known dense granule proteins were selected for further validation as ASP5 substrate. GRA33 has a MW of 40 kDa and is predicted to contain a SP and three internal TM domains. GRA33 migrates as a major form around 55 kDa and is detected in the PVM in WT parasites but is concentrated inside the PV in Δ*asp5* and migrates at a higher MW (Fig 2A-B). GRA34 has a calculated MW of 36 kDa and contains a predicted SP. GRA34, does not appear to be an ASP5 substrate as its migration profile (27-30 kDa) is unchanged in absence of ASP5 (Fig 2C). However, its PV localization changes to vesicular and accumulates around the residual body (RB) in Δ*asp5* parasites (Fig 2D). WNG2 (29, 37) (formerly ROP34 (38, 39)) has a predicted MW of 62 kDa and harbors an N-terminal TM domain and a serine/threonine kinase domain. By WB, WNG2 migrates as two products around 60 kDa, with a predominance of the smaller one (Fig 2E). In absence of ASP5, we observed an accumulation of the larger product. While the protein localizes in the PV and at the PVM in WT parasites, it displays a Golgi/ELC localization pattern and seems to concentrate next to the RB in Δ*asp5* parasites (Fig 2F).

TGME49_293510 has a calculated MW of 44 kDa, contains a predicted SP, in addition to poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region domains. TGME49_293510 migrates as a single product of ~45 kDa and localizes to the parasite nucleus (S4A Fig). TGME49_216060 has a predicted size of 84 kDa with a putative N-terminal TM domain. It migrates as a single product of about 140 kDa and localizes to the perinuclear area (S4B Fig). Both TGME49_293510 and TGME49_216060 are likely false-positive hits, which appear not to be processed by ASP5.

Of note, numerous surface antigen proteins (SAG) were identified in the tachyzoite and bradyzoite lists. SAGs are GPI-anchored and traffic through the Golgi to reach the parasite surface. Since C-terminal tagging is not possible in this case, we introduced epitope tags inside the coding sequence in transgenic lines (S5 Fig). The integration of Ty tags in the WT and Δ*asp5* parasites of type I and II strains was confirmed by sequencing the modified gene locus in the transgenic strains. Out of the four SAGs coding genes examined, only SRS25 was detectable using an anti-Ty antibody in IFA. The tagged SRS25 localized at the parasite plasma membrane and displayed no altered localization or processing in the Δ*asp5* parasites (S4C-S4F Fig). The presented data, corroborated by the co-localization with GRA1, confirms that GRA 65, 66, and 67 are novel dense granule proteins. Together with GRA33 and WNG2, all are *bona fide* substrates of ASP5.

Identification of novel components of the cyst wall

Within the TAILS analysis, six candidates were detected exclusively in the bradyzoite dataset and were further investigated. Although none was a substrate for ASP5 as evaluated by WB, five turned out to reside in the PV or PVM in tachyzoites, and in the cyst matrix or at the CW in bradyzoites. MCP4 (microneme adhesive repeat domain-containing protein 4 (2)) has a predicted MW of 105 kDa, a SP, and two sialic acid binding micronemal adhesive repeats. WB analysis revealed that MCP4 is more abundantly expressed in bradyzoites (after 1 week of *in vitro* differentiation using alkaline treatment (40)) than in tachyzoites, as previously reported (2). The tagged protein is detectable as multiple bands between 80 and 130 kDa in WB that appear unchanged in Δ*asp5* tachyzoites (Fig 3A). MCP4 is hardly detectable by IFA in tachyzoites and localizes to the dense granules in extracellular bradyzoites (Fig 3B-C). MCP4 localization to the cyst wall in WT bradyzoites remains unchanged in Δ*asp5* parasites, despite the overall different CW morphology commonly observed in Δ*asp5* (Fig 3C). GRA68 is a newly identified GRA, which contains a SP and migrates at the predicted MW of 38 kDa in tachyzoites and bradyzoites, but its expression level is reduced in bradyzoites (Fig 3D). GRA68 localizes to the dense granules in extracellular tachyzoites (Fig 3E), and is found in the PV of tachyzoites and in the cyst matrix and CW of bradyzoites (Fig 3F). GRA68 subcellular localization appears altered in Δ*asp5* bradyzoites. GRA69 is a new GRA that contains a SP, an oligopeptidase F and a peptidase family M3 domain that are typical of metalloproteases ("zincins"). GRA69 migrates as a single product at the predicted MW of 75 kDa by WB in tachyzoites and a second product of lower MW appears around 30 kDa in bradyzoites (Fig 3G). It localizes to the dense granules in extracellular parasites (Fig 3H) and to the PV in tachyzoites, in the cyst matrix and the CW in bradyzoites (Fig 3I). The localization of GRA69 is unaltered in Δ*asp5* parasites. TGME49_297160 displayed a mitochondrial pattern, a localization also predicted by LOPIT (S6A Fig). SUSA1 and TGME49_209755 are two PV-resident proteins in tachyzoites and are detected in the cyst matrix in bradyzoites (S6B and S6C Fig). Overall, the analysis of the bradyzoite TAILS led to the identification of two novel GRA proteins.

Export of bradyzoite effector proteins occurs through the immature cyst wall

While secretion, export and subcellular targeting and function in the host cell have been investigated in detail for several GRAs in the tachyzoite stage, little is known about the fate of GRAs in bradyzoites. To investigate the permissiveness of the cyst wall for export to the host cell, we focused on the effector protein IST, which is exported to the host cell nucleus in tachyzoites (18, 19). We first generated an endogenously IST-3Ty tagged strain in a ME49Δ*hx*Δ*ku80* (WT) background (S7A and S7B Fig). As we aimed to express IST-3Ty selectively in mature cysts, we selected the promoter of p21 (TGME49_238440, SAG-related sequence SRS22A), a late bradyzoite marker for which a previously described antibody is available (40). TGME49_238440 was identified as the gene encoding p21 while performing a large-scale screen for a different study. The genetic deletion of TGME49_238440 led to the disappearance of p21 signal, as shown by collecting parasites as tachyzoites or as bradyzoites, at different time points after differentiation *in vitro* (Fig 4A and 4C, S7A-C Fig). We also assessed the impact of *p21* deletion *in vivo* and observed no significant effect on the cyst burden (S7D Fig). p21 localizes to the micronemes, as shown by co-localization with AMA1 (Fig 4B). p21 is expressed from day 4 following differentiation (Fig 4C) and can be considered as a late bradyzoite marker, as compared to SAG4 (Fig 4D) or DBA (Fig 4E), with an expression peaking after 7 days of differentiation (Fig 4F). Importantly, deletion of p21 does not alter appearance of early differentiation markers DBA and SAG4 (Fig 4D-E). We replaced the endogenous IST promoter with the p21 promoter to generate the line P_{p21}-IST-3Ty (S7E and S7F Fig). As anticipated, IST-3Ty under the endogenous promoter was sustainably expressed in tachyzoites and in bradyzoites differentiated *in vitro* for 4, 7 or 10 days, as observed by WB (Fig 4G). Under the p21 promoter, the IST-3Ty product was only detectable after 4 to 7 days of differentiation by WB and IFA (Fig 4G-H). We observed two scenarios for the accumulation of IST-3Ty in the host nucleus: in cells infected by a single cyst, the levels of IST-3Ty or P_{p21}-IST-3Ty in the nucleus were lower than in tachyzoites, suggesting that bradyzoites reduce or stop IST export upon CW maturation (Fig 4I-J); in cells infected with a cluster of small-sized cysts, likely resulting from the rupture of a large cyst in the vicinity, IST-3Ty was increasingly detected in the nucleus over differentiation, while P_{p21}-

IST-3Ty was abundantly found in the nucleus from 4 days of differentiation (Fig 4I and 4K), indicating that newly formed cysts by fully mature bradyzoites are able to secrete IST. The increased IST-Ty signal in the host nucleus over the course of the experiment is likely explained by an accumulation of IST-Ty over time, as newly formed vacuoles have secreted less IST-Ty. Moreover, reduced expression of P_{p21}-IST-3Ty only minimally affects the analysis, as IST-positive host-cell nuclei were not assessed for their signal intensity, and were scored positive even with very faint signal.

Taken together, these data suggest that IST can translocate through an immature CW but its export is prevented upon CW maturation (Fig 4L).

ASP5 substrates participate in residual body constriction in tachyzoites and cyst wall formation in bradyzoites

Given the broad spectrum of ASP5 substrates in tachyzoites and bradyzoites, we investigated the role of ASP5 in type II ME49 and CZ strains. The CZΔ*asp5* line was generated by introducing a selection marker (DHFR) immediately after the *asp5* initiation codon, using the same strategy as for the ME49Δ*asp5* described previously (25). IFAs performed using an α-actin1 antibody on parental and Δ*asp5* parasites from both ME49 and CZ strains showed an enlarged RB with diffuse staining compared with PVs of WT parasites (Fig 5A and 5B, S8A and S8B Fig). Transmission electron microscopy (TEM) confirmed the presence of large RBs in vacuoles of ME49Δ*asp5* (Fig 5C and 5D) and CZΔ*asp5* parasites (S8C and S8D Fig). Although some GRAs have been implicated in formation of the IVN and were shown to accumulate at the basal pole and around the RB in PVs (41), the functional link between ASP5 and the RB is not clear.

TEM revealed that both ME49Δ*asp5* and CZΔ*asp5* *in vitro* differentiated bradyzoites accumulate small electron-dense vesicles on the luminal side of the CW (Fig 5E and 5F, S8E-

S8F Fig). Relevantly, the ASP5 substrate MYR1 is a component of the translocation machinery for parasite effector proteins across the tachyzoite PVM (27) and presumably also the CW in bradyzoites. To address if the translocation machinery participates in CW formation, we selectively deleted *MYR1* in ME49 parasites. TEM analysis confirmed a similar phenotype to those of ME49Δ*asp5* parasites, with accumulation of vesicles and thinner CW in a ME49Δ*myr1* strain after differentiation *in vitro* (Fig 5G).

ASP5 is critical for the generation of morphologically intact tissue cysts

We previously reported that that deletion of ASP5 significantly reduces the virulence of type II parasites, as tested using a lethal dose of 10^5 ME49 parasites as inoculum in mice (25). To assess the ability of ME49Δ*asp5* parasites to form tissue cysts *in vivo*, we analyzed cyst size and number in chronically infected mice inoculated with sub-lethal doses ($5x10^2$) of ME49 (WT) or ME49Δ*asp5* parasites (Fig 6A). At 8 weeks post-inoculation with ME49Δ*asp5* parasites, a 7-8'fold lower number of brain cysts was observed compared with WT parasites, indicating either a defect in dissemination during acute infection, or an altered ability to form and develop tissue cysts (Fig 6B). We addressed this by analyzing the morphology of tissue cysts from the brain of mice chronically infected with WT or ME49Δ*asp5* parasites, fixed 8 weeks p.i. TEM also showed the accumulation of electron-dense vesicles in the matrix of ME49Δ*asp5* cysts in mice, which were absent in cysts formed by WT parasites (Fig 6C and 6D). The morphology of these cysts was comparable to those of ME49Δ*MyoJ* parasites, which also display significantly reduced cyst numbers in mice but are morphologically indistinguishable from WT cysts (42). ME49Δ*MyoJ* cysts appeared morphologically intact, similar to those formed by WT parasites (Fig 6C and 6E). Lastly, although parasites within ME49Δ*asp5* (Fig 6D) and ME49Δ*MyoJ* (Fig 6E) cysts are less tightly packed compared to

WT cysts (Fig 6C), no vesicles accumulating in the matrix are visible in ME49Δ*MyoJ* cysts, indicating that the vesicles formation is specific to ME49Δ*asp5* cysts.

Taken together, the data demonstrate an important role for ASP5 in processes linked to delivery of vesicular content within cysts *in vivo* that result in a significant lower cyst burden in mice upon *asp5* deletion. The ASP5 substrate(s) associated to this particular function remains to be identified.

Assessment of cyst burden in mouse infected brain by 2-photon serial tomography

To investigate the impact of effector GRAs processed by ASP5 on *T. gondii* dissemination during the acute and chronic phases of the infection, we evaluated the localization of cysts at the whole brain scale with a high spatial resolution, using 2-photon serial tomography (43). Mice were infected either with ME49Δ*hx* (WT) or ME49Δ*asp5* *T. gondii* tachyzoites expressing GFP under the control of a bradyzoite specific promoter (BAG1), and the brains were analyzed at 2 or 5 weeks p.i. We first confirmed that the signal detected corresponded to *T. gondii* parasites by staining brain sections containing GFP-fluorescent structures with the parasite inner membrane complex marker GAP45 (Fig 7A and 7Ai). At first glance, we observed tissue cysts widely distributed or sometimes clustered in the brain of 2 (Fig 7B-7Bii) and 5 weeks (Fig 7C-7Cii) infected mice. An unbiased quantification of the cyst number based on fluorescence signals revealed a higher cyst burden in the brains of animals infected for 2 weeks compared to those infected for 5 weeks (Fig 7D). This decrease upon time was observed in both WT- and ME49Δ*asp5*-infected mice and was consistent with the total volume represented by the tissue cysts over the whole brain (Fig 7E). In WT-infected animals, we noticed a predominance of tissue cysts of a small volume at 2 weeks p.i., while a wide range of sizes was observed at 5 weeks p.i. (Fig 7F). The fewer cysts formed by ME49Δ*asp5* parasites at 2 weeks p.i. were slightly larger than the WT, but over time, the majority of the detected cysts tended to be of small sizes. To determine if cysts were clustered, we measured the distance between a given cyst and its closest neighbor. It appeared that a large fraction of WT cysts was highly clustered at 2 weeks p.i., and to a lesser extent at 5 weeks p.i (Fig 7G). However, Δ*asp5* cysts were less condensed than the WT at 2 weeks p.i. and were also more distant towards each other at 5 weeks p.i.

Overall, these data underline the dynamic nature of brain colonization by *T. gondii* and indicate that at the onset of WT parasite entry, a high burden of small-sized and closely located parasites is present in the brain. Only a subfraction of this first pool of cyst successfully persist, increases in size and disseminate in the brain. This pattern is altered during infection with a Δ*asp5* strain, with a lower parasite load initially reaching the brain and mostly small-sized cysts detected at a later time point.

Discussion

Throughout its life cycle in the host, *T. gondii* is surrounded by protective and interactive interfaces. Effectors molecules released by dense granules make critical contributions to the morphology and functionality of the PVM and the PV space, as well as subverting host cellular functions during the tachyzoite stage. The export of proteins across the PVM requires a translocon machinery notably composed of MYR1 (27, 28). Through the maturation of MYR1, ASP5 mediates the transit of all known GRAs exported beyond the PVM in addition to proteolytic processing of numerous GRAs residing in the PV space (29, 44).

To determine to which extent tachyzoites and bradyzoites confined within the PVM and CW communicate with the host cell and to assess the role of ASP5 in these processes, we embarked on a TAILS analysis to identify ASP5 substrates in both stages and dissect the role of ASP5 during the transition to chronic infection. TAILS identified GRA proteins GRA33, GRA65, GRA66, GRA67 and WNG2 as ASP5 substrates (Fig 8). Strikingly, none of the previously characterized exported effectors GRA16, GRA24, GRA28, IST or TEEGR were represented in our TAILS dataset suggesting that these proteins are not as abundant as PV-resident GRAs and therefore are not detected, suggesting that the approach might lack the necessary sensitivity to uncover new members of this family of effectors.

Sequence analysis of the newly identified substrates revealed that the TEXEL motif is variable to a considerable degree. In addition to the RRL sequence, we noted the occurrence of cleavage at TEXEL-like motifs (RHLLT for GRA66, RRLDS for WNG2) as deduced from the enriched N-terminal peptides of several confirmed ASP5 substrates. This observation suggests that ASP5 does not only recognize a specific sequence of amino acids but rather a secondary/tertiary structure that could accommodate different residues, as long as they are of similar charge/polarity/hydrophobicity. Overall, vacuolar and exported GRA effectors processed by ASP5 exhibit a striking imbalance. While a large majority of the TEXEL-containing substrates are resident GRAs of the PV and/or PVM (MYR1, LCAT, WNG1, WNG2, GRA19, GRA20, GRA33, GRA34, GRA44, GRA45, GRA46, GRA65, GRA66, GRA67), the only exported effectors directly cleaved by ASP5 are GRA16 and IST. Apparent for GRA33, GRA34 and GRA66, several PV and/or PVM resident GRA accumulated around the RB in absence of ASP5. Taken together with the enlargement of the RB observed by TEM in type I and type II Δ*asp5* backgrounds, this seems to suggest a role for GRA in RB constriction, likely from the PV side.

We showed that IST also accumulates in the host cell nucleus during intracellular development of bradyzoites. However, the IST signal in the host nucleus decreases upon CW maturation, suggesting that its export beyond the PV occurs mainly early on, shortly after host cell invasion. IST was recently shown to accumulate in the host cell nucleus at the bradyzoite stage, in contrast to GRA16 and GRA24 (32, 45). Concordantly, another study showed that GRA16 export is prevented in the bradyzoite stage (46). Taken together, these data indicate that translocation across the CW in the bradyzoite stage might not be uniform for all GRAs effectors. Additionally, protein translocation seems to be dependent on the maturation state of the CW, with the export of the different GRAs being successively blocked upon CW development (Fig 8). GRAs effectors translocation during the chronic stage might also involve additional factors, such as the catalytic activity of the rhoptry protein kinase ROP17, which deletion compromise the nuclear localization of GRA16 and GRA24 in tachyzoites (47). Nevertheless, given the important changes in mRNA levels after induction of bradyzoite development (30, 32), the amount of protein exported during the early stages might be sufficient to sustainably reprogram host cellular functions. In the absence of ASP5 or MYR1, the CW fails to develop normally both in *in vitro* differentiated bradyzoites and *in vivo* purified cysts from infected mouse brains. This indicates that a functional translocation machinery is required for the formation of a morphologically mature CW. At this stage it is not clear how the accumulated vesicles in type II Δ*asp5* bradyzoites relate to MYR1 and CW formation.

Although the *in vivo* visualization of *T. gondii* using 2-photon serial tomography performed in this study was done on a single animal for each time point, it is in agreement with our previous observations (Boillat et al., 2020). The absence of ASP5 leads to fewer parasites reaching the brain, suggesting that parasite spreading, entry in the brain and subsequent cyst formation are dependent on effector GRAs. As a primary mediator of the response to infection, dendritic cells (DCs) are hijacked by *T. gondii* that increases their mobility and benefit from their ability to cross the blood brain barrier (BBB) to enter the brain. In line with previous studies showing that DCs hypermotility upon *T. gondii* infection is compromised in absence of ASP5 (25) or that GRA24 suppresses maturation of DCs (48), our findings indicate that tachyzoites are greatly dependent on ASP5-related effector GRAs to scavenge DCs functions to disseminate and ultimately enter the brain. The clustering of cysts and their relative proximity to tissue lesions indicates that parasites are readily taking advantage of a breach in the vascular epithelium to cross the BBB and colonize neighboring cells of the parenchyma to disseminate in the brain (49). This observation implies that the transcellular entry is likely the most efficient mode used by *T. gondii* to penetrate in the brain epithelium, as compared to paracellular entry or to the “Trojan horse” method (Fig 8).

Overall, this study underlines the importance of ASP5 substrates for the architecture of tachyzoites and bradyzoites residing compartments. ASP5 not only participate to parasite virulence but also plays an important role in the establishment and maintenance of a chronic infection.

Materials and Methods

Bacteria, parasite and host cell culture

The parental and derived strains of *T. gondii* tachyzoites were maintained by serial passage on confluent monolayers of human foreskin fibroblasts (HFFs) maintained in Dulbecco’s Modified Eagle’s Medium (DMEM, Gibco) supplemented with 5% fetal calf serum (FCS), 2mM glutamine and 25 mg/ml gentamicin. *E. coli* XL-10-Gold chemically competent bacteria were used for all recombinant DNA experiments.

Preparation of *T. gondii* genomic DNA

Genomic DNA (gDNA) from *T. gondii* parasites was extracted using the Wizard SV genomic DNA purification system (Promega) according to the manufacturer’s protocol.

Parasite strains, DNA vector constructs and transfections

- **TASPx-3Ty-HXGPRT (knock-in) strains**

Endogenously Ty tagged strains of candidate genes were made by amplifying the region of a plasmid encompassing the 3ty tags and the HXGPRT selection cassette using KOD DNA polymerase (Novagen, Merck) with primers having 28bp gene homology arms (as shown in S3 Fig). Plasmids TASPx-Cas9-YFP/CRISPR for directing the integration of the 3Ty-HXGPRT fragment at the C-terminus were generated using the Q5 site directed mutagenesis kit (NEB) with primers listed in S3 Table and using the vector pSAG1::CAS9-GFP-U6::sgUPRT as template (50). The amplified 3Ty-HXGPRT PCR products were co-transfected with 20µg of their corresponding gRNA-plasmids as described before (51).

- **RHΔ*hxgprt*Δ*asp5*Δ*ku80* and ME49Δ*asp5*Δ*ku80* strain**

To generate the RHΔ*hxgprt*Δ*asp5*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gKU80(#5944) vector was used to disrupt the *ku80* locus in a RHΔ*hxgprt*Δ*asp5* background strain, previously generated (25). 48 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *ku80* gene was confirmed by sequencing of the *ku80* locus (S2 Fig), using primers listed in S3 Table.

To generate the ME49Δ*asp5*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gKU80(#5944) vector was used to disrupt the *ku80* locus in a ME49Δ*asp5* background strain, previously generated (25). 72 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *ku80* gene was confirmed by sequencing of the *ku80* locus (S2 Fig), using primers listed in S3 Table.

- **ME49Δ*hxgprt*Δ*ku80* strain**

To generate the ME49Δ*hxgprt*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gHXGPRT(#5950) and pSAG1-CAS9gfp-U6gKU80(#5944) vectors were used to disrupt the *hxgprt* and *ku80* loci, respectively, in a ME49 background strain. 72 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *hxgprt* and *ku80* genes was confirmed by sequencing of the *hxgprt* and *ku80* loci (S2 Fig), using primers listed in S3 Table.

- **ME49Δ*hxgprt*Δ*ku80*Δ*p21* strain**

To generate the ME49Δ*hxgprt*Δ*ku80*Δ*p21* strain, a PCR fragment encoding the DHFR-TS selection cassette was generated using the KOD DNA polymerase with the vector p2854-DHFR (52) as template and the primers 6109/6110 that also carry 30 bp homology with the 5' and 3' ends of *p21*. To direct the insertion of the PCR product, the pSAG1-CAS9gfp-U6gP21(#6108) vector was used. The integration of the PCR product was confirmed by PCR of genomic DNA (S7A and S7B Fig) using primers listed in S3 Table.

- **IST-3Ty (knock-in) and P$_{\mathbf{p21}}$-IST-3Ty (promoter replacement) strains**

To generate the 3Ty tagged IST strain controlled by p21 promoter (P$_{p21}$-IST-3Ty), the promoter region of p21 consisting ~1600 bp upstream of its start codon was amplified with primers 8878/8879 having 30 bp IST homology arms. The IST-Cas9-YFP/CRISPR gRNA targeting the 5' region of IST was generated similarly to the TASPx-Cas9-YFP/CRISPR with primers 8877/4883. The PCR-amplified p21 promoter region was co-transfected with 20ug of the IST-Cas9-YFP/CRISPR plasmid into IST-3Ty-KI parasites. Transfected parasites were cloned by FACS-sorting the GFP-positive parasites into 96-well plates 48 hr post-transfection. The integration of the PCR products and promoter swap was confirmed by PCR of genomic DNA (S7E and S7F Fig) using primers listed in S3 Table.

- **ME49Δ*myr1* strain**

To generate the ME49Δ*myr1* strain, a PCR fragment encoding the DHFR-TS selection cassette was targeted to the *myr1* locus using a specific double gRNA (dgRNA) vector, as previously described (30).

- **ME49Δ*hxgprt* P$_{\mathbf{BAG1}}$-GFP strain**

To generate the ME49Δ*hxgprt* P_{BAG1}-GFP strain, a P_{BAG1}-GFP-HXGPRT construct was stably integrated in the genome of ME49Δ*hxgprt* parasites, as previously described (30).

All PCR amplifications for screening of the generated strains were performed using the GoTaq DNA polymerase (Promega). All primers used in this study are listed in S3 Table.

Parasites transfection and selection of clonal stable lines

T. gondii tachyzoites were transfected by electroporation as previously described (53). Transgenic parasites were selected with mycophenolic acid (MPA, 25 mg/mL) and xanthine (50 mg/mL) for HXGPRT selection (52), pyrimethamine (1 μg/ml) for DHFR selection (52). All stable clones were isolated by limiting dilution in 96-well plates and screened for expression of the transgenes by IFA and for genomic integration by GoTaq PCR.

Antibodies

The following primary antibodies were used in this study: monoclonal mouse α-Ty (hybridoma BB2, 1:10 IFA, 1:10 WB (54)), α-actin (hybridoma, 1:10 IFA, 1:10 WB (55)), α-SAG1 (hybridoma, 1:10 WB (56)), α-SAG4 (hybridoma, 1:10 WB (57)), α-p21 (hybridoma, 1:50 IFA, 1:10 WB (40)) and polyclonal rabbit α-catalase (1:2000 WB (58)), α-IMC1 (1:1000 IFA (59)) and α-GAP45 (1:10.000 IFA (60)). *Dolichos biflorus* Agglutinin (DBA) lectin labelled with Rhodamine was used (at 10 μg/mL; Vector) to detect the glycosylated protein CST1, as a marker of the *T. gondii* cyst wall (3). The following secondary antibodies were used in this study: α-mouse and α-rabbit HRP (Sigma) (WB), Alexa-Fluor-488-conjugated goat α-mouse and α-rabbit IgG antibodies and Alexa-Fluor-594-conjugated goat α-mouse and α-rabbit IgG antibodies (Thermofisher) (IFA).

Immunofluorescence assay

HFF monolayers were grown on coverslips and infected with *T. gondii* tachyzoites. The coverslips were subsequently fixed at the appropriate time-points with either 4% paraformaldehyde (PFA) in phosphate-buffered saline (PBS) for 10 min or 4% paraformaldehyde (PFA)/0.001% glutaraldehyde (GA) for 20 min, prior to quenching with 0.1M glycine/PBS. Fixed cells were permeabilized with 0.2% Triton/PBS and blocked with 2% BSA/0.2% Triton/PBS. Cells were then probed with primary antibodies diluted in 2%BSA/0.2%Triton/PBS for 1 hr on an orbital shaker. This is followed by 3 washes with 0.2% Triton/PBS and incubation with secondary antibodies in 2% BSA/0.2% Triton/PBS for 1 hr. After 3 more washes with 0.2% Triton/PBS, the coverslips were stained with DAPI (4',6-diamidino-2-phenylindole; 50 µg/ml in PBS) and mounted on Fluoromount G (Southern Biotech) on glass slides. Images were recorded with a LSM800 confocal microscope (Zeiss) at the Bioimaging core facility of the Faculty of Medicine, University of Geneva. Final image analysis and processing was done with ImageJ Fiji (61).

Western blotting

Freshly egressed parasites were pelleted by centrifugation at 1000g, washed once in PBS, lysed directly in SDS-loading buffer and subjected to SDS-PAGE under reducing conditions. Proteins were transferred to nitrocellulose membrane and immunoblot analysis was performed. Primary and secondary antibodies are diluted in PBS, 0.05% Tween 20 and 5% skimmed milk power, washes are performed in 0.05%Tween/PBS. Following the primary and secondary antibody incubation and washes, the membrane was incubated with a peroxidase-conjugated goat anti-mouse or anti-rabbit antibody. The bound antibodies were visualized using the ECL plus system (GE Healthcare Bio-Sciences).

Competition assay

Parasites to be assessed were mixed with GFP-expressing wild-type parasites and allowed to infect and grow on HFF monolayers. The ratios were quantified over six passages by FACS. Parasites were labeled with Hoechst prior to FACS counting of 10,000 parasites. Data are presented as mean values ± SD from three independent experiments.

In vitro bradyzoite differentiation

Tachyzoite to bradyzoite conversion *in vitro* was induced by exposing parasite cultures to pH 8.2 as described previously (62). Briefly, tachyzoites were allowed to infect HFF monolayers grown on glass coverslips inside 24-well plates. Bradyzoite differentiation was induced 24 hr post infection by replacing normal media with RPMI 1640 buffered with 50 mM HEPES to pH 8.2 and supplemented with 3% fetal bovine serum. Parasites were allowed to grow at 37°C in absence of CO_2 and alkaline media was changed daily. After the required number of days of conversion, infected HFF were fixed and analyzed.

Serial sections transmission electron microscopy on *in vitro* differentiated bradyzoites

Samples for transmission electron microscopy were processes as described previously (25). Briefly, infected HFF cells grown on round glass coverslips were fixed with 2.5% glutaraldehyde (Electron Microscopy Sciences) and 2% paraformaldehyde (Electron Microscopy Sciences) in 0.1 M phosphate buffer (PB) at pH 7.4 for 1 h at room temperature. After extensive washing with 0.1 M sodium cacodylate buffer, pH 7.4 samples were post-fixed with reduced 1% osmium tetroxide (Electron Microscopy Sciences) with 1.5% potassium ferrocyanide in 0.1 M sodium cacodylate buffer, pH 7.4 for 40 min immediately followed by 1% osmium tetroxide alone (Electron Microscopy Sciences) in 0.1 M sodium cacodylate buffer pH 7.4 for 40 min. Cells were then washed in double distilled water twice for 5 min each wash and *en block* stained with aqueous 1% uranyl acetate (Electron

Microscopy Sciences) for 1 h or overnight at 4°C. After 5 min wash in double distilled water cells were dehydrated in graded ethanol series (2 × 50%, 70%, 90%, 95%, and 2 × absolute ethanol) for 3 min each wash and infiltrated with graded series of Durcupan resin (Electron Microscopy Sciences) diluted with ethanol at 1:2, 1:1, 2:1 for 30 min each, and twice with pure Durcupan for 30 min each. Cells were infiltrated with fresh Durcupan resin for additional 2 hours. For flat embedding, 1 mm thick teflon rings were placed on glass slide (3 per slide) coated with mold separating agent (Glorex), filled with fresh resin and covered with coverslip facing grown cell down and then polymerized at 65 °C oven overnight or for 24 h. The glass coverslip was removed from the cured resin disk by immersing alternately into hot (60 °C) water and liquid nitrogen until glass parted. Laser microdissection microscope (Leica Microsystems) was used to select suitable cysts and to outline their positions on the exposed resin surface. Then the selected area was cut out from the disk using a single edged razor blade and glued with superglue (Ted Pella) to a blank resin block. The cutting face was trimmed using a Leica Ultracut UCT microtome (Leica Microsystems) and a glass knife. 70 nm ultrathin serial sections were cut with a diamond knife (DiATOME) and collected onto 2 mm single slot copper grids (Synaptec, Ted Pella) coated with Formvar plastic support film. Sections were examined using a Tecnai 20 TEM (FEI) operating at an acceleration voltage of 80 kV and equipped with a side-mounted MegaView III CCD camera (Olympus Soft-Imaging Systems) controlled by iTEM acquisition software (Olympus Soft-Imaging Systems).

Transmission electron microscopy on *in vivo* cysts

Experimental animals were intraperitoneally infected with ME49, ME49Δ*asp5* or ME49Δ*MyoJ* tachyzoites. 5 weeks post-infection, deeply anesthetized animals were fixed by cardiac perfusion (63) with 150 ml of 2.5% glutaraldehyde (Electron Microscopy Sciences) and 2% paraformaldehyde (Electron Microscopy Sciences) in 0.1 M phosphate buffer (PB) at pH 7.4 at speed of 12 ml/min for 20-30 min. After 2 h, the brain was carefully removed from the skull and kept in 0.01M PBS. Brains were embedded into 5% low melted agarose (Eurobio) in order to cut 80 µm thick vibratome coronal sections. Sections containing the cysts were then processed for electron microscopy as described previously (63, 64). Briefly, vibratome sections were extensively washed with 0.1 M sodium cacodylate buffer, pH 7.4 and post-fixed with reduced 1% osmium tetroxide (Electron Microscopy Sciences) with 1.5% potassium ferrocyanide in 0.1 M sodium cacodylate buffer, pH 7.4 for 1 h immediately followed by 1% osmium tetroxide alone (Electron Microscopy Sciences) in 0.1 M sodium cacodylate buffer pH 7.4 for 1 h. Sections were then washed in double distilled water twice for 5 min each wash and *en block* stained with aqueous 1% uranyl acetate (Electron Microscopy Sciences) for 1 h or overnight at 4°C. After 5 min wash in double distilled water cells were dehydrated in graded ethanol series (2 × 50%, 70%, 90%, 95%, and 2 × absolute ethanol) for 3 min each wash and infiltrated with graded series of Durcupan resin (Electron Microscopy Sciences) diluted with ethanol at 1:2, 1:1, 2:1 for 30 min each, and twice with pure Durcupan for 30 min each. Sections were infiltrated with fresh Durcupan resin for additional 2 h. Finally, brain vibratome sections were placed on glass slide coated with mold separating agent and overlaid with second glass slide coated with mold separating agent. This sandwich was then polymerized at 65 °C oven for 24 h. Cured sections embedded in resin were separated from glass slide using a razor blade.

Using the laser microdissection microscope (Leica Microsystems) to select suitable cysts and to outline their positions on the surface of the cured vibratome section, cutting out selected area from section and gluing with superglue to a blank resin block, trimming the cutting face and serial section ultramicrotomy as well as final ultrathin sections examination was performed in the same way as mentioned in previous section.

Mouse infection

6-weeks old B6CBAF1/J male mice (Janvier laboratories) were intraperitoneally infected with 2.10^2 parasites. The health of mice was monitored daily until they presented severe symptoms of acute toxoplasmosis (bristled hair and complete prostration with incapacity to drink or eat) and were sacrificed on that day.

Processing of the brains, tissue cysts counting and purification

Mice brains were homogenized in 1 ml PBS and syringe passaged 5-10 times through a 18G needle to break up large clumps. Then, the homogenate was sequentially syringe passaged through a 20G needle and a 23G needle (10 times each). Tissue cysts number was estimated by counting 5 fractions of 10 µl from each brain homogenate using the 10× and 20× objectives of an inverted microscope. The procedure for tissue cysts purification was adapted from Watts and colleagues (65), who modified the original Percoll gradient protocol (66). 5 ml of PBS was added to the brain homogenate and the mix was passed once through a cell strainer (Corning) prior to loading on the gradient. The gradient consisted of 4 layers of 90%, 50%, 30% and 10% Percoll diluted in 1× PBS final and supplemented with 1% PFA to avoid premature breakage of tissue cysts during the purification steps. The gradient was centrifuged at 290 × *g* for 20 min at 4°C (with low acceleration and low brake when stopping). The fractions were carefully harvested using a 22G × 2”, 0,7 × 50 mm needle.

Terminal amine isotopic labelling of substrates (TAILS) and LC-MS analysis for identification of ASP5 protease substrates

The candidate substrates were identified according to the methodology described previously (33, 67). Briefly, protein from *T. gondii* cell lysates of tachyzoites (WT and Δ*asp5*) and bradyzoites (Intracellular, WT and Δ*asp5*) was extracted by treatment with RIPA buffer (150 mM NaCl, 1% NP40, 0.5% natriumdeoxycholate, 0.1% SDS, 50 mM Tris-HCl, pH 8.0, 1 mM EDTA) for 30 min at 4°C, high-speed centrifugation for 15 min, and subsequent acetone precipitation. The acetone pellet was processed as previously described, with the only difference being no fraction of the pre-TAILS peptides were sampled for further analysis. LC-MS analysis of the purified TAILS peptides was performed as previously described (33) on an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Scientific) operated with an EASY-nLC 1000 Liquid Chromatography system (Thermo Scientific) in data dependent analysis mode (DDA).

Serial-section two-photon tomography

Anaesthetized mice were transcardially perfused with 15 ml 0.1 M phosphate buffer (pH 7.4) (PB), followed by 50 ml 4% paraformaldehyde in 0.1 M PB. Brains were removed from the skull and post-fixed them in 4% paraformaldehyde 24 hours at 4°C. The fixed brains were then stored in PBS at 4°C until imaging. The fixed brains were embedded in 4% oxidized agarose (derived from type-I agarose (Sigma-Aldrich)) and covalently cross-linked the brain to the agarose by incubation in an excess of 0.5% sodium borohydride (NaBH4, Sigma-Aldrich) in 0.05 M sodium borate buffer overnight at 4°C. Then embedded brains were applied to a TissueVision two-photon scanning microscope, which cut physical sections of the entire brain every 50 µm coronally, and acquired optical sections every 10 µm in three channels (red channel: 560-650 nm; green channel: 500–560 nm; Blue channel: 450-500 nm) by 940-nm excitation laser light (Mai Tai eHP, Spectraphysics). Each imaged section is formed from overlapping 800×800-µm 'tiles' with a resolution of 0.435 µm in x and y. The cysts were segmented and quantified with scripts available from the authors on request.

Ethics statement

All animal experiments were carried out with the authorization GE/150/16 according to the guidelines and regulations issues by the Swiss Federal Veterinary Office. No human samples were used in these experiments.

Data availability

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD034786. All other relevant data are available from the authors on request

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Conflict of interest

The authors declare no conflict of interest.

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Fig 1

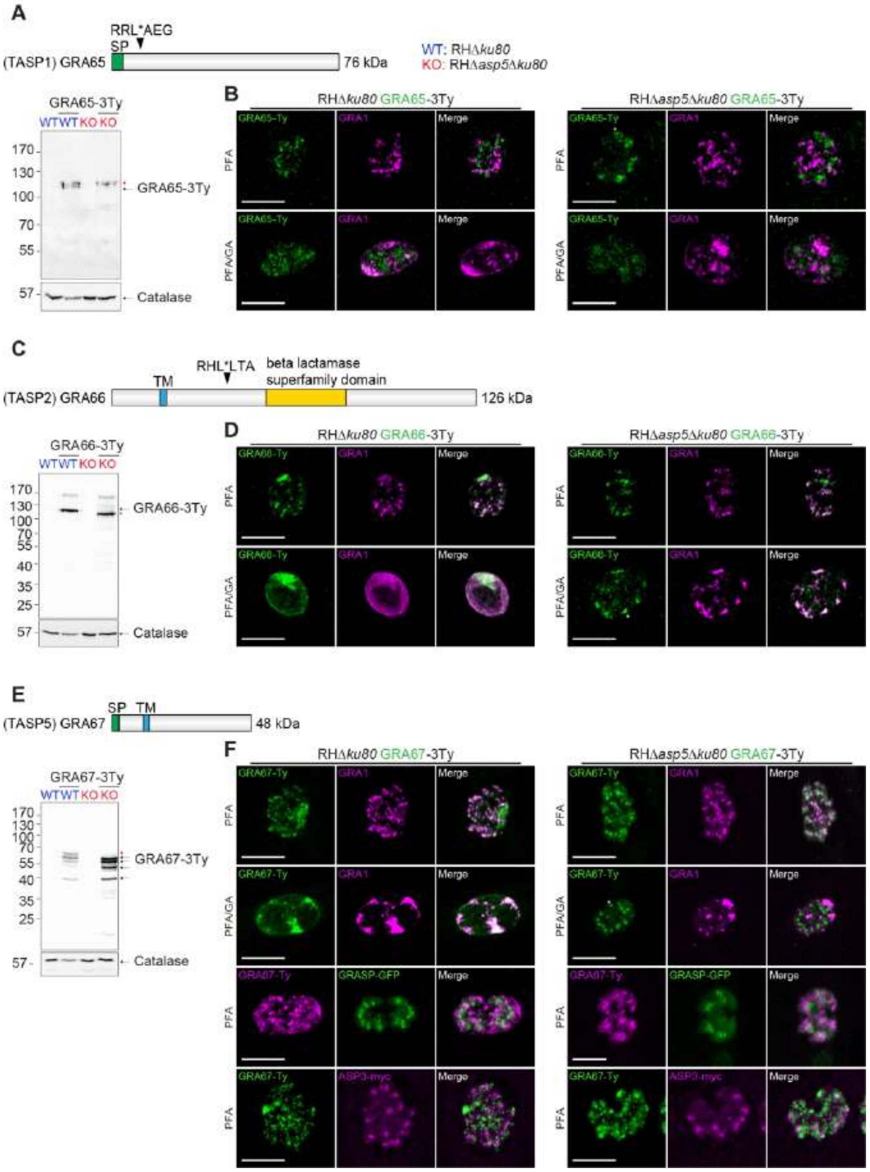

A
RRL*AEG
SP
(TASP1) GRA65
76 kDa
WT: RHΔku80
KO: RHΔasp5Δku80
GRA65-3Ty
WT WT KO KO
170
130
100
70
55
57
GRA65-3Ty
Catalase
B
RHΔku80 GRA65-3Ty
RHΔasp5Δku80 GRA65-3Ty
GRA65-Ty
GRA1
Merge
PFA
PFA/GA
C
TM
RHL*LTA
beta lactamase superfamily domain
(TASP2) GRA66
126 kDa
GRA66-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
GRA66-3Ty
Catalase
D
RHΔku80 GRA66-3Ty
RHΔasp5Δku80 GRA66-3Ty
GRA66-Ty
GRA1
Merge
PFA
PFA/GA
E
SP
TM
(TASP5) GRA67
48 kDa
GRA67-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
GRA67-3Ty
Catalase
F
RHΔku80 GRA67-3Ty
RHΔasp5Δku80 GRA67-3Ty
GRA67-Ty
GRA1
Merge
PFA
PFA/GA
GRA67-Ty
GRASP-GFP
Merge
PFA
GRA67-Ty
ASP3-myc
Merge
PFA

Fig 2

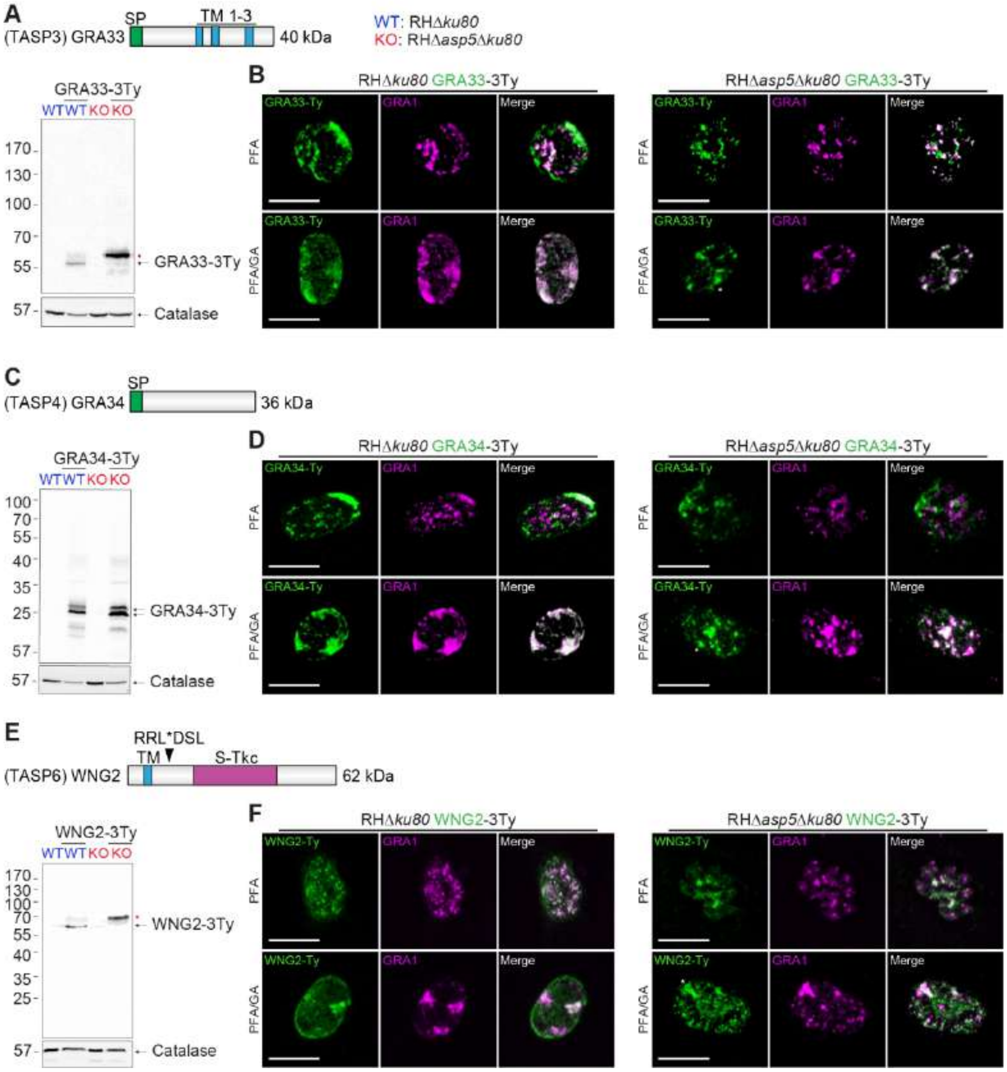

A
(TASP3) GRA33
SP
TM 1-3
40 kDa
WT: RHΔku80
KO: RHΔasp5Δku80
GRA33-3Ty
WT WT KO KO
170
130
100
70
55
57
GRA33-3Ty
Catalase
B
RHΔku80 GRA33-3Ty
RHΔasp5Δku80 GRA33-3Ty
GRA33-Ty
GRA1
Merge
PFA
PFA/GA
C
(TASP4) GRA34
SP
36 kDa
GRA34-3Ty
WT WT KO KO
100
70
55
40
35
25
57
GRA34-3Ty
Catalase
D
RHΔku80 GRA34-3Ty
RHΔasp5Δku80 GRA34-3Ty
GRA34-Ty
GRA1
Merge
PFA
PFA/GA
E
(TASP6) WNG2
RRL*DSL
TM
S-Tkc
62 kDa
WNG2-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
WNG2-3Ty
Catalase
F
RHΔku80 WNG2-3Ty
RHΔasp5Δku80 WNG2-3Ty
WNG2-Ty
GRA1
Merge
PFA
PFA/GA

Fig 3

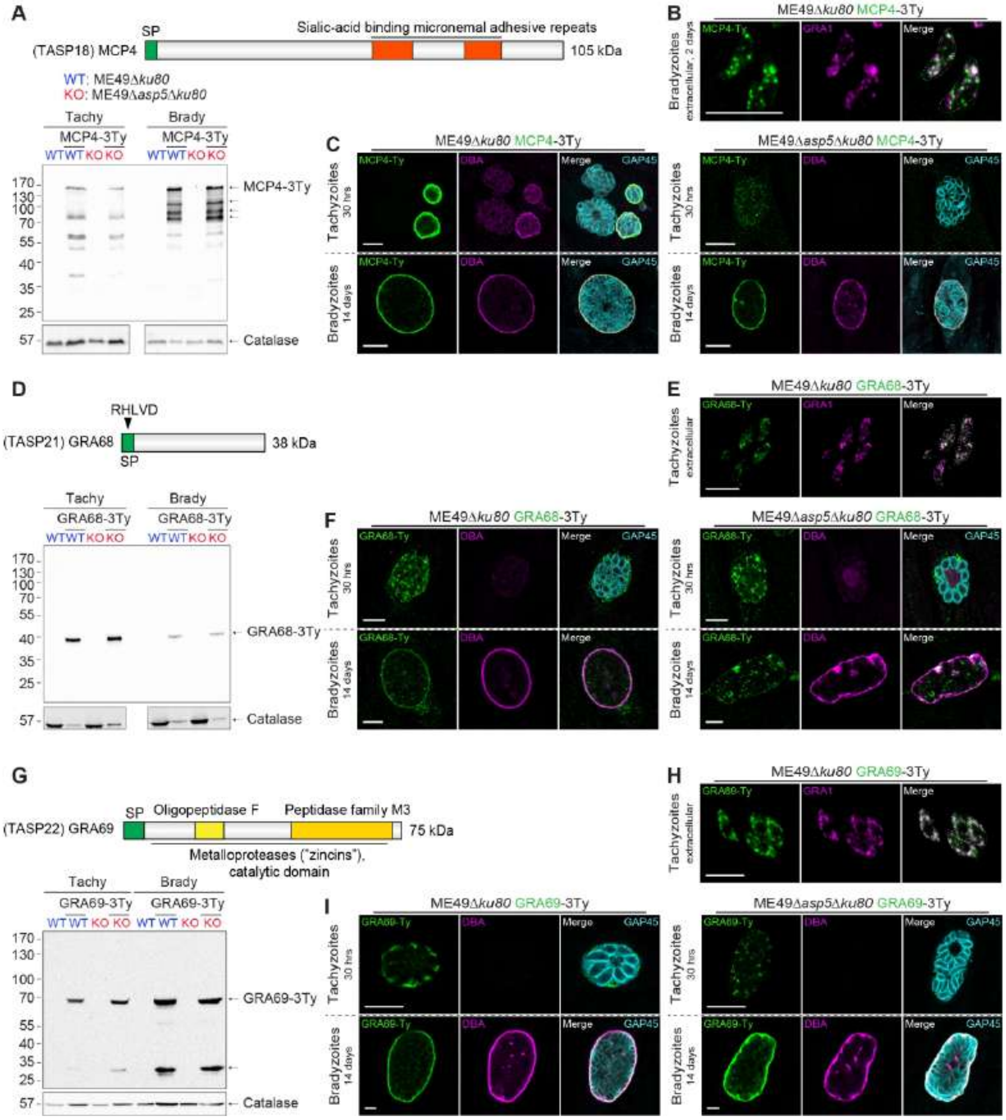

A
SP
Sialic-acid binding micronemal adhesive repeats
(TASP18) MCP4
105 kDa
WT: ME49Δku80
KO: ME49Δasp5Δku80
Tachy
Brady
MCP4-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
MCP4-3Ty
Catalase
B
ME49Δku80 MCP4-3Ty
Bradyzoites extracellular, 2 days
MCP4-Ty
GRA1
Merge
C
ME49Δku80 MCP4-3Ty
ME49Δasp5Δku80 MCP4-3Ty
Tachyzoites 30 hrs
Bradyzoites 14 days
MCP4-Ty
DBA
Merge
GAP45
D
RHLVD
(TASP21) GRA68
SP
38 kDa
GRA68-3Ty
Catalase
E
ME49Δku80 GRA68-3Ty
Tachyzoites extracellular
GRA68-Ty
GRA1
Merge
F
ME49Δku80 GRA68-3Ty
ME49Δasp5Δku80 GRA68-3Ty
GRA68-Ty
DBA
Merge
GAP45
G
SP
Oligopeptidase F
Peptidase family M3
(TASP22) GRA69
75 kDa
Metalloproteases ("zincins"), catalytic domain
GRA69-3Ty
Catalase
H
ME49Δku80 GRA69-3Ty
Tachyzoites extracellular
GRA69-Ty
GRA1
Merge
I
ME49Δku80 GRA69-3Ty
ME49Δasp5Δku80 GRA69-3Ty
GRA69-Ty
DBA
Merge
GAP45

Fig 4

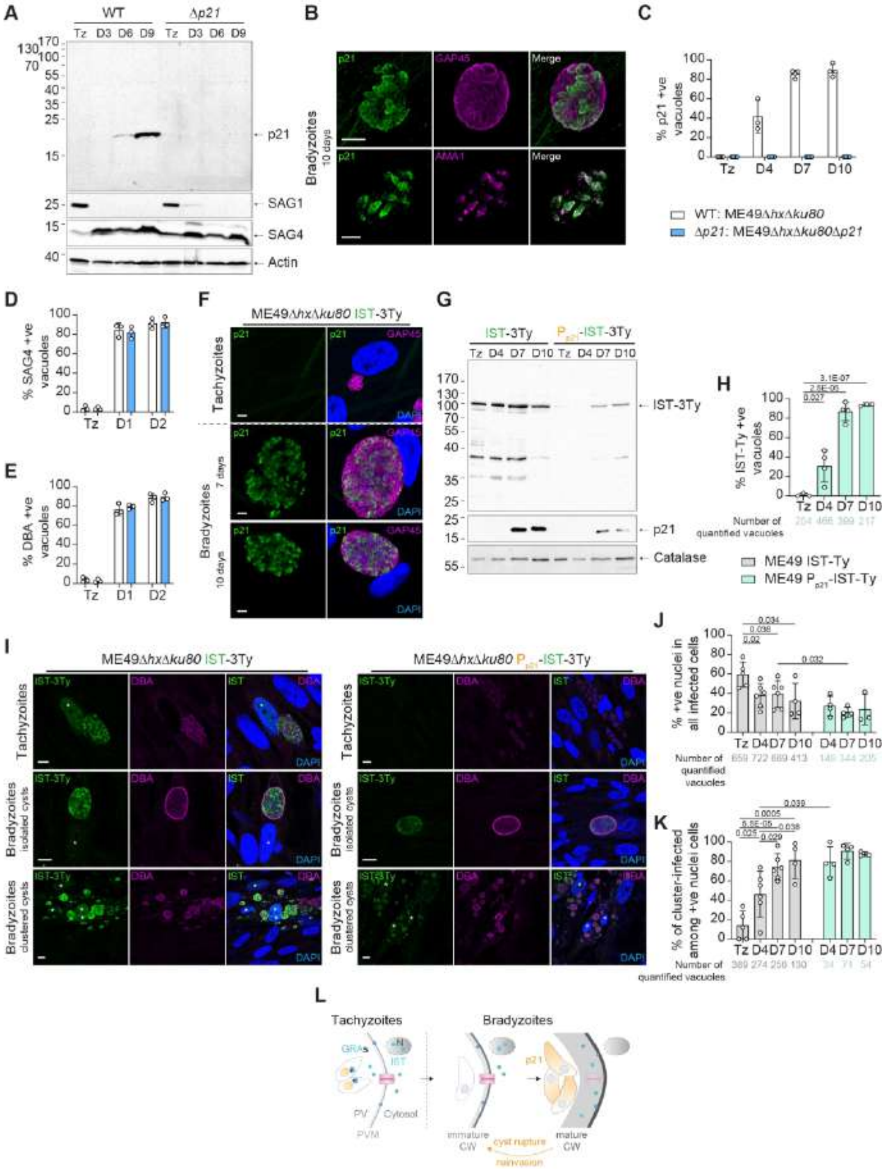

A
WT
Δp21
Tz D3 D6 D9 Tz D3 D6 D9
170
130
100
70
55
40
35
25
15
p21
25
SAG1
15
SAG4
40
Actin
B
Bradyzoites 10 days
p21
GAP45
Merge
p21
MAG1
Merge
C
% p21 +ve vacuoles
100
80
60
40
20
0
Tz D4 D7 D10
WT: ME49ΔhxΔku80
Δp21: ME49ΔhxΔku80Δp21
D
% SAG4 +ve vacuoles
Tz D1 D2
E
% DBA +ve vacuoles
Tz D1 D2
F
ME49ΔhxΔku80 IST-3Ty
Tachyzoites
Bradyzoites 7 days
10 days
p21
GAP45
DAPI
G
IST-3Ty
Pp21-IST-3Ty
Tz D4 D7 D10 Tz D4 D7 D10
IST-3Ty
p21
Catalase
H
% IST-Ty +ve vacuoles
3.1E-07
2.5E-05
0.027
Tz D4 D7 D10
Number of quantified vacuoles
254 466 399 217
ME49 IST-Ty
ME49 Pp21-IST-Ty
I
ME49ΔhxΔku80 IST-3Ty
ME49ΔhxΔku80 Pp21-IST-3Ty
Tachyzoites
Bradyzoites isolated cysts
Bradyzoites clustered cysts
IST-3Ty
DBA
IST
DAPI
J
% +ve nuclei in all infected cells
0.034
0.038
0.02
0.032
Tz D4 D7 D10 D4 D7 D10
Number of quantified vacuoles
659 722 689 413 149 144 205
K
% of cluster-infected among +ve nuclei cells
0.039
0.0005
6.5E-05
0.025
0.038
0.029
Tz D4 D7 D10 D4 D7 D10
Number of quantified vacuoles
389 274 256 130 34 71 54
L
Tachyzoites
Bradyzoites
GRAs
N
IST
p21
PV
Cytosol
PVM
immature CW
mature CW
cyst rupture
reinvasion

Fig 5

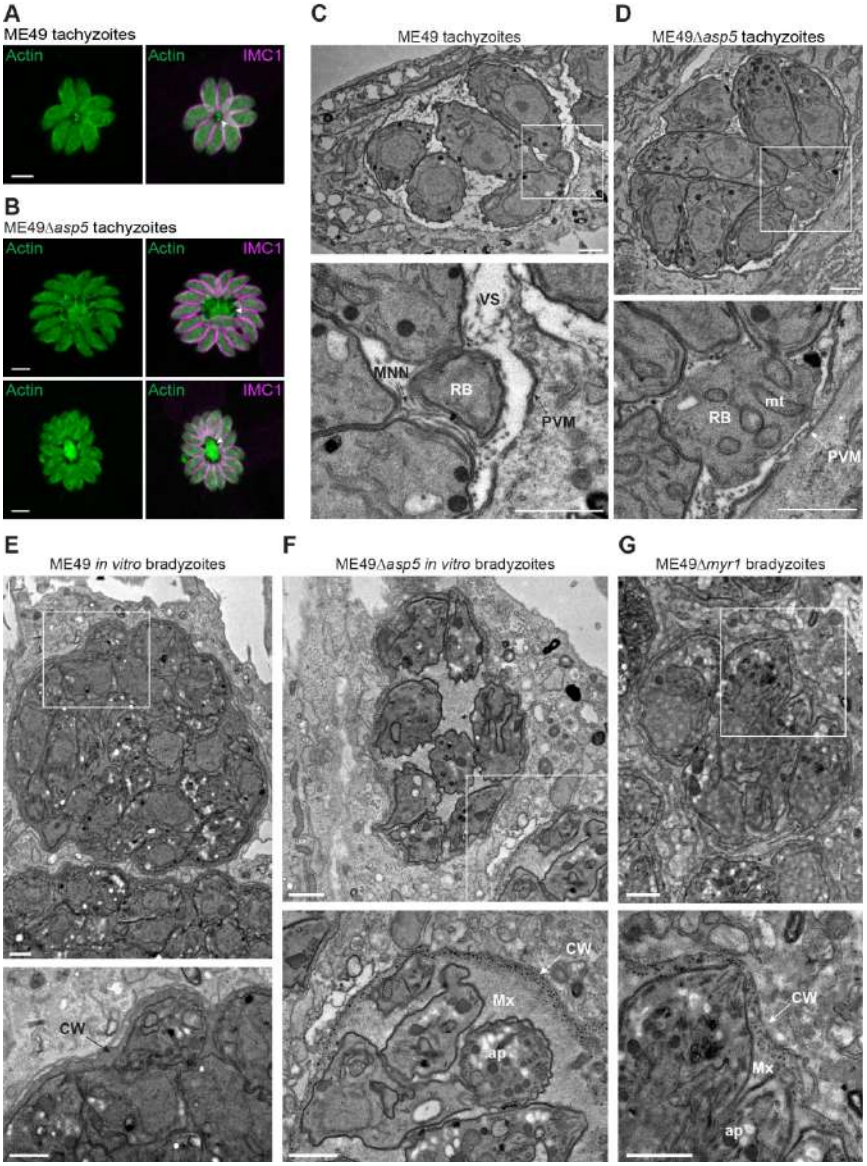

A
ME49 tachyzoites
Actin
Actin IMC1
B
ME49Δasp5 tachyzoites
Actin
Actin IMC1
Actin
Actin IMC1
C
ME49 tachyzoites
VS
MNN
RB
PVM
D
ME49Δasp5 tachyzoites
RB
mt
PVM
E
ME49 in vitro bradyzoites
CW
F
ME49Δasp5 in vitro bradyzoites
CW
Mx
ap
G
ME49Δmyr1 bradyzoites
CW
Mx
ap

Fig 6

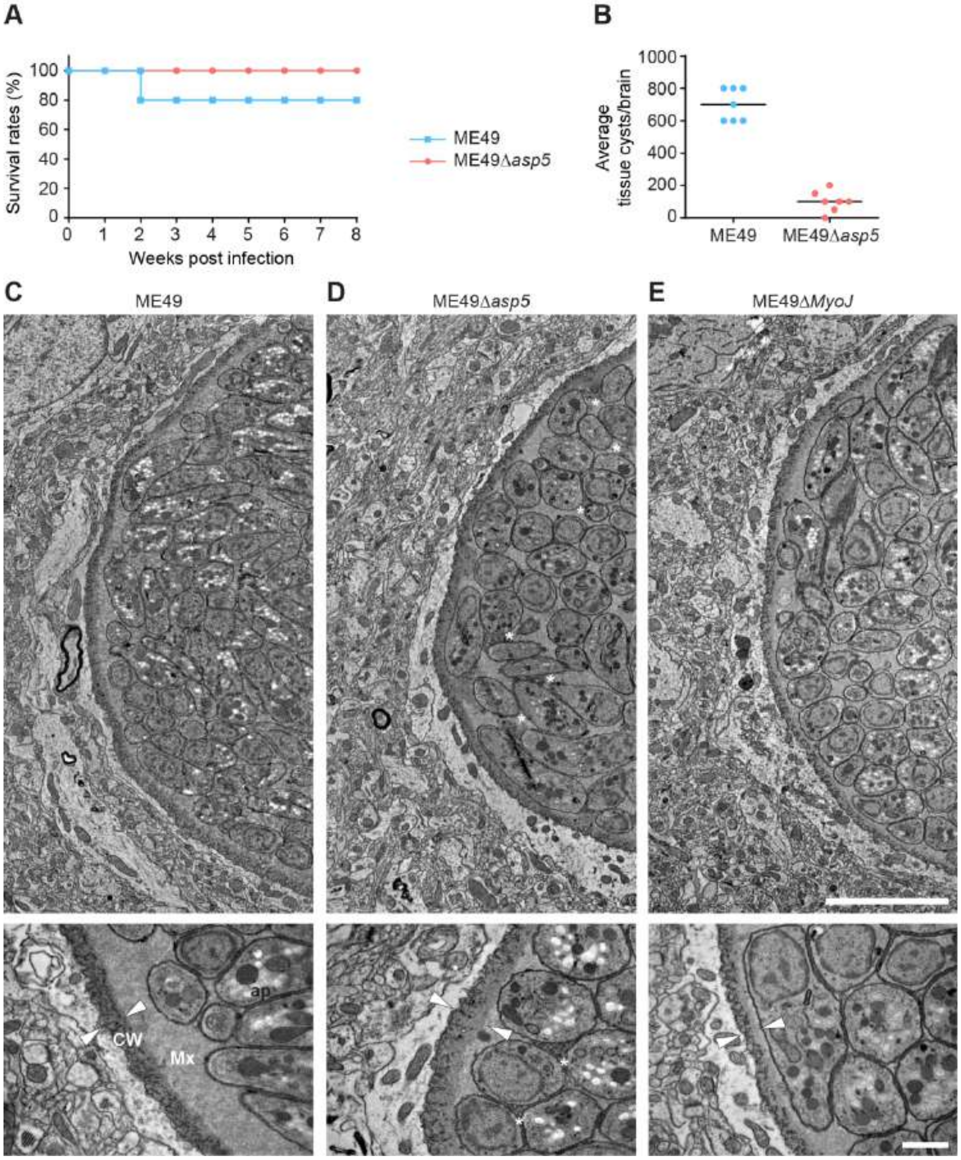

A
Survival rates (%)
100
80
60
40
20
0
0 1 2 3 4 5 6 7 8
Weeks post infection
ME49
ME49Δ*asp5*
B
Average tissue cysts/brain
1000
800
600
400
200
0
ME49
ME49Δ*asp5*
C
ME49
D
ME49Δ*asp5*
E
ME49Δ*MyoJ*
ap
CW
Mx

Fig 7

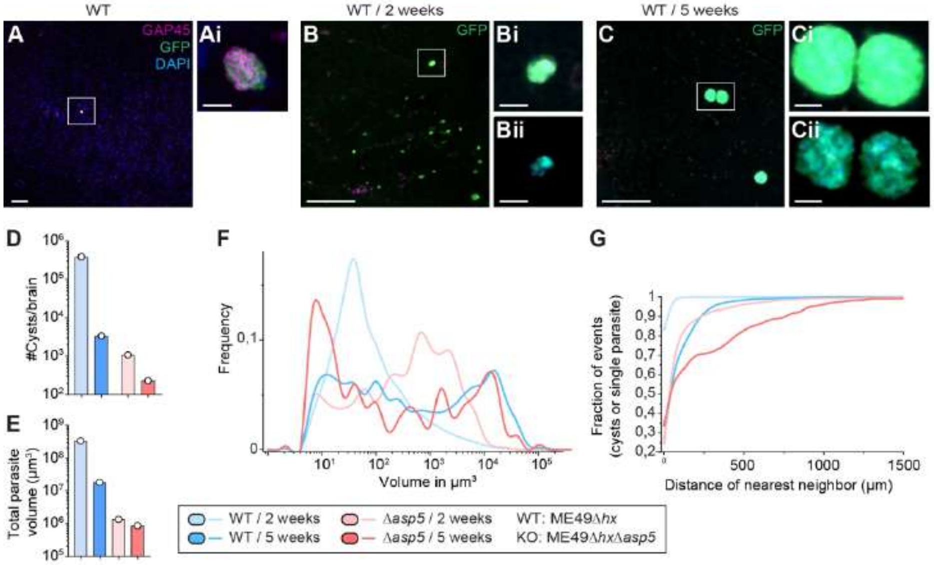

WT
WT / 2 weeks
WT / 5 weeks
A
GAP45
GFP
DAPI
Ai
B
GFP
Bi
Bii
C
GFP
Ci
Cii
D
#Cysts/brain
10²
10³
10⁴
10⁵
10⁶
E
Total parasite volume (µm³)
10⁵
10⁶
10⁷
10⁸
10⁹
F
Frequency
0
0,1
Volume in µm³
10¹
10²
10³
10⁴
10⁵
G
Fraction of events (cysts or single parasite)
0,2
0,3
0,4
0,5
0,6
0,7
0,8
0,9
1
0
500
1000
1500
Distance of nearest neighbor (µm)
WT / 2 weeks
WT / 5 weeks
Δasp5 / 2 weeks
Δasp5 / 5 weeks
WT: ME49Δhx
KO: ME49ΔhxΔasp5

Fig 8

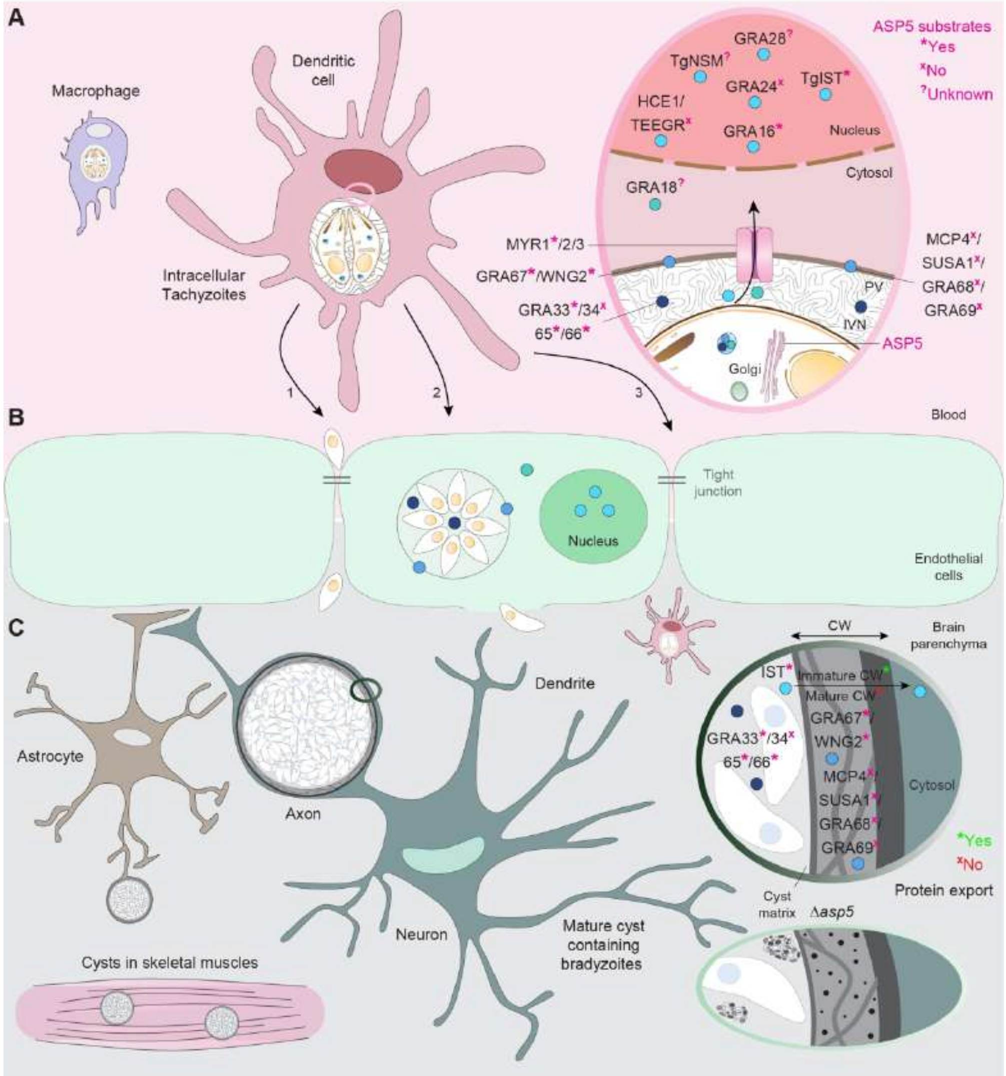

A
Macrophage
Dendritic cell
Intracellular Tachyzoites
ASP5 substrates
*Yes
ˣNo
?Unknown
GRA28?
TgNSM?
GRA24ˣ
TgIST*
HCE1/
TEEGRˣ
GRA16*
Nucleus
Cytosol
GRA18?
MYR1*/2/3
GRA67*/WNG2*
GRA33*/34ˣ
65*/66*
MCP4ˣ/
SUSA1ˣ/
GRA68ˣ/
GRA69ˣ
PV
IVN
ASP5
Golgi
1
2
3
Blood
B
Tight junction
Nucleus
Endothelial cells
C
Astrocyte
Axon
Dendrite
Neuron
Mature cyst containing bradyzoites
Cysts in skeletal muscles
CW
Brain parenchyma
IST*
Immature CW*
Mature CWˣ
GRA67*/
WNG2*
GRA33*/34ˣ
65*/66*
MCP4ˣ/
SUSA1ˣ/
GRA68ˣ/
GRA69ˣ
Cytosol
*Yes
ˣNo
Protein export
Cyst matrix
Δasp5

Figure legends

Fig 1. Localization and migration profile of newly identified GRA among candidate proteins is altered upon *asp5* deletion in tachyzoites.

Subcellular localization by immunofluorescence and migration profiles of 3Ty-tagged GRA65 (A-B), GRA66 (C-D) and GRA67 (E-F) in RHΔ*ku80* (WT) and RHΔ*asp5*Δ*ku80* (KO) parasites. GRA65 (A), GRA66 (C) and GRA67 (E) all display an altered migration profile upon *asp5* deletion, as indicated by the asterisks. GRA67 (E) accumulation in the endosomal-like compartment (ELC) upon *asp5* deletion is visible thanks to the ELC markers GRASP-GFP and ASP3-myc. Parasites were fixed for 3 min in PFA alone or for 20 min in PFA/GA to visualize dense granules or PV space/PVM, respectively. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 2. Localization and migration pattern of GRA is modified by the absence of *asp5* in tachyzoites.

Subcellular localization by immunofluorescence and migration profiles of 3Ty-tagged GRA33 (A-B), GRA34 (C-D) and WNG2 (E-F) in RHΔ*ku80* (WT) and RHΔ*asp5*Δ*ku80* (KO) parasites. GRA33 (A), and WNG2 (E) both display an altered migration profile upon *asp5* deletion. Conversely, the migration profile of GRA34 in KO parasites is unchanged (C). GRA33 (B), GRA34 (D) and WNG2 (F) all display an altered migration profile upon *asp5* deletion, as indicated by the asterisks. Parasites were fixed for 3 min in PFA alone or for 20 min in PFA/GA to visualize dense granules or PV space/PVM, respectively. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 3. Characterization of novel GRA candidate proteins not processed by ASP5.

Migration profile of 3Ty-tagged (A) MCP4, (D) GRA68 and (G) GRA69 in ME49Δ*ku80* (WT) and ME49Δ*asp5*Δ*ku80* (KO) tachyzoites and bradyzoites. (B) MCP4-3Ty, (E) GRA68-3Ty and (H) GRA69-3Ty in ME49Δ*ku80* extracellular tachyzoites or bradyzoites largely colocalizes with the dense granule marker GRA1. Subcellular localization of (C) MCP4-3Ty, (F) GRA68-3Ty and (I) GRA69-3Ty in ME49Δ*ku80* and ME49Δ*asp5*Δ*ku80* intracellular tachyzoites and bradyzoites. Note that the expression of MCP4-3Ty is strongly enhanced in bradyzoites compared to tachyzoites. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 4. IST export by bradyzoites is reduced upon cyst wall maturation.

(A) p21 endogenous expression in ME49Δ*hx*Δ*ku80* (WT) and ME49Δ*ku80*Δ*p21* (Δ*p21*) upon parasite differentiation under alkaline conditions was assessed by western blot. Tachyzoite marker: α-SAG1. Early bradyzoite marker: α-SAG4. Loading control: α-actin. Tz: tachyzoites; D3, D6 and D9: *in vitro* differentiated bradyzoites at 3, 6 or 9 days. All samples were collected intracellularly. (B) immunofluorescence assays (IFA) displaying the localization pattern of p21 using the IMC marker GAP45 and the microneme protein AMA1 after 10 days of differentiation. (C-E) Quantification from IFA of WT or Δ*p21* vacuoles positive for p21 (C), SAG4 (D) and DBA (E) staining upon parasite differentiation under alkaline conditions. (F) IFA of PFA/GA-fixed ME49Δ*hx*Δ*ku80* IST-3Ty tachyzoites and bradyzoites at 7 or 10 days in differentiation conditions. (G) Immunoblot showing IST-3Ty expression driven by endogenous or p21 promoter and upon parasite differentiation under alkaline conditions. Late bradyzoite marker: α-p21. Loading control: α-catalase. Tz: tachyzoites; D4, D7 and D10: *in vitro* differentiated bradyzoites at 4, 7 or 10 days. All samples were collected intracellularly. (H) P_{p21}-IST-3Ty expression kinetics was evaluated from IFA by quantification of IST-3Ty positive vacuoles in tachyzoites or in bradyzoites upon differentiation of P_{p21}-IST-3Ty parasites under alkaline conditions for 4, 7 or 10 days. (I) IFA of PFA/GA-fixed ME49Δ*hx*Δ*ku80* IST-3Ty and P_{p21}-IST-3Ty tachyzoites and bradyzoites at 7 or 10 days in differentiation conditions. Late bradyzoite marker: α-p21. Nuclei: DAPI. IMC: GAP45. Cyst wall: DBA. Asterisk: nucleus of an infected host cell. Scale bars: 10 µm. (J) Quantification from IFA of positive nuclei in infected cells with a single vacuole of tachyzoites or bradyzoites, differentiated for 0, 4, 7 or 10 days. (K) Quantification from IFA of positive nuclei in infected cells with a cluster of tachyzoites or bradyzoites vacuoles, differentiated for 0, 4, 7 or 10 days. (L) Model for IST export during tachyzoite to bradyzoite transition. Scale bars: 10 µm.

Fig 5. ASP5 substrates contributes to the organization of tachyzoite and bradyzoite PVs. Subcellular localization of *T. gondii* actin and immunofluorescence performed on ME49 WT (A) or ME49Δ*asp5* (B) parasites infecting HFFs for 30 h revealed that presence of ASP5 is required for residual body construction. Morphology of parasites was observed by staining of the inner membrane complex (α-IMC1) and the cytosol was visualized using α-actin antibody. The white arrowheads point towards the RB. Scale bars: 5 µm. Section through the residual body in ME49 (C) or ME49Δ*asp5* (D) parasites at 30 h post inoculation in HFF monolayer. Enlarged areas shown below each micrograph are indicated. RB: residual body; VS: vacuolar space; MNN: membranous nanotubular network; mt: mitochondrion; PVM: parasitophorous vacuole membrane. (E-G) TEM analysis documenting that the absence ASP5 and MYR1 results in accumulation of vesicles at the vacuolar membrane of *in vitro* differentiated bradyzoites. Enlarged areas shown below each micrograph are indicated in (E), (F) and (G). CW: cyst wall; Mx; cyst matrix; ap: amylopectin granules. Scale bars: 1 µm.

Fig 6. The absence of ASP5 reduces cyst burden *in vivo* and results in vesicles accumulation in the cyst matrix.

Survival monitoring (A) (n=10) and cyst burden (B) in C57BL/6 mice injected with sub-lethal doses of ME49 WT or ME49Δ*asp5* tachyzoites. (C-E) TEM analysis of ME49 WT (C) Δ*asp5* (D) and Δ*MyoJ* (E) cysts harvested from mice. Δ*asp5* cysts accumulates vesicles in the cyst matrix, indicated by asterisks. As a comparison for a low cyst forming strain, Δ*MyoJ* shows no vesicle accumulation. Asterisk: vesicles clusters. Scale bars: 5 µm. Below, enlarged view of the cyst wall and matrix. CW: cyst wall; Mx; cyst matrix; ap: amylopectin granules. Scale bars: 1 µm.

Fig 7. Cysts behavior in the brain assessed by 2-photon serial tomography.

(A) Immunostaining of brain sections containing ME49Δ*hx* (WT) GFP-fluorescent structures with a parasite membrane marker (α-GAP45). (Ai) Zoom-in the framed area in (A). DAPI: DNA marker. Scale bars: 100 μm (A) and 10 μm (Ai). (B-C) Brain sections showing WT tissue cysts imaged at 2- (B) or 5-weeks (C) post-infection. (Bi-Ci) Zoom-in the framed areas in (B) and (C). (Bii-Cii) Same image as (Bi) or (Ci) taken with a shorter exposure. Scale bars: 100 μm (B and C) and 10 μm (Bi, Bii, Ci and Cii). (D) Fluorescence-based quantification of cysts number in the brain of 2- or 5-weeks-infected mice with WT or ME49Δ*hx*Δ*asp5* (KO) parasites. (E) Total volume (μm^3) represented by the detected parasites in the brain of 2- or 5-weeks-infected mice with WT or KO parasites. (F) Frequency graph showing the volume (μm^3) of the detected cysts in the brain of 2- or 5-weeks-infected mice with WT or KO parasites. (G) Distance (μm) of the nearest neighbor (cyst or single parasite) relative to each cyst or single parasite.

Fig 8. Model for ASP5 functions and targets at the tachyzoite and bradyzoite stage. *T. gondii* tachyzoites multiply in circulating monocytes (A) or endothelial cells (B) within a PV. Secreted GRA proteins are targeted to the vacuolar space, the PVM, or the host cell cytosol or nucleus. ASP5 processes numerous intra- and extravacuolar GRAs: GRA33, GRA65, GRA66, GRA67, WNG2, MYR1, GRA16, GRA24, and IST. Subcellular localization of several GRA is altered as a direct or indirect (e.g. TASP4) effect of ASP5 knockout. The MYR1-2-3 translocation machinery is defective in the absence of ASP5 and the improper maturation of MYR1 is preventing translocation of GRA18, GRA28 and TEEGR to the host cell cytoplasm. (B) Three scenarios are discussed for crossing of the BBB by *T. gondii*: (1) para- or transcellular migration through epithelial cells, (2) infection of endothelial cells and creating a breach or (3) by exploitation of the trans-migration properties of immune cells (Trojan horse hypothesis). ASP5 substrates are involved in inducing hypermotility in infected dendritic cells. (C) Tissue-cysts reside predominantly in axons and dendrites of neurons or astrocytes in the CNS and in skeletal and heart muscle cells. At the onset of host cell infection by bradyzoites, IST and putatively other GRA can translocate through the immature CW. The CW likely becomes impermeable to GRA export upon maturation. This early release of effector proteins by bradyzoites triggers long-term effects on the transcriptome of infected cells and participate in the reprograming of the host cell cycle and immune signaling during the chronic stage of *T. gondii* infection. Of note, ASP5 contributes to the morphology of cysts, and its absence coincides with vesicle accumulation in the cyst matrix and at the PV membrane. PV: parasitophorous vacuole; GRA: dense granule proteins; PVM: parasitophorous vacuole membrane; BBB: blood brain barrier; CNS: central nervous system; IVN: intravacuolar network; CW: cyst wall.

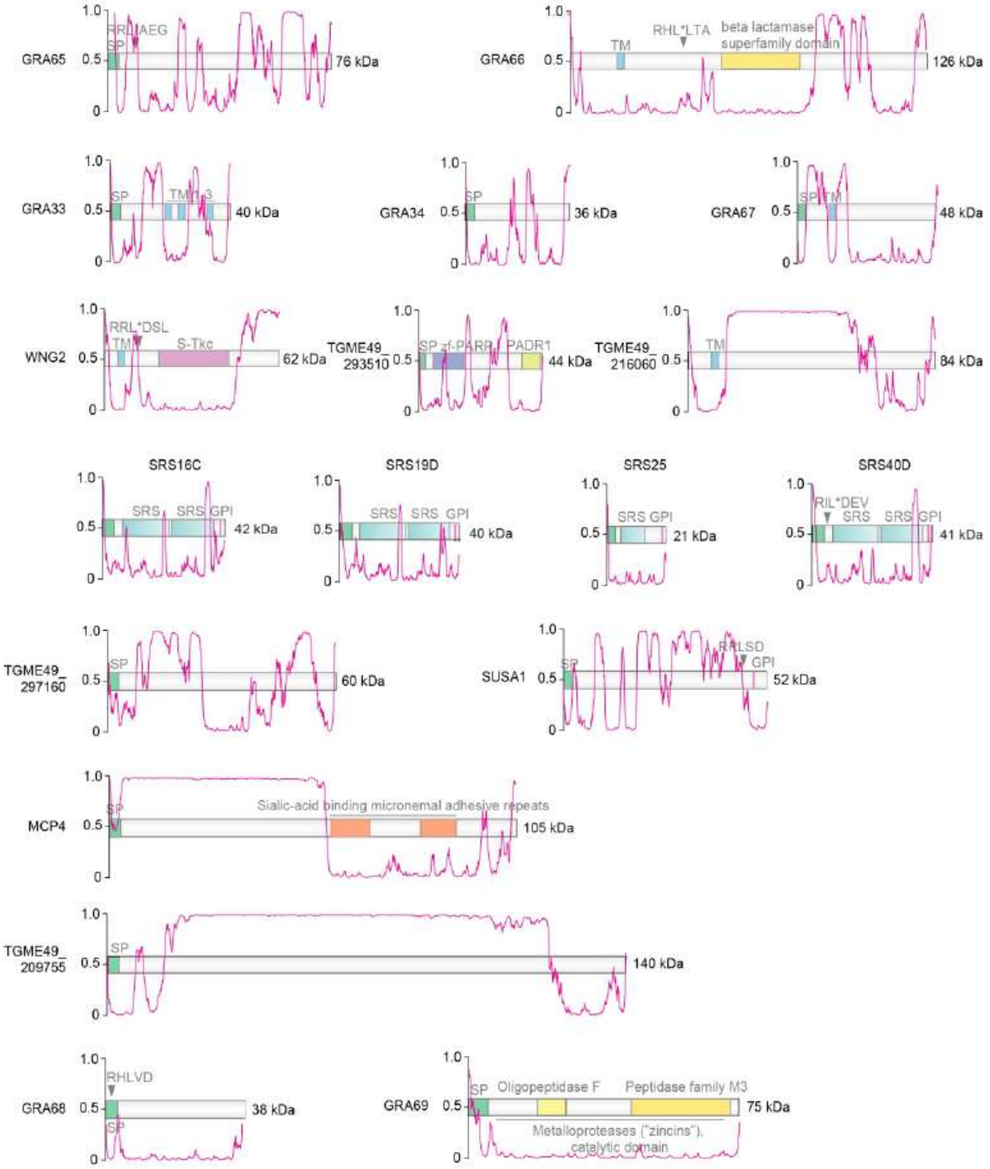
Table 1. Features of candidate TASPs proteins.

Table summarizing the accession number, name, localization, fitness cost and stage expression of candidate proteins selected from the TAILS analysis. Accession numbers, protein sequences, SP, TM, dNdS ratio (Non-synonymous/Synonymous SNPs), conservation in *Eimeria* and transcriptomics RNA-Seq data were obtained from ToxoDB (toxodb.org). For the transcriptomics RNA-Seq data, negative values indicate a lower expression in bradyzoites (Bz) compared to tachyzoites and positive values indicate a higher expression in a bradyzoites compared to tachyzoites. The Localisation of Organelle Proteins by Isotopic Tagging (LOPIT) allocation and probability were obtained from proteome.shinyapps.io/toxolopittzex/. WT: Wild type; KO: Δ*asp5*; CM: Cyst Matrix; CW: Cyst wall; RB: Residual body; PV: Parasitophorous vacuole; PVM: Parasitophorous vacuole membrane; PM: Plasma membrane; ELC: Endosomal-like compartment; SP: Signal peptide; TM: Transmembrane. Additional information on TASPs candidates is available in S1 Table.

Table 1

Gene ID (TGME49_)	Name (Newly assigned)	Processed?	Localization (Red ≠ in Δasp5)	LOPIT		TEXEL (position) or newly identified cleavage motif	SP	TM	Comments	Fitness score	dNdS score	Present in Eimeria?	Bz expression
				Allocation	Probability								
241240	GRA65	●	*WT*: Faint vesicular signal, Cytoplasm, PV *KO*: Parasite Golgi	Dense granules	1	RRLAE (68); RELVD (83)	●	0	Tandemly expanded gene cluster (Adomako-Ankomah et al., 2014)	1.95	1.96	○	-2.83
320490	GRA66	●	*WT*: PV *KO*: RB	Dense granules	1	RHLLT (358)	○	1	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein	0.13	0.92	●	0.01
247440	GRA33	●	*WT*: PV *KO*: RB	Dense granules	1	.	●	4		1.72	3.83	○	0.36
203290	GRA34	○	*WT*: PV *KO*: Vesicular & RB	Dense granules	1	.	●	0		2.26	1.17	○	1.66
279100	GRA67	●	*WT*: PV *KO*: Parasite Golgi	Dense granules	1	RLLRD (250); RGLME (420)	●	1	MAF1 copy (Adomako-Ankomah et al., 2016); Cytoplasmic localization with tubulin driven C-terminal YFP fusion		3.93	○	-0.2
240090	WNG2	●	*WT*: PV & PVM *KO*: Parasite Golgi & ELC	Dense granules	1	RRLDS (109); RELPE (240); RDLKE (277)	○	1	ROP34, renamed as WNG2 (Talevich et al., 2013; Coffey et al., 2018; Beraki et al., 2019)	0.50	1.29	●	-0.73
293510	.	○	*WT*: Parasite Nucleus *KO*: Parasite Nucleus	Nucleus chromatin	1	RELRQ (138)	●	0	poly(ADP-ribose) polymerase and Dna-Ligase Zn-finger region domain-containing protein	1.42	1.50	○	1.19
216060	.	○	*WT*: Parasite Golgi *KO*: Parasite Golgi	Golgi	1	.	○	1		0.12	1.08	○	-1.31
320180	SRS16C	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	RTLQQ (49)	●	1	BSR4 (Knoll et al., 1998; Weiss et al., 2000; Van et al., 2007); GPI (368)	2.49	2.10	○	2.40
301170	SRS19D	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	RSLQQ (49)	●	1	GPI (364)	0.41	3.18	○	0.21
213280	SRS25	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	.	●	0	GPI (167)	2.11	2.50	○	-0.58
224770	SRS40D	○	*WT*: Parasite PM *KO*: Parasite PM	.		RILDE (49)	●	0	GPI (364)		2.11	○	1.82
297160	.	○	*WT*: Parasite Mitochondria *KO*: Parasite Mitochondria	Mitochondrion membranes	1	.	●	0		0.10	0.86	●	0.24
278080	SUSA1	○	*WT*: PV (Tachy); CM (Brady) *KO*: PV (Tachy); CM (Brady)	.		RRLSD (453)	●	0	SAG unrelated surface antigen; GPI (472) (Pollard et al., 2008)	1.43	2.10	○	3.62
208730	MCP4	○	*WT*: PVM (Tachy); CW (Brady) *KO*: PV (Tachy); CW (Brady)	Golgi	1	.	●	1	Cyst wall (Buchholz et al., 2011)	1.09	1.18	●	1.60
209755	.	○	*WT*: PV (Tachy); CM (Brady) *KO*: PV (Tachy); CM (Brady)	.		.	●	0			2.75	○	2.91
308970	GRA68	○	*WT*: PV (Tachy); CW (Brady) *KO*: PV (Tachy); CW (Brady)	Dense granules	1	RHLVD (4)	●	0		2.51	2.00	●	-1.00
226420	GRA69	○	*WT*: PV (Tachy); CM & CW (Brady) *KO*: PV (Tachy); CM & CW (Brady)	Dense granules	0	.	●	0	Peptidase family M3 protein	1.15	2.00	●	1.94

S1 Fig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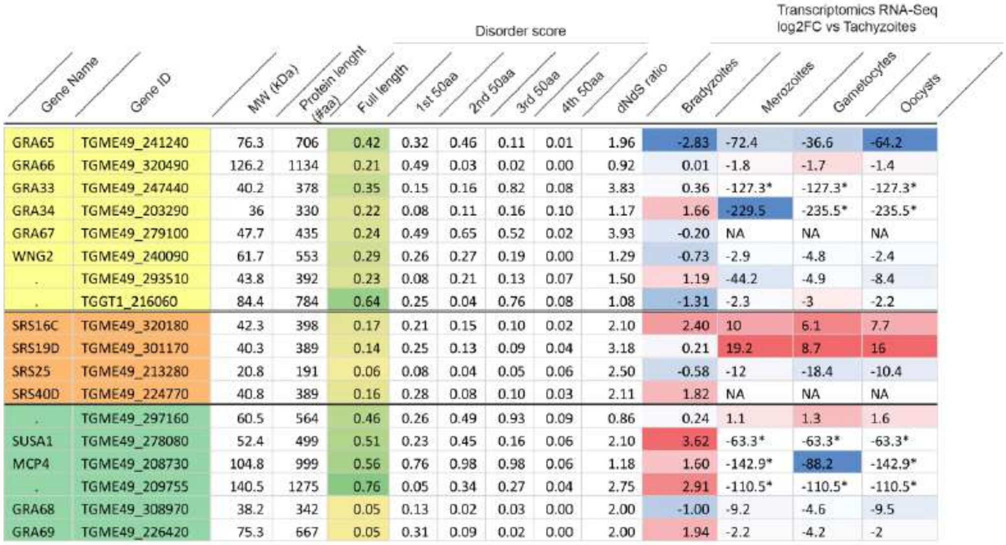
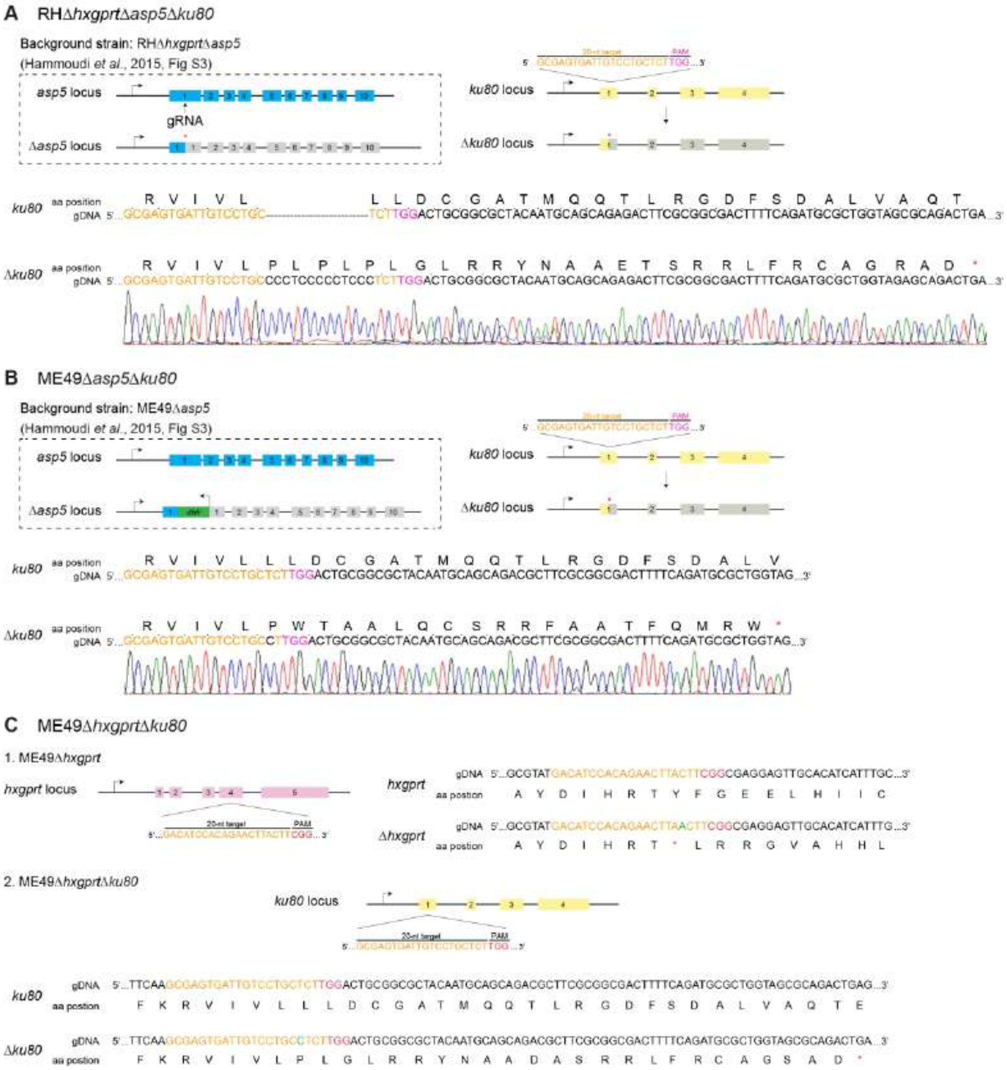
S1 Table



				Disorder score						Transcriptomics RNA-Seq log2FC vs Tachyzoites			
Gene Name	Gene ID	MW (kDa)	Protein lenght (#aa)	Full length	1st 50aa	2nd 50aa	3rd 50aa	4th 50aa	dNdS ratio	Bradyzoites	Merozoites	Gametocytes	Oocysts
GRA65	TGME49_241240	76.3	706	0.42	0.32	0.46	0.11	0.01	1.96	-2.83	-72.4	-36.6	-64.2
GRA66	TGME49_320490	126.2	1134	0.21	0.49	0.03	0.02	0.00	0.92	0.01	-1.8	-1.7	-1.4
GRA33	TGME49_247440	40.2	378	0.35	0.15	0.16	0.82	0.08	3.83	0.36	-127.3*	-127.3*	-127.3*
GRA34	TGME49_203290	36	330	0.22	0.08	0.11	0.16	0.10	1.17	1.66	-229.5	-235.5*	-235.5*
GRA67	TGME49_279100	47.7	435	0.24	0.49	0.65	0.52	0.02	3.93	-0.20	NA	NA	NA
WNG2	TGME49_240090	61.7	553	0.29	0.26	0.27	0.19	0.00	1.29	-0.73	-2.9	-4.8	-2.4
.	TGME49_293510	43.8	392	0.23	0.08	0.21	0.13	0.07	1.50	1.19	-44.2	-4.9	-8.4
.	TGGT1_216060	84.4	784	0.64	0.25	0.04	0.76	0.08	1.08	-1.31	-2.3	-3	-2.2
SRS16C	TGME49_320180	42.3	398	0.17	0.21	0.15	0.10	0.02	2.10	2.40	10	6.1	7.7
SRS19D	TGME49_301170	40.3	389	0.14	0.25	0.13	0.09	0.04	3.18	0.21	19.2	8.7	16
SRS25	TGME49_213280	20.8	191	0.06	0.08	0.04	0.05	0.06	2.50	-0.58	-12	-18.4	-10.4
SRS40D	TGME49_224770	40.8	389	0.16	0.28	0.08	0.10	0.03	2.11	1.82	NA	NA	NA
.	TGME49_297160	60.5	564	0.46	0.26	0.49	0.93	0.09	0.86	0.24	1.1	1.3	1.6
SUSA1	TGME49_278080	52.4	499	0.51	0.23	0.45	0.16	0.06	2.10	3.62	-63.3*	-63.3*	-63.3*
MCP4	TGME49_208730	104.8	999	0.56	0.76	0.98	0.98	0.06	1.18	1.60	-142.9*	-88.2	-142.9*
.	TGME49_209755	140.5	1275	0.76	0.05	0.34	0.27	0.04	2.75	2.91	-110.5*	-110.5*	-110.5*
GRA68	TGME49_308970	38.2	342	0.05	0.13	0.02	0.03	0.00	2.00	-1.00	-9.2	-4.6	-9.5
GRA69	TGME49_226420	75.3	667	0.05	0.31	0.09	0.02	0.00	2.00	1.94	-2.2	-4.2	-2

S2 Fig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TGGT1_319560	microneme protein MIC3	0
TGGT1_356400	cAMP-dependent protein kinase	0
TGGT1_241240	hypothetical protein	0
TGGT1_228170	inner membrane complex protein IMC2A	1
TGGT1_240090	putative rhoptry kinase family protein ROP	1

[SignalP Scores]	[Protein Length]	Annotated Sequence
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[A].TAPGAVLLDAIDAESDKVDNQAEGGER.[M]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[Q].EATAPGAVLLDAIDAESDKVDNQAEGGER.[M]
NN Sum: 4, NN D: .88, HMM Prob: 1	108	[R].AAVVSGLANENGLWR.[R]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[E].ATAPGAVLLDAIDAESDKVDNQAEGGER.[M]
NN Sum: 1, NN D: .41, HMM Prob: .97	398	[A].DNLLEGLLHR.[T]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[Q].EATAPGAVLLDAIDAESDKVDNQAEGGER.[M]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[A].ESDKVDNQAEGGER.[M]
N/A	3700	[S].SLLDLDDAQR.[A]
NN Sum: 4, NN D: .79, HMM Prob: 1	345	[S].FGSHLADMAGLSGR.[H]
NN Sum: 4, NN D: .68, HMM Prob: .97	561	[L].NSHTETPTQSPSAFR.[R]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[L].DAIDAESDKVDNQAEGGER.[M]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[L].LDAIDAESDKVDNQAEGGER.[M]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[P].VDVPFSGKPLDER.[A]
NN Sum: 4, NN D: .68, HMM Prob: .97	561	[N].SHTETPTQSPSAFR.[R]
N/A	175	[SA].FLSEEGR.[HA]
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[T].YNLIKEIR.[K]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[T].SGVQEATAPGAVLLDAIDAESDKVDNQAEGGER
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[K].YADDDIR.[Q]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[G].VVNQGPVDVPFSGKPLDER.[A]
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[T].SFLSHHGEYQNPTSTYNLIKEIR.[K]
NN Sum: 3, NN D: .48, HMM Prob: .73	222	[D].AIDAESDKVDNQAEGGER.[M]
NN Sum: 4, NN D: .61, HMM Prob: .94	436	[A].TVAAGNELFKEALGHQR.[V]
NN Sum: 4, NN D: .55, HMM Prob: .17	378	[A].VTSPAAEEER.[L]
NN Sum: 3, NN D: .46, HMM Prob: .81	256	[Y].ATLNTPKPESPPPVPPPR.[S]
NN Sum: 4, NN D: .61, HMM Prob: .94	436	[R].AATVAAGNELFKEALGHQR.[V]
NN Sum: 3, NN D: .52, HMM Prob: .97	769	[W].SIVDALR.[K]
NN Sum: 1, NN D: .36, HMM Prob: .84	335	[Y].DLNADGAIDVEELQQIIKDPHSHEIR.[M]
N/A	151	[-].MVDTNASKQPAATADR.[K]
NN Sum: 4, NN D: .79, HMM Prob: 1	345	[A].QVVPGTPGHPVQAIPQQPLR.[T]
NN Sum: 4, NN D: .84, HMM Prob: 1	312	[L].GPSLPSFLVAER.[A]
N/A	589	[Q].GLDSRPEKLSSKGLTAR.[R]
NN Sum: 4, NN D: .84, HMM Prob: 1	236	[T].SMDKASVESQLPR.[R]
NN Sum: 4, NN D: .79, HMM Prob: 1	345	[Y].TAQVVPGTPGHPVQAIPQQPLR.[T]
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[A].WDIITTGEPNMGSR.[R]
NN Sum: 1, NN D: .3, HMM Prob: .96	1249	[F].SSTEDEEHASAGGSWWSSLSR.[G]
NN Sum: 4, NN D: .88, HMM Prob: 1	108	[A].SHGTTFQDAGAR.[A]
NN Sum: 4, NN D: .93, HMM Prob: 1	549	[A].DGAGVADETHQEPRPPLR.[K]
NN Sum: 4, NN D: .61, HMM Prob: .94	436	[A].ATVAAGNELFKEALGHQR.[V]
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[K].GAWDIITTGEPNMGSR.[R]
NN Sum: 4, NN D: .93, HMM Prob: 1	549	[A].EEVADMSGGR.[V]
NN Sum: 3, NN D: .64, HMM Prob: .99	1699	[G].SPAADLVASVQTVSNER.[K]
N/A	223	[A].EGDVDPFPVLANEGKSEAR.[G]
NN Sum: 0, NN D: .22, HMM Prob: .86	552	[C].DDFIPEPER.[K]
NN Sum: 4, NN D: .84, HMM Prob: 1	236	[M].DKASVESQLPR.[R]
N/A	389	[M].GGAAPAVFVDEDAEPSPR.[G]

NN Sum: 2, NN D: .27, HMM Prob: .67	621	[F].NLEGKIHVANPVVEMDGDEMTR.[I]
NN Sum: 4, NN D: .55, HMM Prob: .17	378	[Q].SPSAPQHDILWDAR.[K]
NN Sum: 4, NN D: .86, HMM Prob: 1	219	[A].DDAFIDNVKK.[G]
NN Sum: 4, NN D: .93, HMM Prob: 1	549	[A].DETHQEPRPPLR.[K]
NN Sum: 4, NN D: .74, HMM Prob: 1	795	[L].SHHGEYQNPTSTYNLIKEIR.[K]
NN Sum: 4, NN D: .79, HMM Prob: 1	345	[F].VFTPSSVQPGAEVTPGYSGLQLR.[Q]
NN Sum: 4, NN D: .84, HMM Prob: 1	236	[V].DSKGTDDHLTTSMDKASVESQLPR.[R]
N/A	588	[Q].TPEAPASQEPR.[F]
NN Sum: 4, NN D: .84, HMM Prob: 1	236	[K].GTDDHLTTSMDKASVESQLPR.[R]
NN Sum: 4, NN D: .68, HMM Prob: .97	561	[L].LNSHTETPTQSPSAFR.[R]
N/A	131	[A].SLTPGGGRPDGGGGSGSRPR.[F]
NN Sum: 4, NN D: .81, HMM Prob: 1	984	[L].GPTVSDESR.[R]
NN Sum: 3, NN D: .64, HMM Prob: .01	473	[C].ILPEVQAPDR.[K]
NN Sum: 4, NN D: .79, HMM Prob: 1	345	[S].FGSHLADMAGLSGR.[H]
NN Sum: 1, NN D: .32, HMM Prob: .85	336	[A].SDPPLVANQVVTCPDK.[K]
NN Sum: 3, NN D: .64, HMM Prob: .99	1699	[A].GQAAQTDAQPLPKAAQTDAQPLPKVR.[R]
NN Sum: 4, NN D: .72, HMM Prob: .99	183	[A].ADEASSDDRPLLER.[V]
N/A	557	[E].EKTKGQLAGVLR.[L]
NN Sum: 4, NN D: .64, HMM Prob: 1	287	[A].FTLPPLPYAEDALAPHISAETLR.[F]
NN Sum: 4, NN D: .51, HMM Prob: .87	519	[L].NLPDVEEALKR.[D]
NN Sum: 3, NN D: .64, HMM Prob: .99	1699	[Q].AAQTDAQPLPKAAQTDAQPLPKVR.[R]
NN Sum: 3, NN D: .48, HMM Prob: .97	2614	[S].GGVHEYADSQFGHIFATGKNR.[E]
NN Sum: 4, NN D: .93, HMM Prob: 1	549	[E].EVADMSGGR.[V]
NN Sum: 4, NN D: .61, HMM Prob: .94	436	[V].AAGNELFKEALGHQR.[V]
NN Sum: 4, NN D: .74, HMM Prob: .95	435	[A].DASQEAGDVVEER.[T]
NN Sum: 3, NN D: .47, HMM Prob: .38	392	[M].PAKEIVFHCEYAPSGR.[A]
N/A	224	[A].ASAKATHALQPTGTGSVAFTRPGQGSNAQFQT
N/A	588	[Q].GDFLSLSDASLEPHR.[S]
NN Sum: 2, NN D: .41, HMM Prob: .79	377	[A].ASVAPSSSSDSLCSDLSACSTEAAALEALTKR.[R]
N/A	412	[M].VVTASPDTYLHVIDYGLK.[K]
NN Sum: 4, NN D: .72, HMM Prob: .68	1291	[F].VDSTSGQNASPRPTKTDKIR.[K]
N/A	569	[T].ALQCTADKFPDSFGACDVQACKR.[Q]
NN Sum: 4, NN D: .86, HMM Prob: 1	318	[A].DTTEQPSITPSGEEDRPPKDAPKER.[K]
NN Sum: 4, NN D: .63, HMM Prob: 1	383	[F].AVTETHSSVQSPSKQETQLCAISSEGKPCR.[N]
NN Sum: 4, NN D: .63, HMM Prob: 1	383	[G].GDCSCEKQGHR.[C]
NN Sum: 4, NN D: .69, HMM Prob: 1	306	[A].APVQGTLGPDVADTAGEPVVLQVAR.[G]
NN Sum: 4, NN D: .56, HMM Prob: .91	474	[L].AEGKPGEKR.[D]
NN Sum: 2, NN D: .46, HMM Prob: .77	1596	[L].SGIIKTLVLWDPVQR.[L]
N/A	553	[L].DSLIPGFLKR.[R]

Modifications	Modifications in Master Proteins	Positions in Master Proteins	Abundance Ratio: (ko, single) / (wt, single)
2xTMT6plex [N-Term; K17]		TGGT1_227280-t26_1-p1 [85-	100
1xTMT6plex [N-Term]		TGGT1_227280-t26_1-p1 [83-	100
1xTMT6plex [N-Term]		TGGT1_201390-t26_1-p1 [47-	100
2xTMT6plex [N-Term; K18]		TGGT1_227280-t26_1-p1 [84-	30.739
1xTMT6plex [N-Term]		TGGT1_320180-t26_1-p1 [40-	18.861
2xTMT6plex [N-Term; K19]		TGGT1_227280-t26_1-p1 [83-	10.123
2xTMT6plex [N-Term; K4]		TGGT1_227280-t26_1-p1 [98-	9.914
1xTMT6plex [N-Term]		TGGT1_216620-t26_1-p1 [981	9.798
1xTMT6plex [N-Term]		TGGT1_310780-t26_1-p1 [25-	8.695
1xTMT6plex [N-Term]		TGGT1_363030-t26_1-p1 [97-	6.543
2xTMT6plex [N-Term; K9]		TGGT1_227280-t26_1-p1 [93-	5.285
2xTMT6plex [N-Term; K10]		TGGT1_227280-t26_1-p1 [92-	5.163
2xTMT6plex [N-Term; K8]		TGGT1_227620-t26_1-p1 [35-	4.598
1xTMT6plex [N-Term]		TGGT1_363030-t26_1-p1 [98-	4.188
1xTMT6plex [N-Term]		TGGT1_233695-t26_1-p1 [105	4.144
2xTMT6plex [N-Term; K5]		TGGT1_204050-t26_1-p1 [52-	4.089
2xTMT6plex [N-Term; K23]		TGGT1_227280-t26_1-p1 [79-	4.045
1xTMT6plex [N-Term]		TGGT1_204050-t26_1-p1 [85-	3.829
2xTMT6plex [N-Term; K14]		TGGT1_227620-t26_1-p1 [29-	3.616
2xTMT6plex [N-Term; K20]		TGGT1_204050-t26_1-p1 [37-	3.493
1xTMT6plex [K8]		TGGT1_227280-t26_1-p1 [94-	3.465
2xTMT6plex [N-Term; K10]		TGGT1_288650-t26_1-p1 [235	3.138
1xTMT6plex [N-Term]		TGGT1_247440-t26_1-p1 [139	3.065
2xTMT6plex [N-Term; K7]		TGGT1_247520-t26_1-p1 [200	3.014
2xTMT6plex [N-Term; K12]		TGGT1_288650-t26_1-p1 [233	2.897
1xTMT6plex [N-Term]		TGGT1_201780-t26_1-p1 [30-	2.863
2xTMT6plex [N-Term; K18]		TGGT1_229480-t26_1-p1 [240	2.854
1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_25	TGGT1_258730-t26_1-p1 [1-1	2.799
1xTMT6plex [N-Term]		TGGT1_310780-t26_1-p1 [123	2.792
1xTMT6plex [N-Term]		TGGT1_290700-t26_1-p1 [23-	2.677
3xTMT6plex [N-Term; K8; K12]		TGGT1_226020-t26_1-p1 [33-	2.675
2xTMT6plex [N-Term; K4]		TGGT1_203310-t26_1-p1 [72-	2.635
1xTMT6plex [N-Term]		TGGT1_310780-t26_1-p1 [121	2.635
1xTMT6plex [N-Term]		TGGT1_204050-t26_1-p1 [238	2.579
1xTMT6plex [N-Term]		TGGT1_218240-t26_1-p1 [109	2.541
1xTMT6plex [N-Term]		TGGT1_201390-t26_1-p1 [23-	2.483
1xTMT6plex [N-Term]		TGGT1_308090-t26_1-p1 [109	2.482
2xTMT6plex [N-Term; K11]		TGGT1_288650-t26_1-p1 [234	2.476
1xTMT6plex [N-Term]		TGGT1_204050-t26_1-p1 [236	2.45
1xTMT6plex [N-Term]		TGGT1_308090-t26_1-p1 [67-	2.425
1xTMT6plex [N-Term]		TGGT1_311470-t26_1-p1 [35-	2.356
2xTMT6plex [N-Term; K15]		TGGT1_275440-t26_1-p1 [97-	2.325
1xTMT6plex [N-Term]		TGGT1_262380-t26_1-p1 [352	2.304
2xTMT6plex [N-Term; K2]		TGGT1_203310-t26_1-p1 [74-	2.297
1xTMT6plex [N-Term]		TGGT1_219270-t26_1-p1 [40-	2.293

2xTMT6plex [N-Term; K5]		TGGT1_313140-t26_1-p1 [171	2.278
1xTMT6plex [N-Term]		TGGT1_247440-t26_1-p1 [41-	2.264
2xTMT6plex [N-Term; K]		TGGT1_297880-t26_1-p1 [31-	2.26
1xTMT6plex [N-Term]		TGGT1_308090-t26_1-p1 [115	2.254
2xTMT6plex [N-Term; K17]		TGGT1_204050-t26_1-p1 [40-	2.244
1xTMT6plex [N-Term]		TGGT1_310780-t26_1-p1 [164	2.241
3xTMT6plex [N-Term; K3; K15]		TGGT1_203310-t26_1-p1 [61-	2.234
1xTMT6plex [N-Term]		TGGT1_293300-t26_1-p1 [295	2.228
2xTMT6plex [N-Term; K12]		TGGT1_203310-t26_1-p1 [64-	2.224
1xTMT6plex [N-Term]		TGGT1_363030-t26_1-p1 [96-	2.22
1xTMT6plex [N-Term]		TGGT1_316600-t26_1-p1 [102	2.213
1xTMT6plex [N-Term]		TGGT1_229010-t26_1-p1 [882	2.184
1xTMT6plex [N-Term]		TGGT1_269980-t26_1-p1 [17-	2.12
1xTMT6plex [N-Term]; 1xOxidation [M8]		TGGT1_310780-t26_1-p1 [25-	2.108
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13]		TGGT1_233460-t26_1-p1 [48-	2.072
3xTMT6plex [N-Term; K13; K24]		TGGT1_311470-t26_1-p1 [130	2.05
1xTMT6plex [N-Term]		TGGT1_264080-t26_1-p1 [96-	2.032
3xTMT6plex [N-Term; K2; K4]		TGGT1_258870A-t26_1-p1 [38	2.032
1xTMT6plex [N-Term]		TGGT1_316330-t26_1-p1 [87-	2.03
2xTMT6plex [N-Term; K10]		TGGT1_297070-t26_1-p1 [288	2.025
3xTMT6plex [N-Term; K11; K22]		TGGT1_311470-t26_1-p1 [130	2.012
2xTMT6plex [N-Term; K19]		TGGT1_221320-t26_1-p1 [764	2.012
1xTMT6plex [N-Term]		TGGT1_308090-t26_1-p1 [68-	2.004
2xTMT6plex [N-Term; K8]		TGGT1_288650-t26_1-p1 [237	2.002
1xTMT6plex [N-Term]		TGGT1_279100-t26_1-p1 [46-	1.635
2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C9]		TGGT1_293510-t26_1-p1 [36-	0.732
3xTMT6plex [N-Term; K4; K37]		TGGT1_310360-t26_1-p1 [88-	0.496
1xTMT6plex [N-Term]		TGGT1_293300-t26_1-p1 [90-	0.489
2xTMT6plex [N-Term; K31]; 2xCarbamidomethyl [C13; C1		TGGT1_290730-t26_1-p1 [99-	0.487
1xTMT6plex [N-Term]		TGGT1_209800-t26_1-p1 [2-1	0.47
1xAcetyl [N-Term]; 2xTMT6plex [K15; K18]	TGGT1_26	TGGT1_269885A-t26_1-p1 [54	0.456
3xTMT6plex [N-Term; K8; K22]; 3xCarbamidomethyl [C4; C		TGGT1_255260-t26_1-p1 [432	0.404
3xTMT6plex [N-Term; K19; K23]		TGGT1_208450-t26_1-p1 [84-	0.383
3xTMT6plex [N-Term; K14; K27]; 2xCarbamidomethyl [C20		TGGT1_319560-t26_1-p1 [57-	0.383
2xTMT6plex [N-Term; K7]; 2xCarbamidomethyl [C3; C5]		TGGT1_319560-t26_1-p1 [143	0.34
1xTMT6plex [N-Term]		TGGT1_356400-t26_1-p1 [27-	0.255
1xAcetyl [N-Term]; 2xTMT6plex [K4; K8]	TGGT1_241	TGGT1_241240-t26_1-p1 [71-	0.073
2xTMT6plex [N-Term; K5]		TGGT1_228170-t26_1-p1 [86-	0.01
2xTMT6plex [N-Term; K9]		TGGT1_240090-t26_1-p1 [112	0.01

Abundance Ratio (log2): (ko, single) / (wt, single)	Abundances (Grouped): ko, single	Abundances (Grouped): wt, single
6.64	9.9	
6.64	9.3	
6.64	3.6	
4.94	104.7	3.4
4.24	46.8	2.5
3.34	32.1	3.2
3.31	26.5	2.7
3.29	69.3	7.1
3.12	69.2	8
2.71	24.5	3.8
2.4	131.8	24.9
2.37	153.4	29.7
2.2	38.2	8.3
2.07	23.8	5.7
2.05	37.3	9
2.03	189	46.2
2.02	6.9	1.7
1.94	124.9	32.6
1.85	54.3	15
1.8	14.1	4
1.79	14	4
1.65	14.3	4.6
1.62	90.5	29.5
1.59	29.4	9.8
1.53	45.4	15.7
1.52	101.2	35.4
1.51	5.8	2
1.48	43.6	15.6
1.48	14.4	5.2
1.42	330.9	123.6
1.42	50.7	18.9
1.4	238.4	90.4
1.4	4.5	1.7
1.37	5.8	2.2
1.35	7.7	3
1.31	144.8	58.3
1.31	28.3	11.4
1.31	36.1	14.6
1.29	7.3	3
1.28	280.9	115.9
1.24	7	3
1.22	132.7	57.1
1.2	40.3	17.5
1.2	155.5	67.7
1.2	17.5	7.6

1.19	5.1	2.3
1.18	23.1	10.2
1.18	58.4	25.8
1.17	464.8	206.2
1.17	7.5	3.4
1.16	6.2	2.8
1.16	27.7	12.4
1.16	4.4	2
1.15	40.1	18
1.15	20.7	9.3
1.15	8.1	3.7
1.13	7.3	3.3
1.08	39.4	18.6
1.08	9.2	4.4
1.05	25.6	12.4
1.04	22.1	10.8
1.02	28.1	13.8
1.02	78	38.4
1.02	8.4	4.2
1.02	183.5	90.6
1.01	3.4	1.7
1.01	6.6	3.3
1	387.8	193.5
1	117.5	58.7
0.71	165.9	101.5
-0.45	93.4	127.7
-1.01	3.6	7.3
-1.03	1.8	3.6
-1.04	5.1	10.6
-1.09	2.1	4.5
-1.13	3.7	8.1
-1.31	22.4	55.4
-1.39	2.5	6.6
-1.38	6.8	17.8
-1.56	9	26.5
-1.97	1.7	6.7
-3.78	10.8	148.3
-6.64		32.3
-6.64	5.8	717.6

Master Protein Accessions	[Product Description]	[# TM Domains]
TGME49_320180	SAG-related sequence SRS16C	1
TGME49_301170	SAG-related sequence SRS19D	1
TGME49_227620	dense granule protein GRA2	0
TGME49_213280	SAG-related sequence SRS25	0
TGME49_203290	hypothetical protein	0
TGME49_203290	hypothetical protein	0
TGME49_227620	dense granule protein GRA2	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_217740	3-ketoacyl-(acyl-carrier-protein) reductase	0
TGME49_290030	hypothetical protein	1
TGME49_293590	3-oxoacyl-acyl-carrier protein synthase I/II, puta	1
TGME49_305510	hypothetical protein	0
TGME49_253330	Rhoptry kinase family protein, truncated (incom	0
TGME49_244560	heat shock protein 90, putative	1
TGME49_226000	ATP synthase, putative	0
TGME49_215785	rhoptry protein ROP2A	1
TGME49_275440	dense granule protein GRA6	2
TGME49_215590	flavoprotein subunit of succinate dehydrogenas	0
TGME49_250710	microneme protein MIC10	1
TGME49_251540	dense granule protein GRA9	0
TGME49_259550	dihydropteroate synthase	0
TGME49_226420	peptidase family M3 protein	0
TGME49_222840	Ser/Thr phosphatase family protein	0
TGME49_258870	hypothetical protein	2
TGME49_203970	dolichyl-diphosphooligosaccharide--protein glyc	1
TGME49_207160	SAG-related sequence SRS49D	1
TGME49_231100	hypothetical protein	1
TGME49_319560	microneme protein MIC3	0
TGME49_297160	hypothetical protein	0
TGME49_253900	parasite porphobilinogen synthase PBGS	0
TGME49_203290	hypothetical protein	0
TGME49_258390	DnaJ protein, putative	0
TGME49_313390	ribosomal protein RPL6	0
TGME49_209150	non-proton pumping type-II NADH dehydrogena	0
TGME49_292280	SAG-related sequence SRS36D	1
TGME49_219320	acid phosphatase GAP50	2
TGME49_227620	dense granule protein GRA2	0
TGME49_208450	protease inhibitor PI2	0
TGME49_293590	3-oxoacyl-acyl-carrier protein synthase I/II, puta	1
TGME49_254060	SAG-related sequence SRS14A	1
TGME49_236040	fructose-1,6-bisphosphate aldolase	1
TGME49_207160	SAG-related sequence SRS49D	1
TGME49_253330	Rhoptry kinase family protein, truncated (incom	0
TGME49_209755	hypothetical protein	0
TGME49_208730	microneme protein, putative	1
TGME49_206320	hypothetical protein	2

TGME49_292270	SAG-related sequence SRS36C	0
TGME49_237880	hypothetical protein	1
TGME49_224770	SAG-related sequence SRS40D	0
TGME49_214290	DJ-1 family protein	0
TGME49_213670	hypothetical protein	1
TGME49_214780	hydrolase, NUDIX family protein	0
TGME49_208730	microneme protein, putative	1
TGME49_311720	chaperonin protein BiP	1
TGME49_207160	SAG-related sequence SRS49D	1
TGME49_227620	dense granule protein GRA2	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_207130	SAG-related sequence SRS49A	0
TGME49_204530	microneme protein MIC11	0
TGME49_263270	glycerophosphodiester phosphodiesterase fami	6
TGME49_293510	poly(ADP-ribose) polymerase and DNA-Ligase Zr	0
TGME49_214480	replication factor a protein 3 protein	0
TGME49_250710	microneme protein MIC10	1
TGME49_290940	EMP/nonaspanin domain family protein	10
TGME49_207160	SAG-related sequence SRS49D	1
TGME49_215280	succinate dehydrogenase [ubiquinone] iron-sulf	0
TGME49_264080	acyl carrier protein ACP	1
TGME49_236210	peptidase M16 family potein, putative	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_270240	MAG1	1
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_247520	hypothetical protein	1
TGME49_205580	nuclear factor NF4	0
TGME49_254010	serine carboxypeptidase s28 protein	1
TGME49_261740	hypothetical protein	1
TGME49_269190	glyceraldehyde-3-phosphate dehydrogenase GA	1
TGME49_250710	microneme protein MIC10	1
TGME49_286120	prolyl endopeptidase	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_283780	glucose-6-phosphate isomerase GPI	1
TGME49_314250	bradyzoite rhoptry protein BRP1	1
TGME49_311720	chaperonin protein BiP	1
TGME49_229480	calcium binding protein precursor, putative	1
TGME49_219690	hypothetical protein	0
TGME49_278080	Toxoplasma gondii family A protein	0
TGME49_208030	microneme protein MIC4	0
TGME49_255660	EF hand domain-containing protein	0
TGME49_237880	hypothetical protein	1
TGME49_247520	hypothetical protein	1
TGME49_227620	dense granule protein GRA2	0
TGME49_211040	Sec61beta family protein	1
TGME49_219690	hypothetical protein	0
TGME49_319560	microneme protein MIC3	0
TGME49_309160	IgA-specific metalloendopeptidase	0
TGME49_207130	SAG-related sequence SRS49A	0
TGME49_250710	microneme protein MIC10	1
TGME49_283780	glucose-6-phosphate isomerase GPI	1

TGME49_211680	protein disulfide isomerase	0
TGME49_237880	hypothetical protein	1
TGME49_240090	rhoptry kinase family protein ROP34, putative	1
TGME49_291600	gamma interferon inducible lysosomal thiol red	1
TGME49_320490	N-acyl-phosphatidylethanolamine-hydrolyzing p	1
TGME49_208730	microneme protein, putative	1

[SignalP Scores]	[Protein Length]	Annotated Sequence
NN Sum: 1, NN D: .41, HMM Prob: .97	398	[A].DNLLEGLLHR.[T]
NN Sum: 4, NN D: .54, HMM Prob: .98	389	[A].VPDKFLEGLQTR.[S]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[P].VDVPFSGKPLDER.[A]
NN Sum: 4, NN D: .75, HMM Prob: 1	191	[A].EEHFAVFSTCR.[T]
NN Sum: 1, NN D: .3, HMM Prob: .55	330	[S].APYKAYGIPAESTDTTSGDDVEEAFR.[K]
NN Sum: 1, NN D: .3, HMM Prob: .55	330	[P].YKAYGIPAESTDTTSGDDVEEAFR.[K]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[D].VPFSGKPLDER.[A]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[G].LTSAAPDFTVTIPKEGLPADR.[Q]
NN Sum: 4, NN D: .62, HMM Prob: 1	376	[S].AYKLTFGGPETGEKDGR.[V]
NN Sum: 0, NN D: .24, HMM Prob: .83	229	[N].AAAPAAEAAKTLER.[N]
NN Sum: 4, NN D: .73, HMM Prob: .92	551	[R].SSTETCGVKGRPR.[V]
NN Sum: 3, NN D: .44, HMM Prob: .86	418	[M].AVAKLDGKTLPALR.[L]
NN Sum: 4, NN D: .85, HMM Prob: .99	377	[P].NPIDGSKHGQFPSLR.[R]
NN Sum: 4, NN D: .63, HMM Prob: 1	847	[A].TETDAAEPLTAEEAPR.[S]
NN Sum: 1, NN D: .25, HMM Prob: .79	183	[F].ATAAGGANPFKNQLLLTLSSPSEAIYVR.[T]
NN Sum: 4, NN D: .67, HMM Prob: .97	433	[G].HVQQGAGVVRPR.[H]
N/A	224	[S].LGGVAVAADSGGVR.[Q]
NN Sum: 0, NN D: .2, HMM Prob: .98	669	[F].TNVKKPAYR.[V]
NN Sum: 4, NN D: .7, HMM Prob: .42	198	[G].EHDFFNDYDQDEEYR.[K]
NN Sum: 4, NN D: .74, HMM Prob: .99	318	[A].SESDVALKVPEDPVPEEPR.[R]
NN Sum: 1, NN D: .32, HMM Prob: .7	748	[M].TANSHFLQKMR.[E]
NN Sum: 2, NN D: .32, HMM Prob: .97	667	[G].EIANGKGTDTTPAR.[L]
NN Sum: 4, NN D: .53, HMM Prob: .42	433	[M].GIVKVCVR.[Q]
N/A	916	[R].GMDDGAFVR.[G]
N/A	680	[A].AVLPIPSAPPLR.[A]
NN Sum: 0, NN D: .22, HMM Prob: .84	364	[A].NSQSVTCESNASPLVLR.[I]
N/A	492	[A].ELKSSSEEPSQQPASAAGGTDR.[F]
NN Sum: 4, NN D: .63, HMM Prob: 1	383	[Q].SPSKQETQLCAISSEGKPCR.[N]
NN Sum: 4, NN D: .45, HMM Prob: .99	564	[L].SSSQPLTAPSTPTKASR.[S]
NN Sum: 4, NN D: .88, HMM Prob: 1	658	[G].AAAGPTPVGKGTPGGAKGQFR.[G]
NN Sum: 1, NN D: .3, HMM Prob: .55	330	[G].HEPVASAPYKAYGIPAESTDTTSGDDVEEAFR.[K]
NN Sum: 4, NN D: .68, HMM Prob: .81	397	[A].AKQNLYSVLGVKR.[N]
NN Sum: 1, NN D: .19, HMM Prob: .78	282	[M].APTAAALAKKR.[L]
NN Sum: 4, NN D: .56, HMM Prob: .99	618	[C].DSPASPSSPSSPKER.[V]
NN Sum: 4, NN D: .59, HMM Prob: 1	367	[K].GQKEQANTTATLPTCR.[V]
NN Sum: 1, NN D: .35, HMM Prob: .98	431	[F].TVLGVDDWSR.[N]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[V].NQGPVDVPFSGKPLDER.[A]
NN Sum: 4, NN D: .86, HMM Prob: 1	318	[A].SPETKVCSCPR.[N]
NN Sum: 4, NN D: .73, HMM Prob: .92	551	[R].SSTETCGVKGR.[P]
N/A	376	[G].ADSATDHPTCSAADKPVIVSITEPR.[A]
N/A	433	[M].SGYGLPISQEVAKELAENAR.[K]
NN Sum: 0, NN D: .22, HMM Prob: .84	364	[S].QSVTCESNASPLVLR.[I]
NN Sum: 4, NN D: .85, HMM Prob: .99	377	[G].VAWGPNPIDGSKHGQFPSLR.[R]
NN Sum: 3, NN D: .56, HMM Prob: 1	1275	[H].VSTAKGEEPFSSKEEER.[H]
NN Sum: 3, NN D: .69, HMM Prob: .89	999	[A].AGVPKPAAPDGKAVR.[K]
N/A	294	[M].TSVAVSSHSPKPAPQSQSSVR.[S]

NN Sum: 3, NN D: .56, HMM Prob: .87	327	[A].TGQSIVLSCTR.[S]
NN Sum: 3, NN D: .53, HMM Prob: .45	164	[P].DQAQAAVSDKESESR.[V]
NN Sum: 2, NN D: .45, HMM Prob: .96	389	[L].DEVHTADENPHLAIDGR.[T]
NN Sum: 3, NN D: .54, HMM Prob: .99	256	[M].AVKVLVPVAHDSEEIEAVSIIDTLRR.[A]
N/A	790	[L].AAETKVSGDSTAISPNTR.[G]
NN Sum: 4, NN D: .63, HMM Prob: .97	220	[M].SLTAEEPKPAVEAR.[A]
NN Sum: 3, NN D: .69, HMM Prob: .89	999	[G].GKAVKVTPVAR.[K]
NN Sum: 4, NN D: .83, HMM Prob: 1	668	[A].SDAEEGKVK.[D]
NN Sum: 0, NN D: .22, HMM Prob: .84	364	[N].SQSVTCESNASPLVLR.[I]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[G].VVNQGPVDVPFSGKPLDER.[A]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[A].APDFTVTIPKEGLPADR.[Q]
NN Sum: 0, NN D: .14, HMM Prob: .68	367	[A].SEVQSCSGSATPLFLR.[L]
NN Sum: 4, NN D: .82, HMM Prob: .99	204	[T].EDDKSAASIVR.[G]
N/A	866	[R].ANLHPWLPEKPLLIGHR.[G]
NN Sum: 3, NN D: .47, HMM Prob: .38	392	[M].PAKEIVFHCEYAPSGR.[A]
NN Sum: 2, NN D: .36, HMM Prob: .99	205	[T].MYAGIGDPSGGFGAPAYEKYPR.[G]
NN Sum: 4, NN D: .7, HMM Prob: .42	198	[H].DFFNDYDQDEEYR.[K]
NN Sum: 4, NN D: .83, HMM Prob: .99	654	[A].YVPGIAPTDYTR.[G]
NN Sum: 0, NN D: .22, HMM Prob: .84	364	[G].NQANSQSVTCESNASPLVLR.[I]
NN Sum: 0, NN D: .26, HMM Prob: .88	342	[A].SVAHAQTAASEAEAATKVPDFR.[T]
NN Sum: 4, NN D: .72, HMM Prob: .99	183	[F].AADEASSDDRPLLER.[V]
NN Sum: 0, NN D: .31, HMM Prob: .94	509	[G].FFSAAPAAATAGVSPLAR.[S]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[S].TQTYGDAYAFVNGKCDFR.[E]
NN Sum: 4, NN D: .7, HMM Prob: .73	452	[Q].RVPELPEVESFDEVGTGAR.[R]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[S].DAVSTQTYGDAYAFVNGKCDFR.[E]
NN Sum: 3, NN D: .46, HMM Prob: .81	256	[A].SDQKQGSQNPAGGKGGSGPHGGR.[R]
NN Sum: 0, NN D: .36, HMM Prob: .96	497	[M].ASTKSGALPLFWSAAELAANPR.[Q]
NN Sum: 1, NN D: .36, HMM Prob: .69	738	[Q].EGWFLQPLDHGNPLVFNR.[L]
NN Sum: 2, NN D: .63, HMM Prob: .52	131	[R].DGEGEGSEKGPQPSPSGKPLQR.[R]
NN Sum: 3, NN D: .37, HMM Prob: .59	995	[F].GLLGSSSEK.[A]
NN Sum: 4, NN D: .7, HMM Prob: .42	198	[S].IGEHDFFNDYDQDEEYR.[K]
NN Sum: 0, NN D: .35, HMM Prob: .57	825	[M].VAAGVSHGNR.[S]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[S].AAPDFTVTIPKEGLPADR.[Q]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[T].QTYGDAYAFVNGKCDFR.[E]
NN Sum: 1, NN D: .2, HMM Prob: .98	661	[M].APTQLEQCASHGKLLQEK.[K]
NN Sum: 2, NN D: .44, HMM Prob: .87	162	[R].GPKFTLQDMKK.[A]
NN Sum: 4, NN D: .83, HMM Prob: 1	668	[A].SDAEEGKVKDVVIGIDLGTTYSCVGVYR.[H]
NN Sum: 1, NN D: .36, HMM Prob: .84	335	[A].AMPKLSGEKLAELMQMDVK.[D]
NN Sum: 3, NN D: .48, HMM Prob: .95	208	[M].AKPNDLAGLEKALNKNDK.[I]
NN Sum: 4, NN D: .84, HMM Prob: .99	499	[T].SAAPDFTVTIPKEGLPADR.[Q]
NN Sum: 4, NN D: .54, HMM Prob: .98	580	[D].ITPAGDDVSANVTSSEPAKLDLSCVHSDNKGSR.[A
NN Sum: 3, NN D: .58, HMM Prob: 1	149	[A].AAAPQASASGKTAKDASPSTANLQPR.[T]
NN Sum: 3, NN D: .53, HMM Prob: .45	164	[G].APDQAQAAVSDKESESR.[V]
NN Sum: 3, NN D: .46, HMM Prob: .81	256	[Q].GGGPPARPPSPSPEEEPIFGTFVKTDSGGVR.[G]
NN Sum: 4, NN D: .82, HMM Prob: 1	185	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]
N/A	99	[M].VGTNAPSAQASSAQHVGGAR.[T]
NN Sum: 3, NN D: .48, HMM Prob: .95	208	[M].AKPNDLAGLEK.[A]
NN Sum: 4, NN D: .63, HMM Prob: 1	383	[S].EKMNIVFKCPSGYHPR.[Y]
NN Sum: 4, NN D: .83, HMM Prob: 1	847	[A].INSTEPAPYEDAFEVLGR.[T]
NN Sum: 0, NN D: .14, HMM Prob: .68	367	[S].EVQSCSGSATPLFLR.[L]
NN Sum: 4, NN D: .7, HMM Prob: .42	198	[Q].ASIGEHDFFNDYDQDEEYR.[K]
NN Sum: 1, NN D: .2, HMM Prob: .98	661	[M].APTQLEQCASHGK.[L]

NN Sum: 4, NN D: .77, HMM Prob: 1	471	[A].EEEAVTVLTASNFDDTLK.[N]
NN Sum: 3, NN D: .53, HMM Prob: .45	164	[P].DQAQAAVSDKESESR.[V]
N/A	553	[L].DSLIPGFLKR.[R]
NN Sum: 4, NN D: .63, HMM Prob: 1	380	[K].DSQYNWLLCPVPTDNMFR.[D]
N/A	1134	[L].LTANVYEEAR.[S]
NN Sum: 3, NN D: .69, HMM Prob: .89	999	[L].AKSSTDDPTIHDEGHGAAAPSTPR.[A]

Modifications	Modifications in Master Proteins	Positions in Master Proteins
1xTMT6plex [N-Term]		TGME49_320180-t26_1-p1 [40-49]
2xTMT6plex [N-Term; K4]		TGME49_301170-t26_1-p1 [38-49]
1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_227	TGME49_227620-t26_1-p1 [35-47]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10]		TGME49_213280-t26_1-p1 [26-36]
2xTMT6plex [N-Term; K4]		TGME49_203290-t26_1-p1 [138-163]
2xTMT6plex [N-Term; K2]		TGME49_203290-t26_1-p1 [140-163]
1xTMT6plex [K6]		TGME49_227620-t26_1-p1 [37-47]
2xTMT6plex [N-Term; K14]		TGME49_278080-t26_1-p1 [29-49]
3xTMT6plex [N-Term; K3; K14]		TGME49_217740-t26_1-p1 [116-132]
2xTMT6plex [N-Term; K10]		TGME49_290030-t26_1-p1 [38-51]
2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [C6]		TGME49_293590-t26_1-p1 [117-129]
2xTMT6plex [K4; K8]; 1xAcetyl [N-Term]	TGME49_305	TGME49_305510-t26_1-p1 [2-15]
2xTMT6plex [N-Term; K7]		TGME49_253330-t26_1-p1 [32-46]
1xTMT6plex [N-Term]		TGME49_244560-t26_1-p1 [44-59]
2xTMT6plex [N-Term; K11]		TGME49_226000-t26_1-p1 [32-59]
1xTMT6plex [N-Term]		TGME49_215785-t26_1-p1 [27-38]; TGME49
1xTMT6plex [N-Term]		TGME49_275440-t26_1-p1 [37-50]
3xTMT6plex [N-Term; K4; K5]		TGME49_215590-t26_1-p1 [60-68]
1xTMT6plex [N-Term]		TGME49_250710-t26_1-p1 [57-71]
1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_251	TGME49_251540-t26_1-p1 [37-55]
1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_259	TGME49_259550-t26_1-p1 [76-86]
2xTMT6plex [N-Term; K6]		TGME49_226420-t26_1-p1 [50-63]
2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [C6]		TGME49_222840-t26_1-p1 [110-117]
1xTMT6plex [N-Term]		TGME49_258870-t26_1-p1 [354-362]
1xTMT6plex [N-Term]		TGME49_203970-t26_1-p1 [125-136]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]		TGME49_207160-t26_1-p1 [61-77]
2xTMT6plex [N-Term; K3]		TGME49_231100-t26_1-p1 [73-94]
3xTMT6plex [N-Term; K4; K17]; 2xCarbamidomethyl [C10;		TGME49_319560-t26_1-p1 [67-86]
2xTMT6plex [N-Term; K14]		TGME49_297160-t26_1-p1 [99-115]
3xTMT6plex [N-Term; K10; K17]		TGME49_253900-t26_1-p1 [223-243]
2xTMT6plex [N-Term; K10]		TGME49_203290-t26_1-p1 [132-163]
3xTMT6plex [N-Term; K2; K12]		TGME49_258390-t26_1-p1 [47-59]
3xTMT6plex [N-Term; K9; K10]		TGME49_313390-t26_1-p1 [91-101]
2xTMT6plex [N-Term; K13]		TGME49_209150-t26_1-p1 [24-38]
2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C15]		TGME49_292280-t26_1-p1 [316-331]
1xTMT6plex [N-Term]		TGME49_219320-t26_1-p1 [126-135]
2xTMT6plex [N-Term; K12]		TGME49_227620-t26_1-p1 [31-47]
2xTMT6plex [N-Term; K5]; 2xCarbamidomethyl [C7; C9]		TGME49_208450-t26_1-p1 [24-34]
2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [C6]		TGME49_293590-t26_1-p1 [117-127]
1xTMT6plex [K15]; 1xAcetyl [N-Term]; 1xCarb	TGME49_254	TGME49_254060-t26_1-p1 [59-83]
1xTMT6plex [K13]; 1xAcetyl [N-Term]	TGME49_236	TGME49_236040-t26_1-p1 [72-91]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]		TGME49_207160-t26_1-p1 [63-77]
2xTMT6plex [N-Term; K12]		TGME49_253330-t26_1-p1 [27-46]
3xTMT6plex [N-Term; K5; K13]		TGME49_209755-t26_1-p1 [204-220]
3xTMT6plex [N-Term; K5; K12]		TGME49_208730-t26_1-p1 [283-297]
1xTMT6plex [K11]; 1xAcetyl [N-Term]	TGME49_206	TGME49_206320-t26_1-p1 [2-22]

1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]		TGME49_292270-t26_1-p1 [37-47]
2xTMT6plex [N-Term; K10]		TGME49_237880-t26_1-p1 [48-62]
1xTMT6plex [N-Term]		TGME49_224770-t26_1-p1 [52-68]
2xTMT6plex [N-Term; K3]		TGME49_214290-t26_1-p1 [73-98]
2xTMT6plex [N-Term; K5]		TGME49_213670-t26_1-p1 [133-150]
1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_214	TGME49_214780-t26_1-p1 [53-66]
3xTMT6plex [N-Term; K2; K5]		TGME49_208730-t26_1-p1 [217-227]; [347-3
2xTMT6plex [N-Term; K7]		TGME49_311720-t26_1-p1 [30-38]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]		TGME49_207160-t26_1-p1 [62-77]
2xTMT6plex [N-Term; K14]		TGME49_227620-t26_1-p1 [29-47]
2xTMT6plex [N-Term; K10]		TGME49_278080-t26_1-p1 [33-49]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]		TGME49_207130-t26_1-p1 [60-75]
2xTMT6plex [N-Term; K4]		TGME49_204530-t26_1-p1 [58-68]
2xTMT6plex [N-Term; K10]		TGME49_263270-t26_1-p1 [545-561]
2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C9]		TGME49_293510-t26_1-p1 [36-51]
1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_214	TGME49_214480-t26_1-p1 [57-78]
1xTMT6plex [N-Term]		TGME49_250710-t26_1-p1 [59-71]
1xTMT6plex [N-Term]		TGME49_290940-t26_1-p1 [36-47]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10]		TGME49_207160-t26_1-p1 [58-77]
2xTMT6plex [N-Term; K17]		TGME49_215280-t26_1-p1 [22-43]
1xTMT6plex [N-Term]		TGME49_264080-t26_1-p1 [95-109]
1xTMT6plex [N-Term]		TGME49_236210-t26_1-p1 [36-53]
2xTMT6plex [N-Term; K14]; 1xCarbamidomethyl [C15]		TGME49_278080-t26_1-p1 [100-117]
1xTMT6plex [N-Term]		TGME49_270240-t26_1-p1 [32-50]
2xTMT6plex [N-Term; K18]; 1xCarbamidomethyl [C19]		TGME49_278080-t26_1-p1 [96-117]
2xTMT6plex [K4; K14]; 1xAcetyl [N-Term]	TGME49_247	TGME49_247520-t26_1-p1 [36-58]
1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_205	TGME49_205580-t26_1-p1 [2-23]
1xTMT6plex [N-Term]		TGME49_254010-t26_1-p1 [209-226]
2xTMT6plex [K9; K18]		TGME49_261740-t26_1-p1 [86-107]
1xTMT6plex [N-Term]		TGME49_269190-t26_1-p1 [633-641]
1xTMT6plex [N-Term]		TGME49_250710-t26_1-p1 [55-71]
1xTMT6plex [N-Term]		TGME49_286120-t26_1-p1 [94-103]
2xTMT6plex [N-Term; K11]		TGME49_278080-t26_1-p1 [32-49]
2xTMT6plex [N-Term; K13]; 1xCarbamidomethyl [C14]		TGME49_278080-t26_1-p1 [101-117]
2xTMT6plex [N-Term; K]; 1xCarbamidomethyl [C8]		TGME49_283780-t26_1-p1 [100-117]
3xTMT6plex [N-Term; K3; K10]		TGME49_314250-t26_1-p1 [51-61]
3xTMT6plex [N-Term; K7; K9]; 1xCarbamidomethyl [C23]		TGME49_311720-t26_1-p1 [30-57]
3xTMT6plex [N-Term; K4; K9]		TGME49_229480-t26_1-p1 [58-76]
3xTMT6plex [K2; K11; K15]; 1xAcetyl [N-Term	TGME49_219	TGME49_219690-t26_1-p1 [67-84]
2xTMT6plex [N-Term; K12]		TGME49_278080-t26_1-p1 [31-49]
3xTMT6plex [N-Term; K19; K30]; 1xCarbamidomethyl [C24		TGME49_208030-t26_1-p1 [45-77]
2xTMT6plex [K11; K14]; 1xAcetyl [N-Term]	TGME49_255	TGME49_255660-t26_1-p1 [40-65]
2xTMT6plex [N-Term; K12]		TGME49_237880-t26_1-p1 [46-62]
2xTMT6plex [N-Term; K24]		TGME49_247520-t26_1-p1 [67-97]
1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_227	TGME49_227620-t26_1-p1 [24-47]
1xTMT6plex [N-Term]		TGME49_211040-t26_1-p1 [2-21]
1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_219	TGME49_219690-t26_1-p1 [67-77]
3xTMT6plex [N-Term; K2; K8]; 1xCarbamidomethyl [C9]		TGME49_319560-t26_1-p1 [331-346]
1xTMT6plex [N-Term]		TGME49_309160-t26_1-p1 [23-40]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]		TGME49_207130-t26_1-p1 [61-75]
1xTMT6plex [N-Term]		TGME49_250710-t26_1-p1 [53-71]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]		TGME49_283780-t26_1-p1 [100-112]

1xTMT6plex [N-Term]		TGME49_211680-t26_1-p1 [25-42]
1xTMT6plex [N-Term]		TGME49_237880-t26_1-p1 [48-62]
2xTMT6plex [N-Term; K9]		TGME49_240090-t26_1-p1 [112-121]
1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]		TGME49_291600-t26_1-p1 [250-267]
1xTMT6plex [N-Term]		TGME49_320490-t26_1-p1 [361-370]
1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_208	TGME49_208730-t26_1-p1 [37-60]

Abundance Ratio: (ko, single) / (wt, single)	Abundance Ratio (log2): (ko, single) / (wt, single)	Abundances (Grouped): ko, single	Abundances (Grouped): wt, single
0.01	-6.64		11.1
0.054	-4.2	11.9	217.6
0.411	-1.28	69.7	169.6
1.658	0.73	64.1	38.6
1.661	0.73	27.6	16.6
1.666	0.74	33.3	20
1.698	0.76	139.6	82.3
1.998	1	67.1	33.6
2.035	1.02	26.6	13.1
2.044	1.03	93.9	45.9
2.051	1.04	129.9	63.4
2.056	1.04	78.6	38.2
2.082	1.06	67.5	32.4
2.083	1.06	274.7	131.9
2.087	1.06	4.3	2
2.092	1.07	152.8	73
2.094	1.07	69.6	33.2
2.107	1.08	1252.9	594.6
2.117	1.08	20.2	9.6
2.124	1.09	132	62.2
2.127	1.09	86.9	40.8
2.142	1.1	250.4	116.9
2.164	1.11	247.8	114.5
2.185	1.13	62.9	28.8
2.201	1.14	20.4	9.3
2.233	1.16	6.5	2.9
2.235	1.16	20.1	9
2.239	1.16	125.4	56
2.29	1.2	15.8	6.9
2.294	1.2	86.2	37.6
2.298	1.2	6.5	2.8
2.3	1.2	44.5	19.3
2.305	1.2	2015.8	874.5
2.323	1.22	132.3	56.9
2.333	1.22	169.9	72.8
2.351	1.23	191.5	81.5
2.384	1.25	7.1	3
2.388	1.26	785.5	328.9
2.389	1.26	191.2	80
2.39	1.26	10.6	4.5
2.404	1.27	79.4	33
2.406	1.27	6.7	2.8
2.434	1.28	9.5	3.9
2.439	1.29	65.7	26.9
2.479	1.31	291.9	117.7
2.479	1.31	26.9	10.9

2.489	1.32	207.6	83.4
2.548	1.35	79.2	31.1
2.55	1.35	82.4	32.3
2.551	1.35	24	9.4
2.556	1.35	14.1	5.5
2.582	1.37	26.2	10.1
2.602	1.38	1237.4	475.6
2.634	1.4	663.3	251.9
2.753	1.46	118.6	43.1
2.784	1.48	110.4	39.7
2.793	1.48	35	12.5
2.811	1.49	301.6	107.3
2.856	1.51	1096.5	383.9
2.859	1.52	115.3	40.3
2.865	1.52	101.2	35.3
2.882	1.53	30.4	10.6
2.891	1.53	276.4	95.6
2.904	1.54	34.1	11.7
2.906	1.54	9.2	3.2
2.934	1.55	50.1	17.1
2.939	1.56	115.1	39.2
2.941	1.56	97.1	33
2.946	1.56	78.3	26.6
2.978	1.57	42.1	14.1
3.004	1.59	76.6	25.5
3.031	1.6	65.7	21.7
3.035	1.6	5.8	1.9
3.059	1.61	12	3.9
3.063	1.61	12.1	3.9
3.101	1.63	18.1	5.9
3.109	1.64	40.6	13.1
3.113	1.64	21.4	6.9
3.133	1.65	156.3	49.9
3.159	1.66	59.6	18.9
3.2	1.68	35.6	11.1
3.207	1.68	163.3	50.9
3.224	1.69	37.4	11.6
3.333	1.74	35.2	10.6
3.462	1.79	23.8	6.9
3.504	1.81	72.7	20.7
3.535	1.82	7.9	2.2
3.543	1.83	15.2	4.3
3.632	1.86	257.2	70.8
3.644	1.87	9.7	2.7
3.727	1.9	209.4	56.2
3.775	1.92	54.4	14.4
3.833	1.94	28.5	7.4
4.043	2.02	117.2	29
4.166	2.06	79	19
4.34	2.12	20.6	4.8
4.918	2.3	39	7.9
5.968	2.58	41.7	7

6.166	2.62	24.3	3.9
7.651	2.94	11.8	1.5
7.992	3	239.4	30
8.491	3.09	23.6	2.8
9.214	3.2	133.7	14.5
100	6.64	97.4	

Master Protein Accessions	[Product Description]	[# TM Domains]	[SignalP Scores]	[Protein Length]
TGGT1_200230	microneme protein MIC17C	1	NN Sum: 4,	351
TGGT1_200310	hypothetical protein	1	N/A	169
TGGT1_200360	hypothetical protein	0	NN Sum: 3,	186
TGGT1_200400	hypothetical protein	0	N/A	1167
TGGT1_200430	cytidine and deoxycytidylate deaminase zinc-binding	0	N/A	514
TGGT1_201110	hypothetical protein	1	N/A	154
TGGT1_201140	hypothetical protein	0	N/A	1051
TGGT1_201380	putative chorismate synthase	0	N/A	536
TGGT1_201390	hypothetical protein	2	NN Sum: 4,	108
TGGT1_201390	hypothetical protein	2	NN Sum: 4,	108
TGGT1_201390	hypothetical protein	2	NN Sum: 4,	108
TGGT1_201390	hypothetical protein	2	NN Sum: 4,	108
TGGT1_201680	putative eukaryotic initiation factor-3 subunit 10	0	N/A	1031
TGGT1_201680	putative eukaryotic initiation factor-3 subunit 10	0	N/A	1031
TGGT1_201680	putative eukaryotic initiation factor-3 subunit 10	0	N/A	1031
TGGT1_201700	WD domain, G-beta repeat-containing protein	0	N/A	654
TGGT1_201760	hypothetical protein	0	N/A	336
TGGT1_201780	microneme protein MIC2	1	NN Sum: 3,	769
TGGT1_201780	microneme protein MIC2	1	NN Sum: 3,	769
TGGT1_201780	microneme protein MIC2	1	NN Sum: 3,	769
TGGT1_201780	microneme protein MIC2	1	NN Sum: 3,	769
TGGT1_201860	hypothetical protein	1	NN Sum: 4,	157
TGGT1_201880	hypothetical protein	0	N/A	128
TGGT1_202170	hypothetical protein	1	N/A	863
TGGT1_202200	hypothetical protein	0	N/A	793
TGGT1_202200	hypothetical protein	0	N/A	793
TGGT1_202300	putative inosine triphosphate pyrophosphatase	0	N/A	222
TGGT1_202310	O-sialoglycoprotein endopeptidase	0	N/A	580
TGGT1_202370	putative T-complex protein 1, epsilon subunit (TCP-1	0	N/A	536
TGGT1_202390	S15 sporozoite-expressed protein	0	N/A	587
TGGT1_202440	hypothetical protein	1	NN Sum: 2,	281
TGGT1_202460	diacylglycerol kinase accessory domain (presumed) c	0	N/A	679
TGGT1_202500	GAPM1a	6	N/A	305
TGGT1_202500	GAPM1a	6	N/A	305
TGGT1_202510	multi-pass transmembrane protein	6	N/A	305
TGGT1_202510	multi-pass transmembrane protein	6	N/A	305
TGGT1_202610	protein phosphatase 2C domain-containing protein	1	N/A	852
TGGT1_202630	ATP-dependent metallopeptidase HflB subfamily pro	2	NN Sum: 0,	1188
TGGT1_202680	putative peptidase M16, alpha subunit	0	NN Sum: 0,	563
TGGT1_202680	putative peptidase M16, alpha subunit	0	NN Sum: 0,	563
TGGT1_202680	putative peptidase M16, alpha subunit	0	NN Sum: 0,	563
TGGT1_202680	putative peptidase M16, alpha subunit	0	NN Sum: 0,	563
TGGT1_202770	RNA recognition motif-containing protein	0	N/A	532
TGGT1_202770	RNA recognition motif-containing protein	0	N/A	532
TGGT1_202770	RNA recognition motif-containing protein	0	N/A	532
TGGT1_202830	putative Elicitor-responsive protein	1	NN Sum: 3,	306

TGGT1_202830	putative Elicitor-responsive protein	1	NN Sum: 3,	306
TGGT1_202840	FHA domain-containing protein	0	N/A	1042
TGGT1_202870	SAP domain-containing protein	1	NN Sum: 2,	394
TGGT1_202890	hypothetical protein	0	N/A	377
TGGT1_202890	hypothetical protein	0	N/A	377
TGGT1_202890	hypothetical protein	0	N/A	377
TGGT1_202950	hypothetical protein	0	N/A	1414
TGGT1_202980	hypothetical protein	0	N/A	1915
TGGT1_203080	RNA recognition motif-containing protein	0	N/A	302
TGGT1_203220	DEAD/DEAH box helicase domain-containing protein	0	N/A	1144
TGGT1_203240	hypothetical protein	3	N/A	739
TGGT1_203240	hypothetical protein	3	N/A	739
TGGT1_203240	hypothetical protein	3	N/A	739
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203310	dense granule protein GRA7	2	NN Sum: 4,	236
TGGT1_203370	hypothetical protein	0	N/A	774
TGGT1_203390	CRAL/TRIO domain-containing protein	0	N/A	456
TGGT1_203610	putative 3'-5' exoribonuclease csl4	0	N/A	269
TGGT1_203630	ribosomal protein RPL44	0	N/A	105
TGGT1_203630	ribosomal protein RPL44	0	N/A	105
TGGT1_203810	kelch repeat-containing protein	0	N/A	531
TGGT1_203970	dolichyl-diphosphooligosaccharide--protein glycosylt	1	N/A	654
TGGT1_203980	hypothetical protein	0	N/A	1920
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204020	ribosomal protein RPL8	0	N/A	260
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
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TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
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TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795

TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204050	subtilisin SUB1	0	NN Sum: 4,	795
TGGT1_204130	perforin-like protein PLP1	0	N/A	1161
TGGT1_204130	perforin-like protein PLP1	0	N/A	1161
TGGT1_204160	GYF domain-containing protein	0	N/A	1797
TGGT1_204400	putative ATPase synthase subunit alpha	0	NN Sum: 0,	577
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_204530	microneme protein MIC11	0	NN Sum: 4,	204
TGGT1_205010	putative U2 small nuclear ribonucleoprotein family p	0	N/A	1386
TGGT1_205040	PGAP1 family protein	8	N/A	2110
TGGT1_205100	hypothetical protein	2	N/A	556
TGGT1_205130	hypothetical protein	0	N/A	4815
TGGT1_205240	cleft lip and palate transmembrane protein 1 (clptm	4	N/A	794
TGGT1_205250	rhoptry protein ROP18	0	NN Sum: 2,	554
TGGT1_205320	hypothetical protein	0	N/A	739
TGGT1_205320	hypothetical protein	0	N/A	739
TGGT1_205320	hypothetical protein	0	N/A	739
TGGT1_205320	hypothetical protein	0	N/A	739
TGGT1_205340	ribosomal protein RPS12	0	N/A	142
TGGT1_205360	hypothetical protein	2	NN Sum: 3,	2607
TGGT1_205360	hypothetical protein	2	NN Sum: 3,	2607
TGGT1_205440	CCT chaperonin gamma subunit	0	N/A	556
TGGT1_205440	CCT chaperonin gamma subunit	0	N/A	556
TGGT1_205470	putative translation elongation factor 2 family protei	0	N/A	832
TGGT1_205470	putative translation elongation factor 2 family protei	0	N/A	832
TGGT1_205470	putative translation elongation factor 2 family protei	0	N/A	832
TGGT1_205470	putative translation elongation factor 2 family protei	0	N/A	832
TGGT1_205510	putative nucleolar protein 5	0	N/A	490
TGGT1_205510	putative nucleolar protein 5	0	N/A	490
TGGT1_205580	nuclear factor NF4	0	NN Sum: 0,	497
TGGT1_205700	cyclophilin precursor	1	N/A	348
TGGT1_205710	lysine-tRNA ligase	0	NN Sum: 2,	658
TGGT1_205710	lysine-tRNA ligase	0	NN Sum: 2,	658
TGGT1_205710	lysine-tRNA ligase	0	NN Sum: 2,	658
TGGT1_205710	lysine-tRNA ligase	0	NN Sum: 2,	658
TGGT1_205710	lysine-tRNA ligase	0	NN Sum: 2,	658
TGGT1_206320	hypothetical protein	2	N/A	294

TGGT1_206320	hypothetical protein	2	N/A	294
TGGT1_206320	hypothetical protein	2	N/A	294
TGGT1_206320	hypothetical protein	2	N/A	294
TGGT1_206320	hypothetical protein	2	N/A	294
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206510	toxolysin TLN4	1	NN Sum: 4,	2435
TGGT1_206540	hypothetical protein	10	N/A	1295
TGGT1_206590	calcium-dependent protein kinase CDPK2A	0	N/A	786
TGGT1_206670	hypothetical protein	0	N/A	2072
TGGT1_206670	hypothetical protein	0	N/A	2072
TGGT1_206680	hypothetical protein	0	N/A	216
TGGT1_207060	ribonucleoside-diphosphate reductase small subunit	0	N/A	391
TGGT1_207060	ribonucleoside-diphosphate reductase small subunit	0	N/A	391
TGGT1_207060	ribonucleoside-diphosphate reductase small subunit	0	N/A	391
TGGT1_207100	hypothetical protein	0	N/A	1386
TGGT1_207240	hypothetical protein	0	N/A	108
TGGT1_207390	putative coatomer protein complex, gamma sub-uni	0	N/A	517
TGGT1_207640	isoleucyl-tRNA synthetase family protein	0	N/A	1242
TGGT1_207690	programmed cell death 5 protein	0	N/A	122
TGGT1_207770	PCI domain-containing protein	0	N/A	511
TGGT1_207770	PCI domain-containing protein	0	N/A	511
TGGT1_207770	PCI domain-containing protein	0	N/A	511
TGGT1_207770	PCI domain-containing protein	0	N/A	511
TGGT1_207840	ribosomal protein RPS17	0	N/A	132
TGGT1_207840	ribosomal protein RPS17	0	N/A	132
TGGT1_207840	ribosomal protein RPS17	0	N/A	132
TGGT1_207840	ribosomal protein RPS17	0	N/A	132
TGGT1_207950	hypothetical protein	2	NN Sum: 4,	177
TGGT1_207950	hypothetical protein	2	NN Sum: 4,	177
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208030	microneme protein MIC4	0	NN Sum: 4,	580
TGGT1_208200	PHD-finger domain-containing protein	0	N/A	497
TGGT1_208360	hypothetical protein	2	N/A	985
TGGT1_208370	putative myosin heavy chain	2	NN Sum: 4,	1124
TGGT1_208400A	hypothetical protein	0	N/A	227
TGGT1_208440	hypothetical protein	0	NN Sum: 0,	205
TGGT1_208450	protease inhibitor PI2	0	NN Sum: 4,	318
TGGT1_208450	protease inhibitor PI2	0	NN Sum: 4,	318
TGGT1_208500	protein phosphatase 2C domain-containing protein	0	N/A	709
TGGT1_208560	carrier superfamily protein	1	N/A	670
TGGT1_208560	carrier superfamily protein	1	N/A	670

TGGT1_208750	RWD domain-containing protein	0	N/A	268
TGGT1_208750	RWD domain-containing protein	0	N/A	268
TGGT1_208810	hypothetical protein	0	N/A	822
TGGT1_208830	hypothetical protein	0	NN Sum: 4,	505
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209030	actin ACT1	0	N/A	376
TGGT1_209100	PUB domain-containing protein	0	N/A	620
TGGT1_209140	anti-silencing protein, ASF1 family protein	0	N/A	269
TGGT1_209140	anti-silencing protein, ASF1 family protein	0	N/A	269
TGGT1_209150	non-proton pumping type-II NADH dehydrogenase I	0	NN Sum: 4,	618
TGGT1_209170	hypothetical protein	0	NN Sum: 1,	416
TGGT1_209210	hypothetical protein	0	N/A	1492
TGGT1_209250	hypothetical protein	1	N/A	1018
TGGT1_209440	hypothetical protein	0	N/A	3633
TGGT1_209600	hypothetical protein	0	N/A	451
TGGT1_209600	hypothetical protein	0	N/A	451
TGGT1_209600	hypothetical protein	0	N/A	451
TGGT1_209600	hypothetical protein	0	N/A	451
TGGT1_209600	hypothetical protein	0	N/A	451
TGGT1_209680	hypothetical protein	0	N/A	595
TGGT1_209690	small nuclear ribonucleoprotein	0	N/A	233
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209800	formate/nitrite transporter protein	6	N/A	412
TGGT1_209850	RNA recognition motif-containing protein	0	N/A	1412
TGGT1_209910	histone H2Bv	0	N/A	123
TGGT1_210370	hypothetical protein	0	NN Sum: 4,	479
TGGT1_210380	hypothetical protein	6	N/A	657
TGGT1_210440	polynucleotide adenylyltransferase	0	N/A	835
TGGT1_210440	polynucleotide adenylyltransferase	0	N/A	835
TGGT1_210690	ribosomal protein RPS6	0	N/A	256
TGGT1_210690	ribosomal protein RPS6	0	N/A	256
TGGT1_210690	ribosomal protein RPS6	0	N/A	256
TGGT1_210730	putative ATP-dependent hsl protease ATP-binding su	0	NN Sum: 1,	672
TGGT1_210730	putative ATP-dependent hsl protease ATP-binding su	0	NN Sum: 1,	672

TGGT1_210730	putative ATP-dependent hsl protease ATP-binding su	0	NN Sum: 1,	672
TGGT1_210730	putative ATP-dependent hsl protease ATP-binding su	0	NN Sum: 1,	672
TGGT1_210730	putative ATP-dependent hsl protease ATP-binding su	0	NN Sum: 1,	672
TGGT1_210840	arginyl-tRNA synthetase family protein	0	N/A	595
TGGT1_211030	hypothetical protein	0	N/A	191
TGGT1_211040	Sec61beta family protein	1	N/A	99
TGGT1_211040	Sec61beta family protein	1	N/A	99
TGGT1_211040	Sec61beta family protein	1	N/A	99
TGGT1_211040	Sec61beta family protein	1	N/A	99
TGGT1_211040	Sec61beta family protein	1	N/A	99
TGGT1_211250	hypothetical protein	0	N/A	275
TGGT1_211300	putative DUF74 family protein	0	N/A	373
TGGT1_211390	hypothetical protein	0	N/A	405
TGGT1_211440	hypothetical protein	0	N/A	1665
TGGT1_211680	protein disulfide isomerase	0	NN Sum: 4,	471
TGGT1_211680	protein disulfide isomerase	0	NN Sum: 4,	471
TGGT1_211690	AAA family protein	0	NN Sum: 0,	1538
TGGT1_212210	hypothetical protein	0	N/A	280
TGGT1_212210	hypothetical protein	0	N/A	280
TGGT1_212220	hypothetical protein	0	N/A	981
TGGT1_212220	hypothetical protein	0	N/A	981
TGGT1_212260	Sjogren's syndrome/scleroderma autoantigen 1 (Aut	0	N/A	351
TGGT1_212260	Sjogren's syndrome/scleroderma autoantigen 1 (Aut	0	N/A	351
TGGT1_212260	Sjogren's syndrome/scleroderma autoantigen 1 (Aut	0	N/A	351
TGGT1_212260	Sjogren's syndrome/scleroderma autoantigen 1 (Aut	0	N/A	351
TGGT1_212290	ribosomal protein RPS19	0	N/A	313
TGGT1_212290	ribosomal protein RPS19	0	N/A	313
TGGT1_212290	ribosomal protein RPS19	0	N/A	313
TGGT1_212300	hypothetical protein	1	NN Sum: 3,	683
TGGT1_212770	hypothetical protein	0	N/A	940
TGGT1_212820	ubiquitin family protein	0	N/A	1158
TGGT1_212820	ubiquitin family protein	0	N/A	1158
TGGT1_212820	ubiquitin family protein	0	N/A	1158
TGGT1_212950	putative ADP-ribosylation factor family protein 2	0	N/A	185
TGGT1_212980	hypothetical protein	1	N/A	715
TGGT1_212990	hypothetical protein	10	N/A	1064
TGGT1_213030	hypothetical protein	0	N/A	324
TGGT1_213030	hypothetical protein	0	N/A	324
TGGT1_213040	hypothetical protein	0	NN Sum: 0,	1824
TGGT1_213050	hypothetical protein	0	N/A	192
TGGT1_213050	hypothetical protein	0	N/A	192
TGGT1_213240	hypothetical protein	1	N/A	781
TGGT1_213280	SAG-related sequence SRS25	0	NN Sum: 4,	191
TGGT1_213350	ribosomal protein RPS15	0	N/A	150
TGGT1_213350	ribosomal protein RPS15	0	N/A	150
TGGT1_213410	putative small nuclear ribonucleoprotein f (snrnp-f)	0	N/A	87
TGGT1_213570	hypothetical protein	4	NN Sum: 0,	290
TGGT1_213670	hypothetical protein	1	N/A	790
TGGT1_213670	hypothetical protein	1	N/A	790
TGGT1_213670	hypothetical protein	1	N/A	790
TGGT1_213740	hypothetical protein	0	N/A	842
TGGT1_213830	putative Ufm1-conjugating enzyme 1	0	N/A	157

TGGT1_213900	regulator of chromosome condensation RCC1	0	N/A	1155
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214080	toxofilin	1	NN Sum: 4,	245
TGGT1_214090	signal peptidase	0	N/A	1859
TGGT1_214150	putative mitochondrial inner membrane translocase	1	N/A	188
TGGT1_214220	hypothetical protein	0	N/A	212
TGGT1_214260	putative alpha-glucan water dikinase 1	0	N/A	1715
TGGT1_214290	DJ-1 family protein	0	NN Sum: 3,	256
TGGT1_214290	DJ-1 family protein	0	NN Sum: 3,	256
TGGT1_214290	DJ-1 family protein	0	NN Sum: 3,	256
TGGT1_214440	4'-phosphopantetheinyl transferase superfamily pro	0	N/A	437
TGGT1_214480	replication factor a protein 3 protein	0	NN Sum: 2,	205
TGGT1_214590	micro-fibrillar-associated protein 1	0	N/A	438
TGGT1_214750	hypothetical protein	0	NN Sum: 0,	1108
TGGT1_214780	hydrolase, NUDIX family protein	0	NN Sum: 4,	220
TGGT1_214790	glycoprotein	0	N/A	283
TGGT1_214790	glycoprotein	0	N/A	283
TGGT1_214840	AP2 domain transcription factor AP2X-7	0	N/A	1869
TGGT1_214840	AP2 domain transcription factor AP2X-7	0	N/A	1869
TGGT1_214870	ribosomal protein L9, N-terminal domain-containing	0	NN Sum: 0,	491
TGGT1_214880	hypothetical protein	0	N/A	931
TGGT1_214930	hypothetical protein	0	N/A	138
TGGT1_214930	hypothetical protein	0	N/A	138
TGGT1_215010	hypothetical protein	3	NN Sum: 0,	777
TGGT1_215010	hypothetical protein	3	NN Sum: 0,	777
TGGT1_215160	hypothetical protein	0	NN Sum: 3,	269
TGGT1_215220	hypothetical protein	0	N/A	502
TGGT1_215250	thiamin pyrophosphokinase, catalytic domain-contai	1	N/A	816
TGGT1_215260	carbamoylphosphate synthetase	0	N/A	1699
TGGT1_215280	succinate dehydrogenase [ubiquinone] iron-sulfur pr	0	NN Sum: 0,	342
TGGT1_215280	succinate dehydrogenase [ubiquinone] iron-sulfur pr	0	NN Sum: 0,	342
TGGT1_215280	succinate dehydrogenase [ubiquinone] iron-sulfur pr	0	NN Sum: 0,	342
TGGT1_215280	succinate dehydrogenase [ubiquinone] iron-sulfur pr	0	NN Sum: 0,	342
TGGT1_215350	hypothetical protein	0	N/A	145
TGGT1_215380	hypothetical protein	0	N/A	797
TGGT1_215430	hypothetical protein	0	NN Sum: 3,	244
TGGT1_215460	ribosomal protein RPS24	0	N/A	267
TGGT1_215460	ribosomal protein RPS24	0	N/A	267
TGGT1_215460	ribosomal protein RPS24	0	N/A	267
TGGT1_215460	ribosomal protein RPS24	0	N/A	267
TGGT1_215470	ribosomal protein RPL10A	0	N/A	217
TGGT1_215470	ribosomal protein RPL10A	0	N/A	217
TGGT1_215560	histone arginine methyltransferase PRMT5	0	N/A	979
TGGT1_215590	flavoprotein subunit of succinate dehydrogenase	0	NN Sum: 0,	669
TGGT1_215590	flavoprotein subunit of succinate dehydrogenase	0	NN Sum: 0,	669
TGGT1_215740	putative notchless	0	N/A	527

TGGT1_215775	rhoptry protein ROP8	1	NN Sum: 3,	575
TGGT1_215910	hypothetical protein	0	NN Sum: 3,	3029
TGGT1_216000	alveolin domain containing intermediate filament IM	0	N/A	538
TGGT1_216000	alveolin domain containing intermediate filament IM	0	N/A	538
TGGT1_216000	alveolin domain containing intermediate filament IM	0	N/A	538
TGGT1_216030A	hypothetical protein	0	NN Sum: 1,	1127
TGGT1_216060	hypothetical protein	1	N/A	784
TGGT1_216060	hypothetical protein	1	N/A	784
TGGT1_216260	putative eukaryotic initiation factor-2B, gamma subu	0	N/A	525
TGGT1_216260	putative eukaryotic initiation factor-2B, gamma subu	0	N/A	525
TGGT1_216370	hypothetical protein	0	N/A	560
TGGT1_216410	hypothetical protein	0	N/A	188
TGGT1_216450	peptidase, T1 family protein	0	N/A	260
TGGT1_216620	EF hand domain-containing protein	7	N/A	3700
TGGT1_216620	EF hand domain-containing protein	7	N/A	3700
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216670	FUSE-binding protein 2 / KH-type splicing regulatory	0	N/A	941
TGGT1_216720	hypothetical protein	0	NN Sum: 4,	183
TGGT1_216720	hypothetical protein	0	NN Sum: 4,	183
TGGT1_216810	5'-nucleotidase, C-terminal domain-containing prote	0	N/A	710
TGGT1_216880	guanine nucleotide-binding protein	0	N/A	321
TGGT1_216880	guanine nucleotide-binding protein	0	N/A	321
TGGT1_216890	hypothetical protein	7	N/A	999
TGGT1_216920	mediator complex subunit MED8	0	N/A	221
TGGT1_216930	cholinephosphate cytidylyltransferase	0	N/A	329
TGGT1_216950	helicase	0	N/A	939
TGGT1_217030	hypothetical protein	0	N/A	218
TGGT1_217160	Der1 family protein	5	NN Sum: 3,	212
TGGT1_217430	protease inhibitor PI1	0	N/A	439
TGGT1_217460	glutaminyl-tRNA synthetase (GlnRS)	0	NN Sum: 4,	860
TGGT1_217460	glutaminyl-tRNA synthetase (GlnRS)	0	NN Sum: 4,	860
TGGT1_217510	hypothetical protein	0	N/A	380
TGGT1_217570	ribosomal protein RPS27	0	N/A	151
TGGT1_217570	ribosomal protein RPS27	0	N/A	151
TGGT1_217570	ribosomal protein RPS27	0	N/A	151
TGGT1_217570	ribosomal protein RPS27	0	N/A	151
TGGT1_217570	ribosomal protein RPS27	0	N/A	151
TGGT1_217680	hypothetical protein	0	N/A	2213
TGGT1_217680	hypothetical protein	0	N/A	2213
TGGT1_217680	hypothetical protein	0	N/A	2213
TGGT1_217680	hypothetical protein	0	N/A	2213
TGGT1_217680	hypothetical protein	0	N/A	2213
TGGT1_217890	putative alkyl hydroperoxide reductase/ Thiol specifi	0	N/A	196
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249

TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218240	hypothetical protein	1	NN Sum: 1,	1249
TGGT1_218260	histone H3.3	0	N/A	136
TGGT1_218260	histone H3.3	0	N/A	136
TGGT1_218260	histone H3.3	0	N/A	136
TGGT1_218260	histone H3.3	0	N/A	136
TGGT1_218520	microneme protein MIC6	1	NN Sum: 2,	349
TGGT1_218520	microneme protein MIC6	1	NN Sum: 2,	349
TGGT1_218520	microneme protein MIC6	1	NN Sum: 2,	349
TGGT1_218530	proteasome-interacting thioredoxin domain-contain	0	N/A	345
TGGT1_218530	proteasome-interacting thioredoxin domain-contain	0	N/A	345
TGGT1_218530	proteasome-interacting thioredoxin domain-contain	0	N/A	345
TGGT1_218530	proteasome-interacting thioredoxin domain-contain	0	N/A	345
TGGT1_218540	putative peptidase S15	1	NN Sum: 3,	412
TGGT1_218590	protein phosphatase 2C domain-containing protein	0	N/A	901
TGGT1_218600	RNA recognition motif-containing protein	0	N/A	752
TGGT1_218780	putative phosphoserine aminotransferase	0	N/A	481
TGGT1_218820	alba 2	0	N/A	148
TGGT1_218820	alba 2	0	N/A	148
TGGT1_218840	mutS domain protein	0	N/A	2163
TGGT1_218920	putative proteasome subunit beta type	0	N/A	309
TGGT1_218940	hypothetical protein	0	N/A	326
TGGT1_218940	hypothetical protein	0	N/A	326
TGGT1_218960	AP2 domain transcription factor AP2XII-1	0	N/A	2283
TGGT1_219270	multi-pass transmembrane protein	6	N/A	389
TGGT1_219270	multi-pass transmembrane protein	6	N/A	389
TGGT1_219270	multi-pass transmembrane protein	6	N/A	389
TGGT1_219270	multi-pass transmembrane protein	6	N/A	389
TGGT1_219270	multi-pass transmembrane protein	6	N/A	389
TGGT1_219300	ran binding protein	0	N/A	367
TGGT1_219310	DnaK family protein	0	N/A	818
TGGT1_219320	acid phosphatase GAP50	2	NN Sum: 1,	431
TGGT1_219320	acid phosphatase GAP50	2	NN Sum: 1,	431
TGGT1_219320	acid phosphatase GAP50	2	NN Sum: 1,	431
TGGT1_219540	cytosolic tRNA-Ala synthetase	0	NN Sum: 4,	1280
TGGT1_219590	RuvB family 1 protein	0	N/A	492
TGGT1_219690	hypothetical protein	0	NN Sum: 3,	208
TGGT1_219690	hypothetical protein	0	NN Sum: 3,	208
TGGT1_219710	hypothetical protein	0	N/A	1893
TGGT1_219710	hypothetical protein	0	N/A	1893
TGGT1_219790A	pre-mRNA processing factor PRP3	0	N/A	304
TGGT1_219800	putative vacuolar ATP synthase subunit b	0	N/A	505
TGGT1_219800	putative vacuolar ATP synthase subunit b	0	N/A	505
TGGT1_219800	putative vacuolar ATP synthase subunit b	0	N/A	505
TGGT1_219850	prolyl-tRNA synthetase (ProRS)	0	NN Sum: 3,	830
TGGT1_219860	putative replication licensing factor	0	N/A	972
TGGT1_219860	putative replication licensing factor	0	N/A	972
TGGT1_220100	phosphoribosylpyrophosphate synthetase	0	N/A	557
TGGT1_220100	phosphoribosylpyrophosphate synthetase	0	N/A	557
TGGT1_220140	EF hand domain-containing protein	0	N/A	244
TGGT1_220260	hypothetical protein	0	N/A	596

TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220270	alveolin domain containing intermediate filament IV	0	N/A	444
TGGT1_220400	actin depolymerizing factor ADF	0	N/A	118
TGGT1_220400	actin depolymerizing factor ADF	0	N/A	118
TGGT1_220400	actin depolymerizing factor ADF	0	N/A	118
TGGT1_220900	hypothetical protein	0	N/A	706
TGGT1_220910	HEAT repeat-containing protein	0	N/A	1769
TGGT1_221180	hypothetical protein	5	NN Sum: 4,	791
TGGT1_221180	hypothetical protein	5	NN Sum: 4,	791
TGGT1_221180	hypothetical protein	5	NN Sum: 4,	791
TGGT1_221180	hypothetical protein	5	NN Sum: 4,	791
TGGT1_221180	hypothetical protein	5	NN Sum: 4,	791
TGGT1_221210	cyclophilin	0	NN Sum: 4,	179
TGGT1_221230	hypothetical protein	1	N/A	574
TGGT1_221320	acetyl-CoA carboxylase ACC1	1	NN Sum: 3,	2614
TGGT1_221380	alba 1	0	N/A	247
TGGT1_221470	hypothetical protein	0	N/A	552
TGGT1_221470	hypothetical protein	0	N/A	552
TGGT1_221620	putative beta-tubulin	0	N/A	449
TGGT1_221620	putative beta-tubulin	0	N/A	449
TGGT1_221620	putative beta-tubulin	0	N/A	449
TGGT1_221670	transcriptional elongation factor FACT140	0	N/A	1198
TGGT1_221870	hypothetical protein	0	N/A	1373
TGGT1_221922	NifU family domain-containing protein	0	N/A	483
TGGT1_221922	NifU family domain-containing protein	0	N/A	483
TGGT1_221950	putative splicesome-associated protein	0	N/A	559
TGGT1_222020	phosphoglycerate kinase PGKII	0	N/A	593
TGGT1_222100	hypothetical protein	0	N/A	1140
TGGT1_222100	hypothetical protein	0	N/A	1140
TGGT1_222160	aldehyde dehydrogenase	0	N/A	497
TGGT1_222160	aldehyde dehydrogenase	0	N/A	497
TGGT1_222220	alveolin domain containing intermediate filament IV	0	N/A	429
TGGT1_222220	alveolin domain containing intermediate filament IV	0	N/A	429
TGGT1_222220	alveolin domain containing intermediate filament IV	0	N/A	429
TGGT1_222270	hypothetical protein	0	NN Sum: 4,	387
TGGT1_222360	hypothetical protein	0	N/A	774
TGGT1_222840	Ser/Thr phosphatase family protein	0	NN Sum: 4,	433
TGGT1_222840	Ser/Thr phosphatase family protein	0	NN Sum: 4,	433
TGGT1_222840	Ser/Thr phosphatase family protein	0	NN Sum: 4,	433
TGGT1_222970	putative inositol(myo)-1(or 4)-monophosphatase 2	0	N/A	297
TGGT1_223050	ribosomal protein RPS20	0	N/A	233
TGGT1_223110	glycolipid transfer protein GLTP	0	N/A	230
TGGT1_223410	putative eukaryotic initiation factor-4E	0	N/A	225
TGGT1_223540	importin-beta N-terminal domain-containing protein	0	N/A	1095
TGGT1_223580	mediator complex subunit MED4	0	N/A	519
TGGT1_223610	hypothetical protein	0	N/A	1303
TGGT1_223680	ubiquitin family protein	0	N/A	399
TGGT1_223680	ubiquitin family protein	0	N/A	399

TGGT1_223680	ubiquitin family protein	0	N/A	399
TGGT1_223800	hypothetical protein	2	NN Sum: 0,	526
TGGT1_223910	acyltransferase domain-containing protein	3	N/A	388
TGGT1_223930	RNA recognition motif-containing protein	0	N/A	382
TGGT1_223940	GAP45 protein	0	N/A	245
TGGT1_223940	GAP45 protein	0	N/A	245
TGGT1_223940	GAP45 protein	0	N/A	245
TGGT1_223960	ubiquitin interaction motif family protein	0	N/A	388
TGGT1_223960	ubiquitin interaction motif family protein	0	N/A	388
TGGT1_223970	putative translation elongation and release factors (g	0	N/A	1011
TGGT1_224050	AP2 domain transcription factor AP2X-4	0	N/A	896
TGGT1_224060	putative thioredoxin	0	NN Sum: 3,	622
TGGT1_224110	putative adhesion regulating molecule region protein	0	N/A	396
TGGT1_224460	putative aminopeptidase n	0	NN Sum: 1,	970
TGGT1_224460	putative aminopeptidase n	0	NN Sum: 1,	970
TGGT1_224580	RNA recognition motif-containing protein	0	N/A	539
TGGT1_224850	putative polyadenylate binding protein	0	N/A	769
TGGT1_224890	hypothetical protein	0	N/A	1075
TGGT1_224980	hypothetical protein	0	N/A	1132
TGGT1_225050	putative adenosylhomocysteinase	0	N/A	588
TGGT1_225080	ribosomal protein RPS18	0	N/A	156
TGGT1_225080	ribosomal protein RPS18	0	N/A	156
TGGT1_225080	ribosomal protein RPS18	0	N/A	156
TGGT1_225080	ribosomal protein RPS18	0	N/A	156
TGGT1_225200	hypothetical protein	0	NN Sum: 4,	1445
TGGT1_225310	putative ARF1-directed GTPase-activating protein	0	N/A	502
TGGT1_225350	hypothetical protein	3	NN Sum: 3,	399
TGGT1_225360	hypothetical protein	0	N/A	756
TGGT1_225380	hypothetical protein	0	N/A	447
TGGT1_225450	hypothetical protein	0	N/A	579
TGGT1_225790	PDI family protein	0	N/A	189
TGGT1_225790	PDI family protein	0	N/A	189
TGGT1_225860	hypothetical protein	0	N/A	1057
TGGT1_225990	acyl transferase domain-containing protein	1	NN Sum: 4,	502
TGGT1_225990	acyl transferase domain-containing protein	1	NN Sum: 4,	502
TGGT1_226000	putative ATP synthase	0	NN Sum: 1,	183
TGGT1_226020	transporter, major facilitator family protein	12	N/A	589
TGGT1_226020	transporter, major facilitator family protein	12	N/A	589
TGGT1_226072	Ser/Thr phosphatase family protein	0	N/A	807
TGGT1_226072	Ser/Thr phosphatase family protein	0	N/A	807
TGGT1_226220	alveolin domain containing intermediate filament IM	0	N/A	756
TGGT1_226220	alveolin domain containing intermediate filament IM	0	N/A	756
TGGT1_226250	DEAD (Asp-Glu-Ala-Asp) box polypeptide DDX3X	0	N/A	734
TGGT1_226250	DEAD (Asp-Glu-Ala-Asp) box polypeptide DDX3X	0	N/A	734
TGGT1_226250	DEAD (Asp-Glu-Ala-Asp) box polypeptide DDX3X	0	N/A	734
TGGT1_226250	DEAD (Asp-Glu-Ala-Asp) box polypeptide DDX3X	0	N/A	734
TGGT1_226410	EF-1 guanine nucleotide exchange domain-containin	0	N/A	328
TGGT1_226410	EF-1 guanine nucleotide exchange domain-containin	0	N/A	328
TGGT1_226410	EF-1 guanine nucleotide exchange domain-containin	0	N/A	328
TGGT1_226410	EF-1 guanine nucleotide exchange domain-containin	0	N/A	328
TGGT1_226430	reticulon protein	3	N/A	196
TGGT1_226430	reticulon protein	3	N/A	196

TGGT1_226510	Sec23/Sec24 trunk domain-containing protein	0	N/A	1540
TGGT1_226550	TBC domain containing protein	0	N/A	315
TGGT1_226570	hypothetical protein	0	N/A	139
TGGT1_226580	hypothetical protein	1	N/A	380
TGGT1_226730	aconitate hydratase ACN/IRP	0	NN Sum: 4,	1055
TGGT1_226870A	tubulin gamma chain	0	N/A	332
TGGT1_226890	hypothetical protein	0	N/A	2068
TGGT1_226890	hypothetical protein	0	N/A	2068
TGGT1_226970	ribosomal protein RPS11	0	N/A	161
TGGT1_226980	hypothetical protein	0	N/A	227
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227280	dense granule protein GRA3	2	NN Sum: 3,	222
TGGT1_227290	histone deacetylase HDAC3	0	N/A	451
TGGT1_227360	ribosomal protein RPL3	0	N/A	389
TGGT1_227560	putative IWS1 transcription factor	0	N/A	476
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227620	dense granule protein GRA2	0	NN Sum: 4,	185
TGGT1_227650	putative microtubule-associated protein RP/EB famil	0	N/A	413
TGGT1_227810	rhoptry kinase family protein ROP11 (incomplete cat	0	NN Sum: 2,	526
TGGT1_227810	rhoptry kinase family protein ROP11 (incomplete cat	0	NN Sum: 2,	526
TGGT1_227810	rhoptry kinase family protein ROP11 (incomplete cat	0	NN Sum: 2,	526
TGGT1_227810	rhoptry kinase family protein ROP11 (incomplete cat	0	NN Sum: 2,	526
TGGT1_227810	rhoptry kinase family protein ROP11 (incomplete cat	0	NN Sum: 2,	526
TGGT1_227860	hypothetical protein	0	N/A	377
TGGT1_227920	hypothetical protein	0	NN Sum: 2,	85
TGGT1_227948	peptidase M16 inactive domain-containing protein	0	NN Sum: 1,	1306
TGGT1_227952	14-3-3 superfamily protein	0	NN Sum: 1,	422
TGGT1_227960	PCI domain-containing protein	0	N/A	506
TGGT1_227960	PCI domain-containing protein	0	N/A	506

TGGT1_227960	PCI domain-containing protein	0	N/A	506
TGGT1_227970	histone family DNA-binding protein	0	NN Sum: 4,	235
TGGT1_227990	hypothetical protein	0	NN Sum: 1,	900
TGGT1_228160	acid phosphatase	1	NN Sum: 3,	1632
TGGT1_228170	inner membrane complex protein IMC2A	1	NN Sum: 2,	1596
TGGT1_228170	inner membrane complex protein IMC2A	1	NN Sum: 2,	1596
TGGT1_228210	26S proteasome regulatory subunit	0	N/A	398
TGGT1_228210	26S proteasome regulatory subunit	0	N/A	398
TGGT1_228230	hypothetical protein	0	N/A	1256
TGGT1_228290	phospholipase/carboxylesterase	0	N/A	491
TGGT1_228300	CCDC25 protein	0	N/A	222
TGGT1_228360	putative peptidyl-prolyl isomerase FKBP12	1	NN Sum: 0,	362
TGGT1_228360	putative peptidyl-prolyl isomerase FKBP12	1	NN Sum: 0,	362
TGGT1_228360	putative peptidyl-prolyl isomerase FKBP12	1	NN Sum: 0,	362
TGGT1_228360	putative peptidyl-prolyl isomerase FKBP12	1	NN Sum: 0,	362
TGGT1_228470	ribosomal protein RPL15	0	N/A	205
TGGT1_228490	hypothetical protein	0	N/A	394
TGGT1_228490	hypothetical protein	0	N/A	394
TGGT1_229010	rhoptry neck protein RON4	0	NN Sum: 4,	984
TGGT1_229010	rhoptry neck protein RON4	0	NN Sum: 4,	984
TGGT1_229010	rhoptry neck protein RON4	0	NN Sum: 4,	984
TGGT1_229010	rhoptry neck protein RON4	0	NN Sum: 4,	984
TGGT1_229010	rhoptry neck protein RON4	0	NN Sum: 4,	984
TGGT1_229020	putative cell-cycle-associated protein kinase CDK	0	N/A	1259
TGGT1_229140	MaoC family domain-containing protein	0	N/A	324
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229250A	ribosomal protein RPL28	0	N/A	74
TGGT1_229420	putative cytochrome c	0	N/A	163
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229480	putative calcium binding protein precursor	1	NN Sum: 1,	335
TGGT1_229490	tetratricopeptide repeat-containing protein	2	N/A	823
TGGT1_229670	ribosomal protein RPS23	0	N/A	143
TGGT1_229670	ribosomal protein RPS23	0	N/A	143
TGGT1_229680	hypothetical protein	4	NN Sum: 4,	160
TGGT1_229680	hypothetical protein	4	NN Sum: 4,	160
TGGT1_229780	GHMP kinase, N-terminal domain-containing protein	0	N/A	923
TGGT1_229920	hypothetical protein	1	NN Sum: 2,	307
TGGT1_229920	hypothetical protein	1	NN Sum: 2,	307
TGGT1_229930	p25-alpha family protein	0	N/A	163
TGGT1_229930	p25-alpha family protein	0	N/A	163
TGGT1_229950	putative 26S proteasome regulatory subunit 6b	0	N/A	409
TGGT1_229990	putative T-complex protein 1 subunit alpha	0	N/A	548
TGGT1_229990	putative T-complex protein 1 subunit alpha	0	N/A	548

TGGT1_229990	putative T-complex protein 1 subunit alpha	0	N/A	548
TGGT1_230010	hypothetical protein	0	N/A	1295
TGGT1_230140	vacuolar sorting protein 9 (vps9) domain-containing	0	N/A	1326
TGGT1_230160	hypothetical protein	0	N/A	142
TGGT1_230180	hypothetical protein	1	NN Sum: 4,	542
TGGT1_230180	hypothetical protein	1	NN Sum: 4,	542
TGGT1_230210	alveolin domain containing intermediate filament IM	0	N/A	560
TGGT1_230210	alveolin domain containing intermediate filament IM	0	N/A	560
TGGT1_230210	alveolin domain containing intermediate filament IM	0	N/A	560
TGGT1_230210	alveolin domain containing intermediate filament IM	0	N/A	560
TGGT1_230350	hypothetical protein	6	N/A	1254
TGGT1_230410	peroxiredoxin PRX3	0	N/A	283
TGGT1_230420	sarco/endoplasmic reticulum Ca2+-ATPase	7	N/A	1093
TGGT1_230420	sarco/endoplasmic reticulum Ca2+-ATPase	7	N/A	1093
TGGT1_230420	sarco/endoplasmic reticulum Ca2+-ATPase	7	N/A	1093
TGGT1_230420	sarco/endoplasmic reticulum Ca2+-ATPase	7	N/A	1093
TGGT1_230450	bifunctional GMP synthase/glutamine amidotransfer	0	N/A	569
TGGT1_230480	hypothetical protein	2	N/A	171
TGGT1_230705	hypothetical protein	1	NN Sum: 3,	266
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_230940	hypothetical protein	0	N/A	1523
TGGT1_231070	protein kinase	0	N/A	1318
TGGT1_231190	arsenite-activated ATPase family protein	0	N/A	397
TGGT1_231220	hypothetical protein	5	NN Sum: 3,	451
TGGT1_231350	glucosamine-fructose-6-phosphate aminotransferas	0	NN Sum: 0,	898
TGGT1_231430	putative oligosaccharyl transferase stt3 protein	12	N/A	753
TGGT1_231440	LsmAD domain-containing protein	0	N/A	1524
TGGT1_231440	LsmAD domain-containing protein	0	N/A	1524
TGGT1_231440	LsmAD domain-containing protein	0	N/A	1524
TGGT1_231590	SGS domain-containing protein	0	N/A	269
TGGT1_231590	SGS domain-containing protein	0	N/A	269
TGGT1_231600	HEAT repeat-containing protein	0	N/A	1169
TGGT1_231600	HEAT repeat-containing protein	0	N/A	1169
TGGT1_231630	alveolin domain containing intermediate filament IM	0	N/A	452
TGGT1_231630	alveolin domain containing intermediate filament IM	0	N/A	452
TGGT1_231630	alveolin domain containing intermediate filament IM	0	N/A	452
TGGT1_231630	alveolin domain containing intermediate filament IM	0	N/A	452
TGGT1_231630	alveolin domain containing intermediate filament IM	0	N/A	452
TGGT1_231640	alveolin domain containing intermediate filament IM	0	N/A	609
TGGT1_231640	alveolin domain containing intermediate filament IM	0	N/A	609
TGGT1_231640	alveolin domain containing intermediate filament IM	0	N/A	609
TGGT1_231640	alveolin domain containing intermediate filament IM	0	N/A	609
TGGT1_231640	alveolin domain containing intermediate filament IM	0	N/A	609
TGGT1_231850	serine-threonine phosphatase 2C (PP2C)	0	N/A	331
TGGT1_231910	ATP synthase F1 gamma subunit	0	NN Sum: 1,	314
TGGT1_231960	putative omega secalin	0	NN Sum: 3,	1111
TGGT1_232030	hypothetical protein	0	N/A	208
TGGT1_232030	hypothetical protein	0	N/A	208

TGGT1_232030	hypothetical protein	0	N/A	208
TGGT1_232060	hypothetical protein	0	N/A	469
TGGT1_232120	hypothetical protein	10	N/A	2024
TGGT1_232180	UBA/TS-N domain-containing protein	1	N/A	1865
TGGT1_232180	UBA/TS-N domain-containing protein	1	N/A	1865
TGGT1_232250	catalase	0	N/A	502
TGGT1_232300	ribosomal protein RPS3	0	NN Sum: 2,	255
TGGT1_232300	ribosomal protein RPS3	0	NN Sum: 2,	255
TGGT1_232300	ribosomal protein RPS3	0	NN Sum: 2,	255
TGGT1_232300	ribosomal protein RPS3	0	NN Sum: 2,	255
TGGT1_232350	lactate dehydrogenase LDH1	0	N/A	329
TGGT1_232370	CW-type Zinc Finger protein	0	N/A	1156
TGGT1_232390	18S rRNA biogenesis protein RCL1 protein	0	N/A	442
TGGT1_232410	PDI family protein	0	N/A	220
TGGT1_232440	Brf1p family coiled coil protein	0	N/A	468
TGGT1_232520	brix domain-containing protein	0	N/A	401
TGGT1_232550	hypothetical protein	0	N/A	227
TGGT1_232590	glutamate-cysteine ligase, catalytic subunit domain-	0	N/A	1062
TGGT1_232620	hypothetical protein	0	N/A	894
TGGT1_232660	Hsp70 interacting protein HIP	0	N/A	425
TGGT1_232710	ribosomal protein RPS3A	0	N/A	259
TGGT1_232710	ribosomal protein RPS3A	0	N/A	259
TGGT1_232760	protein phosphatase inhibitor IPP2	0	N/A	145
TGGT1_232800	hypothetical protein	0	N/A	1503
TGGT1_233010	putative cell-cycle-assocaited protein kinase ERK7	0	N/A	692
TGGT1_233010	putative cell-cycle-assocaited protein kinase ERK7	0	N/A	692
TGGT1_233110	IMP dehydrogenasa	0	N/A	551
TGGT1_233110	IMP dehydrogenasa	0	N/A	551
TGGT1_233110	IMP dehydrogenasa	0	N/A	551
TGGT1_233160	hypothetical protein	0	N/A	1856
TGGT1_233220	hypothetical protein	2	NN Sum: 4,	1476
TGGT1_233230	RNA-binding protein 8A family protein	0	N/A	162
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233460	SAG-related sequence SRS29B	0	NN Sum: 1,	336
TGGT1_233470	hypothetical protein	2	N/A	568
TGGT1_233480	SAG-related sequence SRS29C	0	NN Sum: 1,	372
TGGT1_233520	ATP-dependent RNA helicase	0	N/A	801
TGGT1_233680	nuclear movement family protein	0	N/A	347
TGGT1_233695	hypothetical protein	2	N/A	175
TGGT1_233695	hypothetical protein	2	N/A	175
TGGT1_233720	DNA-directed RNA polymerase II RPBABC8	0	N/A	149
TGGT1_233820	DNA polymerase epsilon subunit B protein	0	N/A	614
TGGT1_233890	hypothetical protein	0	NN Sum: 0,	683
TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595
TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595

TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595
TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595
TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595
TGGT1_234190	putative serine hydroxymethyltransferase 2	0	N/A	595
TGGT1_234220	hypothetical protein	1	N/A	1072
TGGT1_234270	hypothetical protein	0	N/A	2027
TGGT1_234410	transporter, small conductance mechanosensitive io	8	N/A	3400
TGGT1_234450	ribosomal protein RPS15A	1	N/A	231
TGGT1_234490	kelch repeat-containing protein	0	N/A	1503
TGGT1_234980	hypothetical protein	0	N/A	760
TGGT1_235020	putative COPI protein	0	N/A	1256
TGGT1_235020	putative COPI protein	0	N/A	1256
TGGT1_235020	putative COPI protein	0	N/A	1256
TGGT1_235150	transporter, major facilitator family protein	12	N/A	563
TGGT1_235150	transporter, major facilitator family protein	12	N/A	563
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235340	hypothetical protein	0	N/A	720
TGGT1_235380	hypothetical protein	0	N/A	583
TGGT1_235420	hypothetical protein	0	N/A	4118
TGGT1_235420	hypothetical protein	0	N/A	4118
TGGT1_235470	myosin A	0	N/A	831
TGGT1_235470	myosin A	0	N/A	831
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235930	domain K- type RNA binding proteins family protein	0	N/A	570
TGGT1_235970	putative eukaryotic initiation factor-2 gamma	0	N/A	465
TGGT1_235970	putative eukaryotic initiation factor-2 gamma	0	N/A	465
TGGT1_235980	ARIADNE family protein	0	N/A	655
TGGT1_236010	prenylcysteine oxidase	0	NN Sum: 4,	611
TGGT1_236040	fructose-1,6-bisphosphate aldolase	1	N/A	433
TGGT1_236040	fructose-1,6-bisphosphate aldolase	1	N/A	433
TGGT1_236040	fructose-1,6-bisphosphate aldolase	1	N/A	433
TGGT1_236060	hypothetical protein	0	N/A	507
TGGT1_236080	replication factor-a protein 1 (rpa1) subfamily protei	0	N/A	904
TGGT1_236210	putative peptidase M16 family potein	0	NN Sum: 0,	509
TGGT1_236210	putative peptidase M16 family potein	0	NN Sum: 0,	509
TGGT1_236210	putative peptidase M16 family potein	0	NN Sum: 0,	509
TGGT1_236540	RNA recognition motif-containing protein	0	N/A	508
TGGT1_236540	RNA recognition motif-containing protein	0	N/A	508
TGGT1_236540	RNA recognition motif-containing protein	0	N/A	508
TGGT1_236570	lysine decarboxylase family protein	0	N/A	397
TGGT1_236570	lysine decarboxylase family protein	0	N/A	397
TGGT1_236570	lysine decarboxylase family protein	0	N/A	397
TGGT1_236570	lysine decarboxylase family protein	0	N/A	397
TGGT1_236570	lysine decarboxylase family protein	0	N/A	397

TGGT1_236650	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0	N/A	550
TGGT1_236870	hypothetical protein	2	NN Sum: 2,	214
TGGT1_236870	hypothetical protein	2	NN Sum: 2,	214
TGGT1_236950	hypothetical protein	0	N/A	112
TGGT1_236950	hypothetical protein	0	N/A	112
TGGT1_237015	hypothetical protein	2	N/A	264
TGGT1_237015	hypothetical protein	2	N/A	264
TGGT1_237110	putative replication factor C subunit 2	0	N/A	357
TGGT1_237140	putative ethylene inducible protein	0	N/A	307
TGGT1_237240	hypothetical protein	0	N/A	214
TGGT1_237250	hypothetical protein	0	NN Sum: 1,	259
TGGT1_237880	hypothetical protein	1	NN Sum: 3,	164
TGGT1_238070	glutaredoxin domain-containing protein	0	N/A	238
TGGT1_238070	glutaredoxin domain-containing protein	0	N/A	238
TGGT1_238100	transmembrane protein	2	NN Sum: 4,	240
TGGT1_238110	replication factor a protein 3 protein	0	N/A	111
TGGT1_238130	hypothetical protein	7	N/A	385
TGGT1_238190	DNA-directed RNA polymerase II RPB3	0	N/A	484
TGGT1_238190	DNA-directed RNA polymerase II RPB3	0	N/A	484
TGGT1_238250	ribosomal protein RPL36	0	N/A	101
TGGT1_239010	hypothetical protein	1	NN Sum: 4,	685
TGGT1_239100	ribosomal protein RPS7	0	N/A	196
TGGT1_239100	ribosomal protein RPS7	0	N/A	196
TGGT1_239100	ribosomal protein RPS7	0	N/A	196
TGGT1_239100	ribosomal protein RPS7	0	N/A	196
TGGT1_239100	ribosomal protein RPS7	0	N/A	196
TGGT1_239260	histone H4	0	N/A	103
TGGT1_239260	histone H4	0	N/A	103
TGGT1_239300	hypothetical protein	0	N/A	1232
TGGT1_239310	ribulose 5-phosphate isomerase	0	N/A	259
TGGT1_239530	alanine-glyoxylate aminotransferase	0	N/A	381
TGGT1_239630	cytidine and deoxycytidylate deaminase zinc-binding	0	N/A	445
TGGT1_239630	cytidine and deoxycytidylate deaminase zinc-binding	0	N/A	445
TGGT1_239690	hypothetical protein	2	N/A	158
TGGT1_239760	ribosomal protein RPL22	0	N/A	133
TGGT1_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,	246
TGGT1_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,	246
TGGT1_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,	246
TGGT1_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,	246
TGGT1_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,	246
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240060	hypothetical protein	0	N/A	844
TGGT1_240090	putative rhoptry kinase family protein ROP34	1	N/A	553
TGGT1_240090	putative rhoptry kinase family protein ROP34	1	N/A	553

TGGT1_240090	putative rhoptry kinase family protein ROP34	1	N/A	553
TGGT1_240220	hypothetical protein	0	N/A	1539
TGGT1_240450	Maf family protein	0	N/A	267
TGGT1_240500	hypothetical protein	0	N/A	293
TGGT1_240520	hypothetical protein	1	NN Sum: 4,	399
TGGT1_240540	hypothetical protein	0	N/A	553
TGGT1_240600	putative chaperonin cpn60	1	N/A	667
TGGT1_240660	hypothetical protein	0	N/A	483
TGGT1_240810	hypothetical protein	10	N/A	566
TGGT1_240870	putative beta adaptin protein	0	N/A	924
TGGT1_240870	putative beta adaptin protein	0	N/A	924
TGGT1_240890	6-phosphofructokinase	0	N/A	1399
TGGT1_241000	hypothetical protein	4	N/A	233
TGGT1_241240	hypothetical protein	0	NN Sum: 4,	474
TGGT1_241830	peptidyl-prolyl cis-trans isomerase	0	N/A	575
TGGT1_242000	DUF51 family protein	0	N/A	267
TGGT1_242330	ribosomal protein RPS5	0	N/A	192
TGGT1_242380	fatty acid elongase	7	N/A	350
TGGT1_242660	putative vacuolar sorting protein 35	0	N/A	852
TGGT1_242660	putative vacuolar sorting protein 35	0	N/A	852
TGGT1_242660	putative vacuolar sorting protein 35	0	N/A	852
TGGT1_242660	putative vacuolar sorting protein 35	0	N/A	852
TGGT1_242660	putative vacuolar sorting protein 35	0	N/A	852
TGGT1_242730	guanylate kinase family protein	0	N/A	392
TGGT1_242800	putative ribosome biogenesis protein NSA2	0	N/A	260
TGGT1_242840	membrane protein	1	N/A	119
TGGT1_242860	hypothetical protein	0	N/A	544
TGGT1_242890	hypothetical protein	0	N/A	3144
TGGT1_243200	hypothetical protein	0	N/A	1258
TGGT1_243200	hypothetical protein	0	N/A	1258
TGGT1_243290	hypothetical protein	1	N/A	633
TGGT1_243390	hypothetical protein	2	N/A	337
TGGT1_243440	histone lysine acetyltransferase GCN5-B	0	N/A	1032
TGGT1_243460	hypothetical protein	0	N/A	2011
TGGT1_243460	hypothetical protein	0	N/A	2011
TGGT1_243540	WD domain, G-beta repeat-containing protein	0	N/A	711
TGGT1_243620	hypothetical protein	0	N/A	359
TGGT1_243620	hypothetical protein	0	N/A	359
TGGT1_243690	hypothetical protein	1	N/A	410
TGGT1_243690	hypothetical protein	1	N/A	410
TGGT1_243710	t-complex protein beta subunit	0	N/A	568
TGGT1_243710	t-complex protein beta subunit	0	N/A	568
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243730	rhoptry protein ROP9	1	NN Sum: 1,	353
TGGT1_243760	hypothetical protein	3	NN Sum: 2,	435
TGGT1_243800	putative long-chain fatty acid CoA ligase	0	N/A	758
TGGT1_243910	Cof family hydrolase subfamily protein	0	N/A	374

TGGT1_243920	putative DNA replication licensing factor MCM5	0	N/A	794
TGGT1_243930	hypothetical protein	0	NN Sum: 4,	943
TGGT1_243930	hypothetical protein	0	NN Sum: 4,	943
TGGT1_243950	putative prohibitin	0	NN Sum: 3,	271
TGGT1_243960	nuclear transport factor 2 (ntf2) domain-containing p	0	N/A	797
TGGT1_243960	nuclear transport factor 2 (ntf2) domain-containing p	0	N/A	797
TGGT1_243960	nuclear transport factor 2 (ntf2) domain-containing p	0	N/A	797
TGGT1_243960	nuclear transport factor 2 (ntf2) domain-containing p	0	N/A	797
TGGT1_244110	nucleosome assembly protein (nap) protein	0	N/A	738
TGGT1_244150	glycerate kinase	0	N/A	360
TGGT1_244180	microneme-like protein	0	NN Sum: 1,	717
TGGT1_244280	hypothetical protein	1	NN Sum: 4,	129
TGGT1_244290	adapter-related protein	0	N/A	1116
TGGT1_244390	coatomer epsilon subunit protein	0	N/A	309
TGGT1_244530	hypothetical protein	0	N/A	600
TGGT1_244560	putative heat shock protein 90	1	NN Sum: 4,	853
TGGT1_244560	putative heat shock protein 90	1	NN Sum: 4,	853
TGGT1_244560	putative heat shock protein 90	1	NN Sum: 4,	853
TGGT1_244690	hypothetical protein	0	N/A	623
TGGT1_245450	hypothetical protein	0	N/A	134
TGGT1_245485	microneme protein MIC9	2	NN Sum: 2,	300
TGGT1_245490	microneme protein MIC8	1	NN Sum: 4,	684
TGGT1_245490	microneme protein MIC8	1	NN Sum: 4,	684
TGGT1_245490	microneme protein MIC8	1	NN Sum: 4,	684
TGGT1_246000	large subunit ribosomal protein IMG2	0	N/A	310
TGGT1_246130	serpin (serine proteinase inhibitor) superfamily prote	0	N/A	432
TGGT1_246130	serpin (serine proteinase inhibitor) superfamily prote	0	N/A	432
TGGT1_246170	ARID/BRIGHT DNA binding domain-containing protei	0	N/A	2721
TGGT1_246220	hypothetical protein	2	N/A	811
TGGT1_246330	CRAL/TRIO domain-containing protein	0	N/A	433
TGGT1_246500	surp module domain-containing protein	0	N/A	658
TGGT1_246520	hypothetical protein	0	N/A	980
TGGT1_246540	cytochrome c1, heme protein	1	N/A	398
TGGT1_246550	aspartyl protease ASP3	1	NN Sum: 4,	643
TGGT1_246710	hypothetical protein	3	N/A	463
TGGT1_246740	hypothetical protein	0	N/A	591
TGGT1_246960	hypothetical protein	0	N/A	775
TGGT1_246970	3'-5' exonuclease domain-containing protein	0	N/A	1353
TGGT1_246982	hypothetical protein	2	NN Sum: 4,	1042
TGGT1_246982	hypothetical protein	2	NN Sum: 4,	1042
TGGT1_247220	nudix -type motif 9 isoform a family protein	0	N/A	546
TGGT1_247220	nudix -type motif 9 isoform a family protein	0	N/A	546
TGGT1_247220	nudix -type motif 9 isoform a family protein	0	N/A	546
TGGT1_247300	hypothetical protein	0	N/A	903
TGGT1_247410	hypothetical protein	1	N/A	126
TGGT1_247410	hypothetical protein	1	N/A	126
TGGT1_247440	hypothetical protein	4	NN Sum: 4,	378
TGGT1_247440	hypothetical protein	4	NN Sum: 4,	378
TGGT1_247440	hypothetical protein	4	NN Sum: 4,	378
TGGT1_247440	hypothetical protein	4	NN Sum: 4,	378
TGGT1_247440	hypothetical protein	4	NN Sum: 4,	378
TGGT1_247450	hypothetical protein	0	N/A	2303

TGGT1_247450	hypothetical protein	0	N/A	2303
TGGT1_247460	proliferating cell nuclear antigen PCNA1	0	N/A	317
TGGT1_247460	proliferating cell nuclear antigen PCNA1	0	N/A	317
TGGT1_247460	proliferating cell nuclear antigen PCNA1	0	N/A	317
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247510	fructose-bisphospatase II	0	N/A	381
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247520	hypothetical protein	1	NN Sum: 3,	256
TGGT1_247530	hypothetical protein	1	NN Sum: 4,	213
TGGT1_247610	putative small nuclear ribonucleoprotein E	0	N/A	119
TGGT1_247770	hypothetical protein	1	N/A	167
TGGT1_247770	hypothetical protein	1	N/A	167
TGGT1_248250	putative translation initiation factor IF-2	0	N/A	112
TGGT1_248250	putative translation initiation factor IF-2	0	N/A	112
TGGT1_248340	GTP-binding nuclear protein ran/tc4	0	N/A	229
TGGT1_248340	GTP-binding nuclear protein ran/tc4	0	N/A	229
TGGT1_248340	GTP-binding nuclear protein ran/tc4	0	N/A	229
TGGT1_248340	GTP-binding nuclear protein ran/tc4	0	N/A	229
TGGT1_248370	putative prefoldin subunit 6	0	N/A	123
TGGT1_248390	ribosomal protein RPL26	0	N/A	141
TGGT1_248420	hypothetical protein	10	N/A	728
TGGT1_248460	putative ubiquitin	0	N/A	216
TGGT1_248480	ribosomal protein RPS9	0	N/A	188
TGGT1_248480	ribosomal protein RPS9	0	N/A	188
TGGT1_248600	aspartate aminotransferase	0	N/A	597
TGGT1_248670	V-type H(+)-translocating pyrophosphatase VP1	17	NN Sum: 3,	816
TGGT1_248670	V-type H(+)-translocating pyrophosphatase VP1	17	NN Sum: 3,	816
TGGT1_248700	alveolin domain containing intermediate filament IN	0	N/A	277
TGGT1_248740	hypothetical protein	0	N/A	1283
TGGT1_248770	hypothetical protein	0	N/A	663
TGGT1_248810	nuclear factor NF7	0	N/A	497
TGGT1_248810	nuclear factor NF7	0	N/A	497
TGGT1_248850	methionine aminopeptidase	0	N/A	416
TGGT1_248890	actin-like protein ALP3b	0	NN Sum: 0,	567
TGGT1_249030	endonuclease/exonuclease/phosphatase family prot	0	N/A	541
TGGT1_249180	bifunctional dihydrofolate reductase-thymidylate syr	0	N/A	610
TGGT1_249180	bifunctional dihydrofolate reductase-thymidylate syr	0	N/A	610
TGGT1_249240	putative calmodulin	0	N/A	149
TGGT1_249240	putative calmodulin	0	N/A	149
TGGT1_249240	putative calmodulin	0	N/A	149

TGGT1_249250	ribosomal protein RPL35A	0	N/A	112
TGGT1_249300	hypothetical protein	2	N/A	311
TGGT1_249370	putative translation initiation factor SUI1	0	N/A	325
TGGT1_249390	glutamate/leucine/phenylalanine/valine dehydroger	0	NN Sum: 2,	1206
TGGT1_249390	glutamate/leucine/phenylalanine/valine dehydroger	0	NN Sum: 2,	1206
TGGT1_249480	tetratricopeptide repeat-containing protein	0	N/A	1161
TGGT1_249610	hypothetical protein	0	N/A	1208
TGGT1_249670	cathepsin B	1	NN Sum: 4,	569
TGGT1_249670	cathepsin B	1	NN Sum: 4,	569
TGGT1_249730	hypothetical protein	0	NN Sum: 2,	891
TGGT1_249780	hypothetical protein	0	N/A	328
TGGT1_249780	hypothetical protein	0	N/A	328
TGGT1_249780	hypothetical protein	0	N/A	328
TGGT1_249780	hypothetical protein	0	N/A	328
TGGT1_249780	hypothetical protein	0	N/A	328
TGGT1_249850	GAP40 protein	9	N/A	385
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249900	putative adenine nucleotide translocator	4	N/A	318
TGGT1_249970	hypothetical protein	0	N/A	229
TGGT1_249990	hypothetical protein	0	N/A	838
TGGT1_249990	hypothetical protein	0	N/A	838
TGGT1_250010	Sad1 / UNC family protein	0	N/A	796
TGGT1_250700	hypothetical protein	0	N/A	1509
TGGT1_250700	hypothetical protein	0	N/A	1509
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250710	microneme protein MIC10	1	NN Sum: 4,	198
TGGT1_250770	putative eukaryotic initiation factor-4A	0	N/A	412
TGGT1_250770	putative eukaryotic initiation factor-4A	0	N/A	412
TGGT1_250770	putative eukaryotic initiation factor-4A	0	N/A	412
TGGT1_250820	hypothetical protein	0	N/A	1156
TGGT1_250830	SAC3/GANP family protein	0	N/A	376
TGGT1_250870	DHHC zinc finger domain-containing protein	4	N/A	361

TGGT1_250870	DHHC zinc finger domain-containing protein	4	N/A	361
TGGT1_250880	kinase, pfkB family protein	0	N/A	488
TGGT1_251410	tetratricopeptide repeat-containing protein	0	N/A	2068
TGGT1_251500	putative eukaryotic initiation factor-3, subunit 3	0	NN Sum: 2,	600
TGGT1_251540	dense granule protein GRA9	0	NN Sum: 4,	318
TGGT1_251540	dense granule protein GRA9	0	NN Sum: 4,	318
TGGT1_251620	putative flap structure-specific endonuclease 1	0	N/A	552
TGGT1_251680	putative histamine-releasing factor	0	N/A	171
TGGT1_251680	putative histamine-releasing factor	0	N/A	171
TGGT1_251690	putative seryl-tRNA synthetase, cytoplasmic	0	N/A	482
TGGT1_251690	putative seryl-tRNA synthetase, cytoplasmic	0	N/A	482
TGGT1_251780	heat shock protein	0	NN Sum: 0,	728
TGGT1_251930	enoyl-acyl carrier reductase ENR	0	NN Sum: 4,	417
TGGT1_251930	enoyl-acyl carrier reductase ENR	0	NN Sum: 4,	417
TGGT1_251950	ribosomal protein l7/l12 c-terminal domain-containi	0	N/A	354
TGGT1_252250	ATPase, AAA family protein	0	N/A	1299
TGGT1_252480	hypothetical protein	0	NN Sum: 3,	295
TGGT1_252500	polo kinase	0	NN Sum: 3,	697
TGGT1_252630	hypothetical protein	0	N/A	136
TGGT1_252850	initiation factor, subunit 2 family protein	0	N/A	710
TGGT1_253090	DEAD/DEAH box helicase domain-containing protein	0	N/A	655
TGGT1_253090	DEAD/DEAH box helicase domain-containing protein	0	N/A	655
TGGT1_253090	DEAD/DEAH box helicase domain-containing protein	0	N/A	655
TGGT1_253100	hypothetical protein	4	N/A	519
TGGT1_253100	hypothetical protein	4	N/A	519
TGGT1_253160	hypothetical protein	0	N/A	433
TGGT1_253350	hypothetical protein	0	N/A	811
TGGT1_253420	PQ loop repeat-containing protein	6	N/A	410
TGGT1_253420	PQ loop repeat-containing protein	6	N/A	410
TGGT1_253420	PQ loop repeat-containing protein	6	N/A	410
TGGT1_253470	alveolin domain containing intermediate filament IM	0	N/A	398
TGGT1_253510	transporter/permease protein	8	N/A	357
TGGT1_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,	658
TGGT1_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,	658
TGGT1_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,	658
TGGT1_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,	658
TGGT1_253910	hypothetical protein	0	N/A	887
TGGT1_254000	hypothetical protein	0	N/A	479
TGGT1_254060	SAG-related sequence SRS14A	1	N/A	376
TGGT1_254365	phosphatidate cytidylyltransferase	4	N/A	255
TGGT1_254365	phosphatidate cytidylyltransferase	4	N/A	255
TGGT1_254365	phosphatidate cytidylyltransferase	4	N/A	255
TGGT1_254390	CRAL/TRIO domain-containing protein	0	N/A	683
TGGT1_254410	putative protein phosphatase 2C	0	N/A	626
TGGT1_254440	ribosomal protein RPL12	0	N/A	165
TGGT1_254450	putative Pelota	0	N/A	398
TGGT1_254490	Sel1 repeat-containing protein	2	N/A	1528
TGGT1_254510	ankyrin repeat-containing protein	0	N/A	626
TGGT1_254520	mediator complex subunit MED11	0	N/A	153
TGGT1_254580	UDP-galactose transporter family protein	8	N/A	413
TGGT1_254580	UDP-galactose transporter family protein	8	N/A	413
TGGT1_254610	Tim10/DDP family zinc finger superfamily protein	0	N/A	91

TGGT1_254610	Tim10/DDP family zinc finger superfamily protein	0	N/A	91
TGGT1_254620	ribosomal protein RPL39	0	N/A	68
TGGT1_254650	zinc finger protein	0	N/A	400
TGGT1_254770	Ser/Thr phosphatase family protein	0	N/A	420
TGGT1_254770	Ser/Thr phosphatase family protein	0	N/A	420
TGGT1_254890	hypothetical protein	0	NN Sum: 4,	300
TGGT1_255220	AP2 domain transcription factor AP2VIIb-3	0	N/A	2287
TGGT1_255240	hypothetical protein	0	N/A	2465
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255260	apical membrane antigen AMA1	1	N/A	569
TGGT1_255340	tetratricopeptide repeat-containing protein	0	N/A	1696
TGGT1_255400	hypothetical protein	1	N/A	311
TGGT1_255410	hypothetical protein	2	NN Sum: 1,	165
TGGT1_255420	hypothetical protein	0	N/A	278
TGGT1_255660	EF hand domain-containing protein	0	NN Sum: 3,	149
TGGT1_255690	2-C-methyl-D-erythritol 2,4-cyclodiphosphate syntha	1	NN Sum: 4,	528
TGGT1_255715	hypothetical protein	0	N/A	171
TGGT1_255890	pyridine nucleotide-disulfide oxidoreductase domain	0	N/A	787
TGGT1_255895	hypothetical protein	0	N/A	556
TGGT1_255900	putative Bax inhibitor-1	6	N/A	248
TGGT1_255900	putative Bax inhibitor-1	6	N/A	248
TGGT1_256050	signal recognition particle 14kd protein	0	N/A	172
TGGT1_256060	nucleosome assembly protein (nap) protein	0	N/A	812
TGGT1_256760	pyruvate kinase PyK1	0	N/A	531
TGGT1_256760	pyruvate kinase PyK1	0	N/A	531
TGGT1_256760	pyruvate kinase PyK1	0	N/A	531
TGGT1_256770	putative eukaryotic translation initiation factor 4A, is	0	N/A	395
TGGT1_256840	hypothetical protein	0	N/A	764
TGGT1_256840	hypothetical protein	0	N/A	764
TGGT1_256990	glycyl-tRNA synthetase	0	N/A	771
TGGT1_256990	glycyl-tRNA synthetase	0	N/A	771
TGGT1_257040	TB2/DP1, HVA22 family protein	2	N/A	217
TGGT1_257040	TB2/DP1, HVA22 family protein	2	N/A	217
TGGT1_257100	hypothetical protein	0	N/A	564
TGGT1_257160	hypothetical protein	0	NN Sum: 0,	152
TGGT1_257160	hypothetical protein	0	NN Sum: 0,	152
TGGT1_257160	hypothetical protein	0	NN Sum: 0,	152
TGGT1_257300	hypothetical protein	0	N/A	1152
TGGT1_257310	hypothetical protein	0	N/A	355
TGGT1_257350	putative eukaryotic translation initiation factor	0	N/A	824
TGGT1_257350	putative eukaryotic translation initiation factor	0	N/A	824
TGGT1_257350	putative eukaryotic translation initiation factor	0	N/A	824
TGGT1_257350	putative eukaryotic translation initiation factor	0	N/A	824

TGGT1_257510	CDP-alcohol phosphatidyltransferase superfamily pr	9	N/A	467
TGGT1_257530	transporter, major facilitator family protein	12	N/A	504
TGGT1_257740	UMP-CMP kinase	0	N/A	462
TGGT1_257740	UMP-CMP kinase	0	N/A	462
TGGT1_257750	homocysteine s-methyltransferase domain-containi	0	N/A	434
TGGT1_257990	putative heat shock protein 101	0	N/A	927
TGGT1_257990	putative heat shock protein 101	0	N/A	927
TGGT1_258060	putative myosin heavy chain	0	NN Sum: 0,	208
TGGT1_258060	putative myosin heavy chain	0	NN Sum: 0,	208
TGGT1_258070	hypothetical protein	0	N/A	678
TGGT1_258080	hypothetical protein	0	N/A	1711
TGGT1_258090	hypothetical protein	0	N/A	954
TGGT1_258100	TPR repeat region protein	0	NN Sum: 2,	215
TGGT1_258170	hypothetical protein	0	N/A	408
TGGT1_258170	hypothetical protein	0	N/A	408
TGGT1_258170	hypothetical protein	0	N/A	408
TGGT1_258210	DNA-directed RNA polymerase II RPB2	0	N/A	1259
TGGT1_258360	hypothetical protein	0	NN Sum: 4,	537
TGGT1_258390	putative DnaJ protein	0	NN Sum: 4,	397
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258410	photosensitized INA-labeled protein PHIL1	0	N/A	165
TGGT1_258470	hypothetical protein	0	N/A	284
TGGT1_258580	rhoptry protein ROP17	0	NN Sum: 4,	608
TGGT1_258660	rhoptry protein ROP6	2	NN Sum: 3,	480
TGGT1_258720	putative Ubiquitin family protein	0	N/A	73
TGGT1_258730	hypothetical protein	1	N/A	151
TGGT1_258730	hypothetical protein	1	N/A	151
TGGT1_258770	putative polypeptide n-acetylgalactosaminyltransfer	1	N/A	692
TGGT1_258820	hypothetical protein	2	NN Sum: 4,	129
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_258870A	hypothetical protein	1	N/A	557
TGGT1_259010	putative vacuolar ATP synthase subunit d	0	N/A	396
TGGT1_259040	hypothetical protein	1	N/A	261
TGGT1_259040	hypothetical protein	1	N/A	261
TGGT1_259040	hypothetical protein	1	N/A	261
TGGT1_259040	hypothetical protein	1	N/A	261
TGGT1_259155	hypothetical protein	0	N/A	1206
TGGT1_259260	membrane protein FtsH1	1	N/A	1250
TGGT1_259520	hypothetical protein	0	N/A	436
TGGT1_259550	dihydropteroate synthase	0	NN Sum: 1,	748
TGGT1_259550	dihydropteroate synthase	0	NN Sum: 1,	748
TGGT1_259550	dihydropteroate synthase	0	NN Sum: 1,	748
TGGT1_259640	nucleoporin autopeptidase	0	N/A	2894
TGGT1_259710	protein kinase	0	N/A	251

TGGT1_259710	protein kinase	0	N/A	251
TGGT1_259710	protein kinase	0	N/A	251
TGGT1_259940	hypothetical protein	8	N/A	623
TGGT1_260020	hypothetical protein	1	N/A	186
TGGT1_260180	hypothetical protein	0	N/A	157
TGGT1_260180	hypothetical protein	0	N/A	157
TGGT1_260240	ccr4-associated factor family protein	0	N/A	617
TGGT1_260240	ccr4-associated factor family protein	0	N/A	617
TGGT1_260260	ribosomal protein RPP1	0	N/A	179
TGGT1_260260	ribosomal protein RPP1	0	N/A	179
TGGT1_260370	AtPH1 family protein	0	N/A	130
TGGT1_260440	nuclear factor NF3	0	N/A	312
TGGT1_260440	nuclear factor NF3	0	N/A	312
TGGT1_260500	putative COPI associated protein	4	N/A	270
TGGT1_260500	putative COPI associated protein	4	N/A	270
TGGT1_260520	hypothetical protein	0	N/A	742
TGGT1_260540	alveolin domain containing intermediate filament IV	0	N/A	733
TGGT1_260600	Pumilio-family RNA binding repeat-containing protei	0	N/A	1676
TGGT1_260600	Pumilio-family RNA binding repeat-containing protei	0	N/A	1676
TGGT1_260600	Pumilio-family RNA binding repeat-containing protei	0	N/A	1676
TGGT1_260610	methyltransferase	0	N/A	383
TGGT1_260670	putative centrin	0	N/A	238
TGGT1_260810	hypothetical protein	1	N/A	277
TGGT1_260810	hypothetical protein	1	N/A	277
TGGT1_260820	IMC sub-compartment protein ISP1	0	N/A	176
TGGT1_260820	IMC sub-compartment protein ISP1	0	N/A	176
TGGT1_260825	hypothetical protein	0	N/A	92
TGGT1_261010	putative tat-binding family protein	0	N/A	409
TGGT1_261050	RNB family domain-containing protein	0	N/A	1149
TGGT1_261080	kringle domain-containing protein	9	N/A	3051
TGGT1_261220	transcription elongation factor SPT4	0	N/A	146
TGGT1_261250	histone H2A1	0	N/A	180
TGGT1_261250	histone H2A1	0	N/A	180
TGGT1_261250	histone H2A1	0	N/A	180
TGGT1_261250	histone H2A1	0	N/A	180
TGGT1_261260A	histone lysine demethylase JMJD6a	0	NN Sum: 0,	395
TGGT1_261460	transcriptional elongation factor FACT80	0	N/A	539
TGGT1_261520	putative nucleolar GTP-binding protein 1	0	N/A	719
TGGT1_261720	metal cation transporter, ZIP family protein	8	NN Sum: 2,	448
TGGT1_261740	hypothetical protein	1	NN Sum: 4,	131
TGGT1_261740	hypothetical protein	1	NN Sum: 4,	131
TGGT1_261740	hypothetical protein	1	NN Sum: 4,	131
TGGT1_261740	hypothetical protein	1	NN Sum: 4,	131
TGGT1_261750	rhoptry neck protein RON10	0	N/A	835
TGGT1_261950	ATP synthase beta subunit ATP-B	0	N/A	560
TGGT1_261950	ATP synthase beta subunit ATP-B	0	N/A	560
TGGT1_261950	ATP synthase beta subunit ATP-B	0	N/A	560
TGGT1_262040	SAC3/GANP family protein	0	N/A	269
TGGT1_262040	SAC3/GANP family protein	0	N/A	269
TGGT1_262040	SAC3/GANP family protein	0	N/A	269
TGGT1_262050	rhoptry kinase family protein ROP39	0	NN Sum: 0,	588
TGGT1_262050	rhoptry kinase family protein ROP39	0	NN Sum: 0,	588

TGGT1_262150	kelch repeat and K+ channel tetramerisation domain	0	N/A	818
TGGT1_262380	putative elongation factor Tu	0	NN Sum: 0,	552
TGGT1_262380	putative elongation factor Tu	0	NN Sum: 0,	552
TGGT1_262400	lipase	1	NN Sum: 2,	1409
TGGT1_262480	putative dynein light chain roadblock-type 2	0	N/A	125
TGGT1_262610	hypothetical protein	7	NN Sum: 0,	637
TGGT1_262620	RNA recognition motif-containing protein	0	N/A	293
TGGT1_262620	RNA recognition motif-containing protein	0	N/A	293
TGGT1_262620	RNA recognition motif-containing protein	0	N/A	293
TGGT1_262620	RNA recognition motif-containing protein	0	N/A	293
TGGT1_262640	Cg8 family protein	1	N/A	204
TGGT1_262670	ribosomal protein RPL18A	0	N/A	183
TGGT1_262670	ribosomal protein RPL18A	0	N/A	183
TGGT1_262670	ribosomal protein RPL18A	0	N/A	183
TGGT1_262710	Ctr copper transporter family protein	3	N/A	375
TGGT1_262730	rhoptry protein ROP16	0	NN Sum: 4,	707
TGGT1_262730	rhoptry protein ROP16	0	NN Sum: 4,	707
TGGT1_262730	rhoptry protein ROP16	0	NN Sum: 4,	707
TGGT1_262810	iron donor protein CyaY protein	0	NN Sum: 2,	287
TGGT1_262825	peptidase family c50 protein	0	N/A	6945
TGGT1_262920	trypsin domain-containing protein	1	NN Sum: 4,	972
TGGT1_262920	trypsin domain-containing protein	1	NN Sum: 4,	972
TGGT1_262920	trypsin domain-containing protein	1	NN Sum: 4,	972
TGGT1_262920	trypsin domain-containing protein	1	NN Sum: 4,	972
TGGT1_263040	ribosomal protein RPS16	0	N/A	211
TGGT1_263040	ribosomal protein RPS16	0	N/A	211
TGGT1_263050	ribosomal protein RPL13	0	N/A	355
TGGT1_263050	ribosomal protein RPL13	0	N/A	355
TGGT1_263050	ribosomal protein RPL13	0	N/A	355
TGGT1_263050	ribosomal protein RPL13	0	N/A	355
TGGT1_263050	ribosomal protein RPL13	0	N/A	355
TGGT1_263060	Proteasome/cyclosome repeat-containing protein	0	N/A	988
TGGT1_263070	CMGC kinase, CK2 family	0	N/A	539
TGGT1_263070	CMGC kinase, CK2 family	0	N/A	539
TGGT1_263070	CMGC kinase, CK2 family	0	N/A	539
TGGT1_263070	CMGC kinase, CK2 family	0	N/A	539
TGGT1_263080	hypothetical protein	0	N/A	133
TGGT1_263090	14-3-3 protein	0	N/A	323
TGGT1_263090	14-3-3 protein	0	N/A	323
TGGT1_263180	myosin D	0	N/A	822
TGGT1_263190	putative adenylosuccinate lyase	0	NN Sum: 0,	500
TGGT1_263270	glycerophosphodiester phosphodiesterase family pr	6	N/A	866
TGGT1_263270	glycerophosphodiester phosphodiesterase family pr	6	N/A	866
TGGT1_263300	eukaryotic porin protein	0	N/A	290
TGGT1_263300	eukaryotic porin protein	0	N/A	290
TGGT1_263320	hypothetical protein	0	N/A	403
TGGT1_263323	putative tetratricopeptide repeat protein 11	1	N/A	144
TGGT1_263530	putative chaperonin	0	N/A	127
TGGT1_263530	putative chaperonin	0	N/A	127
TGGT1_263630	hypothetical protein	0	NN Sum: 3,	136
TGGT1_263700	ribosomal protein RPS14	0	N/A	156
TGGT1_263700	ribosomal protein RPS14	0	N/A	156

TGGT1_263700	ribosomal protein RPS14	0	N/A	156
TGGT1_263700	ribosomal protein RPS14	0	N/A	156
TGGT1_263810	hypothetical protein	1	N/A	213
TGGT1_263820	DEAD/DEAH box helicase domain-containing protein	0	N/A	1053
TGGT1_263850	hypothetical protein	0	N/A	229
TGGT1_264020	hypothetical protein	0	N/A	647
TGGT1_264040	hypothetical protein	0	NN Sum: 4,	220
TGGT1_264040	hypothetical protein	0	NN Sum: 4,	220
TGGT1_264060	PCI domain-containing protein	0	N/A	465
TGGT1_264080	acyl carrier protein ACP	1	NN Sum: 4,	183
TGGT1_264080	acyl carrier protein ACP	1	NN Sum: 4,	183
TGGT1_264440	signal recognition particle receptor beta subunit pro	1	N/A	347
TGGT1_264450	putative DNA topoisomerase III beta-1	0	N/A	852
TGGT1_264600	hypothetical protein	4	N/A	217
TGGT1_264610	RNA recognition motif-containing protein	0	N/A	430
TGGT1_264610	RNA recognition motif-containing protein	0	N/A	430
TGGT1_264610	RNA recognition motif-containing protein	0	N/A	430
TGGT1_264610	RNA recognition motif-containing protein	0	N/A	430
TGGT1_264610	RNA recognition motif-containing protein	0	N/A	430
TGGT1_264690	putative cyclin 4	0	N/A	634
TGGT1_264860	zinc finger, C3HC4 type (RING finger) domain-contai	0	N/A	3868
TGGT1_264880	NEDD8-activating enzyme E1 catalytic subunit	0	N/A	589
TGGT1_265020	putative arabinogalactan protein	0	N/A	314
TGGT1_265180	hypothetical protein	0	N/A	452
TGGT1_265220	co-chaperone GrpE protein	0	NN Sum: 1,	347
TGGT1_265250	RNA recognition motif-containing protein	0	N/A	1564
TGGT1_265250	RNA recognition motif-containing protein	0	N/A	1564
TGGT1_265330	putative cell-cycle-associated protein kinase GSK	0	N/A	394
TGGT1_265330	putative cell-cycle-associated protein kinase GSK	0	N/A	394
TGGT1_265330	putative cell-cycle-associated protein kinase GSK	0	N/A	394
TGGT1_265360	hypothetical protein	0	N/A	516
TGGT1_265370	hypothetical protein	0	N/A	142
TGGT1_265420	hypothetical protein	0	N/A	256
TGGT1_265520	hypothetical protein	0	N/A	512
TGGT1_265530	RNA recognition motif-containing protein	0	N/A	492
TGGT1_265530	RNA recognition motif-containing protein	0	N/A	492
TGGT1_265840	hypothetical protein	0	NN Sum: 1,	1332
TGGT1_266060	ribosomal protein RPSA	0	N/A	287
TGGT1_266090	hypothetical protein	4	NN Sum: 3,	451
TGGT1_266280	HEAT repeat-containing protein	0	N/A	910
TGGT1_266620	thioredoxin domain-containing protein	0	NN Sum: 4,	207
TGGT1_266640	putative Acetyl-coenzyme A synthetase 2	0	N/A	714
TGGT1_266640	putative Acetyl-coenzyme A synthetase 2	0	N/A	714
TGGT1_266750	putative transporter/permease protein	7	NN Sum: 3,	355
TGGT1_266760	isocitrate dehydrogenase	0	NN Sum: 4,	594
TGGT1_267050	hydrolase, alpha/beta fold family protein	0	N/A	308
TGGT1_267080	putative 26S protease regulatory subunit 4	0	N/A	441
TGGT1_267080	putative 26S protease regulatory subunit 4	0	N/A	441
TGGT1_267300	hypothetical protein	4	N/A	265
TGGT1_267300	hypothetical protein	4	N/A	265
TGGT1_267390	DNA-directed RNA polymerase I RPAC1	0	N/A	346
TGGT1_267400	ribosomal protein RPL32	0	N/A	134

TGGT1_267420	putative mago nashi family protein 2	1	N/A	202
TGGT1_267420	putative mago nashi family protein 2	1	N/A	202
TGGT1_267420	putative mago nashi family protein 2	1	N/A	202
TGGT1_267430	DnaJ domain-containing protein	4	N/A	425
TGGT1_267700	hypothetical protein	0	N/A	261
TGGT1_267800	dynamin-related protein DRPA	0	N/A	802
TGGT1_268200	RNA recognition motif-containing protein	0	N/A	648
TGGT1_268300	hypothetical protein	0	NN Sum: 2,	124
TGGT1_268560	XPG N-terminal domain-containing protein	0	N/A	2004
TGGT1_268570	zinc finger (CCCH type) motif-containing protein	0	N/A	449
TGGT1_268570	zinc finger (CCCH type) motif-containing protein	0	N/A	449
TGGT1_268580	hypothetical protein	0	N/A	476
TGGT1_268640	BING4CT (NUC141) domain-containing protein	0	N/A	568
TGGT1_268650	putative chaperone clpB protein	0	N/A	1020
TGGT1_268700	hypothetical protein	0	NN Sum: 4,	317
TGGT1_268720	Hrf1 family protein	4	N/A	474
TGGT1_268750	putative peptidyl-prolyl cis-trans isomerase E	0	N/A	145
TGGT1_268790	hypothetical protein	0	NN Sum: 0,	252
TGGT1_268790	hypothetical protein	0	NN Sum: 0,	252
TGGT1_268835	hypothetical protein	0	N/A	669
TGGT1_268835	hypothetical protein	0	N/A	669
TGGT1_268835	hypothetical protein	0	N/A	669
TGGT1_268835	hypothetical protein	0	N/A	669
TGGT1_268835	hypothetical protein	0	N/A	669
TGGT1_268850	enolase 2	0	N/A	475
TGGT1_268850	enolase 2	0	N/A	475
TGGT1_268850	enolase 2	0	N/A	475
TGGT1_268850	enolase 2	0	N/A	475
TGGT1_269180	MIF4G domain-containing protein	0	N/A	2668
TGGT1_269190	glyceraldehyde-3-phosphate dehydrogenase GAPDH	1	NN Sum: 3,	995
TGGT1_269190	glyceraldehyde-3-phosphate dehydrogenase GAPDH	1	NN Sum: 3,	995
TGGT1_269650	FFD and TFG box motifs protein	0	NN Sum: 0,	492
TGGT1_269650	FFD and TFG box motifs protein	0	NN Sum: 0,	492
TGGT1_269650	FFD and TFG box motifs protein	0	NN Sum: 0,	492
TGGT1_269650	FFD and TFG box motifs protein	0	NN Sum: 0,	492
TGGT1_269650	FFD and TFG box motifs protein	0	NN Sum: 0,	492
TGGT1_269680	putative acyl-CoA carboxyltransferase beta chain	0	N/A	812
TGGT1_269800	putative glutamine-dependent NAD(+) synthetase pr	0	N/A	862
TGGT1_269885A	rhoptry metalloprotease toxolysin TLN1	1	NN Sum: 4,	1291
TGGT1_269885A	rhoptry metalloprotease toxolysin TLN1	1	NN Sum: 4,	1291
TGGT1_269885A	rhoptry metalloprotease toxolysin TLN1	1	NN Sum: 4,	1291
TGGT1_269885A	rhoptry metalloprotease toxolysin TLN1	1	NN Sum: 4,	1291
TGGT1_269950	hypothetical protein	0	NN Sum: 4,	944
TGGT1_269980	putative preprotein translocase Sec61	8	NN Sum: 3,	473
TGGT1_269980	putative preprotein translocase Sec61	8	NN Sum: 3,	473
TGGT1_270070	synaptobrevin family protein	1	N/A	225
TGGT1_270140	putative splicing factor DIM1	0	N/A	142
TGGT1_270220	hypothetical protein	7	NN Sum: 2,	1296
TGGT1_270240	MAG1 protein	1	NN Sum: 4,	452
TGGT1_270240	MAG1 protein	1	NN Sum: 4,	452
TGGT1_270240	MAG1 protein	1	NN Sum: 4,	452
TGGT1_270240	MAG1 protein	1	NN Sum: 4,	452

TGGT1_270250	dense granule protein GRA1	0	NN Sum: 4,	190
TGGT1_270250	dense granule protein GRA1	0	NN Sum: 4,	190
TGGT1_270250	dense granule protein GRA1	0	NN Sum: 4,	190
TGGT1_270320	protein phosphatase 2C domain-containing protein	0	NN Sum: 4,	538
TGGT1_270320	protein phosphatase 2C domain-containing protein	0	NN Sum: 4,	538
TGGT1_270360	hypothetical protein	0	N/A	252
TGGT1_270380	ribosomal protein RPS13	0	N/A	151
TGGT1_270380	ribosomal protein RPS13	0	N/A	151
TGGT1_270510	asparaginyl-tRNA synthetase (NOB+tRNA synthase)	0	NN Sum: 3,	676
TGGT1_270560	peptidyl-prolyl cis-trans isomerase family 1	0	NN Sum: 0,	195
TGGT1_270640	RNA recognition motif-containing protein	0	N/A	208
TGGT1_270740	Cwf15/Cwc15 cell cycle control protein	0	N/A	210
TGGT1_270780	DNA-directed RNA polymerase II RPB6	0	N/A	146
TGGT1_270790	hypothetical protein	0	N/A	300
TGGT1_270830	small nuclear ribonucleoprotein	0	N/A	155
TGGT1_270880	RNA recognition motif-containing protein	0	N/A	1374
TGGT1_270880	RNA recognition motif-containing protein	0	N/A	1374
TGGT1_270880	RNA recognition motif-containing protein	0	N/A	1374
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271050	SAG-related sequence SRS34A	0	NN Sum: 4,	186
TGGT1_271060	Sec1 family protein	0	N/A	648
TGGT1_271120	endonuclease/exonuclease/phosphatase family prot	0	N/A	1236
TGGT1_271420	porphobilinogen deaminase	1	N/A	732
TGGT1_271430	hypothetical protein	0	N/A	1314
TGGT1_271760	seryl-tRNA synthetase (SerRS2)	1	NN Sum: 3,	853
TGGT1_271930	hypothetical protein	0	N/A	234
TGGT1_271935	hypothetical protein	0	N/A	89
TGGT1_271935	hypothetical protein	0	N/A	89
TGGT1_272030A	kelch repeat-containing protein	0	N/A	595
TGGT1_272380	hypothetical protein	1	N/A	581
TGGT1_272380	hypothetical protein	1	N/A	581
TGGT1_272400	casein kinase ii regulatory subunit protein	0	N/A	361
TGGT1_272400	casein kinase ii regulatory subunit protein	0	N/A	361
TGGT1_272490	protoporphyrinogen oxidase	0	NN Sum: 0,	1028
TGGT1_272520	hypothetical protein	0	N/A	401
TGGT1_272630	putative U6 snRNA-associated Sm family protein LSm	0	N/A	129
TGGT1_272630	putative U6 snRNA-associated Sm family protein LSm	0	N/A	129
TGGT1_272910	T-complex protein 1 delta subunit	0	N/A	542
TGGT1_273070	putative GTPase activating protein for adp ribosylati	0	NN Sum: 0,	501
TGGT1_273120	SAG-related sequence SRS30C	0	N/A	374
TGGT1_273120	SAG-related sequence SRS30C	0	N/A	374
TGGT1_273150	zinc finger, C3HC4 type (RING finger) domain-contair	0	N/A	779

TGGT1_273320	hypothetical protein	1	NN Sum: 4,	238
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273460	eukaryotic translation initiation factor 3 subunit 6 int	2	N/A	639
TGGT1_273520	PCI domain-containing protein	0	N/A	601
TGGT1_273550	hypothetical protein	0	N/A	858
TGGT1_273630	DnaJ domain-containing protein	1	N/A	232
TGGT1_273760	heat shock protein HSP70	0	N/A	667
TGGT1_273760	heat shock protein HSP70	0	N/A	667
TGGT1_273860	hypothetical protein	0	N/A	343
TGGT1_273885	hypothetical protein	0	NN Sum: 1,	824
TGGT1_273905	hypothetical protein	0	N/A	373
TGGT1_273905	hypothetical protein	0	N/A	373
TGGT1_273950	putative replication factor C subunit 5	0	N/A	396
TGGT1_273950	putative replication factor C subunit 5	0	N/A	396
TGGT1_273960	chaperonin GroS protein	0	N/A	374
TGGT1_273960	chaperonin GroS protein	0	N/A	374
TGGT1_273960	chaperonin GroS protein	0	N/A	374
TGGT1_274060	2-oxoglutarate/malate translocase OMT	1	N/A	323
TGGT1_274060	2-oxoglutarate/malate translocase OMT	1	N/A	323
TGGT1_274060	2-oxoglutarate/malate translocase OMT	1	N/A	323
TGGT1_274100	hypothetical protein	0	NN Sum: 3,	511
TGGT1_275440	dense granule protein GRA6	2	N/A	223
TGGT1_275440	dense granule protein GRA6	2	N/A	223
TGGT1_275440	dense granule protein GRA6	2	N/A	223
TGGT1_275440	dense granule protein GRA6	2	N/A	223
TGGT1_275440	dense granule protein GRA6	2	N/A	223
TGGT1_275630	HECT-domain (ubiquitin-transferase) domain-contair	0	N/A	1709
TGGT1_275650	hypothetical protein	0	N/A	877
TGGT1_275690	putative ClpB	1	N/A	1022
TGGT1_275810	ribosomal protein RPS10	0	N/A	152
TGGT1_275810	ribosomal protein RPS10	0	N/A	152
TGGT1_275810	ribosomal protein RPS10	0	N/A	152
TGGT1_275860	hypothetical protein	1	NN Sum: 4,	383
TGGT1_276120	putative histone lysine methyltransferase, SET	0	N/A	965
TGGT1_276130	cathepsin CPC2	0	NN Sum: 2,	753
TGGT1_276170	phosphatidylinositol 3- and 4-kinase	0	N/A	1228
TGGT1_276890	hypothetical protein	0	N/A	1174
TGGT1_276890	hypothetical protein	0	N/A	1174
TGGT1_276930	hypothetical protein	0	N/A	196
TGGT1_276930	hypothetical protein	0	N/A	196
TGGT1_276940	putative ribosome associated membrane protein RA	1	N/A	68
TGGT1_277000	putative transport protein Sec24	0	N/A	1019
TGGT1_277000	putative transport protein Sec24	0	N/A	1019
TGGT1_277000	putative transport protein Sec24	0	N/A	1019
TGGT1_277000	putative transport protein Sec24	0	N/A	1019
TGGT1_277080	microneme protein MIC5	1	NN Sum: 4,	181
TGGT1_277080	microneme protein MIC5	1	NN Sum: 4,	181
TGGT1_277080	microneme protein MIC5	1	NN Sum: 4,	181

TGGT1_277080	microneme protein MIC5	1	NN Sum: 4,	181
TGGT1_277080	microneme protein MIC5	1	NN Sum: 4,	181
TGGT1_277090	carrier superfamily protein	0	N/A	885
TGGT1_277270	NTPase II	0	N/A	862
TGGT1_277270	NTPase II	0	N/A	862
TGGT1_277760	putative adenylosuccinate lyase	0	N/A	662
TGGT1_277840	Ras family protein	0	N/A	257
TGGT1_277910	thrombospondin type 1 domain-containing protein	0	NN Sum: 0,	1218
TGGT1_277920	hypothetical protein	1	N/A	90
TGGT1_278050	putative proteasome subunit alpha type 1	0	N/A	247
TGGT1_278060	Mre11 DNA-binding domain-containing protein	0	N/A	1243
TGGT1_278090	Toxoplasma gondii family A protein	0	NN Sum: 4,	478
TGGT1_278230	prenyltransferase and squalene oxidase repeat-cont	0	N/A	576
TGGT1_278390	Toxoplasma gondii family A protein	1	NN Sum: 4,	371
TGGT1_278390	Toxoplasma gondii family A protein	1	NN Sum: 4,	371
TGGT1_278490	Zn-finger, RING domain containing protein	0	N/A	289
TGGT1_278530	putative multiprotein bridging factor type 1 family tr	0	N/A	144
TGGT1_278540	hypothetical protein	0	N/A	193
TGGT1_278630	tetratricopeptide repeat-containing protein	1	N/A	981
TGGT1_278720	hypothetical protein	0	NN Sum: 0,	655
TGGT1_278720	hypothetical protein	0	NN Sum: 0,	655
TGGT1_278830	glucose-6-phosphate 1-dehydrogenase	0	N/A	878
TGGT1_278850	DHHC zinc finger domain-containing protein	4	N/A	361
TGGT1_278870	myosin F	0	N/A	1953
TGGT1_278870	myosin F	0	N/A	1953
TGGT1_278870	myosin F	0	N/A	1953
TGGT1_278950	LSM domain-containing protein	0	N/A	121
TGGT1_278950	LSM domain-containing protein	0	N/A	121
TGGT1_278950	LSM domain-containing protein	0	N/A	121
TGGT1_278990	putative phosphate carrier	1	N/A	479
TGGT1_278990	putative phosphate carrier	1	N/A	479
TGGT1_278990	putative phosphate carrier	1	N/A	479
TGGT1_278990	putative phosphate carrier	1	N/A	479
TGGT1_278990	putative phosphate carrier	1	N/A	479
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279100	hypothetical protein	1	NN Sum: 4,	435
TGGT1_279380	hypothetical protein	0	N/A	320
TGGT1_279390	putative proliferation-associated protein 2G4	0	N/A	462
TGGT1_279400	putative glutaredoxin	0	N/A	146
TGGT1_279400	putative glutaredoxin	0	N/A	146
TGGT1_279420	hypothetical protein	0	N/A	1329
TGGT1_279430	cwf18 pre-mRNA splicing factor protein	0	N/A	152
TGGT1_279450	putative adenylosuccinate synthetase	0	N/A	460
TGGT1_280370	hypothetical protein	0	N/A	761
TGGT1_280370	hypothetical protein	0	N/A	761
TGGT1_280480	EF hand domain-containing protein	4	N/A	305
TGGT1_280490	U-box domain-containing protein	0	N/A	1089

TGGT1_280490	U-box domain-containing protein	0	N/A	1089
TGGT1_280550	clathrin adaptor complex small chain subfamily prote	0	NN Sum: 0,	207
TGGT1_280610	signal recognition particle receptor alpha subunit	0	NN Sum: 3,	556
TGGT1_280610	signal recognition particle receptor alpha subunit	0	NN Sum: 3,	556
TGGT1_280660	HECT-domain (ubiquitin-transferase) domain-contai	0	N/A	17226
TGGT1_280750	putative rudimentary enhancer	0	N/A	101
TGGT1_281520	zinc finger, C3HC4 type (RING finger) domain-contai	4	N/A	369
TGGT1_281570	hypothetical protein	0	N/A	483
TGGT1_281610	hypothetical protein	0	N/A	293
TGGT1_281630	hydroxyacylglutathione hydrolase	0	NN Sum: 0,	450
TGGT1_281920	V-type ATPase, D subunit protein	0	N/A	245
TGGT1_281950	putative membrane protein	0	NN Sum: 0,	355
TGGT1_282140	cwf21 protein	0	N/A	681
TGGT1_282180	hypothetical protein	0	N/A	310
TGGT1_283510	hypothetical protein	0	N/A	314
TGGT1_283540	hypothetical protein	0	NN Sum: 4,	376
TGGT1_283550	hypothetical protein	0	N/A	4211
TGGT1_283710	longevity-assurance protein (LAG1) domain-containi	5	NN Sum: 4,	342
TGGT1_283710	longevity-assurance protein (LAG1) domain-containi	5	NN Sum: 4,	342
TGGT1_283730	endomembrane protein 70 subfamily protein	10	N/A	674
TGGT1_283780	glucose-6-phosphate isomerase GPI	1	NN Sum: 1,	661
TGGT1_283810	hypothetical protein	0	N/A	1476
TGGT1_284540	ATP synthase F1, delta subunit protein	0	N/A	252
TGGT1_284560	ribosomal protein RPL9	0	N/A	190
TGGT1_284560	ribosomal protein RPL9	0	N/A	190
TGGT1_284560	ribosomal protein RPL9	0	N/A	190
TGGT1_284560	ribosomal protein RPL9	0	N/A	190
TGGT1_284560	ribosomal protein RPL9	0	N/A	190
TGGT1_285180	hypothetical protein	1	NN Sum: 4,	632
TGGT1_285220	CAP-Gly domain-containing protein	0	N/A	781
TGGT1_285250	hypothetical protein	0	N/A	1151
TGGT1_285500	hypothetical protein	4	N/A	1899
TGGT1_285510	hypothetical protein	0	N/A	166
TGGT1_285680	putative dihydrolipoamide acyltransferase	0	N/A	470
TGGT1_285680	putative dihydrolipoamide acyltransferase	0	N/A	470
TGGT1_285680	putative dihydrolipoamide acyltransferase	0	N/A	470
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_285870	SAG-related sequence SRS20A	1	NN Sum: 3,	328
TGGT1_286090	putative translation initiation factor SUI1	0	N/A	114
TGGT1_286090	putative translation initiation factor SUI1	0	N/A	114
TGGT1_286120	prolyl endopeptidase	0	NN Sum: 0,	825
TGGT1_286120	prolyl endopeptidase	0	NN Sum: 0,	825
TGGT1_286160B	non-specific serine/threonine protein kinase	0	N/A	1844
TGGT1_286160B	non-specific serine/threonine protein kinase	0	N/A	1844
TGGT1_286210	protein phosphatase 4, catalytic subunit	0	N/A	338
TGGT1_286240	putative kelch repeat protein	0	N/A	625
TGGT1_286420A	putative elongation factor 1-alpha (EF-1-ALPHA)	0	N/A	448
TGGT1_286420A	putative elongation factor 1-alpha (EF-1-ALPHA)	0	N/A	448

TGGT1_286420A	putative elongation factor 1-alpha (EF-1-ALPHA)	0	N/A	448
TGGT1_286420A	putative elongation factor 1-alpha (EF-1-ALPHA)	0	N/A	448
TGGT1_286420A	putative elongation factor 1-alpha (EF-1-ALPHA)	0	N/A	448
TGGT1_286580	hypothetical protein	0	N/A	955
TGGT1_286580	hypothetical protein	0	N/A	955
TGGT1_286580	hypothetical protein	0	N/A	955
TGGT1_286590	microtubule associated protein SPM2	0	N/A	357
TGGT1_286590	microtubule associated protein SPM2	0	N/A	357
TGGT1_286600	hypothetical protein	0	N/A	388
TGGT1_286630	redoxin domain-containing protein	1	NN Sum: 3,	292
TGGT1_286630	redoxin domain-containing protein	1	NN Sum: 3,	292
TGGT1_286630	redoxin domain-containing protein	1	NN Sum: 3,	292
TGGT1_286720	heat shock protein HSP28	0	N/A	276
TGGT1_286920	SWIRM domain-containing protein	0	N/A	780
TGGT1_286920	SWIRM domain-containing protein	0	N/A	780
TGGT1_286920	SWIRM domain-containing protein	0	N/A	780
TGGT1_287230	inorganic anion transporter, sulfate permease (SulP)	11	N/A	675
TGGT1_287500	putative T complex chaperonin	0	N/A	556
TGGT1_288210	PUL domain-containing protein	0	NN Sum: 1,	818
TGGT1_288245	hypothetical protein	1	NN Sum: 3,	52
TGGT1_288250	hypothetical protein	0	N/A	1848
TGGT1_288360	tryptophanyl-tRNA synthetase (TrpRS2)	0	NN Sum: 1,	689
TGGT1_288380	heat shock protein HSP90	0	N/A	708
TGGT1_288380	heat shock protein HSP90	0	N/A	708
TGGT1_288500	FAD Malate-dehydrogenase (MDH-FAD)	0	NN Sum: 0,	550
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288650	dense granule protein GRA12	1	NN Sum: 4,	436
TGGT1_288685	Fe-S protein assembly co-chaperone HscB protein	0	N/A	466
TGGT1_288710	hypothetical protein	1	N/A	661
TGGT1_288830	NADH dehydrogenase (NDH2-II)	0	NN Sum: 0,	657
TGGT1_288850	hypothetical protein	2	NN Sum: 3,	99
TGGT1_288860	RuvB family 2 protein	0	N/A	508
TGGT1_288930	hypothetical protein	0	N/A	1185
TGGT1_288990	hypothetical protein	0	N/A	597
TGGT1_289080	HEAT repeat-containing protein	0	NN Sum: 0,	1202
TGGT1_289210	prefoldin subunit protein	0	N/A	330
TGGT1_289300	methionyl-tRNA synthetase	0	N/A	976
TGGT1_289300	methionyl-tRNA synthetase	0	N/A	976
TGGT1_289300	methionyl-tRNA synthetase	0	N/A	976
TGGT1_289330	ubiquitin carboxyl-terminal hydrolase family 2 protei	0	N/A	2291
TGGT1_289360	hypothetical protein	1	NN Sum: 4,	351
TGGT1_289530	ribosomal protein RPL19	0	N/A	187
TGGT1_289540	hypothetical protein	0	NN Sum: 0,	937
TGGT1_289600	heat shock protein HSP29	0	N/A	272
TGGT1_289600	heat shock protein HSP29	0	N/A	272
TGGT1_289630	microneme protein MIC16	1	NN Sum: 1,	668

TGGT1_289690	glyceraldehyde-3-phosphate dehydrogenase GAPDH	0	N/A	489
TGGT1_289690	glyceraldehyde-3-phosphate dehydrogenase GAPDH	0	N/A	489
TGGT1_289750	ribosomal-ubiquitin protein RPL40	0	N/A	129
TGGT1_289800	hypothetical protein	2	NN Sum: 2,	234
TGGT1_289880	hypothetical protein	2	N/A	1326
TGGT1_289880	hypothetical protein	2	N/A	1326
TGGT1_289960	hypothetical protein	1	N/A	607
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_289970	hypothetical protein	0	N/A	232
TGGT1_290030	hypothetical protein	1	NN Sum: 0,	229
TGGT1_290030	hypothetical protein	1	NN Sum: 0,	229
TGGT1_290030	hypothetical protein	1	NN Sum: 0,	229
TGGT1_290160	putative sortilin	1	NN Sum: 0,	1033
TGGT1_290160	putative sortilin	1	NN Sum: 0,	1033
TGGT1_290160	putative sortilin	1	NN Sum: 0,	1033
TGGT1_290200	NAD/NADP octopine/nopaline dehydrogenase, alpha	0	NN Sum: 0,	435
TGGT1_290200	NAD/NADP octopine/nopaline dehydrogenase, alpha	0	NN Sum: 0,	435
TGGT1_290260	thioredoxin family Trp26 protein	0	N/A	208
TGGT1_290290	ubiquitin-activating enzyme E1 family protein	0	N/A	1092
TGGT1_290290	ubiquitin-activating enzyme E1 family protein	0	N/A	1092
TGGT1_290290	ubiquitin-activating enzyme E1 family protein	0	N/A	1092
TGGT1_290290	ubiquitin-activating enzyme E1 family protein	0	N/A	1092
TGGT1_290290	ubiquitin-activating enzyme E1 family protein	0	N/A	1092
TGGT1_290300	hypothetical protein	0	N/A	365
TGGT1_290340	HEAT repeat-containing protein	0	N/A	442
TGGT1_290660	RNA recognition motif-containing protein	0	N/A	446
TGGT1_290660	RNA recognition motif-containing protein	0	N/A	446
TGGT1_290660	RNA recognition motif-containing protein	0	N/A	446
TGGT1_290660	RNA recognition motif-containing protein	0	N/A	446
TGGT1_290660	RNA recognition motif-containing protein	0	N/A	446
TGGT1_290670	leucyl aminopeptidase LAP	0	NN Sum: 1,	781
TGGT1_290700	hypothetical protein	0	NN Sum: 4,	312
TGGT1_290700	hypothetical protein	0	NN Sum: 4,	312
TGGT1_290700	hypothetical protein	0	NN Sum: 4,	312
TGGT1_290730	CS domain-containing protein	0	NN Sum: 2,	377
TGGT1_290730	CS domain-containing protein	0	NN Sum: 2,	377
TGGT1_290850	WD-40 repeat protein	0	N/A	521
TGGT1_290870	patched family protein	12	N/A	1178
TGGT1_290900	hydrolase, NUDIX family protein	0	NN Sum: 2,	300
TGGT1_290940	EMP/nonaspanin domain family protein	10	NN Sum: 4,	654
TGGT1_290950	putative clathrin heavy chain	0	N/A	1731
TGGT1_290950	putative clathrin heavy chain	0	N/A	1731
TGGT1_290950	putative clathrin heavy chain	0	N/A	1731
TGGT1_290950	putative clathrin heavy chain	0	N/A	1731
TGGT1_290950	putative clathrin heavy chain	0	N/A	1731
TGGT1_290980	putative glycine C-acetyltransferase	0	N/A	571

TGGT1_291010	hypothetical protein	0	N/A	216
TGGT1_291180	hypothetical protein	0	N/A	5394
TGGT1_291300	putative RER1 protein	2	N/A	222
TGGT1_291310	putative V-ATPase subunit c' proteolipid	4	N/A	205
TGGT1_291310	putative V-ATPase subunit c' proteolipid	4	N/A	205
TGGT1_291330	RNA recognition motif-containing protein	0	N/A	228
TGGT1_291330	RNA recognition motif-containing protein	0	N/A	228
TGGT1_291330	RNA recognition motif-containing protein	0	N/A	228
TGGT1_291600	gamma interferon inducible lysosomal thiol reductas	1	NN Sum: 4,	379
TGGT1_291640	aspartate carbamoyltransferase	0	N/A	423
TGGT1_291680	Sec23/Sec24 trunk domain-containing protein	0	N/A	791
TGGT1_291820	RNA helicase (UPF2 interacting domain) protein	0	N/A	1539
TGGT1_291850	ribosomal protein RPS30	0	N/A	59
TGGT1_291890	microneme protein MIC1	0	NN Sum: 4,	456
TGGT1_291890	microneme protein MIC1	0	NN Sum: 4,	456
TGGT1_291930	RNA recognition motif-containing protein	0	N/A	705
TGGT1_291950	RNA recognition motif-containing protein	0	N/A	725
TGGT1_291960	rhoptry kinase family protein ROP40 (incomplete cat	0	NN Sum: 0,	525
TGGT1_291960	rhoptry kinase family protein ROP40 (incomplete cat	0	NN Sum: 0,	525
TGGT1_291960	rhoptry kinase family protein ROP40 (incomplete cat	0	NN Sum: 0,	525
TGGT1_291960	rhoptry kinase family protein ROP40 (incomplete cat	0	NN Sum: 0,	525
TGGT1_292020	GCC2 and GCC3 domain-containing protein	9	N/A	7440
TGGT1_292020	GCC2 and GCC3 domain-containing protein	9	N/A	7440
TGGT1_292080	leucyl-tRNA synthetase	0	N/A	1261
TGGT1_292120	membrane occupation and recognition nexus protei	0	N/A	465
TGGT1_292130	ribosomal protein RPL13A	0	N/A	286
TGGT1_292130	ribosomal protein RPL13A	0	N/A	286
TGGT1_292130	ribosomal protein RPL13A	0	N/A	286
TGGT1_292200	RNA recognition motif-containing protein	0	N/A	2069
TGGT1_293180	NADP-specific glutamate dehydrogenase	0	N/A	578
TGGT1_293180	NADP-specific glutamate dehydrogenase	0	N/A	578
TGGT1_293180	NADP-specific glutamate dehydrogenase	0	N/A	578
TGGT1_293230	hypothetical protein	0	N/A	459
TGGT1_293300	Yip1 domain-containing protein	5	N/A	588
TGGT1_293300	Yip1 domain-containing protein	5	N/A	588
TGGT1_293430	hypothetical protein	4	N/A	411
TGGT1_293430	hypothetical protein	4	N/A	411
TGGT1_293430	hypothetical protein	4	N/A	411
TGGT1_293430	hypothetical protein	4	N/A	411
TGGT1_293440	hypothetical protein	4	N/A	538
TGGT1_293510	poly(ADP-ribose) polymerase and DNA-Ligase Zn-fin	0	NN Sum: 3,	392
TGGT1_293580	prefoldin subunit protein	0	N/A	170
TGGT1_293580	prefoldin subunit protein	0	N/A	170
TGGT1_293580	prefoldin subunit protein	0	N/A	170
TGGT1_293580	prefoldin subunit protein	0	N/A	170
TGGT1_293590	putative 3-oxoacyl-acyl-carrier protein synthase I/II	1	NN Sum: 4,	551
TGGT1_293590	putative 3-oxoacyl-acyl-carrier protein synthase I/II	1	NN Sum: 4,	551
TGGT1_293730	DHHC zinc finger domain-containing protein	2	NN Sum: 1,	971
TGGT1_293740	hypothetical protein	0	N/A	96
TGGT1_293770	chitinase-like protein CLP1	0	NN Sum: 3,	714
TGGT1_293770	chitinase-like protein CLP1	0	NN Sum: 3,	714
TGGT1_293770	chitinase-like protein CLP1	0	NN Sum: 3,	714

TGGT1_293870	putative thioredoxin	0	N/A	106
TGGT1_293870	putative thioredoxin	0	N/A	106
TGGT1_294050	hypothetical protein	1	NN Sum: 2,	574
TGGT1_294340	hypothetical protein	1	N/A	345
TGGT1_294340	hypothetical protein	1	N/A	345
TGGT1_294370	hypothetical protein	2	N/A	151
TGGT1_294420	programmed cell death protein 2, c-terminal domain	0	N/A	584
TGGT1_294560	rhoptry kinase family protein ROP37 (incomplete cat	0	NN Sum: 4,	776
TGGT1_294560	rhoptry kinase family protein ROP37 (incomplete cat	0	NN Sum: 4,	776
TGGT1_294620	putative eukaryotic initiation factor-3, subunit 8	0	N/A	971
TGGT1_294620	putative eukaryotic initiation factor-3, subunit 8	0	N/A	971
TGGT1_294620	putative eukaryotic initiation factor-3, subunit 8	0	N/A	971
TGGT1_294670	translation initiation factor 3 subunit	0	N/A	277
TGGT1_294710	RNA recognition motif-containing protein	0	N/A	1151
TGGT1_294730	hypothetical protein	0	N/A	2142
TGGT1_294790	hypothetical protein	0	N/A	351
TGGT1_294812	RNA recognition motif-containing protein	0	N/A	244
TGGT1_294898	tetratricopeptide repeat-containing protein	0	N/A	827
TGGT1_294898	tetratricopeptide repeat-containing protein	0	N/A	827
TGGT1_294898	tetratricopeptide repeat-containing protein	0	N/A	827
TGGT1_295000	hypothetical protein	0	N/A	1053
TGGT1_295010	DEAD/DEAH box helicase domain-containing protein	0	N/A	698
TGGT1_295110	rhoptry protein ROP7	1	NN Sum: 4,	575
TGGT1_295110	rhoptry protein ROP7	1	NN Sum: 4,	575
TGGT1_295125	rhoptry protein ROP4	1	NN Sum: 4,	365
TGGT1_295125	rhoptry protein ROP4	1	NN Sum: 4,	365
TGGT1_295320	putative embryo sac development arrest EDA7	0	N/A	627
TGGT1_295340	UV excision repair protein Rad23 protein	0	N/A	380
TGGT1_295360	hypothetical protein	0	N/A	268
TGGT1_295360	hypothetical protein	0	N/A	268
TGGT1_295450	sjoegren syndrome nuclear autoantigen 1 family pro	0	N/A	150
TGGT1_295710	HECT-domain (ubiquitin-transferase) domain-contair	0	N/A	8007
TGGT1_297060	phosphoglycerate mutase PGMII	0	N/A	339
TGGT1_297070	hypothetical protein	1	NN Sum: 4,	519
TGGT1_297120	hypothetical protein	0	N/A	760
TGGT1_297160	hypothetical protein	0	NN Sum: 4,	564
TGGT1_297270	hypothetical protein	0	NN Sum: 4,	488
TGGT1_297420	putative beta-tubulin cofactor D	0	N/A	2041
TGGT1_297500	T-complex protein 1 eta subunit	0	N/A	546
TGGT1_297650	Ser/Thr phosphatase family protein	1	NN Sum: 4,	651
TGGT1_297690	hypothetical protein	0	N/A	2132
TGGT1_297745	hypothetical protein	1	N/A	3869
TGGT1_297810	hypothetical protein	0	N/A	266
TGGT1_297880	dense granule protein DG32	1	NN Sum: 4,	219
TGGT1_297890	hypothetical protein	0	N/A	1547
TGGT1_297900	hypothetical protein	0	N/A	763
TGGT1_297960B	rhoptry neck protein RON6	0	N/A	718
TGGT1_297960B	rhoptry neck protein RON6	0	N/A	718
TGGT1_297970	aspartyl aminopeptidase	0	N/A	508
TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298610	GYF domain-containing protein	0	N/A	2331

TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298610	GYF domain-containing protein	0	N/A	2331
TGGT1_298970	LSM3, U6 small nuclear RNA associated isoform 2 far	0	N/A	96
TGGT1_298980	RNA pseudouridine synthase superfamily protein	0	N/A	884
TGGT1_299020	AP2 domain transcription factor AP2III-4	0	N/A	1644
TGGT1_299030	RNA recognition motif 2 protein	0	N/A	429
TGGT1_299050	ribosomal protein RPL17	0	N/A	195
TGGT1_299050	ribosomal protein RPL17	0	N/A	195
TGGT1_299050	ribosomal protein RPL17	0	N/A	195
TGGT1_299050	ribosomal protein RPL17	0	N/A	195
TGGT1_299570	Toxoplasma gondii family B protein	1	NN Sum: 4,	150
TGGT1_299670	hypothetical protein	0	N/A	592
TGGT1_299780	hypothetical protein	3	NN Sum: 4,	545
TGGT1_299990	archease family protein	0	N/A	293
TGGT1_300000	ribosomal protein RPL18	0	N/A	187
TGGT1_300040	ubiquitin-conjugating enzyme subfamily protein	0	N/A	240
TGGT1_300100	rhoptry neck protein RON2	3	NN Sum: 4,	1479
TGGT1_300110	hypothetical protein	0	N/A	287
TGGT1_300140	putative elongation factor 1-gamma	0	N/A	394
TGGT1_300150	hypothetical protein	0	N/A	405
TGGT1_300240	putative syntaxin 6 protein	1	N/A	237
TGGT1_300310	26S proteasome regulatory subunit, S6a family AAA	0	N/A	427
TGGT1_301120	acetyl-CoA acetyltransferase	0	N/A	413
TGGT1_301120	acetyl-CoA acetyltransferase	0	N/A	413
TGGT1_301120	acetyl-CoA acetyltransferase	0	N/A	413
TGGT1_301120	acetyl-CoA acetyltransferase	0	N/A	413
TGGT1_301440	calcium-dependent protein kinase CDPK1	0	N/A	582
TGGT1_301440	calcium-dependent protein kinase CDPK1	0	N/A	582
TGGT1_301440	calcium-dependent protein kinase CDPK1	0	N/A	582
TGGT1_301440	calcium-dependent protein kinase CDPK1	0	N/A	582
TGGT1_304670	leucine rich repeat-containing protein	0	N/A	338
TGGT1_304710	putative eukaryotic peptide chain release factor	0	N/A	814
TGGT1_304740	rhoptry kinase family protein ROP35	0	N/A	640
TGGT1_304760	RNA recognition motif-containing protein	0	N/A	1335
TGGT1_304890	hypothetical protein	4	N/A	256
TGGT1_304990	guanylate-binding protein, N-terminal domain-conta	4	N/A	1281
TGGT1_305030	kinase, pfkB family protein	0	N/A	439
TGGT1_305040	HEAT repeat-containing protein	0	N/A	1173
TGGT1_305040	HEAT repeat-containing protein	0	N/A	1173
TGGT1_305070	hypothetical protein	0	N/A	153
TGGT1_305290	putative vacuolar atp synthase subunit e	0	N/A	345
TGGT1_305290	putative vacuolar atp synthase subunit e	0	N/A	345
TGGT1_305320	mRNA capping enzyme	0	N/A	510
TGGT1_305450	acetyltransferase, GNAT family protein	1	N/A	519
TGGT1_305490	programmed cell death protein 2, c-terminal domain	0	N/A	482
TGGT1_305520	ribosomal protein RPS2	0	N/A	269
TGGT1_305600	hypothetical protein	0	N/A	246
TGGT1_305800	6-pyruvoyl tetrahydrobiopterin synthase	0	N/A	475
TGGT1_305810	hypothetical protein	1	N/A	407
TGGT1_305820	SGS domain-containing protein	0	N/A	262

TGGT1_305850	RNA recognition motif-containing protein	0	N/A	372
TGGT1_305850	RNA recognition motif-containing protein	0	N/A	372
TGGT1_305850	RNA recognition motif-containing protein	0	N/A	372
TGGT1_305850	RNA recognition motif-containing protein	0	N/A	372
TGGT1_305860	calcium-dependent protein kinase CDPK3	0	N/A	537
TGGT1_306030	glutathione s-transferase, n-terminal domain contair	0	N/A	333
TGGT1_306030	glutathione s-transferase, n-terminal domain contair	0	N/A	333
TGGT1_306060	rhoptry neck protein RON8	1	NN Sum: 4,	2980
TGGT1_306060	rhoptry neck protein RON8	1	NN Sum: 4,	2980
TGGT1_306220	hypothetical protein	0	N/A	675
TGGT1_306330	phospholipase	0	N/A	582
TGGT1_306380	U1 zinc finger protein	0	N/A	215
TGGT1_306390	hypothetical protein	0	N/A	182
TGGT1_306390	hypothetical protein	0	N/A	182
TGGT1_306410	hypothetical protein	0	N/A	1040
TGGT1_306540	phosphotransferase enzyme family protein	0	N/A	547
TGGT1_306610	3' exoribonuclease family, domain 1 domain-contain	0	N/A	392
TGGT1_306650	hypothetical protein	0	NN Sum: 2,	286
TGGT1_306650	hypothetical protein	0	NN Sum: 2,	286
TGGT1_306650	hypothetical protein	0	NN Sum: 2,	286
TGGT1_306680	hypothetical protein	2	N/A	234
TGGT1_306895	hypothetical protein	4	N/A	169
TGGT1_306910	hypothetical protein	0	NN Sum: 1,	520
TGGT1_306930	putative proteasome subunit beta type 7 precursor	0	N/A	368
TGGT1_306930	putative proteasome subunit beta type 7 precursor	0	N/A	368
TGGT1_307000	hypothetical protein	0	N/A	306
TGGT1_307570	putative glycerol-3-phosphate dehydrogenase (gpdh	0	N/A	846
TGGT1_307570	putative glycerol-3-phosphate dehydrogenase (gpdh	0	N/A	846
TGGT1_307810	hypothetical protein	0	N/A	433
TGGT1_307810	hypothetical protein	0	N/A	433
TGGT1_307810	hypothetical protein	0	N/A	433
TGGT1_307810	hypothetical protein	0	N/A	433
TGGT1_308050	thioredoxin domain-containing protein	0	N/A	198
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549
TGGT1_308090	rhoptry protein ROP5	0	NN Sum: 4,	549

TGGT1_308840	SAG-related sequence SRS51	0	N/A	360
TGGT1_308860	hypothetical protein	0	N/A	654
TGGT1_308860	hypothetical protein	0	N/A	654
TGGT1_308870	hypothetical protein	0	N/A	693
TGGT1_308870	hypothetical protein	0	N/A	693
TGGT1_308950	histidine acid phosphatase superfamily protein	0	NN Sum: 4,	598
TGGT1_308970	hypothetical protein	0	NN Sum: 4,	342
TGGT1_309010	putative elongation factor P	0	NN Sum: 0,	242
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309120	ribosomal protein RPL4	0	N/A	416
TGGT1_309210	putative peroxiredoxin 6	0	N/A	402
TGGT1_309210	putative peroxiredoxin 6	0	N/A	402
TGGT1_309210	putative peroxiredoxin 6	0	N/A	402
TGGT1_309210	putative peroxiredoxin 6	0	N/A	402
TGGT1_309560	nmda receptor glutamate-binding chain	7	N/A	265
TGGT1_309560	nmda receptor glutamate-binding chain	7	N/A	265
TGGT1_309570	DEAD/DEAH box helicase domain-containing protein	0	N/A	834
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309590	rhoptry protein ROP1	0	NN Sum: 4,	456
TGGT1_309610	hypothetical protein	2	N/A	143
TGGT1_309752	putative succinate-Coenzyme A ligase, beta subunit	0	NN Sum: 0,	498
TGGT1_309752	putative succinate-Coenzyme A ligase, beta subunit	0	NN Sum: 0,	498
TGGT1_309760	hypothetical protein	0	NN Sum: 3,	315
TGGT1_309760	hypothetical protein	0	NN Sum: 3,	315
TGGT1_309820	ribosomal protein RPL11	0	N/A	175
TGGT1_310010	rhoptry neck protein RON1	1	NN Sum: 2,	1158
TGGT1_310030	putative cyclase-associated protein	0	N/A	203
TGGT1_310030	putative cyclase-associated protein	0	N/A	203
TGGT1_310050	RNA recognition motif-containing protein	0	N/A	420
TGGT1_310050	RNA recognition motif-containing protein	0	N/A	420
TGGT1_310060	small nuclease	0	N/A	367
TGGT1_310070	putative methyltransferase	0	N/A	224
TGGT1_310070	putative methyltransferase	0	N/A	224
TGGT1_310080	AMP-binding enzyme domain-containing protein	0	N/A	789
TGGT1_310150	AMP-binding enzyme domain-containing protein	0	N/A	866
TGGT1_310235	hypothetical protein	1	N/A	284
TGGT1_310290	regulator of chromosome condensation (RCC1) repe	0	N/A	759
TGGT1_310320	calreticulin family protein	2	NN Sum: 2,	578
TGGT1_310320	calreticulin family protein	2	NN Sum: 2,	578

TGGT1_310320	calreticulin family protein	2	NN Sum: 2,	578
TGGT1_310360	hypothetical protein	3	N/A	224
TGGT1_310360	hypothetical protein	3	N/A	224
TGGT1_310430A	Hsp90 domain-containing protein	0	N/A	686
TGGT1_310430A	Hsp90 domain-containing protein	0	N/A	686
TGGT1_310640	phosphorylase family protein	0	N/A	303
TGGT1_310670	putative glycogen phosphorylase 1	0	N/A	912
TGGT1_310670	putative glycogen phosphorylase 1	0	N/A	912
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310780	dense granule protein GRA4	0	NN Sum: 4,	345
TGGT1_310790	hypothetical protein	0	NN Sum: 4,	219
TGGT1_310840	hypothetical protein	2	N/A	218
TGGT1_310850	MYND finger domain-containing protein	0	N/A	253
TGGT1_310860	U5 snRNP-specific protein	0	NN Sum: 1,	367
TGGT1_310900	AP2 domain transcription factor AP2XI-2	0	N/A	2243
TGGT1_310950	AP2 domain transcription factor AP2XI-3	0	N/A	1399
TGGT1_311160	PWI domain-containing protein	0	N/A	315
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311230	hypothetical protein	1	N/A	4603
TGGT1_311240	putative DnaJ family chaperone	0	N/A	426
TGGT1_311260	putative myosin light chain MLC1	0	N/A	137
TGGT1_311310	protein phosphatase 2B catalytic subunit, calcineurir	0	N/A	501
TGGT1_311400	WD domain, G-beta repeat-containing protein	0	N/A	1585
TGGT1_311400	WD domain, G-beta repeat-containing protein	0	N/A	1585
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699

TGGT1_311470	rhoptry neck protein RON5	0	NN Sum: 3,	1699
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311480	hypothetical protein	0	N/A	386
TGGT1_311500	ThiF family protein	0	NN Sum: 1,	845
TGGT1_311680	FUN14 family protein	0	N/A	184
TGGT1_311690	UBA/TS-N domain-containing protein	0	N/A	417
TGGT1_311690	UBA/TS-N domain-containing protein	0	N/A	417
TGGT1_311690	UBA/TS-N domain-containing protein	0	N/A	417
TGGT1_311720	chaperonin protein BiP	1	NN Sum: 4,	668
TGGT1_311720	chaperonin protein BiP	1	NN Sum: 4,	668
TGGT1_311770	hypothetical protein	0	N/A	2076
TGGT1_311840	hypothetical protein	4	N/A	233
TGGT1_311880	hypothetical protein	0	N/A	728
TGGT1_312100	plasma membrane-type Ca(2+)-ATPase A1 PMCAA1	11	N/A	1822
TGGT1_312200	serine/threonine protein phosphatase	0	N/A	548
TGGT1_312200	serine/threonine protein phosphatase	0	N/A	548
TGGT1_312260	hypothetical protein	0	N/A	904
TGGT1_312270	rhoptry protein ROP13	1	NN Sum: 4,	400
TGGT1_312270	rhoptry protein ROP13	1	NN Sum: 4,	400
TGGT1_312270	rhoptry protein ROP13	1	NN Sum: 4,	400
TGGT1_312270	rhoptry protein ROP13	1	NN Sum: 4,	400
TGGT1_312270	rhoptry protein ROP13	1	NN Sum: 4,	400
TGGT1_312400	putative exosomal 3'-5' exoribonuclease complex sul	0	N/A	275
TGGT1_312420	hypothetical protein	0	NN Sum: 2,	1086
TGGT1_312420	hypothetical protein	0	NN Sum: 2,	1086
TGGT1_312470	hypothetical protein	2	N/A	151
TGGT1_312480	putative uracil phosphoribosyltransferase FUR1	0	N/A	244
TGGT1_312530	splicing factor, CC1 family protein	0	N/A	633
TGGT1_312600	heat shock protein HSP21	0	N/A	195
TGGT1_312600	heat shock protein HSP21	0	N/A	195
TGGT1_312600	heat shock protein HSP21	0	N/A	195
TGGT1_312600	heat shock protein HSP21	0	N/A	195
TGGT1_312600	heat shock protein HSP21	0	N/A	195
TGGT1_312622	DUF803 domain-containing protein	10	N/A	814
TGGT1_312622	DUF803 domain-containing protein	10	N/A	814
TGGT1_312940	hypothetical protein	1	N/A	109
TGGT1_313080	hypothetical protein	1	NN Sum: 4,	455
TGGT1_313100	signal recognition particle SRP54 protein	0	N/A	582
TGGT1_313100	signal recognition particle SRP54 protein	0	N/A	582
TGGT1_313140	isocitrate dehydrogenase	0	NN Sum: 2,	621
TGGT1_313140	isocitrate dehydrogenase	0	NN Sum: 2,	621
TGGT1_313140	isocitrate dehydrogenase	0	NN Sum: 2,	621
TGGT1_313140	isocitrate dehydrogenase	0	NN Sum: 2,	621
TGGT1_313140	isocitrate dehydrogenase	0	NN Sum: 2,	621
TGGT1_313150	DUF89/Fructose bisphosphatase	0	N/A	551
TGGT1_313230	eukaryotic initiation factor-2, alpha subunit	0	N/A	347
TGGT1_313270	hypothetical protein	0	N/A	2799
TGGT1_313270	hypothetical protein	0	N/A	2799

TGGT1_313270	hypothetical protein	0	N/A	2799
TGGT1_313270	hypothetical protein	0	N/A	2799
TGGT1_313370	hypothetical protein	0	N/A	1687
TGGT1_313370	hypothetical protein	0	N/A	1687
TGGT1_313370	hypothetical protein	0	N/A	1687
TGGT1_313370	hypothetical protein	0	N/A	1687
TGGT1_313370	hypothetical protein	0	N/A	1687
TGGT1_313390	ribosomal protein RPL6	0	N/A	322
TGGT1_313390	ribosomal protein RPL6	0	N/A	322
TGGT1_313390	ribosomal protein RPL6	0	N/A	322
TGGT1_313560	putative 60S ribosomal protein L7a	0	N/A	173
TGGT1_313560	putative 60S ribosomal protein L7a	0	N/A	173
TGGT1_313560	putative 60S ribosomal protein L7a	0	N/A	173
TGGT1_313640	hypothetical protein	1	NN Sum: 2,	201
TGGT1_313690	Sel1 repeat-containing protein	0	NN Sum: 4,	1012
TGGT1_313780	hypothetical protein	0	N/A	463
TGGT1_313910	RNA recognition motif 2 protein	0	N/A	903
TGGT1_314000	putative peptide methionine sulfoxide reductase ms	0	N/A	242
TGGT1_314070	hypothetical protein	0	N/A	205
TGGT1_314070	hypothetical protein	0	N/A	205
TGGT1_314070	hypothetical protein	0	N/A	205
TGGT1_314090	proteasome beta subunit	0	N/A	205
TGGT1_314090	proteasome beta subunit	0	N/A	205
TGGT1_314100	tetratricopeptide repeat-containing protein	0	N/A	580
TGGT1_314400	putative pyruvate dehydrogenase E1 component, be	0	NN Sum: 0,	423
TGGT1_314430	serine/threonine specific protein phosphatase	0	N/A	479
TGGT1_314740	PSP protein	0	N/A	758
TGGT1_314740	PSP protein	0	N/A	758
TGGT1_314790	putative small nuclear ribonucleoprotein G	0	N/A	93
TGGT1_314790	putative small nuclear ribonucleoprotein G	0	N/A	93
TGGT1_314810	ribosomal protein RPL7	0	N/A	258
TGGT1_314860	zinc knuckle domain-containing protein	0	NN Sum: 0,	723
TGGT1_314900	LisH protein	0	N/A	468
TGGT1_315110	prefoldin, alpha subunit protein	0	NN Sum: 0,	178
TGGT1_315150	putative eukaryotic initiation factor-4E	0	N/A	455
TGGT1_315220	rhoptry protein ROP14	9	N/A	1061
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315270	hypothetical protein	0	N/A	780
TGGT1_315490	rhoptry protein ROP10	0	NN Sum: 2,	586
TGGT1_315570	hypothetical protein	0	N/A	91
TGGT1_315670	HEAT repeat-containing protein	0	N/A	766
TGGT1_315750	hypothetical protein	0	N/A	231
TGGT1_315770	cytochrome p450 superfamily protein	1	N/A	553
TGGT1_315780	putative myosin regulatory light chain	0	N/A	206
TGGT1_315930	putative integral membrane protein, DUF56 family p	0	N/A	157
TGGT1_315930	putative integral membrane protein, DUF56 family p	0	N/A	157

TGGT1_315930	putative integral membrane protein, DUF56 family p	0	N/A	157
TGGT1_316090	RNAse P Rpr2/Rpp21 subunit domain-containing pro	0	NN Sum: 0,	648
TGGT1_316230	putative SAC1 phosphoinositide phosphatase	3	N/A	1000
TGGT1_316250	hypothetical protein	0	NN Sum: 2,	394
TGGT1_316330	superoxide dismutase SOD2	0	NN Sum: 4,	287
TGGT1_316330	superoxide dismutase SOD2	0	NN Sum: 4,	287
TGGT1_316350	hypothetical protein	0	N/A	391
TGGT1_316360	hypothetical protein	0	NN Sum: 0,	196
TGGT1_316400B	alpha tubulin TUBA1	0	N/A	432
TGGT1_316400B	alpha tubulin TUBA1	0	N/A	432
TGGT1_316600	hypothetical protein	1	N/A	131
TGGT1_316650	hypothetical protein	0	N/A	1278
TGGT1_316890	hypothetical protein	0	NN Sum: 4,	407
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_317720	putative eukaryotic translation initiation factor 3 sub	0	N/A	609
TGGT1_318160	MSP (Major sperm protein) domain-containing prote	1	N/A	239
TGGT1_318170	hypothetical protein	0	N/A	411
TGGT1_318230	phosphoglycerate kinase PGKI	0	N/A	417
TGGT1_318230	phosphoglycerate kinase PGKI	0	N/A	417
TGGT1_318275	peptidyl-prolyl cis-trans isomerase, FKBP-type domai	0	NN Sum: 3,	571
TGGT1_318410	putative TCP-1 chaperonin	0	N/A	537
TGGT1_318410	putative TCP-1 chaperonin	0	N/A	537
TGGT1_318440	helicase associated domain (ha2) protein	0	N/A	2234
TGGT1_318440	helicase associated domain (ha2) protein	0	N/A	2234
TGGT1_318710	ATP-binding cassette sub-family F member 1	0	N/A	811
TGGT1_318710	ATP-binding cassette sub-family F member 1	0	N/A	811
TGGT1_318720	pyridoxal phosphate enzyme, YggS family protein	0	N/A	548
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319560	microneme protein MIC3	0	NN Sum: 4,	383
TGGT1_319570	WD domain, G-beta repeat-containing protein	0	N/A	690
TGGT1_319658	CBF/Mak21 family protein	0	N/A	674
TGGT1_319730	YOU2 family C2C2 zinc finger protein	0	N/A	149
TGGT1_319730	YOU2 family C2C2 zinc finger protein	0	N/A	149
TGGT1_319850	splicing factor U2AF family SnRNP auxilary factor larg	0	N/A	495
TGGT1_319850	splicing factor U2AF family SnRNP auxilary factor larg	0	N/A	495

TGGT1_319850	splicing factor U2AF family SnRNP auxilary factor larg	0	N/A	495
TGGT1_319850	splicing factor U2AF family SnRNP auxilary factor larg	0	N/A	495
TGGT1_319900	hypothetical protein	0	N/A	2426
TGGT1_319910	WD domain, G-beta repeat-containing protein	0	N/A	535
TGGT1_319920	2-oxo acid dehydrogenases acyltransferase (catalytic	0	NN Sum: 1,	669
TGGT1_320000	SCY kinase (incomplete catalytic triad)	0	N/A	1014
TGGT1_320020	transporter, major facilitator family protein	12	N/A	588
TGGT1_320020	transporter, major facilitator family protein	12	N/A	588
TGGT1_320020	transporter, major facilitator family protein	12	N/A	588
TGGT1_320030	hypothetical protein	0	N/A	752
TGGT1_320030	hypothetical protein	0	N/A	752
TGGT1_320100	RNA recognition motif-containing protein	0	N/A	1216
TGGT1_320100	RNA recognition motif-containing protein	0	N/A	1216
TGGT1_320110	proliferating cell nuclear antigen PCNA2	0	N/A	287
TGGT1_320130	hypothetical protein	0	N/A	239
TGGT1_320130	hypothetical protein	0	N/A	239
TGGT1_320140	putative ubiquinol-cytochrome c reductase hinge pr	0	N/A	89
TGGT1_320180	SAG-related sequence SRS16C	1	NN Sum: 1,	398
TGGT1_320200	SAG-related sequence SRS16A	1	NN Sum: 3,	396
TGGT1_320210	WD domain, G-beta repeat domain containing prote	0	N/A	515
TGGT1_320220	putative ubiquinol cytochrome c oxidoreductase	0	N/A	487
TGGT1_320300	putative SWI2/SNF2 Brahma	0	N/A	1628
TGGT1_320440A	hypothetical protein	1	NN Sum: 4,	599
TGGT1_320570	putative elongation factor Tu	0	N/A	586
TGGT1_320570	putative elongation factor Tu	0	N/A	586
TGGT1_320610	hypothetical protein	0	N/A	771
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321500	RNA recognition motif-containing protein	0	N/A	475
TGGT1_321530	cathepsin CPL	1	N/A	422
TGGT1_321530	cathepsin CPL	1	N/A	422
TGGT1_321530	cathepsin CPL	1	N/A	422
TGGT1_321650	hypothetical protein	1	N/A	1375
TGGT1_321660	putative mannosyltransferase	6	N/A	768
TGGT1_321680	hypothetical protein	0	N/A	372
TGGT1_321680	hypothetical protein	0	N/A	372
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_324600	heat shock protein	0	N/A	185
TGGT1_356400	cAMP-dependent protein kinase	0	NN Sum: 4,	306
TGGT1_356400	cAMP-dependent protein kinase	0	NN Sum: 4,	306
TGGT1_359190	leucine rich repeat protein	0	N/A	498

TGGT1_361650	proteasome/cyclosome repeat protein	0	NN Sum: 0,	167
TGGT1_361650	proteasome/cyclosome repeat protein	0	NN Sum: 0,	167
TGGT1_361650	proteasome/cyclosome repeat protein	0	NN Sum: 0,	167
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363030	rhoptry protein ROP8	1	NN Sum: 4,	561
TGGT1_363940	putative transmembrane protein	2	N/A	490
TGGT1_411760	actin	0	N/A	287
TGGT1_411760	actin	0	N/A	287
TGGT1_411760	actin	0	N/A	287
TGGT1_411760	actin	0	N/A	287
TGGT1_411760	actin	0	N/A	287
TGGT1_411760	actin	0	N/A	287

Confidence	Annotated Sequence	Modifications	Modifications in Master Proteins
High	[R].CPLCLVDNYDFR.[G]	2xCarbamidomethyl [C1; C4]	
High	[L].DAATPLPTAPAGTGAVFHSR.[L]	1xTMT6plex [N-Term]	
High	[S].ALQTFGADQR.[L]	1xTMT6plex [N-Term]	
High	[M].ATHFLSGNGPAAR.[V]	1xAcetyl [N-Term]	TGGT1_200
High	[M].VVLGLVGPLQSGKR.[S]	2xTMT6plex [N-Term; K13]	
High	[N].MEGSQALGKPNLR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_201
High	[M].AAVSSFSSTSAR.[A]	1xAcetyl [N-Term]	TGGT1_201
High	[S].ESAASTIKHER.[D]	2xTMT6plex [N-Term; K8]	
High	[R].AAVVSGLANENGLWR.[R]	1xTMT6plex [N-Term]	
High	[A].SHGTTFQDAGAR.[A]	1xTMT6plex [N-Term]	
High	[A].SHGTTFQDAGAR.[A]	1xAcetyl [N-Term]	TGGT1_201
High	[G].TTFQDAGAR.[A]	1xTMT6plex [N-Term]	
High	[-].MQSFQKPENALKR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K6;	TGGT1_201
High	[L].SEHLSAGKEGR.[D]	2xTMT6plex [N-Term; K8]	
High	[A].LSEHLSAGKEGR.[D]	2xTMT6plex [N-Term; K9]	
High	[M].AAPATLSTFETSHAGCLHSVEFDFFATR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_201
High	[K].MEPWKQKVPQCLSLHGSNSLR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_201
High	[G].WSIVDALR.[K]	1xTMT6plex [N-Term]	
High	[G].GWSIVDALR.[K]	1xAcetyl [N-Term]	TGGT1_201
High	[G].GGWSIVDALR.[K]	1xAcetyl [N-Term]	TGGT1_201
High	[W].SIVDALR.[K]	1xTMT6plex [N-Term]	
High	[F].IEDGDQAAMEEDDFDFEGMNDEQAQELANSL	1xTMT6plex [N-Term]	
High	[L].ASESSAAGSKVAKSLPGIR.[F]	3xTMT6plex [N-Term; K10; K13]	
High	[K].MFLVSDGASAAKKR.[T]	1xAcetyl [N-Term]; 2xTMT6plex [K12	TGGT1_202
High	[A].LETAAFVPR.[R]	1xAcetyl [N-Term]	TGGT1_202
High	[S].EAGLEDVDAIR.[V]	1xTMT6plex [N-Term]	
High	[M].AENGGVGLAGTAPDDSRPLIFFCTGNANKLAE	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_202
High	[M].TAPGVVEPLLER.[C]	1xAcetyl [N-Term]	TGGT1_202
High	[-].MNIATDEFGNPFIILR.[E]	1xAcetyl [N-Term]	TGGT1_202
High	[M].ATPFLPLDSGLR.[L]	1xAcetyl [N-Term]	TGGT1_202
High	[A].WHLPEGGSTR.[G]	1xTMT6plex [N-Term]	
High	[S].VLTAEHLGR.[G]	1xTMT6plex [N-Term]	
High	[-].MYFTYVVRPGEAPEGR.[G]	1xTMT6plex [N-Term]	
High	[-].MYFTYVVRPGEAPEGR.[G]	1xAcetyl [N-Term]	TGGT1_202
High	[-].MFLTYVVRPGEAPEGR.[G]	1xAcetyl [N-Term]	TGGT1_202
High	[-].MFLTYVVR.[P]	1xAcetyl [N-Term]	TGGT1_202
High	[A].HSDVWGLR.[R]	1xTMT6plex [N-Term]	
High	[F].SRPPVGFENFYPQR.[S]	1xTMT6plex [N-Term]	
High	[R].SLGHYNPDVIR.[H]	1xTMT6plex [N-Term]	
High	[G].AALQPKAGPAPEYR.[R]	2xTMT6plex [N-Term; K6]	
High	[S].GAALQPKAGPAPEYR.[R]	2xTMT6plex [N-Term; K7]	
High	[L].SGAALQPKAGPAPEYR.[R]	2xTMT6plex [N-Term; K8]	
High	[A].GTSPGSMVNSAQAGAAAATAILAGR.[T]	1xTMT6plex [N-Term]	
High	[T].SMAGTSPGSMVNSAQAGAAAATAILAGR.[T]	1xTMT6plex [N-Term]	
High	[A].AATAILAGR.[T]	1xTMT6plex [N-Term]	
High	[M].SDPNQPTHVTVTVHGAR.[E]	1xAcetyl [N-Term]	TGGT1_202

High	[D].PNQPTHVTVTVHGAR.[E]		
High	[M].VLAPHPSPQNQLLPMQPALR.[V]	1xTMT6plex [N-Term]	
High	[Q].SLPVDKLEEER.[R]	2xTMT6plex [N-Term; K6]	
High	[A].GLSEEFASHLAGR.[Q]	1xTMT6plex [N-Term]	
High	[L].LSVSADAHRPEQFGGDSPR.[Q]	1xTMT6plex [N-Term]	
High	[L].SEEFASHLAGR.[Q]	1xTMT6plex [N-Term]	
High	[-].MHSSSVEPGAPPTPGPSYR.[S]	1xAcetyl [N-Term]	TGGT1_202
High	[M].GTLKAPDR.[L]	2xTMT6plex [N-Term; K4]	
High	[M].ASGAPDKEKTVHLR.[K]	3xTMT6plex [N-Term; K7; K9]	
High	[-].MEHFFLQKGADEEER.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_203
High	[M].APAAPNKEPTR.[R]	2xTMT6plex [N-Term; K7]	
High	[A].PAAPNKEPTR.[R]	2xTMT6plex [N-Term; K6]	
High	[P].AAPNKEPTR.[R]	2xTMT6plex [N-Term; K5]	
High	[T].SMDKASVESQLPR.[R]	2xTMT6plex [N-Term; K4]	
High	[K].GTDDHLTTSMDKASVESQLPR.[R]	2xTMT6plex [N-Term; K12]	
High	[V].DSKGTDDHLTTSMDKASVESQLPR.[R]	3xTMT6plex [N-Term; K3; K15]	
High	[A].ATASDDELMSR.[I]	1xAcetyl [N-Term]	TGGT1_203
High	[E].TEPDEQEEVHFR.[K]	1xTMT6plex [N-Term]	
High	[A].SDDELMSR.[I]	1xTMT6plex [N-Term]	
High	[T].DDNIYEEHTDR.[K]	1xTMT6plex [N-Term]	
High	[R].SDAEVTDDNIYEEHTDR.[K]	1xTMT6plex [N-Term]	
High	[M].DKASVESQLPR.[R]	2xTMT6plex [N-Term; K2]	
High	[R].REPLETEPDEQEEVHFR.[K]	1xTMT6plex [N-Term]	
High	[R].SDAEVTDDNIYEEHTDR.[K]		
High	[A].ATASDDELMSR.[I]	1xAcetyl [N-Term]; 1xOxidation [M9	TGGT1_203
High	[D].SKGTDDHLTTSMDKASVESQLPR.[R]	3xTMT6plex [N-Term; K2; K14]	
High	[P].LETEPDEQEEVHFR.[K]	1xTMT6plex [N-Term]	
High	[A].ATASDDELMSR.[I]	1xTMT6plex [N-Term]	
High	[M].PKESALNSR.[E]	2xTMT6plex [N-Term; K2]	
High	[M].AAPHEREPCPAGDVSR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_203
High	[-].MEANVPSLQHSGMPLLPPGLQGR.[N]	1xAcetyl [N-Term]	TGGT1_203
High	[M].VNVPKLR.[N]	2xTMT6plex [N-Term; K5]	
High	[-].MVNVPKLR.[N]	2xTMT6plex [N-Term; K6]	
High	[M].VTKAGSPSEDGPSR.[K]	2xTMT6plex [N-Term; K3]	
High	[A].AVLPIPSAPPLR.[A]	1xTMT6plex [N-Term]	
High	[-].MQLQQAVR.[S]	1xAcetyl [N-Term]	TGGT1_203
High	[V].SNVEEKAGDR.[G]	2xTMT6plex [N-Term; K6]	
High	[Y].ATIVGHSDDGSKTR.[I]	2xTMT6plex [N-Term; K12]	
High	[S].GTYATIVGHSDDGSKTR.[I]	2xTMT6plex [N-Term; K15]	
High	[A].MNPVEHPHGGGNHQHIGHPSTVSR.[M]	1xTMT6plex [N-Term]	
High	[S].NVEEKAGDR.[G]	2xTMT6plex [N-Term; K5]	
High	[M].AAPGQKVGLIAAR.[R]	2xTMT6plex [N-Term; K6]	
High	[T].SFLSHHGEYQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K20]	
High	[S].HHGEYQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K16]	
High	[R].VVKELNGHVDVLR.[E]	2xTMT6plex [N-Term; K3]	
High	[F].LSHHGEYQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K18]	
High	[H].GEYQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K14]	
High	[E].YQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K12]	
High	[A].WDIITTGEPNMGSR.[R]	1xTMT6plex [N-Term]	
High	[E].NIPVAELEPQDLDR.[E]	1xTMT6plex [N-Term]	
High	[S].ENIPVAELEPQDLDR.[E]	1xTMT6plex [N-Term]	
High	[V].NTSSKGSNDPLLDR.[L]	2xTMT6plex [N-Term; K5]	

High	[L].SSPPTEHSTAQPPKHENDAR.[E]	2xTMT6plex [N-Term; K14]	
High	[T].AQPPKHENDAREEEPPTDEDDFSSVK.[G]	3xTMT6plex [N-Term; K5; K26]	
High	[S].SPPTEHSTAQPPKHENDAR.[E]	2xTMT6plex [N-Term; K13]	
High	[T].AQPPKHENDAR.[E]	2xTMT6plex [N-Term; K5]	
High	[K].GAWDIITTGEPNMGSR.[R]	1xTMT6plex [N-Term]	
High	[R].SDDDDDEETKTSFVETALHSDLAQR.[V]	1xTMT6plex [K10]	
High	[L].NVKGAWDIITTGEPNMGSR.[R]	2xTMT6plex [N-Term; K3]	
High	[R].SDDDDDEETKTSF.[V]	1xTMT6plex [K10]	
High	[T].YNLIKEIR.[K]	2xTMT6plex [N-Term; K5]	
High	[K].YADDDIR.[Q]	1xTMT6plex [N-Term]	
High	[FQY].NLLKELR.[DRK]	2xTMT6plex [N-Term; K4]	
High	[T].SSKGSNDPLLDR.[L]	2xTMT6plex [N-Term; K3]	
High	[L].SHHGEYQNPTSTYNLIKEIR.[K]	2xTMT6plex [N-Term; K17]	
High	[T].APDDDFDFLFEDDTPKKPK.[S]	3xTMT6plex [N-Term; K17; K]	
High	[S].LSPDSSKEDAMLLSAIGGIGPTESR.[L]	2xTMT6plex [N-Term; K7]	
High	[A].APGAPAQGSFASYPGVIGPSR.[G]	1xTMT6plex [N-Term]	
High	[A].AGAKISPSEMSR.[L]	2xTMT6plex [N-Term; K4]	
High	[G].VSEGVVVPVR.[F]	1xTMT6plex [N-Term]	
High	[D].SPKTSEASIRPHGFLQER.[K]	2xTMT6plex [N-Term; K3]	
High	[T].EDDKSAASIVR.[G]	2xTMT6plex [N-Term; K4]	
High	[F].LDSPKTSEASIRPHGFLQER.[K]	2xTMT6plex [N-Term; K5]	
High	[E].TTEDDKSAASIVR.[G]	2xTMT6plex [N-Term; K6]	
High	[S].EGVVVPVR.[F]	1xTMT6plex [N-Term]	
High	[T].GVDKSIAAR.[E]	2xTMT6plex [N-Term; K4]	
High	[M].GALETYSSRPHSGDR.[S]	1xTMT6plex [N-Term]	
High	[D].VAAQGTPPSLAGQSPPR.[T]	1xTMT6plex [N-Term]	
High	[N].MEKLPTIILPGGKAVDETPLSGR.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_205
High	[M].ADTAAVPGGSSGGGPAGDAQAPPQQSFLGR.[	1xAcetyl [N-Term]	TGGT1_205
High	[S].AADSSSRPR.[L]	1xTMT6plex [N-Term]	
High	[M].AAVVSEESSQKVLR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_205
High	[M].AATVLATETQPR.[S]	1xAcetyl [N-Term]	TGGT1_205
High	[T].VAPSDTQSNAHVPEKR.[N]	2xTMT6plex [N-Term; K15]	
High	[T].VVTPEVGEPSGTKVDISR.[E]	2xTMT6plex [N-Term; K13]	
High	[M].SDVESVADEVVAPVEEEEEVKDLMTAIR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K21	TGGT1_205
High	[Q].MEQLFSEVHR.[K]	1xAcetyl [N-Term]	TGGT1_205
High	[F].LSTPEDLLGVR.[S]	1xAcetyl [N-Term]	TGGT1_205
High	[-].MIRPQGPVLVLKQNTKR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K12	TGGT1_205
High	[-].MIRPQGPVLVLKQN.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_205
High	[M].VNFSVEQMR.[E]	1xTMT6plex [N-Term]	
High	[-].MVNFSVEQMR.[E]	1xAcetyl [N-Term]	TGGT1_205
High	[I].DFTVSDPVVSYR.[E]	1xTMT6plex [N-Term]	
High	[L].HVEICLKDLR.[D]	2xTMT6plex [N-Term; K7]; 1xCarbamidomethyl	
High	[-].MLVLVETPAGYGLFR.[V]	1xTMT6plex [N-Term]	
High	[-].MLVLVETPAGY.[G]	1xTMT6plex [N-Term]	
High	[M].ASTKSGALPLFWSAAELAANPR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_205
High	[F].ADVVPKTAENFR.[A]	2xTMT6plex [N-Term; K6]	
High	[P].PAGDVATEAPEKR.[Q]	2xTMT6plex [N-Term; K12]	
High	[P].AGDVATEAPEKR.[Q]	2xTMT6plex [N-Term; K11]	
High	[M].APPAGDVATEAPEKR.[Q]	2xTMT6plex [N-Term; K14]	
High	[A].PPAGDVATEAPEKR.[Q]	2xTMT6plex [N-Term; K13]	
High	[R].SKPELTER.[F]	2xTMT6plex [N-Term; K2]	
High	[M].TSVAVSSHSPKPAPQSQSSVR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_206

High	[M].TSVAVSSHSPKPAPQSQSSVR.[S]	2xTMT6plex [N-Term; K11]	
High	[S].SHSPKPAPQSQSSVR.[S]	2xTMT6plex [N-Term; K5]	
High	[A].VSSHSPKPAPQSQSSVR.[S]	2xTMT6plex [N-Term; K7]	
High	[V].SSHSPKPAPQSQSSVR.[S]	2xTMT6plex [N-Term; K6]	
High	[S].AFPLPPVLACNVAATVALTPR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10	
High	[A].HQPFASLPPAPQLPQEPR.[V]	1xTMT6plex [N-Term]	
High	[G].QSPTVASPSGAAPKRPAPPAGPR.[D]	2xTMT6plex [N-Term; K14]	
High	[R].RGDGQSPTVASPSGAAPKRPAPPAGPR.[D]	2xTMT6plex [N-Term; K18]	
High	[G].AAPKRPAPPAGPR.[D]	2xTMT6plex [N-Term; K4]	
High	[S].QSPAASVKGAGAPPLPLAHQPFASLPPAPQLPQ	2xTMT6plex [N-Term; K8]	
High	[M].ALPSTPAVDR.[S]	1xAcetyl [N-Term]	TGGT1_206
High	[A].TLSPQPYTPTPESHR.[G]	1xTMT6plex [N-Term]	
High	[L].DLPHYPGGGGPDGDGDR.[G]	1xTMT6plex [N-Term]	
High	[A].SVLESEGGEDREEEEREVEYGTGLHEGR.[L]	1xTMT6plex [N-Term]	
High	[M].ADYRPCLHQAINLHAGR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_206
High	[M].APTTPSPCLLNDIASSR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[A].PTTPSPCLLNDIASSR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[P].TTPSPCLLNDIASSR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].GEDEGVAAGAAPTDALQER.[R]	1xTMT6plex [N-Term]	
High	[M].ATDSSSGLSLPPKNAELR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_207
High	[-].MLSQFYVLSPR.[G]	1xAcetyl [N-Term]	TGGT1_207
High	[M].ASPCATTFEPLPERPDFPKEEER.[I]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_207
High	[-].MQPEEFAAAAR.[G]	1xAcetyl [N-Term]	TGGT1_207
High	[M].TSVTAVASGSPPAADDSAKKLEELAAR.[A]	3xTMT6plex [N-Term; K19; K20]	
High	[M].TSVTAVASGSPPAADDSAKKLEELAAR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K19	TGGT1_207
High	[-].MTSVTAVASGSPPAADDSAKKLEELAAR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K20	TGGT1_207
High	[T].AVASGSPPAADDSAKKLEELAAR.[A]	3xTMT6plex [N-Term; K15; K16]	
High	[A].TITVDQDTADMLR.[A]	1xTMT6plex [N-Term]	
High	[I].SLKLQEEER.[E]	2xTMT6plex [N-Term; K3]	
High	[I].SLKLQEEERER.[R]	2xTMT6plex [N-Term; K3]	
High	[S].LKLQEEER.[E]	2xTMT6plex [N-Term; K2]	
High	[A].AGETHVVIPSHQEGR.[H]	1xAcetyl [N-Term]	TGGT1_207
High	[A].AGETHVVIPSHQEGR.[H]	1xTMT6plex [N-Term]	
High	[D].ITPAGDDVSANVTSSEPAKLDLSCVHSDNKGSR.	3xTMT6plex [N-Term; K19; K30]; 1xCarbamidom	
High	[L].DLSCVHSDNKGSR.[A]	2xTMT6plex [N-Term; K10]; 1xCarbamidomethy	
High	[N].VTSSEPAKLDLSCVHSDNKGSR.[A]	3xTMT6plex [N-Term; K8; K19]; 1xCarbamidome	
High	[K].LDLSCVHSDNKGSR.[A]	2xTMT6plex [N-Term; K11]; 1xCarbamidomethy	
High	[S].SEPAKLDLSCVHSDNKGSR.[A]	3xTMT6plex [N-Term; K5; K16]; 1xCarbamidome	
High	[S].EPAKLDLSCVHSDNKGSR.[A]	3xTMT6plex [N-Term; K4; K15]; 1xCarbamidome	
High	[F].TDITPAGDDVSANVTSSEPAKLDLSCVHSDNKG	3xTMT6plex [N-Term; K21; K32]; 1xCarbamidom	
High	[D].ITPAGDDVSANVTSSEPAK.[L]	1xTMT6plex [N-Term]	
High	[T].SSEPAKLDLSCVHSDNKGSR.[A]	3xTMT6plex [N-Term; K6; K17]; 1xCarbamidome	
High	[M].GDPVEQWLEDCLTLPGKLQR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_208
High	[M].SSSGHQGTDEPHLPSR.[L]	1xAcetyl [N-Term]	TGGT1_208
High	[L].SSSAILTGQQIGTYR.[Q]	1xAcetyl [N-Term]	TGGT1_208
High	[-].MEAVCAIHELFSSCR.[G]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_208
High	[A].ASPMLFTDYDNTASPKSELIFMAGNALGYCTER	2xTMT6plex [N-Term; K16]; 1xCarbamidomethy	
High	[A].SPETKVCSCPR.[N]	2xTMT6plex [N-Term; K5]; 2xCarbamidomethyl [	
High	[A].DTTEQPSITPSGEEDRPPKDAPKER.[K]	3xTMT6plex [N-Term; K19; K23]	
High	[M].AAQEAPPLWAAADSNWVAADR.[V]	1xAcetyl [N-Term]	TGGT1_208
High	[A].SAIPLSSSHLSSSLR.[R]	1xTMT6plex [N-Term]	
High	[A].LQTGAQPLVR.[T]	1xTMT6plex [N-Term]	

High	[M].TNHTEEQALELEALEALFTR.[E]	1xTMT6plex [N-Term]	
High	[M].TNHTEEQALELEALEALFTR.[E]	1xAcetyl [N-Term]	TGGT1_208
High	[F].TGPSATDSLDLAR.[V]	1xTMT6plex [N-Term]	
High	[G].IEWNEGKEDFQYTTSPWVIPPDGLVSR.[R]	2xTMT6plex [N-Term; K7]	
High	[L].FQPSFLGKEAAGVHR.[T]	2xTMT6plex [N-Term; K8]	
High	[R].TTFDSIMKCDVDIR.[K]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl [	
High	[L].DSGDGVSHTVPIYEGYALPHAIMR.[L]	1xTMT6plex [N-Term]	
High	[A].DEEVQALVVDNGSGNVK.[A]	1xAcetyl [N-Term]	TGGT1_209
High	[A].DEEVQALVVDNGSGNVKAGVAGDDAPR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K17	TGGT1_209
High	[A].EDSSDIEKSYELPDGNIITVGNER.[F]	2xTMT6plex [N-Term; K8]	
High	[S].FLGKEAAGVHR.[T]	2xTMT6plex [N-Term; K4]	
High	[D].NGSGNVKAGVAGDDAPR.[A]	1xTMT6plex [K7]	
High	[E].EKDCYVGDEAQSKR.[G]	3xTMT6plex [N-Term; K2; K13]; 1xCarbamidome	
High	[V].DNGSGNVKAGVAGDDAPR.[A]	2xTMT6plex [N-Term; K8]	
High	[L].VVDNGSGNVKAGVAGDDAPR.[A]	2xTMT6plex [N-Term; K10]	
High	[M].VGMEEKDCYVGDEAQSKR.[G]	3xTMT6plex [N-Term; K6; K17]; 1xCarbamidome	
High	[M].EEKDCYVGDEAQSKR.[G]	3xTMT6plex [N-Term; K3; K14]; 1xCarbamidome	
High	[A].LDFDEEMKAAEDSSDIEKSYELPDGNIITVGNER.	3xTMT6plex [N-Term; K8; K18]	
High	[N].GSGNVKAGVAGDDAPR.[A]	1xTMT6plex [K6]	
High	[V].SASGTSLSQVAGQHGQMR.[K]	1xTMT6plex [N-Term]	
High	[S].SSGLPSHQSLADGER.[V]	1xTMT6plex [N-Term]	
High	[M].SVVNVTNIR.[L]	1xAcetyl [N-Term]	TGGT1_209
High	[C].DSPASPSSPSSPKER.[V]	2xTMT6plex [N-Term; K13]	
High	[G].NAAPQEAEYMSR.[S]	1xAcetyl [N-Term]	TGGT1_209
High	[-].MDLTGEESGSPAELPR.[E]	1xAcetyl [N-Term]	TGGT1_209
High	[M].GTSTLDASVGHHGPSVQQPFEVAASPPPDR.[G	1xTMT6plex [N-Term]	
High	[F].ALSDHGSFR.[K]	1xTMT6plex [N-Term]	
High	[L].VDDNAIHFIAEAR.[S]	1xTMT6plex [N-Term]	
High	[T].EIVAVKLGR.[D]	2xTMT6plex [N-Term; K6]	
High	[C].AVVDLPQNR.[S]	1xTMT6plex [N-Term]	
High	[M].AKNTLETGDSLR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_209
High	[L].ETVKEEPEEVMGR.[V]	2xTMT6plex [N-Term; K4]	
High	[F].VTGTGQPAR.[T]	1xTMT6plex [N-Term]	
High	[P].AVTQSPGQR.[A]	1xTMT6plex [N-Term]	
High	[N].SLAVSAIPSVFSAPR.[G]	1xTMT6plex [N-Term]	
High	[L].AVSAIPSVFSAPR.[G]	1xTMT6plex [N-Term]	
High	[M].VVTASPDTYLHVIDYGLKKVR.[L]	3xTMT6plex [N-Term; K18; K19]	
High	[M].VVTASPDTYLHVIDYGLK.[K]	1xTMT6plex [N-Term]	
High	[L].VMGDIKR.[Q]	2xTMT6plex [N-Term; K6]	
High	[-].MVVTASPDTYLHVIDYGLKKVR.[L]	3xTMT6plex [N-Term; K19; K20]	
High	[S].AIPSVFSAPR.[G]	1xTMT6plex [N-Term]	
High	[-].METNHSGPEAAR.[S]	1xAcetyl [N-Term]	TGGT1_209
High	[M].SGKGPAQKSQAAK.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_209
High	[N].NPPPLEGASVSPENATDPPETGGSR.[R]	1xAcetyl [N-Term]	TGGT1_210
High	[-].MDDPSLLEAPALDR.[G]	1xAcetyl [N-Term]	TGGT1_210
High	[-].MKDAEHTEKDEGGDPPQR.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_210
High	[-].MKDAEHTEKDEGGDPPQR.[D]	3xTMT6plex [N-Term; K2; K9]	
High	[A].GDSIGDEFKGYIFR.[I]	2xTMT6plex [N-Term; K9]	
High	[-].MKLNLANPQAGMQKTVEVDDEK.[K]	3xTMT6plex [N-Term; K2; K14]	
High	[-].MKLNLANPQAGM.[Q]	2xTMT6plex [N-Term; K2]	
High	[M].LHSATPGVSSHGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K14]	
High	[S].SHGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K5]	

High	[V].SSHGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K6]	
High	[S].HGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K4]	
High	[H].SATPGVSSHGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K12]	
High	[-].MQALNVQVKEAFR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_210
High	[-].MELVSKVEDQDLLPFVGYCR.[I]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_211
High	[M].VGTNAPSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[-].MVGTNAPSAQASSAQHVGGAR.[T]	1xAcetyl [N-Term]	TGGT1_211
High	[N].APSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[V].GTNAPSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[G].TNAPSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[M].ASAAAIPMASTR.[R]	1xAcetyl [N-Term]	TGGT1_211
High	[F].SSYADFGKQLR.[G]	2xTMT6plex [N-Term; K8]	
High	[M].AALPSSPAPAPEETVANSLLSHR.[V]	1xAcetyl [N-Term]	TGGT1_211
High	[A].AAVPSGGEGMRPWLFKR.[L]	2xTMT6plex [N-Term; K16]	
High	[A].EEEAVTVLTASNFDDTLK.[N]	1xTMT6plex [N-Term]	
High	[A].EEEAVTVLTASNFDDTLKNNEIVLVK.[F]	2xTMT6plex [N-Term; K18]	
High	[S].QIFVPQGFQCDFHR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10	
High	[D].PPPLINHGFSR.[Y]		
High	[L].FKTGSSENNEVLPSFQDAEKAAPVR.[R]	3xTMT6plex [N-Term; K2; K20]	
High	[M].SPPGKDDYCGHER.[G]	2xTMT6plex [N-Term; K5]; 1xCarbamidomethyl [	
High	[-].MHFLSCTDGKPHAR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_212
High	[M].SGLSSAAHGGMAASSLAEQR.[R]	1xAcetyl [N-Term]	TGGT1_212
High	[A].SVVGKDDDTSGSLWR.[L]	2xTMT6plex [N-Term; K5]	
High	[V].GKDDDTSGSLWR.[L]	2xTMT6plex [N-Term; K2]	
High	[T].QEDEDVEER.[D]	1xTMT6plex [N-Term]	
High	[M].SNPAYLYETPLETR.[V]	1xAcetyl [N-Term]	TGGT1_212
High	[K].ELAPYDPDWLYIR.[A]	1xTMT6plex [N-Term]	
High	[H].AKELAPYDPDWLYIR.[A]	1xTMT6plex [K/A]	
High	[V].DAAEHAGEDEMTACSPEAAR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C14	
High	[M].AGPLALQPR.[Q]	1xAcetyl [N-Term]	TGGT1_212
High	[C].HGAQADSVQNLLCSLGR.[A]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13	
High	[R].AGEEEEEEPHAGGSIER.[T]		
High	[-].MEPSFFASEESSSSRPEGAASSAGDEILLVNFR.[C	1xAcetyl [N-Term]	TGGT1_212
High	[M].VLLKVLR.[K]	2xTMT6plex [N-Term; K4]	
High	[-].MEELSHASLPR.[F]	1xAcetyl [N-Term]	TGGT1_212
High	[M].SFSSYAADASLGR.[D]	1xAcetyl [N-Term]	TGGT1_212
High	[Y].GLPQDSPLGEATHEEPPKSAPGQQAPR.[M]	2xTMT6plex [N-Term; K18]	
High	[N].GVYGLPQDSPLGEATHEEPPKSAPGQQAPR.[M	2xTMT6plex [N-Term; K21]	
High	[M].ASLQLPVGLSHSSLAHPAVDQQLLR.[T]	1xAcetyl [N-Term]	TGGT1_213
High	[G].ASENPDIVLSSR.[V]	1xAcetyl [N-Term]	TGGT1_213
High	[G].ASENPDIVLSSR.[V]	1xTMT6plex [N-Term]	
High	[A].FLANCLQDER.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].EEHFAVFSTCR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10	
High	[M].ADAGDAAANQPKR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_213
High	[M].ADAGDAAANQPKRR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_213
High	[M].ATVTPVNPKPFLTSLTGR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_213
High	[M].ATGAAPAPAEGHVR.[V]	1xAcetyl [N-Term]	TGGT1_213
High	[L].AAETNVSGDSTAISPNTR.[G]	1xTMT6plex [N-Term]	
High	[AM].VSLEELQR.[LQ]	1xAcetyl [N-Term]	TGGT1_213
High	[AM].VSLEELQR.[LQ]	1xTMT6plex [N-Term]	
High	[-].MNLLPSSIEEFR.[K]	1xAcetyl [N-Term]	TGGT1_213
High	[M].SAHGVEEIPVCSVSAGPR.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_213

High	[-].MDANASVER.[L]	1xAcetyl [N-Term]	TGGT1_213
High	[L].GAVALTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K11]	
High	[V].ALTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K8]	
High	[R].QQELGLLRPEER.[L]	1xTMT6plex [N-Term]	
High	[Q].TVHQLGAVALTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K16]	
High	[L].QTVHQLGAVALTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K17]	
High	[A].LTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K7]	
High	[H].QLGAVALTPEQAKAALLDEILR.[A]	2xTMT6plex [N-Term; K13]	
High	[S].VQLSEGMKR.[L]	2xTMT6plex [N-Term; K8]	
High	[L].HVDFDGLPPEVIPR.[R]	1xTMT6plex [N-Term]	
High	[M].ASALDDDYLR.[T]	1xAcetyl [N-Term]	TGGT1_214
High	[M].ASLLQSLHR.[L]	1xAcetyl [N-Term]	TGGT1_214
High	[M].AQKGHTDAEAPDVR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_214
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLRR.[A]	2xTMT6plex [N-Term; K3]	
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLR.[R]	2xTMT6plex [N-Term; K3]	
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_214
High	[-].MNTELLSLTDEPVILVR.[L]	1xAcetyl [N-Term]	TGGT1_214
High	[T].MYAGIGDPSGGFGAPAYEKYPR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K19	TGGT1_214
High	[M].SAADVHSILYR.[G]	1xAcetyl [N-Term]	TGGT1_214
High	[S].VAPPPLYNGAAPGFR.[E]	1xTMT6plex [N-Term]	
High	[M].SLTAEEPKPAVEAR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_214
High	[F].SSEADSSVEAASKDLLK.[T]	2xTMT6plex [N-Term; K13]	
High	[F].SSEADSSVEAASK.[D]	1xTMT6plex [N-Term]	
High	[A].ATPVIATPSGAAEGATELLTPGGDPR.[G]	1xTMT6plex [N-Term]	
High	[-].MEAMAEPTPPAPGGEILR.[D]	1xAcetyl [N-Term]	TGGT1_214
High	[F].AISHLNPSISKGKVHYR.[V]	3xTMT6plex [N-Term; K11; K13]	
High	[V].AVGGGEKGGPHSHQPPAKGTAGLGPQAR.[G]	3xTMT6plex [N-Term; K7; K18]	
High	[M].SPPTASASVASSGSSPHMDR.[L]	1xTMT6plex [N-Term]	
High	[M].SPPTASASVASSGSSPHMDR.[L]	1xTMT6plex [N-Term]; 1xOxidation [M18]	
High	[M].ALTAVSSASSR.[S]	1xAcetyl [N-Term]	TGGT1_215
High	[M].ALTAVSSASSR.[S]	1xTMT6plex [N-Term]	
High	[G].VPDVTTVADVR.[R]	1xTMT6plex [N-Term]	
High	[A].FQGDDAR.[V]	1xTMT6plex [N-Term]	
High	[L].TTAVKHEETENLR.[D]	2xTMT6plex [N-Term; K5]	
High	[M].GVHHALDDAGEMPHSGGR.[R]	1xTMT6plex [N-Term]	
High	[F].ASVAHAQTAASEAEAATKVPDFR.[T]	2xTMT6plex [N-Term; K18]	
High	[Q].TAASEAEAATKVPDFR.[T]	2xTMT6plex [N-Term; K11]	
High	[A].SVAHAQTAASEAEAATKVPDFR.[T]	2xTMT6plex [N-Term; K17]	
High	[T].DKINHALFR.[E]	2xTMT6plex [N-Term; K2]	
High	[F].SSVKFMDQKR.[S]	3xTMT6plex [N-Term; K4; K9]	
High	[M].ADKDSTPVAASVSAAADPHRPVADMAVSTDLI	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_215
High	[T].SEDVESAVIYNHKELAVDPDFVR.[V]	2xTMT6plex [N-Term; K13]	
High	[A].MIYDNPNAAKKFENR.[F]	3xTMT6plex [N-Term; K10; K11]	
High	[Y].DNPNAAKKFENR.[F]	3xTMT6plex [N-Term; K7; K8]	
High	[M].ADSGAFSLR.[F]	1xAcetyl [N-Term]	TGGT1_215
High	[M].IYDNPNAAKKFENR.[F]	3xTMT6plex [N-Term; K9; K10]	
High	[M].SKLSTDGLKK.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_215
High	[M].SKLSTDGLK.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_215
High	[M].PLHPPSNSCLTGPIYFGVGLPHAAVR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[F].TNVKKPAYR.[V]	3xTMT6plex [N-Term; K4; K5]	
High	[F].FTNVKKPAYR.[V]	3xTMT6plex [N-Term; K5; K6]	
High	[-].MHLAEEVSAPPAKR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_215

High	[W].LEQEAAEDVTPLPGSHTEAQTQSPSAFR.[R]	1xAcetyl [N-Term]	TGGT1_215
High	[G].SSSASFSPEEESLVSHSR.[V]	1xTMT6plex [N-Term]	
High	[M].SDAGTPPAVQGELSQPQER.[V]	1xAcetyl [N-Term]	TGGT1_216
High	[A].GHANEVNLPFEAR.[V]	1xTMT6plex [N-Term]	
High	[N].EVNLPFEAR.[V]	1xTMT6plex [N-Term]	
High	[-].MDGLALAGR.[F]	1xAcetyl [N-Term]	TGGT1_216
High	[M].VTGGIWRPDSLPLYSR.[S]	1xTMT6plex [N-Term]	
High	[-].MVTGGIWRPDSLPLYSR.[S]	1xAcetyl [N-Term]	TGGT1_216
High	[A].PSAATSAPQTPAGSTEAR.[R]	1xTMT6plex [N-Term]	
High	[M].APSAATSAPQTPAGSTEAR.[R]	1xTMT6plex [N-Term]	
High	[M].AAGGNWLENR.[G]	1xAcetyl [N-Term]	TGGT1_216
High	[-].METLDEEKAEALLR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_216
High	[M].AGTGSGYDLSVSTFSPDGR.[V]	1xAcetyl [N-Term]	TGGT1_216
High	[S].SLLDLDDAQR.[A]	1xTMT6plex [N-Term]	
High	[D].FLAESVSHYFTR.[K]	1xTMT6plex [N-Term]	
High	[L].AVVRPEAKATGMASHYAEQEAPLR.[R]	2xTMT6plex [N-Term; K8]	
High	[T].SLVFPVPIAR.[A]	1xTMT6plex [N-Term]	
High	[S].GAGSPGGATSLVFPVPIAR.[A]	1xTMT6plex [N-Term]	
High	[L].AVVRPEAKATGMASHYAEQEAPLRR.[R]	2xTMT6plex [N-Term; K8]	
High	[A].SGAGSPGGATSLVFPVPIAR.[A]	1xTMT6plex [N-Term]	
High	[A].GSPGGATSLVFPVPIAR.[A]	1xTMT6plex [N-Term]	
High	[Q].QATPENAAAAAKR.[L]	2xTMT6plex [N-Term; K12]	
High	[G].SQTSDSSAEVAGHEKTGETDAEKR.[E]	3xTMT6plex [N-Term; K15; K23]	
High	[G].SQTSDSSAEVAGHEKTGETDAEKR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K15	TGGT1_216
High	[M].PLASTESAAPPESDR.[I]	1xTMT6plex [N-Term]	
High	[M].SGESPLEFKGVLEGHTDCVTAISTPSLKSNTIVSS	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_216
High	[R].SFQGHTSDVNSVAFSPDNR.[Q]	1xTMT6plex [N-Term]	
High	[A].IVCGVEAPDGLLAAATAAGSSTPALDIFALPLCR.	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C3;	
High	[-].MENSLTGILDVSEAR.[C]	1xAcetyl [N-Term]	TGGT1_216
High	[-].MEAVSSSSDGLPTKR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K14	TGGT1_216
High	[M].ATLVSDFLLAESER.[L]	1xAcetyl [N-Term]	TGGT1_216
High	[F].ASTLVQPTSSGSVHQDSMAR.[D]	1xTMT6plex [N-Term]	
High	[M].AQVDLFFSHLPPVTR.[F]	1xTMT6plex [N-Term]	
High	[M].TATPAGTLVR.[L]	1xAcetyl [N-Term]	TGGT1_217
High	[A].SEAVDGPDATTSVNFLKQIVEEDLR.[T]	2xTMT6plex [N-Term; K17]	
High	[M].ALSPGAVLR.[I]	1xAcetyl [N-Term]	TGGT1_217
High	[L].AWSTEPAKLVGVPSFNATR.[A]	2xTMT6plex [N-Term; K8]	
High	[C].NIMLCQPTGGKCKLTEGCSFR.[K]	3xTMT6plex [N-Term; K11; K13]; 3xCarbamidom	
High	[M].LCQPTGGKCKLTEGCSFR.[K]	3xTMT6plex [N-Term; K8; K10]; 3xCarbamidome	
High	[K].MEIDLLHPDPKVEASKH.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K11	TGGT1_217
High	[K].MEIDLLHPDPKVEASK.[H]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_217
High	[K].MEIDLLHPDPK.[V]	1xAcetyl [N-Term]	TGGT1_217
High	[A].SATSPEHSTTDESETSGGTIEKR.[G]	2xTMT6plex [N-Term; K22]	
High	[A].SATSPEHSTTDESETSGGTIEKR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K22	TGGT1_217
High	[Q].HSEPLTFER.[Q]	1xTMT6plex [N-Term]	
High	[L].DAEESVAPEEHESVTPKHSEALTFER.[Q]	2xTMT6plex [N-Term; K17]	
High	[A].TSPEHSTTDESETSGGTIEKR.[G]	2xTMT6plex [N-Term; K20]	
High	[M].PAPMVSQPAPAFEAEAVMADGSFGK.[I]	1xTMT6plex [N-Term]	
High	[A].WFGTNGDEDLHAGR.[S]	1xTMT6plex [N-Term]	
High	[L].WLQKISEAPGAR.[E]	2xTMT6plex [N-Term; K4]	
High	[F].SSTEDEEHASAGGSWWSSLSR.[G]	1xTMT6plex [N-Term]	
High	[A].NVASAFSSTEDEEHASAGGSWWSSLSR.[G]	1xTMT6plex [N-Term]	

High	[S].EVGGGLLGSLFR.[R]	1xTMT6plex [N-Term]	
High	[A].NVSSGVQQWFR.[G]	1xTMT6plex [N-Term]	
High	[A].NLVHSGNKAPSPVTGEAAATASADR.[Q]	2xTMT6plex [N-Term; K8]	
High	[F].EDTNLCAIHAKR.[V]	2xTMT6plex [N-Term; K11]; 1xCarbamidomethy	
High	[Y].LVGLFEDTNLCAIHAKR.[V]	2xTMT6plex [N-Term; K16]; 1xCarbamidomethy	
High	[R].VTIMPKDIQLAR.[R]	1xTMT6plex [K6]	
High	[T].NLCAIHAKR.[V]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl [	
High	[G].EIADNCSGNPCGGTAAGTCINTPSGYDCR.[C]	1xTMT6plex [N-Term]; 4xCarbamidomethyl [C6;	
High	[S].ETPAACSSNPCGPEAAGTCKETNSGYICR.[C]	2xTMT6plex [N-Term; K20]; 4xCarbamidomethy	
High	[E].TPAACSSNPCGPEAAGTCKETNSGYICR.[C]	2xTMT6plex [N-Term; K19]; 4xCarbamidomethy	
High	[I].MEGTSLMSLIDKSKVECLNEDAQHSIR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_21
High	[I].MEGTSLMSLIDKSK.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K]	TGGT1_21
High	[I].MEGTSLMSLIDK.[S]	1xAcetyl [N-Term]	TGGT1_21
High	[I].MEGTSLMSLIDKSKVECLNEDAQHSIR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_21
High	[S].ALELQGGELEIWSNR.[V]	1xTMT6plex [N-Term]	
High	[C].DEKTSSPQSSSR.[L]	2xTMT6plex [N-Term; K3]	
High	[-].MKSLTSKGVAAR.[S]	3xTMT6plex [N-Term; K2; K7]	
High	[-].MEEADLSSLAATER.[Q]	1xAcetyl [N-Term]	TGGT1_21
High	[M].ADVAAAPAPNATSQAANSTEGDAAAGSARPD	1xAcetyl [N-Term]; 1xTMT6plex [K40	TGGT1_21
High	[M].ADVAAAPAPNATSQAANSTEGDAAAGSARPD	1xAcetyl [N-Term]; 1xOxidation [M3	TGGT1_21
High	[F].FHTQKRPEAPTR.[D]	2xTMT6plex [N-Term; K5]	
High	[M].AYVADLSFLSDPTR.[L]	1xAcetyl [N-Term]	TGGT1_21
High	[K].ATSMDHGMQYSSIYWETSHR.[T]	1xTMT6plex [N-Term]; 1xOxidation [M]	
High	[K].ATSMDHGMQYSSIYWETSHR.[T]	1xTMT6plex [N-Term]	
High	[C].AESHEVSGFPHGDEDSR.[L]	1xTMT6plex [N-Term]	
High	[M].GGAAPAVFVDEDAEPSPR.[G]	1xTMT6plex [N-Term]	
High	[-].MYSLGVEGDETLLAQNQLSMSSR.[Q]	1xAcetyl [N-Term]	TGGT1_21
High	[L].GVEGDETLLAQNQLSMSSR.[Q]	1xTMT6plex [N-Term]	
High	[V].GHHTMSSTMGGAAPAVFVDEDAEPSPR.[G]	1xTMT6plex [N-Term]	
High	[A].VFVDEDAEPSPR.[G]	1xTMT6plex [N-Term]	
High	[A].DFFPGLFGEAVSEAPGAFR.[G]	1xTMT6plex [N-Term]	
High	[M].AVIGIDLGSLNSVMATVQR.[G]	1xAcetyl [N-Term]	TGGT1_21
High	[F].TVLGVDDWSR.[N]	1xTMT6plex [N-Term]	
High	[T].VLGVDDWSR.[N]	1xTMT6plex [N-Term]	
High	[D].YIIVVADR.[A]	1xTMT6plex [N-Term]	
High	[SM].AMTEEER.[MR]	1xTMT6plex [N-Term]	
High	[-].MEQPLVESAGSAAPAGVPASNATSPADGR.[A]	1xAcetyl [N-Term]	TGGT1_21
High	[M].AKPNDLAGLEKALNKNDK.[I]	1xAcetyl [N-Term]; 3xTMT6plex [K2;	TGGT1_21
High	[M].AKPNDLAGLEK.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_21
High	[Q].ASPVLAAQPLTTAGEKDAFDR.[E]	2xTMT6plex [N-Term; K16]	
High	[A].SHQGASVSPSHAVR.[G]	1xTMT6plex [N-Term]	
High	[-].MEGHQDPVGAAKLR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_21
High	[M].AAQAAKADAALAHAAAASR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_21
High	[Q].AAKADAALAHAAAASR.[D]	2xTMT6plex [N-Term; K3]	
High	[A].AQAAKADAALAHAAAASR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_21
High	[M].ATNSDVSVLSAEEQR.[R]	1xAcetyl [N-Term]	TGGT1_21
High	[A].EGEHAVGSSLEQGDGRDPAR.[M]	1xTMT6plex [N-Term]	
High	[-].MDSLASPSRPASR.[V]	1xAcetyl [N-Term]	TGGT1_21
High	[Q].TAAPVPKTDKGR.[N]	3xTMT6plex [N-Term; K7; K10]	
High	[C].QTAAPVPKTDKGR.[N]	3xTMT6plex [N-Term; K8; K11]	
High	[M].AGPPAVSEQHR.[A]	1xTMT6plex [N-Term]	
High	[M].AVPAAVLSQLR.[Q]	1xAcetyl [N-Term]	TGGT1_22

High	[A].GSEVTPFPMYNWHQNR.[V]	1xTMT6plex [N-Term]	
High	[G].SDSSPETYDR.[S]	1xTMT6plex [N-Term]	
High	[C].GAPQKEPEIEFR.[T]	2xTMT6plex [N-Term; K5]	
High	[S].EVTPFPMYNWHQNR.[V]	1xTMT6plex [N-Term]	
High	[T].EQGFDIVSPPGTLR.[V]	1xTMT6plex [N-Term]	
High	[M].GSVAGSEVTPFPMYNWHQNR.[V]	1xTMT6plex [N-Term]	
High	[M].ASGMGVDENCVAR.[F]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_22
High	[M].ASGMGVDENCVAR.[F]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_22
High	[M].GVDENCVAR.[F]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].ALNITAPPSPLASDTVTSPAAGKPR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K23	TGGT1_22
High	[-].MLAAELADGGEEEDVPTLQR.[V]	1xAcetyl [N-Term]	TGGT1_22
High	[S].FSPDLVLHPPPAPFSR.[V]	1xTMT6plex [N-Term]	
High	[S].VPSADPSVAASQTVVAPAPSTLPASGVPLPQTE	1xTMT6plex [N-Term]	
High	[L].AHAEEDTSSCIDR.[C]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C1	
High	[A].HAEEDTSSCIDR.[C]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[H].IPSPSFSPDLVLHPPPAPFSR.[V]	1xTMT6plex [N-Term]	
High	[A].YMDIDIDGEHAGR.[I]	1xTMT6plex [N-Term]	
High	[-].MELGSYSER.[Q]	1xAcetyl [N-Term]	TGGT1_221
High	[S].GGVHEYADSQFGHIFATGKNR.[E]	2xTMT6plex [N-Term; K19]	
High	[T].TITDVYEPTEEGLDKVKEDR.[V]	3xTMT6plex [N-Term; K15; K17]	
High	[-].MFNPNATMDWIR.[G]	1xAcetyl [N-Term]	TGGT1_221
High	[-].MFNPNATMDWIR.[G]	1xAcetyl [N-Term]; 1xOxidation [M8	TGGT1_221
High	[L].SVHQLVENADEVQVIDNEALYDICFR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2	
High	[A].ELIDSVLDVVR.[K]	1xTMT6plex [N-Term]	
High	[D].SVLDVVR.[K]	1xTMT6plex [N-Term]	
High	[M].ASSEEGAPPIEAKMEMKR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K13	TGGT1_221
High	[S].ALPHWEGDAFASSAHNAEEGVHSPR.[S]	1xTMT6plex [N-Term]	
High	[F].ASSPPAPLSSAGPVAPVADNPFEVYR.[H]	1xTMT6plex [N-Term]	
High	[A].LHLAEAPLFFSTSR.[L]	1xTMT6plex [N-Term]	
High	[M].SASLLEHLR.[A]	1xAcetyl [N-Term]	TGGT1_221
High	[L].ATATSKAGLR.[K]	2xTMT6plex [N-Term; K6]	
High	[L].LQEDATELR.[G]	1xAcetyl [N-Term]	TGGT1_22
High	[G].LSPIQKSFLVQFGR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_22
High	[M].TVKPEDIETR.[L]	2xTMT6plex [N-Term; K3]	
High	[M].TVKPEDIETR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_22
High	[V].DLPLDLVYTVPEVKTR.[M]	2xTMT6plex [N-Term; K14]	
High	[T].HADGSESEIAR.[F]	1xTMT6plex [N-Term]	
High	[T].EDIILCVHR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[G].AAPGCTDTGNDAEATPLAMTLR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[-].MVSLEELQR.[Q]	1xAcetyl [N-Term]	TGGT1_22
High	[A].DDHGATEKAETSDR.[V]	2xTMT6plex [N-Term; K8]	
High	[L].ADDHGATEKAETSDR.[V]	2xTMT6plex [N-Term; K9]	
High	[M].GIVKVCAR.[Q]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl	
High	[M].STVNPADAVGEAKPGPEVTVEFVQAIAR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_22
High	[M].SKLMKGGLEGEEQR.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_22
High	[M].STAATESDLDPTKGEGLFVTLTSGFSKAR.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K13	TGGT1_22
High	[M].AAKFLSFNQELNEAVDLK.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_22
High	[M].AVAPPDPQQLCQVLEGTYSQNEEVR.[R]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_22
High	[M].APPSAPAVAASSPSLQELYNLLR.[S]	1xTMT6plex [N-Term]	
High	[-].MEAELVSQSAGPAAR.[V]	1xAcetyl [N-Term]	TGGT1_22
High	[F].GSMPGNAAADTRPPEER.[F]	1xTMT6plex [N-Term]	
High	[A].AADTRPPEER.[F]	1xTMT6plex [N-Term]	

High	[M].GSFGSMPGNAAADTRPPEER.[F]	1xTMT6plex [N-Term]	
High	[T].SAEASEQHGGLGGKLR.[M]	2xTMT6plex [N-Term; K14]	
High	[M].ANVEDSASGSLSLR.[G]	1xTMT6plex [N-Term]	
High	[Q].SAPNPLDQEPDALQSR.[T]	1xTMT6plex [N-Term]	
High	[A].TQPQKVAEHSSAAVTDR.[S]	2xTMT6plex [N-Term; K5]	
High	[A].EHSSAAVTDR.[S]	1xTMT6plex [N-Term]	
High	[M].ATQPQKVAEHSSAAVTDR.[S]	2xTMT6plex [N-Term; K6]	
High	[M].VLEAVMLCIDNSAYAR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[M].VLEAVMLCIDNSAYAR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[G].SAPSSIFSSSAATVPLSR.[Y]	1xTMT6plex [N-Term]	
High	[M].AEMSSADGVHVLSGTSR.[G]	1xAcetyl [N-Term]	TGGT1_224
High	[V].NVEEASSSGAAR.[S]	1xTMT6plex [N-Term]	
High	[M].AMNFFSSPEGDSVSPESVSFR.[A]	1xAcetyl [N-Term]	TGGT1_224
High	[A].GEEKEEPKAVVR.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_224
High	[A].GEEKEEPKAVVR.[L]	3xTMT6plex [N-Term; K4; K8]	
High	[-].MLAVGGGGHR.[S]	1xAcetyl [N-Term]	TGGT1_224
High	[A].GGPPMQMLQQQQR.[G]	1xTMT6plex [N-Term]	
High	[L].DSNSHFLGVPGSTR.[G]	1xTMT6plex [N-Term]	
High	[-].MWGKLLTDTYNR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_224
High	[M].AEQSKVKDLTLSAFGR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K5;	TGGT1_225
High	[Q].VSNNQDFQHILR.[I]	1xTMT6plex [N-Term]	
High	[M].SIQVSNNQDFQHILR.[I]	1xAcetyl [N-Term]	TGGT1_225
High	[S].NNQDFQHILR.[I]	1xTMT6plex [N-Term]	
High	[A].STPQQFKIPTWFLNR.[Q]	2xTMT6plex [N-Term; K7]	
High	[A].AATPPPLGGTNVR.[A]	1xAcetyl [N-Term]	TGGT1_225
High	[R].MDAQTASFFKQLR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_225
High	[G].SHEAGKPFGVPGHHAR.[A]	2xTMT6plex [N-Term; K6]	
High	[-].MEFLVGDDTGLLKNVSTPR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_225
High	[A].AAALPNPSVPR.[A]	1xTMT6plex [N-Term]	
High	[E].MDEPIHVAITR.[L]	1xAcetyl [N-Term]	TGGT1_225
High	[-].MLAADCFFGPDVVKR.[T]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_225
High	[-].MLAADCFFGPDVVKR.[T]	2xTMT6plex [N-Term; K14]; 1xCarbamidomethy	
High	[S].ESAASGVEHEQKTGGSATEAR.[D]	2xTMT6plex [N-Term; K12]	
High	[Q].GLATASHPGGAADDAFESFR.[A]	1xTMT6plex [N-Term]	
High	[A].VPLPSGHFLSR.[I]	1xTMT6plex [N-Term]	
High	[F].ATAAGGANPFKNQLLLTLSSPSEAIYVR.[T]	2xTMT6plex [N-Term; K11]	
High	[M].VNMSLQKEGR.[Q]	2xTMT6plex [N-Term; K7]	
High	[Q].GLDSRPEKLSSKGLTAR.[R]	3xTMT6plex [N-Term; K8; K12]	
High	[A].SATPVQVIFVVGNNDLPR.[D]	1xTMT6plex [N-Term]	
High	[A].ASATPVQVIFVVGNNDLPR.[D]	1xTMT6plex [N-Term]	
High	[-].MEHGGFLSSR.[G]	1xAcetyl [N-Term]	TGGT1_226
High	[C].SAPQEDMRPPSAPFQPR.[D]	1xTMT6plex [N-Term]	
High	[-].MDSQQQLSPAVDSAVGSR.[V]	1xAcetyl [N-Term]	TGGT1_226
High	[A].GNAQGGVYNAR.[A]	1xTMT6plex [N-Term]	
High	[N].ALSSQAHGQTYSPTDR.[T]	1xTMT6plex [N-Term]	
High	[L].SSQAHGQTYSPTDR.[T]	1xTMT6plex [N-Term]	
High	[K].MVVPDFGNLKSDIGVGKLNEYLASR.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K10	TGGT1_226
High	[M].VVPDFGNLKSDIGVGKLNEYLASR.[S]	3xTMT6plex [N-Term; K9; K16]	
High	[M].VVPDFGNLKSDIGVGK.[L]	2xTMT6plex [N-Term; K9]	
High	[M].VVPDFGNLK.[S]	1xTMT6plex [N-Term]	
High	[M].SKISAGSSSPTR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_226
High	[M].SKISAGSSSPTR.[E]	2xTMT6plex [N-Term; K2]	

High	[A].GGADGGDLGPGHGGTAKR.[H]	2xTMT6plex [N-Term; K17]	
High	[-].MIGSEEFWKTEADAPLLNR.[N]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_226
High	[M].SQPTSPTVSPGTPLNCGASER.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_226
High	[M].AETMAVCPR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_226
High	[S].MKALSNIVLPR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_226
High	[I].QTSEYKNLYNPENFFISKEGGGAGNNWGSGYA	3xTMT6plex [N-Term; K6; K18]	
High	[P].APPFGVFFASAGEER.[F]	1xTMT6plex [N-Term]	
High	[M].APAPPFGVFFASAGEER.[F]	1xTMT6plex [N-Term]	
High	[M].ATADVQTER.[A]	1xAcetyl [N-Term]	TGGT1_226
High	[M].SSWEDEADEILEAEER.[R]	1xAcetyl [N-Term]	TGGT1_226
High	[L].LDAIDAESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K10]	
High	[A].TAPGAVLLDAIDAESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K17]	
High	[T].SGVQEATAPGAVLLDAIDAESDKVDNQAEGGE	2xTMT6plex [N-Term; K23]	
High	[E].ATAPGAVLLDAIDAESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K18]	
High	[E].ATAPGAVLLDAIDAESDKVDNQAEGGER.[M]	1xTMT6plex [N-Term]	
High	[Q].EATAPGAVLLDAIDAESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K19]	
High	[Q].EATAPGAVLLDAIDAESDKVDNQAEGGER.[M]	1xTMT6plex [N-Term]	
High	[S].GVQEATAPGAVLLDAIDAESDKVDNQAEGGER.	2xTMT6plex [N-Term; K22]	
High	[A].TSGVQEATAPGAVLLDAIDAESDKVDNQAEGG	2xTMT6plex [N-Term; K24]	
High	[S].ATSGVQEATAPGAVLLDAIDAESDKVDNQAEG	2xTMT6plex [N-Term; K25]	
High	[L].DAIDAESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K9]	
High	[D].AIDAESDKVDNQAEGGER.[M]	1xTMT6plex [K8]	
High	[T].SGVQEATAPGAVLLDAIDAESDKVDNQAEGGE	1xTMT6plex [N-Term]	
High	[D].AESDKVDNQAEGGER.[M]	1xTMT6plex [K5]	
High	[Y].SSATSGVQEATAPGAVLLDAIDAESDKVDNQAE	2xTMT6plex [N-Term; K27]	
High	[A].ESDKVDNQAEGGER.[M]	2xTMT6plex [N-Term; K4]	
High	[R].SEASGFCYINDIVLGILELLKYHAR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_227
High	[R].TEMNKKVYR.[V]	3xTMT6plex [N-Term; K5; K6]	
High	[M].ADAGDEGDALR.[A]	1xAcetyl [N-Term]	TGGT1_227
High	[V].NQGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K12]	
High	[N].QGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K11]	
High	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K19]	
High	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K19	TGGT1_227
High	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]	1xAcetyl [N-Term]	TGGT1_227
High	[G].VVNQGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K14]	
High	[V].AEKGFTAAKTHTVR.[G]	3xTMT6plex [N-Term; K3; K9]	
High	[P].VDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K8]	
High	[D].VPFSGKPLDER.[A]	1xTMT6plex [K6]	
High	[Q].GPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K10]	
High	[G].PVDVPFSGKPLDER.[A]	1xTMT6plex [K9]	
High	[M].ALAHASSGTVR.[D]	1xAcetyl [N-Term]	TGGT1_227
High	[Y].LQQSSLPSNISPALELAALGQDPVR.[R]	1xAcetyl [N-Term]	TGGT1_227
High	[S].SLPSNISPALELAALGQDPVR.[R]	1xTMT6plex [N-Term]	
High	[Q].QSSLPSNISPALELAALGQDPVR.[R]	1xAcetyl [N-Term]	TGGT1_227
High	[Q].QSSLPSNISPALELAALGQDPVRR.[R]	1xAcetyl [N-Term]	TGGT1_227
High	[Q].QSSLPSNISPALELAALGQDPVR.[R]	1xTMT6plex [N-Term]	
High	[M].GKGAVHYTGTNFR.[R]	2xTMT6plex [N-Term; K2]	
High	[M].APSTTPKDASTDAQSWR.[S]	2xTMT6plex [N-Term; K7]	
High	[F].SVMPAAALSSGSR.[G]	1xTMT6plex [N-Term]	
High	[M].SISLATLPLAGGLAVPPQEKTQR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K20	TGGT1_227
High	[P].SAQPSETPEAPPEEKR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_227
High	[P].SAQPSETPEAPPEEKR.[G]	2xTMT6plex [N-Term; K15]	

High	[M].PPSAQPSETPEAPPEEKR.[G]	2xTMT6plex [N-Term; K17]	
High	[Q].AASAPSETTEEDETTKEVAGSAVTR.[K]	2xTMT6plex [N-Term; K16]	
High	[F].STGVTDEKATTVAEKGASSADIPSELR.[S]	3xTMT6plex [N-Term; K8; K15]	
High	[R].EEELELPFDQDIDVKDSDIDMDAL.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_228
High	[L].SGIIKTLVLWDPVQR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_228
High	[L].SGIIKTLVLWDPVQR.[L]	2xTMT6plex [N-Term; K5]	
High	[M].VTSTAQPGGGDDER.[A]	1xTMT6plex [N-Term]	
High	[-].MVTSTAQPGGGDDER.[A]	1xAcetyl [N-Term]	TGGT1_228
High	[-].MDKLNLLSLHVPPIYGER.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_228
High	[M].ASLQPGDGYGGEGFHR.[F]	1xAcetyl [N-Term]	TGGT1_228
High	[M].VYTFTCSDPR.[Y]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].APLASLQHQVIKPGSGSPLQR.[G]	2xTMT6plex [N-Term; K12]	
High	[P].LASLQHQVIKPGSGSPLQR.[G]	2xTMT6plex [N-Term; K10]	
High	[Q].HQVIKPGSGSPLQR.[G]	2xTMT6plex [N-Term; K5]	
High	[A].GIGQVIAGWDQGVLGMTVGETR.[R]	1xTMT6plex [N-Term]	
High	[M].GAYKYLEELWK.[K]	2xTMT6plex [N-Term; K4]	
High	[-].MKGSNKTAEAAVSGEGDR.[R]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_228
High	[-].MKGSNKTAEAAVSGEGDR.[R]	3xTMT6plex [N-Term; K2; K6]	
High	[A].QVLHPLPAKGVTR.[R]	2xTMT6plex [N-Term; K9]	
High	[Q].VLHPLPAKGVTR.[R]	2xTMT6plex [N-Term; K8]	
High	[A].AQVLHPLPAKGVTR.[R]	2xTMT6plex [N-Term; K10]	
High	[L].GPTVSDESR.[R]	1xTMT6plex [N-Term]	
High	[L].HPLPAKGVTR.[R]	2xTMT6plex [N-Term; K6]	
High	[M].SLDDFKADLIDQVVPFR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_229
High	[-].MKPEKVIR.[D]	3xTMT6plex [N-Term; K2; K5]	
High	[-].MVSSELLWQCVR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10	
High	[-].MVSSELLWQCVR.[R]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_229
High	[M].VSSELLWQCVR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[A].LVTVQKCSR.[A]	2xTMT6plex [N-Term; K6]; 1xCarbamidomethyl [	
High	[I].ALVTVQKCSR.[A]	2xTMT6plex [N-Term; K7]; 1xCarbamidomethyl [	
High	[-].MVSSELLWQ.[C]	1xTMT6plex [N-Term]	
High	[A].HKQPLGLNR.[H]	2xTMT6plex [N-Term; K2]	
High	[M].AQKPGSSNGKTVRPSR.[F]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_229
High	[A].AMPKLSGEKLAELMQMDVK.[D]	3xTMT6plex [N-Term; K4; K9]	
High	[A].AMPKLSGEKLAELMQMDVK.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_229
High	[Y].DLNADGAIDVEELQQIIKDPHSHEIR.[M]	2xTMT6plex [N-Term; K18]	
High	[V].DKDNDGLLDLSEIR.[I]	2xTMT6plex [N-Term; K2]	
High	[E].ELQQIIKDPHSHEIR.[M]	2xTMT6plex [N-Term; K7]	
High	[E].EILNAQDKNGDR.[K]	2xTMT6plex [N-Term; K8]	
High	[M].GGVSKAKGATR.[S]	3xTMT6plex [N-Term; K5; K7]	
High	[N].YIDENDEVLVAGFGR.[S]	1xTMT6plex [N-Term]	
High	[R].SGHAVGDIPGVR.[F]	1xTMT6plex [N-Term]	
High	[-].MDDDAASPVLAVITR.[W]	1xTMT6plex [N-Term]	
High	[-].MDDDAASPVLAVITR.[W]	1xAcetyl [N-Term]	TGGT1_229
High	[M].AKTENAPAEAASLAAEAVR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_229
High	[M].SGGHDEYPPELTR.[G]	1xTMT6plex [N-Term]	
High	[G].MSGGHDEYPPELTR.[G]	1xTMT6plex [N-Term]	
High	[M].SIAGVFQSYTQGKGDMDSR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_229
High	[M].SIAGVFQSYTQGKGDMDSR.[T]	1xAcetyl [N-Term]; 1xOxidation [M1	TGGT1_229
High	[M].SSAVVDHPAAEASLCPSDASGDSLHTR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_229
High	[R].SVHDALCAVSR.[A]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[Q].VDNPEELEKIR.[Q]	2xTMT6plex [N-Term; K9]	

High	[M].ALAIFGDR.[Q]	1xAcetyl [N-Term]	TGGT1_22
High	[-].MWAAHAGAPPGDFTSLR.[W]	1xAcetyl [N-Term]	TGGT1_23
High	[K].MQGSLEALHLGSGNSR.[C]	1xAcetyl [N-Term]	TGGT1_23
High	[A].EVVYATGLKYTDPATR.[C]	2xTMT6plex [N-Term; K9]	
High	[A].SDPLLHAPKER.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_23
High	[A].SDPLLHAPKER.[E]	2xTMT6plex [N-Term; K9]	
High	[M].SEFQQPQSPAGGSMFITGTTENAEVER.[V]	1xAcetyl [N-Term]	TGGT1_23
High	[L].TACCPGTATHKVVTTDR.[L]	2xTMT6plex [N-Term; K11]; 2xCarbamidomethy	
High	[Q].ADQPVVPVPVYQDVYKR.[D]	2xTMT6plex [N-Term; K16]	
High	[Q].FVPKWDVR.[E]	2xTMT6plex [N-Term; K4]	
High	[F].SEIHSEQSEDAEEPESQDSSSSR.[N]	1xAcetyl [N-Term]	TGGT1_23
High	[F].STADSPNGLCLVTR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C1	
High	[A].GTEVAKEAADMVLADDNFSTIVAAVEEGR.[S]	2xTMT6plex [N-Term; K6]	
High	[-].MDLSNEKAVGALSKHR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K7;	TGGT1_23
High	[S].SSPDLLSSLQDVNIHTKAHVLDAEEVVR.[Q]	2xTMT6plex [N-Term; K17]	
High	[L].GFNPPDLDVMKR.[E]	2xTMT6plex [N-Term; K11]	
High	[M].ANAAGVGCDGSSAAAEFDGGR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_23
High	[M].SCDEVIR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2]	
High	[A].GATHEPDASSETATVTSASGAHR.[L]	1xAcetyl [N-Term]	TGGT1_23
High	[L].GQAPHGVVVVGAR.[A]	1xTMT6plex [N-Term]	
High	[L].SSAQGQHFAQGGR.[G]	1xTMT6plex [N-Term]	
High	[A].GMEPDAEGATRPPVSPR.[Q]	1xTMT6plex [N-Term]	
High	[A].GGSQPSSFSSYSHSQQR.[E]	1xTMT6plex [N-Term]	
High	[A].GAPTGQTAPATPVLR.[V]	1xTMT6plex [N-Term]	
High	[M].APVMTASAASDR.[M]	1xTMT6plex [N-Term]	
High	[F].SQCHPTLPAAPGR.[F]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C3]	
High	[-].MEDLELEGSLKELFETPSLR.[W]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_231
High	[M].SGEDPVSELLTRPR.[D]	1xTMT6plex [N-Term]	
High	[C].CGIVGYVGDKEAEPVLMEGLEILQNR.[G]	2xTMT6plex [N-Term; K10]; 1xCarbamidomethy	
High	[M].AGQDSSTSGGGLAVAPSR.[R]	1xTMT6plex [N-Term]	
High	[M].GKTDAQSPSSGPAGRPESGR.[K]	2xTMT6plex [N-Term; K2]	
High	[V].SLGAPGGTGSLGDHAQVPVPHSVSGSR.[H]	1xTMT6plex [N-Term]	
High	[S].GAHANKSGAAGGGLSATGER.[G]	2xTMT6plex [N-Term; K6]	
High	[M].SVSNCAPASKAGESAASGPAHR.[T]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_231
High	[S].NCAPASKAGESAASGPAHR.[T]	2xTMT6plex [N-Term; K7]; 1xCarbamidomethyl	
High	[M].SAAGTPHPAMADLQLQLEQLLLASLDPAQVKP	1xAcetyl [N-Term]; 1xTMT6plex [K31	TGGT1_231
High	[L].GTLAEEVGPAIFFSR.[E]	1xTMT6plex [N-Term]	
High	[V].EVLKEEIQER.[V]	2xTMT6plex [N-Term; K4]	
High	[-].MFSECCQPCAPCGEGEPGAAQPTQVPGSR.[L]	1xAcetyl [N-Term]; 4xCarbamidomet	TGGT1_231
High	[Q].IVQEYLCPKIEPR.[Y]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl	
High	[A].AVGSAPASPAR.[G]	1xTMT6plex [N-Term]	
High	[M].AQQGYPTMPVPQGWDGAAPPAGWEGWSK	2xTMT6plex [N-Term; K28]	
High	[-].MFKDCADPCSDCCQPAEQQR.[G]	1xAcetyl [N-Term]; 4xCarbamidomet	TGGT1_231
High	[T].AYQPIDTVTKTVEVPVVR.[T]	2xTMT6plex [N-Term; K10]	
High	[L].QQLHGTQESVR.[S]	1xTMT6plex [N-Term]	
High	[S].DSPAIHVTAEASQR.[L]	1xTMT6plex [N-Term]	
High	[S].VQVPVLKFR.[D]	2xTMT6plex [N-Term; K7]	
High	[-].MKSSAEIR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_231
High	[F].GAGDLKIVAAR.[M]	2xTMT6plex [N-Term; K6]	
High	[T].SLSLGTAHR.[N]	1xTMT6plex [N-Term]	
High	[T].EKETLLTHDSDSTFLR.[M]	2xTMT6plex [N-Term; K2]	
High	[K].MTDETEPQEQMPLPEPPESITQR.[L]	1xAcetyl [N-Term]	TGGT1_23

High	[M].TDETEPQEQMPLPEPPESITQR.[L]	1xAcetyl [N-Term]	TGGT1_232
High	[-].MWAGSGVAFLCHVEKPALQELESETASSPDGKR	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_232
High	[A].ARPPEAGVHGTQVDAPAVQSPEVR.[G]	1xTMT6plex [N-Term]	
High	[T].MESLVSVER.[A]	1xTMT6plex [N-Term]	
High	[T].MESLVSVER.[A]	1xAcetyl [N-Term]	TGGT1_232
High	[S].GTVACHPQEHPNSDFEQPGNFYR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[C].EVVVSGKLR.[A]	2xTMT6plex [N-Term; K7]	
High	[S].EDGYSGVEVR.[V]	1xTMT6plex [N-Term]	
High	[L].SEDGYSGVEVR.[V]	1xTMT6plex [N-Term]	
High	[K].GCEVVVSGKLR.[A]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [	
High	[R].NDLLPFNSKIIR.[E]	1xTMT6plex [K9]	
High	[L].SLAGHPTAAR.[V]	1xTMT6plex [N-Term]	
High	[-].MKHLCYEGSAFLR.[Q]	2xTMT6plex [N-Term; K2]; 1xCarbamidomethyl [	
High	[M].SQPVFASPLNVEKR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_232
High	[S].SFEETSVYPLR.[A]	1xTMT6plex [N-Term]	
High	[G].AKNLNLAVSR.[V]	2xTMT6plex [N-Term; K2]	
High	[M].SAAVDAQAVPLGGQR.[V]	1xAcetyl [N-Term]	TGGT1_232
High	[M].GFLEEGAPLAWR.[D]	1xTMT6plex [N-Term]	
High	[-].MNFFTAVR.[S]	1xAcetyl [N-Term]	TGGT1_232
High	[M].AALSPQKVAELKAFIGMCER.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_232
High	[A].DLNNDEDQGFR.[K]	1xTMT6plex [N-Term]	
High	[Y].EVNLADLNNDEDQGFR.[K]	1xTMT6plex [N-Term]	
High	[-].MQVIGKDQPNGSSGQPTHSALR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_232
High	[M].ADSGPVSSTDRPVAASAQGSAR.[N]	1xAcetyl [N-Term]	TGGT1_232
High	[M].SDEVDKHVLR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_233
High	[A].GQSAEGVAAHAVSR.[G]	1xTMT6plex [N-Term]	
High	[S].DLVVGHEPVQLAEANELLR.[E]	1xTMT6plex [N-Term]	
High	[S].EASPSAKSEASR.[T]	2xTMT6plex [N-Term; K7]	
High	[M].TSDLVVGHEPVQLAEANELLR.[E]	1xTMT6plex [N-Term]	
High	[M].AEGAETPGKGALSAQEEER.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_233
High	[A].EAANENAAAGVWTQPSVSR.[E]	1xTMT6plex [N-Term]	
High	[M].ADVDMTLDR.[R]	1xAcetyl [N-Term]	TGGT1_233
High	[A].SDPPLVANQVVTCPDK.[K]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13	
High	[A].SDPPLVANQVVTCPDK.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_233
High	[A].SDPPLVANQVVTCPDKK.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_233
High	[A].SDPPLVANQVVTCPDKK.[S]	2xTMT6plex [N-Term; K]; 1xCarbamidomethyl [C	
High	[D].PPLVANQVVTCPDKK.[S]	1xCarbamidomethyl [C11]; 1xTMT6plex [K]	
High	[D].PPLVANQVVTCPDK.[K]	1xCarbamidomethyl [C11]	
High	[A].SDPPLVANQVVTCPDKKSTAAVILTPTENHFTLK	3xTMT6plex [N-Term; K16; K17]; 1xCarbamidom	
High	[C].PKTALTEPPTLAYSPNR.[Q]	2xTMT6plex [N-Term; K2]	
High	[S].SVVNNVAR.[C]	1xTMT6plex [N-Term]	
High	[A].LSFEDNRPSPVRPLLR.[L]	1xTMT6plex [N-Term]	
High	[Q].LGGEDPSEGSRPGGGSGGGKR.[G]	2xTMT6plex [N-Term; K20]	
High	[-].MDGPAPKLDLGSKR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K7;	TGGT1_233
High	[-].MDTPTLDEAMTDSR.[F]	1xAcetyl [N-Term]	TGGT1_233
High	[A].ASLFPGDSGLHSTCAFLSEEGR.[A]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C14	
High	[SA].FLSEEGR.[HA]	1xTMT6plex [N-Term]	
High	[M].SIPCLFEDR.[F]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_233
High	[-].MKPPSGLSGASAQGVGAEETSVSLLAR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_233
High	[F].SSEKKDTTEQPLSPAVDTSSSSCR.[G]	3xTMT6plex [N-Term; K4; K5]; 1xCarbamidomet	
High	[V].GTDHEEADVTMLQSATPR.[G]	1xTMT6plex [N-Term]	
High	[A].PQSVPPVGNFSGLAAAVGTDHEEADVTMLQSA	1xTMT6plex [N-Term]	

High	[P].QSVPPVGNFSGLAAAVGTDHEEADVTMLQSAT	1xTMT6plex [N-Term]	
High	[A].AAVGTDHEEADVTMLQSATPR.[G]	1xTMT6plex [N-Term]	
High	[A].AVGTDHEEADVTMLQSATPR.[G]	1xTMT6plex [N-Term]	
High	[L].AAAVGTDHEEADVTMLQSATPR.[G]	1xTMT6plex [N-Term]	
High	[Q].EAGVSPVKLVADR.[M]	2xTMT6plex [N-Term; K8]	
High	[M].AHLVFFPPVVDSADQAACPTVPSGPSAKR.[R]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_234
High	[G].FELPALFGSGTVAAADPSEKAPQPGLEAPR.[T]	2xTMT6plex [N-Term; K20]	
High	[L].ADCLKTLVNAEKR.[G]	3xTMT6plex [N-Term; K5; K12]; 1xCarbamidome	
High	[M].AGDTMASFLR.[R]	1xAcetyl [N-Term]	TGGT1_234
High	[A].TPEEALPASTSKKQR.[K]	3xTMT6plex [N-Term; K12; K13]	
High	[F].DETLSGVPADMHR.[L]	1xTMT6plex [N-Term]	
High	[S].GSASVAYSDIR.[S]	1xTMT6plex [N-Term]	
High	[A].SVAYSDIR.[S]	1xTMT6plex [N-Term]	
High	[R].YHSAAEADTGVCGETKSR.[D]	2xTMT6plex [N-Term; K16]; 1xCarbamidomethy	
High	[Y].HSAAEADTGVCGETKSR.[D]	2xTMT6plex [N-Term; K15]; 1xCarbamidomethy	
High	[Q].ALPVHFISGKPR.[D]	2xTMT6plex [N-Term; K10]	
High	[S].HVVSGVSVAEGGTR.[G]	1xTMT6plex [N-Term]	
High	[Q].GLPSSLPAGETGHGKR.[Y]	2xTMT6plex [N-Term; K15]	
High	[F].SSASHVVSGVSVAEGGTR.[G]	1xTMT6plex [N-Term]	
High	[A].SHVVSGVSVAEGGTR.[G]	1xTMT6plex [N-Term]	
High	[M].EGCVSKVAPVSPTFYR.[R]	2xTMT6plex [N-Term; K6]; 1xCarbamidomethyl	
High	[R].SAFGHTPDAVAQLLR.[S]	1xTMT6plex [N-Term]	
High	[S].NVAPFAQAGAYIHR.[E]	1xTMT6plex [N-Term]	
High	[C].GVSNVAPFAQAGAYIHR.[E]	1xTMT6plex [N-Term]	
High	[M].ASKTTSEELKTATALK.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_235
High	[M].ASKTTSEELK.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_235
High	[A].QEEAEDVKMDR.[R]	2xTMT6plex [N-Term; K8]	
High	[M].AQEEAEDVKMDR.[R]	2xTMT6plex [N-Term; K9]	
High	[M].AQEEAEDVK.[M]	1xTMT6plex [N-Term]	
High	[M].AQEEAEDVKMDRR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_235
High	[M].AQEEAEDVKMDRR.[S]	2xTMT6plex [N-Term; K9]	
High	[M].AQEEAEDVKMDR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_235
High	[M].ANATTDHLRPQDLETLDISKLTPLSPDVISR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K20	TGGT1_235
High	[M].ANATTDHLRPQDLETLDISK.[L]	1xAcetyl [N-Term]	TGGT1_235
High	[-].MEDVESAAVENETEKQHESR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_235
High	[G].TPLQAFNSASFPR.[C]	1xTMT6plex [N-Term]	
High	[M].SGYGLPISQEVAKELAENAR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_236
High	[R].ANGEAQLGKYGGGAGGAAAASSLFEKR.[Y]	2xTMT6plex [K9; K26]	
High	[M].SGYGLPISQEVAK.[E]	1xAcetyl [N-Term]	TGGT1_236
High	[-].MNILPLHFSEGLR.[E]	1xAcetyl [N-Term]	TGGT1_236
High	[P].YHGTAECSEVNSSFSSR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[G].FFSAAPAAATAGVSPLAR.[S]	1xTMT6plex [N-Term]	
High	[A].AATAGVSPLAR.[S]	1xTMT6plex [N-Term]	
High	[F].SAAPAAATAGVSPLAR.[S]	1xTMT6plex [N-Term]	
High	[Y].GGGGGYGGGGGFGSGGYGGGGGYSPAGPHH	1xTMT6plex [N-Term]	
High	[Q].ASPEEEKPSNGDER.[L]	2xTMT6plex [N-Term; K7]	
High	[A].GPHHGGMDTANWSAQVLR.[L]	1xTMT6plex [N-Term]	
High	[-].MKAKMSHEALTETAR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_236
High	[-].MKAKMSHEALTETAR.[K]	3xTMT6plex [N-Term; K2; K4]	
High	[M].SHEALTETAR.[K]	1xTMT6plex [N-Term]	
High	[-].MKAKMSHEALTETAR.[K]	1xAcetyl [N-Term]; 1xOxidation [M5]	TGGT1_236
High	[M].SHEALTETAR.[K]	1xAcetyl [N-Term]	TGGT1_236

High	[R].GLDVKDIR.[H]	2xTMT6plex [N-Term; K5]	
High	[M].LLGDSPHDTPGHEEDKLGAHR.[R]	2xTMT6plex [N-Term; K16]	
High	[A].APFQQTETR.[A]	1xTMT6plex [N-Term]	
High	[-].MNVLAYGTAEQR.[S]	1xAcetyl [N-Term]	TGGT1_236
High	[-].MNVLAYGTAEQR.[S]	1xTMT6plex [N-Term]	
High	[C].SAANDMDVAVSDGGHESAGLVEDIAQGHKTR.	1xAcetyl [N-Term]; 1xTMT6plex [K29	TGGT1_237
High	[S].DGGHESAGLVEDIAQGHKTR.[S]	2xTMT6plex [N-Term; K18]	
High	[M].TAAVSASSVEKAPSPFSTAAPPR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_237
High	[-].MDQAATSAAASQR.[G]	1xAcetyl [N-Term]	TGGT1_237
High	[M].TVLDKDEVFR.[R]	2xTMT6plex [N-Term; K5]	
High	[A].VLFEVPGSGR.[E]	1xTMT6plex [N-Term]	
High	[G].APDQAQAAVSDKESESR.[V]	2xTMT6plex [N-Term; K12]	
High	[M].AGCVQMLKNGDEATAFR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_238
High	[M].AGCVQMLKNGDEATAFR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_238
High	[A].AYFYVQESQDK.[C]	1xTMT6plex [N-Term]	
High	[M].SAVYCQALPATHLAEQVGKTVGVTGR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_238
High	[M].SELATAPR.[H]	1xAcetyl [N-Term]	TGGT1_238
High	[-].MDSFFSQPVPGHGSTQR.[E]	1xAcetyl [N-Term]	TGGT1_238
High	[A].SAGFLDLGCPMPVPLLR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[M].SGIAVGLKR.[G]	2xTMT6plex [N-Term; K8]	
High	[A].GTGKEQGQKPDSPPSPYVSQR.[Q]	3xTMT6plex [N-Term; K4; K9]	
High	[Q].DGMLEDIVSPTEIVGKR.[M]	2xTMT6plex [N-Term; K16]	
High	[L].TAVQDGMLEDIVSPTEIVGKR.[M]	2xTMT6plex [N-Term; K20]	
High	[S].SVKEVEVPQGR.[K]	2xTMT6plex [N-Term; K3]	
High	[L].FDIETSSQSDLKGDVR.[H]	2xTMT6plex [N-Term; K12]	
High	[K].EVEVPQGR.[K]	1xTMT6plex [N-Term]	
High	[F].LENIIKDSVTYTEHAR.[R]	2xTMT6plex [N-Term; K6]	
High	[Q].GITKPAIR.[R]	2xTMT6plex [N-Term; K4]	
High	[M].ADLTLEPR.[G]	1xAcetyl [N-Term]	TGGT1_239
High	[-].MNPQDKAKQAVGYFAVDTYVR.[S]	3xTMT6plex [N-Term; K6; K8]	
High	[-].MEGTTKINEELRPAVRPLEVPQR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_239
High	[M].GQHGAESAPLSHAGISCR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C17	
High	[M].GQHGAESAPLSHAGISCR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_239
High	[-].MEGAGVSGVQMR.[D]	1xAcetyl [N-Term]	TGGT1_239
High	[K].FTVDCQKPVDDNIIEAKGLER.[F]	3xTMT6plex [N-Term; K7; K17]; 1xCarbamidome	
High	[T].QSGATFEDVTDECLTLHNKFR.[T]	2xTMT6plex [N-Term; K19]; 1xCarbamidomethy	
High	[Q].SGATFEDVTDECLTLHNKFR.[T]	2xTMT6plex [N-Term; K18]; 1xCarbamidomethy	
High	[G].ATFEDVTDECLTLHNKFR.[T]	2xTMT6plex [N-Term; K16]; 1xCarbamidomethy	
High	[R].AEAETGLQTFQHER.[S]	1xAcetyl [N-Term]	TGGT1_239
High	[R].AEAETGLQTFQHER.[S]	1xTMT6plex [N-Term]	
High	[Q].SHPGSASLEVPAAFGKVEEGPR.[R]	2xTMT6plex [N-Term; K16]	
High	[A].GSEAIADGGHLAVYAGTVTASAR.[G]	1xTMT6plex [N-Term]	
High	[A].GSEAIADGGHLAVYAGTVTASAR.[G]	1xAcetyl [N-Term]	TGGT1_240
High	[L].QAGSLSAPQLIQSQR.[S]	1xTMT6plex [N-Term]	
High	[V].SAPGVSPSVGSAPSASPPVR.[L]	1xTMT6plex [N-Term]	
High	[L].SAPQLIQSQR.[S]	1xTMT6plex [N-Term]	
High	[L].EVPAAFGKVEEGPR.[R]	2xTMT6plex [N-Term; K8]	
High	[A].SMPGPSPKSEPPLLPTQR.[T]	2xTMT6plex [N-Term; K8]	
High	[Q].AGSLSAPQLIQSQR.[S]	1xTMT6plex [N-Term]	
High	[A].SLHSEPGAASMPGPSPKSEPPLLPTQR.[T]	2xTMT6plex [N-Term; K17]	
High	[A].AHAEHPEDSATNFLFSFAENSLANR.[E]	1xAcetyl [N-Term]	TGGT1_240
High	[A].HAEHPEDSATNFLFSFAENSLANR.[E]	1xTMT6plex [N-Term]	

High	[L].DSLIPGFLKR.[R]	2xTMT6plex [N-Term; K9]	
High	[S].SSPVAPSARPPSDSSDSKR.[L]	2xTMT6plex [N-Term; K18]	
High	[M].ANNGELASFFR.[K]	1xAcetyl [N-Term]	TGGT1_240
High	[M].ANIDSTAANTNR.[M]	1xAcetyl [N-Term]	TGGT1_240
High	[Y].AIPLVTGLTR.[S]	1xTMT6plex [N-Term]	
High	[-].MIKSLSQLPLDR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_240
High	[C].FQLPAPNAFLGHSLLR.[S]	1xTMT6plex [N-Term]	
High	[M].GHPQIASGGPR.[G]	1xTMT6plex [N-Term]	
High	[M].ASSDSNAKLASQR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_240
High	[M].TDGNYFQPAKR.[G]	2xTMT6plex [N-Term; K10]	
High	[M].TDGNYFQPAKR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_240
High	[M].AYPPSGVDADKTNLR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_240
High	[M].AVQTAVDDPEAPAEDQPLLGGSLKKPSTYR.[Q	3xTMT6plex [N-Term; K24; K25]	
High	[L].AEGKPGEKR.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_241
High	[M].SEVYVHEPSTR.[G]	1xAcetyl [N-Term]	TGGT1_241
High	[M].GKNENSNPVGR.[G]	2xTMT6plex [N-Term; K2]	
High	[M].ATEAKLFGR.[W]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_242
High	[M].APTIVDAPLIQLLADGYGQYR.[Q]	1xTMT6plex [N-Term]	
High	[-].MIMEHDQEKLLDEASAVVKEQAR.[Y]	3xTMT6plex [N-Term; K9; K19]	
High	[-].MIMEHDQEKLLDEASAVVKEQAR.[Y]	1xAcetyl [N-Term]; 2xTMT6plex [K9;	TGGT1_242
High	[M].IMEHDQEKLLDEASAVVKEQAR.[Y]	3xTMT6plex [N-Term; K8; K18]	
High	[I].MEHDQEKLLDEASAVVKEQAR.[Y]	1xAcetyl [N-Term]; 2xTMT6plex [K7;	TGGT1_242
High	[-].MIMEHDQEKLLDEASAVVKEQAR.[Y]	1xAcetyl [N-Term]; 1xOxidation [M3	TGGT1_242
High	[R].MLAAAADANALSAAATKSR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K17	TGGT1_242
High	[M].PQNEYIELHQKR.[F]	2xTMT6plex [N-Term; K11]	
High	[M].GVYPPVAGGPVYWALR.[N]	1xTMT6plex [N-Term]	
High	[M].AFSPEFLSR.[L]	1xAcetyl [N-Term]	TGGT1_242
High	[-].MEEATAAVAR.[C]	1xAcetyl [N-Term]	TGGT1_242
High	[-].MEALPVNSDVLDSR.[L]	1xAcetyl [N-Term]	TGGT1_243
High	[M].GGLDETALYQAAVQSETPGR.[A]	1xTMT6plex [N-Term]	
High	[S].SPSPVDVTATAPSPSPSASPAAGAAR.[N]	1xTMT6plex [N-Term]	
High	[C].TPSSPSLASFCASTSPSAPLLSGR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C11	
High	[S].AEPSSSETPSSAVSSHSPHR.[A]	1xTMT6plex [N-Term]	
High	[A].SSVGAPGKLHAR.[G]	2xTMT6plex [N-Term; K8]	
High	[M].TDPLSSEPKELLESAAAASSLLSSSPLSLSR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_243
High	[-].MESASPAGSGQAPGVAKSFHDGPR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K17	TGGT1_243
High	[M].AGTEVQASSPPSSALALR.[T]	1xTMT6plex [N-Term]	
High	[M].AGTEVQASSPPSSALALR.[T]	1xAcetyl [N-Term]	TGGT1_243
High	[T].LINAISDVHR.[T]	1xTMT6plex [N-Term]	
High	[S].ETLINAISDVHR.[T]	1xTMT6plex [N-Term]	
High	[-].MISEGGVPDVLQR.[G]	1xAcetyl [N-Term]	TGGT1_243
High	[S].EGGVPDVLQR.[G]	1xTMT6plex [N-Term]	
High	[A].IQLGKPQGSPPASQKEAIR.[D]	3xTMT6plex [N-Term; K5; K15]	
High	[A].ETPGAASAAAAEVGRPSR.[S]	1xTMT6plex [N-Term]	
High	[Q].LGKPQGSPPASQKEAIR.[D]	3xTMT6plex [N-Term; K3; K13]	
High	[S].AAAAEVGRPSR.[S]	1xTMT6plex [N-Term]	
High	[A].AAAEVGRPSR.[S]	1xTMT6plex [N-Term]	
High	[R].GPSLFTEETMGPSKR.[H]	2xTMT6plex [N-Term; K14]	
High	[Q].LGKPQGSPPASQKEAIR.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_243
High	[M].AAFVVDGLAALSR.[F]	1xAcetyl [N-Term]	TGGT1_243
High	[Q].SGPQIVYNVPIEDPVPAGKKR.[T]	3xTMT6plex [N-Term; K19; K20]	
High	[M].ASFCSSSCTSGPVGSEKYFSR.[S]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_243

High	[-].MEETPVYFNTSR.[L]	1xAcetyl [N-Term]	TGGT1_243
High	[L].SALGALDAR.[G]	1xTMT6plex [N-Term]	
High	[K].VDPQQLQPVAPISVPTQLAPQMPTPVSPLPL.[A	1xTMT6plex [N-Term]	
High	[R].AEGEAEAATLISEAIKQHGTGLIEVR.[R]	1xTMT6plex [K16]	
High	[V].AQQGPEAEHAVHAAAKPR.[M]	2xTMT6plex [N-Term; K16]	
High	[T].SVAQQGPEAEHAVHAAAKPR.[M]	2xTMT6plex [N-Term; K18]	
High	[Q].QGPEAEHAVHAAAKPR.[M]	2xTMT6plex [N-Term; K14]	
High	[A].QQGPEAEHAVHAAAKPR.[M]	2xTMT6plex [N-Term; K15]	
High	[S].DIELISNR.[L]	1xTMT6plex [N-Term]	
High	[M].ADAPAAASPSAAALPAELDALLHALELDRR.[V]	1xAcetyl [N-Term]	TGGT1_244
High	[A].SELDTALVSVPTSKAVSFTEFDIQQPPSDNSWLC	2xTMT6plex [N-Term; K14]; 1xCarbamidomethy	
High	[R].ATPQIASDSEQEKGTSSEEDAGPVAPEVAEEESR	2xTMT6plex [N-Term; K13]	
High	[K].MNAAGSNVSKEFFHLIKAIGEAR.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K10	TGGT1_244
High	[-].MEEDELSQCR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_244
High	[G].SEEASTLDTPEGR.[D]	1xAcetyl [N-Term]	TGGT1_244
High	[A].TETDAAEPLTAEEAPR.[S]	1xTMT6plex [N-Term]	
High	[L].SHPEVLEPKKNLDIR.[I]	3xTMT6plex [N-Term; K9; K10]	
High	[D].AAEPLTAEEAPR.[S]		
High	[-].MEDSGVSAAASSCVAR.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_244
High	[-].MLNFIPKR.[C]	2xTMT6plex [N-Term; K7]	
High	[K].GVLSVTGICDR.[N]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_245
High	[R].QNVQHTHSALLAKLKEPPDPDDENSWLCR.[I]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_245
High	[K].HKPEDNKGR.[Y]	3xTMT6plex [N-Term; K2; K7]	
High	[D].PDDENSWLCR.[I]	1xCarbamidomethyl [C9]	
High	[S].LVEVKFAQQR.[G]	2xTMT6plex [N-Term; K5]	
High	[M].SNFLEGLASIFSGKKPEKSDEMASMSTPAAELQ	1xAcetyl [N-Term]; 3xTMT6plex [K14	TGGT1_246
High	[M].ASMSTPAAELQR.[A]	1xAcetyl [N-Term]	TGGT1_246
High	[-].MDREQFLESLEKYHLER.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_246
High	[M].PHGWPIHVTR.[T]	1xTMT6plex [N-Term]	
High	[M].ASSAPSDAAVSDPVVGPPPVLCIFPFR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_246
High	[M].SAAVLPPPVAPGDSNAGVGDPKASGSAVNPSS	1xAcetyl [N-Term]; 1xTMT6plex [K22	TGGT1_246
High	[-].MEEGGAVIGR.[L]	1xAcetyl [N-Term]	TGGT1_246
High	[C].LEKEPPHPPSYPFWFKSLFHSHDIPSVR.[R]	3xTMT6plex [N-Term; K3; K16]	
High	[A].LIPAGKSAGSSFLAATSSQSSEEAPR.[E]	2xTMT6plex [N-Term; K6]	
High	[F].AEIVESDDWLR.[S]	1xAcetyl [N-Term]	TGGT1_246
High	[M].SDLDKTPESAGPSPWVEAATASR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_246
High	[M].ALHGLTAATKSLDQMSPADSR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_246
High	[-].MNFSIPSLDR.[L]	1xAcetyl [N-Term]	TGGT1_246
High	[M].AALSFSQESPWR.[A]	1xTMT6plex [N-Term]	
High	[A].GLLPAHNEDGWR.[A]	1xTMT6plex [N-Term]	
High	[A].EAAGNVEAALSHVDSHR.[S]	1xTMT6plex [N-Term]	
High	[A].AGNVEAALSHVDSHR.[S]	1xAcetyl [N-Term]	TGGT1_247
High	[T].MQKKLVVPEDSFPSSSSLYHR.[I]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_247
High	[G].SVPSPLLPSPQSQQPR.[A]	1xTMT6plex [N-Term]	
High	[M].ATPPLQDGAPTNGGAATKPSCGAR.[L]	2xTMT6plex [N-Term; K18]; 1xCarbamidomethy	
High	[M].ATPPLQDGAPTNGGAATKPSCGAR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_247
High	[Q].SPSAPQHDILWDAR.[K]	1xTMT6plex [N-Term]	
High	[F].SVQSPSAPQHDILWDAR.[K]	1xTMT6plex [N-Term]	
High	[C].SDGVFSVQSPSAPQHDILWDAR.[K]	1xTMT6plex [N-Term]	
High	[C].SDGVFSVQSPSAPQHDILWDAR.[K]	1xAcetyl [N-Term]	TGGT1_247
High	[A].VTSPAAEEER.[L]	1xTMT6plex [N-Term]	
High	[A].GAGAAPPGNPTKPQKEER.[E]	3xTMT6plex [N-Term; K12; K15]	

High	[L].SLASAGLQALR.[D]	1xTMT6plex [N-Term]	
High	[-].MLEAKLQHASVLR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_247
High	[-].MLEAKLQHASVLR.[R]	2xTMT6plex [N-Term; K5]	
High	[-].MLEAKLQH.[A]	2xTMT6plex [N-Term; K5]	
High	[M].AASGHPIPELGEFIIANKEKLR.[N]	1xAcetyl [N-Term]; 2xTMT6plex [K18	TGGT1_247
High	[A].ASGHPIPELGEFIIANKEKLR.[N]	1xAcetyl [N-Term]; 2xTMT6plex [K17	TGGT1_247
High	[M].AASGHPIPELGEFIIANKEK.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K]	TGGT1_247
High	[M].AASGHPIPELGEFIIANK.[E]	1xAcetyl [N-Term]	TGGT1_247
High	[L].GAAGNQNVQGEEQQKLDVFANHKFIQALVNR.	3xTMT6plex [N-Term; K15; K23]	
High	[M].DIQPSELHQR.[V]	1xTMT6plex [N-Term]	
High	[S].GHPIPELGEFIIANKEKLR.[N]	3xTMT6plex [N-Term; K15; K17]	
High	[Y].ATLNTPKPESPPPVPPPR.[S]	2xTMT6plex [N-Term; K7]	
High	[Q].GGGPPARPPSPSPEEEPIFGTFVKTDGGGVR.[G	2xTMT6plex [N-Term; K24]	
High	[A].SDQKQGSQNPAGGKGGSGPHGGR.[R]	3xTMT6plex [N-Term; K4; K14]	
High	[A].SDQKQGSQNPAGGKGGSGPHGGR.[R]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_247
High	[R].GVADSGGNKGR.[G]	2xTMT6plex [N-Term; K9]	
High	[Q].GSQNPAGGKGGSGPHGGR.[R]	2xTMT6plex [N-Term; K9]	
High	[Q].NPAGGKGGSGPHGGR.[R]	2xTMT6plex [N-Term; K6]	
High	[F].VKTDGGGVR.[G]	2xTMT6plex [N-Term; K2]	
High	[F].VTASDQKQGSQNPAGGKGGSGPHGGR.[R]	1xTMT6plex [K17]	
High	[A].SQENKNLGKSR.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K5;	TGGT1_247
High	[M].SAAAPKATSAPATSGVVSGGPSYLPLALVDKCI	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_247
High	[R].SYATEHGHFPFAPAR.[T]	1xTMT6plex [N-Term]	
High	[L].GGNHIYLGR.[F]	1xTMT6plex [N-Term]	
High	[M].AAKHHPDLIMCR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_248
High	[M].AAKHHPDLIMCR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_248
High	[M].AAAAAQAVPEFKLILVGDGGVGK.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_248
High	[M].AAAAAQAVPEFK.[L]	1xAcetyl [N-Term]	TGGT1_248
High	[C].ENIPIVLVGNKVDVKDR.[Q]	3xTMT6plex [N-Term; K11; K15]	
High	[M].AAAAAQAVPEFKLILVGDGGVGKTTLVK.[R]	1xAcetyl [N-Term]; 2xTMT6plex [K23	TGGT1_248
High	[M].SQEQLTEAMR.[E]	1xAcetyl [N-Term]	TGGT1_248
High	[-].MKFSSQVSSSR.[R]	2xTMT6plex [N-Term; K2]	
High	[L].EYFPTAPVR.[E]	1xTMT6plex [N-Term]	
High	[-].MEPCTVTVTDFTGGR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_248
High	[H].IRVGKHIVDIPSFMVR.[V]		
High	[L].GEYGLKNKR.[E]	3xTMT6plex [N-Term; K6; K8]	
High	[M].ATQSSLFDGVQEAPPDPILGLEVAFR.[A]	1xTMT6plex [N-Term]	
High	[A].EMAGLGPEVR.[S]	1xTMT6plex [N-Term]	
High	[S].FPLLSSSSPESEGDR.[F]	1xTMT6plex [N-Term]	
High	[M].ATEFVVPPSMLAVPNAGNMQTGTVGNIVPPS	1xAcetyl [N-Term]	TGGT1_248
High	[-].MENTEREDAPR.[E]	1xAcetyl [N-Term]	TGGT1_248
High	[S].AQTPGHLGADEEGPLPTVTLTQEDLDFYR.[E]	1xTMT6plex [N-Term]	
High	[M].TVATLFPKEEGVGFSLTTQSHGECKVR.[V]	3xTMT6plex [N-Term; K8; K25]; 1xCarbamidome	
High	[M].TVATLFPKEEGVGFSLTTQSHGECK.[V]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl	
High	[M].VDTAASADSAR.[A]	1xAcetyl [N-Term]	TGGT1_248
High	[-].MFSSSPLPAAPLVFDWGTHTLR.[A]	1xAcetyl [N-Term]	TGGT1_248
High	[M].ATPLTSGGQVQLAR.[Q]	1xAcetyl [N-Term]	TGGT1_249
High	[-].MQKPVCLVVAMTPKR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_249
High	[-].MQKPVCLVVAMTPKR.[G]	3xTMT6plex [N-Term; K3; K14]; 1xCarbamidome	
High	[D].GTITTKELGTVMR.[S]	1xTMT6plex [K6]	
High	[M].ADQLTEEQIAEFK.[E]	1xAcetyl [N-Term]	TGGT1_249
High	[M].ADQLTEEQIAEFKEAFSLFDK.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_249

High	[L].QLEGVNDR.[K]	1xTMT6plex [N-Term]	
High	[M].SSTADDELPR.[I]	1xAcetyl [N-Term]	TGGT1_249
High	[M].SVEVHNFGISDPFANDTSQFSVGGSSTHLIHIR.[	1xAcetyl [N-Term]	TGGT1_249
High	[K].METTLNGGGR.[A]	1xAcetyl [N-Term]	TGGT1_249
High	[H].ASFSCYDGASGTSPSTTSGGSAGDLGAPVSR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[-].MEDLSNATLAR.[L]	1xAcetyl [N-Term]	TGGT1_249
High	[-].MEFAGAPPVDDEADPTNCLPAEETVER.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_249
High	[T].EPVPAHFDAR.[T]	1xTMT6plex [N-Term]	
High	[A].TEPVPAHFDAR.[T]	1xTMT6plex [N-Term]	
High	[M].ADQAVLLALSSLCGSSVR.[Y]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_249
High	[M].AAASTASPPASR.[D]	1xAcetyl [N-Term]	TGGT1_249
High	[S].ATPEASLASQESAKHAPEQPGIR.[D]	2xTMT6plex [N-Term; K14]	
High	[Q].ESAKHAPEQPGIR.[D]	2xTMT6plex [N-Term; K4]	
High	[A].SQESAKHAPEQPGIR.[D]	2xTMT6plex [N-Term; K6]	
High	[C].GVSATPEASLASQESAKHAPEQPGIR.[D]	2xTMT6plex [N-Term; K17]	
High	[-].MSTLQDIR.[L]	1xTMT6plex [N-Term]	
High	[L].IQTQDSIPEIKEGKIPR.[Y]	3xTMT6plex [N-Term; K11; K14]	
High	[S].SLVIVYPLDFAR.[T]	1xTMT6plex [N-Term]	
High	[A].GVASYPFDTVR.[R]	1xTMT6plex [N-Term]	
High	[S].AGVSKTIVAPIER.[V]	2xTMT6plex [N-Term; K5]	
High	[Q].DSIPEIKEGKIPR.[Y]	3xTMT6plex [N-Term; K7; K10]	
High	[Q].TQDSIPEIKEGKIPR.[Y]	3xTMT6plex [N-Term; K9; K12]	
High	[L].VIVYPLDFAR.[T]	1xTMT6plex [N-Term]	
High	[A].GASSLVIVYPLDFAR.[T]	1xTMT6plex [N-Term]	
High	[A].SYPFDTVR.[R]	1xTMT6plex [N-Term]	
High	[A].SDVGKGNER.[E]	2xTMT6plex [N-Term; K5]	
High	[A].GVSKTIVAPIER.[V]	2xTMT6plex [N-Term; K4]	
High	[A].ASPGAAAPVPERPMR.[R]	1xTMT6plex [N-Term]	
High	[S].SSLPGGESEDFKDR.[E]	2xTMT6plex [N-Term; K12]	
High	[S].SLPGGESEDFKDR.[E]	2xTMT6plex [N-Term; K11]	
High	[E].QAQQLLADVDNLQEEIRGLEK.[R]	1xTMT6plex [N-Term]	
High	[-].MDDFELQPLEPDDAEADAFNDDTFGDVGGVV	1xAcetyl [N-Term]; 1xTMT6plex [K36	TGGT1_25
High	[F].EALHATIR.[D]	1xTMT6plex [N-Term]	
High	[G].EHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[E].HDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[L].QASIGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[Q].ASIGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[F].FNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[D].FFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[H].DFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[S].IGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[Q].SPEEVEEAKR.[K]	2xTMT6plex [N-Term; K9]	
High	[A].SIGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[Q].NQSPEEVEEAKR.[K]	2xTMT6plex [N-Term; K11]	
High	[N].QSPEEVEEAKR.[K]	2xTMT6plex [N-Term; K10]	
High	[D].YDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[A].AVAAPTPANDEVIETNYDEVVDSFDALKLNESLL	2xTMT6plex [N-Term; K28]	
High	[A].VAAPTPANDEVIETNYDEVVDSFDALKLNESLLR	2xTMT6plex [N-Term; K27]	
High	[V].AAPTPANDEVIETNYDEVVDSFDALKLNESLLR.[	2xTMT6plex [N-Term; K26]	
High	[A].EAVASSETGVGDTHHR.[S]	1xTMT6plex [N-Term]	
High	[M].APGVTQAEFQR.[E]	1xTMT6plex [N-Term]	
High	[M].ANLPHLDGSVAGPSAPAGR.[S]	1xTMT6plex [N-Term]	

High	[M].ANLPHLDGSVAGPSAPAGR.[S]	1xAcetyl [N-Term]	TGGT1_250
High	[M].AVDSSNSATGPMR.[V]	1xAcetyl [N-Term]	TGGT1_250
High	[-].MELFGDQYIR.[I]	1xAcetyl [N-Term]	TGGT1_251
High	[K].MNSGGKYIPPSMR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_251
High	[A].SESDVALKVPEDPVPEEPR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_251
High	[L].GDSPGFHFPR.[L]	1xTMT6plex [N-Term]	
High	[M].GIKGLGKFVGDFAPR.[A]	3xTMT6plex [N-Term; K3; K7]	
High	[D].PSLSEVAFEVATKR.[I]	1xTMT6plex [K13]	
High	[A].DNSEEDGGGVDSTSETVVDVVDAFR.[L]	1xTMT6plex [N-Term]	
High	[M].TIDVNLLR.[A]	1xTMT6plex [N-Term]	
High	[-].MTIDVNLLR.[A]	1xAcetyl [N-Term]	TGGT1_251
High	[R].TDLQEKITQLR.[S]	1xTMT6plex [K6]	
High	[R].AADSAAGVGAAQSAFPIDLR.[G]	1xTMT6plex [N-Term]	
High	[I].GKSGEKSFIDYAIDYSYNNAPLR.[R]	3xTMT6plex [N-Term; K2; K6]	
High	[D].PPEAGEDAGATAKKR.[K]	2xTMT6plex [K13; K14]	
High	[M].GHQSAPNSSYPTGR.[H]	1xTMT6plex [N-Term]	
High	[M].AHLHFGAAVPVVFR.[L]	1xAcetyl [N-Term]	TGGT1_252
High	[F].FFLHSKPPHGFPPNER.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_252
High	[M].STHSCGNVAGGAGSSGAAKCNMFR.[G]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_252
High	[-].MLTDGILPPSGR.[G]	1xAcetyl [N-Term]	TGGT1_252
High	[P].SADVLSVLLR.[G]	1xTMT6plex [N-Term]	
High	[S].ADVLSVLLR.[G]	1xAcetyl [N-Term]	TGGT1_253
High	[P].SADVLSVLLR.[G]	1xAcetyl [N-Term]	TGGT1_253
High	[A].SSSSPHIIVPR.[L]	1xAcetyl [N-Term]	TGGT1_253
High	[S].SSPHIIVPR.[L]	1xAcetyl [N-Term]	TGGT1_253
High	[-].METLSSAAGVR.[T]	1xAcetyl [N-Term]	TGGT1_253
High	[A].HIFSNLWR.[S]	1xTMT6plex [N-Term]	
High	[S].AAVPTASPAEGGGFLLVNPR.[C]	1xTMT6plex [N-Term]	
High	[M].AKLSAAVPTASPAEGGGFLLVNPR.[C]	2xTMT6plex [N-Term; K2]	
High	[M].AKLSAAVPTASPAEGGGFLLVNPR.[C]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_253
High	[M].AQQSGFCQPPGSPVNGAPSNTIYVPLINQTIR.[	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_253
High	[M].AFDLDAEPPPTIGPVVLR.[S]	1xTMT6plex [N-Term]	
High	[A].AAGPTPVGKGTPGGAKGQFR.[G]	3xTMT6plex [N-Term; K9; K16]	
High	[G].AAAGPTPVGKGTPGGAKGQFR.[G]	3xTMT6plex [N-Term; K10; K17]	
High	[A].AHPSALLPEVCSFVSR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C11	
High	[A].LLQSSSVAGSFPTPASVASSGR.[S]	1xTMT6plex [N-Term]	
High	[M].AADFPHSLDLR.[E]	1xAcetyl [N-Term]	TGGT1_253
High	[C].MAPPPPNQIGDIKR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_254
High	[G].ADSATDHPTCSAADKPVIVSITEPR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_254
High	[A].ELFGHLEVAPISSGAAKAGPVAAEEYR.[R]	2xTMT6plex [N-Term; K17]	
High	[A].ELFGHLEVAPISSGAAKAGPVAAEEYRR.[D]	2xTMT6plex [N-Term; K17]	
High	[F].GHLEVAPISSGAAKAGPVAAEEYR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K14	TGGT1_254
High	[M].SAATSPSGLPEQPATVHADDFR.[E]	1xAcetyl [N-Term]	TGGT1_254
High	[F].LFFDSCR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[D].PSEVKYIYLR.[Q]	1xTMT6plex [K5]	
High	[-].MKLVKQNYER.[D]	3xTMT6plex [N-Term; K2; K5]	
High	[A].EEVVLGR.[E]	1xTMT6plex [N-Term]	
High	[M].AAPAAFSAAR.[R]	1xAcetyl [N-Term]	TGGT1_254
High	[M].ASSKPGGASKAGVDAVQEISMMAR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_254
High	[M].AAGSAMVDKGVSPVAR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_254
High	[M].AAGSAMVDKGVSPVAR.[R]	2xTMT6plex [N-Term; K9]	
High	[-].MDSDIPADKMQEMETQLAMLLEGQR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_254

High	[-].MDSDIPADKMQEMETQLAMLLEGQR.[Q]	1xAcetyl [N-Term]; 1xOxidation [M];	TGGT1_254
High	[K].GLSLKKHLGR.[K]	3xTMT6plex [N-Term; K5; K6]	
High	[M].SGLEKSGFGIAHDFKGR.[T]	1xAcetyl [N-Term]; 2xTMT6plex [K5;	TGGT1_254
High	[T].SDPLDFHWPGSR.[I]	1xTMT6plex [N-Term]	
High	[A].VTSDPLDFHWPGSR.[I]	1xTMT6plex [N-Term]	
High	[A].TNDNHIGEESSEFLEWHGGKVTAR.[E]	2xTMT6plex [N-Term; K20]	
High	[-].MEAPGLPSNEDNIQLFLAGGEESPVDKPAIVKHF	1xAcetyl [N-Term]; 2xTMT6plex [K27	TGGT1_255
High	[M].ALSELPGTLETAGLER.[S]	1xAcetyl [N-Term]	TGGT1_255
High	[S].TSGNPFQANVEMKTFMER.[F]	2xTMT6plex [N-Term; K13]	
High	[Q].CTADKFPDSFGACDVQACKR.[Q]	3xTMT6plex [N-Term; K5; K19]; 3xCarbamidome	
High	[Q].ASWNDWWPLHQSDQPHSGGVGR.[N]	1xTMT6plex [N-Term]	
High	[T].SQASWNDWWPLHQSDQPHSGGVGR.[N]	1xTMT6plex [N-Term]	
High	[S].GNPFQANVEMKTFMER.[F]	2xTMT6plex [N-Term; K11]	
High	[Q].AAHHEHEFQSDR.[G]	1xTMT6plex [N-Term]	
High	[R].CLDYTELTDTVIER.[V]	1xCarbamidomethyl [C1]	
High	[T].ALQCTADKFPDSFGACDVQACKR.[Q]	3xTMT6plex [N-Term; K8; K22]; 3xCarbamidome	
High	[R].ESQTLSASTSGNPFQANVEMKTFMER.[F]	2xTMT6plex [N-Term; K21]	
High	[A].HHEHEFQSDR.[G]	1xTMT6plex [N-Term]	
High	[S].TSGNPFQANVEMKTFMER.[F]	2xTMT6plex [N-Term; K13]; 1xOxidation [M]	
High	[-].MEEAAFSMVR.[H]	1xAcetyl [N-Term]	TGGT1_255
High	[-].MDVVFEFTR.[V]	1xAcetyl [N-Term]	TGGT1_255
High	[L].DLATAADSAPAMPHEEVGLSKR.[K]	2xTMT6plex [N-Term; K21]	
High	[A].ENKTENAGIER.[A]	2xTMT6plex [N-Term; K3]	
High	[A].AAAPQASASGKTAKDASPSTANLQPR.[T]	1xAcetyl [N-Term]; 2xTMT6plex [K11	TGGT1_255
High	[R].SSSVGGESEGEGGGETETTGEAGER.[R]	1xTMT6plex [N-Term]	
High	[M].GWITSTLKDLR.[Q]	2xTMT6plex [N-Term; K8]	
High	[M].VSLSGTLNGEEALER.[Q]	1xTMT6plex [N-Term]	
High	[M].TTASAIIGPSGGR.[D]	1xAcetyl [N-Term]	TGGT1_255
High	[-].MNVFEQYNQR.[Q]	1xTMT6plex [N-Term]	
High	[-].MNVFEQYNQR.[Q]	1xAcetyl [N-Term]	TGGT1_255
High	[M].VLADNNVFLEELGR.[L]	1xTMT6plex [N-Term]	
High	[M].APEEKKGSR.[N]	3xTMT6plex [N-Term; K5; K6]	
High	[M].ASKQPQTLSAGAVESGR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_256
High	[R].SEEDWTAHR.[T]	1xTMT6plex [N-Term]	
High	[S].SVMTQQLGKSTNIR.[M]	2xTMT6plex [N-Term; K9]	
High	[F].ETSEDCQVLPTFDAMGFKEDLLR.[G]	2xTMT6plex [N-Term; K18]; 1xCarbamidomethy	
High	[A].SLLASPASAFFR.[L]	1xTMT6plex [N-Term]	
High	[A].ALSVDPEVLPSPASLLASPASAFFR.[L]	1xTMT6plex [N-Term]	
High	[M].TTLNGVTPADEAATEQLAEQLR.[E]	1xTMT6plex [N-Term]	
High	[M].TTLNGVTPADEAATEQLAEQLR.[E]	1xAcetyl [N-Term]	TGGT1_256
High	[Q].VAGFDLQR.[M]	1xTMT6plex [N-Term]	
High	[E].ECPSIQVAGFDLQR.[M]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2]	
High	[-].MQGSSAPAEIGDCLFAISADSIGR.[I]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_257
High	[A].ANAVQAHGGAHAPAATVTPR.[Y]	1xTMT6plex [N-Term]	
High	[F].AANAVQAHGGAHAPAATVTPR.[Y]	1xTMT6plex [N-Term]	
High	[Q].AHGGAHAPAATVTPR.[Y]	1xTMT6plex [N-Term]	
High	[-].MNCSWDTAVWGDALPPCTHPPFR.[R]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_257
High	[M].VDYSKWER.[L]	2xTMT6plex [N-Term; K5]	
High	[S].MVDINEIR.[T]	1xTMT6plex [N-Term]	
High	[V].GHAPPPPGGGPGASAASPQHHAER.[K]	1xTMT6plex [N-Term]	
High	[M].SHQPPTQTYSAGER.[G]	1xAcetyl [N-Term]	TGGT1_257
High	[A].SAVPLSPAPEVAR.[E]	1xTMT6plex [N-Term]	

High	[M].MVGGVFGCFITR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_257
High	[-].MESTEATMVER.[K]	1xAcetyl [N-Term]	TGGT1_257
High	[M].AATNTIESGTTR.[C]	1xAcetyl [N-Term]	TGGT1_257
High	[M].AATNTIESGTTR.[C]	1xTMT6plex [N-Term]	
High	[M].PHAGFTDDILLLDGGLGTHLR.[A]	1xTMT6plex [N-Term]	
High	[-].MDADSWTTLVKKAF.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K11	TGGT1_257
High	[-].MDADSWTTLVKKAFLAGQEVCR.[E]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_257
High	[M].TALPPPPSANVAVSFTAAPAEPLSR.[G]	1xTMT6plex [N-Term]	
High	[M].TALPPPPSANVAVSFTAAPAEPLSR.[G]	1xAcetyl [N-Term]	TGGT1_258
High	[M].AEALEAERPEGAFR.[S]	1xAcetyl [N-Term]	TGGT1_258
High	[-].MHSLFKSALEAAR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_258
High	[M].ATKQMLPGEGADR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_258
High	[F].SSLSLQDGICGSDEKSVIR.[A]	2xTMT6plex [N-Term; K15]; 1xCarbamidomethy	
High	[M].TDNAQTTSAEAGAANPSGEHPSAGAKR.[R]	2xTMT6plex [N-Term; K26]	
High	[-].MTDNAQTTSAEAGAANPSGEHPSAGAKR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K27	TGGT1_258
High	[M].TDNAQTTSAEAGAANPSGEHPSAGAKR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K26	TGGT1_258
High	[-].MEDPWKGGSGGYGEPSYGAEGVGTR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_258
High	[Q].SASEADEEEESGGSSKR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_258
High	[A].AKQNLYSVLGVKR.[N]	3xTMT6plex [N-Term; K2; K12]	
High	[M].SQPNLQYAHTGAIEDYYR.[L]	1xAcetyl [N-Term]	TGGT1_258
High	[A].HTGAIEDYYR.[L]	1xTMT6plex [N-Term]	
High	[G].AIEDYYR.[L]	1xTMT6plex [N-Term]	
High	[Q].YAHTGAIEDYYR.[L]	1xTMT6plex [N-Term]	
High	[V].SNALFDASGAFR.[S]	1xTMT6plex [N-Term]	
High	[A].GTPGPLHYGVPLSDGCDPGVYAVSNALFDASG	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C16	
High	[A].ESVETEEELKER.[Q]	2xTMT6plex [N-Term; K10]	
High	[R].SPTSNDVFGELVASAER.[A]	1xTMT6plex [N-Term]	
High	[Q].QPQLPQEAMPTENADLLGNQPGMR.[N]	1xTMT6plex [N-Term]	
High	[-].MIEVILNDR.[L]	1xTMT6plex [N-Term]	
High	[M].VDTNASKQPAATADR.[K]	2xTMT6plex [N-Term; K7]	
High	[-].MVDTNASKQPAATADR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_258
High	[M].PVECPVGGGQETPR.[A]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C4]	
High	[M].ASLVQPAR.[F]	1xTMT6plex [N-Term]	
High	[T].WIAEHLADTDSGKDSHDYR.[F]	2xTMT6plex [N-Term; K13]	
High	[A].EHLADTDSGKDSHDYR.[F]	2xTMT6plex [N-Term; K10]	
High	[L].NDDQHNHVEEGDGEVGGR.[T]	1xTMT6plex [N-Term]	
High	[E].EKTKGQLAGVLR.[L]	3xTMT6plex [N-Term; K2; K4]	
High	[A].EVVEDDSKDSR.[A]	2xTMT6plex [N-Term; K8]	
High	[Q].EFVKAMTVPR.[I]	2xTMT6plex [N-Term; K4]	
High	[-].MELSFFNVDDGYLEGICR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_259
High	[S].TSSSEGGVWEFLSGVCGR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C16	
High	[S].SSEGGVWEFLSGVCGR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C14	
High	[T].SSSEGGVWEFLSGVCGR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C15	
High	[S].SEGGVWEFLSGVCGR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13	
High	[S].NSPSSFLSSSSSLLWEAVEQCVVSLEGREPGQYE	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_259
High	[S].SSHVSNESHSFQR.[I]	1xTMT6plex [N-Term]	
High	[-].MEDAIHQLR.[D]	1xAcetyl [N-Term]	TGGT1_259
High	[T].MTANSHFLQKMR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_259
High	[M].TANSHFLQKMR.[E]	2xTMT6plex [N-Term; K9]	
High	[M].TANSHFLQKMR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_259
High	[T].ALGDTGLLGSVGSSVWR.[S]	1xTMT6plex [N-Term]	
High	[A].AGGAYYWAR.[D]	1xTMT6plex [N-Term]	

High	[S].AAGGAYYWAR.[D]	1xTMT6plex [N-Term]	
High	[S].AAGGAYYWAR.[D]	1xAcetyl [N-Term]	TGGT1_259
High	[-].MEVCLPTR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_259
High	[M].VVVVNGELLPDSDPR.[A]	1xTMT6plex [N-Term]	
High	[M].AFAGAAAPLGVKGR.[S]	2xTMT6plex [N-Term; K12]	
High	[M].AFAGAAAPLGVKGR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_260
High	[L].SAAGPQGAPASTLHSKASR.[Q]	2xTMT6plex [N-Term; K16]	
High	[S].AAGPQGAPASTLHSKASR.[Q]	2xTMT6plex [N-Term; K15]	
High	[M].AAVATSALPEAQK.[Q]	1xAcetyl [N-Term]	TGGT1_260
High	[M].AAVATSALPEAQKQELLCTYAALILSDDK.[M]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_260
High	[-].MNAFQSPSLDITISR.[G]	1xAcetyl [N-Term]	TGGT1_260
High	[-].MFYGVVVKPGQTVTLSPEDGGEVLHLSQVCMP	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_260
High	[-].MFYGVVVKPGQTVTLSPEDGGEVLHLS.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_260
High	[-].MYADAPIAGHPTEALVGGQNGYPAIPTSAAHIA	1xAcetyl [N-Term]	TGGT1_260
High	[-].MYADAPIAGHPTEALVGGQNGYPAIPTSAAH.[I	1xAcetyl [N-Term]	TGGT1_260
High	[A].QRPDATLPDLVTAR.[V]	1xTMT6plex [N-Term]	
High	[-].MELCESPCCEPR.[E]	1xAcetyl [N-Term]; 3xCarbamidomet	TGGT1_260
High	[A].SSLGGHDLYFGGLQHQR.[G]	1xTMT6plex [N-Term]	
High	[L].GGHDLYFGGLQHQR.[G]	1xTMT6plex [N-Term]	
High	[L].SAQGLESTGTDAHFR.[A]	1xTMT6plex [N-Term]	
High	[M].SRPEYEAPADVFYNALEAKKYAR.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K19	TGGT1_260
High	[S].GGAAAPGAVGR.[R]	1xTMT6plex [N-Term]	
High	[-].MEPSQMQEHHPPPGPVAAEEALR.[C]	1xAcetyl [N-Term]	TGGT1_260
High	[Q].EHHPPPGPVAAEEALR.[C]	1xTMT6plex [N-Term]	
High	[A].SAPQVTAADIEDLHR.[R]	1xTMT6plex [N-Term]	
High	[S].HAASAPQVTAADIEDLHR.[R]	1xTMT6plex [N-Term]	
High	[M].AYLYYPTVTLQR.[V]	1xAcetyl [N-Term]	TGGT1_260
High	[M].SALAGPLRPPCATEGEDGPSSGLQTYYEQKIDN	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_261
High	[M].AYSLLPGSTAR.[R]	1xAcetyl [N-Term]	TGGT1_261
High	[A].VEVSSPEALKTTFEER.[E]	2xTMT6plex [N-Term; K10]	
High	[-].MEGGSGSLYDVDDTAASLAGDPSTVATVPR.[G]	1xAcetyl [N-Term]	TGGT1_261
High	[K].SAKAGLQFPVGR.[I]	2xTMT6plex [N-Term; K3]	
High	[S].SSKSAKAGLQFPVGR.[I]	3xTMT6plex [N-Term; K3; K6]	
High	[S].SKSAKAGLQFPVGR.[I]	3xTMT6plex [N-Term; K2; K5]	
High	[L].EYLCAEILELAGNAAR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C4]	
High	[M].SGQALAAATAAVPSGAATSPGSR.[E]	1xAcetyl [N-Term]	TGGT1_261
High	[M].AETTDAPAAAPLPASAPPGGSAGPAIALGNIR.[	1xAcetyl [N-Term]	TGGT1_261
High	[-].MEAGSFFR.[L]	1xAcetyl [N-Term]	TGGT1_261
High	[M].ATVADDVMSAASWGSR.[V]	1xAcetyl [N-Term]	TGGT1_261
High	[R].DGEGEGSEKGSQPSPPGKPLQR.[R]	2xTMT6plex [K9; K18]	
High	[R].ASHSSSKGEGGDEEKHK.[D]	1xAcetyl [N-Term]; 2xTMT6plex [K7;	TGGT1_261
High	[G].SQPSPPGKPLQR.[R]	2xTMT6plex [N-Term; K8]	
High	[R].EEDRDGEGEGSEKGSQPSPPGKPLQR.[R]	2xTMT6plex [K13; K22]	
High	[Q].TDASPSSGGIWAGVKKYVELGTSGER.[H]	1xAcetyl [N-Term]; 2xTMT6plex [K15	TGGT1_261
High	[S].SAAPNPGKKPASAAPPAGTNHGR.[I]	3xTMT6plex [N-Term; K8; K9]	
High	[S].AAPNPGKKPASAAPPAGTNHGR.[I]	3xTMT6plex [N-Term; K7; K8]	
High	[L].SSAAPNPGKKPASAAPPAGTNHGR.[I]	3xTMT6plex [N-Term; K9; K10]	
High	[S].ATTPPLAAQVQALLQAPELR.[Y]	1xTMT6plex [N-Term]	
High	[A].SATTPPLAAQVQALLQAPELR.[Y]	1xTMT6plex [N-Term]	
High	[M].SGAASATTPPLAAQVQALLQAPELR.[Y]	1xAcetyl [N-Term]	TGGT1_262
High	[Q].AVGGVGGPPYAGDGSPLLASR.[L]	1xAcetyl [N-Term]	TGGT1_262
High	[R].SALLGQSR.[G]	1xTMT6plex [N-Term]	

High	[A].MNSTGNASPSSLLR.[R]	1xAcetyl [N-Term]	TGGT1_262
High	[K].TIQDLMQACDDFIPEPER.[K]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[C].DDFIPEPER.[K]	1xTMT6plex [N-Term]	
High	[A].ATVQDAEEVER.[R]	1xAcetyl [N-Term]	TGGT1_262
High	[M].SEVEETLNR.[I]	1xAcetyl [N-Term]	TGGT1_262
High	[M].TLSHPSGAQGAGGPNNSR.[S]	1xTMT6plex [N-Term]	
High	[M].PADEQQQQLPR.[E]	1xTMT6plex [N-Term]	
High	[M].PADEQQQQLPR.[E]		
High	[-].MPADEQQQQLPR.[E]	1xMet-loss [N-Term]	TGGT1_262
High	[V].EYTNVEDAQKAIKELTDTELFDR.[L]	3xTMT6plex [N-Term; K10; K13]	
High	[Q].IANLPYHSQVPSPPPR.[E]	1xTMT6plex [N-Term]	
High	[D].PTLQQKISQYQVVGR.[K]	1xTMT6plex [K6]	
High	[-].MKADPTLQQKISQY.[Q]	3xTMT6plex [N-Term; K2; K10]	
High	[-].MKADPTLQQKISQYQVVGR.[K]	3xTMT6plex [N-Term; K2; K10]	
High	[S].SASNSPVSSDNEVPDPQR.[N]	1xTMT6plex [N-Term]	
High	[F].EEAQKASEAAKR.[Q]	1xAcetyl [N-Term]; 2xTMT6plex [K5;	TGGT1_262
High	[M].SFEEAQKASEAAKR.[Q]	1xAcetyl [N-Term]; 2xTMT6plex [K7;	TGGT1_262
High	[L].DSGIQSPAQKR.[R]	2xTMT6plex [N-Term; K10]	
High	[N].ISSGVSGGKPADPR.[R]	2xTMT6plex [N-Term; K9]	
High	[N].GDKPGKPESLER.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_262
High	[Q].VTPKHILANR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_262
High	[S].SFPAQEALSEKASEAVEEGPR.[S]	2xTMT6plex [N-Term; K11]	
High	[Q].VTPKHILANR.[S]	2xTMT6plex [N-Term; K4]	
High	[Q].TQVTPKHILANR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_262
High	[C].TQGKGLLR.[V]	2xTMT6plex [N-Term; K4]	
High	[V].ALCTQGKGLLR.[V]	2xTMT6plex [N-Term; K7]; 1xCarbamidomethyl	
High	[S].GLLRPIVHPPTQR.[Y]	1xTMT6plex [N-Term]	
High	[S].TAMPIPKASKR.[C]	3xTMT6plex [N-Term; K7; K10]	
High	[L].SIGVAVDHR.[R]	1xTMT6plex [N-Term]	
High	[A].LSIGVAVDHR.[R]	1xTMT6plex [N-Term]	
High	[M].VSKNNVLPNVHLHKWWQR.[Y]	3xTMT6plex [N-Term; K3; K14]	
High	[R].QEAAVGFCLAFQLWYWYPLIHMV.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_263
High	[R].PTADAGAPPATVAPAAR.[G]	1xTMT6plex [N-Term]	
High	[A].PPRPTADAGAPPATVAPAAR.[G]	1xTMT6plex [N-Term]	
High	[M].APPRPTADAGAPPATVAPAAR.[G]	1xTMT6plex [N-Term]	
High	[P].TADAGAPPATVAPAAR.[G]	1xTMT6plex [N-Term]	
High	[M].PAPAASGAAAVLSKDIAR.[S]	2xTMT6plex [N-Term; K14]	
High	[R].DEYVYKAKLAEQAER.[Y]	2xTMT6plex [K6; K8]	
High	[M].AEEIKNLR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_263
High	[M].AAKPEQDCKTAAALIR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_263
High	[M].APPSACAAPTSAGVCAAEFELLAIGPLDGR.[Y]	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C6;	
High	[R].ANLHPWLPEKPLLIGHR.[G]	2xTMT6plex [N-Term; K10]	
High	[N].LHPWLPEKPLLIGHR.[G]	2xTMT6plex [N-Term; K8]	
High	[M].VLFKDLNKSCADLLTK.[G]	3xTMT6plex [N-Term; K4; K8]; 1xCarbamidomet	
High	[M].VLFKDLNK.[S]	2xTMT6plex [N-Term; K4]	
High	[M].TTTSGSTMMSMESQLNCSLDDLVKMQR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_263
High	[-].MEDSNFSLQAETQQLR.[E]	1xAcetyl [N-Term]	TGGT1_263
High	[M].AANAASKFIPLLDR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K7]	TGGT1_263
High	[A].SKFIPLLDR.[V]	2xTMT6plex [N-Term; K2]	
High	[M].AHYGLLFAR.[G]	1xTMT6plex [N-Term]	
High	[Y].ASFNDTFIHVTDLSGR.[E]	1xTMT6plex [N-Term]	
High	[A].TGEEGEAQGSGLGPATR.[D]	1xTMT6plex [N-Term]	

High	[R].SKTPGPGAQSALR.[A]	2xTMT6plex [N-Term; K2]	
High	[K].ADRDESSPYAAMMAAADVAAR.[C]	1xTMT6plex [N-Term]	
High	[V].AVDAPVVGGGKR.[K]	2xTMT6plex [N-Term; K11]	
High	[P].SSLLKAEADEEEATKR.[D]	3xTMT6plex [N-Term; K5; K15]	
High	[M].SYNPSYGGQFQGLNAAR.[G]	1xAcetyl [N-Term]	TGGT1_263
High	[A].GSHSTIKQNASR.[V]	2xTMT6plex [N-Term; K7]	
High	[R].GPTTPFSSTPAPY.[S]	1xTMT6plex [N-Term]	
High	[R].GPTTPFSSTPAPYSAISR.[A]	1xTMT6plex [N-Term]	
High	[-].MLADGLPSR.[G]	1xAcetyl [N-Term]	TGGT1_264
High	[F].AADEASSDDRPLLER.[V]	1xTMT6plex [N-Term]	
High	[A].ADEASSDDRPLLER.[V]	1xTMT6plex [N-Term]	
High	[M].AASSPENSAGAAGTQR.[Q]	1xTMT6plex [N-Term]	
High	[M].APAVLMVAEKPSIAETIAR.[I]	2xTMT6plex [N-Term; K10]	
High	[M].ADILQENFQDLVHSPGGGR.[S]	1xAcetyl [N-Term]	TGGT1_264
High	[L].QGQNHQSLEQDAAAPADGANAGDVAHAFGE	1xTMT6plex [N-Term]	
High	[G].APAYGVGSEEGGYGGSPASGGAER.[G]	1xTMT6plex [N-Term]	
High	[A].GDVAHAFGENADSR.[E]	1xTMT6plex [N-Term]	
High	[A].GAPAYGVGSEEGGYGGSPASGGAER.[G]	1xTMT6plex [N-Term]	
High	[G].SEEGGYGGSPASGGAER.[G]	1xTMT6plex [N-Term]	
High	[M].ANHIVLPPQKLLKVPPSVR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K10	TGGT1_264
High	[M].APNEKIPATSASR.[G]	2xTMT6plex [N-Term; K5]	
High	[M].SETKGTQGCHPGSVYR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_264
High	[M].AVNPVLAQDASTKETFPLPVPGEVFFLKR.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K13	TGGT1_265
High	[-].MDAVMVVHQLQR.[L]	1xAcetyl [N-Term]	TGGT1_265
High	[L].STASAGPSNAAPESGGVSEGDSSR.[G]	1xTMT6plex [N-Term]	
High	[S].SPVHDFPQAEKSFR.[R]	2xTMT6plex [N-Term; K11]	
High	[A].DLHQQAASLPYR.[S]	1xTMT6plex [N-Term]	
High	[M].PDPQYDPAAAQKSSNAR.[G]	2xTMT6plex [N-Term; K12]	
High	[D].PQYDPAAAQKSSNAR.[G]	1xTMT6plex [K10]	
High	[D].PAAAQKSSNAR.[G]	1xTMT6plex [K6]	
High	[F].STCDLLSGSSLR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C3]	
High	[-].MQSAEITALESPAIKAALECSPEINPAR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_265
High	[M].ASTTASSSGTDLSWLPSDAEEQLALGFR.[I]	1xAcetyl [N-Term]	TGGT1_265
High	[M].APPTVAENGGENR.[T]	1xTMT6plex [N-Term]	
High	[A].HQPHVPPPGGYYAPPR.[S]	1xTMT6plex [N-Term]	
High	[T].ATASATGATNTAAR.[G]	1xTMT6plex [N-Term]	
High	[M].AHPSEPPPHVR.[G]	1xAcetyl [N-Term]	TGGT1_265
High	[M].AADKQAKLSLQEDSIAK.[M]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_266
High	[-].MLGTFCGESNR.[D]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_266
High	[M].AAASPSAPPPPPPTHHVVVPRPPAGPQFFVDQ	1xAcetyl [N-Term]; 1xTMT6plex [K33	TGGT1_266
High	[Q].GLNAENVQLFR.[M]	1xTMT6plex [N-Term]	
High	[R].SLHDADSFWR.[E]	1xTMT6plex [N-Term]	
High	[T].MEGGAEHVER.[G]	1xAcetyl [N-Term]	TGGT1_266
High	[M].GQAGGDLLR.[A]	1xTMT6plex [N-Term]	
High	[A].TVTHPETVPETR.[I]	1xTMT6plex [N-Term]	
High	[M].PQTNIPSWHFANEKGR.[F]	2xTMT6plex [N-Term; K14]	
High	[V].FIDEIDAVGTKR.[Y]	2xTMT6plex [N-Term; K11]	
High	[E].SLDPALIRPGR.[I]	1xTMT6plex [N-Term]	
High	[-].MDPYLASSYAPPR.[G]	1xAcetyl [N-Term]	TGGT1_267
High	[A].PVGAETPFGAQEAGAQFTCAALEGTMR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C19	
High	[M].SLPGHEGRPSASIPLHSNR.[L]	1xAcetyl [N-Term]	TGGT1_267
High	[M].APVSTVKR.[S]	2xTMT6plex [N-Term; K7]	

High	[M].TSGEEEDFYLR.[Y]	1xTMT6plex [N-Term]	
High	[T].MTSGEEEDFYLR.[Y]	1xAcetyl [N-Term]	TGGT1_267
High	[M].TSGEEEDFYLR.[Y]	1xAcetyl [N-Term]	TGGT1_267
High	[-].MDEVLQR.[S]	1xTMT6plex [N-Term]	
High	[M].PASSLGDLPYLLR.[Q]	1xTMT6plex [N-Term]	
High	[-].MEELIPVVNR.[L]	1xAcetyl [N-Term]	TGGT1_267
High	[A].HLGAQGPKAASPAPAKAGDR.[G]	3xTMT6plex [N-Term; K8; K16]	
High	[M].CYEVKCTHCGKR.[T]	3xTMT6plex [N-Term; K5; K11]; 3xCarbamidome	
High	[M].GVKGLWDLLEPAGR.[R]	2xTMT6plex [N-Term; K3]	
High	[S].SIVASAAPSTVVSGR.[S]	1xTMT6plex [N-Term]	
High	[V].ASAAPSTVVSGR.[S]	1xTMT6plex [N-Term]	
High	[M].ASSSDPVTLPANAAQLR.[E]	1xAcetyl [N-Term]	TGGT1_268
High	[M].GTAKASGNEGVASSR.[Q]	2xTMT6plex [N-Term; K4]	
High	[A].AANTPGFSLKGDDYTDR.[A]	2xTMT6plex [N-Term; K10]	
High	[P].ADLTPIVEAIR.[Q]	1xAcetyl [N-Term]	TGGT1_268
High	[M].AAPNSFAFSADQQR.[A]	1xAcetyl [N-Term]	TGGT1_268
High	[-].MLPVQGQTSLLANTGEER.[L]	1xAcetyl [N-Term]	TGGT1_268
High	[C].SIWRPQGTPEVGSLGHDAADTAAAEAAR.[D]	1xTMT6plex [N-Term]	
High	[C].SIWRPQGTPEVGSLGHDAADTAAAEAAR.[D]	1xAcetyl [N-Term]	TGGT1_268
High	[R].DSWMSLAPF.[V]	1xTMT6plex [N-Term]	
High	[R].DSWMSLAPFVAPN.[N]	1xTMT6plex [N-Term]	
High	[R].DSWMSLAPFVAPNNAAAWR.[K]	1xTMT6plex [N-Term]	
High	[R].DSWMSLAPFVAPNNAAAWR.[K]	1xTMT6plex [N-Term]; 1xOxidation [M4]	
High	[R].DSWMSLAPF.[V]	1xTMT6plex [N-Term]; 1xOxidation [M4]	
High	[R].SGETEDSFIADLVVGLR.[CT]	1xTMT6plex [N-Term]	
High	[M].VAIKDITAR.[Q]	2xTMT6plex [N-Term; K4]	
High	[K].MVAIKDITAR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_268
High	[M].VAIKDITAR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_268
High	[T].EHAEGAPGASPAPAKTGATSGAQER.[A]	2xTMT6plex [N-Term; K15]	
High	[F].GLLGSSSEKASAPIR.[L]	2xTMT6plex [N-Term; K9]	
High	[F].GLLGSSSEKASAPIR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_269
High	[M].AAAPLGSATAAGSDAAGTPDVGPGAELPYLGS	1xAcetyl [N-Term]	TGGT1_269
High	[L].GNASAQPSSPPSQHAGR.[G]	1xTMT6plex [N-Term]	
High	[L].NEEDILHAR.[D]	1xTMT6plex [N-Term]	
High	[A].AAPLGSATAAGSDAAGTPDVGPGAELPYLGSR.	1xAcetyl [N-Term]	TGGT1_269
High	[A].GSDAAGTPDVGPGAELPYLGSR.[I]	1xTMT6plex [N-Term]	
High	[R].SALAEFKPLYGETLVCGFAHLNGYPIGVMANNG	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_269
High	[M].AVVGSSGVGASHSSFPSANGWIGDEQDIQETL	1xAcetyl [N-Term]	TGGT1_269
High	[D].STSGQNASPRPTKTDKIR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K13	TGGT1_269
High	[F].VDSTSGQNASPRPTKTDKIR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K15	TGGT1_269
High	[G].QNASPRPTKTDKIR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K9;	TGGT1_269
High	[T].SGQNASPRPTKTDKIR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K11	TGGT1_269
High	[G].APANLSPAAHPAVPAVISEHPFGTSPVHMATSA	1xTMT6plex [N-Term]	
High	[I].QVDQSLKEDR.[A]	2xTMT6plex [N-Term; K7]	
High	[C].ILPEVQAPDR.[K]	1xTMT6plex [N-Term]	
High	[M].CDITFVSR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_270
High	[M].SYMLQHLHSGWQVDQAILTEEER.[L]	1xAcetyl [N-Term]	TGGT1_270
High	[M].PTSAQVGKPLKAR.[T]	3xTMT6plex [N-Term; K8; K11]	
High	[E].GMPPPVLPPAPVVHPR.[F]	1xTMT6plex [N-Term]	
High	[G].EVVPDCEER.[Q]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[R].VPELPEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[L].GVDAVEKELR.[R]	2xTMT6plex [N-Term; K7]	

High	[A].AEGGDNQSSAVSDR.[A]	1xAcetyl [N-Term]	TGGT1_270
High	[A].AEGGDNQSSAVSDR.[A]	1xTMT6plex [N-Term]	
High	[A].YAAEGGDNQSSAVSDR.[A]	1xTMT6plex [N-Term]	
High	[A].GESAAELSTSIDDDDFDSSSGVAVPSLTTEQEVH	1xAcetyl [N-Term]	TGGT1_270
High	[A].GESAAELSTSIDDDDFDSSSGVAVPSLTTEQEVH	1xTMT6plex [N-Term]	
High	[M].AASTIPISQWPSLLYAPPSSPANPAVEALPEMQ	1xAcetyl [N-Term]	TGGT1_270
High	[K].SVTGNKILR.[I]	2xTMT6plex [N-Term; K6]	
High	[M].SASALPWR.[R]	1xTMT6plex [N-Term]	
High	[M].AQPQGESKSFTPGHLEDQVPTSCKQAIPVFGC	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_270
High	[-].MFSLASAPASR.[K]	1xAcetyl [N-Term]	TGGT1_270
High	[M].ATGCSLLIR.[N]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_270
High	[M].TTAHRPTWHQALGGEHQGGNR.[L]	1xAcetyl [N-Term]	TGGT1_270
High	[M].ADDEIDHMFAGEPGGLGDDFGEDFGDDELID	1xAcetyl [N-Term]	TGGT1_270
High	[M].ALSASPLSTQAVAKSR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K14	TGGT1_270
High	[N].MDEKIVALNPNR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_270
High	[S].GGSSFAGESGGGVHGGAPR.[G]	1xTMT6plex [N-Term]	
High	[A].WHQGSGDFLEHPNADGGSGAHSQR.[H]	1xTMT6plex [N-Term]	
High	[L].GLHSGVSGGSSFAGESGGGVHGGAPR.[G]	1xTMT6plex [N-Term]	
High	[D].KLTISPSGEGDVFYGKECTDSR.[K]	2xTMT6plex [K16; K]; 1xCarbamidomethyl [C18]	
High	[D].VFYGKECTDSR.[K]	1xCarbamidomethyl [C7]; 1xTMT6plex [K5]	
High	[R].NNDGSSAPTPKDCKLIVR.[V]	1xCarbamidomethyl [C13]; 2xTMT6plex [K11; K1	
High	[R].NNDGSSAPTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K11; K14]; 1xCarbamidom	
High	[N].NDGSSAPTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K10; K13]; 1xCarbamidom	
High	[N].DGSSAPTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K9; K12]; 1xCarbamidome	
High	[G].SSAPTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K7; K10]; 1xCarbamidome	
High	[S].SAPTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K6; K9]; 1xCarbamidomet	
High	[S].APTPKDCKLIVR.[V]	3xTMT6plex [N-Term; K5; K8]; 1xCarbamidomet	
High	[A].STTETPAPIECTAGATKTVDAPSSGSVVFQCGD	2xTMT6plex [N-Term; K17]; 2xCarbamidomethy	
High	[Y].KCVAEAGAPAGR.[N]	1xCarbamidomethyl [C2]; 1xTMT6plex [K]	
High	[T].ETPAPIECTAGATKTVDAPSSGSVVFQCGDK.[L]	2xTMT6plex [N-Term; K14]; 2xCarbamidomethy	
High	[M].AGMCTDLVSLVSQHIR.[A]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_271
High	[A].VASTPKAPVDASR.[E]	2xTMT6plex [N-Term; K6]	
High	[A].FLPVSASQNAVQTTPPFSGASEKTPLR.[V]	2xTMT6plex [N-Term; K23]	
High	[-].MESDLESGSDLLR.[E]	1xAcetyl [N-Term]	TGGT1_271
High	[A].HASSPDPTSSLR.[V]	1xTMT6plex [N-Term]	
High	[-].MENPPQIPVYR.[T]	1xAcetyl [N-Term]	TGGT1_271
High	[-].MEKHVTKPLSR.[Q]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_271
High	[-].MEKHVTKPL.[S]	1xAcetyl [N-Term]; 2xTMT6plex [K3;	TGGT1_271
High	[M].ADKPVCTPVCGSPGDSPFR.[G]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_272
High	[A].STDDDDLAVEEHR.[V]	1xTMT6plex [N-Term]	
High	[A].ENASTDDDDLAVEEHR.[V]	1xTMT6plex [N-Term]	
High	[A].SSLLPAVEER.[E]	1xTMT6plex [N-Term]	
High	[M].TLTSSASR.[G]	1xTMT6plex [N-Term]	
High	[L].TSSSHCVSSVSPSPSSDR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].AYVEEPSSALQR.[Q]	1xAcetyl [N-Term]	TGGT1_272
High	[M].AQVLQTLVDQKVEIVTVDGR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_272
High	[M].AQVLQTLVDQK.[V]	1xAcetyl [N-Term]	TGGT1_272
High	[R].SLHDALCVVR.[C]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[-].MQASFSASAAAQQAPPNASSHPASR.[A]	1xAcetyl [N-Term]	TGGT1_273
High	[Q].GGETPPSDPTCVVEGAVTKCTCR.[N]	2xTMT6plex [N-Term; K19]; 3xCarbamidomethy	
High	[A].AKAQGGETPPSDPTCVVEGAVTKCTCR.[N]	1xAcetyl [N-Term]; 3xCarbamidomet	TGGT1_273
High	[M].PSSSLGALPAGERPEVHR.[E]	1xTMT6plex [N-Term]	

High	[A].DTPSLDSDPSASPLR.[A]	1xTMT6plex [N-Term]	
High	[A].DAGSLPVEKR.[E]	2xTMT6plex [N-Term; K9]	
High	[M].SGEGQVADAGSLPVEKR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_273
High	[R].SQHLFNSIQNSAR.[S]	1xTMT6plex [N-Term]	
High	[M].SGEGQVADAGSLPVEKR.[E]	2xTMT6plex [N-Term; K16]	
High	[-].MSGEGQVADAGSLPVEKR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K17	TGGT1_273
High	[A].GSLPVEKR.[E]	2xTMT6plex [N-Term; K7]	
High	[-].MVSDSNMANGAAPSQGGLGLIKL.[M]	1xAcetyl [N-Term]; 1xTMT6plex [K22	TGGT1_273
High	[A].TVSPAALQDVCYAFGNISR.[K]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C11	
High	[M].SNEKSNHYVTLGVSR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_273
High	[M].ADSPAVGIDLGTTYSCVGVWKNDAVEIIANDQ	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_273
High	[D].AVEIIANDQGNR.[T]		
High	[T].TKKDEDEDGSEDSEDDEAER.[A]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_273
High	[F].SSSAPSAEAFATLLR.[D]	1xTMT6plex [N-Term]	
High	[M].ANSGINWPGLYR.[W]	1xAcetyl [N-Term]	TGGT1_273
High	[S].AVHAPEESR.[D]	1xTMT6plex [N-Term]	
High	[-].MLWVDKHAPR.[E]	2xTMT6plex [N-Term; K6]	
High	[-].MLWVDKHAPR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_273
High	[R].SASNFSFEGEDIR.[G]	1xTMT6plex [N-Term]	
High	[G].TVYKQPGSVAPTSLHCAGSDSGGEGFVR.[S]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl	
High	[R].SASNFSFEGEDIRGPIKPLR.[G]	2xTMT6plex [N-Term; K17]	
High	[L].SGCVATTCVQPIDMIKVR.[I]	2xTMT6plex [N-Term; K16]; 2xCarbamidomethy	
High	[V].ATTCVQPIDMIKVR.[I]	2xTMT6plex [N-Term; K12]; 1xCarbamidomethy	
High	[A].TTCVQPIDMIKVR.[I]	2xTMT6plex [N-Term; K11]; 1xCarbamidomethy	
High	[C].ASPTDSQEKPQPPR.[R]	2xTMT6plex [N-Term; K9]	
High	[A].EGDVDPFPVLANEGKSEAR.[G]	2xTMT6plex [N-Term; K15]	
High	[M].GGGQGDSLAEDDTTSEAAEGDVDPFPVLANE	2xTMT6plex [N-Term; K33]	
High	[S].SVQEPQAKVPSKR.[T]	3xTMT6plex [N-Term; K8; K12]	
High	[Q].EPQAKVPSKR.[T]	3xTMT6plex [N-Term; K5; K9]	
High	[D].PFPVLANEGKSEAR.[G]	1xTMT6plex [K10]	
High	[-].MFSDFTHSSNR.[R]	1xAcetyl [N-Term]	TGGT1_275
High	[M].VSEAPGVPSSPSTEVR.[T]	1xTMT6plex [N-Term]	
High	[M].AEDGLVLNSEDYTEK.[A]	1xTMT6plex [N-Term]	
High	[M].TVPGMKFSLIPKANR.[K]	3xTMT6plex [N-Term; K6; K12]	
High	[M].TVPGMKFSLIPK.[A]	2xTMT6plex [N-Term; K6]	
High	[M].TVPGMKFSLIPKANR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K6;	TGGT1_275
High	[A].EVGLTHGIMSTEFEVELR.[G]	1xTMT6plex [N-Term]	
High	[M].PLHSLVDVR.[H]	1xTMT6plex [N-Term]	
High	[G].DLPAHCLVR.[H]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].ACAKMGEGGGAAPAASGGLASHPLYYYSTHN	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_276
High	[M].PVPVAVSPQPLALSTPPLPVAPTIDLASLSAR.[N	1xTMT6plex [N-Term]	
High	[L].SPAPESVSLGTGHELSAGAR.[W]	1xTMT6plex [N-Term]	
High	[S].SATHPESIDRPAVAETVSR.[E]	1xTMT6plex [N-Term]	
High	[M].AVSSATHPESIDRPAVAETVSR.[E]	1xTMT6plex [N-Term]	
High	[S].QFEKNITHR.[G]	2xTMT6plex [N-Term; K4]	
High	[Y].ASTGSAAQQVLQEIQQFNSPR.[Y]	1xTMT6plex [N-Term]	
High	[L].DCVHPDVAAASIGDSQDPVGLR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2]	
High	[A].ALPADSGAYASTGSAAQQVLQEIQQFNSPR.[Y]	1xTMT6plex [N-Term]	
High	[S].GVSHSAALPADSGAYASTGSAAQQVLQEIQQF	1xTMT6plex [N-Term]	
High	[K].EGVEETKHEDDPEMTR.[L]	2xTMT6plex [N-Term; K7]	
High	[E].ETKHEDDPEMTR.[L]	2xTMT6plex [N-Term; K3]; 1xOxidation [M10]	
High	[E].ETKHEDDPEMTR.[L]	2xTMT6plex [N-Term; K3]	

High	[K].EGVEETKHEDDPEMTR.[L]	2xTMT6plex [N-Term; K7]; 1xOxidation [M14]	
High	[T].MDTQNDVESAGR.[Q]	1xAcetyl [N-Term]	TGGT1_277
High	[T].HATLAPIAEEEFR.[V]	1xTMT6plex [N-Term]	
High	[V].EVGGASAQIVFPLQEGTVLPSSVR.[A]	1xTMT6plex [N-Term]	
High	[N].SIDPTKPLAER.[M]	2xTMT6plex [N-Term; K6]	
High	[M].ALYEPPGDEDGCR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_277
High	[M].ATGANFPILR.[I]	1xAcetyl [N-Term]	TGGT1_277
High	[A].HTANPGDSSKSR.[R]	2xTMT6plex [N-Term; K10]	
High	[K].MMFPGMLR.[E]	1xAcetyl [N-Term]	TGGT1_277
High	[R].SDTHVVLCSLKR.[A]	2xTMT6plex [N-Term; K11]; 1xCarbamidomethy	
High	[K].MDTNAIAAFIDR.[N]	1xAcetyl [N-Term]	TGGT1_278
High	[A].SEITEPTMTTNPDFTVTIPKGGLPQDVEEVFFLQ	2xTMT6plex [N-Term; K20]	
High	[M].VVEAPLAAAR.[H]	1xTMT6plex [N-Term]	
High	[A].SETNHLTPEADFTATIPKSGLER.[N]	2xTMT6plex [N-Term; K18]	
High	[A].SETNHLTPEADFTATIPKSGLER.[N]	1xAcetyl [N-Term]; 1xTMT6plex [K18	TGGT1_278
High	[V].ENTPSAPPEEAKPPKR.[S]	3xTMT6plex [N-Term; K12; K15]	
High	[M].SFQDWTPVSWNKTGQR.[Q]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_278
High	[T].MEQPGHPGSSVAPASGR.[S]	1xAcetyl [N-Term]	TGGT1_278
High	[M].ASKVEQHTAPTPGPR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_278
High	[C].SSPHSALPHLNFR.[N]	1xTMT6plex [N-Term]	
High	[Y].STTNSSPSGPDFR.[T]	1xTMT6plex [N-Term]	
High	[K].MKSANEEASPSGSSSGR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_278
High	[-].MYHGPSPMAPGLLYHQPEGYAPAPTGPPLPQY	1xAcetyl [N-Term]	TGGT1_278
High	[M].TASSADGASAPGGGDPGEEEVR.[C]	1xTMT6plex [N-Term]	
High	[L].GASAVGGQENGVEKSSSGVSAHR.[Q]	2xTMT6plex [N-Term; K14]	
High	[A].SAAPLSPPVALEPELWESVLHDQR.[W]	1xTMT6plex [N-Term]	
High	[M].VLPLTLLR.[A]	1xTMT6plex [N-Term]	
High	[-].MVLPLTLLR.[A]	1xTMT6plex [N-Term]	
High	[-].MVLPLTLLR.[A]	1xAcetyl [N-Term]	TGGT1_278
High	[L].SVAAASPLAAAKSQWDAR.[L]	2xTMT6plex [N-Term; K12]	
High	[M].SSLSVAAASPLAAAKSQWDAR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_278
High	[A].ASPLAAAKSQWDAR.[L]	2xTMT6plex [N-Term; K8]	
High	[A].AASPLAAAKSQWDAR.[L]	2xTMT6plex [N-Term; K9]	
High	[A].SPLAAAKSQWDAR.[L]	2xTMT6plex [N-Term; K7]	
High	[A].DASQEAGDVVEER.[T]	1xTMT6plex [N-Term]	
High	[A].SQEAGDVVEER.[T]	1xAcetyl [N-Term]	TGGT1_279
High	[G].SQMSDSVGR.[N]	1xTMT6plex [N-Term]	
High	[G].LGSQMSDSVGR.[N]	1xTMT6plex [N-Term]	
High	[G].SQMSDSVGR.[N]	1xAcetyl [N-Term]	TGGT1_279
High	[R].SLDSIGR.[A]	1xTMT6plex [N-Term]	
High	[G].SQMSDSVGR.[N]	1xAcetyl [N-Term]; 1xOxidation [M3]	TGGT1_279
High	[M].ASSGFSSSLTKSMSCVDTSNEKVNGEASGR.[G]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_279
High	[M].ADATGSEVETEVVQDLSNPDVVTKYR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K24	TGGT1_279
High	[M].AETLASEAHVAEWADR.[L]	1xAcetyl [N-Term]	TGGT1_279
High	[L].ASEAHVAEWADR.[L]	1xTMT6plex [N-Term]	
High	[A].EESLTSMER.[N]	1xTMT6plex [N-Term]	
High	[M].TQRPLDYLDVGEHSQVILR.[F]	1xAcetyl [N-Term]	TGGT1_279
High	[M].AVSVEGSQDER.[H]	1xAcetyl [N-Term]	TGGT1_279
High	[G].EIVDVPGESKTKDNR.[S]	3xTMT6plex [N-Term; K10; K12]	
High	[T].QHTTSYIDPQAFAVLQELHR.[T]	1xTMT6plex [N-Term]	
High	[M].TDQEPLLPQMVER.[E]	1xAcetyl [N-Term]	TGGT1_280
High	[-].MQDSPQSSAAACGAAATIGPAKEDHFLQLVLR.[	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_280

High	[A].ATIGPAKEDHFLQLVLR.[L]	2xTMT6plex [N-Term; K7]	
High	[M].AGLSVSGVALLDSEGER.[L]	1xAcetyl [N-Term]	TGGT1_280
High	[-].MIDAICAFSR.[G]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[-].MIDAICAF.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[T].GGPPQGETVGASASQR.[A]	1xTMT6plex [N-Term]	
High	[M].SHTILLVQFSDR.[K]	1xAcetyl [N-Term]	TGGT1_280
High	[-].MEAAEAEAIALQIQR.[D]	1xAcetyl [N-Term]	TGGT1_281
High	[M].SLGSHAFLQR.[V]	1xAcetyl [N-Term]	TGGT1_281
High	[M].GYLHAEAETLSR.[S]	1xTMT6plex [N-Term]	
High	[S].LHSAAVPPSAALSSR.[S]	1xTMT6plex [N-Term]	
High	[M].PQDIRPAPNR.[M]	1xTMT6plex [N-Term]	
High	[M].ASAASSSLQGGGSSSSSAGAAGVSSGR.[A]	1xAcetyl [N-Term]	TGGT1_281
High	[-].MYNGVGLQTAR.[G]	1xAcetyl [N-Term]	TGGT1_282
High	[F].SGGAAKPSWHVAR.[E]	2xTMT6plex [N-Term; K6]	
High	[-].MDCCGLCADDDRDVWMTDR.[I]	1xAcetyl [N-Term]; 3xCarbamidomet	TGGT1_283
High	[T].TQPISNVTR.[Y]	1xTMT6plex [N-Term]	
High	[M].AHVTDYYGKSPR.[R]	2xTMT6plex [N-Term; K9]	
High	[M].SDLHSPTVSEEEPSVVER.[R]	1xTMT6plex [N-Term]	
High	[D].LHSPTVSEEEPSVVER.[R]	1xTMT6plex [N-Term]	
High	[-].MKDGIELSSLGGEGR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_283
High	[G].AFDGNREDLDDFLHR.[S]	1xAcetyl [N-Term]	TGGT1_283
High	[S].QAIQSFDGFAAKGLYPMGEVVQSLNVILNRPFLI	2xTMT6plex [N-Term; K12]; 1xOxidation [M17]	
High	[F].STAAAEDSGASQTLEGR.[Y]	1xTMT6plex [N-Term]	
High	[C].ETITIPAGVTVDVKSR.[V]	2xTMT6plex [N-Term; K14]	
High	[-].MKSVYACETITIPAGVTVDVKSR.[V]	3xTMT6plex [N-Term; K2; K21]; 1xCarbamidome	
High	[T].GTDVELVSR.[S]	1xTMT6plex [N-Term]	
High	[K].CEKATNVKDEIALTGTDVELVSR.[S]	3xTMT6plex [N-Term; K3; K8]; 1xCarbamidomet	
High	[A].ALIHQSTLVR.[R]	1xTMT6plex [N-Term]	
High	[P].WILTPSSQDSGNDFPVSGASSSFSSPSSR.[N]	1xTMT6plex [N-Term]	
High	[-].MEEAAASLEAAGACAESTFLHR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_285
High	[L].DLLTIAPGTR.[H]	1xTMT6plex [N-Term]	
High	[M].ASWLSAKISALGER.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K7]	TGGT1_285
High	[M].SGDSVAPHQR.[A]	1xAcetyl [N-Term]	TGGT1_285
High	[S].AAGPTEHVIKVPSLGDSITEGGLLEWR.[K]	2xTMT6plex [N-Term; K10]	
High	[S].SSAAGPTEHVIKVPSLGDSITEGGLLEWR.[K]	2xTMT6plex [N-Term; K12]	
High	[S].SAAGPTEHVIKVPSLGDSITEGGLLEWR.[K]	2xTMT6plex [N-Term; K11]	
High	[G].ADPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K5]; 1xCarbamidomethyl [	
High	[A].IAGADPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl [	
High	[D].PEKCDQDGSLLNLR.[V]	1xCarbamidomethyl [C4]; 1xTMT6plex [K3]	
High	[A].DPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [	
High	[G].ADPEKCDQDGSLLNLR.[V]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_285
High	[A].GADPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K6]; 1xCarbamidomethyl [	
High	[M].SLDIQNFGVSDPFANDTSQAGGAGGSSTHLIHI	1xAcetyl [N-Term]	TGGT1_286
High	[D].PFANDTSQAGGAGGSSTHLIHIR.[N]		
High	[M].VAAGVSHGNR.[S]	1xTMT6plex [N-Term]	
High	[M].VAAGVSHGNR.[S]	1xAcetyl [N-Term]	TGGT1_286
High	[Q].AVQQSPSEGREDEGEEGGKR.[R]	2xTMT6plex [N-Term; K19]	
High	[V].QQSPSEGREDEGEEGGKR.[R]	2xTMT6plex [N-Term; K17]	
High	[M].AGIEGPAAGEGAGGAALGSCEGPGENATKAAS	2xTMT6plex [N-Term; K29]; 1xCarbamidomethy	
High	[M].SGPEEDVSGEAASFGR.[C]	1xAcetyl [N-Term]	TGGT1_286
High	[I].DIALWQFETPKYHYTVIDAPGHR.[D]	2xTMT6plex [N-Term; K11]	
High	[V].NMEPSKPMVVEAFTDYPPLGR.[F]	2xTMT6plex [N-Term; K6]	

High	[W].QFETPKYHYTVIDAPGHR.[D]	2xTMT6plex [N-Term; K6]	
High	[L].DTMEAPKRPSDKPLR.[L]	3xTMT6plex [N-Term; K7; K12]	
High	[W].VLDKLKAER.[E]	2xTMT6plex [K4; K6]	
High	[L].CLGSVTSHSGESAHENSEAR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C1]	
High	[C].SSVICGSETKLEEWPYPR.[L]	2xTMT6plex [N-Term; K10]; 1xCarbamidomethy	
High	[R].DSSHPLGGLMGFR.[M]	1xTMT6plex [N-Term]	
High	[-].MELPLDAWATAAHGSKAYVAR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_286
High	[-].MELPLDAWATAAHGSKAY.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_286
High	[M].ATSVGGPLAVPIPGTAQPR.[V]	1xAcetyl [N-Term]	TGGT1_286
High	[R].DDAEDDPFVASDVASVLKYLR.[D]	1xTMT6plex [K18]	
High	[K].AASALGSR.[S]	1xTMT6plex [N-Term]	
High	[F].SSSALKAASALGSR.[S]	2xTMT6plex [N-Term; K6]	
High	[M].SSSSGSAADSGNTLEGQR.[Q]	1xAcetyl [N-Term]	TGGT1_286
High	[M].SNEDAIPPPQKPEFAPSAGASGEDPAR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_286
High	[L].VSTATFATVSVPSEDFR.[E]	1xTMT6plex [N-Term]	
High	[M].SNEDAIPPPQKPEFAPSAGASGEDPAR.[G]	2xTMT6plex [N-Term; K11]	
High	[A].NAFAELDDLRR.[S]	1xTMT6plex [N-Term]	
High	[R].SFTGIDEVTAKNIDACKALTDLTR.[T]	3xTMT6plex [N-Term; K11; K17]; 1xCarbamidom	
High	[M].ASSPFLLAFEGAVHSKAVR.[C]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_288
High	[-].MFALQDAEQLQLQR.[M]	1xAcetyl [N-Term]	TGGT1_288
High	[-].MVADGILPR.[A]	1xAcetyl [N-Term]	TGGT1_288
High	[R].CLIPQAIDQDPYFR.[M]	1xCarbamidomethyl [C1]	
High	[L].TIEDDGIGMTKAELVNNLGTIAR.[S]	2xTMT6plex [N-Term; K11]	
High	[R].QSVASSPFLEALR.[K]		
High	[A].AAPTATAADTKPASATPLQKPGSSTGGMTSGP	3xTMT6plex [N-Term; K11; K20]	
High	[A].TVAAGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K10]	
High	[A].ATVAAGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K11]	
High	[R].AATVAAGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K12]	
High	[A].GNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K6]	
High	[N].ELFKEALGHQR.[V]	2xTMT6plex [N-Term; K4]	
High	[A].AGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K7]	
High	[V].AAGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K8]	
High	[T].VAAGNELFKEALGHQR.[V]	2xTMT6plex [N-Term; K9]	
High	[F].SEATGGKTSR.[E]	2xTMT6plex [N-Term; K7]	
High	[F].SSSKPPGTEDSTDSLPGVR.[T]	2xTMT6plex [N-Term; K4]	
High	[C].AGTLSPLSCIEPVR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[-].MDDSLWER.[V]	1xAcetyl [N-Term]	TGGT1_288
High	[M].AAAAPAVGGGIR.[V]	1xAcetyl [N-Term]	TGGT1_288
High	[A].TDGGDTGAPAGSETHPVVR.[L]	1xTMT6plex [N-Term]	
High	[R].LQRPKPAGLSMETPAR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_288
High	[M].SLSPLMASTGPLLDR.[A]	1xAcetyl [N-Term]	TGGT1_289
High	[K].MDVEVTEEAQSR.[I]	1xAcetyl [N-Term]	TGGT1_289
High	[M].TGSSPKSAASSTPLR.[L]	2xTMT6plex [N-Term; K6]	
High	[M].STMTGSSPKSAASSTPLR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_289
High	[T].MTGSSPKSAASSTPLR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K7]	TGGT1_289
High	[T].MEEDDAALFKVEKGSSR.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K10	TGGT1_289
High	[A].VTPPAVSPQTSLWISSGLVGGSDKAVR.[G]	2xTMT6plex [N-Term; K24]	
High	[M].SLQLQKR.[L]	2xTMT6plex [N-Term; K6]	
High	[A].AGLVASMKR.[A]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_289
High	[C].GTTTGPTTSATDFAFDDLKR.[Y]	2xTMT6plex [N-Term; K19]	
High	[T].TGPTTSATDFAFDDLKR.[Y]	2xTMT6plex [N-Term; K16]	
High	[G].GPSDEVAIPSDR.[L]	1xTMT6plex [N-Term]	

High	[M].VCKLGINGFGR.[I]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl	
High	[K].MVCKLGINGFGR.[I]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl	
High	[G].IIEPSLALLAQK.[Y]	2xTMT6plex [N-Term; K12]	
High	[A].FQAVIELAPGQKR.[C]	2xTMT6plex [N-Term; K12]	
High	[L].GVPAAPEASPAPDQR.[S]	1xTMT6plex [N-Term]	
High	[S].ASLVGEQWNASESVPGTVDR.[E]	1xAcetyl [N-Term]	TGGT1_28
High	[Y].LHSFVSSSSTSPSHR.[Q]	1xTMT6plex [N-Term]	
High	[A].ASPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[A].SPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[A].SAAASPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[G].SVTPAIAAAKKSTANR.[L]	3xTMT6plex [N-Term; K10; K11]	
High	[F].NNEVNFASAAASPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[A].EKGGVFNNEVNFASAAASPAHFATATTTR.[A]	2xTMT6plex [N-Term; K2]	
High	[N].EVNFASAAASPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[A].AASPAHFATATTTR.[A]	1xTMT6plex [N-Term]	
High	[A].AAPAAEAAKTLER.[N]	2xTMT6plex [N-Term; K9]	
High	[L].NAAAPAAEAAKTLER.[N]	2xTMT6plex [N-Term; K11]	
High	[N].AAAPAAEAAKTLER.[N]	2xTMT6plex [N-Term; K10]	
High	[S].AGGPGGWLDQEAGESR.[R]	1xTMT6plex [N-Term]	
High	[Q].SQQDCNHQLFYTR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].ASYANKKVSVSEVSFDSHIEDIQWCGTDHR.[T]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_29
High	[M].GAPSPVAAGVAAR.[T]	1xAcetyl [N-Term]	TGGT1_29
High	[M].GAPSPVAAGVAAR.[T]	1xTMT6plex [N-Term]	
High	[M].PGVHGPQCGCVHETDLKGAQFLLPYINLEGIR.[	2xTMT6plex [N-Term; K17]; 2xCarbamidomethy	
High	[R].SQHIIVNALDNIQAR.[Q]	1xTMT6plex [N-Term]	
High	[A].AHIDTDLYSR.[Q]	1xTMT6plex [N-Term]	
High	[A].AAHIDTDLYSR.[Q]	1xTMT6plex [N-Term]	
High	[A].HIDTDLYSR.[Q]	1xTMT6plex [N-Term]	
High	[M].ATPQESSGAAAHIDTDLYSR.[Q]	1xAcetyl [N-Term]	TGGT1_29
High	[S].SPPSDLSCTVAFEGPISR.[A]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[M].NLILESLNHDEGSVLFR.[H]	1xTMT6plex [N-Term]	
High	[-].MEEKTTTAPPESFR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_29
High	[A].GIQPPPPAHAIGHHAAPVHHGVR.[L]	1xTMT6plex [N-Term]	
High	[T].GDLPPPGQAPGAAVPAGVNNGR.[N]	1xTMT6plex [N-Term]	
High	[A].VAGIQPPPPAHAIGHHAAPVHHGVR.[L]	1xTMT6plex [N-Term]	
High	[V].AGIQPPPPAHAIGHHAAPVHHGVR.[L]	1xTMT6plex [N-Term]	
High	[L].ATFSSGSSPR.[L]	1xTMT6plex [N-Term]	
High	[A].LGPSLPSFLVAER.[A]	1xAcetyl [N-Term]	TGGT1_29
High	[L].GPSLPSFLVAER.[A]	1xTMT6plex [N-Term]	
High	[A].LGPSLPSFLVAER.[A]	1xTMT6plex [N-Term]	
High	[A].ASVAPSSSSDSLCSDLSACSTEAAALEALTKR.[R]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_29
High	[A].ASVAPSSSSDSLCSDLSACSTEAAALEALTKR.[R]	2xTMT6plex [N-Term; K31]; 2xCarbamidomethy	
High	[M].ATNLEIDSADVIR.[L]	1xAcetyl [N-Term]	TGGT1_29
High	[-].MEKNCNSVAGHAGTLIKASSR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_29
High	[M].PLPKIPSAAR.[L]	2xTMT6plex [N-Term; K4]	
High	[A].YVPGIAPTDYTR.[G]	1xTMT6plex [N-Term]	
High	[M].AQQFPIQLHSVVNLADQGVSASSFR.[F]	1xAcetyl [N-Term]	TGGT1_29
High	[N].SANAPLVIGTLIDQDAAEDFIR.[N]	1xTMT6plex [N-Term]	
High	[L].ELVRPVAVQGR.[K]	1xTMT6plex [N-Term]	
High	[E].SLELVRPVAVQGR.[K]	1xTMT6plex [N-Term]	
High	[L].HSPQVAETIFQMEMLTHFDR.[A]	1xTMT6plex [N-Term]	
High	[M].ASGATYFTR.[G]	1xAcetyl [N-Term]	TGGT1_29

High	[M].THADVSACPAR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[-].MLEALVER.[L]	1xTMT6plex [N-Term]	
High	[-].MMASTSAQEDLVSAPFSSR.[L]	1xAcetyl [N-Term]	TGGT1_291
High	[-].MEVPVPSGVQPVAAIPQSR.[Y]	1xAcetyl [N-Term]	TGGT1_291
High	[-].MEVPVPSGVQPVAAIPQSR.[Y]	1xTMT6plex [N-Term]	
High	[M].TQSMLDMSLDDIVAAHR.[E]	1xTMT6plex [N-Term]	
High	[M].TQSMLDMSLDDIVAAHR.[E]	1xAcetyl [N-Term]	TGGT1_291
High	[L].DMSLDDIVAAHR.[E]	1xTMT6plex [N-Term]	
High	[K].DSQYNWLLCPVPTDNMFR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[-].MEDSKDKAAFSTFCGQLSAAFR.[H]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_291
High	[-].MDVHEHEAATGCR.[F]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_291
High	[L].AAAAVSGADHQTLR.[A]	1xTMT6plex [N-Term]	
High	[M].GKVHGSLAR.[A]	2xTMT6plex [N-Term; K2]	
High	[A].SHSHSPASGR.[Y]	1xTMT6plex [N-Term]	
High	[R].CQEIAAELCQSGLR.[K]	2xCarbamidomethyl [C1; C9]	
High	[Q].TKGGGVVDKLR.[T]	3xTMT6plex [N-Term; K2; K9]	
High	[-].MDPTVSLAAGAEPVAGEKR.[K]	1xAcetyl [N-Term]; 1xTMT6plex [K18	TGGT1_291
High	[G].LATDSDSEPEGKGGYQR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_291
High	[A].TDSDSEPEGKGGYQR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_291
High	[A].TDSDSEPEGKGGYQR.[L]	2xTMT6plex [N-Term; K10]	
High	[G].LATDSDSEPEGKGGYQR.[L]	2xTMT6plex [N-Term; K12]	
High	[F].YQTTAAPWLQPDIR.[Q]	1xTMT6plex [N-Term]	
High	[R].TVQGLAAGAAPAAGLR.[S]	1xTMT6plex [N-Term]	
High	[M].AAAPAAPQSR.[G]	1xAcetyl [N-Term]	TGGT1_292
High	[A].EAKTGDAAEGDKDANAAAGGYHMSAEPEMD	3xTMT6plex [N-Term; K3; K12]	
High	[M].TFKKVVVIDCQGHLLGR.[L]	3xTMT6plex [N-Term; K3; K4]; 1xCarbamidomet	
High	[E].DINISGSLHR.[N]	1xTMT6plex [N-Term]	
High	[Q].VFEGVPTMVER.[K]	1xTMT6plex [N-Term]	
High	[S].AAGAVPPLLLTPALNGVER.[G]	1xTMT6plex [N-Term]	
High	[K].MITDKNLSVVTPPELVTDDPGDMPDCKISPR.[C	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_293
High	[D].PEEVDAFVKQIETANR.[F]	1xTMT6plex [K9]	
High	[D].PGDMPDCKISPR.[C]	1xCarbamidomethyl [C7]; 1xTMT6plex [K8]	
High	[-].MDSLRPPVGVDELQSSLVACYER.[I]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_293
High	[Q].GDFLSLSDASLEPHR.[S]	1xTMT6plex [N-Term]	
High	[Q].TPEAPASQEPR.[F]	1xTMT6plex [N-Term]	
High	[A].ELTSIEAVAR.[Q]	1xTMT6plex [N-Term]	
High	[M].PATLEEQAVVAPPGDQTAMSSLPFEDTAAGR.	1xTMT6plex [N-Term]	
High	[S].SLPFEDTAAGR.[Q]	1xTMT6plex [N-Term]	
High	[M].SSLPFEDTAAGR.[Q]	1xAcetyl [N-Term]	TGGT1_293
High	[K].SKENGGSLIGGMATAALLKECK.[K]	3xTMT6plex [N-Term; K2; K19]; 1xCarbamidome	
High	[M].PAKEIVFHCEYAPSGR.[A]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl	
High	[M].ALAAASSASASSDQKR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_293
High	[M].ALAAASSASASSDQKR.[E]	2xTMT6plex [N-Term; K15]	
High	[A].GLAELEKKEWTVPELQQALHR.[V]	3xTMT6plex [N-Term; K7; K8]	
High	[A].ELEKKEWTVPELQQALHR.[V]	3xTMT6plex [N-Term; K4; K5]	
High	[R].SSTETCGVKGRPR.[V]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl	
High	[R].SSTETCGVKGR.[P]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl	
High	[Q].ATPIGAFEALFAEAAR.[R]	1xTMT6plex [N-Term]	
High	[M].DVAEEPQIQATADR.[V]	1xTMT6plex [N-Term]	
High	[Q].TQALALPSTLTR.[F]	1xAcetyl [N-Term]	TGGT1_293
High	[Q].ALALPSTLTR.[F]	1xAcetyl [N-Term]	TGGT1_293
High	[L].ALPSTLTR.[F]	1xTMT6plex [N-Term]	

High	[M].PVHHVTTEAQFK.[S]	1xTMT6plex [N-Term]	
High	[F].VKIDVDELADVAER.[E]	1xTMT6plex [V/K]	
High	[A].EADAAPLCR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[-].MKEGSFMIAGSPSHPER.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_294
High	[-].MKEGSFMIAGSPSHPER.[L]	2xTMT6plex [N-Term; K2]	
High	[M].SAELFPLGEAALPSNQMR.[D]	1xAcetyl [N-Term]	TGGT1_294
High	[-].MDAEETNLGFLVAAHPQR.[L]	1xAcetyl [N-Term]	TGGT1_294
High	[Q].ISPAISAASASSAQSPESQAMSESIDR.[M]	1xAcetyl [N-Term]	TGGT1_294
High	[T].SPYFPAAGPQTR.[R]	1xAcetyl [N-Term]	TGGT1_294
High	[K].DMESLFDTNDLDASVIR.[K]	1xTMT6plex [N-Term]	
High	[L].ASSDAVDAALVAPDAQVVSSGILTSFVER.[L]	1xTMT6plex [N-Term]	
High	[A].LVAPDAQVVSSGILTSFVER.[L]	1xTMT6plex [N-Term]	
High	[A].GGDGDEETGLR.[S]	1xTMT6plex [N-Term]	
High	[-].MLGGASGLGAAPTR.[A]	1xAcetyl [N-Term]	TGGT1_294
High	[S].ELPLAEALVGGAGVSGPR.[E]	1xTMT6plex [N-Term]	
High	[Q].EVQHTLDGVNAVVSITELMGKVR.[E]	2xTMT6plex [N-Term; K21]	
High	[F].STEPISHMQEKPATLR.[L]	2xTMT6plex [N-Term; K11]	
High	[M].APQHPAAAVSTADPAEKDATLEAAATGASACP	2xTMT6plex [N-Term; K17]; 1xCarbamidomethy	
High	[A].PQHPAAAVSTADPAEKDATLEAAATGASACPR.	2xTMT6plex [N-Term; K16]; 1xCarbamidomethy	
High	[P].QHPAAAVSTADPAEKDATLEAAATGASACPR.[	2xTMT6plex [N-Term; K15]; 1xCarbamidomethy	
High	[-].MISFPSHSPR.[S]	1xAcetyl [N-Term]	TGGT1_295
High	[-].MEGSALHKLR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_295
High	[D].PPDLETNSLYYR.[D]		
High	[W].LEQEGVELRPPLLDSQTGTSTASPTGFR.[R]	1xAcetyl [N-Term]	TGGT1_295
High	[W].LEQEGVELR.[S]	1xTMT6plex [N-Term]	
High	[W].LEQEGVELR.[S]	1xAcetyl [N-Term]	TGGT1_295
High	[M].VLVTSNADNNKIYNLSGGR.[S]	2xTMT6plex [N-Term; K11]	
High	[A].GTGGFAAPGIIQMTAEEMEALQR.[L]	1xTMT6plex [N-Term]	
High	[N].ELPAGQQGSPLAER.[Q]	1xTMT6plex [N-Term]	
High	[-].MEQQQDELKHSWGANELPAGQQGSPLAER.[Q	1xAcetyl [N-Term]; 1xTMT6plex [K9]	TGGT1_295
High	[M].TSTTNSNLHNYNHELVACIDDLRR.[K]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_295
High	[M].GKIPLSLSDNFQLAVSSLPETQR.[Q]	2xTMT6plex [N-Term; K2]	
High	[M].AKAKYTLVLIR.[H]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_297
High	[L].NLPDVEEALKR.[D]	2xTMT6plex [N-Term; K10]	
High	[K].MHTEYSAQQAAR.[S]	1xAcetyl [N-Term]	TGGT1_297
High	[L].SSSQPLTAPSTPTKASR.[S]	2xTMT6plex [N-Term; K14]	
High	[M].VWGYPIFGDDPKKLR.[R]	3xTMT6plex [N-Term; K12; K13]	
High	[-].MDAIPVSQWQDVPAATGGAAR.[G]	1xAcetyl [N-Term]	TGGT1_297
High	[M].SHLLNAPIILLKDGVDTSQGR.[G]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_297
High	[F].ASHGLCCSDREEAFMR.[S]	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C6;	
High	[M].ADPPLHLSAR.[A]	1xAcetyl [N-Term]	TGGT1_297
High	[A].AAAPSEQPQLKIGPAQVLLPSPAQAAGR.[L]	2xTMT6plex [N-Term; K11]	
High	[L].ATAAAAGPAR.[A]	1xTMT6plex [N-Term]	
High	[A].DDAFIDNVKK.[G]	2xTMT6plex [N-Term; K]	
High	[H].APTAARVALKK.[R]	2xTMT6plex [N-Term; K]	
High	[A].HGPSDSPATKQPQVQR.[K]	2xTMT6plex [N-Term; K10]	
High	[A].WEAAVHPHEQGR.[V]	1xTMT6plex [N-Term]	
High	[Q].DVTQHHQLQEATQMAGKLTR.[H]	2xTMT6plex [N-Term; K17]	
High	[N].MLGTSSAVAAALLEGGR.[R]	1xAcetyl [N-Term]	TGGT1_297
High	[A].ATSGAGPAAGFWSDEPIIKR.[R]	2xTMT6plex [N-Term; K19]	
High	[A].GHQGPFLER.[E]	1xTMT6plex [N-Term]	
High	[L].TPAPAAAGPAAASGSHRPGAAGGAQVGEKSG	2xTMT6plex [N-Term; K29]	

High	[L].GASASASSSGHLR.[V]	1xTMT6plex [N-Term]	
High	[A].QVCIGGAATGHR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C3]	
High	[M].SIAPSPGHR.[S]	1xTMT6plex [N-Term]	
High	[L].ADTADFPFLVNPSR.[S]	1xTMT6plex [N-Term]	
High	[D].PTLLLQEPLDIVR.[V]		
High	[M].SRPEDSADAHEAEASCHGCLGQVGSR.[E]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_298
High	[S].PSSCCPHHSQAEGGGELQGDSAAGCADESDPM	3xCarbamidomethyl [C4; C5; C25]	
High	[-].MEPGELIVHR.[T]	1xAcetyl [N-Term]	TGGT1_299
High	[L].DVDNLVIEHIQVNR.[A]	1xTMT6plex [N-Term]	
High	[K].NLDVDNLVIEHIQVNR.[A]	1xTMT6plex [N-Term]	
High	[M].VKYAKEPSNENK.[C]	3xTMT6plex [N-Term; K2; K5]	
High	[L].VIEHIQVNR.[A]	1xTMT6plex [N-Term]	
High	[K].TVTVTTAGVLLTAVVGMLMASG.[K]	1xAcetyl [N-Term]	TGGT1_299
High	[P].MDVSNFSR.[S]	1xAcetyl [N-Term]	TGGT1_299
High	[G].VDSISPGAER.[G]	1xTMT6plex [N-Term]	
High	[-].MEENVSGSEASAKADPPVIEVAGVSVR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K13	TGGT1_299
High	[L].TFDQLALR.[R]	1xTMT6plex [N-Term]	
High	[M].AGSTISNHQVSSNR.[K]	1xAcetyl [N-Term]	TGGT1_300
High	[A].AEPDSDATPGLRPQPSPR.[T]	1xAcetyl [N-Term]	TGGT1_300
High	[M].ADAASAACKPR.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_300
High	[-].MKLLTPKDDVR.[G]	3xTMT6plex [N-Term; K2; K7]	
High	[-].MNCTEETVQQFMAATGVSDR.[E]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_300
High	[M].ASTAPSSLAAR.[A]	1xAcetyl [N-Term]	TGGT1_300
High	[-].MDSAAVWSDESEDVATAELAGLSASDLR.[M]	1xAcetyl [N-Term]	TGGT1_300
High	[M].ASTQVASLHAQPLLR.[R]	1xAcetyl [N-Term]	TGGT1_301
High	[A].SLHAQPLLR.[R]	1xTMT6plex [N-Term]	
High	[Q].VASLHAQPLLR.[R]	1xTMT6plex [N-Term]	
High	[S].LHAQPLLR.[R]	1xTMT6plex [N-Term]	
High	[S].GGPGDHLHATPGMFVQHSTAIFSDR.[Y]	1xTMT6plex [N-Term]	
High	[T].SGGPGDHLHATPGMFVQHSTAIFSDR.[Y]	1xTMT6plex [N-Term]	
High	[Q].HSTAIFSDR.[Y]	1xTMT6plex [N-Term]	
High	[A].GTSGGPGDHLHATPGMFVQHSTAIFSDR.[Y]	1xTMT6plex [N-Term]	
High	[M].ATFNPVNAAR.[T]	1xAcetyl [N-Term]	TGGT1_304
High	[M].ASDGDVDTNIEQWKIKR.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K14	TGGT1_304
High	[A].TVAAPQVETGPLLSVR.[A]	1xTMT6plex [N-Term]	
High	[F].GVGGESKHAEFR.[Y]	2xTMT6plex [N-Term; K7]	
High	[M].AAVAAAVGGGGPPPAR.[V]	1xAcetyl [N-Term]	TGGT1_304
High	[A].SPLASAAGLAGGAVALGAR.[Q]	1xTMT6plex [N-Term]	
High	[M].ALDTPATSLAAR.[D]	1xAcetyl [N-Term]	TGGT1_305
High	[M].GHPTATVQEALKALQSPDNAVR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_305
High	[M].GHPTATVQEALKALQSPDNAVR.[S]	2xTMT6plex [N-Term; K12]	
High	[-].METSLSAASASPGR.[H]	1xAcetyl [N-Term]	TGGT1_305
High	[M].AMDDAEAQR.[Q]	1xAcetyl [N-Term]	TGGT1_305
High	[M].AMDDAEAQR.[Q]	1xAcetyl [N-Term]; 1xOxidation [M2]	TGGT1_305
High	[-].MNALHSEAIPPPPEDGRR.[T]	1xAcetyl [N-Term]	TGGT1_305
High	[M].ASSPKAAELEPEQSAAATGR.[F]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_305
High	[M].GSKSEPATFLGFLGDR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_305
High	[K].DCFSNSKGSTKTR.[G]	3xTMT6plex [N-Term; K7; K11]; 1xCarbamidome	
High	[-].MDDLVALQR.[Q]	1xAcetyl [N-Term]	TGGT1_305
High	[P].TKPESPGASR.[R]	2xTMT6plex [N-Term; K2]	
High	[C].GGQGAVSETQKHR.[K]	2xTMT6plex [N-Term; K11]	
High	[M].AATEQKRPQETSISR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_305

High	[L].GHCPPTLAFVPR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C3]	
High	[Y].GNFAVNVHPNFAR.[G]	1xTMT6plex [N-Term]	
High	[F].AVNVHPNFAR.[G]	1xTMT6plex [N-Term]	
High	[A].VNVHPNFAR.[G]	1xTMT6plex [N-Term]	
High	[T].QQKAHLSDR.[Y]	2xTMT6plex [N-Term; K3]	
High	[-].MKLAHHIYR.[D]	2xTMT6plex [N-Term; K2]	
High	[-].MKLAHHIYR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_306
High	[N].ELGPVWHQSIPKADGGLR.[K]	2xTMT6plex [N-Term; K12]	
High	[L].TAGPQQHLAPLKALR.[Q]	2xTMT6plex [N-Term; K12]	
High	[A].EAAGANGWTEHVGKDGR.[R]	2xTMT6plex [N-Term; K14]	
High	[M].APQETAPR.[T]	1xTMT6plex [N-Term]	
High	[M].PKYYCEYCDIYLTHSSPAGR.[R]	2xTMT6plex [N-Term; K2]; 2xCarbamidomethyl	
High	[M].TDSNTNPALKFQR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_306
High	[K].MTDSNTNPALKFQR.[S]	2xTMT6plex [N-Term; K11]	
High	[-].MHLSSPPRPAALASAVTPGDQR.[R]	1xAcetyl [N-Term]	TGGT1_306
High	[M].ALHTACTPSPLGGAASASR.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_306
High	[-].MKPEIANVASESDGAHPPTSASTEVFLRPDGR.[E	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_306
High	[F].STASAPATPETVCRPQVSASQSFSSAAPAAAPKS	2xTMT6plex [N-Term; K33]; 1xCarbamidomethy	
High	[A].EDVAAHDFPQLLHR.[E]	1xTMT6plex [N-Term]	
High	[S].SAAPAAAPKSR.[E]	2xTMT6plex [N-Term; K9]	
High	[A].YPWFDDMDDVGDER.[Y]	1xTMT6plex [N-Term]	
High	[-].MEDTAQSTPTTAVSAKKNAWMQASR.[L]	1xAcetyl [N-Term]; 2xTMT6plex [K16	TGGT1_306
High	[-].MLSAFDHSSQAAAPR.[V]	1xAcetyl [N-Term]	TGGT1_306
High	[G].TTICGVVCKDGVVLGADTR.[A]	2xTMT6plex [N-Term; K9]; 2xCarbamidomethyl	
High	[T].MDSISQLALQR.[G]	1xAcetyl [N-Term]	TGGT1_306
High	[M].PQFVPVYDPERPR.[A]	1xTMT6plex [N-Term]	
High	[A].MESFLRPIQPKR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K11	TGGT1_307
High	[S].FLRPIQPKR.[S]	2xTMT6plex [N-Term; K8]	
High	[-].MWSIFAPEALTSTSEPATKPAGGATR.[M]	1xAcetyl [N-Term]; 1xTMT6plex [K19	TGGT1_307
High	[L].TSTSEPATKPAGGATR.[M]	2xTMT6plex [N-Term; K9]	
High	[A].YVQKGQDANAPESAAETAPPR.[D]	2xTMT6plex [N-Term; K4]	
High	[A].SGTSGNAQGAAASKQKPR.[R]	3xTMT6plex [N-Term; K14; K16]	
High	[M].AISSALIQQR.[V]	1xAcetyl [N-Term]	TGGT1_308
High	[L].DPSFHGLEAGDSFMR.[D]	1xTMT6plex [N-Term]	
High	[D].PSFHGLEAGDSFMR.[D]		
High	[Q].RPLLDPSFHGLEAGDSFMR.[D]	1xTMT6plex [N-Term]	
High	[Q].SGTGDDSDFPQAVAEEVADMSGGR.[V]	1xTMT6plex [N-Term]	
High	[T].ADGAGVADETHQEPRPPLR.[K]	1xTMT6plex [N-Term]	
High	[V].ADETHQEPRPPLR.[K]	1xTMT6plex [N-Term]	
High	[N].DLASGTPHVAR.[G]	1xTMT6plex [N-Term]	
High	[A].GVADETHQEPRPPLR.[K]	1xTMT6plex [N-Term]	
High	[R].TNDLASGTPHVAR.[G]	1xTMT6plex [N-Term]	
High	[A].EEVADMSGGR.[V]	1xTMT6plex [N-Term]	
High	[A].DGAGVADETHQEPRPPLR.[K]	1xTMT6plex [N-Term]	
High	[A].DETHQEPRPPLR.[K]	1xTMT6plex [N-Term]	
High	[E].EVADMSGGR.[V]	1xTMT6plex [N-Term]	
High	[T].TSASEGIFR.[R]	1xTMT6plex [N-Term]	
High	[T].TTSASEGIFR.[R]	1xTMT6plex [N-Term]	
High	[D].LASGTPHVAR.[G]	1xTMT6plex [N-Term]	
High	[T].SASEGIFR.[R]	1xTMT6plex [N-Term]	
High	[A].VQLSPPNSR.[T]	1xTMT6plex [N-Term]	
High	[R].SVVFLVR.[D]	1xTMT6plex [N-Term]	

High	[S].SKDSQTVTCAYGSASNADVHR.[V]	2xTMT6plex [N-Term; K2]; 1xCarbamidomethyl [	
High	[F].GANSQSSLAPPDGR.[G]	1xTMT6plex [N-Term]	
High	[A].SGSVEHMPQNVPEHLAALGTNLLEKQR.[A]	2xTMT6plex [N-Term; K25]	
High	[S].ESPLSGGPAGSHGEKATGESFLGAR.[G]	2xTMT6plex [N-Term; K15]	
High	[S].ALSNEADLSR.[G]	1xTMT6plex [N-Term]	
High	[G].SVDNGGLDDPNASR.[M]	1xTMT6plex [N-Term]	
High	[G].LVGKQESGCHVSLR.[Q]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [	
High	[F].ATVGVGDIR.[Q]	1xTMT6plex [N-Term]	
High	[F].LSPLRPDLVR.[F]	1xTMT6plex [N-Term]	
High	[S].AVAATGLPALVMAR.[G]	1xTMT6plex [N-Term]	
High	[L].VSVYKPEDGTASGTSLMPSVFLSPLRPDLVR.[F]	2xTMT6plex [N-Term; K5]	
High	[T].SLMPSVFLSPLRPDLVR.[F]	1xTMT6plex [N-Term]	
High	[S].GTSLMPSVFLSPLRPDLVR.[F]	1xTMT6plex [N-Term]	
High	[A].ATGLPALVMAR.[G]	1xTMT6plex [N-Term]	
High	[V].AATGLPALVMAR.[G]	1xTMT6plex [N-Term]	
High	[A].TGLPALVMAR.[G]	1xTMT6plex [N-Term]	
High	[L].SPLRPDLVR.[F]	1xTMT6plex [N-Term]	
High	[T].MLVLGSTFPDVHADASGVPGDK.[I]	1xTMT6plex [N-Term]	
High	[T].MLVLGSTFPDVHADASGVPGDKIK.[L]	2xTMT6plex [N-Term; K]	
High	[T].MLVLGSTFPDVHADASGVPGDK.[I]	1xAcetyl [N-Term]	TGGT1_309
High	[L].SGDLPFPIIADPER.[K]	1xTMT6plex [N-Term]	
High	[-].MDTKSENSIATGVGPTPVGR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K4]	TGGT1_309
High	[A].TGVGPTPVGR.[V]	1xTMT6plex [N-Term]	
High	[M].APETAKSR.[F]	2xTMT6plex [N-Term; K6]	
High	[S].SHNGVPAYPSYAQVSLSSNGEPR.[H]	1xTMT6plex [N-Term]	
High	[Q].QLLLEPTEEQQEGPQEPLPPPPPPTR.[G]	1xTMT6plex [N-Term]	
High	[M].SVKPHANADDFASDDNYEPLPSFVEAPVR.[G]	2xTMT6plex [N-Term; K3]	
High	[Q].ELPPPTEQELPPSTEQELPPPVGEGQR.[L]	1xTMT6plex [N-Term]	
High	[E].APVRGPDQVPAR.[G]	1xAcetyl [N-Term]	TGGT1_309
High	[A].LSSHNGVPAYPSYAQVSLSSNGEPR.[H]	1xTMT6plex [N-Term]	
High	[F].VEAPVRGPDQVPAR.[G]	1xAcetyl [N-Term]	TGGT1_309
High	[Q].ELPPPVGEGQR.[L]	1xTMT6plex [N-Term]	
High	[-].MLGASPEVEVLADEGSAGCIASAGASELR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_309
High	[F].LNLHEYQSMR.[I]	1xTMT6plex [N-Term]	
High	[F].LNLHEYQSMR.[I]	1xTMT6plex [N-Term]; 1xOxidation [M9]	
High	[S].TIFGGASLQGR.[N]	1xTMT6plex [N-Term]	
High	[S].TIFGGASLQGR.[N]	1xAcetyl [N-Term]	TGGT1_309
High	[M].VKKGEENPMR.[K]	3xTMT6plex [N-Term; K2; K3]	
High	[R].AAANGSEGGVAQSEQER.[A]	1xAcetyl [N-Term]	TGGT1_310
High	[M].AKTGAEQLELHGDTWR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K2]	TGGT1_310
High	[M].AKTGAEQLELHGDTWR.[V]	2xTMT6plex [N-Term; K2]	
High	[-].MYHIPVAAPLGVYGTPAVPVPYSPAPYGAPAHP	1xAcetyl [N-Term]	TGGT1_310
High	[Y].GTPAVPVPYSPAPYGAPAHPGAYPR.[G]	1xTMT6plex [N-Term]	
High	[E].MEGMMEAPAR.[F]	1xAcetyl [N-Term]	TGGT1_310
High	[M].TAYGKVDYWDER.[Y]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_310
High	[M].TAYGKVDYWDER.[Y]	2xTMT6plex [N-Term; K5]	
High	[M].ALQYAYPVDSPRPGESAIWR.[C]	1xAcetyl [N-Term]	TGGT1_310
High	[T].MIYATPVGSPGPGESATWQSTGFAAYSASPMP	1xAcetyl [N-Term]	TGGT1_310
High	[A].QFHPDAYESANVR.[G]	1xAcetyl [N-Term]	TGGT1_310
High	[C].AGLQAGDAETGR.[T]	1xTMT6plex [N-Term]	
High	[A].ALPDFSEEASFSR.[E]	1xAcetyl [N-Term]	TGGT1_310
High	[A].ALPDFSEEASFSR.[E]	1xTMT6plex [N-Term]	

High	[A].LPDFSEEASFSR.[E]	1xTMT6plex [N-Term]	
High	[A].AASAKATHALQPTGTGSVAFTRPGQGSNAQFQ	3xTMT6plex [N-Term; K5; K38]	
High	[A].ASAKATHALQPTGTGSVAFTRPGQGSNAQFQT	3xTMT6plex [N-Term; K4; K37]	
High	[A].AGVQAGEKGAAPAPEIFPFQAEVKR.[V]	3xTMT6plex [N-Term; K8; K24]	
High	[Q].AGEKGAAPAPEIFPFQAEVKR.[V]	3xTMT6plex [N-Term; K4; K20]	
High	[M].SELKGKNIFLTPDGR.[T]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_310
High	[M].ANAADENVFANDSSYHWEMR.[R]	1xAcetyl [N-Term]	TGGT1_310
High	[M].ANAADENVFANDSSYHWEMR.[R]	1xAcetyl [N-Term]; 1xOxidation [M1	TGGT1_310
High	[S].FGSHLADMAGLSGR.[H]	1xTMT6plex [N-Term]	
High	[C].SFGSHLADMAGLSGR.[H]	1xTMT6plex [N-Term]; 1xOxidation [M9]	
High	[C].SFGSHLADMAGLSGR.[H]	1xTMT6plex [N-Term]	
High	[C].SFGSHLADMAGLSGR.[H]	1xAcetyl [N-Term]; 1xOxidation [M9	TGGT1_310
High	[C].SFGSHLADMAGLSGR.[H]	1xAcetyl [N-Term]	TGGT1_310
High	[Y].TAQVVPGTPGHPVQAIPQQPLR.[T]	1xTMT6plex [N-Term]	
High	[A].QVVPGTPGHPVQAIPQQPLR.[T]	1xTMT6plex [N-Term]	
High	[F].VFTPSSVQPGAEVTPGYSGLQLR.[Q]	1xTMT6plex [N-Term]	
High	[T].STPTPPPPASYGYPVFPAFPR.[L]	1xTMT6plex [N-Term]	
High	[S].SVQPGAEVTPGYSGLQLR.[Q]	1xTMT6plex [N-Term]	
High	[T].GVKDSSSSESTVTPADEAASESEEGDKTSR.[K]	3xTMT6plex [N-Term; K3; K27]	
High	[S].FGSHLADMAGLSGR.[H]	1xTMT6plex [N-Term]; 1xOxidation [M8]	
High	[A].DMAGLSGR.[H]	1xTMT6plex [N-Term]	
High	[G].SHLADMAGLSGR.[H]	1xTMT6plex [N-Term]	
High	[F].TPSSVQPGAEVTPGYSGLQLR.[Q]	1xTMT6plex [N-Term]	
High	[A].ATEQGAAEVDEATDEHEEDDDDDHR.[A]	1xTMT6plex [N-Term]	
High	[A].METPESLAAALAEADDPLSPAAVR.[E]	1xAcetyl [N-Term]	TGGT1_310
High	[M].SLDDVVHKKFTFVFVPADINDPVEER.[T]	1xAcetyl [N-Term]; 2xTMT6plex [K8;	TGGT1_310
High	[M].ALVAANAAGAALSVAPADAPSALAQNAR.[D]	1xAcetyl [N-Term]	TGGT1_310
High	[S].ASPGGAGALVGSSLLALR.[G]	1xTMT6plex [N-Term]	
High	[A].GLGGDVVVLDER.[Q]	1xTMT6plex [N-Term]	
High	[M].SGGPGFYR.[G]	1xAcetyl [N-Term]	TGGT1_311
High	[Q].QESLEPESEEHAHLYQLQEVR.[E]	1xTMT6plex [N-Term]	
High	[L].EVLGQSEHLPGLR.[Q]	1xTMT6plex [N-Term]	
High	[K].MQASSPLSNAPR.[V]	1xAcetyl [N-Term]	TGGT1_311
High	[M].QAPGAPVETPVWAPAHGGR.[S]	1xTMT6plex [N-Term]	
High	[L].SMPQDFNPLQPLVAR.[G]	1xTMT6plex [N-Term]	
High	[L].GSSLSGSMQNLPTLTGEQTR.[G]	1xTMT6plex [N-Term]	
High	[S].ANLVESESR.[R]	1xTMT6plex [N-Term]	
High	[A].TFPAYPQGAYVPSYPGWNSSHR.[T]	1xTMT6plex [N-Term]	
High	[T].TVPVEGGPSR.[K]	1xTMT6plex [N-Term]	
High	[A].EFFPDDPPR.[Q]	1xTMT6plex [N-Term]	
High	[S].GSSSSLAADSR.[V]	1xTMT6plex [N-Term]	
High	[-].MYFGSFPFGDDMR.[G]	1xAcetyl [N-Term]	TGGT1_311
High	[M].SSDADIQMAFQDCSEGSKIPAAKVGAAAR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_311
High	[-].MEPLADPLHDR.[V]	1xAcetyl [N-Term]	TGGT1_311
High	[N].GTGEASGSAKGLLASVPVHR.[N]	2xTMT6plex [N-Term; K10]	
High	[N].GVEPQQAFR.[Q]	1xTMT6plex [N-Term]	
High	[A].DDIFGSEDFSPPPMNVAGAPLR.[D]	1xTMT6plex [N-Term]	
High	[G].SPAADLVASVQTVSNER.[K]	1xTMT6plex [N-Term]	
High	[A].GSPAADLVASVQTVSNER.[K]	1xTMT6plex [N-Term]	
High	[A].GQAAQTDAQPLPKAAQTDAQPLPKVR.[R]	3xTMT6plex [N-Term; K13; K24]	
High	[A].GARPPFFR.[G]	1xTMT6plex [N-Term]	
High	[Q].DIDINASSDSLKSHAVMR.[I]	2xTMT6plex [N-Term; K12]	

High	[Q].AAQTDAQPLPKAAQTDAQPLPKVR.[R]	3xTMT6plex [N-Term; K11; K22]	
High	[Q].EINDPEGDSHWHDR.[D]	1xTMT6plex [N-Term]	
High	[V].QEINDPEGDSHWHDR.[D]	1xTMT6plex [N-Term]	
High	[V].SHQPIKPDFSR.[K]	2xTMT6plex [N-Term; K6]	
High	[M].ALSDLYCLAYAPIQSTCLDSIGDEDCSPEVIVKEL	1xAcetyl [N-Term]; 3xCarbamidomet	TGGT1_311
High	[S].MIASEPDHDDGSVVSHQPIKPDFSR.[K]	2xTMT6plex [N-Term; K20]	
High	[V].QEINDPEGDSHWHDRDR.[H]	1xTMT6plex [N-Term]	
High	[M].APASSVSAIFNPLLVPTLSPACHSHSSSAPLR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C22	
High	[M].ASSTPTQVNAAKPEELASSSSTLSPISSPPSSQGE	1xAcetyl [N-Term]; 1xTMT6plex [K12	TGGT1_311
High	[M].TMEGQQDLTVIPPLSHQDADRR.[W]	1xTMT6plex [N-Term]	
High	[T].MEGQQDLTVIPPLSHQDADRR.[W]	1xAcetyl [N-Term]	TGGT1_311
High	[M].TMEGQQDLTVIPPLSHQDADRR.[W]	1xAcetyl [N-Term]	TGGT1_311
High	[A].SDAEEGKVKDVVIGIDLGTTYSCVGVYR.[H]	3xTMT6plex [N-Term; K7; K9]; 1xCarbamidomet	
High	[A].SDAEEGKVK.[D]	2xTMT6plex [N-Term; K7]	
High	[-].MDTLESVDSLAAR.[K]	1xAcetyl [N-Term]	TGGT1_311
High	[-].MVGTTALR.[M]	1xAcetyl [N-Term]	TGGT1_311
High	[-].MDKLLQPIAISSR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K3]	TGGT1_311
High	[-].MEDWKEQFR.[V]	2xTMT6plex [N-Term; K5]	
High	[M].AEGEGVSGEAATSQDTR.[A]	1xTMT6plex [N-Term]	
High	[M].AEGEGVSGEAATSQDTR.[A]	1xAcetyl [N-Term]	TGGT1_312
High	[M].AASTLADSKVGQPASQAQELPQQR.[E]	2xTMT6plex [N-Term; K9]	
High	[E].GTNETNPPTSRPPGWKYEGSDLHR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K16	TGGT1_312
High	[G].TNETNPPTSRPPGWKYEGSDLHR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_312
High	[F].TEGTNETNPPTSRPPGWKYEGSDLHR.[R]	1xAcetyl [N-Term]; 1xTMT6plex [K18	TGGT1_312
High	[E].GTNETNPPTSRPPGWKYEGSDLHR.[R]	2xTMT6plex [N-Term; K16]	
High	[E].TNPPTSRPPGWKYEGSDLHR.[R]	2xTMT6plex [N-Term; K12]	
High	[M].APTPAGASSGPSSPAVFLPGDMLLR.[I]	1xTMT6plex [N-Term]	
High	[L].GDVISAAPSDCPFGGLR.[K]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C11	
High	[A].ALGDVISAAPSDCPFGGLR.[K]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13	
High	[-].MEANSSSSSLPSVQKFFSDIR.[T]	1xAcetyl [N-Term]; 1xTMT6plex [K15	TGGT1_312
High	[M].AQVPASGKLLVDPR.[Y]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_312
High	[M].GDLDFDEVEKLLDSR.[D]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_312
High	[T].HTYNWDEFR.[Q]	1xTMT6plex [N-Term]	
High	[L].GAPASAAPNTIFELAPTAAEAGR.[A]	1xTMT6plex [N-Term]	
High	[M].ASPTSASSKAPGTESEACGHR.[H]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_312
High	[A].SSKAPGTESEACGHR.[H]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [	
High	[T].SASSKAPGTESEACGHR.[H]	2xTMT6plex [N-Term; K5]; 1xCarbamidomethyl [	
High	[A].LAPAGLADASQVR.[R]	1xAcetyl [N-Term]	TGGT1_312
High	[A].LAPAGLADASQVR.[R]	1xTMT6plex [N-Term]	
High	[M].SYGNGTVLMPIVR.[R]	1xTMT6plex [N-Term]	
High	[A].AASAQSSFKDKR.[G]	3xTMT6plex [N-Term; K9; K11]	
High	[M].VLAELGEQISGALR.[R]	1xTMT6plex [N-Term]	
High	[-].MVLAELGEQISGALR.[R]	1xTMT6plex [N-Term]	
High	[F].NLEGKIHVANPVVEMDGDEMTR.[I]	2xTMT6plex [N-Term; K5]	
High	[S].AASVATGGAFNLEGKIHVANPVVEMDGDEMTR	2xTMT6plex [N-Term; K15]	
High	[A].TGGAFNLEGKIHVANPVVEMDGDEMTR.[I]	2xTMT6plex [N-Term; K10]	
High	[A].SVATGGAFNLEGKIHVANPVVEMDGDEMTR.[I	2xTMT6plex [N-Term; K13]	
High	[A].ASVATGGAFNLEGKIHVANPVVEMDGDEMTR.	2xTMT6plex [N-Term; K14]	
High	[M].TWTPKNVDSAR.[A]	2xTMT6plex [N-Term; K5]	
High	[A].AVPKADLGDCR.[F]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [	
High	[S].ESNAQPDVHAPEDGASR.[H]	1xTMT6plex [N-Term]	
High	[L].GDTPHQATDGDGAVTR.[G]	1xTMT6plex [N-Term]	

High	[M].SGTGGAGSGPLGSAGGAR.[G]	1xAcetyl [N-Term]	TGGT1_313
High	[A].SQPGASPLLQGGTER.[G]	1xTMT6plex [N-Term]	
High	[S].SLDASAGLGLLHER.[D]	1xTMT6plex [N-Term]	
High	[L].DASAGLGLLHER.[D]	1xTMT6plex [N-Term]	
High	[L].GTSADGSAYFHCTPAR.[C]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C12	
High	[M].SANPCPLPAPSVLFGR.[H]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_313
High	[T].FLPPLIGTGFTNEAFLR.[E]	1xTMT6plex [N-Term]	
High	[M].APTAAALAKKR.[L]	3xTMT6plex [N-Term; K9; K10]	
High	[M].APTAAALAK.[K]	2xTMT6plex [N-Term; K9]	
High	[A].PTAAALAKKR.[L]	3xTMT6plex [N-Term; K8; K9]	
High	[M].ANEDGETAASKMTYLSPIASPLLDGKSLR.[R]	3xTMT6plex [N-Term; K11; K26]	
High	[M].ANEDGETAASKMTYLSPIASPLLDGKSLR.[R]	1xAcetyl [N-Term]; 2xTMT6plex [K11	TGGT1_313
High	[M].ANEDGETAASKMTYLSPIASPLLDGKSLR.[R]	1xAcetyl [N-Term]; 1xOxidation [M1	TGGT1_313
High	[Q].FSVVCTETR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].FVKSGEER.[R]	2xTMT6plex [N-Term; K3]	
High	[M].SLDEPCCPPPSR.[H]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_313
High	[M].GGSVESDPR.[S]	1xTMT6plex [N-Term]	
High	[M].SVPSNEVPAPPR.[G]	1xAcetyl [N-Term]	TGGT1_314
High	[M].AAAAEKVAYGPEDEAR.[E]	1xAcetyl [N-Term]; 1xTMT6plex [K6]	TGGT1_314
High	[L].FDAGKFTHWTDLYR.[Q]	2xTMT6plex [N-Term; K5]	
High	[A].EKVAYGPEDEAR.[E]	2xTMT6plex [N-Term; K2]	
High	[-].MDAYNGSAVVAMAGKDCVGIASDTR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_314
High	[-].MDAYNGSAVVAMAGKDCVGIASDTR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_314
High	[-].MEANTSENSKLSESPVANAEESR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K10	TGGT1_314
High	[N].VGGSAIDFTVACR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C12	
High	[M].AGTSIFQGSSWAR.[I]	1xAcetyl [N-Term]	TGGT1_314
High	[M].ATESASALSNGTSADR.[G]	1xAcetyl [N-Term]	TGGT1_314
High	[T].VSLNPNEMEQEGVFTADVIR.[Q]	1xTMT6plex [N-Term]	
High	[M].PGVMGKAGPAADLR.[R]	2xTMT6plex [N-Term; K6]	
High	[M].GKAGPAADLR.[R]	2xTMT6plex [N-Term; K2]	
High	[K].LLRPMEGVPVPER.[T]	1xTMT6plex [N-Term]	
High	[M].SMEQLMALVPLEAALAGKEKGGR.[K]	1xAcetyl [N-Term]; 2xTMT6plex [K18	TGGT1_314
High	[T].AVAGPWPHGVGAAGR.[S]	1xTMT6plex [N-Term]	
High	[M].AAIAAGAASQAPR.[S]	1xAcetyl [N-Term]	TGGT1_315
High	[-].MKEAVAVPLASVEEKER.[Q]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_315
High	[-].MYSSPQSEEAGLVNSR.[G]	1xAcetyl [N-Term]	TGGT1_315
High	[R].QQEEDLDFAEVR.[K]	1xTMT6plex [N-Term]	
High	[R].EDDEDLDFAAVR.[D]		
High	[S].GSPAAGAGFTGEDEEELKR.[Q]	2xTMT6plex [N-Term; K18]	
High	[T].LLPSAPKPVDEAALAAAEKER.[E]	3xTMT6plex [N-Term; K7; K19]	
High	[E].SVAPSSDSRPEHLR.[S]	1xTMT6plex [N-Term]	
High	[T].GAAPGACTPSSSSPGER.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[A].QAFSEENKPGAGPGQNASSSFSAR.[V]	2xTMT6plex [N-Term; K8]	
High	[A].ESVAPSSDSRPEHLR.[S]	1xTMT6plex [N-Term]	
High	[L].VDVSSPGDR.[G]	1xAcetyl [N-Term]	TGGT1_315
High	[-].MKGPSKMAAR.[P]	3xTMT6plex [N-Term; K2; K6]	
High	[M].AEHLSFLEEELVGLPDTPAAFKPSQSQQVSALTF	1xAcetyl [N-Term]; 1xTMT6plex [K22	TGGT1_315
High	[M].SSQNGMQSADGAEQQVTAGLER.[S]	1xAcetyl [N-Term]	TGGT1_315
High	[M].SELSTPSDLLR.[Y]	1xAcetyl [N-Term]	TGGT1_315
High	[M].SNVVRPIKLQEQHLR.[L]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_315
High	[M].GKLVVPSDISLLEEKQTVGR.[R]	3xTMT6plex [N-Term; K2; K15]	
High	[M].GKLVVPSDISLLEEKQTVGR.[R]	1xAcetyl [N-Term]; 2xTMT6plex [K2;	TGGT1_315

High	[M].GKLVVPSDISLLEEK.[Q]	2xTMT6plex [N-Term; K2]	
High	[M].ASLLQIAAALR.[G]	1xAcetyl [N-Term]	TGGT1_316
High	[-].MDASAVLAAPFVCEVHHDR.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_316
High	[A].DNVATAENVQSGFPPLGVSPLEGTTQVGSSPR.	1xTMT6plex [N-Term]	
High	[A].FTLPPLPYAEDALAPHISAETLR.[F]	1xTMT6plex [N-Term]	
High	[F].STNACAFTLPPLPYAEDALAPHISAETLR.[F]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[M].AVKTPTSDAPVR.[V]	2xTMT6plex [N-Term; K3]	
High	[M].AAFSAALAATR.[S]	1xAcetyl [N-Term]	TGGT1_316
High	[F].FSETGAGKHVPR.[C]	2xTMT6plex [N-Term; K8]	
High	[R].CVFLDLEPTVVDEVR.[T]	1xCarbamidomethyl [C1]	
High	[A].SLTPGGGRPDGGGGSGSRPR.[F]	1xTMT6plex [N-Term]	
High	[M].VALEEAPPSSEDRR.[S]	1xTMT6plex [N-Term]	
High	[Q].NFPETLPKSTSLTIEVQDATTDEMEDRPILFVYH	1xAcetyl [N-Term]; 1xOxidation [M2	TGGT1_316
High	[-].MEQASEERPHFEHIANPGSLFGCHPQSAGWGP	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_317
High	[-].MEQASEERPHFEHIANPGSLFGCHPQ.[S]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_317
High	[F].ADEEQQFQTVDNRPLLR.[R]	1xTMT6plex [N-Term]	
High	[A].FADEEQQFQTVDNRPLLR.[R]	1xTMT6plex [N-Term]	
High	[-].MEQASEERPHFEHIANPGSLF.[G]	1xAcetyl [N-Term]	TGGT1_317
High	[C].DFTFHVQQR.[Q]	1xTMT6plex [N-Term]	
High	[A].SGSQGGSYSADLKSR.[Y]	2xTMT6plex [N-Term; K13]	
High	[F].AHDAGSLFSFR.[S]	1xTMT6plex [N-Term]	
High	[-].MLANKLGIQDVGAQLTGK.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K5]	TGGT1_318
High	[-].MLANKLGIQDVGAQLTGKSVLIR.[V]	1xAcetyl [N-Term]; 2xTMT6plex [K5;	TGGT1_318
High	[A].VVEEYAELEETGEQSHHR.[R]	1xTMT6plex [N-Term]	
High	[-].MVSIVNAKADVLR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K8]	TGGT1_318
High	[M].VSIVNAKADVLR.[S]	1xAcetyl [N-Term]; 1xTMT6plex [K7]	TGGT1_318
High	[Q].EVGAPAYR.[R]	1xTMT6plex [N-Term]	
High	[S].ADLTSPGVPSSAPVGR.[R]	1xTMT6plex [N-Term]	
High	[M].GQDSESIIDALR.[T]	1xTMT6plex [N-Term]	
High	[M].GQDSESIIDALR.[T]	1xAcetyl [N-Term]	TGGT1_318
High	[M].AFDASSLDLLIR.[E]	1xAcetyl [N-Term]	TGGT1_318
High	[E].GSLSEKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K6; K12]; 1xCarbamidome	
High	[L].SEKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K3; K9]; 1xCarbamidomet	
High	[S].EKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K2; K8]; 1xCarbamidomet	
High	[Q].SPSKQETQLCAISSEGKPCRNR.[Q]	3xTMT6plex [N-Term; K4; K17]; 2xCarbamidome	
High	[F].AVTETHSSVQSPSKQETQLCAISSEGKPCR.[N]	3xTMT6plex [N-Term; K14; K27]; 2xCarbamidom	
High	[Q].SPSKQETQLCAISSEGKPCR.[N]	2xTMT6plex [N-Term; K4]; 2xCarbamidomethyl [	
High	[Q].SPSKQETQLCAISSEGKPCR.[N]	3xTMT6plex [N-Term; K4; K17]; 2xCarbamidome	
High	[A].LPIQKSVQLGSFDKVVPSR.[E]	3xTMT6plex [N-Term; K5; K14]	
High	[P].SKQETQLCAISSEGKPCR.[N]	3xTMT6plex [N-Term; K2; K15]; 2xCarbamidome	
High	[S].YGGDCSCEKQGHR.[C]	2xTMT6plex [N-Term; K9]; 2xCarbamidomethyl [	
High	[G].GDCSCEKQGHR.[C]	2xTMT6plex [N-Term; K7]; 2xCarbamidomethyl [	
High	[R].CIDDASHENGYTCECPTGYSR.[E]	3xCarbamidomethyl [C1; C13; C15]	
High	[G].ESGSEGSLSEKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K11; K17]; 1xCarbamidom	
High	[F].AVTETHSSVQSPSKQETQLCAISSEGKPCR.[N]	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_319
High	[G].SLSEKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K5; K11]; 1xCarbamidome	
High	[S].ADASSGGNLENEGASPGR.[E]	1xTMT6plex [N-Term]	
High	[M].SVKDAGPVSTGNAAVVAEAKALLAECR.[E]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_319
High	[M].AFGSSSSSER.[Y]	1xTMT6plex [N-Term]	
High	[M].AFGSSSSSER.[Y]	1xAcetyl [N-Term]	TGGT1_319
High	[Q].AAAMLIGQLAAPGGPPAGTTR.[F]	1xTMT6plex [N-Term]	
High	[M].LIGQLAAPGGPPAGTTR.[F]	1xTMT6plex [N-Term]	

High	[M].GMEDGREPYSSR.[G]	1xTMT6plex [N-Term]	
High	[M].GMEDGREPYSSR.[G]	1xTMT6plex [N-Term]; 1xOxidation [M2]	
High	[A].LEKPEDDDFQLVLPPSPAALR.[R]	2xTMT6plex [N-Term; K3]	
High	[M].VADLSPVSPSR.[A]	1xTMT6plex [N-Term]	
High	[L].AVKTFKLADIGEGIAQVELLK.[W]	3xTMT6plex [N-Term; K3; K6]	
High	[-].MLQSLLGR.[F]	1xAcetyl [N-Term]	TGGT1_320
High	[Q].ETAMVVPNGSGLELQNR.[S]	1xTMT6plex [N-Term]	
High	[M].AAAQETAMVVPNGSGLELQNR.[S]	1xAcetyl [N-Term]	TGGT1_320
High	[Q].EAASDEKQDDDSPKR.[R]	3xTMT6plex [N-Term; K7; K14]	
High	[-].MKHESSGFCHR.[T]	2xTMT6plex [N-Term; K2]; 1xCarbamidomethyl	
High	[-].MKHESSGFCHR.[T]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_320
High	[A].FLHSPFPSSSSPAFVHASDGDPR.[G]	1xTMT6plex [N-Term]	
High	[S].GIHPQPLR.[T]	1xTMT6plex [N-Term]	
High	[-].MFECTIEGLLLKR.[L]	2xTMT6plex [N-Term; K12]; 1xCarbamidomethy	
High	[-].MMEDFSAVAR.[A]	1xAcetyl [N-Term]	TGGT1_320
High	[M].MEDFSAVAR.[A]	1xAcetyl [N-Term]	TGGT1_320
High	[M].SYPYYCEFFVKFPNYIPPKDPAER.[L]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_320
High	[A].DNLLEGLLHR.[T]	1xTMT6plex [N-Term]	
High	[M].SVEDSHQTIEPSISGTR.[A]	1xTMT6plex [N-Term]	
High	[M].ASLVCAISGVIPEEPVFSVK.[T]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_320
High	[F].SVHSHNIRPDKHELPASEVPLYYNR.[F]	2xTMT6plex [N-Term; K11]	
High	[-].MEGGGPVAVSPSARPEVSSKNR.[V]	1xAcetyl [N-Term]; 1xTMT6plex [K20	TGGT1_320
High	[A].GIPGLHNWLR.[Q]	1xTMT6plex [N-Term]	
High	[M].SGFVFNPNASVFVPGGVSSAPPPPPPASEDPA	1xAcetyl [N-Term]	TGGT1_320
High	[S].SAPPPPPPASEDPAR.[A]	1xTMT6plex [N-Term]	
High	[M].SGQNSFVLGR.[G]	1xAcetyl [N-Term]	TGGT1_320
High	[S].NMGGMGGPAMGMGSSTQMGTPNNSNPR.[	1xTMT6plex [N-Term]	
High	[-].MEGAIPQAGEMENGATVGAPVSGVPR.[P]	1xAcetyl [N-Term]	TGGT1_321
High	[M].GSSTQMGTPNNSNPR.[A]	1xTMT6plex [N-Term]	
High	[T].QMGTPNNSNPR.[A]	1xTMT6plex [N-Term]	
High	[-].MEGAIPQAGEMENGATVGAPVSGVPR.[P]	1xAcetyl [N-Term]; 1xOxidation [M1	TGGT1_321
High	[M].GSSTQMGTPNNSNPR.[A]	1xTMT6plex [N-Term]; 1xOxidation [M6]	
High	[M].GGMGGPAMGMGSSTQMGTPNNSNPR.[A]	1xTMT6plex [N-Term]	
High	[S].ELPAGVDWR.[S]	1xTMT6plex [N-Term]	
High	[E].LPAGVDWR.[S]	1xTMT6plex [N-Term]	
High	[E].LPAGVDWR.[S]	1xAcetyl [N-Term]	TGGT1_321
High	[F].AEHKSGGEKASR.[E]	1xAcetyl [N-Term]; 2xTMT6plex [K4;	TGGT1_321
High	[M].VSVEGELAR.[E]	1xTMT6plex [N-Term]	
High	[Q].GEENEENVEQTFGVR.[R]	1xTMT6plex [N-Term]	
High	[A].AGKKANEGVSAHHDSER.[R]	3xTMT6plex [N-Term; K3; K4]	
High	[L].SIHERPTGFFFR.[S]	1xTMT6plex [N-Term]	
High	[A].EIQAPAEIR.[S]	1xTMT6plex [N-Term]	
High	[A].EHEVVLDNTGDMDEMLPDQLIPSVPR.[S]	1xTMT6plex [N-Term]	
High	[A].EHEVVLDNTGDMDEMLPDQLIPSVPR.[S]	1xTMT6plex [N-Term]; 1xOxidation [M]	
High	[M].SCCGGTVAEHEVVLDNTGDMDEMLPDQLIPS	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_324
High	[H].ERPTGFFFR.[S]	1xTMT6plex [N-Term]	
High	[G].EGQLFISGPR.[S]	1xTMT6plex [N-Term]	
High	[M].SCCGGTVAEHEVVLDNTGDMDEMLPDQLIPS	1xAcetyl [N-Term]; 2xCarbamidomet	TGGT1_324
High	[V].AEHEVVLDNTGDMDEMLPDQLIPSVPR.[S]	1xTMT6plex [N-Term]	
High	[A].APVQGTLGPDVADTAGEPVVLQVAR.[G]	1xTMT6plex [N-Term]	
High	[A].APVQGTLGPDVADTAGEPVVLQVAR.[G]	1xAcetyl [N-Term]	TGGT1_356
High	[M].SASPCSIPSLR.[E]	1xAcetyl [N-Term]; 1xCarbamidomet	TGGT1_359

High	[M].AFAPPASSAAGVLALLHER.[D]	1xTMT6plex [N-Term]	
High	[M].SAGAVTAQPLPSPKAGLGAAMAFAPPASSAA	1xAcetyl [N-Term]; 1xTMT6plex [K14	TGGT1_361
High	[M].AFAPPASSAAGVLALLHER.[D]	1xAcetyl [N-Term]	TGGT1_361
High	[W].LEQEAAEEVTPLLNSHTETPTQSPSAFR.[R]	1xTMT6plex [N-Term]	
High	[W].LEQEAAEEVTPLLNSHTETPTQSPSAFR.[R]	1xAcetyl [N-Term]	TGGT1_363
High	[E].QEAAEEVTPLLNSHTETPTQSPSAFR.[R]	1xAcetyl [N-Term]	TGGT1_363
High	[N].SHTETPTQSPSAFR.[R]	1xTMT6plex [N-Term]	
High	[L].NSHTETPTQSPSAFR.[R]	1xTMT6plex [N-Term]	
High	[L].LNSHTETPTQSPSAFR.[R]	1xTMT6plex [N-Term]	
High	[G].HVQQGAGVVRPR.[H]	1xTMT6plex [N-Term]	
High	[M].AHVLISSPSTVELDEETQVFTSLQNAALIPR.[D]	1xAcetyl [N-Term]	TGGT1_363
High	[D].GQVITIGNER.[F]	1xTMT6plex [N-Term]	
High	[M].GQKDSYVGDEAQSKR.[G]	3xTMT6plex [N-Term; K3; K14]	
High	[G].MGQKDSYVGDEAQSKR.[G]	3xTMT6plex [N-Term; K4; K15]	
High	[L].TEAPLNPKANR.[E]	2xTMT6plex [N-Term; K8]	
High	[T].EAPLNPKANR.[E]	2xTMT6plex [N-Term; K7]	
High	[SC].YVGDEAQSKR.[G]	2xTMT6plex [N-Term; K9]	

Contaminant	spike-in std	Qvality PEP	Qvality q-value	# Protein Groups	# Proteins	# PSMs	Positions in Master Proteins	# Missed Cleavages
FALSE	FALSE	0.18872	0.005483	1	3	7	TGGT1_200	0
FALSE	FALSE	1.53E-05	0	1	1	14	TGGT1_200	0
FALSE	FALSE	0.062214	0.001175	1	1	9	TGGT1_200	0
FALSE	FALSE	0.094782	0.001557	1	1	6	TGGT1_200	0
FALSE	FALSE	0.004519	0	1	1	7	TGGT1_200	1
FALSE	FALSE	0.178124	0.005258	1	1	1	TGGT1_201	0
FALSE	FALSE	0.013454	0	1	1	9	TGGT1_201	0
FALSE	FALSE	0.043229	0.000606	1	1	6	TGGT1_201	1
FALSE	FALSE	0.003043	0	1	1	9	TGGT1_201	0
FALSE	FALSE	0.001414	0	1	1	9	TGGT1_201	0
FALSE	FALSE	0.029036	0.000606	1	1	9	TGGT1_201	0
FALSE	FALSE	0.083436	0.001557	1	1	3	TGGT1_201	0
FALSE	FALSE	0.065345	0.001175	1	1	6	TGGT1_201	1
FALSE	FALSE	0.062214	0.001175	1	1	7	TGGT1_201	1
FALSE	FALSE	0.195339	0.005483	1	1	1	TGGT1_201	1
FALSE	FALSE	8.68E-05	0	1	1	8	TGGT1_201	0
FALSE	FALSE	0.021785	0	1	1	7	TGGT1_201	2
FALSE	FALSE	0.026941	0	1	1	30	TGGT1_201	0
FALSE	FALSE	0.083436	0.001557	1	1	5	TGGT1_201	0
FALSE	FALSE	0.074309	0.001557	1	1	9	TGGT1_201	0
FALSE	FALSE	0.201008	0.00584	1	1	2	TGGT1_201	0
FALSE	FALSE	0.00174	0	1	1	7	TGGT1_201	0
FALSE	FALSE	0.0004	0	1	1	1	TGGT1_201	2
FALSE	FALSE	0.100694	0.001981	1	1	3	TGGT1_202	2
FALSE	FALSE	0.020337	0	1	1	8	TGGT1_202	0
FALSE	FALSE	0.128061	0.002851	1	1	3	TGGT1_202	0
FALSE	FALSE	0.084458	0.001557	1	1	3	TGGT1_202	1
FALSE	FALSE	0.182298	0.005483	1	1	2	TGGT1_202	0
FALSE	FALSE	0.001544	0	1	1	8	TGGT1_202	0
FALSE	FALSE	0.013709	0	1	1	9	TGGT1_202	0
FALSE	FALSE	0.059962	0.001175	1	1	6	TGGT1_202	0
FALSE	FALSE	0.079468	0.001557	1	1	5	TGGT1_202	0
FALSE	FALSE	0.017391	0	1	1	6	TGGT1_202	0
FALSE	FALSE	0.000547	0	1	1	19	TGGT1_202	0
FALSE	FALSE	0.00034	0	1	1	20	TGGT1_202	0
FALSE	FALSE	0.173026	0.005258	1	1	8	TGGT1_202	0
FALSE	FALSE	0.113596	0.001981	1	1	9	TGGT1_202	0
FALSE	FALSE	0.003673	0	1	1	7	TGGT1_202	0
FALSE	FALSE	0.003605	0	1	1	9	TGGT1_202	0
FALSE	FALSE	0.016336	0	1	1	9	TGGT1_202	1
FALSE	FALSE	2.26E-05	0	1	1	13	TGGT1_202	1
FALSE	FALSE	3.02E-05	0	1	1	17	TGGT1_202	1
FALSE	FALSE	0.007799	0	1	1	6	TGGT1_202	0
FALSE	FALSE	0.031097	0.000606	1	1	9	TGGT1_202	0
FALSE	FALSE	0.029769	0.000606	1	1	4	TGGT1_202	0
FALSE	FALSE	5.56E-05	0	1	1	9	TGGT1_202	0

FALSE	FALSE	0.069901	0.001557	1	1	8	TGGT1_202	0
FALSE	FALSE	0.001468	0	1	1	12	TGGT1_202	0
FALSE	FALSE	0.004036	0	1	1	9	TGGT1_202	1
FALSE	FALSE	0.001303	0	1	1	6	TGGT1_202	0
FALSE	FALSE	0.005286	0	1	1	1	TGGT1_202	0
FALSE	FALSE	0.026442	0	1	1	4	TGGT1_202	0
FALSE	FALSE	0.220108	0.006954	1	1	1	TGGT1_202	0
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FALSE	FALSE	0.0032	0	1	1	5	TGGT1_203	0
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FALSE	FALSE	0.118474	0.002459	1	1	9	TGGT1_203	0
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FALSE	FALSE	0.065345	0.001175	1	1	3	TGGT1_209	2
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FALSE	FALSE	0.030331	0.000606	1	1	2	TGGT1_216	0
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FALSE	FALSE	0.022618	0	1	1	4	TGGT1_216	0
FALSE	FALSE	0.118474	0.002459	1	1	2	TGGT1_216	0
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FALSE	FALSE	0.009532	0	1	1	9	TGGT1_216	0
FALSE	FALSE	0.001478	0	1	1	8	TGGT1_216	0
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FALSE	FALSE	0.015344	0	1	1	9	TGGT1_230	0
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FALSE	FALSE	0.097695	0.001981	1	1	5	TGGT1_243	0
FALSE	FALSE	0.17003	0.005258	1	1	1	TGGT1_243	0
FALSE	FALSE	0.227657	0.007305	1	1	1	TGGT1_243	1
FALSE	FALSE	0.001255	0	1	1	5	TGGT1_243	0
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FALSE	FALSE	0.003936	0	1	1	3	TGGT1_243	0
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FALSE	FALSE	0.036108	0.000606	1	1	8	TGGT1_244	0
FALSE	FALSE	0.047143	0.000606	1	1	4	TGGT1_244	1
FALSE	FALSE	0.127299	0.002851	1	1	1	TGGT1_244	1
FALSE	FALSE	0.022477	0	1	1	2	TGGT1_244	1
FALSE	FALSE	0.017944	0	1	1	8	TGGT1_244	2
FALSE	FALSE	0.112238	0.001981	1	1	7	TGGT1_244	0
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FALSE	FALSE	2.59E-07	0	1	1	17	TGGT1_244	0
FALSE	FALSE	0.032281	0.000606	1	1	2	TGGT1_244	2
FALSE	FALSE	0.186558	0.005483	1	1	1	TGGT1_244	0
FALSE	FALSE	0.000426	0	1	1	9	TGGT1_244	0
FALSE	FALSE	0.009296	0	1	1	8	TGGT1_245	1
FALSE	FALSE	0.042962	0.000606	1	1	3	TGGT1_245	0
FALSE	FALSE	0.032686	0.000606	1	1	3	TGGT1_245	2
FALSE	FALSE	0.119903	0.002851	1	1	2	TGGT1_245	1
FALSE	FALSE	0.158504	0.004951	1	1	2	TGGT1_245	0
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FALSE	FALSE	0.114281	0.001981	1	1	3	TGGT1_246	0
FALSE	FALSE	0.008841	0	1	1	6	TGGT1_246	2
FALSE	FALSE	0.106959	0.001981	1	1	2	TGGT1_246	0
FALSE	FALSE	0.010603	0	1	1	2	TGGT1_246	0
FALSE	FALSE	0.039634	0.000606	1	1	8	TGGT1_246	1
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FALSE	FALSE	0.039389	0.000606	1	1	2	TGGT1_246	1
FALSE	FALSE	0.004491	0	1	1	9	TGGT1_246	0
FALSE	FALSE	0.028144	0	1	1	5	TGGT1_246	1
FALSE	FALSE	0.228936	0.007683	1	1	3	TGGT1_246	1
FALSE	FALSE	0.093075	0.001557	1	1	8	TGGT1_246	0
FALSE	FALSE	0.005993	0	1	1	12	TGGT1_246	0
FALSE	FALSE	0.045144	0.000606	1	1	5	TGGT1_246	0
FALSE	FALSE	1.89E-05	0	1	1	9	TGGT1_247	0
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FALSE	FALSE	0.047143	0.000606	1	1	1	TGGT1_247	2
FALSE	FALSE	0.018748	0	1	1	2	TGGT1_247	0
FALSE	FALSE	0.020464	0	1	1	4	TGGT1_247	0
FALSE	FALSE	0.043498	0.000606	1	1	5	TGGT1_247	0
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FALSE	FALSE	4.15E-06	0	1	1	9	TGGT1_247	0
FALSE	FALSE	0.000633	0	1	1	10	TGGT1_247	0
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FALSE	FALSE	0.086013	0.001557	1	1	4	TGGT1_247	1

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FALSE	FALSE	0.000311	0	1	1	9	TGGT1_247	1
FALSE	FALSE	1.05E-05	0	1	1	11	TGGT1_247	1
FALSE	FALSE	0.209182	0.00624	1	1	7	TGGT1_247	1
FALSE	FALSE	6.29E-07	0	1	1	22	TGGT1_247	2
FALSE	FALSE	0.001311	0	1	1	4	TGGT1_247	2
FALSE	FALSE	0.027623	0	1	1	10	TGGT1_247	1
FALSE	FALSE	0.023046	0	1	1	8	TGGT1_247	0
FALSE	FALSE	0.008098	0	1	1	3	TGGT1_247	2
FALSE	FALSE	0.057082	0.000606	1	1	5	TGGT1_247	0
FALSE	FALSE	0.115663	0.001981	1	1	1	TGGT1_247	2
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FALSE	FALSE	0.000217	0	1	1	4	TGGT1_247	1
FALSE	FALSE	0.012401	0	1	1	5	TGGT1_247	2
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FALSE	FALSE	0.057789	0.000606	1	1	7	TGGT1_247	1
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FALSE	FALSE	0.125036	0.002851	1	1	3	TGGT1_247	2
FALSE	FALSE	0.000397	0	1	1	4	TGGT1_247	2
FALSE	FALSE	0.000572	0	1	1	4	TGGT1_247	0
FALSE	FALSE	0.168058	0.005258	1	1	8	TGGT1_247	0
FALSE	FALSE	0.005664	0	1	1	9	TGGT1_248	1
FALSE	FALSE	0.030712	0.000606	1	1	21	TGGT1_248	1
FALSE	FALSE	0.009354	0	1	1	9	TGGT1_248	1
FALSE	FALSE	0.013882	0	1	1	9	TGGT1_248	0
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FALSE	FALSE	0.000745	0	1	1	8	TGGT1_248	1
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FALSE	FALSE	0.023046	0	1	1	4	TGGT1_248	0
FALSE	FALSE	0.166107	0.005258	1	1	3	TGGT1_248	2
FALSE	FALSE	0.190904	0.005483	1	1	2	TGGT1_248	2
FALSE	FALSE	0.000774	0	1	1	13	TGGT1_248	0
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FALSE	FALSE	0.02728	0	1	1	7	TGGT1_248	0
FALSE	FALSE	0.198723	0.005483	1	1	6	TGGT1_248	0
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FALSE	FALSE	0.020852	0	1	1	3	TGGT1_248	0
FALSE	FALSE	0.000254	0	1	1	4	TGGT1_248	2
FALSE	FALSE	0.158504	0.004951	1	1	1	TGGT1_248	1
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FALSE	FALSE	0.030521	0.000606	1	1	4	TGGT1_248	0
FALSE	FALSE	0.066151	0.001557	1	1	6	TGGT1_249	0
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FALSE	FALSE	0.06905	0.001557	1	1	4	TGGT1_249	1
FALSE	FALSE	0.074309	0.001557	1	1	8	TGGT1_249	0
FALSE	FALSE	0.107605	0.001981	1	1	2	TGGT1_249	1

FALSE	FALSE	0.074764	0.001557	1	1	7	TGGT1_249	0
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FALSE	FALSE	0.005918	0	1	1	9	TGGT1_249	0
FALSE	FALSE	0.040379	0.000606	1	1	6	TGGT1_249	0
FALSE	FALSE	0.004842	0	1	1	6	TGGT1_249	0
FALSE	FALSE	0.005736	0	1	1	6	TGGT1_249	0
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FALSE	FALSE	0.019834	0	1	1	9	TGGT1_249	0
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FALSE	FALSE	0.012095	0	1	1	2	TGGT1_249	1
FALSE	FALSE	7.37E-05	0	1	1	9	TGGT1_249	1
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FALSE	FALSE	0.225117	0.007305	1	1	2	TGGT1_249	0
FALSE	FALSE	0.00312	0	1	1	1	TGGT1_249	2
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FALSE	FALSE	0.003101	0	1	1	8	TGGT1_250	0
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FALSE	FALSE	0.000495	0	1	1	19	TGGT1_250	0
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FALSE	FALSE	0.005808	0	1	1	9	TGGT1_251	1
FALSE	FALSE	0.114281	0.001981	1	1	2	TGGT1_251	0
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FALSE	FALSE	0.057434	0.000606	1	1	4	TGGT1_252	0
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FALSE	FALSE	0.106959	0.001981	1	3	2	TGGT1_252	0
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FALSE	FALSE	0.061833	0.001175	1	1	6	TGGT1_253	0
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FALSE	FALSE	0.081926	0.001557	1	1	5	TGGT1_253	0
FALSE	FALSE	0.073856	0.001557	1	1	5	TGGT1_253	0
FALSE	FALSE	0.238058	0.008344	1	1	1	TGGT1_253	0
FALSE	FALSE	0.171023	0.005258	1	1	1	TGGT1_253	0
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FALSE	FALSE	0.039634	0.000606	1	1	2	TGGT1_254	0
FALSE	FALSE	0.190904	0.005483	1	1	7	TGGT1_254	0
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FALSE	FALSE	0.230221	0.008066	1	1	1	TGGT1_254	2
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FALSE	FALSE	0.125036	0.002851	1	1	5	TGGT1_258	0
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FALSE	FALSE	0.001686	0	1	1	7	TGGT1_258	1
FALSE	FALSE	0.000325	0	1	1	8	TGGT1_258	0
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FALSE	FALSE	0.091397	0.001557	1	1	3	TGGT1_258	1
FALSE	FALSE	0.135119	0.003322	1	2	1	TGGT1_258	1
FALSE	FALSE	0.11636	0.002459	1	1	3	TGGT1_259	0
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FALSE	FALSE	0.000855	0	1	1	9	TGGT1_259	0
FALSE	FALSE	0.000982	0	1	1	9	TGGT1_259	0
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FALSE	FALSE	0.235421	0.008344	1	1	1	TGGT1_259	1
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FALSE	FALSE	0.111565	0.001981	1	1	3	TGGT1_259	0
FALSE	FALSE	0.010805	0	1	1	9	TGGT1_259	1
FALSE	FALSE	0.000281	0	1	1	9	TGGT1_259	1
FALSE	FALSE	0.011869	0	1	1	9	TGGT1_259	1
FALSE	FALSE	0.228936	0.007683	1	1	4	TGGT1_259	0
FALSE	FALSE	0.024077	0	1	1	7	TGGT1_259	0

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FALSE	FALSE	0.04599	0.000606	1	1	3	TGGT1_259	0
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FALSE	FALSE	0.001263	0	1	1	10	TGGT1_260	0
FALSE	FALSE	1.77E-05	0	1	1	6	TGGT1_260	1
FALSE	FALSE	0.000492	0	1	1	18	TGGT1_260	1
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FALSE	FALSE	0.035884	0.000606	1	1	16	TGGT1_260	1
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FALSE	FALSE	6.67E-05	0	1	1	18	TGGT1_260	1
FALSE	FALSE	0.196462	0.005483	1	1	5	TGGT1_260	0
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FALSE	FALSE	0.012796	0	1	1	8	TGGT1_260	0
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FALSE	FALSE	0.007464	0	1	1	6	TGGT1_260	0
FALSE	FALSE	0.000231	0	1	1	8	TGGT1_260	0
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FALSE	FALSE	0.000492	0	1	1	8	TGGT1_264	0
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FALSE	FALSE	0.007848	0	1	1	5	TGGT1_293	1
FALSE	FALSE	0.00014	0	1	1	8	TGGT1_293	1
FALSE	FALSE	0.036787	0.000606	1	1	6	TGGT1_293	0
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FALSE	FALSE	0.079954	0.001557	1	1	8	TGGT1_293	0
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FALSE	FALSE	0.000883	0	1	1	9	TGGT1_294	0
FALSE	FALSE	0.138371	0.004241	1	1	2	TGGT1_294	1
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FALSE	FALSE	0.011869	0	1	1	4	TGGT1_294	1
FALSE	FALSE	0.000221	0	1	1	3	TGGT1_294	1
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FALSE	FALSE	0.000104	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.121349	0.002851	1	1	4	TGGT1_312	0
FALSE	FALSE	0.001149	0	1	1	1	TGGT1_312	1
FALSE	FALSE	0.000995	0	1	1	9	TGGT1_312	1
FALSE	FALSE	0.006752	0	1	1	6	TGGT1_312	1
FALSE	FALSE	0.000057	0	1	1	7	TGGT1_312	1
FALSE	FALSE	0.064153	0.001175	1	1	1	TGGT1_312	1
FALSE	FALSE	0.216413	0.006605	1	1	1	TGGT1_312	1
FALSE	FALSE	0.006462	0	1	1	8	TGGT1_312	0
FALSE	FALSE	0.076613	0.001557	1	1	1	TGGT1_312	0
FALSE	FALSE	0.212772	0.006605	1	1	2	TGGT1_312	0
FALSE	FALSE	0.058866	0.000606	1	1	9	TGGT1_312	1
FALSE	FALSE	0.083945	0.001557	1	1	13	TGGT1_312	1
FALSE	FALSE	0.000669	0	1	1	9	TGGT1_312	1
FALSE	FALSE	0.026277	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.0004	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.001795	0	1	1	7	TGGT1_312	1
FALSE	FALSE	0.016133	0	1	1	5	TGGT1_312	1
FALSE	FALSE	0.232809	0.008344	1	1	2	TGGT1_312	1
FALSE	FALSE	0.001864	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.01067	0	1	1	7	TGGT1_312	0
FALSE	FALSE	0.000182	0	1	1	16	TGGT1_312	0
FALSE	FALSE	0.023778	0	1	1	5	TGGT1_313	2
FALSE	FALSE	0.001114	0	1	1	17	TGGT1_313	0
FALSE	FALSE	0.103781	0.001981	1	1	1	TGGT1_313	0
FALSE	FALSE	0.02138	0	1	1	2	TGGT1_313	1
FALSE	FALSE	0.010022	0	1	1	1	TGGT1_313	1
FALSE	FALSE	0.016336	0	1	1	5	TGGT1_313	1
FALSE	FALSE	1.23E-05	0	1	1	6	TGGT1_313	1
FALSE	FALSE	0.028856	0.000606	1	1	1	TGGT1_313	1
FALSE	FALSE	0.032081	0.000606	1	1	6	TGGT1_313	1
FALSE	FALSE	0.106959	0.001981	1	1	1	TGGT1_313	1
FALSE	FALSE	0.003605	0	1	1	9	TGGT1_313	0
FALSE	FALSE	0.024686	0	1	1	8	TGGT1_313	0

FALSE	FALSE	0.054003	0.000606	1	1	4	TGGT1_313	0
FALSE	FALSE	0.151216	0.004951	1	1	2	TGGT1_313	0
FALSE	FALSE	0.024996	0	1	1	6	TGGT1_313	0
FALSE	FALSE	0.000292	0	1	1	9	TGGT1_313	0
FALSE	FALSE	0.005559	0	1	1	9	TGGT1_313	0
FALSE	FALSE	0.061454	0.001175	1	1	7	TGGT1_313	0
FALSE	FALSE	0.221351	0.006954	1	1	2	TGGT1_313	0
FALSE	FALSE	2.63E-05	0	1	1	12	TGGT1_313	2
FALSE	FALSE	0.002986	0	1	1	17	TGGT1_313	0
FALSE	FALSE	0.077081	0.001557	1	1	4	TGGT1_313	2
FALSE	FALSE	1.4E-06	0	1	1	4	TGGT1_313	2
FALSE	FALSE	4.53E-06	0	1	1	12	TGGT1_313	2
FALSE	FALSE	0.089749	0.001557	1	1	3	TGGT1_313	2
FALSE	FALSE	0.094782	0.001557	1	1	1	TGGT1_313	0
FALSE	FALSE	0.092513	0.001557	1	1	4	TGGT1_313	1
FALSE	FALSE	0.02021	0	1	1	9	TGGT1_313	0
FALSE	FALSE	0.206818	0.00584	1	1	4	TGGT1_313	0
FALSE	FALSE	0.211569	0.006605	1	1	2	TGGT1_314	0
FALSE	FALSE	0.000311	0	1	1	16	TGGT1_314	1
FALSE	FALSE	0.01761	0	1	1	9	TGGT1_314	1
FALSE	FALSE	0.103781	0.001981	1	1	3	TGGT1_314	1
FALSE	FALSE	7.06E-05	0	1	1	9	TGGT1_314	1
FALSE	FALSE	0.203315	0.00584	1	1	1	TGGT1_314	1
FALSE	FALSE	0.000583	0	1	1	8	TGGT1_314	1
FALSE	FALSE	0.000194	0	1	1	18	TGGT1_314	0
FALSE	FALSE	0.005489	0	1	1	9	TGGT1_314	0
FALSE	FALSE	0.000911	0	1	1	8	TGGT1_314	0
FALSE	FALSE	0.140857	0.004678	1	1	4	TGGT1_314	0
FALSE	FALSE	0.023482	0	1	1	9	TGGT1_314	1
FALSE	FALSE	0.067793	0.001557	1	1	6	TGGT1_314	1
FALSE	FALSE	0.013203	0	1	1	2	TGGT1_314	0
FALSE	FALSE	0.007654	0	1	1	12	TGGT1_314	2
FALSE	FALSE	0.008461	0	1	1	4	TGGT1_314	0
FALSE	FALSE	0.000531	0	1	1	9	TGGT1_315	0
FALSE	FALSE	7.63E-06	0	1	1	14	TGGT1_315	2
FALSE	FALSE	0.018631	0	1	1	4	TGGT1_315	0
FALSE	FALSE	0.007654	0	1	1	7	TGGT1_315	0
FALSE	FALSE	0.013795	0	1	1	9	TGGT1_315	0
FALSE	FALSE	0.001396	0	1	1	2	TGGT1_315	1
FALSE	FALSE	4.2E-06	0	1	1	5	TGGT1_315	1
FALSE	FALSE	0.019587	0	1	1	1	TGGT1_315	0
FALSE	FALSE	0.027451	0	1	1	1	TGGT1_315	0
FALSE	FALSE	0.063761	0.001175	1	1	1	TGGT1_315	0
FALSE	FALSE	0.079954	0.001557	1	1	2	TGGT1_315	0
FALSE	FALSE	0.145091	0.004951	1	1	4	TGGT1_315	0
FALSE	FALSE	0.025153	0	1	1	8	TGGT1_315	2
FALSE	FALSE	5.52E-05	0	1	1	9	TGGT1_315	0
FALSE	FALSE	0.1802	0.005483	1	1	2	TGGT1_315	0
FALSE	FALSE	0.014323	0	1	1	9	TGGT1_315	0
FALSE	FALSE	4.01E-05	0	1	1	8	TGGT1_315	1
FALSE	FALSE	0.000108	0	1	1	3	TGGT1_315	2
FALSE	FALSE	2.33E-05	0	1	1	18	TGGT1_315	2

FALSE	FALSE	0.083945	0.001557	1	1	4	TGGT1_315	1
FALSE	FALSE	0.051402	0.000606	1	1	4	TGGT1_316	0
FALSE	FALSE	0.122078	0.002851	1	1	2	TGGT1_316	0
FALSE	FALSE	0.005091	0	1	1	10	TGGT1_316	0
FALSE	FALSE	0.000237	0	1	1	9	TGGT1_316	0
FALSE	FALSE	8.98E-06	0	1	1	17	TGGT1_316	0
FALSE	FALSE	0.006381	0	1	1	8	TGGT1_316	1
FALSE	FALSE	0.002822	0	1	1	9	TGGT1_316	0
FALSE	FALSE	0.031487	0.000606	1	1	2	TGGT1_316	1
FALSE	FALSE	0.205645	0.00584	1	1	2	TGGT1_316	0
FALSE	FALSE	0.079954	0.001557	1	1	2	TGGT1_316	0
FALSE	FALSE	0.066558	0.001557	1	1	1	TGGT1_316	1
FALSE	FALSE	0.158504	0.004951	1	1	1	TGGT1_316	1
FALSE	FALSE	3.12E-05	0	1	1	13	TGGT1_317	1
FALSE	FALSE	0.0082	0	1	1	9	TGGT1_317	0
FALSE	FALSE	0.007325	0	1	1	6	TGGT1_317	0
FALSE	FALSE	0.066967	0.001557	1	1	6	TGGT1_317	0
FALSE	FALSE	0.158504	0.004951	1	1	3	TGGT1_317	0
FALSE	FALSE	0.225117	0.007305	1	1	1	TGGT1_317	0
FALSE	FALSE	0.078028	0.001557	1	1	2	TGGT1_318	1
FALSE	FALSE	0.001423	0	1	1	9	TGGT1_318	0
FALSE	FALSE	0.021114	0	1	1	7	TGGT1_318	1
FALSE	FALSE	6.48E-06	0	1	1	15	TGGT1_318	2
FALSE	FALSE	0.001295	0	1	1	2	TGGT1_318	0
FALSE	FALSE	0.00102	0	1	1	7	TGGT1_318	1
FALSE	FALSE	0.003062	0	1	1	16	TGGT1_318	1
FALSE	FALSE	0.182298	0.005483	1	1	3	TGGT1_318	0
FALSE	FALSE	0.231512	0.008344	1	1	1	TGGT1_318	0
FALSE	FALSE	0.00023	0	1	1	18	TGGT1_318	0
FALSE	FALSE	0.007325	0	1	1	5	TGGT1_318	0
FALSE	FALSE	0.001554	0	1	1	8	TGGT1_318	0
FALSE	FALSE	0.000195	0	1	1	6	TGGT1_319	2
FALSE	FALSE	0.013795	0	1	1	3	TGGT1_319	2
FALSE	FALSE	0.001066	0	1	1	10	TGGT1_319	2
FALSE	FALSE	0.000483	0	1	1	5	TGGT1_319	2
FALSE	FALSE	0.005387	0	1	1	2	TGGT1_319	1
FALSE	FALSE	0.001912	0	1	1	4	TGGT1_319	1
FALSE	FALSE	2.5E-08	0	1	1	24	TGGT1_319	1
FALSE	FALSE	0.000113	0	1	1	3	TGGT1_319	2
FALSE	FALSE	0.003407	0	1	1	1	TGGT1_319	1
FALSE	FALSE	0.060703	0.001175	1	1	3	TGGT1_319	1
FALSE	FALSE	0.103781	0.001981	1	1	4	TGGT1_319	1
FALSE	FALSE	0.149443	0.004951	1	1	5	TGGT1_319	0
FALSE	FALSE	0.148563	0.004951	1	1	1	TGGT1_319	2
FALSE	FALSE	0.196462	0.005483	1	1	1	TGGT1_319	1
FALSE	FALSE	0.192005	0.005483	1	1	1	TGGT1_319	2
FALSE	FALSE	0.001121	0	1	1	5	TGGT1_319	0
FALSE	FALSE	0.001841	0	1	1	4	TGGT1_319	2
FALSE	FALSE	0.002181	0	1	1	8	TGGT1_319	0
FALSE	FALSE	0.064153	0.001175	1	1	4	TGGT1_319	0
FALSE	FALSE	0.015734	0	1	1	3	TGGT1_319	0
FALSE	FALSE	2.82E-05	0	1	1	9	TGGT1_319	0

FALSE	FALSE	0.000333	0	1	1	9	TGGT1_319	1
FALSE	FALSE	0.105677	0.001981	1	1	2	TGGT1_319	1
FALSE	FALSE	0.013203	0	1	1	6	TGGT1_319	0
FALSE	FALSE	0.131155	0.002851	1	1	1	TGGT1_319	0
FALSE	FALSE	0.057434	0.000606	1	1	2	TGGT1_319	2
FALSE	FALSE	0.144235	0.004951	1	1	8	TGGT1_320	0
FALSE	FALSE	0.0011	0	1	1	9	TGGT1_320	0
FALSE	FALSE	0.000134	0	1	1	6	TGGT1_320	0
FALSE	FALSE	0.153009	0.004951	1	1	2	TGGT1_320	2
FALSE	FALSE	0.009354	0	1	1	5	TGGT1_320	1
FALSE	FALSE	0.028498	0	1	1	4	TGGT1_320	1
FALSE	FALSE	0.098884	0.001981	1	1	1	TGGT1_320	0
FALSE	FALSE	0.17505	0.005258	1	1	2	TGGT1_320	0
FALSE	FALSE	0.04191	0.000606	1	1	6	TGGT1_320	1
FALSE	FALSE	0.03544	0.000606	1	1	9	TGGT1_320	0
FALSE	FALSE	0.029769	0.000606	1	1	8	TGGT1_320	0
FALSE	FALSE	0.025311	0	1	1	8	TGGT1_320	2
FALSE	FALSE	0.007848	0	1	1	9	TGGT1_320	0
FALSE	FALSE	0.109568	0.001981	1	1	2	TGGT1_320	0
FALSE	FALSE	0.236737	0.008344	1	1	1	TGGT1_320	0
FALSE	FALSE	0.000508	0	1	1	29	TGGT1_320	1
FALSE	FALSE	0.007011	0	1	1	8	TGGT1_320	1
FALSE	FALSE	0.095937	0.001557	1	1	1	TGGT1_320	0
FALSE	FALSE	0.001459	0	1	1	7	TGGT1_320	0
FALSE	FALSE	0.153912	0.004951	1	1	2	TGGT1_320	0
FALSE	FALSE	0.236737	0.008344	1	1	1	TGGT1_320	0
FALSE	FALSE	8.05E-05	0	1	1	9	TGGT1_321	0
FALSE	FALSE	0.001432	0	1	1	18	TGGT1_321	0
FALSE	FALSE	0.007799	0	1	1	9	TGGT1_321	0
FALSE	FALSE	0.044313	0.000606	1	1	5	TGGT1_321	0
FALSE	FALSE	0.04404	0.000606	1	1	16	TGGT1_321	0
FALSE	FALSE	0.128061	0.002851	1	1	6	TGGT1_321	0
FALSE	FALSE	0.174035	0.005258	1	1	2	TGGT1_321	0
FALSE	FALSE	0.146818	0.004951	1	1	4	TGGT1_321	0
FALSE	FALSE	0.168058	0.005258	1	1	5	TGGT1_321	0
FALSE	FALSE	0.225117	0.007305	1	1	1	TGGT1_321	0
FALSE	FALSE	0.216413	0.006605	1	1	1	TGGT1_321	2
FALSE	FALSE	0.007654	0	1	1	9	TGGT1_321	0
FALSE	FALSE	0.002181	0	1	1	9	TGGT1_321	0
FALSE	FALSE	0.193111	0.005483	1	1	1	TGGT1_321	2
FALSE	FALSE	0.000686	0	1	1	9	TGGT1_324	0
FALSE	FALSE	0.028498	0	1	1	6	TGGT1_324	0
FALSE	FALSE	1.34E-07	0	1	1	19	TGGT1_324	0
FALSE	FALSE	0.000621	0	1	1	56	TGGT1_324	0
FALSE	FALSE	0.01067	0	1	1	16	TGGT1_324	0
FALSE	FALSE	0.164176	0.004951	1	1	1	TGGT1_324	0
FALSE	FALSE	0.199863	0.005483	1	1	2	TGGT1_324	0
FALSE	FALSE	0.202159	0.00584	1	1	28	TGGT1_324	0
FALSE	FALSE	0.243405	0.009409	1	1	3	TGGT1_324	0
FALSE	FALSE	0.000025	0	1	1	10	TGGT1_356	0
FALSE	FALSE	0.041393	0.000606	1	1	13	TGGT1_356	0
FALSE	FALSE	0.101918	0.001981	1	1	8	TGGT1_359	0

FALSE	FALSE	0.002412	0	1	1	8	TGGT1_361	0
FALSE	FALSE	0.060331	0.001175	1	1	8	TGGT1_361	1
FALSE	FALSE	0.194222	0.005483	1	1	2	TGGT1_361	0
FALSE	FALSE	0.000976	0	1	1	7	TGGT1_363	0
FALSE	FALSE	4.21E-05	0	1	1	15	TGGT1_363	0
FALSE	FALSE	0.003386	0	1	1	9	TGGT1_363	0
FALSE	FALSE	0.001864	0	1	1	8	TGGT1_363	0
FALSE	FALSE	0.00265	0	1	1	9	TGGT1_363	0
FALSE	FALSE	0.003961	0	1	1	7	TGGT1_363	0
FALSE	FALSE	0.004191	0	2	2	9	TGGT1_363	0
FALSE	FALSE	0.013795	0	1	1	10	TGGT1_363	0
FALSE	FALSE	0.09652	0.001557	1	1	5	TGGT1_411	0
FALSE	FALSE	0.112238	0.001981	1	1	5	TGGT1_411	2
FALSE	FALSE	0.153009	0.004951	1	1	1	TGGT1_411	2
FALSE	FALSE	0.000261	0	2	2	9	TGGT1_411	1
FALSE	FALSE	0.000153	0	2	2	9	TGGT1_411	1
FALSE	FALSE	0.203315	0.00584	2	2	3	TGGT1_411	1

Theo. MH+ [Da]	20171104_04_S65989_asp5_tmt10_tails_po.raw	20171104_05_S65989_asp5_tmt10_tails_po.raw	20171104_07_S65989_asp5_tmt10_tails_po.raw	Found in Sample: [S51] F6: 126, Sample, wt, pool	Found in Sample: [S52] F6: 127N, Sample, wt, single	Found in Sample: [S54] F6: 128N, Sample, wt, single	Found in Sample: [S56] F6: 129N, Sample, wt, single	Found in Sample: [S58] F6: 130N, Sample, wt, single
1571.698	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2166.15	High	High	High	High	High	High	High	High
1335.722	High	High	High	High	High	High	High	High
1340.671	High	High	High	High	Not Found	High	High	Not Found
1881.205	High	High	High	High	High	High	High	High
1671.905	Not Found	High	Not Found	Not Found	High	High	High	High
1212.586	High	High	High	High	High	High	High	High
1686.954	High	High	High	High	High	High	High	High
1785.981	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1476.739	High	High	High	High	High	High	High	High
1289.587	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1195.627	High	High	High	High	High	High	High	High
2077.163	High	High	High	High	High	High	High	High
1628.912	High	High	High	High	High	High	High	High
1741.996	High	Not Found	Not Found	High	High	High	High	High
3112.447	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2995.601	High	High	High	High	High	High	High	High
1188.694	High	High	High	High	High	High	High	High
1058.563	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1115.584	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1002.615	High	Not Found	Not Found	High	High	High	High	High
4263.793	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2503.481	High	Not Found	Not Found	High	High	High	High	High
1981.13	High	High	High	High	High	High	High	High
1045.568	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1416.753	High	High	High	High	High	High	High	High
4799.426	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1322.731	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1892.957	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1328.721	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1368.722	High	High	High	High	High	High	High	High
1224.726	High	High	High	High	High	High	High	High
2101.074	High	High	High	High	High	High	High	High
1913.921	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1863.942	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1070.57	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1198.653	High	High	High	High	High	High	High	High
1923.007	High	High	High	High	High	High	High	High
1499.817	High	High	High	High	High	High	High	High
1927.117	High	High	High	High	High	High	High	High
1984.138	High	High	High	High	High	High	High	High
2071.17	High	High	High	High	High	High	High	High
2459.287	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2748.397	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1072.668	High	Not Found	High	High	High	High	High	High
1857.92	High	High	High	Not Found	High	Not Found	Not Found	High

1613.851	High	High	High	High	High	High	High	High
2436.375	High	High	High	High	High	High	High	High
1773.016	High	High	High	High	High	High	High	High
1602.844	High	High	High	High	High	High	High	High
2255.137	Not Found	Not Found	High	High	High	High	High	High
1432.738	High	High	High	High	High	High	High	High
1995.923	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1315.81	Not Found	Not Found	High	High	High	High	High	High
2196.307	Not Found	Not Found	High	High	High	High	High	High
2137.022	High	High	High	High	High	High	High	High
1609.943	High	High	High	High	High	High	High	High
1538.905	High	High	High	High	High	High	High	High
1441.853	High	High	High	High	High	High	High	High
1906.047	High	High	High	High	High	High	High	High
2746.408	High	High	High	High	High	High	High	High
3305.725	High	High	Not Found	High	High	High	High	High
1237.537	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1744.834	High	Not Found	High	High	High	High	High	High
1181.567	High	High	High	High	High	High	High	High
1635.745	High	High	High	High	High	High	High	High
2238	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1687.974	High	High	Not Found	High	High	High	High	High
2369.157	High	High	High	High	High	High	High	High
2008.837	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1253.531	High	High	High	High	High	High	High	High
3190.698	Not Found	High	Not Found	High	High	High	High	High
1986.961	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1424.689	Not Found	High	Not Found	High	High	High	High	High
1459.863	High	High	High	High	High	High	High	High
1790.824	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2471.253	High	High	High	Not Found	Not Found	High	High	Not Found
1283.856	Not Found	High	High	High	High	High	High	High
1414.897	Not Found	High	Not Found	High	High	High	High	High
1846.007	High	High	High	High	High	High	High	High
1459.92	High	High	High	High	High	High	High	High
1015.535	High	High	High	Not Found	Not Found	Not Found	High	High
1562.854	High	Not Found	High	High	High	High	High	High
1902.045	High	High	High	High	High	High	High	High
2223.177	High	Not Found	Not Found	High	Not Found	High	High	High
2811.381	High	High	High	High	High	High	High	High
1475.822	High	Not Found	Not Found	High	High	High	High	High
1710.079	Not Found	Not Found	High	High	High	High	High	High
3192.684	High	High	Not Found	High	Not Found	High	High	High
2758.468	High	High	High	High	High	High	High	High
1936.174	High	High	High	High	High	High	High	High
2958.584	High	High	High	High	High	High	High	High
2484.35	High	High	Not Found	High	High	High	High	High
2298.286	High	High	High	High	High	High	High	High
1805.905	High	High	High	High	Not Found	High	Not Found	High
1837.986	Not Found	Not Found	High	Not Found	Not Found	High	Not Found	High
1967.028	High	High	High	High	High	High	High	High
1962.066	High	High	High	High	High	High	High	High

2644.348	High	Not Found	High	High	High	High	High	High
3654.813	High	High	Not Found	High	High	High	High	High
2557.316	High	High	High	High	High	High	High	High
1720.949	High	High	High	High	High	High	High	High
1933.964	High	High	Not Found	High	High	High	High	High
3053.402	High	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
2504.333	High	High	High	High	High	High	High	High
1732.723	High	High	High	High	High	High	High	High
1506.941	High	Not Found	High	High	High	High	High	High
1096.547	High	High	High	High	High	High	High	High
1343.877	High	High	High	High	High	High	High	High
1746.975	Not Found	High	Not Found	High	High	High	High	High
2845.5	High	Not Found	Not Found	High	Not Found	High	High	High
2927.528	Not Found	Not Found	High	High	High	Not Found	Not Found	Not Found
2989.592	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
2216.166	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1691.951	High	High	High	High	High	High	High	High
1269.773	High	High	High	High	High	High	High	High
2498.388	Not Found	High	High	High	High	High	High	High
1648.927	High	High	High	High	High	High	High	High
2726.499	Not Found	Not Found	High	High	High	High	High	High
1851.022	Not Found	High	High	High	High	High	High	High
1083.672	High	High	High	High	High	High	High	High
1374.847	Not Found	High	Not Found	High	High	High	High	High
1861.935	Not Found	High	High	High	High	High	High	High
1863.029	High	High	High	High	High	High	High	High
2922.674	High	High	High	High	High	High	High	High
2766.308	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1175.633	High	High	Not Found	High	High	High	High	High
1773.991	High	High	High	High	High	High	High	High
1299.69	High	High	High	Not Found	Not Found	High	High	High
2194.198	Not Found	High	High	High	High	Not Found	High	High
2328.317	High	Not Found	High	High	High	High	High	High
3359.661	High	Not Found	High	Not Found	High	High	Not Found	High
1317.626	High	High	High	High	High	Not Found	Not Found	High
1241.674	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2478.511	High	High	High	High	High	High	High	High
1864.104	High	High	Not Found	High	High	High	High	High
1338.704	High	High	High	High	High	High	High	High
1282.592	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1613.837	High	High	High	High	High	High	High	High
1741.019	High	Not Found	High	High	High	High	High	High
1895.066	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1421.791	High	High	High	High	High	High	High	High
2529.366	High	High	High	High	High	High	High	High
1805.032	High	High	High	High	High	High	High	High
1799.006	High	High	High	High	High	High	High	High
1701.954	High	High	High	High	High	High	High	High
1967.096	Not Found	Not Found	High	High	High	High	High	High
1896.059	Not Found	High	High	High	High	High	High	High
1417.842	High	High	High	High	High	High	High	High
2408.273	High	High	High	High	High	High	High	High

2595.425	Not Found	High	High	High	High	High	High	High
2051.14	High	High	High	High	High	High	High	High
2237.24	High	High	Not Found	High	High	High	High	High
2138.172	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2407.373	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2239.219	Not Found	High	High	Not Found	High	High	High	High
2655.509	High	High	High	High	High	High	High	High
3040.68	Not Found	Not Found	High	High	High	Not Found	High	High
1744.075	High	Not Found	Not Found	High	High	High	High	High
4081.275	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1068.568	High	High	High	High	High	High	High	High
1940.008	High	High	High	Not Found	High	High	High	High
1910.883	High	High	High	High	High	High	High	High
3406.583	High	Not Found	High	High	High	High	High	High
2034.009	High	High	High	High	High	High	High	High
2029.059	High	High	High	High	High	High	High	High
1958.021	High	High	High	High	High	High	High	High
1860.969	Not Found	High	Not Found	Not Found	Not Found	High	High	Not Found
2086.025	High	Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found
2114.129	High	High	High	High	High	High	High	High
1382.714	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2974.445	High	High	High	High	High	High	High	High
1262.583	High	High	High	High	High	High	High	High
3329.852	Not Found	High	High	High	High	High	High	High
3142.7	High	High	Not Found	High	High	High	High	High
3273.74	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2941.656	High	Not Found	Not Found	High	High	High	Not Found	High
1707.878	High	High	High	High	High	High	High	High
1589.926	High	High	High	High	High	High	High	High
1875.07	High	High	High	High	High	High	High	High
1502.894	High	High	High	High	High	High	High	High
1658.825	High	High	High	High	High	High	High	High
1845.977	Not Found	Not Found	High	High	High	High	High	High
4115.128	High	Not Found	High	High	High	High	High	High
1932.996	High	High	High	High	High	High	High	High
3074.651	Not Found	High	Not Found	High	High	High	High	High
2046.08	High	Not Found	Not Found	High	High	High	High	High
2787.503	High	High	Not Found	High	High	High	High	High
2700.471	High	Not Found	High	High	High	High	High	High
4331.203	High	Not Found	High	High	High	High	High	High
2088.066	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2874.535	Not Found	High	Not Found	High	High	High	High	High
2625.354	High	High	High	High	High	High	High	High
1733.784	High	Not Found	High	High	High	High	High	High
1623.834	Not Found	Not Found	High	Not Found	High	Not Found	High	Not Found
1851.819	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
4129.012	High	High	High	Not Found	Not Found	Not Found	High	High
1778.929	High	High	High	High	High	High	High	High
3467.822	High	High	High	Not Found	Not Found	High	Not Found	High
2252.073	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1770.991	High	High	High	High	High	High	High	High
1311.795	Not Found	High	High	High	High	High	High	High

2544.314	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2357.162	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1532.812	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3621.863	High	High	Not Found	Not Found	Not Found	High	Not Found	Not Found
2102.191	High	High	High	High	High	High	High	High
2159.124	High	High	High	High	High	High	High	High
2814.408	High	High	Not Found	Not Found	Not Found	High	Not Found	Not Found
1814.877	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2953.47	High	High	High	High	High	High	High	High
3138.584	High	High	High	High	High	High	High	High
1642.979	High	High	High	High	High	High	High	High
1813.935	High	High	High	High	High	High	High	High
2372.248	High	High	High	High	High	High	High	High
2158.125	High	High	High	High	High	High	High	High
2356.262	High	High	High	High	High	High	High	High
2788.421	High	Not Found	High	High	High	High	High	High
2501.291	High	Not Found	Not Found	High	High	High	High	High
4517.248	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1699.892	High	High	Not Found	High	High	High	High	High
2031.024	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1769.898	High	Not Found	High	Not Found	Not Found	High	High	Not Found
1043.584	High	High	High	High	High	High	High	High
1987.05	High	High	High	High	High	High	High	High
1408.616	Not Found	High	High	Not Found	High	High	High	High
1730.79	High	High	High	Not Found	High	Not Found	Not Found	Not Found
3270.634	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1218.643	Not Found	Not Found	High	High	High	High	High	High
1699.896	High	High	High	High	High	High	High	High
1442.946	High	High	High	High	High	High	High	High
1240.721	Not Found	High	Not Found	High	High	High	High	High
1575.854	High	High	High	High	High	High	High	High
1991.052	High	High	High	High	High	High	High	High
1115.637	Not Found	High	High	High	High	High	High	High
1172.659	High	High	High	High	High	High	High	High
1731	High	High	High	High	Not Found	Not Found	High	Not Found
1530.884	High	High	High	High	High	High	High	High
3061.802	Not Found	High	High	High	High	High	High	High
2220.211	High	High	High	Not Found	High	High	Not Found	High
1276.781	High	High	High	High	High	High	High	High
3192.842	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
1273.747	Not Found	High	Not Found	High	High	High	High	High
1341.585	High	High	Not Found	Not Found	High	Not Found	High	High
1758.027	High	High	High	High	High	High	High	High
2518.169	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1584.757	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
2540.245	High	High	Not Found	High	High	High	High	High
2727.398	Not Found	Not Found	High	High	High	High	High	High
2062.101	High	High	High	High	High	High	High	High
3146.716	Not Found	High	High	High	High	High	High	High
1745.981	High	High	High	High	High	High	High	High
3410.657	High	High	Not Found	High	High	High	High	High
2561.223	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	High

2648.255	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2474.191	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3160.514	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1804.994	High	High	High	High	High	High	High	High
2669.352	High	High	High	High	High	High	High	High
2095.084	High	High	High	High	High	High	High	High
2038.972	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1723.904	High	High	Not Found	High	High	Not Found	Not Found	Not Found
1996.016	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
1938.994	Not Found	High	Not Found	High	High	High	Not Found	Not Found
1188.604	High	High	High	Not Found	High	High	High	High
1729.964	High	High	High	High	High	High	High	High
2357.21	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2317.3	Not Found	High	Not Found	High	High	High	High	High
2211.123	High	High	High	High	High	High	High	High
3349.814	High	Not Found	High	High	Not Found	High	Not Found	Not Found
2008.006	Not Found	High	High	High	Not Found	Not Found	High	High
1234.669	High	High	High	High	High	High	High	High
3408.837	High	High	Not Found	High	High	High	High	High
1975.97	High	High	High	High	High	High	High	High
1927.947	Not Found	High	Not Found	High	High	High	High	High
1929.908	High	High	High	Not Found	Not Found	High	High	High
2080.108	High	High	Not Found	High	High	High	High	High
1794.939	Not Found	Not Found	High	High	High	High	High	High
1377.633	High	Not Found	High	High	High	High	High	High
1695.822	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1879.979	High	High	Not Found	High	High	High	Not Found	High
2079.111	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
2347.013	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
964.5574	High	High	High	Not Found	High	High	High	Not Found
2055.06	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
1825.783	High	Not Found	Not Found	High	Not Found	High	Not Found	Not Found
3546.633	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1298.929	High	High	High	High	High	High	High	High
1311.636	High	High	High	High	High	High	High	High
1373.633	High	High	High	High	High	High	High	High
3252.701	Not Found	High	High	High	High	High	High	High
3571.855	Not Found	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
2679.458	High	High	High	Not Found	Not Found	High	Not Found	Not Found
1329.664	Not Found	Not Found	High	High	High	High	High	High
1516.817	High	High	Not Found	High	High	High	High	High
1494.757	Not Found	High	Not Found	High	High	High	High	High
1611.779	High	High	High	High	High	High	High	High
1555.803	High	High	High	High	High	High	High	High
1711.904	High	High	High	High	High	High	High	High
2170.243	High	High	High	High	High	High	High	High
1346.681	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2020.014	High	High	High	High	High	High	High	High
1015.542	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1202.694	Not Found	High	Not Found	High	High	High	High	High
1477.736	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1893.912	High	High	High	High	High	High	High	High

1034.457	High	Not Found	High	Not Found	Not Found	High	Not Found	Not Found
2537.507	High	High	High	High	High	High	High	High
2310.38	High	High	High	High	High	High	High	High
1696.954	High	High	High	High	High	High	High	High
3115.824	High	High	High	High	High	High	High	High
3243.883	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	High
2239.343	High	High	High	High	High	High	High	High
2778.649	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1505.887	Not Found	High	High	High	High	High	High	High
1819.99	Not Found	Not Found	High	Not Found	Not Found	High	Not Found	Not Found
1180.548	High	High	High	Not Found	High	Not Found	High	Not Found
1066.6	High	High	High	Not Found	High	Not Found	Not Found	Not Found
1765.903	High	High	High	High	High	High	High	High
3317.92	High	High	High	High	High	High	High	High
3161.819	High	High	High	High	High	High	High	High
2974.666	High	High	High	High	High	High	High	High
1985.062	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2575.249	High	High	High	High	High	High	High	High
1273.654	High	High	High	High	High	High	High	High
1755.974	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1768.964	High	High	High	High	High	High	High	High
2195.181	High	High	High	High	High	High	High	High
1496.728	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2678.42	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1908.919	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2594.55	High	High	High	High	High	High	High	High
3306.839	Not Found	Not Found	High	High	High	High	High	High
2158.04	High	High	High	High	High	High	High	High
2174.035	High	High	Not Found	High	High	High	High	High
1091.569	High	High	High	High	Not Found	Not Found	High	High
1278.721	Not Found	High	High	High	High	High	High	High
1400.795	High	Not Found	High	High	High	High	High	High
1037.521	High	Not Found	Not Found	High	High	High	High	High
1986.102	High	High	High	High	High	High	High	High
2071.993	High	High	High	High	High	High	High	High
2786.484	High	Not Found	High	High	High	High	High	Not Found
2122.154	High	High	High	High	High	High	High	High
2715.447	High	High	High	High	High	High	High	High
1571.942	Not Found	High	High	High	High	High	High	High
1913.125	High	High	High	High	High	High	High	High
3589.812	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
3090.615	High	High	Not Found	High	High	High	High	High
2498.379	High	Not Found	Not Found	High	High	High	High	High
2091.191	High	High	High	High	High	High	High	High
965.4687	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2367.339	High	Not Found	Not Found	High	High	High	High	High
1576.967	High	High	High	High	High	High	High	High
1219.71	Not Found	High	High	High	High	High	High	High
2986.592	High	High	High	High	High	High	High	High
1764.11	High	High	High	High	High	High	High	High
1911.178	High	High	High	High	High	High	High	High
1806.973	High	High	High	High	High	High	High	High

3038.434	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2152.036	High	High	High	High	High	High	High	High
2008.957	High	High	High	Not Found	Not Found	High	High	High
1682.881	High	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
1303.721	High	High	High	High	High	High	High	High
945.4822	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2046.133	High	High	High	High	High	High	High	High
1990.021	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1928.987	High	High	High	High	High	High	High	High
2000.025	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1129.538	High	High	High	High	Not Found	Not Found	High	High
1918.999	High	High	High	High	High	High	High	High
1915.867	High	High	High	Not Found	High	High	Not Found	High
1374.743	High	High	High	High	High	High	High	High
1685.885	High	High	Not Found	Not Found	High	Not Found	High	High
3040.64	High	High	High	High	High	High	High	High
1327.83	High	High	High	High	High	High	High	High
1983.122	High	High	High	Not Found	Not Found	Not Found	Not Found	High
3196.741	Not Found	Not Found	High	High	High	High	High	High
2070.155	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1855.064	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1757.007	High	Not Found	High	High	High	High	High	High
3207.633	Not Found	Not Found	High	High	High	High	High	High
3020.481	Not Found	Not Found	High	High	High	High	High	High
1756.891	Not Found	High	High	High	High	High	High	High
4391.28	Not Found	High	Not Found	High	High	High	High	High
2294.1	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3626.912	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1676.816	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1835.937	High	High	High	High	High	High	High	High
1592.817	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2288.15	High	High	High	Not Found	High	High	High	High
1956.09	Not Found	Not Found	High	Not Found	High	Not Found	Not Found	High
1028.573	High	High	High	High	High	High	High	High
3191.684	High	High	High	Not Found	Not Found	Not Found	Not Found	High
925.5465	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2489.392	High	Not Found	Not Found	High	High	High	High	High
3144.639	High	Not Found	Not Found	High	High	High	High	High
2786.472	High	Not Found	High	High	High	High	High	High
2459.337	High	High	High	High	High	High	High	High
2093.115	High	High	High	High	High	High	High	High
1349.677	Not Found	High	High	High	High	High	High	High
2865.411	High	High	High	High	High	High	High	High
2678.259	High	High	High	High	High	High	High	High
1344.711	High	High	High	High	High	High	High	High
3382.68	High	Not Found	High	High	Not Found	Not Found	Not Found	High
2707.342	Not Found	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
2734.342	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1803.861	High	High	High	High	High	High	High	High
1814.069	High	High	High	High	High	High	High	High
2495.127	Not Found	High	High	High	High	High	Not Found	High
3084.413	High	High	High	High	High	High	High	High

1433.831	High	High	High	High	High	High	High	High
1536.812	High	High	High	High	High	High	High	High
2879.538	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1886.032	High	Not Found	High	High	High	High	High	High
2415.358	Not Found	Not Found	High	Not Found	High	High	Not Found	High
1613.961	Not Found	High	Not Found	High	High	High	High	High
1540.915	Not Found	High	High	High	High	High	High	High
3304.392	High	High	High	High	High	High	High	High
3603.634	High	High	High	High	High	High	High	High
3474.591	Not Found	High	Not Found	Not Found	High	High	High	High
3591.822	High	High	High	High	High	High	High	High
1810.949	High	High	High	High	High	High	High	High
1366.659	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3607.817	High	Not Found	High	High	Not Found	High	High	High
1944.039	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
1766.928	High	Not Found	High	High	High	High	High	High
1936.198	High	High	Not Found	High	High	High	High	High
1564.716	High	High	High	Not Found	Not Found	Not Found	High	Not Found
4888.401	High	High	High	Not Found	Not Found	Not Found	High	High
4904.396	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1926.107	High	High	High	High	High	High	High	High
1596.79	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2632.176	High	High	High	Not Found	High	High	High	High
2616.181	High	High	High	High	High	High	High	High
2084.947	High	Not Found	High	High	High	High	High	High
2014.008	High	High	High	High	High	High	High	High
2571.207	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2264.139	Not Found	High	High	High	Not Found	High	Not Found	Not Found
2983.388	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1589.801	High	High	High	High	High	High	High	High
2243.133	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1986.069	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1376.737	High	Not Found	High	High	High	High	High	High
1275.689	High	Not Found	High	High	High	High	High	High
1177.714	Not Found	High	High	High	High	High	High	High
1094.535	High	High	High	High	High	High	High	High
2780.316	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2668.56	High	Not Found	Not Found	High	High	High	High	High
1426.81	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	High
2616.44	Not Found	High	High	High	High	High	High	High
1648.872	High	Not Found	Not Found	Not Found	Not Found	High	High	High
1779.937	High	High	High	High	High	High	High	High
2007.093	High	High	High	High	High	High	High	High
1924.113	High	High	High	High	High	High	High	High
1936.056	Not Found	High	Not Found	High	High	High	High	High
1647.782	High	High	High	Not Found	High	High	Not Found	High
2296.112	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1416.69	Not Found	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1928.19	High	High	High	High	High	High	High	High
2056.248	High	High	High	High	High	High	High	High
1377.744	High	High	High	High	High	High	High	High
1166.689	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found

2192.054	High	High	High	Not Found	High	Not Found	Not Found	High
1385.638	High	High	High	High	High	High	High	High
1859.043	High	High	High	High	High	High	High	High
2048.001	High	High	High	Not Found	High	High	High	High
1744.943	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	High
2506.213	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1407.599	High	High	High	High	High	High	High	High
1423.594	High	High	High	High	High	High	High	High
1248.62	High	High	High	High	High	High	High	High
2703.488	High	High	High	High	High	High	High	High
2186.028	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2006.106	High	High	High	High	High	High	High	High
3766.022	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1719.781	High	High	High	High	High	High	High	High
1648.743	High	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
2487.36	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
1720.816	Not Found	Not Found	High	High	High	High	High	High
1113.488	High	High	High	Not Found	Not Found	Not Found	High	High
2749.421	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
3024.634	Not Found	High	Not Found	High	High	High	High	High
1537.693	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1553.688	High	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
3305.631	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1486.868	High	High	High	High	High	High	High	High
1016.63	High	High	High	High	High	High	High	High
2461.283	High	High	High	High	High	High	High	High
2901.387	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
2825.467	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1818.011	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1067.584	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1433.884	High	High	High	High	High	High	High	High
1116.553	High	Not Found	High	High	Not Found	Not Found	High	High
1891.1	High	High	High	Not Found	Not Found	Not Found	High	High
1645.953	High	High	High	High	High	High	High	High
1458.8	High	High	High	High	High	High	High	High
2316.358	High	High	Not Found	High	High	High	High	High
1400.697	High	High	High	High	High	High	High	High
1383.762	High	High	High	High	High	Not Found	Not Found	High
2462.185	High	High	High	Not Found	High	High	High	Not Found
1146.582	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1989.988	High	High	High	High	High	High	High	High
2061.025	High	High	High	High	High	High	High	High
1360.85	High	High	High	High	High	High	High	High
3123.652	High	Not Found	High	High	High	High	High	High
2062.137	High	High	High	High	High	High	High	High
3486.837	High	High	High	High	High	High	High	High
2308.239	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2870.363	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2581.419	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1558.753	High	High	High	High	High	High	High	High
1984.971	High	High	Not Found	Not Found	High	High	High	High
1370.723	High	High	Not Found	High	High	High	High	High

2276.093	High	Not Found	High	High	High	High	High	High
2055.135	Not Found	Not Found	High	High	High	High	High	High
1634.855	High	Not Found	High	Not Found	Not Found	High	High	High
1967.003	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
2283.246	Not Found	Not Found	High	High	Not Found	Not Found	High	High
1301.665	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2354.283	Not Found	Not Found	High	High	High	Not Found	High	Not Found
2054.061	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2070.056	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1994.076	High	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
1745.812	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1406.707	High	High	High	High	High	High	High	High
2319.023	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1871.064	High	High	High	High	High	High	High	High
2058.216	Not Found	High	Not Found	High	High	High	High	High
996.5044	High	High	Not Found	High	High	High	High	High
1727.888	High	Not Found	High	Not Found	Not Found	High	High	High
1702.871	Not Found	Not Found	High	High	High	High	High	High
1768.925	High	High	Not Found	High	High	High	High	High
2250.286	High	High	High	High	High	High	High	High
1699.908	High	High	High	High	High	High	High	High
1840.93	High	High	High	High	High	High	Not Found	Not Found
1513.807	High	High	High	High	High	High	High	High
2321.317	Not Found	Not Found	High	High	High	High	High	High
1292.696	Not Found	Not Found	High	High	High	Not Found	Not Found	High
1813.947	High	High	High	High	High	High	High	High
2142.172	Not Found	Not Found	High	High	High	High	High	High
2363.248	High	High	High	High	High	High	High	High
1321.779	Not Found	High	High	High	High	High	High	High
1323.673	High	High	High	High	High	High	High	High
1997.019	High	High	High	High	High	High	High	High
2184.171	High	High	Not Found	High	High	High	High	High
2560.3	High	Not Found	High	Not Found	Not Found	Not Found	High	High
2206.073	High	High	High	High	High	High	High	High
1438.837	High	High	High	High	High	High	High	Not Found
3347.873	High	High	High	High	High	High	High	High
1619.93	High	High	Not Found	High	High	High	High	High
2502.497	High	Not Found	Not Found	High	High	High	High	High
2155.207	High	High	Not Found	High	High	Not Found	High	High
2226.244	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1162.531	High	High	High	Not Found	High	High	High	High
2140.081	Not Found	Not Found	High	High	High	High	High	High
1917.897	High	High	High	Not Found	Not Found	Not Found	High	High
1335.697	High	High	High	High	High	High	High	High
1947.972	High	High	High	High	High	High	High	High
1763.851	High	High	High	High	High	High	High	High
3222.76	High	High	High	High	High	High	High	High
3278.872	High	High	High	High	High	High	High	High
2103.221	High	High	High	High	High	High	High	High
1217.709	High	High	Not Found	High	High	High	High	High
1448.791	High	High	High	High	High	High	High	High
1635.943	High	High	High	High	High	High	High	High

2038.083	High	Not Found	Not Found	Not Found	High	High	High	High
2478.254	High	High	High	High	High	High	High	High
2185.019	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1076.486	High	High	High	High	High	High	High	High
1512.913	High	High	High	High	Not Found	Not Found	Not Found	Not Found
4671.311	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1810.933	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1979.022	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1032.496	High	High	High	High	High	High	High	High
1949.825	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2590.3	High	High	High	High	High	High	High	High
3199.648	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3770.908	High	High	Not Found	High	Not Found	High	Not Found	High
3270.685	High	High	High	Not Found	High	Not Found	High	High
3041.522	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3399.728	High	High	High	High	High	High	High	High
3170.565	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3683.876	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3871.956	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
3942.993	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2477.216	High	High	High	High	High	High	High	High
2133.026	High	High	High	High	Not Found	Not Found	High	High
3541.746	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1833.878	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
4117.057	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1992.003	Not Found	Not Found	High	Not Found	High	High	Not Found	High
3152.665	Not Found	High	Not Found	Not Found	Not Found	High	High	High
1856.103	High	High	High	High	High	High	High	High
1131.491	High	High	High	High	High	High	High	High
2313.26	High	High	High	High	High	High	High	High
2199.217	High	High	High	High	High	High	High	High
3002.599	High	High	High	High	High	High	High	High
2815.446	High	High	High	High	High	High	High	High
2586.283	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2511.397	High	High	High	High	High	High	High	High
2204.312	Not Found	High	Not Found	High	High	High	High	High
1917.085	Not Found	High	High	High	High	High	High	High
1473.826	High	High	High	High	High	High	High	High
2071.159	High	High	High	High	High	High	High	High
1784.974	High	Not Found	High	High	Not Found	High	High	High
1111.585	High	High	High	Not Found	Not Found	Not Found	High	High
2646.41	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2377.329	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2405.267	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2561.368	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2592.419	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1866.039	High	High	High	High	High	High	High	High
2277.188	High	High	High	High	High	High	High	High
1462.789	High	High	High	High	High	High	High	High
2618.508	High	High	High	High	High	High	High	High
2024.013	High	High	High	High	High	High	High	High
2211.166	High	High	High	High	High	High	High	High

2405.271	Not Found	Not Found	High	Not Found	Not Found	High	High	High
2995.511	High	High	High	High	High	High	High	High
3407.847	Not Found	High	High	High	High	High	High	High
3065.423	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1996.179	High	High	High	High	High	Not Found	High	High
2183.332	Not Found	High	High	High	High	High	High	High
1618.787	High	High	High	High	High	High	High	High
1562.675	High	High	High	Not Found	High	Not Found	Not Found	High
2366.31	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1689.762	High	High	High	High	Not Found	High	Not Found	High
1474.72	High	High	High	High	High	High	High	High
2642.551	High	High	High	High	High	High	High	High
2474.461	High	High	High	High	High	High	High	High
1962.165	High	High	Not Found	High	High	High	High	High
2473.307	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1858.051	High	High	High	High	High	High	High	High
2308.197	High	High	Not Found	High	High	High	High	High
2495.349	High	Not Found	High	High	High	High	High	High
1874.174	High	High	High	High	High	High	High	High
1746.115	High	High	High	High	High	High	High	High
1945.211	High	High	High	High	High	High	High	High
1176.606	High	Not Found	Not Found	High	High	High	High	High
1533.963	High	Not Found	Not Found	High	High	High	High	High
2249.202	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
1688.086	High	High	High	High	High	High	High	High
1736.903	High	High	High	High	High	High	High	High
1549.75	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1605.862	High	High	High	High	High	High	High	High
1548.93	High	High	High	High	High	High	High	High
1619.967	High	High	High	High	High	High	High	High
1321.702	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1520.943	Not Found	Not Found	High	High	High	High	High	High
2170.246	Not Found	High	High	High	High	High	High	High
2806.585	High	High	High	High	High	High	High	High
2619.432	High	Not Found	High	High	High	High	High	High
3413.807	High	High	Not Found	High	Not Found	Not Found	High	Not Found
2061.123	High	Not Found	High	High	High	High	High	High
2301.308	Not Found	High	High	High	High	High	High	High
1831.007	High	Not Found	High	High	High	High	High	High
1719.084	High	High	Not Found	High	High	High	High	High
1925.981	High	High	High	High	High	High	Not Found	Not Found
1393.775	High	High	High	High	High	High	High	High
1802.952	High	High	High	High	High	High	High	High
1615.8	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2141.14	High	High	High	High	High	High	High	High
1686.828	High	High	High	High	High	High	High	High
1817.869	Not Found	High	High	High	High	High	High	High
2318.128	High	High	High	High	High	High	High	High
2334.123	High	High	High	High	High	High	High	High
2779.259	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1443.758	Not Found	High	High	High	High	High	High	High
1800.027	High	Not Found	High	High	High	High	High	High

904.4887	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1826.864	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1698.823	High	High	High	Not Found	Not Found	Not Found	High	High
2242.248	High	High	High	High	High	High	High	High
1533.859	High	High	High	High	High	High	High	High
1721.011	High	High	High	High	High	High	High	High
2940.332	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2333.211	High	Not Found	Not Found	High	Not Found	Not Found	High	Not Found
2431.375	Not Found	High	Not Found	High	High	High	High	High
1504.904	Not Found	High	Not Found	High	High	High	High	High
2592.045	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1719.89	High	High	High	High	High	High	High	High
3466.778	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2256.253	High	High	High	High	High	High	High	High
3530.922	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
1847.025	High	High	High	High	High	High	High	High
1981.83	High	High	High	High	High	High	High	High
1107.567	High	High	High	High	High	High	High	High
2282.028	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1475.864	High	High	High	High	High	High	High	High
1559.788	High	High	High	High	High	High	High	High
1996.012	High	High	High	High	High	High	High	High
2055.968	Not Found	High	High	High	Not Found	High	Not Found	Not Found
1665.949	High	High	High	High	High	High	High	High
1405.731	High	High	High	High	High	High	High	High
1620.848	High	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
2607.343	High	High	High	High	High	High	High	High
1784.97	High	High	High	High	High	High	High	High
3347.774	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1846.946	High	High	High	High	High	High	High	High
2400.263	High	High	High	High	High	High	High	High
2756.428	Not Found	Not Found	High	High	Not Found	High	High	High
2227.194	Not Found	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
2383.162	High	High	Not Found	High	High	High	High	High
2297.182	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
4279.296	High	High	High	Not Found	High	Not Found	High	Not Found
1822.99	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1731.005	High	High	High	High	High	High	High	High
3207.306	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2103.204	High	Not Found	High	High	High	High	High	High
1212.69	High	High	High	High	High	High	High	High
4345.202	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2774.13	High	High	High	High	High	High	High	High
2473.443	High	High	High	High	High	High	High	High
1511.813	High	High	High	High	High	High	High	High
1710.897	Not Found	High	High	High	High	High	High	High
1544.009	Not Found	Not Found	High	High	High	High	High	High
1192.656	High	Not Found	High	High	High	High	High	High
1528.958	High	High	High	High	High	High	High	High
1170.679	High	High	High	High	High	High	High	High
2350.265	High	High	High	High	High	High	High	High
2725.233	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found

2594.193	High	High	High	Not Found	Not Found	Not Found	Not Found	High
4088.062	High	High	Not Found	High	High	High	High	High
2697.427	High	Not Found	High	High	High	High	High	High
1278.693	High	High	High	High	High	High	High	High
1091.54	High	Not Found	High	High	High	High	High	High
2916.332	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1444.925	High	High	High	High	High	High	High	High
1339.669	High	High	High	High	High	High	High	High
1426.701	Not Found	High	High	High	High	High	High	High
1661.977	High	High	Not Found	High	High	High	High	High
1658.979	High	High	High	High	High	High	High	High
1209.69	High	High	High	High	High	High	High	High
2070.103	High	High	High	High	High	High	High	High
1843.028	High	High	High	High	High	High	High	High
1556.816	High	High	High	High	High	High	High	High
1543.968	High	High	High	High	High	High	High	High
1481.771	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1574.853	High	High	High	High	High	High	High	High
1027.503	High	High	High	Not Found	High	Not Found	Not Found	Not Found
2719.504	High	High	High	High	High	High	High	High
1551.724	High	High	High	High	High	High	High	High
2077.999	Not Found	High	High	High	Not Found	High	Not Found	Not Found
2579.32	High	High	High	Not Found	High	High	High	High
2129.022	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1468.796	High	High	High	High	High	High	High	High
1568.834	Not Found	High	Not Found	Not Found	High	High	Not Found	High
2331.287	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1677.917	Not Found	High	High	High	High	High	High	High
2519.367	Not Found	High	Not Found	High	High	High	High	High
2201.088	Not Found	High	Not Found	High	High	Not Found	High	High
2187.099	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1077.488	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1969.026	High	High	High	High	High	High	High	High
1781.874	High	High	High	Not Found	High	High	High	High
2139.132	High	High	High	High	High	High	High	High
2326.284	High	High	High	High	High	High	High	High
1895.062	High	High	High	High	High	High	High	High
1537.804	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
4379.425	High	Not Found	Not Found	High	High	High	High	High
2314.317	High	High	High	High	Not Found	High	High	High
1087.642	High	High	High	High	High	High	High	High
2125.208	High	High	High	High	High	High	High	High
2372.232	Not Found	High	Not Found	High	High	High	High	High
1985.125	High	High	High	High	High	High	High	High
1624.683	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2567.24	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1066.573	Not Found	Not Found	High	High	High	High	High	High
1178.551	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2871.508	High	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
3284.688	Not Found	High	Not Found	High	Not Found	High	High	Not Found
2187.055	High	High	High	Not Found	High	High	Not Found	High
3778.891	High	High	High	Not Found	High	High	Not Found	High

3681.838	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2428.198	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2357.16	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
2499.235	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1799.079	Not Found	Not Found	High	High	High	High	High	High
3292.699	High	High	High	High	High	High	High	Not Found
3481.873	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2205.299	High	Not Found	Not Found	High	High	High	High	High
1110.525	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2330.365	Not Found	Not Found	High	High	High	High	High	High
1656.821	High	High	Not Found	High	High	High	High	High
1354.716	High	High	Not Found	High	High	High	High	High
1139.626	High	High	High	High	High	High	High	High
2397.187	High	High	Not Found	High	High	High	High	High
2234.124	High	Not Found	Not Found	Not Found	High	Not Found	High	High
1780.1	High	High	High	High	High	High	High	High
1583.87	High	Not Found	High	High	High	High	High	High
2022.15	Not Found	High	Not Found	High	High	High	High	High
1916.003	High	High	High	Not Found	Not Found	High	Not Found	High
1670.902	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
2255.226	High	High	Not Found	High	High	High	High	High
1811.997	Not Found	Not Found	High	High	High	High	High	Not Found
1743.949	High	High	High	High	Not Found	High	High	High
1987.071	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2179.259	High	High	High	High	High	High	High	High
1364.747	High	High	High	High	High	High	High	High
1807.926	High	High	Not Found	High	High	High	High	High
1878.963	High	High	High	High	High	High	High	High
1247.632	High	High	High	High	High	High	High	High
1847.912	Not Found	High	High	High	High	High	High	High
2035.064	Not Found	High	Not Found	High	High	High	High	High
1691.811	High	High	High	High	High	High	High	High
3687.975	High	High	High	High	High	High	High	High
2280.147	High	High	High	Not Found	High	Not Found	Not Found	Not Found
2589.194	Not Found	High	Not Found	Not Found	Not Found	High	High	Not Found
1664.896	High	High	High	Not Found	Not Found	High	Not Found	High
2403.272	High	High	High	High	High	High	High	High
2996.595	High	High	High	High	High	High	High	High
1390.721	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1568.825	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2146.966	High	High	High	Not Found	High	High	High	High
1934.07	High	High	High	High	High	High	High	High
1242.737	Not Found	High	High	High	High	High	High	High
1639.933	High	Not Found	Not Found	High	High	High	High	High
4167.87	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2003.008	High	High	High	High	High	High	High	High
2163.072	High	High	High	High	High	High	High	High
2204.193	High	High	High	High	High	High	High	High
2391.346	High	High	High	High	High	High	High	High
1343.712	Not Found	High	High	High	High	High	High	High
2220.188	High	Not Found	High	High	High	High	High	High
1156.559	High	High	High	High	Not Found	Not Found	Not Found	High

1373.852	High	Not Found	High	High	High	High	High	High
2739.421	High	High	High	High	High	High	High	High
1306.695	High	High	High	High	High	High	High	High
1394.673	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1581.826	High	High	High	High	High	High	High	High
3408.629	High	High	High	High	High	High	High	High
2535.332	Not Found	Not Found	High	High	High	High	High	High
2500.324	High	Not Found	Not Found	High	High	Not Found	High	High
1349.611	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1679.973	High	High	High	High	High	High	High	High
1289.742	High	High	High	High	High	High	High	High
2247.162	High	High	High	High	High	High	High	High
2139.052	High	High	High	High	High	High	High	High
2155.047	Not Found	Not Found	High	High	High	High	High	High
1606.795	High	High	High	High	High	Not Found	High	High
2984.583	High	High	High	High	High	High	High	High
886.4629	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
1919.87	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2072.123	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1358.888	High	High	High	High	High	High	High	High
2930.594	Not Found	High	Not Found	High	High	High	High	High
2317.284	High	High	High	High	High	High	High	High
2716.496	High	High	High	High	High	High	High	High
1685.995	High	Not Found	High	High	High	High	High	High
2255.192	High	High	High	High	High	High	High	High
1142.637	Not Found	High	High	High	High	High	High	High
2347.302	High	High	Not Found	High	High	High	High	High
1313.867	High	High	High	High	High	High	High	High
956.5047	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3088.686	High	Not Found	High	High	High	High	High	High
2934.603	High	High	High	High	High	High	High	High
2064.024	High	High	High	High	High	High	High	High
1876.872	High	High	High	High	High	High	High	High
1263.582	High	High	High	High	High	High	High	High
3134.712	High	High	Not Found	High	High	High	High	High
2926.477	High	High	Not Found	High	Not Found	Not Found	High	Not Found
2798.418	High	High	High	High	High	High	High	High
2654.365	High	High	High	High	High	High	High	High
1658.777	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1845.929	High	High	High	High	High	High	High	High
2680.446	High	High	High	High	High	High	High	High
2403.247	High	High	High	Not Found	Not Found	High	Not Found	High
2216.094	High	High	High	High	High	High	High	Not Found
1813.013	High	High	High	High	High	High	High	High
2036.097	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1356.78	High	High	High	High	High	High	High	High
1944.095	Not Found	High	High	High	High	High	High	High
2377.331	Not Found	High	Not Found	High	High	High	High	High
1684.954	Not Found	High	Not Found	Not Found	Not Found	High	High	Not Found
3226.729	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
2817.286	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2933.402	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found

1603.994	High	High	High	High	High	High	High	High
2386.273	High	High	High	High	High	High	High	High
1267.607	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1289.608	High	High	High	High	High	High	High	Not Found
1269.809	High	High	High	High	High	High	High	High
1671.966	High	High	Not Found	High	High	High	High	High
2010.149	Not Found	High	Not Found	Not Found	Not Found	High	Not Found	Not Found
1305.722	High	High	High	High	High	High	High	High
1605.839	High	High	High	High	High	High	High	High
1754.959	High	High	High	High	High	High	High	High
1567.807	High	High	High	High	High	High	High	High
1874.981	High	High	High	High	High	High	High	High
3841.095	High	Not Found	High	Not Found	High	High	High	Not Found
1471.863	High	High	Not Found	High	High	High	High	High
1345.638	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1629.907	High	High	High	High	High	High	High	High
1263.726	High	High	High	High	High	High	High	High
2503.376	High	High	High	Not Found	Not Found	High	Not Found	High
3357.811	High	Not Found	High	High	High	High	High	High
3170.659	High	High	High	High	High	High	High	High
3226.771	High	High	Not Found	High	High	High	High	High
2926.534	High	High	High	High	High	High	High	High
3186.654	High	Not Found	High	High	High	High	High	High
2075.112	High	High	High	High	High	High	High	High
2013.128	High	High	High	High	High	High	High	High
1931.074	High	High	High	High	High	High	High	High
1095.547	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1090.52	High	High	High	Not Found	Not Found	Not Found	High	High
1587.768	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
2292.167	High	High	Not Found	Not Found	High	Not Found	High	Not Found
2578.331	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2607.329	High	High	High	Not Found	High	High	High	High
2266.09	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1637.985	High	Not Found	High	High	High	High	High	High
3414.805	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2612.272	High	High	High	High	High	High	High	High
1971.071	High	High	High	High	Not Found	High	High	High
1783.918	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1366.8	High	Not Found	High	High	Not Found	High	High	High
1596.891	High	Not Found	Not Found	Not Found	Not Found	High	High	Not Found
1442.731	High	High	High	Not Found	Not Found	High	Not Found	Not Found
1298.727	High	High	High	High	High	High	High	High
2692.608	High	High	High	High	High	High	High	High
1927.019	High	High	High	High	High	High	High	High
2451.465	High	High	High	High	High	High	High	High
1313.749	High	High	High	High	High	High	High	High
1242.712	Not Found	High	High	High	High	High	High	High
2095.126	Not Found	High	Not Found	High	High	High	High	High
2264.313	Not Found	Not Found	High	High	High	High	High	High
1331.732	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2951.729	Not Found	Not Found	High	High	High	Not Found	High	High
2572.165	High	High	High	High	High	High	High	High

1515.678	High	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1102.642	High	High	High	High	High	High	High	High
3487.944	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2922.573	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
2326.278	High	High	Not Found	High	High	High	High	High
2512.378	High	High	High	High	High	High	High	High
2127.182	Not Found	High	High	High	High	High	High	High
2255.241	Not Found	High	Not Found	High	High	High	High	High
1188.679	High	High	High	High	High	High	High	High
3038.591	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
4383.222	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3988.915	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2990.629	High	High	High	High	Not Found	High	High	High
1338.53	High	High	High	High	High	High	High	High
1433.639	High	Not Found	High	Not Found	Not Found	Not Found	High	High
1929.96	High	High	High	High	High	High	High	High
2462.47	Not Found	High	High	High	High	High	High	High
1254.632	High	Not Found	Not Found	High	High	High	High	High
1639.705	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1476.912	High	High	High	High	High	High	High	High
1218.615	High	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
3898.991	Not Found	High	High	High	High	High	High	High
1768.043	Not Found	Not Found	High	High	High	High	High	High
1291.537	High	High	Not Found	High	Not Found	High	High	High
1676.026	High	High	Not Found	High	High	High	High	High
4386.293	High	High	Not Found	High	Not Found	Not Found	High	High
1303.631	High	High	Not Found	High	High	High	High	High
2494.26	High	High	High	High	High	High	High	High
1428.806	Not Found	Not Found	High	High	High	High	High	High
2795.407	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
4179.192	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1060.509	High	Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found
4062.2	Not Found	Not Found	High	High	High	High	High	High
3007.61	High	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
1374.654	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2643.31	High	High	High	High	High	High	High	High
2441.266	High	High	Not Found	High	High	Not Found	High	High
1221.593	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1607.838	High	High	High	High	High	High	High	High
1593.834	High	High	High	High	High	High	High	High
1992.01	High	High	High	High	High	High	High	High
1604.778	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2935.575	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
1947.086	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2753.44	High	High	High	Not Found	High	High	High	Not Found
2566.288	High	High	High	High	High	High	High	High
1821.945	High	High	High	High	High	High	High	High
2136.104	High	High	Not Found	High	High	High	High	High
2641.321	High	High	High	High	High	High	High	High
2454.168	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1317.685	High	High	High	High	High	High	High	High
2492.419	Not Found	High	High	High	High	High	High	High

1315.79	High	Not Found	Not Found	High	High	High	High	High
1767.015	High	High	High	High	High	High	High	High
1954.167	High	High	High	High	High	High	High	High
1427.844	High	High	High	High	High	High	High	High
2890.655	High	High	High	High	High	High	High	High
2819.618	High	Not Found	High	High	High	High	High	High
2392.307	High	High	High	High	High	High	High	High
1906.007	High	High	High	Not Found	Not Found	High	Not Found	Not Found
4111.24	High	Not Found	High	High	High	High	High	High
1451.78	High	High	High	High	High	High	High	High
2848.702	High	Not Found	Not Found	High	High	High	High	High
2353.364	High	High	High	High	High	High	High	High
3550.869	Not Found	High	High	High	High	High	High	High
2851.513	Not Found	High	High	High	High	High	High	High
2664.36	High	High	High	High	High	High	High	High
1475.833	High	High	High	High	High	High	High	High
2036.079	High	High	High	High	High	High	High	High
1763.967	High	High	High	High	High	High	High	High
1346.816	High	High	High	High	High	High	High	High
2664.34	High	High	High	High	High	High	High	High
1761.002	High	High	High	High	High	High	High	High
3957.152	High	High	High	High	High	High	High	High
1916.96	High	High	Not Found	High	High	High	High	High
1215.68	High	High	High	High	High	High	High	High
1719.898	High	High	High	High	High	High	High	High
1735.893	High	High	High	High	High	High	High	High
2453.397	High	High	High	High	High	High	High	High
1215.637	High	High	High	High	High	High	High	High
2595.58	Not Found	Not Found	High	High	High	High	High	High
3224.902	High	High	High	Not Found	High	Not Found	Not Found	High
1234.573	High	High	High	Not Found	High	High	High	High
1701.936	High	High	High	High	High	High	High	High
1308.715	High	High	Not Found	High	High	High	High	High
1712.762	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1867.073	High	High	Not Found	High	High	High	High	High
1752.074	Not Found	High	High	High	High	High	High	High
2986.572	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1287.693	High	High	High	High	High	High	High	High
1836.918	High	High	High	High	Not Found	High	Not Found	Not Found
3522.772	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1389.606	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3399.691	High	High	High	Not Found	Not Found	Not Found	High	Not Found
3665.993	High	Not Found	High	High	High	High	High	High
3181.66	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1105.512	High	High	High	High	High	High	High	High
2472.238	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1440.781	High	High	Not Found	High	High	High	High	High
2258.295	High	High	High	High	High	High	High	High
2445.447	High	High	High	High	High	High	High	High
1635.93	High	Not Found	High	High	High	High	High	High
1563.754	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2730.371	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found

1159.627	High	High	High	High	High	High	High	High
1132.512	High	High	Not Found	High	High	High	High	High
3597.736	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1077.499	High	High	High	High	High	Not Found	Not Found	Not Found
3136.433	High	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
1262.605	High	High	High	High	Not Found	High	High	Not Found
3002.303	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1367.727	High	High	High	High	High	High	High	High
1468.775	High	High	High	High	High	High	High	High
1888.98	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1128.564	High	High	High	High	High	High	High	High
2833.521	Not Found	High	High	High	High	High	High	High
1878.06	Not Found	High	High	High	High	High	High	High
2093.15	High	High	High	High	High	High	High	High
3076.643	High	High	Not Found	High	High	High	Not Found	High
1192.656	High	Not Found	High	High	High	High	High	High
2639.57	Not Found	High	Not Found	High	High	High	High	High
1621.951	High	High	High	High	High	High	High	High
1440.768	High	High	High	High	High	High	High	High
1799.115	High	High	High	High	High	High	High	High
2169.321	High	High	Not Found	High	High	High	High	High
2398.427	High	Not Found	Not Found	High	High	High	High	High
1421.835	High	High	High	High	High	High	High	High
1837.042	High	High	High	High	High	High	High	High
1213.641	High	High	High	High	High	High	High	High
1419.796	High	High	High	High	High	High	High	High
1728.078	High	Not Found	Not Found	High	High	High	High	High
1735.947	High	High	High	High	High	High	High	High
1982.023	High	High	High	High	High	High	High	High
1894.991	Not Found	Not Found	High	High	High	High	High	High
2639.42	High	Not Found	Not Found	High	High	High	High	High
4655.052	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1139.673	High	High	Not Found	High	High	High	High	High
2250.941	High	High	High	High	High	High	High	High
2121.899	High	High	High	High	High	High	High	High
2707.175	High	High	High	High	High	High	High	High
2579.116	High	High	High	High	High	High	High	High
1722.744	Not Found	High	High	High	High	High	High	High
1869.813	High	High	High	High	High	High	High	High
1984.84	High	High	High	High	High	High	High	High
2421.047	High	High	High	High	High	High	High	High
1631.9	High	High	High	High	High	High	High	High
2508.079	High	High	High	Not Found	High	High	High	High
1874.002	High	High	High	High	High	High	High	High
1759.959	High	Not Found	Not Found	High	High	High	High	High
1346.606	Not Found	Not Found	High	High	High	High	High	High
4277.223	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
4206.186	High	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
4107.117	Not Found	Not Found	High	Not Found	Not Found	High	Not Found	Not Found
1881.925	High	High	High	High	High	High	High	High
1432.775	High	High	High	High	High	High	High	High
2016.082	High	High	High	High	High	High	High	High

1828.93	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1334.601	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1313.619	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1708.871	High	High	High	High	High	High	High	High
2364.213	High	High	High	High	High	High	High	High
1345.685	Not Found	High	Not Found	High	High	High	High	High
2249.374	High	Not Found	Not Found	High	High	High	High	High
1762.99	High	High	High	High	High	High	High	High
2828.291	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1172.72	High	High	High	High	High	High	High	High
1116.608	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1573.911	High	High	High	High	High	High	High	High
2117.119	High	High	High	High	High	High	High	High
3295.757	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
1956.091	High	High	High	High	High	High	High	High
1687.835	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1562.859	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2178.145	High	High	Not Found	High	High	High	High	High
2655.202	High	High	Not Found	High	High	High	High	High
1298.677	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1301.799	High	High	High	High	High	High	High	High
1027.615	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1114.647	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1221.659	High	High	High	High	Not Found	High	Not Found	High
1047.595	High	High	High	High	High	High	High	High
1163.572	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1301.732	High	Not Found	Not Found	High	High	High	High	High
2153.192	High	High	High	High	Not Found	High	High	High
2781.603	High	High	High	Not Found	High	High	High	High
2594.45	High	High	High	High	High	High	High	High
3453.722	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2136.19	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2541.487	High	High	Not Found	High	High	High	High	High
2612.524	High	High	Not Found	High	High	High	High	High
1999.063	Not Found	Not Found	High	Not Found	High	Not Found	High	Not Found
2335.246	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
1283.638	High	High	High	High	High	High	High	High
1804.994	High	High	High	High	High	High	High	High
2909.451	High	High	High	Not Found	Not Found	Not Found	High	High
3227.746	High	High	High	High	High	High	High	High
3383.848	Not Found	High	Not Found	Not Found	High	Not Found	High	High
2651.399	High	High	Not Found	High	High	High	High	High
2296.084	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1173.592	High	High	High	High	High	High	High	High
1496.867	High	High	High	High	High	High	High	High
1996.198	Not Found	Not Found	High	High	High	High	High	High
1030.609	High	High	Not Found	High	High	High	High	High
974.5054	High	High	High	Not Found	Not Found	High	High	High
2848.506	High	High	High	High	High	High	High	High
1786.968	High	High	High	High	High	High	High	High
1974.121	High	High	High	High	High	High	High	High
3151.498	High	High	High	High	High	High	High	High

3167.493	High	High	High	Not Found	High	High	Not Found	Not Found
1796.184	High	High	High	High	High	High	High	High
2306.266	High	High	High	High	High	High	High	High
1642.818	High	High	High	High	High	High	High	High
1842.934	Not Found	High	High	High	High	High	High	High
3171.586	Not Found	High	Not Found	Not Found	High	High	High	High
4159.19	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1698.891	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2545.294	High	High	High	High	High	High	High	High
3020.5	High	High	High	High	High	High	High	High
2746.307	High	High	High	High	High	High	High	High
2961.398	High	High	High	High	High	High	High	High
2357.215	High	High	High	High	High	High	High	High
1692.804	Not Found	High	High	High	High	High	High	High
1727.816	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3332.679	Not Found	High	High	High	High	High	High	High
3348.66	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1550.73	Not Found	Not Found	High	High	High	High	High	High
2561.289	High	High	Not Found	High	High	High	High	High
1212.539	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1185.561	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2724.439	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1718.944	Not Found	High	High	High	High	High	High	High
2996.617	High	High	High	High	High	High	High	High
2585.128	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1748.047	High	High	Not Found	High	High	High	High	High
1803.965	High	High	High	High	High	High	High	High
1229.648	Not Found	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
1557.768	High	High	High	High	High	High	High	High
1370.616	High	High	High	High	High	High	High	High
1817.996	High	High	High	High	High	High	High	High
1689.026	High	High	High	High	High	High	High	High
1958.05	High	High	High	High	High	High	High	High
1359.649	High	High	High	High	High	High	High	High
2021.158	Not Found	High	High	High	High	High	High	High
3159.574	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1495.847	High	High	High	High	High	High	High	High
2771.518	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2557.331	High	High	High	High	High	High	High	High
2370.178	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1134.647	High	High	High	High	High	High	High	High
1848.948	Not Found	High	High	High	High	High	High	High
2495.154	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2126.142	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
2197.179	High	High	High	High	High	High	High	High
1642.898	High	High	Not Found	High	High	High	High	High
2757.201	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1540.852	High	Not Found	High	High	High	High	High	High
1218.671	Not Found	High	High	High	High	High	High	High
2469.233	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1600.735	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1522.879	Not Found	High	High	High	High	High	High	High

1385.67	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1325.571	High	High	High	Not Found	Not Found	High	High	High
1263.618	High	High	Not Found	Not Found	High	High	High	High
1450.77	Not Found	High	High	High	High	High	High	High
2447.324	High	High	High	High	High	High	High	High
2113.14	High	High	High	High	High	High	High	High
3026.584	High	High	Not Found	High	High	High	High	High
2690.471	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2503.319	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1587.776	High	High	High	High	High	Not Found	High	High
1731.941	High	High	High	High	High	High	High	High
1644.858	Not Found	High	High	High	High	High	High	High
2509.333	High	High	High	High	High	High	High	High
3054.524	High	High	Not Found	High	High	High	High	High
2998.412	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2867.372	Not Found	High	High	High	Not Found	Not Found	Not Found	High
2815.283	High	High	High	High	High	High	High	High
2025.905	High	High	High	High	High	High	High	High
2163.358	High	High	High	High	High	High	High	High
2168.004	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1453.727	High	Not Found	High	High	High	High	High	High
1158.599	High	High	High	High	High	High	High	High
1687.828	Not Found	High	High	High	High	High	High	High
1484.77	High	High	High	High	High	High	High	High
3793.848	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1936.028	High	High	Not Found	High	High	High	High	High
2008.018	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2864.423	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1331.755	High	High	High	High	High	High	High	High
2003.092	Not Found	Not Found	High	High	High	High	High	High
1946.98	High	High	High	High	High	High	High	High
1711.863	High	High	High	High	High	High	High	High
1070.652	High	High	High	High	High	High	High	High
2674.326	High	High	High	High	High	High	High	High
2304.126	High	High	High	High	High	High	High	High
2192.975	High	High	High	Not Found	Not Found	High	High	Not Found
1987.263	Not Found	Not Found	High	High	High	High	High	High
1736.907	High	High	High	High	High	High	High	High
1635.966	Not Found	Not Found	High	High	High	High	High	High
2206.978	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2144.028	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1955.948	High	High	High	High	High	High	High	High
2042.98	High	High	High	High	High	High	High	High
1868.916	High	High	High	Not Found	High	Not Found	High	High
4989.373	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1730.841	High	High	Not Found	Not Found	Not Found	Not Found	High	High
1154.562	High	High	High	High	High	High	High	High
1734.898	High	High	High	High	High	High	High	High
1791.01	High	High	High	High	High	High	High	High
1603.858	High	High	High	High	High	High	High	High
1904.044	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1243.642	High	High	High	High	High	High	High	High

1314.679	High	High	High	High	High	High	High	High
1127.527	High	High	Not Found	Not Found	High	High	High	High
1047.496	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1838.022	High	High	High	High	High	High	High	High
1744.063	High	High	High	High	High	High	High	High
1556.911	High	High	High	High	High	High	High	High
2252.251	High	High	High	High	High	High	High	High
2165.219	Not Found	Not Found	High	High	High	High	High	High
1298.695	High	High	High	High	Not Found	Not Found	Not Found	Not Found
3361.776	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1721.853	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
4713.424	High	High	High	High	High	High	High	High
3130.633	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
4249.008	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3119.489	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1782.007	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
1609.611	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2101.078	Not Found	Not Found	High	High	High	High	High	High
1813.93	High	High	High	High	High	High	High	High
1805.898	High	Not Found	High	Not Found	Not Found	High	High	High
3188.678	High	High	High	High	High	High	High	High
1112.637	High	Not Found	High	High	High	High	High	High
2580.197	High	High	High	High	Not Found	High	High	Not Found
1936.024	High	High	High	High	High	High	High	High
1851.976	High	High	High	High	High	High	High	High
2131.109	Not Found	Not Found	High	Not Found	High	Not Found	High	High
1529.8	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
4190.066	High	High	High	High	High	High	High	High
1177.621	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2280.249	Not Found	High	Not Found	High	High	High	High	High
2981.368	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1689.021	High	High	High	High	High	High	High	High
2220.343	High	High	High	High	High	High	High	High
2133.311	High	High	High	High	High	High	High	High
2022.053	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2041.031	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2924.511	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
986.44	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1665.754	High	High	High	Not Found	High	Not Found	High	Not Found
2695.405	High	High	High	High	High	High	High	High
2270.141	Not Found	High	High	High	High	High	High	High
1750.038	High	Not Found	High	High	High	High	High	High
3224.618	Not Found	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
3152.663	High	Not Found	Not Found	High	High	High	High	High
2841.605	High	High	High	High	High	High	High	High
2754.573	High	High	High	High	High	High	High	High
2928.637	Not Found	High	High	High	High	High	High	High
2317.344	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2404.376	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2503.351	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1939.987	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1060.631	High	High	Not Found	High	High	High	High	High

1476.711	High	High	High	High	High	High	High	High
2407.147	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1346.679	Not Found	High	High	High	High	High	High	High
1288.602	High	High	High	High	High	High	High	High
1118.532	High	High	High	High	Not Found	High	High	High
1936.979	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
1538.812	High	High	High	High	High	High	High	High
1309.65	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1309.65	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
3415.82	Not Found	High	Not Found	High	High	High	High	High
2002.107	High	High	High	High	High	High	High	High
1974.133	High	High	High	High	High	High	High	High
2338.341	Not Found	High	Not Found	High	High	High	High	High
2877.659	High	High	High	High	High	High	High	High
2115.015	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1818.012	Not Found	Not Found	High	High	High	High	High	High
2052.113	High	High	Not Found	High	High	High	High	High
1644.943	High	Not Found	High	High	High	High	High	High
1786.022	High	High	Not Found	High	High	High	High	High
1813.022	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
1419.863	High	High	High	High	High	High	High	High
2690.404	High	Not Found	High	Not Found	Not Found	Not Found	High	High
1607.016	Not Found	High	High	High	High	High	High	High
1648.97	Not Found	Not Found	High	Not Found	High	High	High	High
1330.857	High	High	High	High	High	High	High	High
1675.009	Not Found	High	Not Found	High	High	High	High	High
1713.049	High	High	High	High	High	High	High	High
1887.182	Not Found	High	High	High	High	High	High	High
1182.679	High	High	Not Found	High	Not Found	High	High	High
1295.763	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
2942.72	High	Not Found	Not Found	High	High	High	High	High
2900.394	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1762.965	High	High	High	High	High	High	High	High
2113.172	High	High	High	High	High	High	High	High
2184.209	High	High	High	High	High	High	High	High
1665.912	High	High	High	High	High	High	High	High
2124.254	High	High	High	High	High	High	High	High
2271.239	High	High	High	High	High	High	High	High
1243.721	High	High	High	High	High	High	High	High
2243.258	High	High	High	High	High	High	High	High
3198.612	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2449.46	Not Found	High	Not Found	High	High	High	High	High
2264.38	High	High	Not Found	Not Found	High	High	Not Found	Not Found
2552.509	High	High	Not Found	High	High	High	High	High
1434.908	High	High	High	High	High	High	High	High
3322.529	High	High	Not Found	High	High	High	Not Found	Not Found
1938.886	High	High	High	Not Found	Not Found	High	Not Found	Not Found
1758.011	High	High	High	High	High	High	High	High
1546.972	Not Found	Not Found	High	High	High	High	High	High
1276.736	High	High	High	High	High	High	High	High
2009.029	High	High	High	High	High	High	High	High
1845.914	High	High	High	Not Found	High	High	Not Found	High

1728.017	High	High	High	High	High	High	High	High
2398.133	High	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
1583.963	Not Found	Not Found	High	High	High	High	High	High
2464.386	Not Found	Not Found	High	High	High	High	High	High
1871.867	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1743.987	Not Found	High	Not Found	High	High	High	High	High
1551.789	High	High	High	High	High	High	High	High
2066.076	High	High	High	High	High	High	High	High
1001.508	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1873.945	High	High	High	High	High	High	High	High
1802.908	High	High	High	High	High	High	High	High
1703.851	High	High	High	High	High	High	High	High
2425.425	High	High	High	High	High	High	High	High
2095.02	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3748.713	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2412.127	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1674.803	High	High	High	High	High	High	High	High
2469.148	High	High	High	Not Found	Not Found	Not Found	High	High
1796.825	Not Found	High	High	High	High	High	High	High
2606.627	High	High	High	High	High	High	High	High
1800.038	High	High	High	High	High	High	High	High
2034.986	High	High	High	High	High	High	High	High
3671.061	High	High	High	High	High	High	High	High
1468.74	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2407.117	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2103.139	Not Found	Not Found	High	High	High	High	High	High
1627.875	Not Found	Not Found	High	High	High	High	High	High
2274.188	High	High	High	High	High	High	High	High
1832.945	Not Found	High	High	High	High	High	High	High
1329.744	High	Not Found	Not Found	High	High	High	High	High
1524.789	High	High	High	High	High	High	High	High
3268.675	High	High	High	High	High	High	High	High
2939.391	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1540.792	High	High	High	High	High	High	High	High
1999.05	High	High	High	High	High	High	High	High
1492.792	Not Found	High	High	High	High	High	High	High
1265.639	High	Not Found	High	Not Found	Not Found	High	High	High
2316.317	High	High	Not Found	High	High	High	High	High
1313.561	High	High	High	High	High	High	High	High
3821.06	Not Found	High	Not Found	Not Found	High	Not Found	High	Not Found
1489.832	High	High	High	High	High	High	High	High
1462.728	High	High	High	High	High	High	High	High
1156.505	High	High	High	High	Not Found	High	High	High
1115.637	High	High	High	High	High	High	High	High
1595.859	High	High	High	High	High	High	High	High
2340.261	High	High	High	High	High	High	High	High
1822.047	High	High	Not Found	High	High	High	High	High
1423.858	Not Found	High	Not Found	High	High	High	High	High
1509.704	High	High	Not Found	Not Found	Not Found	High	High	High
2996.444	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2054.053	High	High	High	High	High	High	High	High
1315.846	High	High	High	High	High	High	High	High

1574.754	High	High	Not Found	High	High	High	High	High
1518.642	High	High	High	Not Found	High	High	High	High
1387.601	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1119.603	Not Found	High	High	High	High	High	High	High
1630.937	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
1241.656	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2587.504	High	Not Found	High	High	High	High	High	High
2285.192	High	High	Not Found	High	High	High	High	High
1969.164	High	High	High	High	High	High	High	High
1630.933	High	High	High	High	High	High	High	High
1331.748	Not Found	Not Found	High	High	High	High	High	High
1739.892	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1850.013	Not Found	High	High	High	High	High	High	High
2286.177	High	High	Not Found	High	High	High	High	High
1239.694	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1551.719	High	High	High	Not Found	Not Found	High	High	High
1985.996	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
3063.545	High	High	High	Not Found	High	High	High	High
2876.392	High	High	High	High	Not Found	Not Found	High	High
1282.634	High	High	High	High	High	High	High	High
1663.835	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2333.17	Not Found	High	High	High	Not Found	High	High	High
2349.165	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1298.629	High	High	High	Not Found	Not Found	High	High	Not Found
2037.07	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1444.925	High	High	High	High	High	High	High	High
1388.813	High	Not Found	High	High	High	High	High	High
1257.773	Not Found	Not Found	High	High	High	High	High	High
2806.448	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1931.133	High	High	High	High	High	High	High	High
1743.98	High	High	High	High	High	High	High	High
3010.475	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1877.942	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1325.701	Not Found	Not Found	High	High	High	High	High	High
2939.438	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2316.167	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
4207.088	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3471.641	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2444.362	High	Not Found	High	High	High	High	High	High
2658.458	Not Found	High	High	High	High	High	High	High
2112.229	Not Found	High	High	High	High	High	High	High
2256.282	Not Found	Not Found	High	High	High	High	High	High
3909.007	High	High	High	Not Found	High	High	High	High
1675.938	High	High	High	High	High	High	High	High
1366.789	Not Found	High	High	High	High	High	High	High
1039.488	High	High	High	High	Not Found	Not Found	Not Found	High
2812.336	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2040.29	High	Not Found	High	High	High	High	High	High
1890.099	High	High	High	High	High	High	High	High
1361.657	High	High	High	High	High	High	High	High
2160.102	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
1573.931	High	High	High	High	High	High	High	High

1434.609	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1621.762	High	High	High	High	High	High	High	High
1855.862	High	High	Not Found	Not Found	High	Not Found	High	High
3693.652	High	High	High	Not Found	Not Found	High	Not Found	Not Found
3880.805	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
4519.228	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1445.92	High	High	High	High	High	High	High	High
1116.636	Not Found	High	High	High	High	High	High	High
4402.196	High	High	High	High	High	High	High	High
1179.583	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1032.551	High	High	High	High	High	High	High	High
2353.129	High	High	High	High	High	High	High	High
4116.672	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1858.06	Not Found	High	High	High	Not Found	High	High	High
1670.91	High	High	High	High	High	High	High	High
1872.915	High	High	High	Not Found	High	High	High	High
2776.277	High	High	High	High	High	High	High	High
2510.233	High	High	High	Not Found	High	Not Found	High	High
2904.481	High	High	High	High	High	High	High	High
1590.778	High	High	High	High	High	High	High	High
2430.318	Not Found	High	High	High	High	High	High	High
2659.48	High	High	High	High	High	High	High	High
2545.438	Not Found	Not Found	High	High	High	High	High	High
2431.395	High	Not Found	High	High	High	High	High	High
2259.346	Not Found	High	High	High	High	High	High	High
2172.314	High	Not Found	High	High	High	High	High	High
2085.282	High	High	High	High	High	High	High	High
3927.936	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1415.763	Not Found	High	High	High	High	High	High	High
3638.808	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1828.904	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1757.032	High	High	High	High	High	High	High	High
3288.799	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1493.679	High	High	Not Found	Not Found	Not Found	High	Not Found	Not Found
1483.77	High	High	High	High	High	High	High	High
1385.688	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1826.072	High	High	High	High	High	High	High	High
1582.939	High	High	High	High	High	High	High	High
2318.111	High	High	High	Not Found	High	High	High	High
1730.803	High	High	High	Not Found	High	High	High	High
2044.926	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1329.758	Not Found	High	High	High	High	High	High	High
1051.595	Not Found	High	High	High	High	High	High	High
2092.977	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1391.68	High	High	High	High	High	High	Not Found	Not Found
2482.408	High	High	High	High	High	High	High	High
1284.716	High	High	High	High	High	High	High	High
1398.772	High	High	High	High	High	High	High	High
2512.163	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2936.432	High	High	High	High	Not Found	High	High	High
3376.67	High	High	High	Not Found	High	High	High	High
2089.135	High	Not Found	High	Not Found	Not Found	High	High	High

1786.902	High	High	High	High	High	High	High	High
1529.905	High	High	High	High	High	High	High	High
1971.034	High	High	High	High	High	High	High	High
1730.914	High	High	High	High	High	High	High	High
2158.187	High	High	Not Found	High	High	High	High	High
2102.075	Not Found	High	Not Found	High	Not Found	High	Not Found	High
1343.841	High	Not Found	High	High	High	High	High	High
2502.289	High	High	High	High	High	High	High	High
2298.175	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1962.024	Not Found	Not Found	High	High	High	High	High	High
3976.955	High	High	High	Not Found	High	High	High	High
1299.665	High	High	Not Found	Not Found	Not Found	High	High	High
2799.233	Not Found	Not Found	High	High	High	High	High	High
1736.938	High	High	High	Not Found	High	High	High	High
1389.691	High	High	High	High	High	High	High	High
1224.653	High	High	Not Found	High	High	High	High	High
1710.988	High	High	High	High	High	High	High	High
1523.835	High	High	High	High	High	High	High	High
1687.812	High	High	High	High	High	High	High	High
3322.689	High	Not Found	Not Found	High	High	High	High	High
2678.467	Not Found	Not Found	High	High	High	High	High	High
2493.339	Not Found	High	Not Found	High	High	Not Found	High	High
2090.187	Not Found	Not Found	High	High	High	High	High	High
2019.15	Not Found	High	High	High	High	High	High	High
1996.086	Not Found	Not Found	High	High	High	High	High	High
2488.308	High	High	High	High	High	High	High	High
4149.974	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2141.301	Not Found	Not Found	High	High	High	High	High	High
1827.142	High	High	High	High	High	High	High	High
1743.959	High	High	High	High	High	High	High	High
1370.579	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1827.965	High	High	High	High	High	High	High	High
1911.938	High	High	High	High	High	High	High	High
2346.43	High	High	High	High	High	High	High	High
1776.086	High	Not Found	High	High	High	High	High	High
2159.277	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2276.179	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1264.757	Not Found	High	Not Found	High	High	High	High	High
1309.725	High	High	High	High	High	High	High	High
3677.779	High	High	High	Not Found	High	High	Not Found	Not Found
3403.977	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2152.12	High	High	High	Not Found	Not Found	High	High	High
2252.183	High	High	High	High	High	High	High	High
2509.321	High	High	Not Found	High	High	High	High	High
1630.943	High	Not Found	High	High	High	High	High	High
2489.295	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2508.235	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3334.687	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3872.936	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2360.144	High	High	Not Found	High	High	High	High	High
1961.964	High	High	High	High	High	High	High	High
1945.969	High	High	High	High	High	High	High	High

2376.139	Not Found	Not Found	High	High	High	Not Found	High	High
1364.575	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1712.917	High	High	Not Found	High	High	High	High	High
2670.466	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1685	High	Not Found	Not Found	High	High	High	High	Not Found
1520.632	High	High	High	Not Found	Not Found	High	High	Not Found
1101.605	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1714.924	Not Found	High	High	High	High	High	High	High
1024.478	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1873.073	High	High	High	High	High	High	High	High
1379.662	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
4933.595	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1225.747	High	High	Not Found	High	High	High	High	High
2972.573	High	High	Not Found	High	High	High	High	High
2785.421	High	High	High	High	High	High	High	High
2435.386	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
2208.104	High	High	Not Found	High	High	High	High	High
1706.791	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1846.997	High	High	High	High	High	High	High	High
1691.918	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
1581.771	Not Found	High	Not Found	High	High	High	High	High
1952.918	High	High	High	High	High	High	High	High
3914.878	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2246.037	High	High	High	High	Not Found	High	High	High
2629.369	High	High	Not Found	High	High	High	Not Found	High
2870.525	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1153.787	High	High	High	High	High	High	High	High
1284.827	High	High	High	High	High	High	High	High
1097.675	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2258.266	High	High	High	High	High	High	High	High
2358.261	High	High	High	High	High	High	High	High
1930.091	High	High	High	High	High	High	High	High
2001.128	High	High	Not Found	High	High	High	High	High
1859.054	High	Not Found	High	High	High	High	High	High
1633.787	High	High	High	High	High	High	High	High
1260.57	High	High	High	Not Found	Not Found	High	Not Found	High
1195.594	High	High	High	High	High	High	High	High
1365.699	High	High	High	High	High	High	High	High
1008.441	High	High	High	High	High	High	High	High
976.5625	High	High	High	High	High	High	High	High
1024.436	High	High	High	Not Found	High	High	High	High
3580.726	Not Found	High	Not Found	High	High	High	High	Not Found
3093.543	High	High	High	High	High	High	High	High
1797.84	High	High	High	High	Not Found	High	Not Found	High
1570.781	Not Found	High	High	High	Not Found	High	High	High
1310.646	High	High	Not Found	High	High	High	High	High
2281.194	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1218.56	High	High	High	High	High	High	High	High
2374.354	High	Not Found	Not Found	High	High	High	High	High
2583.352	Not Found	High	High	High	Not Found	Not Found	Not Found	Not Found
1597.789	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3611.815	High	Not Found	Not Found	Not Found	Not Found	High	High	Not Found

2366.396	High	High	Not Found	High	High	High	High	High
1701.865	High	High	High	Not Found	High	Not Found	High	Not Found
1412.723	High	High	High	High	High	High	High	High
1169.59	High	High	High	High	High	High	High	High
1727.887	High	Not Found	Not Found	Not Found	High	High	Not Found	High
1457.775	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1685.853	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1157.606	High	High	High	High	High	High	High	High
1575.833	High	High	High	High	High	High	High	High
1692.959	Not Found	High	High	High	High	High	High	High
1392.791	Not Found	High	High	High	High	High	High	High
2283.044	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1251.615	Not Found	Not Found	High	High	Not Found	Not Found	High	High
1782.018	High	High	High	High	High	High	High	High
2432.903	Not Found	High	High	Not Found	Not Found	High	Not Found	Not Found
1244.716	High	High	High	High	High	High	High	High
1852.012	High	Not Found	High	High	High	High	High	High
2226.109	High	Not Found	High	Not Found	Not Found	High	High	High
2024.05	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1819.942	High	High	High	High	High	High	High	High
1861.846	High	High	Not Found	High	High	High	High	High
4666.548	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1879.919	High	High	High	High	High	High	High	High
2144.269	High	High	High	High	High	High	High	High
3212.799	High	High	High	High	High	High	High	High
1204.673	High	High	High	High	High	High	High	High
3235.781	Not Found	Not Found	High	High	High	High	High	High
1366.837	High	High	High	High	High	High	High	High
3216.528	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2364.059	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1285.768	High	High	High	High	High	High	High	High
1759.99	High	Not Found	High	Not Found	High	High	Not Found	Not Found
1095.518	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3290.815	High	High	High	High	High	High	High	High
3464.879	High	High	High	High	High	High	High	High
3377.847	Not Found	Not Found	High	High	High	High	High	High
2289.191	High	High	High	High	High	High	High	High
2530.334	High	High	High	High	High	High	High	High
1873.964	High	High	High	High	High	High	High	High
2218.154	Not Found	High	High	High	High	High	High	High
2102.039	High	High	High	High	High	High	High	High
2346.212	High	High	High	High	High	High	High	High
3511.684	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2294.127	High	High	High	High	High	High	High	High
1196.67	High	High	High	High	High	High	High	High
1009.517	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2603.306	Not Found	Not Found	High	High	High	High	High	High
2433.201	Not Found	Not Found	High	High	Not Found	High	Not Found	High
4045.996	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
1636.709	High	High	High	High	High	High	High	High
3215.704	High	High	High	Not Found	High	Not Found	High	High
2836.478	High	High	Not Found	High	High	Not Found	High	High

2617.393	Not Found	High	High	Not Found	High	High	Not Found	High
2428.395	Not Found	High	High	High	High	High	High	High
1529.978	High	Not Found	High	High	High	High	High	High
2344.079	High	Not Found	High	Not Found	Not Found	High	High	High
2596.348	Not Found	High	Not Found	High	High	High	High	High
1602.826	High	High	High	High	High	Not Found	Not Found	High
2529.312	High	High	High	High	High	High	High	High
2203.106	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1831.007	High	High	High	Not Found	Not Found	High	Not Found	High
2554.287	High	High	High	High	Not Found	High	High	High
961.5628	High	High	High	High	High	High	High	High
1764.038	High	High	Not Found	High	High	High	High	High
1752.763	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3006.464	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2043.06	Not Found	High	High	High	Not Found	Not Found	Not Found	High
3193.617	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1548.833	High	High	High	High	High	High	High	High
3326.823	High	High	High	High	High	High	High	High
2258.249	High	High	High	High	High	High	High	High
1732.869	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1013.545	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1735.847	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2889.576	High	Not Found	Not Found	High	High	High	High	High
1404.748	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
4113.185	High	High	High	High	High	High	High	High
2299.292	High	Not Found	Not Found	High	High	High	High	High
2370.329	High	High	High	High	High	High	High	High
2441.367	High	High	High	High	High	High	High	High
1957.102	High	High	High	High	High	High	High	High
1786.038	High	High	High	High	High	High	High	High
2028.139	High	High	High	High	High	High	High	High
2099.176	High	High	High	High	High	High	High	High
2198.245	Not Found	Not Found	High	High	High	High	High	High
1451.822	High	Not Found	High	High	High	High	High	High
2375.245	Not Found	High	High	High	High	High	High	High
1728.952	High	Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found
1093.462	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1052.585	High	High	High	Not Found	High	High	High	High
2053.015	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2023.132	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1599.841	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1435.637	High	High	High	High	High	High	High	High
1905.081	High	High	High	High	High	High	High	High
2037.048	High	High	High	High	High	High	High	High
1848.969	High	High	High	High	High	High	High	High
2412.248	High	High	Not Found	High	High	High	High	High
3167.783	High	High	High	Not Found	High	High	Not Found	Not Found
1330.857	High	High	High	High	High	High	High	High
1203.708	High	High	Not Found	High	High	High	High	High
2560.33	High	High	High	High	High	High	High	High
2301.213	High	High	High	High	High	High	High	High
1471.759	Not Found	High	High	High	High	High	High	High

1678.983	High	High	High	High	High	High	High	High
1810.023	Not Found	High	High	High	High	High	High	High
1754.119	High	High	High	High	High	Not Found	High	High
1915.153	High	High	High	High	High	High	High	High
1691.891	High	High	Not Found	High	High	High	High	High
2144.025	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1844.945	Not Found	Not Found	High	High	High	High	High	High
1560.833	High	High	High	High	High	High	High	High
1489.796	High	High	High	High	High	High	High	High
1789.939	High	High	High	High	High	High	High	High
2273.391	High	High	High	High	High	High	High	High
2578.285	High	Not Found	Not Found	High	Not Found	Not Found	Not Found	High
3424.765	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
2350.199	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1631.87	Not Found	Not Found	High	Not Found	High	High	High	High
1757.032	High	High	High	High	High	High	High	High
1942.112	High	High	High	High	High	High	High	High
1828.069	High	High	High	High	High	High	High	High
1815.882	High	High	Not Found	High	High	High	High	High
1925.913	High	Not Found	High	Not Found	High	High	High	Not Found
3965.949	Not Found	High	High	Not Found	High	High	High	High
1165.632	High	High	High	Not Found	Not Found	High	Not Found	High
1352.785	High	High	High	High	High	High	High	High
4034.114	Not Found	High	High	Not Found	High	High	High	Not Found
1921.082	High	High	High	Not Found	High	High	High	High
1419.743	High	High	High	High	High	High	High	High
1490.78	High	High	High	High	High	High	High	High
1348.706	Not Found	High	High	High	High	High	High	High
2131.989	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2149.08	High	High	High	High	Not Found	High	High	High
2185.181	High	Not Found	High	Not Found	High	High	Not Found	Not Found
1894.942	High	High	High	High	High	High	High	High
2582.417	High	High	High	High	High	High	High	High
2241.194	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	High
2752.522	High	Not Found	High	High	High	High	High	High
2653.454	High	Not Found	High	High	Not Found	High	High	High
1225.637	High	High	High	High	High	High	High	High
1427.789	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1501.858	High	High	High	High	High	High	High	High
1614.942	High	High	High	High	High	High	High	High
3513.689	High	High	High	Not Found	High	High	Not Found	High
3700.841	High	High	Not Found	High	High	High	High	High
1458.743	High	High	High	Not Found	High	High	High	High
2731.438	High	High	High	High	High	High	High	High
1507.972	High	High	High	High	High	High	High	High
1581.847	High	High	High	High	High	High	High	High
2741.401	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2558.366	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1452.885	High	High	High	High	High	High	High	High
1653.001	High	High	High	High	High	High	High	High
2646.301	Not Found	High	High	High	Not Found	Not Found	Not Found	Not Found
1015.484	High	High	High	High	High	High	High	High

1413.711	High	High	High	High	High	High	High	High
1189.681	High	High	High	High	High	High	High	High
2056.931	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2004.058	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2191.211	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2132.068	High	High	High	High	High	High	High	High
1944.915	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1571.805	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
2485.184	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2967.474	High	High	High	Not Found	High	High	Not Found	High
1554.642	High	High	High	High	High	High	High	High
1596.866	High	Not Found	Not Found	Not Found	High	Not Found	High	High
1382.863	High	High	High	High	High	High	High	High
1251.639	High	High	High	High	High	High	High	High
1634.763	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1817.158	High	High	High	High	High	High	High	High
2170.138	Not Found	High	High	Not Found	High	High	High	High
2080.998	High	High	High	High	High	High	High	High
1896.877	High	High	High	High	High	High	High	High
2084.03	High	High	High	High	High	High	High	High
2268.151	High	High	High	High	High	High	High	High
1889.012	High	High	Not Found	Not Found	High	High	High	High
1652.965	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
981.5112	High	High	High	High	High	High	High	High
3951.906	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	High
2657.589	High	High	High	High	High	High	High	High
1340.748	High	High	High	High	High	High	High	High
1492.803	High	Not Found	Not Found	High	High	High	High	High
2088.238	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3941.011	High	High	High	High	High	High	High	High
2075.097	High	High	Not Found	High	High	High	High	High
1601.798	High	High	High	High	High	High	High	High
2663.28	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1872.965	High	High	High	Not Found	High	Not Found	Not Found	High
1411.738	Not Found	Not Found	High	Not Found	High	High	High	High
1317.758	High	High	High	High	High	High	High	High
3385.678	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1392.732	High	High	High	High	High	High	High	High
1292.612	High	High	Not Found	High	High	High	High	High
2922.636	High	Not Found	High	High	Not Found	High	High	High
2319.232	High	High	High	High	High	High	High	High
1791.94	High	High	High	High	High	High	High	High
1979.092	High	High	High	High	High	High	High	High
3162.824	Not Found	Not Found	High	High	High	Not Found	Not Found	Not Found
2921.682	Not Found	High	Not Found	High	Not Found	High	High	High
1893.038	High	High	High	High	High	High	High	High
1639.884	High	High	High	High	High	High	High	High
1864.017	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1771.902	High	Not Found	High	High	High	High	High	High
1313.742	High	High	High	Not Found	Not Found	High	Not Found	Not Found
1084.636	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1087.667	High	High	High	High	High	High	High	High

1622.885	High	High	High	High	High	High	High	High
1800.99	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1231.63	High	High	High	High	High	High	High	High
2132.047	Not Found	High	High	High	High	High	High	High
2319.199	High	High	High	High	High	High	High	High
1972.98	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2040.981	High	High	High	Not Found	High	High	High	High
2720.268	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
1333.654	High	High	High	High	Not Found	High	High	High
2170.054	High	High	High	Not Found	Not Found	Not Found	High	Not Found
3104.631	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2317.296	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1334.639	High	High	High	High	High	High	High	High
1300.668	High	High	High	Not Found	Not Found	High	High	Not Found
1922.091	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2953.654	High	High	Not Found	Not Found	Not Found	High	Not Found	Not Found
2283.253	High	Not Found	Not Found	High	High	High	High	High
3661.864	High	Not Found	High	Not Found	High	High	High	Not Found
3590.827	High	High	High	High	High	High	High	High
3493.775	High	High	High	High	High	High	Not Found	High
1200.583	High	High	Not Found	High	High	High	High	High
1412.788	High	High	High	High	High	High	High	High
1467.711	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
3028.522	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1301.726	High	Not Found	High	High	High	High	High	High
1114.574	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2493.383	High	High	High	High	High	High	High	High
2607.311	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1681.907	High	High	High	High	High	High	High	High
3505.697	High	High	High	High	High	High	High	High
2885.359	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2958.666	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1776.151	High	Not Found	High	High	High	High	High	High
1742.021	High	High	High	High	High	High	High	High
1434.643	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2174.218	High	High	High	High	High	High	High	High
2478.448	High	Not Found	High	High	High	High	High	High
2183.055	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2518.419	High	High	High	High	High	High	High	High
2154.968	High	High	Not Found	High	High	High	High	High
1118.595	Not Found	Not Found	High	High	High	High	High	High
3224.852	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1085.626	High	High	High	High	High	High	High	High
1622.915	High	High	High	High	High	High	High	High
1584.036	High	High	High	High	High	High	High	High
2191.198	High	High	Not Found	High	High	High	High	High
1645.84	High	High	High	High	High	High	High	High
2750.477	Not Found	High	High	High	High	High	High	High
1645.858	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2489.355	High	High	High	High	High	High	High	High
1269.69	High	High	High	High	High	High	High	High
3327.767	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found

1416.739	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1455.769	High	High	High	High	High	High	High	High
1150.653	High	High	High	High	High	High	High	High
1778.927	High	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1506.889	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2825.196	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
4116.666	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1222.625	High	High	High	High	High	High	High	High
1893.039	High	High	High	High	High	High	High	High
2120.166	Not Found	Not Found	High	High	Not Found	High	High	Not Found
2094.216	High	Not Found	Not Found	High	High	High	High	High
1336.79	High	High	High	High	High	High	High	High
2134.15	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
997.4408	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1259.679	High	High	High	High	High	High	High	High
2999.519	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1192.689	High	Not Found	High	High	High	High	High	High
1499.72	High	High	High	Not Found	High	Not Found	High	High
1932.941	High	High	High	Not Found	High	High	High	Not Found
1388.715	High	High	High	High	High	High	High	High
2003.229	High	High	High	High	High	High	High	High
2316.989	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1073.559	Not Found	High	High	High	High	High	High	High
2938.326	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1633.902	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1263.773	High	High	High	High	High	High	High	High
1433.879	High	High	High	High	High	High	High	High
1176.741	High	High	High	High	High	High	High	High
2864.41	High	High	High	High	High	High	High	High
2951.442	Not Found	High	High	Not Found	Not Found	Not Found	High	High
1262.669	High	High	High	High	High	High	High	High
3109.511	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1102.564	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2475.324	Not Found	High	Not Found	High	High	High	High	High
1867.085	High	High	High	High	High	High	High	High
1731.954	Not Found	High	High	High	High	High	High	High
1360.733	High	High	Not Found	Not Found	High	High	High	Not Found
1839.065	High	High	High	High	High	High	High	High
1228.653	High	High	High	High	High	High	High	High
2574.384	High	Not Found	High	High	High	High	High	High
2761.536	Not Found	Not Found	High	Not Found	Not Found	High	Not Found	High
1406.658	High	High	High	High	Not Found	Not Found	Not Found	Not Found
1048.436	High	High	High	High	High	High	High	High
1064.431	High	Not Found	High	High	High	High	High	High
2028.992	Not Found	High	High	High	High	High	High	High
2242.151	High	High	High	High	High	High	High	Not Found
1953.028	High	Not Found	High	High	High	High	High	High
2175.18	High	Not Found	Not Found	High	High	High	High	High
1102.556	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1487.858	Not Found	Not Found	High	High	High	High	High	High
1813.008	High	High	High	High	High	High	High	High
1973.061	High	High	High	High	High	High	High	High

1580.857	High	High	High	High	High	High	High	High
1671.892	High	High	High	High	High	High	High	High
1353.759	Not Found	Not Found	High	High	High	High	High	High
1282.722	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1540.896	High	Not Found	Not Found	High	High	High	High	High
1626.967	High	High	High	High	High	High	High	High
1439.814	High	High	High	High	High	High	High	High
2418.366	Not Found	High	High	High	High	High	High	High
2059.254	High	High	High	High	High	High	High	High
2213.146	Not Found	Not Found	High	Not Found	Not Found	High	High	High
1098.61	High	High	High	High	High	High	High	High
2938.427	High	High	High	High	High	High	High	High
1762.929	High	High	High	High	High	High	High	High
2081.121	Not Found	High	High	High	High	High	High	High
2301.177	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1866.913	High	High	High	Not Found	Not Found	High	High	High
3637.812	High	High	Not Found	Not Found	Not Found	High	High	Not Found
3932.034	High	High	High	High	High	High	High	High
1876.987	High	High	Not Found	High	High	High	High	High
1484.895	Not Found	High	Not Found	High	High	High	High	High
1988.853	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
3210.629	High	High	High	High	High	High	High	High
1630.764	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2479.341	High	High	High	High	High	High	High	High
1303.667	High	High	High	High	Not Found	Not Found	High	High
1828.991	Not Found	Not Found	High	High	High	Not Found	High	High
1773.004	High	High	High	High	High	High	High	High
1613.042	Not Found	High	High	High	High	High	High	High
2948.503	High	High	High	High	High	High	High	High
1990.097	High	High	High	High	High	High	High	High
2658.389	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
2403.367	High	High	Not Found	High	High	High	High	High
1128.637	High	High	High	High	High	Not Found	Not Found	Not Found
1894.896	High	High	High	High	High	High	High	High
1550.706	High	High	High	High	Not Found	High	High	Not Found
2374.218	High	High	Not Found	High	Not Found	Not Found	High	High
2627.173	High	High	High	Not Found	Not Found	Not Found	Not Found	High
2245.152	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
1774.94	High	Not Found	High	High	High	High	High	High
1352.748	High	High	High	High	High	High	High	High
1931.03	High	High	High	High	High	High	High	High
1567.839	High	High	High	High	High	High	High	High
1279.615	High	High	High	High	High	High	High	High
2174.115	High	High	High	High	High	High	High	High
1703.903	High	High	High	High	High	High	High	High
1150.572	High	High	High	High	High	High	High	High
1196.647	High	High	High	High	High	High	High	High
1297.695	High	High	High	High	High	High	High	High
1237.721	Not Found	High	High	High	High	High	High	High
1095.6	High	High	High	High	High	High	High	High
1226.705	High	High	High	High	High	High	High	High
1048.672	High	High	High	High	High	High	High	High

2712.341	High	High	High	High	High	High	High	High
1585.813	High	Not Found	Not Found	Not Found	High	Not Found	High	High
3413.836	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2857.484	High	Not Found	High	High	High	High	High	High
1304.701	Not Found	High	Not Found	High	High	High	High	High
1645.798	High	High	High	High	High	High	High	High
2028.142	High	High	High	High	High	High	High	High
1116.657	Not Found	High	High	High	High	High	High	High
1394.868	High	High	High	High	High	High	High	High
1569.935	High	High	High	Not Found	Not Found	Not Found	Not Found	High
3777.066	High	High	High	High	High	High	High	High
2156.246	High	High	High	High	High	High	High	High
2314.315	High	High	High	High	High	High	High	High
1328.792	High	High	High	High	High	High	High	High
1399.829	High	High	Not Found	High	High	High	High	High
1257.755	High	High	Not Found	High	High	High	High	High
1281.784	High	High	High	High	High	High	High	High
2442.254	High	High	High	High	High	High	High	High
2912.596	High	Not Found	High	High	Not Found	High	High	High
2255.101	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1755.948	High	High	High	High	High	High	High	High
2288.175	High	High	High	High	High	High	High	High
1169.684	High	High	High	High	High	High	High	High
1317.789	High	High	High	High	High	High	High	High
2646.311	High	High	High	Not Found	High	Not Found	Not Found	Not Found
3146.657	High	High	High	Not Found	High	Not Found	High	High
3645.823	High	High	High	Not Found	High	High	High	High
3180.626	High	High	High	High	High	Not Found	Not Found	High
1304.707	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2846.427	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1532.818	High	High	High	Not Found	High	High	Not Found	Not Found
1407.779	High	High	High	Not Found	High	High	Not Found	High
2889.36	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1519.789	High	High	High	High	High	High	High	High
1535.784	High	High	High	High	High	High	High	High
1335.758	High	High	High	High	High	High	High	High
1148.606	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1875.109	High	High	High	High	High	High	High	High
1702.763	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2083.077	High	High	High	High	High	High	High	High
2270.229	High	Not Found	Not Found	High	High	High	High	High
3943.999	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2719.419	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1164.485	High	High	High	High	High	High	High	High
1773.865	High	High	High	High	High	High	High	High
1961.017	High	High	High	High	High	High	High	High
2318.156	High	High	High	High	Not Found	Not Found	High	High
4050.852	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1575.719	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1374.717	High	High	High	High	High	High	High	High
1497.686	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1684.838	High	High	High	High	High	High	High	High

1613.801	High	High	Not Found	High	High	High	High	High
4717.538	High	Not Found	Not Found	High	High	High	High	High
4646.501	Not Found	High	High	High	High	High	High	Not Found
3255.846	High	Not Found	Not Found	High	High	High	High	High
2900.66	High	Not Found	Not Found	High	High	High	High	High
2175.254	High	High	High	High	High	High	High	High
2368.989	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2384.984	High	High	High	Not Found	High	Not Found	Not Found	Not Found
1647.847	High	High	High	High	High	High	High	High
1750.874	High	High	High	High	High	High	High	High
1734.879	High	High	High	High	High	High	High	High
1563.722	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1547.727	High	High	High	High	High	High	High	High
2520.425	High	High	High	Not Found	Not Found	Not Found	High	High
2348.34	High	High	High	High	High	High	Not Found	High
2619.398	High	High	High	Not Found	High	Not Found	High	High
2475.291	High	High	High	High	High	High	High	High
2088.129	Not Found	High	Not Found	High	Not Found	Not Found	Not Found	High
3730.835	Not Found	Not Found	High	Not Found	Not Found	High	High	High
1663.842	High	High	High	Not Found	High	High	High	High
1035.545	High	High	High	High	High	High	High	High
1443.758	Not Found	High	Not Found	High	High	High	High	High
2373.261	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
3028.236	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2467.202	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3516.878	High	High	High	High	High	High	High	High
2574.363	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1826.07	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1457.816	High	Not Found	Not Found	High	High	High	High	High
882.4104	High	High	High	High	Not Found	High	High	High
2780.369	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1663.933	High	High	High	High	High	High	High	High
1300.631	High	High	High	High	High	High	High	High
2127.13	High	High	High	High	High	High	High	High
1942.042	High	High	High	High	High	High	Not Found	High
2293.166	High	High	High	Not Found	Not Found	High	High	High
1233.664	High	High	High	High	High	High	High	High
2711.32	High	High	High	Not Found	High	High	Not Found	High
1227.689	High	Not Found	Not Found	High	High	High	High	High
1348.673	Not Found	Not Found	High	High	High	High	High	High
1266.649	High	Not Found	Not Found	High	High	High	High	High
1611.661	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3481.746	High	High	High	High	High	High	High	High
1335.636	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2352.34	Not Found	Not Found	High	Not Found	Not Found	High	High	Not Found
1260.69	High	Not Found	Not Found	High	High	High	High	High
2561.254	High	High	High	Not Found	Not Found	Not Found	High	Not Found
1973.05	High	High	High	High	High	Not Found	High	High
2030.072	High	High	High	Not Found	Not Found	High	High	High
3387.932	Not Found	High	High	High	High	High	High	High
1176.684	High	High	High	High	High	High	High	High
2417.286	Not Found	High	Not Found	High	High	Not Found	High	Not Found

3202.852	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	High
1935.878	High	High	High	High	High	High	High	High
2063.937	High	High	High	High	High	High	High	High
1770.006	High	High	High	High	High	High	High	High
4372.124	High	High	High	High	High	High	High	High
3222.625	Not Found	Not Found	High	Not Found	High	High	High	High
2335.065	High	High	Not Found	High	High	High	High	High
3500.852	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
4582.227	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2736.394	High	High	High	High	High	High	High	High
2448.194	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2549.241	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3717.998	High	High	High	High	High	High	High	High
1420.805	High	High	High	High	High	High	High	High
1449.689	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
890.4764	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1743.004	High	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
1726.899	Not Found	High	Not Found	High	High	High	High	High
1893.899	High	High	High	High	High	High	High	High
1706.746	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2939.595	Not Found	High	Not Found	Not Found	High	Not Found	High	High
2967.455	High	High	High	High	High	High	High	High
2910.433	High	High	High	High	High	High	High	High
3197.545	High	High	High	High	High	High	High	High
3154.607	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	Not Found
2753.452	High	Not Found	Not Found	High	High	High	High	High
2625.391	High	High	High	High	Not Found	High	Not Found	High
1947.98	Not Found	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
2132.101	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2588.286	High	High	High	High	Not Found	High	High	High
1722.011	High	High	High	High	High	High	High	High
2022.023	High	High	High	High	High	High	High	High
1496.712	High	High	High	High	High	High	High	High
2412.272	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2359.115	High	High	High	High	High	High	High	High
2032.028	High	High	High	High	High	High	High	High
2190.097	Not Found	High	Not Found	High	High	High	High	High
1310.706	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1497.859	High	High	High	High	Not Found	Not Found	Not Found	High
1635.909	High	High	High	High	High	High	High	High
1983.159	High	High	High	High	High	High	High	High
1684.98	High	High	High	High	High	High	High	High
1816.02	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2912.501	High	High	Not Found	Not Found	Not Found	High	High	High
3744.909	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
3345.697	High	High	High	High	Not Found	High	High	Not Found
3602.835	High	High	High	High	High	High	High	High
3673.872	High	Not Found	Not Found	Not Found	Not Found	High	Not Found	High
1732.975	High	High	High	High	High	High	High	High
1659.925	Not Found	Not Found	High	High	High	High	High	High
2008.952	High	High	High	Not Found	High	Not Found	Not Found	High
1826.883	High	High	High	High	Not Found	Not Found	High	High

1458.693	High	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1726.929	High	High	Not Found	High	Not Found	Not Found	Not Found	High
1667.928	High	High	High	High	High	High	High	High
1467.812	High	High	High	High	High	High	High	High
1926.897	High	High	High	High	High	High	High	High
1724.879	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2122.19	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1785.168	High	High	High	High	High	High	High	High
1271.809	High	High	High	High	High	High	High	High
1714.131	High	High	High	High	High	High	High	High
3723.024	Not Found	High	High	High	High	High	High	High
3535.872	High	High	High	High	High	High	High	High
3551.867	Not Found	High	High	Not Found	Not Found	Not Found	High	Not Found
1327.688	High	Not Found	Not Found	High	High	High	High	High
1409.815	High	High	High	High	High	High	High	High
1456.62	High	High	High	High	Not Found	Not Found	High	High
1132.58	High	High	High	High	High	High	High	High
1291.664	High	Not Found	High	Not Found	High	High	High	High
1918.971	High	High	High	High	High	High	High	High
2215.17	High	High	High	High	High	High	High	High
1821.975	High	High	Not Found	High	High	High	High	High
2830.337	High	High	High	High	High	High	High	High
2846.332	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2751.294	High	High	High	High	High	High	High	High
1581.826	High	High	High	High	High	High	High	High
1409.681	High	High	High	High	High	High	High	High
1579.719	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2477.254	High	High	High	Not Found	Not Found	Not Found	Not Found	High
1798.041	High	High	High	High	High	High	High	High
1413.858	Not Found	High	High	High	High	High	High	High
1721.993	Not Found	High	High	High	High	High	High	High
2899.615	High	High	High	High	High	High	High	High
1631.897	Not Found	High	High	High	High	High	High	High
1196.638	High	High	High	High	High	High	High	High
2386.342	High	High	High	High	High	High	High	High
1796.812	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1707.839	High	High	High	High	High	High	High	High
1394.607	High	High	High	High	Not Found	High	High	High
2379.219	Not Found	High	High	High	High	High	High	High
2863.686	High	High	High	High	High	High	High	High
1766.935	Not Found	Not Found	High	High	Not Found	High	High	High
1817.865	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2882.443	Not Found	Not Found	High	Not Found	High	High	Not Found	Not Found
1895.977	High	Not Found	High	High	High	High	High	High
973.4585	High	High	High	High	High	High	High	High
1764.059	High	High	High	High	High	High	High	High
3967.065	High	High	High	High	High	Not Found	High	High
2306.031	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1259.648	High	High	High	High	High	High	High	High
2088.224	High	High	High	High	High	High	High	High
2855.717	High	Not Found	High	High	High	High	High	High
2668.565	High	High	High	High	High	High	High	High

2085.257	High	High	High	High	High	High	High	High
1168.705	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2167.006	High	Not Found	Not Found	High	High	Not Found	Not Found	Not Found
3440.75	High	High	High	Not Found	Not Found	High	Not Found	Not Found
2751.492	High	High	High	High	High	High	High	High
3355.719	High	High	High	Not Found	Not Found	Not Found	High	High
1700.011	High	High	High	High	High	High	High	High
1091.584	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1743.991	Not Found	High	High	High	High	High	High	High
1790.899	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2054.069	High	Not Found	High	High	High	High	High	High
1784.934	High	Not Found	Not Found	Not Found	High	High	Not Found	High
4988.415	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
4807.204	High	High	High	High	High	High	High	High
3047.352	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2288.183	High	High	High	High	High	High	High	High
2435.252	High	High	High	High	High	High	High	High
2468.13	High	High	Not Found	Not Found	Not Found	Not Found	High	High
1406.738	Not Found	High	Not Found	High	High	High	High	High
1958.034	High	Not Found	Not Found	High	High	High	High	High
1436.748	High	High	High	High	High	High	High	High
2128.2	High	High	High	High	Not Found	Not Found	High	Not Found
2925.732	High	High	High	High	High	High	High	High
2371.136	Not Found	High	High	High	Not Found	High	High	High
1686.977	High	High	High	High	High	High	High	High
1555.937	High	High	High	High	High	High	High	High
1091.605	High	Not Found	High	High	High	High	High	High
1739.949	High	Not Found	Not Found	High	Not Found	Not Found	High	High
1532.812	High	High	High	High	High	High	High	High
1345.659	High	High	High	High	High	High	High	High
1362.726	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2994.626	High	High	High	High	High	High	High	High
2737.489	High	Not Found	High	High	High	High	High	High
2650.456	High	High	High	High	High	High	High	High
3220.713	High	High	High	High	High	High	High	High
3990.063	Not Found	Not Found	High	High	High	High	High	High
2721.406	High	High	Not Found	High	High	High	High	High
2950.569	High	High	High	High	High	High	High	High
2785.691	Not Found	High	High	High	High	High	High	High
2766.485	High	Not Found	Not Found	High	High	High	High	High
2011.948	High	High	High	High	High	High	High	High
1791.863	High	High	High	High	High	High	High	High
2491.955	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3483.797	Not Found	High	Not Found	High	High	High	High	High
3802.91	Not Found	Not Found	High	High	Not Found	High	Not Found	Not Found
2937.605	High	Not Found	Not Found	Not Found	High	High	Not Found	High
1917.91	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3184.74	High	High	High	High	High	High	High	High
1243.612	High	High	High	High	High	High	High	High
1056.459	High	Not Found	High	High	High	High	High	High
2150.195	High	Not Found	High	High	High	High	High	High
1806.043	High	High	High	Not Found	High	High	High	High

1612.759	High	High	High	High	High	High	High	High
1628.754	Not Found	High	High	High	High	High	High	High
2808.555	High	High	High	Not Found	Not Found	High	Not Found	Not Found
1356.768	Not Found	Not Found	High	High	High	High	High	High
2930.79	High	Not Found	High	High	High	Not Found	Not Found	High
959.5343	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2044.069	High	High	High	High	High	Not Found	High	High
2198.087	High	High	High	High	Not Found	Not Found	Not Found	Not Found
2378.24	Not Found	High	High	Not Found	High	High	High	High
1833.925	High	High	High	High	High	High	High	High
1646.773	High	High	High	High	High	High	High	High
2671.31	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1146.694	High	High	Not Found	High	High	High	High	High
2068.17	High	High	High	High	High	High	High	High
1198.523	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1067.483	High	High	High	Not Found	Not Found	High	High	Not Found
3527.775	High	High	High	High	High	High	High	High
1408.811	High	High	High	Not Found	Not Found	High	Not Found	High
2072.046	Not Found	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
2144.131	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
3416.823	High	High	High	High	High	High	High	High
2483.287	High	High	High	High	High	High	High	High
1391.811	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
3290.612	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1714.896	High	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
1106.559	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2868.252	High	High	High	Not Found	Not Found	Not Found	High	Not Found
2567.223	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1776.85	High	High	High	High	High	High	High	High
1444.716	High	High	High	High	High	High	High	High
2583.218	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1792.845	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2623.168	High	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1271.695	High	High	High	High	High	High	High	High
1142.652	High	High	High	High	High	High	High	High
955.4996	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1756.971	High	Not Found	Not Found	High	High	High	High	High
1188.679	High	High	High	High	High	High	High	High
1965.935	High	High	High	High	High	High	High	High
2480.357	Not Found	Not Found	High	High	Not Found	High	High	High
1722.928	High	High	High	High	High	High	High	High
1255.721	High	High	High	High	High	High	High	High
3178.56	High	High	High	High	High	High	High	High
3194.555	High	High	High	Not Found	High	Not Found	Not Found	Not Found
3783.697	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1385.753	High	Not Found	Not Found	High	High	High	High	High
1332.747	High	Not Found	Not Found	High	High	High	High	High
3799.692	High	High	High	Not Found	High	Not Found	Not Found	Not Found
3249.597	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2689.472	High	High	High	High	High	High	High	High
2502.32	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1216.599	High	High	High	High	High	High	High	High

2107.186	High	High	High	Not Found	Not Found	Not Found	High	Not Found
4025.184	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1920.034	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3311.659	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
3124.507	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2882.38	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1774.892	High	High	High	High	High	High	High	High
1888.935	High	High	High	High	High	Not Found	High	High
2002.019	High	High	High	High	High	High	High	High
1532.897	High	High	High	High	High	High	High	High
3407.769	High	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1315.753	High	High	High	High	High	High	High	High
2355.287	High	High	Not Found	High	High	High	High	High
2486.328	Not Found	Not Found	High	High	High	High	High	High
1668.98	High	High	High	High	High	High	High	High
1567.932	High	High	High	High	High	High	High	High
1610.89	High	Not Found	High	High	High	High	High	High

Found in Sample: [S53] F6: 127C, Sample, ko, single	Found in Sample: [S55] F6: 128C, Sample, ko, single	Found in Sample: [S57] F6: 129C, Sample, ko, single	Found in Sample: [S59] F6: 130C, Sample, ko, single	Found in Sample: [S60] F6: 131, Sample, ko, pool	Found in Sample Group: wt, pool	Found in Sample Group: wt, single	Found in Sample Group: ko, single	Found in Sample Group: ko, pool
Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	Not Found
High	High	High	High	High	High	High	High	High
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Abundance Ratio: (ko, pool) / (wt, pool)	Abundance Ratio: (ko, single) / (wt, single)	Abundance Ratio (log2): (ko, pool) / (wt, pool)	Abundance Ratio (log2): (ko, single) / (wt,	Abundances (Grouped): wt, pool	Abundances (Grouped): wt, single	Abundances (Grouped): ko, single	Abundances (Grouped): ko, pool	Abundances (Grouped) Standard Error [%]: wt, pool
2.074	1.177	1.05	0.24	21.4	31.1	36.6	44.4	
2.014	1.609	1.01	0.69	72.2	83.2	133.9	145.4	
0.722	0.77	-0.47	-0.38	150.1	132.6	102	108.4	
100	1.618	6.64	0.69		2.2	3.5	4.2	
0.86	1.042	-0.22	0.06	113.9	99.6	103.8	98	
100	100	6.64	6.64			3.6	1.9	
2.82	2.483	1.5	1.31	47.9	58.3	144.8	135	
1.25	0.994	0.32	-0.01	45.6	50.2	49.9	57	
0.844	0.869	-0.24	-0.2	135.1	146.4	127.3	114.1	
0.999	1.192	0	0.25	141.9	125.8	150	141.8	
1.393	1.161	0.48	0.22	15.1	18.2	21.1	21	
1.138	1.497	0.19	0.58	35.5	34.6	51.8	40.4	
1.058	0.871	0.08	-0.2	1510.7	1681.6	1464.3	1598.7	
2.644	2.863	1.4	1.52	37.3	35.4	101.2	98.7	
1.113	0.859	0.15	-0.22	26	37.2	31.9	28.9	
0.573	0.853	-0.8	-0.23	22.7	25.1	21.4	13	
4.844	3.617	2.28	1.85	17.8	21	76	86.4	
2.068	1.92	1.05	0.94	28.4	36	69.1	58.7	
1.056	0.651	0.08	-0.62	26	36.2	23.6	27.4	
1.799	1.826	0.85	0.87	35	40.7	74.3	63	
1.163	1.05	0.22	0.07	128.6	127.9	134.3	149.6	
1.113	0.802	0.15	-0.32	82.1	98.7	79.2	91.4	
1.317	1.009	0.4	0.01	70.4	80.6	81.3	92.7	
1.217	1.252	0.28	0.32	79.6	74.8	93.6	96.9	
0.984	0.935	-0.02	-0.1	708.6	685.4	640.8	697.4	
0.961	0.879	-0.06	-0.19	532.2	531.5	467.4	511.3	
	1.096		0.13		1.6	1.8		
100	1.246	6.64	0.32		1.6	2	1.5	
1.083	1.09	0.12	0.12	106.3	100.5	109.6	115.1	

1.955	1.194	0.97	0.26	5.8	10.9	13	11.4
1.038	1.171	0.05	0.23	265.2	246.6	288.8	275.2
1.472	1.103	0.56	0.14	12.5	9.3	10.2	18.4
0.01	0.991	-6.64	-0.01	4.5	2.7	2.7	
0.861	0.937	-0.22	-0.09	102.2	90.7	85	88
1.102	1.197	0.14	0.26	28.7	26.4	31.6	31.6
0.761	0.803	-0.39	-0.32	96.4	91.9	73.8	73.3
0.598	0.523	-0.74	-0.93	408	411.7	215.5	243.8
0.83	0.718	-0.27	-0.48	183.8	208	149.4	152.6
0.657	0.605	-0.61	-0.72	127.8	131.2	79.4	83.9
2.401	2.635	1.26	1.4	97.5	90.4	238.4	234.1
4.814	2.224	2.27	1.15	10.1	18	40.1	48.4
1.803	2.234	0.85	1.16	14.4	12.4	27.7	26
2.601	1.855	1.38	0.89	7.5	8.3	15.4	19.4
1.782	1.775	0.83	0.83	198.9	193.5	343.6	354.3
2.127	1.975	1.09	0.98	37.5	39.1	77.2	79.7
100	100	6.64	6.64			3.4	2.5
2.331	2.297	1.22	1.2	68.1	67.7	155.5	158.8
2.647	1.441	1.4	0.53	4.1	5.4	7.8	10.7
1.158	1.291	0.21	0.37	15.1	16.6	21.4	17.5
	1.005		0.01		3.1	3.1	
0.814	0.852	-0.3	-0.23	201.5	215.3	183.5	164
0.745	0.825	-0.42	-0.28	1583.1	1508.1	1244.2	1180.2
0.633	0.637	-0.66	-0.65	311.3	307.5	196	197
0.926	0.846	-0.11	-0.24	99.3	101.6	85.9	91.9
1.593	1.35	0.67	0.43	42.5	50.2	67.8	67.7
1.343	1.303	0.43	0.38	70.4	70.2	91.5	94.5
1.895	1.141	0.92	0.19	2.1	2.9	3.3	4
1.584	1.636	0.66	0.71	2.6	2.4	4	4.1
1.259	1.43	0.33	0.52	5.4	9.5	13.5	6.7
1.612	3.493	0.69	1.8	6.2	4	14.1	9.9
1.3	1.226	0.38	0.29	34.9	41.9	51.3	45.3
1.208	1.167	0.27	0.22	221.6	205	239.2	267.7
1.068	1.204	0.09	0.27	38.9	33.6	40.4	41.6
1.127	1.476	0.17	0.56	58.1	44.3	65.3	65.4
1.153	1.286	0.21	0.36	289.1	257.1	330.7	333.4
3.52	2.579	1.82	1.37	2.4	2.2	5.8	8.6
100	1.353	6.64	0.44		3.5	4.7	2.2
1.181	1.333	0.24	0.41	115.2	106.9	142.4	136
1.698	1.799	0.76	0.85	176.2	172.9	310.9	299.2

1.887	1.45	0.92	0.54	26.9	33.1	48	50.8
0.795	1.338	-0.33	0.42	5	4.6	6.1	4
1.574	1.854	0.65	0.89	29.5	25.6	47.6	46.5
1.518	1.469	0.6	0.56	114	118.9	174.7	173.1
3.203	2.45	1.68	1.29	3.2	3	7.3	10.4
100	0.952	6.64	-0.07		1.8	1.7	1.6
3.586	1.557	1.84	0.64	10.4	16.9	26.3	37.2
1.209	1.283	0.27	0.36	18.3	20.3	26	22.2
4.019	4.089	2.01	2.03	44.1	46.2	189	177.3
3.154	3.829	1.66	1.94	41.9	32.6	124.9	132
1.393	1.62	0.48	0.7	260.4	227.1	367.9	362.6
1.469	1.256	0.56	0.33	26	25.6	32.2	38.1
3.614	2.244	1.85	1.17	2.4	3.4	7.5	8.8
0.01	1.091	-6.64	0.13	2.9	2.3	2.5	
	0.01		-6.64		1.5		
0.832	0.98	-0.26	-0.03	344.7	299.3	293.2	287
1.14	1.262	0.19	0.34	264.9	232.7	293.7	301.9
1.302	1.029	0.38	0.04	111.3	129.5	133.2	144.9
0.929	0.722	-0.11	-0.47	650.5	802.1	579.1	604.3
0.974	1.053	-0.04	0.07	14	14.9	15.7	13.6
1.457	1.323	0.54	0.4	32.4	34.7	45.9	47.3
1.113	1.184	0.15	0.24	207	188.3	222.8	230.3
1.325	1.328	0.41	0.41	34.6	40.4	53.7	45.8
1.291	1.19	0.37	0.25	6.8	7.8	9.3	8.8
2.387	1.353	1.26	0.44	7.5	10.2	13.8	17.8
0.827	0.757	-0.27	-0.4	140.6	127.6	96.6	116.2
3.866	1.634	1.95	0.71	10.9	23.5	38.3	42
0.962	0.997	-0.06	-0.01	146.6	138.6	138.1	141
1.184	1.482	0.24	0.57	7.1	4	5.9	8.5
1.106	1.673	0.15	0.74	12.5	8.4	14	13.8
	0.01		-6.64		2.2		
0.752	0.805	-0.41	-0.31	205.9	187.4	150.8	154.8
1.446	0.662	0.53	-0.59	11.8	15.7	10.4	17.1
0.89	0.812	-0.17	-0.3	362.6	385.4	313.1	322.8
2.178	1.894	1.12	0.92	32.6	34.7	65.8	71
1.447	1.27	0.53	0.34	37.5	44.3	56.2	54.2
	100		6.64			2	
0.77	0.727	-0.38	-0.46	10.4	11	8	8
0.44	0.628	-1.18	-0.67	5.2	8.8	5.6	2.3
0.722	0.552	-0.47	-0.86	355.4	342.8	189.2	256.5
0.689	0.784	-0.54	-0.35	351.2	354.8	278.2	241.9
0.711	0.734	-0.49	-0.45	185.7	182.1	133.6	132
0.412	0.556	-1.28	-0.85	18	16.7	9.3	7.4
0.544	0.621	-0.88	-0.69	64.1	64.6	40.1	34.8
0.734	0.72	-0.45	-0.47	288.4	309.9	223.1	211.8
1.53	0.981	0.61	-0.03	14.9	25.5	25	22.8

0.973	0.799	-0.04	-0.32	28.9	28.4	22.7	28.1
2.181	1.598	1.12	0.68	18.2	18.4	29.4	39.6
1.58	1.385	0.66	0.47	7.3	8.3	11.5	11.5
100	1.06	6.64	0.08		2.4	2.5	4.2
2.437	1.095	1.28	0.13	8.4	11.8	12.9	20.6
0.626	0.793	-0.68	-0.34	2.9	2.8	2.2	1.8
0.774	0.943	-0.37	-0.09	36	29.3	27.6	27.9
	1.044		0.06		2.4	2.5	
100	1.13	6.64	0.18		3.2	3.6	2.3
5.92	5.125	2.57	2.36	6.3	9.5	48.8	37.5
0.66	0.887	-0.6	-0.17	2.6	2.9	2.6	1.7
0.657	0.592	-0.61	-0.76	19.5	17.2	10.2	12.8
1.417	1.131	0.5	0.18	24.3	26	29.3	34.5
1.002	0.874	0	-0.19	47	44.7	39.1	47.2
2.659	0.747	1.41	-0.42	11.7	31	23.1	31.1
0.899	0.809	-0.15	-0.31	2.9	3.5	2.9	2.6
0.531	0.57	-0.91	-0.81	25.1	28	16	13.4
	100		6.64			2.4	
1.538	0.99	0.62	-0.01	4.4	7.2	7.1	6.7
1.058	1.346	0.08	0.43	106.3	93.4	125.7	112.4
0.977	1.161	-0.03	0.21	658.6	601.1	697.7	643.7
1.059	1.144	0.08	0.19	497.4	466	533.1	526.5
0.95	1.189	-0.07	0.25	255.3	220.2	261.9	242.7
0.704	0.515	-0.51	-0.96	5	8.1	4.2	3.5
0.733	0.909	-0.45	-0.14	23.7	23.2	21.1	17.4
0.75	0.64	-0.41	-0.64	118.9	124.6	79.7	89.2
1.105	1.203	0.14	0.27	16.2	17	20.5	17.9
0.614	0.555	-0.7	-0.85	22.9	20.5	11.4	14
0.463	0.537	-1.11	-0.9	26.1	27.9	15	12.1
0.535	0.528	-0.9	-0.92	78.4	68.3	36.1	41.9
0.773	0.715	-0.37	-0.48	13.3	12.4	8.9	10.3
	100		6.64			4.5	
1.031	1.083	0.04	0.11	11.5	6.8	7.4	11.9
0.792	0.842	-0.34	-0.25	2.6	5.8	4.9	2.1
	0.998		0		1.6	1.6	
0.668	0.817	-0.58	-0.29	432.5	363.9	297.3	288.9
100	0.383	6.64	-1.39		6.6	2.5	4.2
1.001	1.06	0	0.08	44.9	43.2	45.8	45
0.991	0.858	-0.01	-0.22	27.1	26.5	22.7	26.8

100	0.01	6.64	-6.64		2.1		1.6
2.075	1.95	1.05	0.96	52.4	56.2	109.5	108.7
0.796	0.79	-0.33	-0.34	305.9	339.5	268.1	243.7
100	1.229	6.64	0.3		2.8	3.5	3.5
1.235	0.952	0.3	-0.07	219.6	267.5	254.7	271.3
2.081	2.384	1.06	1.25	21.9	19.3	46.1	45.6
1.826	1.84	0.87	0.88	74.3	83.5	153.7	135.7
0.921	0.695	-0.12	-0.52	23.2	19	13.2	21.4
1.569	1.817	0.65	0.86	145.2	141	256.1	227.8
1.948	2.002	0.96	1	77.4	82.6	165.4	150.7
1.911	2.177	0.93	1.12	140.5	128.4	279.4	268.5
1.481	1.581	0.57	0.66	77.5	80.2	126.7	114.9
1.374	1.719	0.46	0.78	50.4	37.4	64.3	69.3
	100		6.64			2.5	
2.542	0.797	1.35	-0.33	2.9	4.6	3.7	7.4
	1.054		0.08		2.9	3	
1.187	1.211	0.25	0.28	372	375.1	454.3	441.6
0.776	1.155	-0.37	0.21	14.3	11	12.7	11.1
11.615	1.545	3.54	0.63	2.6	16.5	25.5	30.1
1.301	1.376	0.38	0.46	752.5	748.4	1030.1	979
1.294	1.278	0.37	0.35	16.1	14.6	18.7	20.8
1.085	1.106	0.12	0.15	303.3	292.2	323.1	329.2
1.492	1.411	0.58	0.5	66.7	65.1	91.9	99.5
0.709	0.87	-0.5	-0.2	67.6	58.7	51.1	48
0.933	0.851	-0.1	-0.23	183.6	180.9	154	171.4
0.01	1.045	-6.64	0.06	2.4	1.5	1.6	
1.069	1.035	0.1	0.05	72.8	70.4	72.8	77.9
0.905	0.606	-0.14	-0.72	22.7	23.9	14.5	20.6
100	0.47	6.64	-1.09		4.5	2.1	5
0.948	0.992	-0.08	-0.01	767.3	713.8	708.1	727.3
	0.839		-0.25		2.7	2.3	
2.056	1.012	1.04	0.02	6.2	10.6	10.7	12.7
1.85	1.3	0.89	0.38	32.3	22.9	29.7	59.7
4.192	0.941	2.07	-0.09	3.6	11.3	10.6	15
1.305	1.306	0.38	0.39	355.7	353.5	461.7	464.3
0.665	1.143	-0.59	0.19	35.4	18.3	20.9	23.5
0.984	0.813	-0.02	-0.3	36.7	39.1	31.8	36.1
0.433	0.563	-1.21	-0.83	13.5	12.2	6.9	5.8
	0.871		-0.2		1.7	1.5	

	100		6.64			3.3	
	0.01		-6.64		2.6		
1.044	0.806	0.06	-0.31	249	276.1	222.6	260
0.908	0.872	-0.14	-0.2	25.8	33.7	29.4	23.4
0.673	0.57	-0.57	-0.81	70.9	71.2	40.6	47.7
0.469	1.375	-1.09	0.46	4.9	2.1	2.9	2.3
0.01		-6.64		2.6			
1.01	1.11	0.01	0.15	3.7	2.9	3.3	3.8
0.776	0.809	-0.36	-0.31	310	288	233.1	240.7
0.634	1.411	-0.66	0.5	4.9	5.5	7.8	3.1
1.876	1.033	0.91	0.05	30.5	39.5	40.8	57.2
1.1	1.576	0.14	0.66	2.6	2.3	3.6	2.9
0.01	100	-6.64	6.64	2.1		2.1	
2.703	1.785	1.43	0.84	4.1	4.3	7.7	11
1.059	1.117	0.08	0.16	17.4	14.3	16	18.4
1.76	0.965	0.82	-0.05	6.2	11.9	11.4	10.8
0.975	0.866	-0.04	-0.21	61.2	63.5	55	59.6
2.464	0.998	1.3	0	4.2	8.2	8.2	10.4
1.54	1.59	0.62	0.67	2.6	2.5	4.1	4
	100		6.64			2.6	
100	1.08	6.64	0.11		3.2	3.5	4.3
0.652	0.727	-0.62	-0.46	170.7	169.7	123.4	111.3
1.311	1.562	0.39	0.64	4.7	5.5	8.5	6.2
	0.791		-0.34		2.7	2.2	
0.569	0.712	-0.81	-0.49	46.6	37.4	26.7	26.5
1.479	1.12	0.56	0.16	11.2	10.1	11.3	16.6
1.303	1.061	0.38	0.09	104.5	143.4	152.1	136.1
0.763	0.829	-0.39	-0.27	893.5	856.2	709.5	681.9
0.682	0.793	-0.55	-0.33	86.6	91.1	72.3	59
0.81	0.865	-0.3	-0.21	75.1	79.1	68.4	60.9
2.519	1.233	1.33	0.3	3.1	4.6	5.6	7.8

1.05	0.877	0.07	-0.19	103	100.5	88.1	108.1
0.947	1.055	-0.08	0.08	104	100.8	106.3	98.4
0.944	1.019	-0.08	0.03	160.6	148.2	151	151.5
0.01	0.928	-6.64	-0.11	6.3	4.9	4.5	
	0.63		-0.67		2.1	1.3	
1.074	1.202	0.1	0.27	66.3	62.6	75.2	71.3
	100		6.64			2.2	
0.652	0.909	-0.62	-0.14	70.2	64.9	59	45.8
100	1.497	6.64	0.58		1.8	2.8	1.7
0.804	0.677	-0.32	-0.56	124.6	129.7	87.8	100.1
2.953	1.819	1.56	0.86	5.8	5.7	10.3	17.2
2.105	1.043	1.07	0.06	33.7	56.5	59	71
1.129	1.179	0.17	0.24	18	18.2	21.4	20.3
1.23	0.962	0.3	-0.06	32.1	38.7	37.2	39.5
1.094	0.957	0.13	-0.06	58.9	63.8	61.1	64.4
1.187	1.571	0.25	0.65	31.5	19.6	30.8	37.3
100	1.058	6.64	0.08		2.4	2.5	1.5
0.773	0.761	-0.37	-0.39	190.9	187.6	142.8	147.5
0.684	1.057	-0.55	0.08	22.5	16.8	17.7	15.4
2.313	0.919	1.21	-0.12	4.5	13.8	12.7	10.5
1.245	2.747	0.32	1.46	2.1	2.7	7.3	2.6
2.035	0.822	1.02	-0.28	10.4	21.8	17.9	21.1
1.405	1.196	0.49	0.26	38.4	40.3	48.2	54
1.184	1.186	0.24	0.25	30.7	30.4	36.1	36.3
1.051	1.002	0.07	0	97.3	94.5	94.6	102.3
0.812	0.816	-0.3	-0.29	270.4	265.2	216.5	219.6
1.512	1.401	0.6	0.49	4.4	2.8	3.9	6.6
1.363	1.603	0.45	0.68	64.1	65.8	105.4	87.4
0.899	1.03	-0.15	0.04	84.2	76.4	78.7	75.7
1.391	1.341	0.48	0.42	20.8	21.3	28.5	28.9
0.881	0.912	-0.18	-0.13	1538.6	1532.8	1398.4	1355.9
0.533	0.721	-0.91	-0.47	6	4.8	3.5	3.2
1.34	1.766	0.42	0.82	18.5	15.1	26.7	24.8
1.389	1.505	0.47	0.59	291.5	264.5	397.9	404.8
1.016	1.445	0.02	0.53	11.4	7.8	11.3	11.5
0.879	0.871	-0.19	-0.2	118.6	82.6	72	104.3
0.986	1.012	-0.02	0.02	19.5	11.6	11.8	19.2
1.114	1.869	0.16	0.9	12.8	8.9	16.7	14.3
0.79	0.85	-0.34	-0.23	2385.9	2470.6	2100.4	1885.6
0.748	0.84	-0.42	-0.25	399.9	411.5	345.7	299.2
0.723	0.843	-0.47	-0.25	149.2	140.2	118.2	107.9

0.58	1.304	-0.79	0.38	2.8	2.2	2.8	1.6
0.01	100	-6.64	6.64	2.1		2.4	
1.468	1.479	0.55	0.56	109.3	111	164.1	160.6
0.525	0.522	-0.93	-0.94	100.9	98.2	51.3	53
2.534	0.958	1.34	-0.06	2.4	11.8	11.3	6.2
0.886	0.84	-0.17	-0.25	196.6	187.3	157.3	174.3
30.352	9.798	4.92	3.29	2.8	7.1	69.3	83.7
	100		6.64			1.7	
0.917	0.894	-0.13	-0.16	27.9	28.4	25.4	25.6
0.958	0.969	-0.06	-0.05	234.1	213	206.5	224.2
100	0.694	6.64	-0.53		2.8	1.9	1.6
0.837	0.936	-0.26	-0.1	9.4	10.4	9.8	7.9
0.01	100	-6.64	6.64	2.1		1.8	
0.652	0.666	-0.62	-0.59	4.4	5.4	3.6	2.9
2.992	1.63	1.58	0.7	3.9	6.5	10.6	11.6
0.858	0.662	-0.22	-0.6	5.2	7.4	4.9	4.5
3.52	0.802	1.82	-0.32	3.1	9.4	7.5	10.8
0.767	0.797	-0.38	-0.33	36	39.4	31.4	27.6
100		6.64					5.6
1.09	0.76	0.12	-0.4	61.2	67.7	51.5	66.7
100	1.355	6.64	0.44		3.6	4.9	1.5
	1.215		0.28		2.2	2.7	
100	1.26	6.64	0.33		2.1	2.6	2.1
1.223	1.358	0.29	0.44	3.1	4.6	6.3	3.8
0.609	0.999	-0.71	0	30.2	25.3	25.3	18.4
1.027	1.223	0.04	0.29	83.4	83.6	102.2	85.6
0.987	0.823	-0.02	-0.28	129.5	137.3	113	127.8
1.892	0.969	0.92	-0.05	33.7	28.4	27.5	63.8
0.797	0.898	-0.33	-0.15	24.7	24.6	22.1	19.6
1.455	1.239	0.54	0.31	9.7	12	14.9	14.2
1.739	1.651	0.8	0.72	22.4	21.5	35.5	38.9
0.01	1.495	-6.64	0.58	6.2	2.5	3.8	
	0.01		-6.64		2.3		
100	0.838	6.64	-0.25		1.7	1.4	1.5
1.786	0.985	0.84	-0.02	34.7	45	44.3	62
0.865	1.034	-0.21	0.05	59.5	52.8	54.6	51.5
3.251	2.541	1.7	1.35	3.4	3	7.7	11.1
1.434	1	0.52	0	30.2	39.7	39.7	43.3

1.11	1.063	0.15	0.09	241.5	241.8	257.2	268.2
0.983	1.084	-0.02	0.12	36.8	40.1	43.5	36.2
	100		6.64			1.9	
1.226	1.354	0.29	0.44	80.9	79.3	107.3	99.2
100	1.286	6.64	0.36		2.4	3.1	2.2
1.025	1.214	0.04	0.28	13.1	10.7	13	13.5
1.028	0.725	0.04	-0.46	90.7	99.3	72	93.2
0.616	0.878	-0.7	-0.19	14.3	11.2	9.9	8.8
0.981	0.782	-0.03	-0.35	64.2	69.9	54.7	63
100	0.937	6.64	-0.09		2.7	2.6	2.1
1.027	0.858	0.04	-0.22	103.8	114.6	98.3	106.7
1.903	0.501	0.93	-1	4.4	6.2	3.1	8.3
0.576	0.541	-0.8	-0.89	3.6	3.5	1.9	2.1
	0.01		-6.64		1.9		
0.914	0.898	-0.13	-0.15	109.3	114.1	102.5	99.9
0.894	0.879	-0.16	-0.19	296.9	310.3	272.7	265.4
	0.566		-0.82		3.7	2.1	
0.868	0.798	-0.2	-0.33	265.1	271	216.3	230
100	0.831	6.64	-0.27		10.8	9	9.6
1.337	0.79	0.42	-0.34	8.1	9.4	7.4	10.8
0.395	1.149	-1.34	0.2	6.7	5.5	6.3	2.6
2.062	2.293	1.04	1.2	9.1	7.6	17.5	18.7
0.01	1.503	-6.64	0.59	2.9	1.6	2.3	
2.017	1.784	1.01	0.84	12	11.9	21.2	24.2
0.847	0.761	-0.24	-0.39	76.7	87.8	66.9	65
0.791	0.815	-0.34	-0.3	60.2	60.7	49.5	47.6
1.455	1.53	0.54	0.61	26.4	28.6	43.7	38.5
0.707	0.712	-0.5	-0.49	336.4	298.5	212.7	238
1.799	1.511	0.85	0.6	5.8	4.4	6.7	10.5
0.01	1.406	-6.64	0.49	3.4	1.8	2.6	
4.836	1.433	2.27	0.52	3.7	10.2	14.6	18
100	0.01	6.64	-6.64		3.4		2.2
0.874	0.877	-0.2	-0.19	134	134.9	118.2	117
1.757	0.756	0.81	-0.4	22.9	37.6	28.4	40.2
1.864	1.221	0.9	0.29	41.5	62.7	76.5	77.4
2.062	0.849	1.04	-0.24	4.5	5.3	4.5	9.4
2.112	100	1.08	6.64	2.1		2.8	4.5
1.036	1.044	0.05	0.06	397.3	401.3	419	411.8
0.884	0.952	-0.18	-0.07	969.7	948.8	902.8	857.6
2.429	1.451	1.28	0.54	24.5	35.8	52	59.5

100	2.23	6.64	1.16		3.3	7.3	8.9
2.328	1.958	1.22	0.97	45.4	55.7	109	105.7
1.393	1.473	0.48	0.56	46.7	46.6	68.6	65.1
100	1.779	6.64	0.83		4	7.1	12
100	2.406	6.64	1.27		1.8	4.4	2.2
0.837	0.874	-0.26	-0.19	241.9	222.6	194.5	202.3
3.872	1.372	1.95	0.46	5.8	14.4	19.7	22.6
1.136	0.774	0.18	-0.37	11.4	10.1	7.8	12.9
100		6.64					1.8
13.727	1.6	3.78	0.68	2.9	18.5	29.5	40.1
0.66		-0.6		2.6			1.7
100	1.41	6.64	0.5		2	2.8	2.5
1.035	0.991	0.05	-0.01	2.8	3.5	3.5	2.9
100	2.012	6.64	1.01		3.3	6.6	2.9
4.646	1.345	2.22	0.43	2.4	6.6	8.9	11.3
2.116	1.211	1.08	0.28	28.1	39.4	47.7	59.4
1.71	1.307	0.77	0.39	203.6	300.1	392.1	348.1
0.924	0.884	-0.11	-0.18	73.8	77.8	68.8	68.2
	0.01		-6.64		1.9		
100		6.64					1.4
1.089	1.085	0.12	0.12	1840	1790.5	1943.3	2004.4
100	0.907	6.64	-0.14		1.9	1.7	1.9
0.616	0.718	-0.7	-0.48	461.8	453.6	325.9	284.4
0.762	0.802	-0.39	-0.32	166.3	156.3	125.3	126.6
100	0.976	6.64	-0.03		5.9	5.8	7.8
1.03	1.593	0.04	0.67	58.6	40.3	64.2	60.3
0.626	1.247	-0.68	0.32	2.9	3.7	4.6	1.8
100	1.399	6.64	0.48		4	5.6	1.7
1.128	1.325	0.17	0.41	40.4	36.3	48.2	45.6
1.387	1.16	0.47	0.21	108.4	122	141.5	150.3
0.714	0.795	-0.49	-0.33	3208.8	3069.5	2439.4	2291.7
0.91	0.943	-0.14	-0.08	6.7	5.8	5.5	6.1
0.73	0.838	-0.45	-0.25	780.1	746.4	625.8	569.8
1.282	0.842	0.36	-0.25	15.4	23.8	20.1	19.8
100	1.779	6.64	0.83		6.4	11.3	11.3
1.047	0.952	0.07	-0.07	13	11.1	10.5	13.6

0.832	1.308	-0.27	0.39	5.4	4.3	5.7	4.5
1.584	0.96	0.66	-0.06	4.5	5.4	5.1	7.2
100	1.491	6.64	0.58		3.5	5.2	4.5
	1.115		0.16		1.9	2.1	
0.446	1.362	-1.17	0.45	9.7	3	4.1	4.3
0.01	1.049	-6.64	0.07	3.7	2.8	3	
	1.146		0.2		1.7	1.9	
1.456	1.438	0.54	0.52	35.9	39	56	52.2
1.128	1.182	0.17	0.24	170.3	188.3	222.5	192.1
1.415	1.438	0.5	0.52	187.7	202.4	291	265.6
100	1.186	6.64	0.25		3.7	4.4	1.8
0.909	1.099	-0.14	0.14	3.9	3.3	3.6	3.5
0.827	0.806	-0.27	-0.31	65	70	56.5	53.8
0.78	0.814	-0.36	-0.3	409.4	404.3	328.9	319.3
1.599	1.253	0.68	0.33	71.5	90.1	113	114.4
0.988	1.099	-0.02	0.14	145.7	155.2	170.5	144
1.294	1.378	0.37	0.46	10.1	9.9	13.6	13
0.851	0.865	-0.23	-0.21	350.4	317.8	274.7	298.2
1.303	1.097	0.38	0.13	10.9	10.3	11.3	14.2
1.491	0.823	0.58	-0.28	19.3	32.5	26.8	28.8
1.537	0.509	0.62	-0.98	7.9	16.6	8.5	12.2
0.752	0.658	-0.41	-0.6	277.9	311.7	204.9	209
0.605	0.781	-0.73	-0.36	93.4	91.3	71.3	56.5
100	0.996	6.64	-0.01		4.3	4.2	4.8
1.254	1.099	0.33	0.14	41.5	39.4	43.3	52.1
1.801	1.987	0.85	0.99	5.5	6	12	9.9
1.32	0.892	0.4	-0.16	40.2	49.1	43.8	53.1
0.97	0.867	-0.04	-0.21	99.3	111.7	96.9	96.3
1.954	2.675	0.97	1.42	23.8	18.9	50.7	46.6
1.137	1.179	0.19	0.24	2.1	2.6	3	2.4
0.01		-6.64		2.1			
0.782	1.102	-0.35	0.14	2.9	2.1	2.4	2.3
0.971	1.007	-0.04	0.01	106.1	98.8	99.5	103
1.934	1.394	0.95	0.48	14.8	18.7	26.1	28.5
0.689	0.992	-0.54	-0.01	23	19.6	19.4	15.9
2.331	3.283	1.22	1.72	29.7	21.2	69.5	69.2
0.804	0.74	-0.31	-0.43	60.5	58.4	43.2	48.6
0.922	1.16	-0.12	0.21	56	28.6	33.2	51.6
1.035	0.996	0.05	-0.01	118.6	97.6	97.2	122.8
1.067	0.905	0.09	-0.14	555.8	585.2	529.6	592.8
0.935	0.842	-0.1	-0.25	540.5	591.4	497.8	505.2

1.516	0.799	0.6	-0.32	23.2	45.8	36.6	35.2
0.01	100	-6.64	6.64	2.6		1.7	
	100		6.64			1.6	
	100		6.64			3.5	
100	100	6.64	6.64			4.8	2.7
4.453	5.163	2.15	2.37	35.9	29.7	153.4	159.6
100	100	6.64	6.64			9.9	11.1
3.628	4.045	1.86	2.02	2.1	1.7	6.9	7.7
100	30.739	6.64	4.94		3.4	104.7	108.7
100	100	6.64	6.64			2.7	8.2
9.972	10.123	3.32	3.34	2.9	3.2	32.1	29.1
100	100	6.64	6.64			9.3	19.8
100	100	6.64	6.64			4.7	7.7
100	1.521	6.64	0.61		2.2	3.3	5.6
	100		6.64			2.1	
7.699	5.285	2.94	2.4	15.4	24.9	131.8	118.6
6.985	3.465	2.8	1.79	2.1	4	14	14.7
100	100	6.64	6.64			3.6	4.7
100	100	6.64	6.64			1.6	1.7
100	9.914	6.64	3.31		2.7	26.5	27.2
100	0.815	6.64	-0.29		3.1	2.5	7.1
0.635	0.707	-0.66	-0.5	1874.8	1938.4	1370.4	1190.5
1.459	1.484	0.55	0.57	90.8	86.9	129	132.6
1.729	1.596	0.79	0.67	112.4	121.1	193.4	194.4
1.05	0.996	0.07	-0.01	152	156.1	155.5	159.5
1.124	1.021	0.17	0.03	169.8	171	174.7	190.9
5.496	3.616	2.46	1.85	12.7	15	54.3	69.5
1.519	1.163	0.6	0.22	26.8	34.3	39.9	40.7
8.538	4.598	3.09	2.2	5	8.3	38.2	42.9
0.983	1.104	-0.03	0.14	192.9	178.7	197.3	189.6
1.707	1.742	0.77	0.8	67.6	68.6	119.4	115.4
0.616	1.418	-0.7	0.5	2.6	1.9	2.7	1.6
	0.01		-6.64		1.8		
0.799	0.864	-0.32	-0.21	78.2	78.4	67.7	62.5
0.879	0.936	-0.19	-0.1	215.1	211.2	197.7	189.1
0.77	0.823	-0.38	-0.28	107.1	92.3	76	82.4
0.46	1.809	-1.12	0.86	4.2	3	5.4	1.9
1.507	0.924	0.59	-0.11	23	36.3	33.5	34.7
0.778	0.681	-0.36	-0.55	122	134.6	91.6	94.9

100	0.569	6.64	-0.81		3.7	2.1	2.5
3.52	1.073	1.82	0.1	2.4	5.5	5.9	8.6
0.848	0.682	-0.24	-0.55	7.9	17.8	12.1	6.7
0.01	0.01	-6.64	-6.64	3.1	4.4		
0.056	0.01	-4.17	-6.64	30.8	32.3		1.7
0.596	0.525	-0.75	-0.93	109.3	118.2	62	65.2
0.766	0.779	-0.38	-0.36	149.9	147.9	115.3	114.9
0.721	0.707	-0.47	-0.5	136.9	143.4	101.4	98.8
0.635	0.74	-0.66	-0.43	59.4	47.7	35.3	37.7
0.514	1.148	-0.96	0.2	18	11	12.7	9.2
1.08	0.862	0.11	-0.21	147.5	119	102.6	159.3
0.875	0.941	-0.19	-0.09	75.9	68.2	64.2	66.5
0.73	0.914	-0.45	-0.13	86.9	78.4	71.7	63.5
1.409	1.548	0.49	0.63	97.7	89.4	138.3	137.6
1.512	1.412	0.6	0.5	140.8	141.9	200.4	213
1.438	1.486	0.52	0.57	214.8	208.2	309.4	308.9
1.476	2.184	0.56	1.13	5	3.3	7.3	7.4
2.27	1.786	1.18	0.84	13	17.8	31.8	29.5
100	0.01	6.64	-6.64		2.2		1.9
1.401	1.584	0.49	0.66	1962.8	1956.9	3099.4	2750.3
1.123	1.16	0.17	0.21	237.3	245.7	285.1	266.6
0.726	0.753	-0.46	-0.41	506.8	494.6	372.4	368
0.942	0.995	-0.09	-0.01	294.4	270.8	269.5	277.5
0.957	1.012	-0.06	0.02	58.7	58.5	59.2	56.2
100	100	6.64	6.64			3	3
0.944	1.016	-0.08	0.02	271.1	249	252.8	256
0.713	0.673	-0.49	-0.57	174.1	170.8	114.9	124.1
0.755	0.732	-0.4	-0.45	159.8	113.8	83.4	120.7
1.306	1.503	0.39	0.59	59.4	32.7	49.1	77.5
1.971	2.854	0.98	1.51	2.4	2	5.8	4.8
2.062	1.566	1.04	0.65	20.8	28.4	44.5	42.8
1.258	1.359	0.33	0.44	38.8	36.3	49.3	48.8
1.272	1.149	0.35	0.2	36.2	38.5	44.2	46
0.727	0.74	-0.46	-0.43	539.1	529	391.6	391.7
0.01	0.01	-6.64	-6.64	2.6	2.6		
1.125	0.844	0.17	-0.25	65.7	82.4	69.5	73.9
0.66	0.589	-0.6	-0.76	7.8	5.1	3	5.1
1.605	0.852	0.68	-0.23	8.1	8.9	7.6	13
1.491	0.962	0.58	-0.06	49.5	59.5	57.3	73.8
1.54	1.044	0.62	0.06	5.2	6.7	6.9	8
0.718	0.71	-0.48	-0.49	146.5	148.4	105.4	105.2
0.968	0.683	-0.05	-0.55	25.5	31.1	21.2	24.7
1.625	1.132	0.7	0.18	25.8	33.3	37.7	41.9
1.22	1.287	0.29	0.36	26.1	28.8	37.1	31.9

2.24	2.003	1.16	1	66.8	79	158.3	149.7
0.564	0.606	-0.83	-0.72	382.5	332.8	201.6	215.8
0.762	0.724	-0.39	-0.47	131.2	138.6	100.3	100
0.737	1.75	-0.44	0.81	3.4	1.8	3.1	2.5
2.615	1.781	1.39	0.83	3.4	4.5	8	8.9
1.309	1.211	0.39	0.28	11.5	9.6	11.6	15.1
0.923	0.863	-0.12	-0.21	448.2	450	388.4	413.6
0.906	0.811	-0.14	-0.3	331.1	348.9	282.8	299.9
100	1.617	6.64	0.69		2.8	4.4	3.5
1.004	1.286	0.01	0.36	110.8	88.5	113.7	111.2
0.565	0.616	-0.82	-0.7	594.2	569	350.7	335.5
1.175	1.625	0.23	0.7	37.3	31.1	50.6	43.8
1.187	1.176	0.25	0.23	11.4	9.1	10.7	13.5
1.064	1.093	0.09	0.13	28.2	27.2	29.7	30
0.682	0.739	-0.55	-0.44	5.2	5	3.7	3.5
0.929	1.581	-0.11	0.66	7.6	5.3	8.4	7.1
0.583	0.531	-0.78	-0.91	107.7	106.1	56.3	62.8
	0.9		-0.15		2.4	2.2	
0.966	0.648	-0.05	-0.63	15.2	14.9	9.6	14.7
1.528	0.87	0.61	-0.2	25.6	34.2	29.8	39.2
1.508	0.939	0.59	-0.09	19.5	22	20.6	29.3
0.837	0.9	-0.26	-0.15	91.8	79.6	71.6	76.9
0.616	0.942	-0.7	-0.09	2.6	3.9	3.7	1.6
100	0.942	6.64	-0.09		2.6	2.4	3.2
2.675	0.837	1.42	-0.26	3.2	8.4	7.1	8.7
100	100	6.64	6.64			2	2.5
100	0.01	6.64	-6.64		4		1.7
1.233	1.467	0.3	0.55	137.9	122.5	179.7	170
1.395	1.575	0.48	0.66	42.8	40	63	59.7
1.477	1.566	0.56	0.65	36.2	31.7	49.7	53.4
	100		6.64			1.6	
1.179	0.999	0.24	0	14	17.4	17.3	16.4
1.325	1.555	0.41	0.64	76.9	69.1	107.4	101.9
4.827	2.51	2.27	1.33	3.4	4.7	11.9	16.4
0.866	0.998	-0.21	0	4.2	7.6	7.6	3.7
1.48	1.582	0.57	0.66	15.7	17.4	27.6	23.3
0.883	0.886	-0.18	-0.17	238.6	220.6	195.6	210.8
0.937	0.938	-0.09	-0.09	1640.7	1692	1586.7	1536.5
0.923	1.192	-0.12	0.25	73.5	61.9	73.8	67.8
2.506	2.016	1.33	1.01	14.8	19.8	40	37

0.01	0.741	-6.64	-0.43	2.3	3.6	2.6	
1.425	1.405	0.51	0.49	6.5	3.3	4.7	9.2
1.056	0.918	0.08	-0.12	226.8	228.1	209.3	239.5
1.125	1.298	0.17	0.38	1246.2	1149.1	1491.9	1402.5
1.785	1.555	0.84	0.64	42.7	45.1	70.1	76.2
1.305	1.292	0.38	0.37	36.7	40.2	51.9	47.8
1.084	1.152	0.12	0.2	40.6	39.8	45.8	44
2.944	1.273	1.56	0.35	7.1	13.8	17.5	21
1.79	1.479	0.84	0.56	14.9	16.8	24.8	26.7
1.419	0.939	0.5	-0.09	21.3	23	21.6	30.1
0.952	0.955	-0.07	-0.07	424	415.9	397	403.8
1.524	1.322	0.61	0.4	50.1	57	75.4	76.4
0.896	0.915	-0.16	-0.13	473.8	471	431.1	424.8
0.88	0.672	-0.18	-0.57	70.7	76.2	51.2	62.2
0.741	0.791	-0.43	-0.34	244.5	221.9	175.6	181.1
1.202	1.458	0.26	0.54	120.7	104.1	151.7	145
0.866	0.967	-0.21	-0.05	2.1	3.3	3.1	1.8
100	0.419	6.64	-1.25		5.7	2.4	4.8
1.074	1.07	0.1	0.1	192.1	192.3	205.8	206.3
100	1.218	6.64	0.28		2.5	3.1	3.3
	100		6.64			2.1	
1.111	1.102	0.15	0.14	18.5	20.7	22.8	20.6
1.86	1.249	0.9	0.32	2.3	2.2	2.8	4.2
100	100	6.64	6.64			3.3	5.4
4.864	2.072	2.28	1.05	16.2	12.4	25.6	78.9
1.996	0.87	1	-0.2	16.7	15.6	13.6	33.3
2.256	1.338	1.17	0.42	44.4	20.4	27.3	100.3
5.683	1.949	2.51	0.96	11	9.8	19.2	62.7
4.18	0.973	2.06	-0.04	2.6	4.3	4.2	10.8
1.83	0.72	0.87	-0.47	2.4	7	5	4.5
0.897	0.997	-0.16	0	304.3	282.6	281.8	273
1.169	1.074	0.23	0.1	45.9	45.7	49.1	53.7
1.25	1.189	0.32	0.25	39.7	35.7	42.5	49.7
0.815	0.807	-0.3	-0.31	311.5	304.5	245.8	253.8
100	100	6.64	6.64			7.3	11.6
3.285	4.144	1.72	2.05	10.7	9	37.3	35.2
	0.01		-6.64		2.4		
0.01	1.005	-6.64	0.01	3.7	3.6	3.6	
100	0.963	6.64	-0.05		4.5	4.4	4.8
	0.598		-0.74		2.2	1.3	

	0.01		-6.64		3		
100	0.64	6.64	-0.64		7.5	4.8	8.8
	1.21		0.28		1.8	2.2	
100	1.198	6.64	0.26		1.5	1.8	1.6
1.085	0.956	0.12	-0.06	15.6	15.7	15.1	16.9
1.006	0.824	0.01	-0.28	2.3	3.7	3	2.3
1.519	1.085	0.6	0.12	25.8	34.3	37.2	39.2
0.839	1.083	-0.25	0.12	4.2	3.5	3.8	3.5
2.928	1.202	1.55	0.27	4.1	8.1	9.7	11.9
1.191	1.088	0.25	0.12	13.1	15.7	17.1	15.6
0.918	1.093	-0.12	0.13	54.5	47.9	52.4	50
2.938	1.807	1.55	0.85	3.7	2.5	4.5	11
	0.01		-6.64		2.7		
1.417	1.516	0.5	0.6	90.7	89.1	135	128.5
1.243	0.678	0.31	-0.56	7.6	12.3	8.4	9.5
2.197	1.761	1.14	0.82	5.4	7.2	12.7	11.8
	1.832		0.87		2	3.6	
	1.187		0.25		2.4	2.9	
1.272	1.594	0.35	0.67	30.3	24.3	38.7	38.6
0.751	0.73	-0.41	-0.45	2.4	3.5	2.5	1.8
1.698	2.524	0.76	1.34	2.8	3.1	7.9	4.7
100	100	6.64	6.64			2.2	2.3
1.347	1.13	0.43	0.18	65.9	53	59.9	88.7
1.784	1.071	0.84	0.1	106.6	79.2	84.8	190.1
1.191	1.086	0.25	0.12	43.8	47	51	52.2
0.715	0.822	-0.48	-0.28	367.1	351.1	288.6	262.3
0.976	0.877	-0.03	-0.19	66.7	50.3	44.2	65.1
2.728	1.332	1.45	0.41	3.9	9.7	12.9	10.6
0.734	1.202	-0.45	0.26	15.4	11	13.2	11.3
1.007	1.063	0.01	0.09	80.3	71.1	75.6	80.8
1.09	0.831	0.12	-0.27	103.2	118.6	98.5	112.5
	1.008		0.01		2.5	2.5	
	0.01		-6.64		2.8		
0.673	0.704	-0.57	-0.51	182.8	170.2	119.8	123
0.932	0.772	-0.1	-0.37	54.7	61.9	47.8	50.9
100	0.978	6.64	-0.03		3	2.9	1.7
1.071	0.937	0.1	-0.09	274.5	284.5	266.5	294
1.751	1.397	0.81	0.48	24.7	23	32.1	43.2
0.839	0.952	-0.25	-0.07	19.5	15.3	14.6	16.3
1.269	1.391	0.34	0.48	157	148.9	207.1	199.3
2.793	1.319	1.48	0.4	10.1	11.9	15.7	28.1
0.917	0.87	-0.13	-0.2	118.6	121	105.2	108.7
0.867	0.948	-0.21	-0.08	214.6	202.7	192.1	186
1.408	0.705	0.49	-0.5	10.9	19.5	13.7	15.3
0.995	1.226	-0.01	0.29	14.9	10.3	12.6	14.8

1.108	1.129	0.15	0.17	58.2	59.6	67.3	64.5
1.525	1.397	0.61	0.48	124.4	127.3	177.9	189.8
0.934	0.972	-0.1	-0.04	106.7	95.6	92.9	99.7
1.151	1.357	0.2	0.44	34.2	40.9	55.5	39.4
3.388	1.408	1.76	0.49	2.6	6.1	8.6	8.8
2.393	1.223	1.26	0.29	14.6	22.3	27.3	34.9
0.921	0.975	-0.12	-0.04	4.2	4.5	4.4	3.9
0.492	0.557	-1.02	-0.84	201.2	201.6	112.4	98.9
0.886	0.819	-0.18	-0.29	576.2	583.8	478.4	510.3
1.176	1.556	0.23	0.64	91	79.5	123.7	107
0.808	0.991	-0.31	-0.01	78.7	72.7	72.1	63.6
1.006	0.919	0.01	-0.12	5.7	4.4	4	5.7
1.284	0.663	0.36	-0.59	5.5	4.5	3	7.1
0.532	1.266	-0.91	0.34	7.9	6.2	7.8	4.2
0.808	0.899	-0.31	-0.15	4105.1	4027.3	3620.8	3316.2
1.17	1.096	0.23	0.13	20.6	20.6	22.6	24.1
1.804	1.426	0.85	0.51	61.2	74.2	105.8	110.3
1.491	1.61	0.58	0.69	26.1	25.1	40.3	38.9
1.017	1.236	0.02	0.31	101.7	87.1	107.7	103.5
1.885	1.462	0.91	0.55	18.7	24.6	36	35.2
1.212	1.573	0.28	0.65	49	42.7	67.2	59.4
3.989	0.945	2	-0.08	2.9	7.5	7	11.6
1.198	1.238	0.26	0.31	539.5	540.2	669	646.4
1.089	0.817	0.12	-0.29	41.5	53	43.3	45.2
0.722	0.794	-0.47	-0.33	192.9	180.3	143.1	139.2
1.406	0.8	0.49	-0.32	55.3	76.3	61	77.8
1.201	1.278	0.26	0.35	20.9	24.9	31.9	25.1
0.657	0.715	-0.61	-0.48	2.4	2.4	1.7	1.6
0.943	1.119	-0.08	0.16	50.1	45.4	50.8	47.3
1.249	1.178	0.32	0.24	25.1	26.1	30.8	31.4
2.208	1.187	1.14	0.25	3.6	6.7	8	7.9
3.002	1.692	1.59	0.76	5.5	11	18.5	16.6
100	4.171	6.64	2.06		2.6	10.9	10.8
1.538	1.287	0.62	0.36	6.2	7.2	9.3	9.5
	1.969		0.98		2.7	5.3	
2.187	1.249	1.13	0.32	27.4	40.4	50.5	59.9
1.08	1.3	0.11	0.38	30.7	26.8	34.9	33.1
1.33	1.521	0.41	0.6	4.4	4	6.1	5.8
	1.099		0.14		2.2	2.4	
0.01	100	-6.64	6.64	2.3		1.6	
	100		6.64			2	

0.014	0.01	-6.14	-6.64	700.3	717.6	5.8	9.9
1.748	1.48	0.81	0.57	9.7	12.4	18.4	17
1.01	1.077	0.01	0.11	220.3	189.8	204.4	222.4
0.01	0.483	-6.64	-1.05	2.9	3.4	1.6	
	0.01		-6.64		1.7		
0.869	0.841	-0.2	-0.25	94.9	93.5	78.6	82.4
1.461	1.304	0.55	0.38	288.6	300.7	392	421.7
0.766	0.765	-0.39	-0.39	116.5	134.6	103	89.2
1.028	0.815	0.04	-0.3	93.1	110.4	89.9	95.7
1.541	1.344	0.62	0.43	24	27.8	37.4	37
100	0.609	6.64	-0.72		3.1	1.9	2.5
0.052	0.073	-4.28	-3.78	150.7	148.3	10.8	7.8
0.536	0.613	-0.9	-0.71	637.2	570.9	349.8	341.8
0.898	0.858	-0.16	-0.22	872.9	864.1	741.7	783.7
100	0.679	6.64	-0.56		2.9	2	2.4
0.27	0.623	-1.89	-0.68	25.8	25.9	16.2	7
0.938	0.71	-0.09	-0.49	51.3	62.9	44.7	48.1
1.079	0.683	0.11	-0.55	7.3	7.3	5	7.9
1.18	0.884	0.24	-0.18	6	7.8	6.9	7.1
2.581	1.073	1.37	0.1	2.9	9.2	9.9	7.5
0.704	0.694	-0.51	-0.53	13.8	19	13.2	9.7
0.722	0.864	-0.47	-0.21	75.3	58.2	50.3	54.4
1.454	1.153	0.54	0.21	81.6	97.7	112.7	118.6
	1.595		0.67		1.9	3	
100	0.88	6.64	-0.18		5	4.4	4.2
	0.01		-6.64		1.8		
1.955	1.944	0.97	0.96	7.3	7.7	15	14.3
0.558	0.731	-0.84	-0.45	12.5	20.3	14.8	7
0.538	1.589	-0.89	0.67	2.8	4.3	6.9	1.5
1.81	1.88	0.86	0.91	2.3	2.8	5.2	4.1
100	0.852	6.64	-0.23		2.9	2.5	1.8
1.088	1.125	0.12	0.17	158.2	146.8	165.2	172.1
0.7	0.769	-0.51	-0.38	284	265.8	204.3	198.8
1.304	1.271	0.38	0.35	62.6	64	81.4	81.6
0.803	0.862	-0.32	-0.21	82.9	82	70.7	66.6
1.224	1.136	0.29	0.18	119.6	127.8	145.1	146.3
1.251	1.175	0.32	0.23	49.5	47.8	56.1	61.9
1.552	1.039	0.63	0.05	15.1	22.1	22.9	23.4
0.944	0.891	-0.08	-0.17	7.6	5.2	4.6	7.2
0.497	1.433	-1.01	0.52	5.5	5.9	8.4	2.7
0.781	0.832	-0.36	-0.27	79.8	78.2	65	62.3

1.024	0.946	0.03	-0.08	54.2	55.1	52.1	55.5
	0.01		-6.64		1.6		
1.33	0.871	0.41	-0.2	30.7	40.3	35.1	40.8
1.196	1.12	0.26	0.16	68.3	56.4	63.2	81.6
0.921	1.125	-0.12	0.17	36.8	31	34.9	33.9
1.108	1.011	0.15	0.02	32.8	38	38.5	36.3
1.269	1.294	0.34	0.37	190.1	195.8	253.5	241.3
0.826	0.64	-0.28	-0.64	7.5	5.8	3.7	6.2
0.848	0.831	-0.24	-0.27	593.4	592.9	492.8	503.2
1.56	1.352	0.64	0.43	102.8	123.3	166.7	160.4
1.148	1.179	0.2	0.24	498.3	489.5	577	572.3
2.022	1.13	1.02	0.18	6.3	8.5	9.6	12.8
0.843	0.939	-0.25	-0.09	125.7	130.3	122.4	106
0.761	0.72	-0.39	-0.47	71.9	82.4	59.3	54.7
0.905	0.706	-0.14	-0.5	2.3	3.5	2.4	2.1
1.647	0.943	0.72	-0.09	8.1	15.8	14.9	13.4
1.265	0.966	0.34	-0.05	9.6	10.8	10.4	12.1
0.943	0.918	-0.09	-0.12	18.7	21.1	19.3	17.6
100	1.011	6.64	0.02		1.8	1.8	1.8
1.496	0.542	0.58	-0.88	2.6	5.2	2.8	3.9
0.778	1.267	-0.36	0.34	3.1	2.9	3.6	2.4
1.036	0.864	0.05	-0.21	109.3	114.5	98.9	113.3
3.975	1.362	1.99	0.45	2.8	6.2	8.4	11
1.568	1.064	0.65	0.09	7.1	11	11.7	11.2
	0.99		-0.01		2.2	2.2	
	100		6.64			1.4	
100	0.68	6.64	-0.56		3.7	2.5	7.8
0.917	0.736	-0.13	-0.44	12.3	15.9	11.7	11.3
2.105	2.264	1.07	1.18	16.2	10.2	23.1	34.1
1.889	1.409	0.92	0.49	6.7	8.3	11.6	12.6
3.754	1.234	1.91	0.3	5.8	15.8	19.5	21.9
2.998	3.065	1.58	1.62	32.6	29.5	90.5	97.7
1.889	2.047	0.92	1.03	3.1	3.9	7.9	5.8

1.16	1.279	0.21	0.35	14.8	13.4	17.1	17.1
0.848	0.82	-0.24	-0.29	92.8	87.5	71.7	78.7
0.848	0.836	-0.24	-0.26	871.6	909.9	760.3	739
0.884	0.804	-0.18	-0.32	118.9	120.1	96.5	105.2
1.062	0.824	0.09	-0.28	170.8	207.3	170.9	181.3
3.715	0.626	1.89	-0.68	2.9	12.2	7.6	10.8
1.7	0.75	0.77	-0.42	20	11.6	8.7	33.9
3.102	1.028	1.63	0.04	5.2	7.8	8	16.1
6.39	1.627	2.68	0.7	2.1	5.2	8.4	13.5
0.01	1.014	-6.64	0.02	2.9	3.2	3.2	
4.996	3.014	2.32	1.59	6.7	9.8	29.4	33.2
1.216	1.481	0.28	0.57	69.8	59.3	87.9	84.8
0.7	0.836	-0.51	-0.26	29.5	27.9	23.3	20.7
0.979	1.099	-0.03	0.14	102.8	97.9	107.6	100.7
1.329	1.527	0.41	0.61	463.9	419.1	639.9	616.5
2.024	1.424	1.02	0.51	14.3	23.7	33.7	28.9
1.001	1.144	0	0.19	30	29.4	33.6	30
1.231	1.46	0.3	0.55	2307.2	2038.5	2976	2839.3
0.736	0.774	-0.44	-0.37	166.9	143.2	110.9	122.9
2.5	0.71	1.32	-0.5	4.7	7.9	5.6	11.8
2.74	0.619	1.45	-0.69	4.5	10.2	6.3	12.4
1.118	1.037	0.16	0.05	727.1	731.1	758	812.9
0.801	0.939	-0.32	-0.09	308.2	284.5	267.2	246.8
1.02	0.982	0.03	-0.03	213	222.3	218.4	217.3
1.097	0.675	0.13	-0.57	8.4	5.3	3.6	9.2
2.567	1.729	1.36	0.79	2.8	3	5.3	7.1
100	0.01	6.64	-6.64		2.1		2.7
0.659	0.782	-0.6	-0.35	533.7	481.1	376.4	351.8
1.87	1.588	0.9	0.67	41	42.6	67.6	76.7
1.211	1.187	0.28	0.25	205.9	213.3	253.2	249.3
0.01	100	-6.64	6.64	2.1		1.5	
1.863	1.413	0.9	0.5	50.4	59.8	84.5	94
0.54	100	-0.89	6.64	4.9		2.5	2.6
	0.01		-6.64		1.7		
1.008	1.16	0.01	0.21	22.5	32.1	37.2	22.7
100	100	6.64	6.64			1.6	1.7
0.583	0.932	-0.78	-0.1	39.6	43.6	40.6	23.1
0.907	1.031	-0.14	0.04	62	58.6	60.4	56.2
1	0.716	0	-0.48	8.1	10.6	7.6	8.1
100	100	6.64	6.64			1.6	1.5

1.055	1.139	0.08	0.19	143.9	140.9	160.4	151.8
0.01		-6.64		1.9			
0.586	0.582	-0.77	-0.78	265.6	236	137.4	155.6
0.686	0.747	-0.54	-0.42	37.8	30.3	22.6	25.9
0.784	1.806	-0.35	0.85	8.6	4.4	8	6.7
1.625	1.341	0.7	0.42	11	12.1	16.3	17.9
1.229	1.273	0.3	0.35	113.7	114.1	145.2	139.8
0.01	1.141	-6.64	0.19	6	3.4	3.9	
1.355	1.131	0.44	0.18	21.4	24.5	27.7	29
1.454	1.417	0.54	0.5	12.3	12.1	17.2	17.9
2.776	1.896	1.47	0.92	34.2	44.6	84.6	95
1.711	1.527	0.77	0.61	90.4	92.6	141.4	154.6
1.304	1.226	0.38	0.29	358.2	368.9	452.1	467
1.121	1.319	0.16	0.4	69.6	69.4	91.6	78
1.986	1.206	0.99	0.27	10.9	15.9	19.1	21.6
1.867	1.649	0.9	0.72	75.6	83.3	137.3	141.1
5.052	1.629	2.34	0.7	2.8	5.5	9	13.9
1.62	1.59	0.7	0.67	237.2	233	370.5	384.3
1.495	1.483	0.58	0.57	174.5	170.4	252.7	260.9
1.107	1.308	0.15	0.39	40.6	32.7	42.8	44.9
1.246	1.154	0.32	0.21	68.5	70	80.8	85.3
2.155	2.033	1.11	1.02	74.8	78.9	160.3	161.1
1.529	1.413	0.61	0.5	4.7	5.2	7.4	7.2
4.885	3.416	2.29	1.77	10.7	13.8	47.3	52.3
1.856	1.193	0.89	0.25	10.7	16.1	19.2	19.9
0.663	0.736	-0.59	-0.44	36.5	31.8	23.4	24.2
4.112	1.415	2.04	0.5	3.1	6.2	8.8	12.7
1.203	1.579	0.27	0.66	14	13.3	21.1	16.8
0.786	0.771	-0.35	-0.37	64.1	60.7	46.8	50.4
1.129	1.138	0.18	0.19	159.1	152.1	173.1	179.7
1.072	0.864	0.1	-0.21	164.7	201.8	174.4	176.5
0.922	0.908	-0.12	-0.14	837.4	797.5	723.9	772.3
0.638	0.81	-0.65	-0.3	77.5	64.6	52.3	49.4
0.853	1.048	-0.23	0.07	187.4	159.6	167.3	159.8
100	1.353	6.64	0.44		7.6	10.3	12.7
1.382	1.045	0.47	0.06	70.1	86.2	90.1	96.8
1.088	1	0.12	0	19.3	17.3	17.3	21
1.854	0.973	0.89	-0.04	6.7	9.6	9.3	12.3
	100		6.64			1.8	
0.01	100	-6.64	6.64	2.6		1.3	
	0.01		-6.64		2.5		
1.812	1.468	0.86	0.55	7.6	12	17.6	13.8
0.645	0.862	-0.63	-0.21	500.3	356.9	307.6	322.6
1.897	1.291	0.92	0.37	11.7	13.2	17.1	22.2

1.211	0.783	0.28	-0.35	33.6	31.8	24.9	40.7
0.955	1.136	-0.07	0.18	21.4	14	15.9	20.4
0.978	1.116	-0.03	0.16	20.4	20.4	22.8	20
0.913	0.967	-0.13	-0.05	118.1	121.7	117.8	107.8
1.204	1.025	0.27	0.04	48.7	58.6	60.1	58.6
	1.143		0.19		2.2	2.5	
0.827	0.847	-0.27	-0.24	853.3	848.5	718.4	705.6
1.433	0.884	0.52	-0.18	13.6	15.2	13.5	19.5
1.417	1.755	0.5	0.81	38.6	31.7	55.7	54.7
100	1.118	6.64	0.16		2	2.3	2.4
0.75	0.834	-0.41	-0.26	130.7	121.2	101.1	98.1
2.029	1.859	1.02	0.89	2.8	3.7	6.8	5.6
0.768	0.687	-0.38	-0.54	37.1	47.5	32.6	28.5
0.843	0.835	-0.25	-0.26	231.2	225.9	188.6	194.9
1.008	0.8	0.01	-0.32	8.3	8.2	6.5	8.3
100	1.197	6.64	0.26		4.8	5.8	6.1
1.908	1.03	0.93	0.04	6.2	9.2	9.4	11.8
0.982	1.219	-0.03	0.29	147.8	123.1	150.1	145.1
1.224	1.377	0.29	0.46	35.4	33.8	46.5	43.3
	0.896		-0.16		1.7	1.5	
	0.01		-6.64		1.8		
1.016	0.834	0.02	-0.26	24.5	44.8	37.4	24.9
100	0.532	6.64	-0.91		3.1	1.6	3.1
0.971	0.762	-0.04	-0.39	26.9	34.2	26	26.1
100	0.86	6.64	-0.22		2.8	2.4	3.1
0.422	0.915	-1.24	-0.13	3.2	2.7	2.5	1.4
0.982	1	-0.03	0	378.1	375.7	375.6	371.5
0.865	0.855	-0.21	-0.23	372	364.9	312.1	321.9
0.856	0.872	-0.22	-0.2	99.1	97.9	85.4	84.8
0.958	0.874	-0.06	-0.19	399.7	402.8	352.2	382.8
0.822	0.854	-0.28	-0.23	343.6	312.5	266.9	282.4
2.207	1.662	1.14	0.73	26.4	31.1	51.7	58.4
0.709	0.725	-0.5	-0.46	203.6	199.1	144.3	144.3
1.087	1.067	0.12	0.09	12.8	11.3	12.1	13.9

	1.272		0.35		2.2	2.8	
1.062	1.177	0.09	0.23	527.5	497.7	585.6	560.3
0.869	0.836	-0.2	-0.26	110.8	109.1	91.2	96.3
0.759	0.713	-0.4	-0.49	80.3	71.8	51.2	61
0.239	0.968	-2.06	-0.05	8.6	5.4	5.2	2.1
0.984	0.964	-0.02	-0.05	321.2	338.4	326.1	316
0.462	0.533	-1.11	-0.91	74.6	79	42.1	34.5
1.006	1.04	0.01	0.06	17	14.4	15	17.1
0.909	1.008	-0.14	0.01	7.8	9.1	9.1	7.1
0.904	0.952	-0.15	-0.07	70.9	69.6	66.3	64.1
	100		6.64			3.5	
0.493	0.404	-1.02	-1.31	54.7	55.4	22.4	26.9
100	100	6.64	6.64			2.5	1.9
1.188	1.31	0.25	0.39	65.4	61.9	81.2	77.6
0.927	0.912	-0.11	-0.13	67.6	66.9	61	62.7
100	1.17	6.64	0.23		3.7	4.3	9.7
1.087	1.306	0.12	0.39	69.4	58.8	76.7	75.5
0.849	0.829	-0.24	-0.27	111.3	113.6	94.1	94.4
0.991	0.755	-0.01	-0.4	41	48	36.2	40.7
0.602	1.056	-0.73	0.08	8.9	5.5	5.8	5.4
1.053	0.773	0.08	-0.37	139.8	159	122.8	147.3
0.818	0.827	-0.29	-0.27	236	232.6	192.2	193.1
0.653	0.714	-0.62	-0.49	1511.5	1452.6	1036.8	986.5
1	1.06	0	0.08	344.9	316.3	335.2	345
1.175	0.898	0.23	-0.16	77.5	87.6	78.7	91.1
1.471	1.505	0.56	0.59	27.3	28.6	43.1	40.1
100	100	6.64	6.64			1.5	1.6
1.112	1.021	0.15	0.03	192.4	186.4	190.4	213.9
0.704	0.886	-0.51	-0.17	3.2	8.1	7.2	2.3
1.559	1.467	0.64	0.55	84.8	88	129.1	132.2
0.482	0.767	-1.05	-0.38	3.1	3.2	2.4	1.5
100	0.754	6.64	-0.41		2.6	2	2.3
1.435	1.006	0.52	0.01	55.2	65	65.3	79.1
1.299	0.962	0.38	-0.06	16.7	19.3	18.6	21.7
0.715	0.727	-0.48	-0.46	123.4	127.1	92.4	88.3
1.605	1.673	0.68	0.74	29.5	29.9	50	47.4
100	100	6.64	6.64			2.9	1.9
0.648	1.572	-0.63	0.65	8.1	4.1	6.4	5.3

0.785	0.579	-0.35	-0.79	35.2	30.4	17.6	27.6
1.807	0.56	0.85	-0.84	6	9.5	5.3	10.8
0.624	0.587	-0.68	-0.77	70.1	85.2	50.1	43.7
0.173	0.591	-2.53	-0.76	10.5	14.8	8.7	1.8
	0.814		-0.3		2.1	1.7	
0.955	0.821	-0.07	-0.29	94.2	95	77.9	90
1.12	1.16	0.16	0.21	24.2	24	27.9	27.1
0.757	0.859	-0.4	-0.22	182.2	172.9	148.5	137.9
0.372	0.469	-1.43	-1.09	5.8	4.6	2.1	2.2
0.921	1.331	-0.12	0.41	2.1	1.6	2.1	1.9
2.413	0.527	1.27	-0.92	2.3	6.2	3.2	5.5
0.812	0.875	-0.3	-0.19	19	12.6	11.1	15.4
0.758	0.867	-0.4	-0.21	472.4	431.1	373.7	357.9
1.161	1.116	0.21	0.16	6	5	5.6	7
1.424	1.582	0.51	0.66	114.5	113.1	178.9	163.1
2.163	1.778	1.11	0.83	26.8	29.1	51.8	57.9
1.76	1.451	0.82	0.54	43.8	57.2	83	77.1
0.778	0.798	-0.36	-0.33	400.8	387	308.8	311.7
0.848	0.899	-0.24	-0.15	56.9	55.4	49.9	48.3
3.357	2.799	1.75	1.48	14.8	15.6	43.6	49.6
1.426	1.301	0.51	0.38	6.3	9.1	11.9	9
0.823	0.918	-0.28	-0.12	194.8	201.8	185.2	160.4
2.397	1.593	1.26	0.67	28.1	36.6	58.3	67.3
1.953	1.622	0.97	0.7	90	100.5	163	175.9
100	1.604	6.64	0.68		2.3	3.7	8.3
2.106	2.032	1.07	1.02	37.8	38.4	78	79.6
2.362	1.981	1.24	0.99	15.1	17.7	35.1	35.6
1.677	1.831	0.75	0.87	15.2	13.9	25.5	25.6
1.493	1.226	0.58	0.29	5.4	3.9	4.7	8
4.324	1.525	2.11	0.61	2.3	3.8	5.8	9.8
	0.01		-6.64		1.9		
100	0.936	6.64	-0.1		2.6	2.4	2.2
2.126	1.55	1.09	0.63	47	54.7	84.8	100
0.702	0.767	-0.51	-0.38	816.4	743.1	569.9	572.9
0.914	0.99	-0.13	-0.02	164.2	154.9	153.2	150
100		6.64					1.7
0.948	0.907	-0.08	-0.14	361.1	353.8	321.1	342.3

0.892	0.89	-0.16	-0.17	522.7	500.9	446.1	466.4
1.84	0.822	0.88	-0.28	7.1	11.7	9.6	13.1
1.028	0.962	0.04	-0.06	191.9	199.1	191.6	197.3
1.011	0.938	0.02	-0.09	406.8	422.8	396.8	411.3
1.334	1.446	0.42	0.53	3.1	4.2	6.1	4.1
1.186	1.622	0.25	0.7	3.1	3.5	5.7	3.7
	100		6.64			2	
1.057	0.892	0.08	-0.17	54.3	54.2	48.3	57.4
	1.027		0.04		2.2	2.2	
1.251	1.098	0.32	0.14	2.9	3.7	4.1	3.7
2.924	0.821	1.55	-0.28	2.1	5.3	4.3	6.2
100	0.951	6.64	-0.07		3.6	3.4	3.1
0.645	0.743	-0.63	-0.43	26.9	29	21.5	17.4
1.408	1.491	0.49	0.58	27.1	29.8	44.4	38.1
6.065	1.446	2.6	0.53	2.1	5.7	8.3	12.8
1.588	1.735	0.67	0.8	14.6	12.1	21	23.2
100	1.834	6.64	0.87		2.6	4.7	2.6
0.352	0.764	-1.51	-0.39	10.4	7.8	6	3.7
1.126	1.16	0.17	0.21	152.5	153.4	178	171.6
1.091	1.163	0.12	0.22	222.7	226.3	263.2	242.9
1.037	1.128	0.05	0.17	121.5	111.3	125.5	126
1.03	1.089	0.04	0.12	32.6	33.7	36.7	33.6
0.986	1.234	-0.02	0.3	142.9	80.4	99.2	140.9
1.048	1.221	0.07	0.29	43.8	50.3	61.5	45.9
100	0.824	6.64	-0.28		3	2.5	2.9
1.615	1.81	0.69	0.86	5.5	4.6	8.4	8.9
0.906	0.866	-0.14	-0.21	114.9	123.3	106.8	104
1.154	1.158	0.21	0.21	152	147.1	170.3	175.4
0.67	0.91	-0.58	-0.14	30.2	29	26.4	20.2
100		6.64					1.4
1.574	1.089	0.65	0.12	23.4	27.8	30.2	36.8

2.464	2.304	1.3	1.2	15.2	17.5	40.3	37.6
	1.232		0.3		1.5	1.8	
0.808	0.87	-0.31	-0.2	510.3	517.7	450.5	412.6
1.212	1.011	0.28	0.02	15.7	17.3	17.5	19.1
1.508	1.097	0.59	0.13	81.9	97.1	106.6	123.6
1.994	0.962	1	-0.06	14.6	27	26	29.1
0.787	0.869	-0.35	-0.2	152.5	145.2	126.2	120
0.798	0.823	-0.32	-0.28	814.2	798.4	656.8	650.1
	100		6.64			1.3	
0.852	0.905	-0.23	-0.14	54.8	57	51.5	46.7
0.805	1.086	-0.31	0.12	71.1	61.1	66.3	57.2
1.31	1.303	0.39	0.38	53.7	55.4	72.1	70.3
0.788	0.813	-0.34	-0.3	89.7	87.1	70.8	70.7
100	1.122	6.64	0.17		1.7	1.9	3.3
1.185	1.103	0.25	0.14	409.8	419.3	462.7	485.8
	1.545		0.63		1.8	2.7	
0.823	1.045	-0.28	0.06	68	61.3	64.1	56
100	0.844	6.64	-0.24		3.8	3.2	3.9
0.934	1.041	-0.1	0.06	668.2	616.7	641.8	624.4
1.028	1.022	0.04	0.03	45.7	45.5	46.5	47
3.548	1.51	1.83	0.59	12	24	36.2	42.6
1.063	1.165	0.09	0.22	188.2	170.6	198.7	199.9
2.195	1.404	1.13	0.49	2.8	4.2	5.9	6.1
	0.558		-0.84		2.9	1.6	
1.145	1.131	0.2	0.18	23	22.6	25.5	26.4
1.449	1.131	0.53	0.18	14	16.8	19	20.2
2.31	1.601	1.21	0.68	5.2	7.7	12.4	12
0.366	0.358	-1.45	-1.48	51.7	58.8	21.1	19
0.897	0.774	-0.16	-0.37	43.8	50.6	39.1	39.3
0.832	0.911	-0.26	-0.13	210.7	227.9	207.7	175.4
0.98	1.237	-0.03	0.31	34.7	35.5	43.9	34
0.927	0.908	-0.11	-0.14	225.2	225.9	205.1	208.7
1.145	1.074	0.19	0.1	217.7	216.9	232.8	249.2
2.464	1.075	1.3	0.1	2.6	3.3	3.6	6.4
	0.01		-6.64		2.3		
1.009	1.138	0.01	0.19	120.9	65.4	74.4	122
1.062	1.095	0.09	0.13	566.6	337.5	369.6	601.7
0.804	0.675	-0.31	-0.57	3.4	4.3	2.9	2.7
1.077	1.044	0.11	0.06	622.8	589.2	615.1	671
1.74	1.756	0.8	0.81	22.7	24.3	42.6	39.5
0.837	1.091	-0.26	0.13	182.8	155.8	169.9	153
1.777	1.727	0.83	0.79	16.4	16.6	28.7	29.1
	1.941		0.96		2.2	4.2	

0.976	1.199	-0.03	0.26	126.7	117.2	140.6	123.7
0.88	100	-0.18	6.64	2.6		2.4	2.3
0.826	1.735	-0.28	0.8	16.9	12.3	21.4	13.9
1.056	1.177	0.08	0.23	13	9.4	11.1	13.7
1.499	0.98	0.58	-0.03	12.5	16.5	16.2	18.7
1.303	1.006	0.38	0.01	77.5	98.9	99.5	101.1
1.157	1.244	0.21	0.32	174.1	164.9	205.2	201.3
2.255	2.032	1.17	1.02	17.5	13.8	28.1	39.5
0.668	0.832	-0.58	-0.27	19.3	18.9	15.7	12.9
0.818	0.821	-0.29	-0.28	160.6	155	127.3	131.3
	100		6.64			1.9	
2.834	1.893	1.5	0.92	6.3	10.4	19.6	17.9
100	2.238	6.64	1.16		1.8	4	3.2
0.67	1.071	-0.58	0.1	6.8	4.3	4.6	4.6
1.564	1.423	0.64	0.51	16.9	19.9	28.3	26.4
0.786	0.756	-0.35	-0.4	132.4	125.9	95.2	104
1.368	0.612	0.45	-0.71	22.7	39	23.9	31.1
0.771	0.762	-0.37	-0.39	11.8	14.2	10.8	9.1
	0.874		-0.19		1.9	1.7	
1.474	1.01	0.56	0.01	5.2	5.2	5.2	7.7
0.587	1.318	-0.77	0.4	3.9	3.1	4	2.3
0.811	0.794	-0.3	-0.33	159.9	173.3	137.7	129.7
1.689	0.961	0.76	-0.06	10.5	20.5	19.7	17.8
0.745	0.715	-0.43	-0.48	72.7	77.1	55.1	54.1
1.044	0.983	0.06	-0.02	64.4	56.7	55.8	67.3
1.703	1.376	0.77	0.46	19	17.4	24	32.3
1.79	0.891	0.84	-0.17	13.1	20.1	17.9	23.5
2.089	0.899	1.06	-0.15	9.9	19.4	17.5	20.7
0.381	1.626	-1.39	0.7	6	4.7	7.6	2.3
1.106	0.937	0.15	-0.09	53.4	39.3	36.8	59
100	1.326	6.64	0.41		2	2.6	1.6
1.639	1.289	0.71	0.37	31.1	34.2	44.1	51
0.669	0.761	-0.58	-0.39	109.2	110.7	84.2	73.1
1.327	1.143	0.41	0.19	183.5	183.2	209.4	243.5
1.608	1.114	0.69	0.16	26.3	45.1	50.2	42.3
0.658	0.683	-0.6	-0.55	42.3	50.4	34.4	27.9
1.276	1.288	0.35	0.36	71.9	72.1	92.8	91.7
1.13	1.373	0.18	0.46	23	19.4	26.7	26
100	0.615	6.64	-0.7		4.1	2.5	3.4
0.753	0.814	-0.41	-0.3	5326.4	5065.3	4124.3	4011.6

0.701	0.661	-0.51	-0.6	45.7	48.7	32.2	32.1
1.007	0.845	0.01	-0.24	113.6	127.2	107.5	114.3
	0.01		-6.64		2		
0.977	0.972	-0.03	-0.04	21.7	20.9	20.3	21.2
0.654	0.729	-0.61	-0.46	102.5	126.6	92.3	67
0.841	0.911	-0.25	-0.13	34.2	34.3	31.2	28.8
2.723	2.001	1.45	1	19.8	27.3	54.7	53.9
0.788	1.175	-0.34	0.23	27.1	17	19.9	21.4
0.747	0.777	-0.42	-0.36	100.7	98.9	76.9	75.3
0.869	0.758	-0.2	-0.4	62.3	65.9	49.9	54.1
	0.01		-6.64		2.3		
0.894	1.082	-0.16	0.11	16.2	16.2	17.5	14.5
	100		6.64			1.5	
0.863	0.95	-0.21	-0.07	5	2.3	2.2	4.3
100		6.64					1.5
100	0.597	6.64	-0.74		4	2.4	4
	100		6.64			2.1	
1.026	0.947	0.04	-0.08	5148.6	5572	5277.4	5281.1
2.127	2.518	1.09	1.33	59	48.6	122.3	125.6
1.069	1.106	0.1	0.14	55.3	49.6	54.8	59.2
1.049	1.105	0.07	0.14	183.1	179.1	197.9	192.1
1.939	1.304	0.96	0.38	9.2	11.5	15	17.9
100		6.64					1.6
2.112	1.523	1.08	0.61	8.8	9.5	14.4	18.5
100	1.879	6.64	0.91		1.8	3.4	2.3
0.493	1.026	-1.02	0.04	6.5	5	5.1	3.2
0.664	0.456	-0.59	-1.13	5.7	8.1	3.7	3.8
1.115	1.077	0.16	0.11	81.8	76.2	82.1	91.1
1.126	0.685	0.17	-0.55	7.3	10.2	7	8.2
	1.008		0.01		1.9	1.9	
1.682	1.689	0.75	0.76	126.4	131.4	221.9	212.5
2.676	2.12	1.42	1.08	14.8	18.6	39.4	39.5
0.937	0.781	-0.09	-0.36	65.2	80.8	63.1	61.1
2.707	1.39	1.44	0.48	12.7	22	30.6	34.3
1.429	1.316	0.52	0.4	148.1	146.1	192.3	211.7
	0.854		-0.23		2	1.7	
1.126	1.064	0.17	0.09	43.3	41.3	44	48.8

1.436	1.247	0.52	0.32	49	49.8	62.1	70.3
100	1.602	6.64	0.68		2	3.2	4.5
1.092	1.243	0.13	0.31	313.6	289.6	359.8	342.6
1.245	1.446	0.32	0.53	95.2	80.3	116.1	118.5
0.902	0.914	-0.15	-0.13	62.1	71	64.9	56.1
0.682	0.384	-0.55	-1.38	5.2	6.7	2.6	3.5
0.805	0.928	-0.31	-0.11	517.2	457.6	424.5	416.1
100	0.943	6.64	-0.08		6.2	5.9	3.2
0.991	1.416	-0.01	0.5	24.7	21.4	30.3	24.4
	0.664		-0.59		2.8	1.8	
1.386	1.201	0.47	0.26	15.4	22	26.5	21.4
1.865	1.103	0.9	0.14	53.7	85.8	94.7	100.1
1.723	1.142	0.78	0.19	6.2	11.1	12.7	10.6
0.83	0.866	-0.27	-0.21	90.5	95.9	83.1	75.1
1.296	1.044	0.37	0.06	15.2	18	18.8	19.8
1.001	0.91	0	-0.14	276.6	285.5	259.7	276.8
0.726	0.818	-0.46	-0.29	51.3	59.4	48.6	37.2
0.585	0.635	-0.77	-0.66	121.3	122.7	77.8	71
0.634	0.583	-0.66	-0.78	523.8	557.4	325.2	332.1
2.156	1.404	1.11	0.49	2.6	3.1	4.4	5.6
1.227	0.985	0.29	-0.02	61.2	75.1	74	75
0.994	0.91	-0.01	-0.14	113.6	104.3	94.9	112.8
0.909	1.004	-0.14	0.01	1210.6	1359.8	1364.8	1100.1
1.09	1.148	0.12	0.2	52.4	55.7	64	57.1
100	0.9	6.64	-0.15		6.6	5.9	5
100	0.985	6.64	-0.02		8.9	8.8	9.6
1.422	1.294	0.51	0.37	31.6	32.2	41.6	45
0.796	0.727	-0.33	-0.46	178	187.9	136.7	141.6
	0.01		-6.64		1.8		
1.006	0.865	0.01	-0.21	17	15.8	13.6	17.1
1.51	0.941	0.59	-0.09	11.2	17.9	16.8	16.9
4.019	1.672	2.01	0.74	5	11.1	18.6	20.2
100	2.11	6.64	1.08		2	4.3	5.7
100	1.44	6.64	0.53		2.1	3	4.3

0.974	0.993	-0.04	-0.01	47.7	50.3	49.9	46.5
1.176	1.293	0.23	0.37	295.6	281.1	363.5	347.7
0.981	0.854	-0.03	-0.23	124.4	137.4	117.3	122.1
1.317	1.21	0.4	0.28	10.1	10.7	12.9	13.2
1.413	0.971	0.5	-0.04	20.3	29.3	28.4	28.7
0.88	0.01	-0.18	-6.64	2.6	3.1		2.3
1.234	1.283	0.3	0.36	226.9	209.9	269.3	280
0.924	0.938	-0.11	-0.09	16.1	13.3	12.5	14.8
	1.225		0.29		1.8	2.2	
2.257	1.823	1.17	0.87	4.7	6.2	11.3	10.6
	1.059		0.08		3	3.2	
0.816	1.55	-0.29	0.63	10.2	5.7	8.9	8.3
100	1.289	6.64	0.37		3.4	4.3	8.6
0.828	1.017	-0.27	0.02	8.3	6.5	6.6	6.9
0.952	0.867	-0.07	-0.21	547.2	590.4	511.6	520.7
1.641	1.026	0.71	0.04	24.5	29.1	29.9	40.2
0.91	0.947	-0.14	-0.08	314.1	281.3	266.3	285.8
1.272	1.355	0.35	0.44	5	2.7	3.6	6.4
5.585	1.715	2.48	0.78	2.4	5.9	10.2	13.6
0.929	1.263	-0.11	0.34	4.1	3.4	4.3	3.8
2.686	1.826	1.43	0.87	6.2	9.3	16.9	16.6
3.62	1.786	1.86	0.84	2.3	4.1	7.4	8.2
1.21	0.951	0.27	-0.07	16.7	18.8	17.9	20.2
2.115	2.325	1.08	1.22	71.1	57.1	132.7	150.3
	100		6.64			2.9	
2.136	1.966	1.09	0.98	33.1	39.8	78.2	70.7
1.146	1.268	0.2	0.34	1296.4	1257.4	1594.2	1485.4
1.265	0.967	0.34	-0.05	62.9	84.7	81.9	79.6
0.931	0.925	-0.1	-0.11	90.4	81.8	75.7	84.2
1.738	1.337	0.8	0.42	12.8	7	9.4	22.3
0.757	0.824	-0.4	-0.28	681.2	682.5	562.2	515.9
1.177	0.921	0.24	-0.12	9.9	7.8	7.2	11.6
	1.085		0.12		1.8	1.9	
0.523	0.766	-0.93	-0.38	6.3	5.8	4.4	3.3
1.134	1.033	0.18	0.05	225	248.4	256.5	255.2
100	1.728	6.64	0.79		3.4	5.9	2.1
	100		6.64			1.3	
100	2.128	6.64	1.09		2.1	4.6	5.5
1.772	1.911	0.83	0.93	22.5	18.7	35.7	40
1.659	1.803	0.73	0.85	2.3	2.3	4.2	3.8
0.827	1.137	-0.27	0.19	185.1	153.6	174.7	153
	0.01		-6.64		1.8		
1.18	1.279	0.24	0.35	150.5	128.6	164.5	177.6
1.626	1.245	0.7	0.32	61.2	88.2	109.8	99.5
1.39	1.533	0.47	0.62	232.8	210	321.9	323.5

0.979	0.957	-0.03	-0.06	3.7	3.9	3.7	3.7
1.196	0.713	0.26	-0.49	10.2	9.6	6.9	12.2
100	100	6.64	6.64			3	1.6
0.866	1.012	-0.21	0.02	16.9	12.8	12.9	14.6
1.014	0.701	0.02	-0.51	27.6	46.6	32.7	28
0.73	0.905	-0.45	-0.14	13.1	13.5	12.2	9.6
1.383	1.607	0.47	0.68	32	29.8	47.9	44.2
1.372	1.085	0.46	0.12	47.9	52.9	57.4	65.7
100	1.437	6.64	0.52		1.9	2.8	2.6
0.936	1.317	-0.09	0.4	34.4	27.2	35.8	32.2
1.004	0.947	0.01	-0.08	25.1	31.3	29.6	25.2
	1.246		0.32		1.7	2.1	
0.747	0.822	-0.42	-0.28	10.7	7.9	6.5	8
1.361	1.416	0.44	0.5	9.7	8	11.3	13.2
3.036	0.734	1.6	-0.45	2.6	7.1	5.2	7.9
3.297	1.998	1.72	1	3.1	3.6	7.2	10.2
0.617	0.699	-0.7	-0.52	595.7	558.1	389.9	367.5
1.657	1.678	0.73	0.75	120.2	118.7	199.3	199.1
1.215	1.105	0.28	0.14	131.2	136	150.3	159.4
1.066	0.709	0.09	-0.5	48.5	59.3	42	51.7
1.149	1.077	0.2	0.11	122.8	126.6	136.3	141.1
1.156	1.128	0.21	0.17	72.7	69.4	78.2	84
1.32	1.051	0.4	0.07	16.9	20.2	21.2	22.3
1.605	1.635	0.68	0.71	115.2	101.5	165.9	184.9
1.483	1.44	0.57	0.53	157.4	154.1	221.9	233.4
1.116	1.041	0.16	0.06	110.3	111.6	116.2	123.1
0.992	0.948	-0.01	-0.08	202.1	220	208.5	200.5
0.905	0.797	-0.14	-0.33	3.4	2.8	2.3	3.1
1.071	0.776	0.1	-0.37	29.5	29.1	22.5	31.6
1.443	1.552	0.53	0.63	3.2	3	4.7	4.7
0.892	1.528	-0.16	0.61	27.3	19.3	29.6	24.3
0.804	0.714	-0.31	-0.49	3.4	3.4	2.4	2.7
0.01	100	-6.64	6.64	2.4		2.1	
100	0.768	6.64	-0.38		2.3	1.8	1.8

2.346	0.937	1.23	-0.09	1.9	4.8	4.5	4.6
1.202	0.961	0.27	-0.06	64.2	61.9	59.5	77.2
8.122	0.859	3.02	-0.22	2.1	12.1	10.4	17.1
100	0.644	6.64	-0.63		2.6	1.6	1.6
1.214	0.837	0.28	-0.26	27.7	34	28.4	33.7
1.281	1.273	0.36	0.35	19.8	21	26.7	25.4
0.915	0.948	-0.13	-0.08	82.7	85.9	81.5	75.7
0.927	0.91	-0.11	-0.14	1384.2	1372.9	1249.3	1282.6
1.267	1.384	0.34	0.47	141.9	130.8	181.1	179.8
0.966	0.971	-0.05	-0.04	15.2	16.4	15.9	14.7
100	1.138	6.64	0.19		4.3	4.9	3.1
0.823	0.755	-0.28	-0.41	129.9	132.4	99.9	106.9
1.252	0.853	0.32	-0.23	53.5	62.7	53.5	67
0.944	1.151	-0.08	0.2	68	64.4	74.1	64.2
1.526	0.826	0.61	-0.28	25.1	42.6	35.2	38.4
1.095	1.05	0.13	0.07	63.1	68.8	72.2	69.1
2.408	1.097	1.27	0.13	3.1	9.8	10.7	7.4
1.004	1.361	0.01	0.44	113.4	89.3	121.6	113.8
0.01		-6.64		1.9			
1.487	1.578	0.57	0.66	58.1	50.4	79.5	86.3
100	0.01	6.64	-6.64		2.6		2.2
3.032	1.035	1.6	0.05	2.1	6	6.2	6.4
0.743	0.773	-0.43	-0.37	23.2	25	19.4	17.2
0.864	0.857	-0.21	-0.22	3.6	5.3	4.6	3.1
0.964	0.986	-0.05	-0.02	455.2	438.3	432.1	438.8
0.918	0.953	-0.12	-0.07	257.6	252.4	240.5	236.5
1.414	0.971	0.5	-0.04	19.5	23.7	23	27.5
0.901	0.993	-0.15	-0.01	45.7	43.4	43.2	41.2
0.778	0.79	-0.36	-0.34	9.2	10.7	8.5	7.2
0.954	1.012	-0.07	0.02	92.8	89.6	90.7	88.5
0.827	0.728	-0.27	-0.46	39.9	43.5	31.6	33
1.188	1.275	0.25	0.35	15.6	12.8	16.3	18.5
0.217	1.739	-2.21	0.8	10.5	2.8	4.9	2.3
	0.01		-6.64		1.8		
100	1.722	6.64	0.78		3.8	6.5	4.7
4.259	2.936	2.09	1.55	3.2	4	11.9	13.8

100	1.687	6.64	0.75		2.6	4.3	4.2
1.095	1.328	0.13	0.41	26.3	26.6	35.3	28.8
0.804	0.929	-0.32	-0.11	83.5	86.3	80.2	67.1
100	1.467	6.64	0.55		3.4	5	4.8
1.219	1.634	0.29	0.71	10.9	10.8	17.6	13.2
1.674	1.903	0.74	0.93	7.3	5	9.5	12.2
1.255	1.151	0.33	0.2	16.4	18.4	21.2	20.6
100	2.252	6.64	1.17		2.1	4.7	2.2
0.544	0.728	-0.88	-0.46	3.6	2.9	2.1	1.9
1.107	1.102	0.15	0.14	807.5	724.5	798.3	893.9
1.193	1.224	0.26	0.29	41.5	36.1	44.3	49.6
	0.98		-0.03		1.8	1.8	
0.01	1.064	-6.64	0.09	2.1	2.1	2.2	
	100		6.64			1.7	
1.453	0.849	0.54	-0.24	30.2	41.6	35.4	43.8
0.706	0.714	-0.5	-0.49	50.3	59.1	42.2	35.5
0.715	0.718	-0.48	-0.48	9.9	12.6	9	7.1
1.022	1.244	0.03	0.32	20.4	18.1	22.5	20.9
0.664	0.797	-0.59	-0.33	11.5	8.4	6.7	7.7
3.687	3.138	1.88	1.65	3.4	4.6	14.3	12.6
7.537	2.476	2.91	1.31	6.7	14.6	36.1	50.1
5.441	2.897	2.44	1.53	10.2	15.7	45.4	55.6
1.898	1.837	0.92	0.88	167.9	160.1	294.2	318.7
1.738	1.888	0.8	0.92	101.4	96.2	181.6	176.2
2.08	1.984	1.06	0.99	152.8	159.9	317.1	317.8
1.827	2.002	0.87	1	67	58.7	117.5	122.4
1.841	1.456	0.88	0.54	2.1	3.3	4.8	3.9
0.743	0.809	-0.43	-0.31	221.4	207.5	167.8	164.5
1.029	0.839	0.04	-0.25	19.3	20.2	16.9	19.9
1.408	100	0.49	6.64	2.9		3.2	4.1
0.678	0.699	-0.56	-0.52	395.3	409.8	286.5	268
1.116	0.615	0.16	-0.7	20.8	26.9	16.6	23.2
1.163	1.023	0.22	0.03	7.5	7	7.2	8.7
1.039	0.857	0.06	-0.22	41.5	54.7	46.9	43.2
100	0.01	6.64	-6.64		3.3		1.8
0.903	0.948	-0.15	-0.08	2429.4	2424.6	2297.6	2194.6
1.051	1.09	0.07	0.12	115.3	104.3	113.7	121.3
1.237	1.07	0.31	0.1	60.2	70	74.8	74.5
0.925	1.026	-0.11	0.04	84.4	73.7	75.6	78
0.915	1.107	-0.13	0.15	55.8	48.7	54	51

0.982	0.76	-0.03	-0.4	1224.4	1508.4	1146.5	1202.4
2.258	1.931	1.17	0.95	25.8	28.6	55.2	58.2
0.01	0.576	-6.64	-0.8	3.1	3.6	2.1	
0.844	0.824	-0.25	-0.28	350.4	368.4	303.5	295.6
0.503	1.58	-0.99	0.66	3.4	3.1	4.9	1.7
1.359	1.169	0.44	0.23	20.9	22.6	26.4	28.4
1.665	1.648	0.74	0.72	30.2	33	54.3	50.2
1.294	1.412	0.37	0.5	40.1	34.1	48.2	51.8
2.273	1.826	1.18	0.87	17.7	17.1	31.2	40.2
1.243	1.296	0.31	0.37	83.2	74.9	97.1	103.5
0.955	0.909	-0.07	-0.14	2.3	2.5	2.3	2.2
100	1.06	6.64	0.08		1.5	1.6	4.2
	1.59		0.67		1.9	3.1	
100	0.834	6.64	-0.26		2.9	2.4	3.1
1.083	1.063	0.11	0.09	208	202.8	215.6	225.2
0.856	0.875	-0.22	-0.19	104.1	98.6	86.2	89.2
0.844	0.911	-0.24	-0.13	473.7	454.9	414.3	399.9
1.383	1.173	0.47	0.23	23.2	20.9	24.6	32.1
100	0.644	6.64	-0.64		3.1	2	2.7
	1.387		0.47		2.3	3.2	
0.658	0.605	-0.6	-0.73	657.3	654.5	395.9	432.8
	0.667		-0.58		2.4	1.6	
100	1.499	6.64	0.58		4.4	6.6	7.8
1.001	0.925	0	-0.11	171.6	182.1	168.5	171.7
2.112	0.922	1.08	-0.12	10.7	16.1	14.9	22.6
1.59	1.141	0.67	0.19	25.1	29.7	33.9	40
0.01	1.403	-6.64	0.49	2.4	3.3	4.6	
100	1.437	6.64	0.52		2.4	3.4	1.7
0.94	0.877	-0.09	-0.19	305.5	299.4	262.7	287.2
1.286	1.161	0.36	0.22	210.6	240.1	278.9	270.7
100	1.846	6.64	0.88		2.1	3.8	1.8
5.891	1.372	2.56	0.46	3.1	8.1	11.1	18.2
1.284	1.255	0.36	0.33	2.8	2.7	3.4	3.5
0.996	0.87	-0.01	-0.2	57.1	55.6	48.4	56.9
3.381	2.677	1.76	1.42	105.8	123.6	330.9	357.6
1.16	1.081	0.21	0.11	319.9	326.9	353.3	371.1
100	1.976	6.64	0.98		2.8	5.5	4.1
0.469	0.487	-1.09	-1.04	11.2	10.6	5.1	5.3
0.768	0.656	-0.38	-0.61	14.3	14.6	9.6	11
0.882	0.915	-0.18	-0.13	442	488.6	446.9	389.7
0.833	0.831	-0.26	-0.27	219.3	219.6	182.6	182.6
	100		6.64			1.8	
1.256	1.353	0.33	0.44	128.5	120.2	162.7	161.4
1.755	2.002	0.81	1	23	17.5	35	40.4
0.01		-6.64		2.6			

2.445	1.616	1.29	0.69	6.2	11.3	18.3	15.1
0.952	0.855	-0.07	-0.23	371.5	409.7	350.4	353.5
1.064	1.468	0.09	0.55	7	3.9	5.7	7.4
	0.01		-6.64		1.4		
	0.77		-0.38		3.9	3	
100	0.982	6.64	-0.03		3.2	3.1	2.2
0.677	0.835	-0.56	-0.26	1345.3	1178.5	983.9	910.6
0.9	0.943	-0.15	-0.09	132.2	132.8	125.2	119
1.223	1.122	0.29	0.17	200.5	247.9	278.3	245.2
100	0.995	6.64	-0.01		2.9	2.9	2.7
0.921	0.805	-0.12	-0.31	54.7	55.3	44.5	50.4
1.307	1.149	0.39	0.2	126.2	131.7	151.3	164.9
0.888	0.844	-0.17	-0.25	95.4	102	86	84.7
0.974	0.864	-0.04	-0.21	106.7	110.3	95.3	103.9
100	1.028	6.64	0.04		4.8	4.9	7
0.821	1.1	-0.28	0.14	1.9	1.9	2.1	1.6
1.348	0.919	0.43	-0.12	9.6	16.7	15.3	12.9
1.073	1.002	0.1	0	83.9	84.1	84.3	90
1.686	1.072	0.75	0.1	6.2	7.5	8	10.4
1.738	0.99	0.8	-0.01	21.4	30.9	30.6	37.2
0.934	0.715	-0.1	-0.48	8.4	11.1	7.9	7.9
1.474	1.174	0.56	0.23	29.5	38.4	45.2	43.5
	0.489		-1.03		3.6	1.8	
100	2.228	6.64	1.16		2	4.4	5.5
1.673	1.281	0.74	0.36	120.9	142.4	182.5	202.2
100		6.64					4
2.553	1.741	1.35	0.8	47.4	62.7	109.1	120.9
1.83	1.12	0.87	0.16	2.4	2.5	2.8	4.5
0.657	0.732	-0.61	-0.45	125.4	127.7	93.4	82.3
0.904	0.727	-0.15	-0.46	131.4	137.6	100.1	118.8
0.835	0.745	-0.26	-0.42	131.4	134.2	100	109.7
0.978	0.893	-0.03	-0.16	2.9	3.6	3.2	2.9
0.889	1.182	-0.17	0.24	3.1	2.7	3.2	2.7
0.782	0.964	-0.36	-0.05	99.9	90.8	87.5	78.1
0.922	1.006	-0.12	0.01	529.2	514.6	517.9	488.1
1.432	0.921	0.52	-0.12	4.7	4.2	3.9	6.7
0.865	0.875	-0.21	-0.19	421.9	415.5	363.5	364.8

0.899	1.167	-0.15	0.22	36.3	25.9	30.3	32.7
1.002	0.819	0	-0.29	138.5	136.2	111.5	138.9
100	0.554	6.64	-0.85		3.9	2.1	3.5
1.828	1.509	0.87	0.59	19.3	27.1	41	35.3
	1.045		0.06		1.5	1.6	
1.392	1.301	0.48	0.38	35.5	37.7	49	49.4
100	100	6.64	6.64			2	1.7
100	1.406	6.64	0.49		2.1	3	2.1
0.976	0.788	-0.03	-0.34	20.1	19.3	15.2	19.6
	0.01		-6.64		2.7		
0.995	0.952	-0.01	-0.07	4.7	4.9	4.7	4.7
0.743	1.022	-0.43	0.03	2.9	3.7	3.8	2.2
0.977	0.819	-0.03	-0.29	138.5	151.2	123.9	135.3
0.994	0.724	-0.01	-0.47	43.6	50.2	36.3	43.4
0.991	0.906	-0.01	-0.14	50.4	50.5	45.8	50
0.804	100	-0.31	6.64	2.3		1.8	1.8
0.966	1.621	-0.05	0.7	18.3	11.7	19	17.7
1.868	1.343	0.9	0.43	8.4	19.2	25.8	15.8
100	100	6.64	6.64			4.3	3.7
0.814	0.945	-0.3	-0.08	209.6	199.6	188.6	170.6
2.036	2.025	1.03	1.02	89.1	90.6	183.5	181.3
0.961	0.925	-0.06	-0.11	72.8	68.8	63.6	70
1.408	1.061	0.49	0.08	2.8	4.3	4.6	3.9
1.024	0.731	0.03	-0.45	115.5	145.9	106.6	118.3
1.977	1.183	0.98	0.24	7.6	10.2	12	15.1
	100		6.64			3.5	
0.954	1.013	-0.07	0.02	372.8	333.7	337.9	355.7
3.564	2.26	1.83	1.18	26	25.8	58.4	92.5
1.023	1.012	0.03	0.02	127.5	122.4	124	130.4
0.991	0.902	-0.01	-0.15	4.4	5.6	5	4.3
2.086	1.131	1.06	0.18	26.9	46	52	56.2
2.048	1.74	1.03	0.8	3.6	6.5	11.2	7.3
1.209	1.342	0.27	0.42	83.1	70.6	94.7	100.4
0.884	1.164	-0.18	0.22	181.7	143.7	167.3	160.7
	100		6.64			3.2	

	100		6.64			1.8	
0.984	1.819	-0.02	0.86	12.7	8	14.5	12.4
0.928	1.151	-0.11	0.2	55.2	44.2	50.9	51.2
	0.01		-6.64		2.3		
2.306	2.265	1.21	1.18	15.2	15.6	35.4	35.2
0.709	0.986	-0.5	-0.02	41.2	24.8	24.4	29.2
1.632	1.171	0.71	0.23	48.8	62	72.6	79.7
1.518	1.424	0.6	0.51	240.2	237.2	337.7	364.6
0.981	1.323	-0.03	0.4	28.9	31	41	28.3
0.747	0.8	-0.42	-0.32	139.3	122.8	98.3	104.1
0.89	0.678	-0.17	-0.56	3310.9	4330.8	2935.9	2946.2
1.589	1.584	0.67	0.66	47.9	47.9	75.8	76.1
1.348	1.191	0.43	0.25	11.4	13.2	15.8	15.3
2.387	1.405	1.26	0.49	37.8	61.5	86.5	90.2
2.188	1.603	1.13	0.68	7.5	10.5	16.8	16.3
100	1.908	6.64	0.93		3.7	7.1	7.4
1.206	1.239	0.27	0.31	208.5	210.1	260.4	251.3
100	100	6.64	6.64			2.3	2.2
1.556	0.927	0.64	-0.11	6.2	9.9	9.2	9.6
1.663	1.562	0.73	0.64	47.4	52.6	82.1	78.8
0.937	1.037	-0.09	0.05	213	202.3	209.7	199.6
3.754	1.709	1.91	0.77	2.4	3.7	6.2	9.1
2.431	0.973	1.28	-0.04	14	19.3	18.7	33.9
100	0.837	6.64	-0.26		2.8	2.3	1.6
1.173	0.742	0.23	-0.43	4.4	3.5	2.6	5.1
2.425	0.469	1.28	-1.09	2.9	5.7	2.7	7.1
1.277	1.624	0.35	0.7	30.5	26.4	42.9	38.9
0.735	0.796	-0.44	-0.33	55	58.9	46.9	40.4
1.331	1.079	0.41	0.11	29.5	36.9	39.8	39.3
0.766	0.776	-0.38	-0.37	358.7	330.4	256.4	274.9

1.168	1.078	0.22	0.11	33.7	29.3	31.6	39.4
1.323	1.251	0.4	0.32	37.6	35.3	44.2	49.8
0.848	1.056	-0.24	0.08	45.9	33.2	35	38.9
100	100	6.64	6.64			2.2	1.7
1.357	1.282	0.44	0.36	60.8	64.7	83	82.6
1.075	0.997	0.1	0	156.1	160.5	160.1	167.7
1.55	1.524	0.63	0.61	95.7	98.7	150.4	148.3
2.715	1.987	1.44	0.99	5.7	6.7	13.2	15.4
2.454	1.791	1.3	0.84	18	22.3	40	44.2
100	1.675	6.64	0.74		2	3.4	2.1
0.77	0.776	-0.38	-0.37	376.2	352.3	273.5	289.8
0.75	0.754	-0.42	-0.41	22.4	29.2	22	16.8
0.938	1.059	-0.09	0.08	217.7	201.6	213.5	204.3
1.283	1.291	0.36	0.37	23.8	22.5	29.1	30.6
100	1.122	6.64	0.17		2	2.3	2.3
1.389	0.834	0.47	-0.26	6.2	10.2	8.5	8.6
4.576	1.212	2.19	0.28	1.9	7.3	8.8	8.9
1.156	1.123	0.21	0.17	20.4	20.5	23	23.6
1.879	1.27	0.91	0.34	25.5	30	38	47.8
0.777	0.92	-0.36	-0.12	142.9	139.6	128.4	111.1
1.118	1.305	0.16	0.38	2.8	2.4	3.2	3.1
0.814	0.761	-0.3	-0.39	123.4	119.7	91.1	100.5
0.917	0.853	-0.13	-0.23	89.5	103.1	87.9	82.1
0.794	0.784	-0.33	-0.35	25.5	20.7	16.2	20.2
1.043	1.178	0.06	0.24	91.2	90.5	106.6	95.1
1.102	1.307	0.14	0.39	35.9	30.1	39.3	39.5
3.534	1.093	1.82	0.13	7.8	22.7	24.9	27.5
3.872	0.828	1.95	-0.27	1.9	5.6	4.6	7.5
100	0.766	6.64	-0.38		4	3.1	5.8
	1.018		0.03		2.4	2.5	
2.218	1.68	1.15	0.75	37.5	45.1	75.8	83.1
1.571	1.538	0.65	0.62	268.8	258.3	397.2	422.4
1.885	1.808	0.91	0.85	97.3	91.6	165.5	183.5
2.922	1.32	1.55	0.4	17.2	26.5	35	50.2
2.529	2.425	1.34	1.28	117	115.9	280.9	295.8
1.888	2.482	0.92	1.31	14.3	11.4	28.3	26.9
2.508	2.254	1.33	1.17	196.9	206.2	464.8	494
2.159	2.004	1.11	1	196.4	193.5	387.8	424.2
1.839	1.864	0.88	0.9	251.1	239.7	446.8	461.9
1.772	1.714	0.83	0.78	153.8	163.2	279.7	272.6
1.949	1.68	0.96	0.75	11.2	14.1	23.6	21.8
1.923	1.786	0.94	0.84	259.1	264.6	472.5	498.1
1.22	1.073	0.29	0.1	146.5	149	159.9	178.7
1.259	1.051	0.33	0.07	107.6	136.8	143.8	135.4

2.195	1.361	1.13	0.45	2.8	2.1	2.9	6.1
	1.028		0.04		2.1	2.2	
100	100	6.64	6.64			2.6	1.7
2.902	1.367	1.54	0.45	6.7	12.5	17.1	19.3
1.87	1.209	0.9	0.27	5.7	10.5	12.7	10.6
0.79	1.33	-0.34	0.41	14.6	11.7	15.5	11.5
1.327	1.306	0.41	0.39	550.2	549.8	718.2	729.9
1.06	0.901	0.08	-0.15	62	61.2	55.1	65.7
0.995	1.266	-0.01	0.34	208.6	172.1	218	207.5
	0.01		-6.64		2.3		
1.31	1.096	0.39	0.13	16.4	20.3	22.3	21.5
1.257	1.229	0.33	0.3	87.8	85.8	105.4	110.3
1.294	1.548	0.37	0.63	35.2	26.6	41.2	45.6
1.016	1.162	0.02	0.22	147.3	137.3	159.5	149.6
1.054	1.139	0.08	0.19	31.3	26.3	29.9	33
0.946	0.662	-0.08	-0.6	19.8	22.7	15	18.7
100	1.488	6.64	0.57		3.9	5.7	8.7
0.62	0.821	-0.69	-0.28	9.6	6	4.9	5.9
1.101	0.367	0.14	-1.45	23.8	27.5	10.1	26.3
1.04	0.778	0.06	-0.36	18.3	24.1	18.7	19.1
1.389	1.268	0.47	0.34	227.9	228.2	289.4	316.5
0.965	0.953	-0.05	-0.07	1122.6	1098	1046.3	1083
	0.747		-0.42		2.1	1.6	
100	0.595	6.64	-0.75		2.7	1.6	1.8
	0.691		-0.53		3.3	2.3	
1.596	1.388	0.67	0.47	2.4	2.8	3.9	3.9
100	1.906	6.64	0.93		1.8	3.4	1.8
0.948	1.004	-0.08	0.01	266.5	272.5	273.7	252.6
1.607	1.184	0.68	0.24	139.8	172.2	203.8	224.7
1.329	1.164	0.41	0.22	135.5	153.7	178.8	180
0.666	0.739	-0.59	-0.44	3156.4	3202.2	2365.3	2102
1.71	0.921	0.77	-0.12	67.6	99.8	91.9	115.7
1.427	1.747	0.51	0.8	5.8	3.6	6.3	8.3
0.852	0.958	-0.23	-0.06	236	212.4	203.4	201.2
0.711	0.736	-0.49	-0.44	67.8	65.7	48.3	48.2
0.804	0.866	-0.31	-0.21	113.9	94.1	81.5	91.6
0.867	0.66	-0.21	-0.6	105.9	114.6	75.7	91.8

0.797	0.88	-0.33	-0.18	49.2	40.6	35.7	39.2
1.568	0.999	0.65	0	3.6	3.3	3.3	5.6
1.54	0.496	0.62	-1.01	2.6	7.3	3.6	4
0.533	0.971	-0.91	-0.04	5.4	3.2	3.1	2.9
0.785	1.91	-0.35	0.93	4.2	3.5	6.7	3.3
0.992	0.909	-0.01	-0.14	449.7	491.6	447	446.3
13.918	8.695	3.8	3.12	5.7	8	69.2	79
1.76	1.622	0.82	0.7	42.5	42.8	69.3	74.8
1.222	1.343	0.29	0.43	131.7	106.6	143.2	161
100	2.635	6.64	1.4		1.7	4.5	5.7
1.848	2.792	0.89	1.48	7.8	5.2	14.4	14.4
100	2.241	6.64	1.16		2.8	6.2	2.2
1.208	1.046	0.27	0.06	10.9	14.4	15	13.1
0.667	1.492	-0.58	0.58	3.1	2.1	3.1	2.1
100	1.779	6.64	0.83		2.9	5.1	7.2
100	2.108	6.64	1.08		4.4	9.2	11.6
1.909	1.936	0.93	0.95	186.7	175.9	340.5	356.4
0.681	1.694	-0.55	0.76	5	3.5	6	3.4
100	1.26	6.64	0.33		1.7	2.1	1.9
1.234	0.86	0.3	-0.22	15.1	15.5	13.4	18.6
1.012	1.868	0.02	0.9	10.4	5.7	10.6	10.5
	100		6.64			3.5	
1.573	1.468	0.65	0.55	34.6	38	55.8	54.4
1.1	1.237	0.14	0.31	5.2	4.4	5.5	5.7
100	1.274	6.64	0.35		4.4	5.7	3.9
100	1.028	6.64	0.04		6.8	7	2.3
1.541	1.3	0.62	0.38	59.4	58.1	75.6	91.5
100	0.985	6.64	-0.02		3	2.9	1.5
0.828	1.29	-0.27	0.37	11	8.6	11	9.1
1.456	1.217	0.54	0.28	7.1	5.9	7.2	10.4
0.425	1.281	-1.24	0.36	10.2	7.4	9.4	4.3
1.26	1.059	0.33	0.08	13.1	12.6	13.3	16.6
100	1.173	6.64	0.23		2	2.3	2.1
1.245	1.34	0.32	0.42	14.8	11.9	15.9	18.4
100	1.622	6.64	0.7		1.8	2.9	3.2
0.01	2.356	-6.64	1.24	4.2	3	7	
100	1.331	6.64	0.41		2.1	2.8	5.1
10.505	2.05	3.39	1.04	2.1	10.8	22.1	22.2
1.616	1.606	0.69	0.68	205	204.3	328.1	331.3
1.354	1.744	0.44	0.8	2.1	2.3	4.1	2.9

100	2.012	6.64	1.01		1.7	3.4	1.8
2.07	1.739	1.05	0.8	24.7	29.2	50.7	51
2.205	1.827	1.14	0.87	18.3	19.8	36.1	40.4
1.595	1.423	0.67	0.51	81.8	87.8	124.9	130.4
0.589	0.855	-0.76	-0.23	7.9	7.5	6.4	4.7
100	1.14	6.64	0.19		4.3	4.9	7.9
1.173	1.018	0.23	0.03	13.6	16.9	17.2	16
2.816	0.755	1.49	-0.41	2.3	3.7	2.8	6.4
1.255	1.07	0.33	0.1	24.7	28.2	30.1	30.9
0.823	0.895	-0.28	-0.16	1020.2	758.9	679.3	840.1
	1.265		0.34		1.7	2.1	
0.988	0.988	-0.02	-0.02	61.5	62	61.3	60.7
1.813	0.5	0.86	-1	5.4	10.6	5.3	9.7
100	0.845	6.64	-0.24		2.1	1.8	1.8
1.405	1.135	0.49	0.18	38.6	41	46.5	54.2
3.232	1.508	1.69	0.59	7.1	10.3	15.6	23.1
1.494	0.876	0.58	-0.19	27.7	32.5	28.4	41.5
	0.892		-0.17		2.7	2.4	
0.828	0.955	-0.27	-0.07	13.8	10.3	9.8	11.4
0.01	1.277	-6.64	0.35	2.1	1.8	2.3	
0.01	100	-6.64	6.64	2.6		2.2	
	100		6.64			1.2	
0.845	0.991	-0.24	-0.01	4.9	3.7	3.7	4.1
0.99	0.892	-0.01	-0.17	131.1	137.6	122.7	129.7
1.53	0.886	0.61	-0.17	32.8	51.1	45.3	50.1
1.223	1.273	0.29	0.35	36.5	36	45.9	44.6
100	3.168	6.64	1.66		1.5	4.8	2.9
0.984	0.863	-0.02	-0.21	23.7	19	16.4	23.3
0.717	2.014	-0.48	1.01	8.9	3.3	6.7	6.4
0.97	0.949	-0.04	-0.08	8.6	7.4	7	8.3
1.57	0.951	0.65	-0.07	2.1	3	2.8	3.3
0.792	1.111	-0.34	0.15	243.3	190.3	211.5	192.6
1.629	1.725	0.7	0.79	101.5	93.2	160.9	165.5
0.774	0.689	-0.37	-0.54	70.6	90.2	62.1	54.6
100	2.278	6.64	1.19		2.3	5.1	1.8
	0.01		-6.64		1.9		
2.328	0.882	1.22	-0.18	2.1	3.1	2.7	4.9
1.76	1.146	0.82	0.2	2.3	4.9	5.7	4
100	1.108	6.64	0.15		1.9	2.1	2.2
0.874	0.829	-0.19	-0.27	148.8	154.3	127.8	130.1
0.994	1.084	-0.01	0.12	13.8	11.5	12.5	13.7
100	2.051	6.64	1.04		1.9	3.9	7.5
0.621	2.101	-0.69	1.07	2.8	3.5	7.3	1.7

1.516	0.9	0.6	-0.15	2.1	4.4	3.9	3.2
1.269	1.2	0.34	0.26	27.1	17.6	21.1	34.4
1.389	1.5	0.47	0.59	6	6.7	10	8.3
0.795	0.718	-0.33	-0.48	1643.8	1779.9	1278.8	1306.1
0.792	0.856	-0.34	-0.22	658	612.3	524.3	520.9
0.796	0.839	-0.33	-0.25	287.9	301.9	253.2	229.1
0.727	0.968	-0.46	-0.05	63.8	56.8	55	46.4
1.19	0.891	0.25	-0.17	56.6	70.8	63.1	67.4
	1.669		0.74		1.9	3.2	
1.661	0.67	0.73	-0.58	6.3	13.9	9.3	10.5
0.951	1.018	-0.07	0.03	206.8	196.5	200.1	196.8
0.366	0.783	-1.45	-0.35	16.5	14.2	11.1	6.1
0.84	0.906	-0.25	-0.14	111.8	103	93.3	93.9
1.075	1.333	0.1	0.41	84.5	67.1	89.4	90.9
1.643	1.286	0.72	0.36	14.1	13.3	17.1	23.2
1.521	0.805	0.6	-0.31	34.4	58.5	47.1	52.3
0.853	0.734	-0.23	-0.45	31.5	27.1	19.9	26.8
1.041	0.944	0.06	-0.08	357.2	361.6	341.2	371.7
	1.302		0.38		1.8	2.4	
0.734	0.801	-0.45	-0.32	369.7	386.8	309.8	271.2
1.064	1.226	0.09	0.29	400.2	384.4	471.2	425.7
1.541	1.086	0.62	0.12	9.4	13.8	15	14.5
0.587	0.55	-0.77	-0.86	5.8	8.6	4.8	3.4
1.311	0.832	0.39	-0.27	9.4	12.4	10.3	12.3
1.137	0.954	0.19	-0.07	96.2	116.2	110.8	109.4
1.107	1.302	0.15	0.38	32.6	22.9	29.9	36.1
1.07	1.554	0.1	0.64	39.3	32.3	50.3	42
0.863	1.239	-0.21	0.31	128.6	108.6	134.6	111
0.804	1.883	-0.31	0.91	5.7	3.4	6.5	4.6
100	100	6.64	6.64			2.1	1.5
	0.72		-0.47		2.5	1.8	
0.522	1.188	-0.94	0.25	5	7.2	8.6	2.6
0.981	1.109	-0.03	0.15	5334.1	5066.3	5618.1	5233.5
0.01	0.646	-6.64	-0.63	2.3	4.1	2.6	
1.182	1.083	0.24	0.11	237.2	264.9	286.7	280.3
0.829	0.932	-0.27	-0.1	65.9	61.4	57.3	54.6
1.003	0.83	0	-0.27	362.2	408.1	338.8	363.4

3.296	1.353	1.72	0.44	10.2	9.6	13	33.7
	1.245		0.32		2.1	2.6	
0.813	2.03	-0.3	1.02	7.3	4.2	8.4	5.9
100	1.763	6.64	0.82		2	3.6	3.7
0.774	0.868	-0.37	-0.2	281.8	263.1	228.3	218.2
2.397	1.443	1.26	0.53	12	18.8	27.1	28.8
1.834	2.213	0.88	1.15	5.4	3.7	8.1	9.8
100	1.03	6.64	0.04		2.7	2.8	2.3
1.201	0.853	0.26	-0.23	32.6	44.3	37.7	39.2
1.363	1.477	0.45	0.56	30.5	29.7	43.8	41.6
3.313	1.886	1.73	0.92	13.8	20.5	38.7	45.7
2.179	1.456	1.12	0.54	3.4	3.3	4.9	7.4
1.256	1.194	0.33	0.26	29.4	33.1	39.5	36.9
1.753	0.939	0.81	-0.09	16.5	26	24.4	29
1.532	1.268	0.62	0.34	2.8	2.8	3.6	4.2
0.978	1.07	-0.03	0.1	243	230.4	246.6	237.7
1.035	0.838	0.05	-0.25	2.8	4	3.4	2.9
1.714	1.728	0.78	0.79	93	98.6	170.4	159.3
0.738	0.74	-0.44	-0.43	325.7	319.3	236.4	240.3
1.042	1.307	0.06	0.39	45.6	37.6	49.1	47.5
1.09	0.856	0.12	-0.22	274.5	296.6	254	299.2
0.67	0.772	-0.58	-0.37	61.5	51.5	39.7	41.2
1.014	0.621	0.02	-0.69	30.2	47.3	29.3	30.6
0.48	0.59	-1.06	-0.76	192.6	174.9	103.2	92.5
1.651	0.766	0.72	-0.38	14.1	27.7	21.2	23.3
0.324	0.383	-1.63	-1.38	18.3	17.8	6.8	5.9
1.074	1.847	0.1	0.89	3.1	2.1	3.8	3.3
0.695	0.681	-0.52	-0.55	788.9	800.7	545.1	548.3
0.697	0.719	-0.52	-0.48	122.3	131.7	94.7	85.3
1.173	0.776	0.23	-0.37	17	20.2	15.7	20
0.925	0.735	-0.11	-0.44	14.4	12.2	9	13.4
0.282	0.34	-1.82	-1.56	24.7	26.5	9	7
0.48	1.066	-1.06	0.09	3.6	2.9	3.1	1.7
0.01	0.01	-6.64	-6.64	2.1	2.3		
100	1.335	6.64	0.42		2.2	3	2.1
	100		6.64			2	
1.32	0.425	0.4	-1.23	2.6	7.4	3.2	3.4
0.767	0.856	-0.38	-0.22	392.9	346.8	296.9	301.3
7.906	1.503	2.98	0.59	2.1	8.9	13.4	16.7
100	1.231	6.64	0.3		8	9.8	8.7

0.75	0.821	-0.41	-0.28	239.3	226.7	186.2	179.5
1.152	0.656	0.2	-0.61	7.1	17.1	11.2	8.2
100	1.377	6.64	0.46		2.1	2.9	2.1
3.55	1.723	1.83	0.78	3.7	5.5	9.4	13.2
100	1.964	6.64	0.97		4.6	9	11.4
1.011	1.388	0.02	0.47	36.8	32.3	44.8	37.2
2.511	1.217	1.33	0.28	9.7	24.7	30	24.4
1.064	0.68	0.09	-0.56	20	25.4	17.3	21.2
1.03	1.019	0.04	0.03	109	134	136.5	112.2
1.537	0.924	0.62	-0.11	28.2	32.9	30.4	43.4
100	18.861	6.64	4.24		2.5	46.8	67.9
0.821	100	-0.28	6.64	2.9		3.4	2.4
1.272	1.061	0.35	0.09	164.5	175.9	186.6	209.2
0.792	0.608	-0.34	-0.72	5.2	4.3	2.6	4.1
	1.246		0.32		1.7	2.1	
100	100	6.64	6.64			1.8	1.7
100	0.01	6.64	-6.64		2.4		1.6
1.234	0.841	0.3	-0.25	15.1	20.5	17.2	18.6
0.63	0.939	-0.67	-0.09	125.9	105.1	98.7	79.4
100	100	6.64	6.64			1.5	1.7
0.752	0.945	-0.41	-0.08	90.8	75	70.8	68.3
0.792	0.958	-0.34	-0.06	365.6	310.9	298	289.7
0.829	1.152	-0.27	0.2	41.9	37.4	43	34.7
0.823	0.795	-0.28	-0.33	268.5	269.6	214.2	221.1
3.52	2.553	1.82	1.35	7.1	8.4	21.5	25.1
0.648	1.326	-0.63	0.41	4.1	3.1	4.1	2.6
1.523	1.56	0.61	0.64	84	79.3	123.8	128
1.947	2.183	0.96	1.13	64.6	59.8	130.6	125.7
2.503	2.33	1.32	1.22	4.4	5.5	12.9	11
100	0.722	6.64	-0.47		2.1	1.5	3.2
2.549	2.088	1.35	1.06	4.7	5.2	10.9	12
1.739	1.656	0.8	0.73	30.7	26.2	43.4	53.3
0.01	0.255	-6.64	-1.97	12.2	6.7	1.7	

	0.832		-0.27		2.7	2.2	
	100		6.64			1.6	
	100		6.64			2.4	
9.453	4.188	3.24	2.07	2.3	5.7	23.8	21.5
10.129	6.543	3.34	2.71	2.9	3.8	24.5	29.6
4.074	2.22	2.03	1.15	5.4	9.3	20.7	21.8
0.811	0.774	-0.3	-0.37	194.3	193.1	149.5	157.7
4.919	6.516	2.3	2.7	26.1	18.7	122.1	128.5
6.593	5.808	2.72	2.54	24.8	29.3	169.9	163.6
5.144	4.63	2.36	2.21	4.2	5.4	25.2	21.7
4.296	4.481	2.1	2.16	102.7	102.8	460.6	441.1
1.966	2.204	0.98	1.14	712.9	679.3	1496.8	1401.6
1.603	2.01	0.68	1.01	72.5	61.5	123.6	116.2

Abundances (Grouped) Standard Error [%]: wt, single	Abundances (Grouped) Standard Error [%]: ko, single	Abundances (Grouped) Standard Error [%]: ko, pool	Abundances (Grouped) Count: wt, pool	Abundances (Grouped) Count: wt, single	Abundances (Grouped) Count: ko, single	Abundances (Grouped) Count: ko, pool	Abundances (Normalized): F6: 126, Sample,	Abundances (Normalized): F6: 127N, Sample,
18.34	11		1	4	4	1	21.4	35.3
14.6	6.49		1	4	4	1	72.2	85
2.63	5.26		1	4	4	1	150.1	137.4
22.67	38.07			4	3	1		2.9
6.66	8.9		1	4	4	1	113.9	107.5
	64.83				4	1		
9.62	13.45		1	4	4	1	47.9	54.4
5.2	18.1		1	4	4	1	45.6	52.1
4.8	4.6		1	4	4	1	135.1	140.4
11.23	2.51		1	4	4	1	141.9	116.5
17.64	17.79		1	4	4	1	15.1	19.4
9.15	8.78		1	4	4	1	35.5	34.4
12.22	6.22		1	4	4	1	1510.7	1962.3
5.62	14.2		1	4	4	1	37.3	37
6.18	11.38		1	4	4	1	26	35.6
15.25	13.77		1	4	4	1	22.7	25.7
28.57	15.91		1	4	4	1	17.8	21.4
27.06	17.21		1	4	4	1	28.4	26.4
17.27	17.59		1	4	4	1	26	30.7
11.85	12.28		1	4	4	1	35	33.5
4.24	10.29		1	4	4	1	128.6	127.2
11.95	10.85		1	4	4	1	82.1	108.6
16.13	14.58		1	4	4	1	70.4	91.9
19.49	24.45		1	4	4	1	79.6	66.8
2.25	6.13		1	4	4	1	708.6	687.6
9.39	16.58		1	4	4	1	532.2	493.7
				1	1			
				1	1	1		
16.07	9.28		1	4	4	1	106.3	99.6

32.78	10.17	1	4	4	1	5.8	14.7
14.78	12.44	1	4	4	1	265.2	240.5
37.79	41.34	1	4	4	1	12.5	5.8
41	11.24	1	4	4		4.5	2.3
8.1	12.04	1	4	4	1	102.2	90.3
13.05	7.04	1	4	4	1	28.7	25.4
8.48	8.32	1	4	4	1	96.4	82.7
6.44	7.63	1	4	4	1	408	432.1
3.93	5.53	1	4	4	1	183.8	217.2
8.99	12.28	1	4	4	1	127.8	136.8
12.82	10.01	1	4	4	1	97.5	100.1
28.44	8.24	1	4	4	1	10.1	19.5
66.7	22.84	1	4	4	1	14.4	3.6
21.43	41.74	1	4	4	1	7.5	9.8
15.63	14.17	1	4	4	1	198.9	214.6
31.76	14.25	1	4	4	1	37.5	30.1
	72.79			2	1		
24.04	13.91	1	4	4	1	68.1	75.3
38.13	20.02	1	4	4	1	4.1	2.6
22.31	15.65	1	4	4	1	15.1	14.5
52.39	41.95		2	4			
6.6	9.44	1	4	4	1	201.5	214.1
6.77	6.29	1	4	4	1	1583.1	1444.9
5.77	4.7	1	4	4	1	311.3	292.7
6.14	11.11	1	4	4	1	99.3	102.5
22.35	26.81	1	4	4	1	42.5	50.7
12.35	12.19	1	4	4	1	70.4	64.7
32.45	4.46	1	3	2	1	2.1	
25.4	27.77	1	4	3	1	2.6	2.4
5.75	27.8	1	4	4	1	5.4	9.4
18.28	30.98	1	3	4	1	6.2	
27.29	5.54	1	4	4	1	34.9	28.9
10.11	9.55	1	4	4	1	221.6	174.8
8.28	7.92	1	4	4	1	38.9	36.5
23.15	11.92	1	4	4	1	58.1	30.7
7.53	12.7	1	4	4	1	289.1	236.1
10.78	52.57	1	2	4	1	2.4	
26.4	7.48		2	2	1		
11.18	13.61	1	4	4	1	115.2	102.1
4.49	4.7	1	4	4	1	176.2	163.1

19.94	6.44	1	4	4	1	26.9	26.4
53.11	45.22	1	4	4	1	5	2.6
17.96	5.45	1	4	4	1	29.5	19.8
9.83	7.63	1	4	4	1	114	104
44.54	52.3	1	4	4	1	3.2	3.6
			1	1	1		
24.88	21.79	1	4	4	1	10.4	12
23.5	26.5	1	4	4	1	18.3	18.3
16.66	15.87	1	4	4	1	44.1	47.6
15.04	13.49	1	4	4	1	41.9	28.9
12.38	12.07	1	4	4	1	260.4	210.8
9.27	7.84	1	4	4	1	26	28.5
45.39	31.3	1	3	4	1	2.4	
	20.39	1	1	3		2.9	2.3
			1				
3.5	4.27	1	4	4	1	344.7	284.6
3.14	7.85	1	4	4	1	264.9	226.3
10.08	7.17	1	4	4	1	111.3	117.5
24.9	5.77	1	4	4	1	650.5	1095.5
21.12	10.86	1	4	4	1	14	12.6
20.36	13.82	1	4	4	1	32.4	24.8
9.3	6.68	1	4	4	1	207	203.4
3.29	12.55	1	4	4	1	34.6	40.4
21.21	15.6	1	4	4	1	6.8	6.1
34.34	37.08	1	4	4	1	7.5	5.5
7.42	1.56	1	4	4	1	140.6	124.8
9.07	6.91	1	4	4	1	10.9	22.3
8.04	11.88	1	4	4	1	146.6	131.8
38.86	50.28	1	3	4	1	7.1	2.7
42.57	27.51	1	4	4	1	12.5	6.5
16.26			3				2.6
6.9	9.47	1	4	4	1	205.9	171.3
9.79	34.46	1	4	4	1	11.8	14.8
10.84	5.81	1	4	4	1	362.6	433.1
40.93	31.43	1	4	4	1	32.6	21.5
29.55	16.85	1	4	4	1	37.5	37.7
				1			
29.54	45.89	1	4	4	1	10.4	6.8
21.09	66.19	1	4	4	1	5.2	8.8
22.49	24.7	1	4	4	1	355.4	391.9
5.06	10.9	1	4	4	1	351.2	363
4.44	7.98	1	4	4	1	185.7	178.7
20.25	39.63	1	4	4	1	18	17.4
11.6	19.62	1	4	4	1	64.1	65.3
11	7.35	1	4	4	1	288.4	338.9
23.4	10.85	1	4	4	1	14.9	25

17.87	31.08	1	4	4	1	28.9	22.4
28.79	21.41	1	4	4	1	18.2	19.8
46.83	33.98	1	4	4	1	7.3	4.8
14.5	19.81		4	4	1		2.3
29.71	16.62	1	4	4	1	8.4	14.8
18.33	9.08	1	3	2	1	2.9	3.3
8.85	20.72	1	4	4	1	36	26.8
			1	1			
26.22	5.25		4	3	1		3
43.82	17.98	1	4	4	1	6.3	6.8
43.71	25.67	1	4	3	1	2.6	2.9
21.22	34.55	1	4	4	1	19.5	20
26.44	10.76	1	4	4	1	24.3	22.1
15.89	17.18	1	4	4	1	47	35
16.86	11.38	1	4	4	1	11.7	26.2
24.19	12.47	1	4	3	1	2.9	4.2
28.87	24.21	1	4	4	1	25.1	16.7
	35.23			4			
60.65	21.94	1	3	4	1	4.4	2.9
12.33	8.85	1	4	4	1	106.3	102.8
9.02	10.05	1	4	4	1	658.6	596.8
8.08	8.38	1	4	4	1	497.4	470.2
16.81	9.42	1	4	4	1	255.3	209.4
48.25	21.76	1	4	4	1	5	4.1
9.21	16.75	1	4	4	1	23.7	23.2
9.92	6.64	1	4	4	1	118.9	124.3
4.68	11.95	1	4	4	1	16.2	16.2
12.64	40.34	1	4	4	1	22.9	24.1
14.74	12.6	1	4	4	1	26.1	23.5
16.84	11.77	1	4	4	1	78.4	80.4
19.24	13.76	1	4	4	1	13.3	13.8
				1			
44.85	46.35	1	4	4	1	11.5	4.5
35.12	64.36	1	4	4	1	2.6	8.5
12.74			2	1			
9.06	10.8	1	4	4	1	432.5	408.7
20.42	30.03		2	4	1		
13.33	18.21	1	4	4	1	44.9	51.3
14.51	19.55	1	4	4	1	27.1	21.7

			1		1		
18.12	24.78	1	4	4	1	52.4	54.8
11.79	19.91	1	4	4	1	305.9	385.1
	47.83		1	2	1		
10.63	12.8	1	4	4	1	219.6	242.9
27.14	33.71	1	4	4	1	21.9	20.6
13.22	20.88	1	4	4	1	74.3	87.2
19.93	14.41	1	4	4	1	23.2	18.6
16.22	23.6	1	4	4	1	145.2	128.3
19.13	19.93	1	4	4	1	77.4	83.7
23.84	25.75	1	4	4	1	140.5	109.5
18.12	21.06	1	4	4	1	77.5	77.2
16.56	17.21	1	4	4	1	50.4	32.7
				1			
54.36	17.33	1	4	4	1	2.9	4.7
53.53	42.16		2	4			
4.52	4.29	1	4	4	1	372	365.4
6.1	23.81	1	4	4	1	14.3	10.3
32.69	32.87	1	4	4	1	2.6	19.8
21.23	16.66	1	4	4	1	752.5	720.1
20.69	12.38	1	4	4	1	16.1	19.1
10.13	5.58	1	4	4	1	303.3	319.8
17.21	15.38	1	4	4	1	66.7	63.9
7.45	4.98	1	4	4	1	67.6	61
7.18	7.7	1	4	4	1	183.6	176.3
		1	1	1		2.4	
16.53	21.26	1	4	4	1	72.8	67.4
41.57	77.63	1	4	4	1	22.7	18.3
25.59	44.16		3	3	1		3.2
17.01	17.21	1	4	4	1	767.3	673.6
	15.33		1	2			
22.16	14.93	1	4	4	1	6.2	9.8
38.95	56.37	1	4	4	1	32.3	14.4
29.94	66.61	1	4	4	1	3.6	11.7
13.6	14.44	1	4	4	1	355.7	324.2
33.56	49.9	1	4	4	1	35.4	12.7
22.05	13.05	1	4	4	1	36.7	27.1
38.25	21.94	1	4	4	1	13.5	7.3
9.59			2	1			

	31.32			3			
24.95			2				
8.08	8.05	1	4	4	1	249	257.9
17.04	21.42	1	4	4	1	25.8	26
10.26	11.63	1	4	4	1	70.9	66.8
	54.69	1	1	3	1	4.9	2.1
		1				2.6	
18.91	20.25	1	2	4	1	3.7	3.3
6.76	6.58	1	4	4	1	310	283.8
36.69	43.26	1	4	4	1	4.9	5.5
20.33	22.59	1	4	4	1	30.5	32.1
	14.53	1	1	2	1	2.6	
		1		1		2.1	
39.7	25.59	1	4	4	1	4.1	2.4
10.89	23.66	1	4	4	1	17.4	12.7
32.59	13.02	1	4	4	1	6.2	17
13.25	12.86	1	4	4	1	61.2	54.4
46.05	13.43	1	4	4	1	4.2	10.3
34.32	27.7	1	3	4	1	2.6	2
				1			
	56.52		1	4	1		
5.65	5.3	1	4	4	1	170.7	171.9
31.79	35.09	1	4	4	1	4.7	5.1
	16.75		1	2			2.7
32.65	10.92	1	4	4	1	46.6	21.8
44.61	9.02	1	4	4	1	11.2	14.8
7.72	12.18	1	4	4	1	104.5	144.3
4.04	6.83	1	4	4	1	893.5	844.9
10.05	10.53	1	4	4	1	86.6	83.7
29.79	9.34	1	4	4	1	75.1	49.4
44.56	56.99	1	4	4	1	3.1	3.5

24.81	15.82	1	4	4	1	103	85.9
16.23	13.19	1	4	4	1	104	98.7
12.99	6.8	1	4	4	1	160.6	127.2
32.98	60.35	1	4	3		6.3	2.7
			1	1			
32.75	13.88	1	4	4	1	66.3	60
				1			
2.43	11.8	1	4	4	1	70.2	62.8
			1	1	1		
1.02	9.97	1	4	4	1	124.6	131
48.22	42.28	1	4	4	1	5.8	5.6
19.21	2.86	1	4	4	1	33.7	69.5
17.1	21.59	1	4	4	1	18	14.4
22.44	4.29	1	4	4	1	32.1	29.7
7.96	11.07	1	4	4	1	58.9	62.1
28.22	32.41	1	4	4	1	31.5	23.2
			1	1	1		
9.85	7.15	1	4	4	1	190.9	170.4
20.38	17.66	1	4	4	1	22.5	13
30.85	11.18	1	4	4	1	4.5	7.4
54.97		1	4	1	1	2.1	2
13.95	27.37	1	4	4	1	10.4	17.6
7.5	12.35	1	4	4	1	38.4	36.8
9.08	12.75	1	4	4	1	30.7	30.3
5.06	4.96	1	4	4	1	97.3	96.6
2.16	5.21	1	4	4	1	270.4	269.3
49.32	31.72	1	3	4	1	4.4	4.4
14.31	10.81	1	4	4	1	64.1	58.2
15.37	24.52	1	4	4	1	84.2	68.1
22.25	17.03	1	4	4	1	20.8	23
4.31	6.93	1	4	4	1	1538.6	1461
31.73	81.01	1	4	4	1	6	6.8
20.1	13.45	1	4	4	1	18.5	11.2
11.54	14.56	1	4	4	1	291.5	272.4
44.21	21.98	1	4	4	1	11.4	11.4
6.1	29.33	1	4	4	1	118.6	75.1
39.02	55.15	1	4	4	1	19.5	7.6
16.23	16.35	1	4	4	1	12.8	9.1
2.69	2.88	1	4	4	1	2385.9	2452
16.32	22.84	1	4	4	1	399.9	385.1
8.57	8.68	1	4	4	1	149.2	143

29.74	51.17	1	4	3	1	2.8	2
	22.4	1		3		2.1	
11.15	4.38	1	4	4	1	109.3	98.3
10.14	5.17	1	4	4	1	100.9	112.4
16.17	16.42	1	4	4	1	2.4	9.8
6.82	2.63	1	4	4	1	196.6	175.5
52.06	12.22	1	4	4	1	2.8	5.1
				1			
25.52	28.28	1	4	4	1	27.9	25
12.57	12.77	1	4	4	1	234.1	213.1
	5.71		1	4	1		
39.33	27.33	1	4	4	1	9.4	6.8
	7.31	1		2		2.1	
42.64	17.74	1	4	4	1	4.4	5
48.44	21.66	1	4	4	1	3.9	5
30.02	30.29	1	4	4	1	5.2	6.7
34.89	52.46	1	4	4	1	3.1	5.6
6.67	16.78	1	4	4	1	36	36.3
					1		
7.51	12.52	1	4	4	1	61.2	61.8
57.52	14.44		4	2	1		2
23.74			2	1			2.6
			1	1	1		
37.05	34.95	1	4	4	1	3.1	5.8
9.87	17.3	1	4	4	1	30.2	24.7
20.22	15.45	1	4	4	1	83.4	71.6
11.08	10.66	1	4	4	1	129.5	122.2
29.9	44.39	1	4	4	1	33.7	23
28.61	23.93	1	4	4	1	24.7	22.7
18.3	19.78	1	4	4	1	9.7	9.8
37.7	22.09	1	4	4	1	22.4	24.8
	8.64	1	1	2		6.2	
			1				2.3
			1	1	1		
22.94	20.5	1	4	4	1	34.7	33.9
13.54	20.64	1	4	4	1	59.5	55.4
30.96	34.74	1	3	4	1	3.4	3.8
13.56	25.48	1	4	4	1	30.2	41.5

9.47	11.97	1	4	4	1	241.5	234.1
15.32	23.05	1	4	4	1	36.8	38.2
				1			
31.68	19.77	1	4	4	1	80.9	73.5
39.75	24.29		3	4	1		3.5
33.19	31.12	1	4	4	1	13.1	15.8
24.52	20.83	1	4	4	1	90.7	114.5
41.81	36.35	1	4	4	1	14.3	6.5
13.53	11.75	1	4	4	1	64.2	69.5
19.6	35.75		4	3	1		3.5
10.79	3.05	1	4	4	1	103.8	109.5
53.3	60.95	1	4	4	1	4.4	3
21.91		1	3	1	1	3.6	
			1				
1.53	7.57	1	4	4	1	109.3	112.2
7.95	5.63	1	4	4	1	296.9	295.2
58.24			2	1			
3.86	4.13	1	4	4	1	265.1	268.5
29.52	54.15		4	4	1		11.2
10.19	22.91	1	4	4	1	8.1	9.7
55.7	37.7	1	4	4	1	6.7	2.6
9.12	26.49	1	4	4	1	9.1	7
	3.73	1	1	2		2.9	
39.35	26.79	1	4	4	1	12	18.2
10.43	20.79	1	4	4	1	76.7	100.9
7.06	8.63	1	4	4	1	60.2	57.5
12.53	17.05	1	4	4	1	26.4	26.4
7.12	3.88	1	4	4	1	336.4	307.1
10.08	48.26	1	4	4	1	5.8	5
	25.98	1	1	4		3.4	
16.71	37.55	1	4	4	1	3.7	10.8
28.49			3		1		
6.96	8.62	1	4	4	1	134	124.6
8.46	23.34	1	4	4	1	22.9	40.3
16.82	11.09	1	4	4	1	41.5	56.9
13.07	36.76	1	4	3	1	4.5	4.4
	11.62	1		2	1	2.1	
2.68	7.13	1	4	4	1	397.3	386.5
2.62	4.14	1	4	4	1	969.7	918.7
17.72	12.03	1	4	4	1	24.5	34.2

56.47	42.13		2	4	1		2
15.19	4.31	1	4	4	1	45.4	61.8
11.32	8.44	1	4	4	1	46.7	46.3
54.4	47.85		4	4	1		3
	65.6		1	4	1		
2.88	6.87	1	4	4	1	241.9	231
18.78	32.3	1	4	4	1	5.8	10.6
59.65	29.75	1	4	4	1	11.4	6.7
					1		
14.03	25.35	1	4	4	1	2.9	17
		1			1	2.6	
	50.76		1	4	1		
55.8	40.36	1	4	4	1	2.8	3.8
26.23	34.21		2	4	1		
14.59	24.45	1	4	4	1	2.4	6.4
33.3	39.02	1	4	4	1	28.1	29.7
41.07	32.67	1	4	4	1	203.6	438.1
11.68	12.35	1	4	4	1	73.8	80.1
			1				
					1		
2.13	3.32	1	4	4	1	1840	1816.1
2.97			2	1	1		
1.82	6.25	1	4	4	1	461.8	465.4
7.27	11.7	1	4	4	1	166.3	151
42.54	23.31		4	4	1		4.7
14.32	10.12	1	4	4	1	58.6	34.5
54.27	35.64	1	2	4	1	2.9	5.1
51.16	6.13		3	3	1		6.4
28.7	10.33	1	4	4	1	40.4	35.7
15.67	11.97	1	4	4	1	108.4	114.9
2.03	2.09	1	4	4	1	3208.8	3100.2
43.45	41.34	1	4	4	1	6.7	4.8
5.12	8.59	1	4	4	1	780.1	720.9
30.5	42.14	1	4	4	1	15.4	19.2
28.88	33.8		4	4	1		5.5
41.51	25.2	1	4	4	1	13	5.6

42.61	50.69	1	4	4	1	5.4	6.4
25.52	79.9	1	4	4	1	4.5	5
29.71	44.28		3	4	1		
	11.06		1	2			
38.81	11.13	1	2	4	1	9.7	
32.91	36.37	1	2	4		3.7	3.5
			1	1			
36.74	12.82	1	4	4	1	35.9	29.5
4.26	8.51	1	4	4	1	170.3	199.9
2.35	7.41	1	4	4	1	187.7	198.5
43.92	34.85		3	4	1		
17.71	17.76	1	4	4	1	3.9	3.9
7.47	8.37	1	4	4	1	65	72.7
5.1	0.5	1	4	4	1	409.4	377.4
10.49	18.65	1	4	4	1	71.5	92.2
6.19	10.22	1	4	4	1	145.7	161.9
39.66	14.6	1	4	4	1	10.1	10.1
5.84	5.14	1	4	4	1	350.4	300.6
46.43	2.68	1	4	4	1	10.9	3.6
11.84	13.62	1	4	4	1	19.3	27
16.04	5.42	1	4	4	1	7.9	15.6
5.02	13.64	1	4	4	1	277.9	334.5
9.27	9.42	1	4	4	1	93.4	80.6
19.56	48.03		2	3	1		
3.66	9.68	1	4	4	1	41.5	38.6
27.81	35.25	1	3	4	1	5.5	7.1
11.22	11.44	1	4	4	1	40.2	43.6
8.82	5.71	1	4	4	1	99.3	105.9
28.62	8.13	1	4	4	1	23.8	21.1
21.49	14.89	1	3	4	1	2.1	2.1
		1				2.1	
21.28	20.4	1	4	3	1	2.9	2.3
6.9	8.43	1	4	4	1	106.1	91.2
29.42	37.29	1	4	4	1	14.8	18.8
9.84	15.93	1	4	4	1	23	18.3
20.7	30.18	1	4	4	1	29.7	17.3
14.39	12.67	1	4	4	1	60.5	48.8
23.67	28.71	1	4	4	1	56	22.4
6.82	20.95	1	4	4	1	118.6	101.2
4.1	12	1	4	4	1	555.8	609.9
7.29	11.66	1	4	4	1	540.5	574.4

14.86	21.35	1	4	4	1	23.2	37.4
	2.44	1		2		2.6	
				1			
				1			
	61.09			4	1		
9.12	12.73	1	4	4	1	35.9	32
	19.91			4	1		
	51.53	1	1	4	1	2.1	
27.22	22.06		3	4	1		4.2
	21.66			2	1		
28.27	13.9	1	4	4	1	2.9	3.5
	51.27			3	1		
	26.02			4	1		
	53.06		1	4	1		
	35.56			3			
38.52	12.86	1	4	4	1	15.4	28.3
81.34	31.23	1	2	4	1	2.1	
	43.86			4	1		
				1	1		
37.52	18.95		3	4	1		3.8
11.49	29.34		3	3	1		
14.02	16.81	1	4	4	1	1874.8	2116.7
24.87	15.98	1	4	4	1	90.8	76.5
16.43	9.48	1	4	4	1	112.4	130.7
9.47	10.69	1	4	4	1	152	140.4
16.04	13.17	1	4	4	1	169.8	207.5
13.75	36.43	1	4	4	1	12.7	15.4
23.96	9.7	1	4	4	1	26.8	46.3
47.65	20.74	1	4	4	1	5	13.9
4.22	7.24	1	4	4	1	192.9	167.8
16.16	8.23	1	4	4	1	67.6	69.1
11.49	35.76	1	3	3	1	2.6	
			1				
9.92	16.11	1	4	4	1	78.2	78.6
3.71	7.79	1	4	4	1	215.1	215.1
4.67	9.65	1	4	4	1	107.1	95.3
66.58	6.04	1	4	3	1	4.2	3
15.29	23.96	1	4	4	1	23	37.7
7.26	8.36	1	4	4	1	122	131.3

24.06	30.81		3	3	1		
42.24	48.85	1	4	4	1	2.4	2.3
29.52	52.47	1	4	4	1	7.9	22.6
43.8		1	3			3.1	6.1
21.77		1	4		1	30.8	28
5.11	5.24	1	4	4	1	109.3	109.2
3.78	11.09	1	4	4	1	149.9	150.8
6.95	10.3	1	4	4	1	136.9	133.7
10.42	19.76	1	4	4	1	59.4	53.6
26.36	17.33	1	4	4	1	18	15.3
9.09	28.25	1	4	4	1	147.5	104.3
11.65	5.95	1	4	4	1	75.9	70.4
14.48	13.81	1	4	4	1	86.9	75.4
18.45	5.49	1	4	4	1	97.7	73.6
10.36	7.16	1	4	4	1	140.8	123.1
11.17	2.31	1	4	4	1	214.8	202.3
7.52	35.64	1	4	4	1	5	3.5
23.79	8.44	1	4	4	1	13	23.6
			1		1		
3.31	4.98	1	4	4	1	1962.8	2034.3
14.53	14.9	1	4	4	1	237.3	216.6
4.55	4.44	1	4	4	1	506.8	503.4
13.49	7.78	1	4	4	1	294.4	245
6.86	16.57	1	4	4	1	58.7	57.5
	25.31			3	1		
12.95	14.85	1	4	4	1	271.1	224.3
5.77	9.48	1	4	4	1	174.1	160.8
9.33	26.1	1	4	4	1	159.8	108.7
24.12	37.23	1	4	4	1	59.4	32.1
	20.9	1	1	3	1	2.4	
5.41	8.96	1	4	4	1	20.8	29.2
18.63	15.95	1	4	4	1	38.8	33.8
12.24	11.96	1	4	4	1	36.2	41.3
6.45	6.2	1	4	4	1	539.1	529.7
26.8		1	2			2.6	2.1
18.16	9.13	1	4	4	1	65.7	94
13.7	29.95	1	4	4	1	7.8	5.5
40.85	44.92	1	4	4	1	8.1	5.6
6.14	18.23	1	4	4	1	49.5	55.9
31.2	22.49	1	4	4	1	5.2	3.6
2.94	17.66	1	4	4	1	146.5	143.3
14.3	35.2	1	4	4	1	25.5	33.6
23.92	12.06	1	4	4	1	25.8	27
22.62	22.94	1	4	4	1	26.1	28.3

16.01	9.14	1	4	4	1	66.8	96.5
4.79	6.35	1	4	4	1	382.5	340.1
5.34	2.52	1	4	4	1	131.2	143
	32.56	1	1	3	1	3.4	
45.28	30.64	1	4	4	1	3.4	3.6
33.75	36.85	1	4	4	1	11.5	10.9
3.7	11.14	1	4	4	1	448.2	474.6
2.92	2.25	1	4	4	1	331.1	336.8
	44.55		1	4	1		
16.24	9.62	1	4	4	1	110.8	77.4
8.71	12.29	1	4	4	1	594.2	617.7
13.48	10.15	1	4	4	1	37.3	30
59.75	48.29	1	4	4	1	11.4	5.3
26.8	5.1	1	4	4	1	28.2	19.1
	49.12	1	1	4	1	5.2	
41.68	26.62	1	4	4	1	7.6	2.3
10.5	15.23	1	4	4	1	107.7	113.3
	5.35		1	2			2.4
17.09	50.92	1	4	4	1	15.2	12.6
8.06	16.87	1	4	4	1	25.6	31.8
20.62	25.39	1	4	4	1	19.5	16.2
11.97	11.72	1	4	4	1	91.8	73.3
50.74	54.91	1	3	4	1	2.6	
	46.09		1	2	1		2.6
18.33	34.19	1	4	4	1	3.2	7.7
	0.39			2	1		
9.65			2		1		4.2
6.83	8.1	1	4	4	1	137.9	118.6
20.67	4.27	1	4	4	1	42.8	33.6
28.13	8.12	1	4	4	1	36.2	36.8
	7.7			3			
26.92	39.28	1	4	4	1	14	16.2
22.77	11.45	1	4	4	1	76.9	48.9
39.76	40.02	1	4	4	1	3.4	5.5
60.32	33.62	1	4	4	1	4.2	4.5
22.13	16.12	1	4	4	1	15.7	16.2
2.51	0.68	1	4	4	1	238.6	223.5
2.87	2.63	1	4	4	1	1640.7	1648.9
27.79	14.67	1	4	4	1	73.5	49.5
28.03	15.06	1	4	4	1	14.8	19.1

50.09	15.39	1	4	4		2.3	4.1
26.92	59.74	1	4	4	1	6.5	2.6
5.08	7.32	1	4	4	1	226.8	231.4
11.12	12.96	1	4	4	1	1246.2	1103.6
13.1	13.62	1	4	4	1	42.7	43.5
12.73	10.97	1	4	4	1	36.7	34.4
17.46	20.41	1	4	4	1	40.6	42.7
15.65	28.39	1	4	4	1	7.1	11.1
26.34	15.79	1	4	4	1	14.9	14.8
18.73	22.02	1	4	4	1	21.3	24.5
8.45	7.6	1	4	4	1	424	464.3
8.26	12.3	1	4	4	1	50.1	58.9
4.41	2.71	1	4	4	1	473.8	475.8
7.5	18.13	1	4	4	1	70.7	71.6
7.95	2.58	1	4	4	1	244.5	212.3
7.55	11.33	1	4	4	1	120.7	94.7
	14.94	1	1	3	1	2.1	
37.75	45.43		4	4	1		2.6
7.66	7.04	1	4	4	1	192.1	173.7
31.38	19.85		3	3	1		1.8
	3.05			2			
30.74	20.27	1	4	4	1	18.5	14.2
25.08	46.38	1	3	3	1	2.3	2.4
	35.56			3	1		
56.72	39.17	1	4	4	1	16.2	2.9
39.02	44.59	1	4	4	1	16.7	15.9
38.95	55.34	1	4	4	1	44.4	16.4
82.03	17.59	1	4	4	1	11	4.1
51.02	19.66	1	4	4	1	2.6	2.3
34.03	54.61	1	3	3	1	2.4	
2.55	6.19	1	4	4	1	304.3	274.6
15.43	9.53	1	4	4	1	45.9	39.2
18.12	9.96	1	4	4	1	39.7	30.6
2.02	5.61	1	4	4	1	311.5	312.6
	58.62			4	1		
32.89	11.31	1	4	4	1	10.7	9.2
			1				2.4
45.95	13.52	1	2	4		3.7	
34.67	56.11		3	4	1		2.7
8.24			3	1			2

			1				
	8.68		1	2	1		
	30.16		1	2			
	10.27		1	2	1		
17.54	10.18	1	4	4	1	15.6	11.7
71.46	47.41	1	3	2	1	2.3	6.7
3.38	11.44	1	4	4	1	25.8	34.4
15.98	22.39	1	4	4	1	4.2	2.9
37.71	42.84	1	4	4	1	4.1	5.1
32.65	13.13	1	4	4	1	13.1	10.9
9.95	8.51	1	4	4	1	54.5	47.1
19.36	69.65	1	3	4	1	3.7	2.7
49.3			3				4.2
23.6	5.81	1	4	4	1	90.7	81.2
25.3	24.87	1	4	4	1	7.6	15.9
34.82	28.59	1	4	4	1	5.4	3.5
1.12			2	1			
	17.67		1	2			
22.52	12.37	1	4	4	1	30.3	20.7
33.25	6.42	1	3	2	1	2.4	4.7
62.14	30.45	1	3	4	1	2.8	
	0.91			2	1		
17.52	31	1	4	4	1	65.9	51
6.11	34.8	1	4	4	1	106.6	79.8
13.22	22.84	1	4	4	1	43.8	56
3.77	8.71	1	4	4	1	367.1	362.4
13.86	39.12	1	4	4	1	66.7	50.9
10.56	44.85	1	4	4	1	3.9	10.9
10.38	12.39	1	4	4	1	15.4	11.8
8.18	10.27	1	4	4	1	80.3	77.5
7.46	8.96	1	4	4	1	103.2	124.2
18.7	30.45		2	3			
35.7			2				
6.89	11.85	1	4	4	1	182.8	163.4
7.95	11.43	1	4	4	1	54.7	58
45.04	44.92		3	2	1		4.5
4.6	8.22	1	4	4	1	274.5	277
20	13.72	1	4	4	1	24.7	24.4
8.56	12.76	1	4	4	1	19.5	14.8
19.9	10.9	1	4	4	1	157	148
60.91	18.06	1	4	4	1	10.1	6.7
2.48	8.79	1	4	4	1	118.6	122.7
8.01	8.08	1	4	4	1	214.6	183.2
24.44	7.67	1	4	4	1	10.9	12.9
17.69	15.09	1	4	4	1	14.9	10.1

7.87	8.22	1	4	4	1	58.2	61.8
13.75	5.87	1	4	4	1	124.4	107.4
10.52	14.32	1	4	4	1	106.7	104.5
20.09	24.39	1	4	4	1	34.2	41.8
33.28	22.39	1	4	4	1	2.6	6.4
25.09	6.48	1	4	4	1	14.6	23.5
38.47	21.1	1	3	4	1	4.2	3
6.78	7.9	1	4	4	1	201.2	206
3.29	7.42	1	4	4	1	576.2	583.4
18.85	12.87	1	4	4	1	91	71.8
7.61	4.6	1	4	4	1	78.7	76.2
48.87	34.92	1	4	4	1	5.7	3.2
34.12	45.79	1	3	2	1	5.5	3
30.58	57.12	1	4	4	1	7.9	4.8
6.06	10.56	1	4	4	1	4105.1	3789.1
13.72	9.59	1	4	4	1	20.6	17.1
21.55	11.45	1	4	4	1	61.2	56.5
26.35	12.7	1	4	4	1	26.1	19.4
12.1	19.43	1	4	4	1	101.7	80.9
14.35	10.54	1	4	4	1	18.7	20
18.63	9.59	1	4	4	1	49	41.9
13.23	9.78	1	4	4	1	2.9	7.3
31.47	23.02	1	4	4	1	539.5	467.8
15.29	7.42	1	4	4	1	41.5	45
6.41	3.84	1	4	4	1	192.9	163.7
12.18	22.2	1	4	4	1	55.3	69.4
7.77	15.15	1	4	4	1	20.9	23.8
	19.03	1	1	2	1	2.4	
19.72	13.14	1	4	4	1	50.1	34.4
27.35	15.02	1	4	4	1	25.1	24.1
38.94	26.36	1	4	4	1	3.6	3.5
24.94	10.01	1	4	4	1	5.5	9.1
19.36	25.47		2	4	1		
34.83	23.67	1	4	4	1	6.2	8.9
15.14	2.73		2	2			
28.88	6.32	1	4	4	1	27.4	28.5
23.97	11.87	1	4	4	1	30.7	25.3
29.87	40.21	1	4	4	1	4.4	5.8
14.23	49.43		2	3			
		1		1		2.3	
				1			

5.5	90.13	1	4	4	1	700.3	712.1
35.93	4.1	1	4	4	1	9.7	9.5
5.12	9.01	1	4	4	1	220.3	186.6
44.26	24.15	1	4	3		2.9	2.4
			1				
11.81	11.9	1	4	4	1	94.9	79.1
5.02	7.49	1	4	4	1	288.6	286.8
7.97	4.14	1	4	4	1	116.5	137.5
6.19	10.99	1	4	4	1	93.1	112.2
9.89	20.99	1	4	4	1	24	28.3
63.31	29.54		3	3	1		2.3
7.62	53.75	1	4	4	1	150.7	156.7
6.27	7.43	1	4	4	1	637.2	561.1
6.19	7.98	1	4	4	1	872.9	822.9
51.88			2	1	1		
40.75	13.94	1	4	4	1	25.8	13.9
17.57	12.19	1	4	4	1	51.3	50.9
53.6	30.78	1	4	4	1	7.3	5.6
30.73	30.03	1	4	4	1	6	9.5
20.81	38.8	1	4	4	1	2.9	6.5
5.82	41.36	1	4	4	1	13.8	17.7
14.89	12.91	1	4	4	1	75.3	63.9
8.73	17.93	1	4	4	1	81.6	87.1
6.9	48.55		2	2			2
48.06	37.75		4	4	1		2.3
			1				
26.96	7.08	1	4	4	1	7.3	6.1
15.56	20.7	1	4	4	1	12.5	23.6
69.33	29.37	1	3	4	1	2.8	
35.25	7.04	1	3	3	1	2.3	
12.06	51.31		2	4	1		
19.27	19.25	1	4	4	1	158.2	136.9
3.85	4.23	1	4	4	1	284	268.5
8.1	2.47	1	4	4	1	62.6	60.1
12.32	8.28	1	4	4	1	82.9	71.8
12.59	4.41	1	4	4	1	119.6	125.7
16.28	11.36	1	4	4	1	49.5	48
14.56	22.29	1	4	4	1	15.1	24.1
30.28	13.47	1	4	4	1	7.6	4.5
27.81	36.68	1	3	4	1	5.5	5.5
6.12	9.29	1	4	4	1	79.8	80.3

16.88	8.45	1	4	4	1	54.2	43.6
			1				
28.18	20.3	1	4	4	1	30.7	35.3
26.16	6.86	1	4	4	1	68.3	36
9.26	12.8	1	4	4	1	36.8	28.5
10.03	7.05	1	4	4	1	32.8	35.6
19.31	11.39	1	4	4	1	190.1	186.9
30.19	43.11	1	3	4	1	7.5	
3.67	6.79	1	4	4	1	593.4	609.7
10.49	10.72	1	4	4	1	102.8	125.5
2.27	7.07	1	4	4	1	498.3	485.4
36.51	23.69	1	4	4	1	6.3	8.6
3.38	8.47	1	4	4	1	125.7	133.6
8.01	10	1	4	4	1	71.9	80.4
19.84	23.14	1	2	3	1	2.3	
11.97	37.63	1	4	4	1	8.1	14.2
27.4	34.17	1	4	4	1	9.6	8.3
16.09	23.2	1	4	4	1	18.7	25.9
	16.02		1	2	1		
26.3	48.74	1	4	4	1	2.6	4.8
25.44	45.31	1	3	4	1	3.1	2.1
6.39	9.92	1	4	4	1	109.3	118.9
20.77	33.11	1	4	4	1	2.8	5.1
26.92	16.61	1	4	4	1	7.1	6.8
	43.04		1	2			
				1			
15.61	13.83		3	2	1		3
18.48	10.69	1	4	4	1	12.3	19.1
20.1	24.06	1	4	4	1	16.2	10.1
32.38	21.06	1	4	4	1	6.7	5.5
29.12	12.12	1	4	4	1	5.8	9.4
19.11	19.47	1	4	4	1	32.6	25.1
74.45	16.8	1	4	4	1	3.1	2.6

8.56	22.97	1	4	4	1	14.8	12.1
7.95	2.86	1	4	4	1	92.8	81.9
5.2	5.93	1	4	4	1	871.6	887.5
6.96	5.85	1	4	4	1	118.9	111
7.97	3.98	1	4	4	1	170.8	199.6
22.27	63.26	1	4	4	1	2.9	10.4
32.09	50.27	1	4	4	1	20	13.9
29.49	40.94	1	4	4	1	5.2	4.4
20	15.19	1	4	4	1	2.1	5.1
27.67	19.16	1	4	4		2.9	3
49.87	11.32	1	4	4	1	6.7	8.5
18.95	4.78	1	4	4	1	69.8	56.9
13.43	22.92	1	4	4	1	29.5	26.2
2.92	12.59	1	4	4	1	102.8	97.7
17.85	4.62	1	4	4	1	463.9	363
13.37	22.43	1	4	4	1	14.3	20.4
17.12	10.57	1	4	4	1	30	26.7
13.16	7.69	1	4	4	1	2307.2	2010.4
7.74	11.91	1	4	4	1	166.9	156
40.63	20.48	1	4	4	1	4.7	11.5
36.34	22.59	1	4	4	1	4.5	11.8
4.65	8.63	1	4	4	1	727.1	727.5
4.55	6.21	1	4	4	1	308.2	299.4
9.48	6.14	1	4	4	1	213	204
51.34	37.26	1	4	3	1	8.4	6.4
33.79	57.55	1	4	4	1	2.8	2.9
24.01			2		1		2.4
7.32	7.41	1	4	4	1	533.7	464.2
18.54	9.25	1	4	4	1	41	39.4
10.02	7.74	1	4	4	1	205.9	210.4
		1		1		2.1	
10.93	6.71	1	4	4	1	50.4	67.2
	46.46	1		3	1	4.9	
			1				
11.33	13.43	1	4	4	1	22.5	28.5
	28.85			2	1		
16.73	9.46	1	4	4	1	39.6	39.2
10.17	5.94	1	4	4	1	62	50.1
21.41	29.45	1	4	4	1	8.1	12.6
				1	1		

28.74	24.04	1	4	4	1	143.9	123.6
		1				1.9	
2.86	6.27	1	4	4	1	265.6	233.4
16.25	9.87	1	4	4	1	37.8	35.1
26.66	13.49	1	4	4	1	8.6	3.5
51.92	27.9	1	4	4	1	11	8.5
11.72	10.89	1	4	4	1	113.7	116.2
7.12	45.85	1	3	4		6	3.3
5.59	16.83	1	4	4	1	21.4	26.2
29.72	24.18	1	4	4	1	12.3	11.4
24.27	11.48	1	4	4	1	34.2	41.6
11.29	9.21	1	4	4	1	90.4	88.9
15.02	13.26	1	4	4	1	358.2	366.9
13.6	15.35	1	4	4	1	69.6	66.3
19.06	5.04	1	4	4	1	10.9	15
22.11	10.54	1	4	4	1	75.6	82.1
56.39	35.4	1	4	4	1	2.8	3.5
10.14	8.2	1	4	4	1	237.2	248.8
10.49	8.43	1	4	4	1	174.5	182.8
17.8	10.1	1	4	4	1	40.6	28.9
14.24	10.49	1	4	4	1	68.5	71
10.73	6.97	1	4	4	1	74.8	68.9
38.61	43.02	1	4	4	1	4.7	4.1
18.75	17.37	1	4	4	1	10.7	16.8
33.1	21.9	1	4	4	1	10.7	8.2
24.44	26.57	1	4	4	1	36.5	25.7
37.92	13.85	1	4	4	1	3.1	2.7
24.79	8.16	1	4	4	1	14	9.1
9.04	20.3	1	4	4	1	64.1	60
7.63	8.49	1	4	4	1	159.1	151.3
13.75	15.33	1	4	4	1	164.7	216.7
5.26	8.17	1	4	4	1	837.4	740.1
17.94	22.28	1	4	4	1	77.5	50.9
10.26	5.29	1	4	4	1	187.4	142.4
25.1	44.28		4	4	1		5.9
6.29	14.37	1	4	4	1	70.1	84.8
23.39	18.03	1	4	4	1	19.3	11.5
17.14	41.53	1	4	4	1	6.7	8.8
	10.27			2			
		1		1		2.6	
			1				
29.58	20.65	1	4	4	1	7.6	9.5
3.6	3.48	1	4	4	1	500.3	358.8
15.99	9.63	1	4	4	1	11.7	13.3

15.32	28.12	1	4	4	1	33.6	30.9
18.97	27.87	1	4	4	1	21.4	15.8
21.18	12.69	1	4	4	1	20.4	26.2
6.75	6.23	1	4	4	1	118.1	114.5
13.02	4.67	1	4	4	1	48.7	51
	56.26		1	2			
2.31	3.81	1	4	4	1	853.3	832.3
18.64	14.84	1	4	4	1	13.6	18
24.78	22.72	1	4	4	1	38.6	22.1
	1.16		1	2	1		
7.69	11.62	1	4	4	1	130.7	113.4
47.15	48.07	1	4	4	1	2.8	5.3
9.95	19.32	1	4	4	1	37.1	40.7
3.2	12.63	1	4	4	1	231.2	224.7
67.57	37.68	1	3	4	1	8.3	
44.46	23.43		3	4	1		5.1
49.04	53.02	1	4	4	1	6.2	4.2
2.8	4.75	1	4	4	1	147.8	118.4
17.14	14.68	1	4	4	1	35.4	27.3
12.12			2	1			1.8
			1				
13.07	4.82	1	4	4	1	24.5	42.3
51.9	20.5		2	2	1		
15.48	28.01	1	4	4	1	26.9	28.6
22.94			3	1	1		2.7
40.02	24.54	1	4	4	1	3.2	2.3
1.91	10.27	1	4	4	1	378.1	384.1
6.74	7.41	1	4	4	1	372	346.5
8.53	7.16	1	4	4	1	99.1	86.8
3.81	7.9	1	4	4	1	399.7	415.3
4.58	6.54	1	4	4	1	343.6	292.3
15.22	20.66	1	4	4	1	26.4	28
9.76	5.49	1	4	4	1	203.6	202.6
29.32	7.92	1	4	4	1	12.8	14.1

14.23			2	1			2.4
21.59	21.1	1	4	4	1	527.5	488
3.4	15.29	1	4	4	1	110.8	104
10.39	15.8	1	4	4	1	80.3	62.2
14.44	44.5	1	4	3	1	8.6	4.5
5.82	4.89	1	4	4	1	321.2	315.2
14.61	7.85	1	4	4	1	74.6	78.8
25.13	21.9	1	4	4	1	17	13.8
27.14	19.48	1	4	4	1	7.8	10.9
6.42	4.56	1	4	4	1	70.9	71.2
				1			
13.8	15.82	1	4	4	1	54.7	59.1
				1	1		
5.31	9.23	1	4	4	1	65.4	57.1
5.09	8.57	1	4	4	1	67.6	67.1
36.52	26.24		2	4	1		
9.62	5.99	1	4	4	1	69.4	59.1
7.68	13.98	1	4	4	1	111.3	106.6
15.17	10.1	1	4	4	1	41	45.1
22.67	31.35	1	4	4	1	8.9	6.2
11.18	8.48	1	4	4	1	139.8	179.2
3	4.5	1	4	4	1	236	222.5
3.39	3.68	1	4	4	1	1511.5	1466.3
4.76	2.87	1	4	4	1	344.9	323.3
9.73	9.73	1	4	4	1	77.5	89.7
21.19	8.25	1	4	4	1	27.3	28
				1	1		
3.13	9.32	1	4	4	1	192.4	190.4
39.18	25.74	1	4	4	1	3.2	6.2
13.11	8.16	1	4	4	1	84.8	85
35.32	34.45	1	3	3	1	3.1	2.1
18.37	13.95		2	4	1		
12.42	17.75	1	4	4	1	55.2	58.9
26.03	22.76	1	4	4	1	16.7	11.8
10.26	13.35	1	4	4	1	123.4	120.4
23.32	2.24	1	4	4	1	29.5	22.9
	4.96			2	1		
40.89	30.16	1	4	4	1	8.1	2.3

8.76	18.64	1	4	4	1	35.2	27.3
26.13	73.94	1	4	4	1	6	6.4
11.83	23.38	1	4	4	1	70.1	98.4
28.51	54.92	1	4	4	1	10.5	13.9
	11.21		1	3			
9.1	6.62	1	4	4	1	94.2	86.8
8.03	11.69	1	4	4	1	24.2	26.5
2.35	5.94	1	4	4	1	182.2	171.9
48.11	16.1	1	4	2	1	5.8	2.1
		1	1	1	1	2.1	
36.61	59.5	1	4	4	1	2.3	5.3
62.28	37.84	1	4	4	1	19	2.6
4.83	1.14	1	4	4	1	472.4	403.3
41.95	31.05	1	4	4	1	6	3.2
6.37	9.44	1	4	4	1	114.5	116.9
38.02	17.33	1	4	4	1	26.8	40.7
9.48	16.55	1	4	4	1	43.8	53.3
2.57	6.77	1	4	4	1	400.8	375
8.5	11.48	1	4	4	1	56.9	58.9
28.93	17.74	1	4	4	1	14.8	9.1
37.62	19.34	1	4	4	1	6.3	6.1
7.84	5.18	1	4	4	1	194.8	211.6
14.51	11.31	1	4	4	1	28.1	38.6
18.18	13.98	1	4	4	1	90	100
29.45	84.66		2	3	1		
13.29	14.97	1	4	4	1	37.8	37.9
28.78	15.41	1	4	4	1	15.1	20.6
20.51	17.78	1	4	4	1	15.2	17.3
51.34	19.53	1	4	3	1	5.4	5.1
39.06	60.52	1	4	3	1	2.3	4.1
21.11			3				2
40.68	28.21		2	3	1		
14.49	11.78	1	4	4	1	47	57.5
4.7	7.86	1	4	4	1	816.4	763.6
8.19	4.46	1	4	4	1	164.2	171.4
					1		
5.71	12.09	1	4	4	1	361.1	373.8

5.26	9.53	1	4	4	1	522.7	509.9
45.52	25.18	1	4	4	1	7.1	5.6
3.41	3.64	1	4	4	1	191.9	189.2
3.35	9.05	1	4	4	1	406.8	408.1
40.44	14.83	1	4	4	1	3.1	2.3
14.17	47.6	1	4	4	1	3.1	3
				1			
27.37	8.39	1	4	4	1	54.3	38.9
	20.25		1	4			
71.38	74.8	1	4	4	1	2.9	2.4
26.28	26.26	1	4	4	1	2.1	5
40.99	46.21		3	3	1		
10.16	4.78	1	4	4	1	26.9	24.7
9.47	13.56	1	4	4	1	27.1	29.8
35.91	54.19	1	4	4	1	2.1	2.7
37.11	17.91	1	4	4	1	14.6	6.2
21.37	34.88		3	4	1		2.9
46.25	32.54	1	4	4	1	10.4	12.1
33.66	20.83	1	4	4	1	152.5	123.3
20.34	14.54	1	4	4	1	222.7	189.6
31.43	19.83	1	4	4	1	121.5	80.3
12.25	20.46	1	4	4	1	32.6	33.3
25.92	45.88	1	4	4	1	142.9	68.1
19.36	21.61	1	4	4	1	43.8	58.8
	36.62		1	4	1		3
73.92	7.74	1	4	4	1	5.5	2.3
9.47	11.82	1	4	4	1	114.9	106.8
10.47	15.24	1	4	4	1	152	134.9
27.12	19.33	1	4	4	1	30.2	18
					1		
16.52	20.56	1	4	4	1	23.4	34.4

43.89	4.36	1	4	4	1	15.2	14.1
	20.29		1	2			
9.25	5.67	1	4	4	1	510.3	552
8.43	22.92	1	4	4	1	15.7	17.9
10.41	5.55	1	4	4	1	81.9	98.9
22.08	9.52	1	4	4	1	14.6	18.5
11.15	4.3	1	4	4	1	152.5	124.9
6.81	6.18	1	4	4	1	814.2	735.6
				1			
8.2	12.38	1	4	4	1	54.8	55.9
7.15	2.83	1	4	4	1	71.1	65.6
5.56	3.9	1	4	4	1	53.7	52.1
12.13	5.91	1	4	4	1	89.7	95.4
	29.4		1	2	1		
6.17	6.74	1	4	4	1	409.8	415.9
2.65	16.06		2	2			
7.58	18.95	1	4	4	1	68	55.6
16.87	25.61		4	2	1		3.6
7.68	10.58	1	4	4	1	668.2	606.8
21.15	6.04	1	4	4	1	45.7	46
32.4	26.15	1	4	4	1	12	18
18.94	7.85	1	4	4	1	188.2	142.7
55.95	44.74	1	3	4	1	2.8	
			1	1			
10.45	10.71	1	4	4	1	23	19.5
23.6	12.27	1	4	4	1	14	13
27.36	30.63	1	4	4	1	5.2	8.2
31.03	27.17	1	4	4	1	51.7	43.5
10.13	20.4	1	4	4	1	43.8	51.6
7.15	2.74	1	4	4	1	210.7	235.9
22.46	17.89	1	4	4	1	34.7	25.7
3.94	8.08	1	4	4	1	225.2	219
5.68	3.39	1	4	4	1	217.7	224.9
30.59	37.73	1	4	4	1	2.6	3
30.79			2				1.8
16.4	32.59	1	4	4	1	120.9	60.7
15.75	37.14	1	4	4	1	566.6	340.9
57.72	49.15	1	2	4	1	3.4	6.1
3.04	9.78	1	4	4	1	622.8	580.3
26.11	17.64	1	4	4	1	22.7	19.8
7.4	6.59	1	4	4	1	182.8	146.7
41.25	23.45	1	4	4	1	16.4	9.7
22.35	46.7		3	4			2.1

13.58	5.02	1	4	4	1	126.7	99.6
	8.69	1		3	1	2.6	
17.11	10.37	1	4	4	1	16.9	13
39.6	18.32	1	4	4	1	13	3.9
13.18	18.54	1	4	4	1	12.5	17.7
2.77	8.98	1	4	4	1	77.5	96.9
6.29	6.88	1	4	4	1	174.1	166.9
21.8	9.18	1	4	4	1	17.5	14.4
37	11.83	1	4	4	1	19.3	8.5
8.16	6.78	1	4	4	1	160.6	143.9
	2.45			2			
28.36	7.59	1	4	4	1	6.3	11.4
22.03	46.1		2	3	1		
24.36	44.21	1	4	3	1	6.8	5.6
10.76	23.82	1	4	4	1	16.9	17.4
6.86	5.58	1	4	4	1	132.4	123.3
22.4	3.02	1	4	4	1	22.7	26.8
30.39	29.81	1	4	4	1	11.8	8.2
			1	1			
64.38	53.62	1	4	4	1	5.2	2.6
10.13	8.86	1	4	4	1	3.9	3.3
5.75	6.56	1	4	4	1	159.9	181
31.54	11.24	1	4	4	1	10.5	15.3
15.62	14.54	1	4	4	1	72.7	79.7
5.51	8.65	1	4	4	1	64.4	57.1
22.15	30.42	1	4	4	1	19	17.1
3.26	23.94	1	4	4	1	13.1	20
19.47	19.24	1	4	4	1	9.9	22.4
62.14	42.74	1	4	4	1	6	2.7
16.03	30.37	1	4	4	1	53.4	36.5
12.45	66.48		2	2	1		1.8
23.08	12.77	1	4	4	1	31.1	32.7
9.27	23.62	1	4	4	1	109.2	124.9
6.92	11.75	1	4	4	1	183.5	171.1
14.36	8.82	1	4	4	1	26.3	42.9
15.12	41.13	1	4	4	1	42.3	42.9
21.62	20.89	1	4	4	1	71.9	69.1
27.38	11.17	1	4	4	1	23	15.8
	58.9		1	3	1		
4.56	7.18	1	4	4	1	5326.4	4931

11.27	8.75	1	4	4	1	45.7	52.7
9.79	2.71	1	4	4	1	113.6	142.2
			1				
36.53	11.73	1	4	4	1	21.7	10.3
7.38	14.57	1	4	4	1	102.5	124.3
16.56	12.13	1	4	4	1	34.2	26.2
11.94	12.58	1	4	4	1	19.8	23.8
27.25	20.09	1	4	4	1	27.1	16.5
12.28	9.91	1	4	4	1	100.7	95.7
5.41	15.98	1	4	4	1	62.3	62.2
25.99			4				2.3
23.3	29.62	1	4	4	1	16.2	14.4
				1			
3.27	28.17	1	3	3	1	5	
					1		
77.12	10.88		2	2	1		
	5.88			2			
12.85	4.44	1	4	4	1	5148.6	6561.9
14.67	22.17	1	4	4	1	59	40.3
10.31	7.63	1	4	4	1	55.3	54.2
3.37	3.08	1	4	4	1	183.1	176.1
41.78	29	1	4	4	1	9.2	7.1
					1		
57.74	31.18	1	4	4	1	8.8	8.3
	44.55		1	3	1		
38.65	54.23	1	4	4	1	6.5	4.1
32.22	27.05	1	4	4	1	5.7	9.5
8.17	7.8	1	4	4	1	81.8	79.1
29.11	28.51	1	4	4	1	7.3	6.4
19.82	4.48		3	2			2
21.03	14.82	1	4	4	1	126.4	122.7
35.16	16.06	1	4	4	1	14.8	12.3
3.08	3.7	1	4	4	1	65.2	81.8
27.35	8.55	1	4	4	1	12.7	14.4
17.08	13.39	1	4	4	1	148.1	171.6
3.24			2	1			
20.25	11.25	1	4	4	1	43.3	47.4

24.93	11.5	1	4	4	1	49	31.7
23.66	67.55		3	4	1		2.1
6.66	5.81	1	4	4	1	313.6	277.3
9.73	4.78	1	4	4	1	95.2	80
1.6	8.29	1	4	4	1	62.1	70
27.3	37.82	1	3	4	1	5.2	
3.53	3.69	1	4	4	1	517.2	455.2
48.03	83.72		4	3	1		2.3
11.22	19.87	1	4	4	1	24.7	21.7
2.04			2	1			2.7
10.95	13.74	1	4	4	1	15.4	19.4
7.13	9.47	1	4	4	1	53.7	82.2
45.84	6.56	1	4	4	1	6.2	13.2
5.3	21.66	1	4	4	1	90.5	103.1
16.09	12.25	1	4	4	1	15.2	20
6.58	19.77	1	4	4	1	276.6	289.3
9.82	12.64	1	4	4	1	51.3	66.6
8.89	5.73	1	4	4	1	121.3	127.1
2.06	5.69	1	4	4	1	523.8	563.1
28.7	34.53	1	4	4	1	2.6	2.9
6.23	9.77	1	4	4	1	61.2	76.3
2.01	7.76	1	4	4	1	113.6	104
3.47	2.34	1	4	4	1	1210.6	1307.4
11.83	9.14	1	4	4	1	52.4	47.1
14.72	23.13		4	4	1		5.5
36.51	55.79		4	4	1		10.9
8.47	17.16	1	4	4	1	31.6	28.2
8.97	10.32	1	4	4	1	178	207
			1				
25.9	18.61	1	4	4	1	17	13.2
25.51	29.95	1	4	4	1	11.2	19.2
34.86	29.62	1	3	4	1	5	
17.55	49.45		4	4	1		2.6
40.78	37.59		3	4	1		

18.4	23.66	1	4	4	1	47.7	38.8
10.18	9.6	1	4	4	1	295.6	269.9
5.77	14.95	1	4	4	1	124.4	129.6
48.25	31.62	1	4	4	1	10.1	3.3
23.82	19.89	1	4	4	1	20.3	29.1
0.37		1	2		1	2.6	
14.94	8.16	1	4	4	1	226.9	204.9
34.74	31.23	1	4	4	1	16.1	8
	20.21		1	2			
39.59	25.95	1	4	4	1	4.7	4.5
24.75	57.63		4	3			2.1
41.76	2.6	1	4	4	1	10.2	5.6
58.5	8.82		4	4	1		2.1
25.59	42.78	1	4	4	1	8.3	8
7.56	1.64	1	4	4	1	547.2	612
10.88	13.25	1	4	4	1	24.5	29.1
2.02	4.44	1	4	4	1	314.1	289.9
33.5	14.62	1	4	4	1	5	2.3
34.63	15.05	1	4	4	1	2.4	3.6
31.41	23.45	1	3	4	1	4.1	3
31.6	27.55	1	4	4	1	6.2	12.6
14.06	41.1	1	4	4	1	2.3	4.7
18.55	10.54	1	4	4	1	16.7	14.5
33.67	15.5	1	4	4	1	71.1	56.5
				1			
15.67	12.81	1	4	4	1	33.1	44.1
18.99	8.51	1	4	4	1	1296.4	1233.2
10.63	7.05	1	4	4	1	62.9	83.4
17.78	12.23	1	4	4	1	90.4	68.3
21.57	69.19	1	4	4	1	12.8	7
6.48	7.36	1	4	4	1	681.2	634.5
40.87	50.57	1	4	4	1	9.9	7.6
	4.57		1	2			
50.77	11.86	1	4	4	1	6.3	4.2
2.9	3.98	1	4	4	1	225	252.8
59.37			2	1	1		4.8
				1			
10.8	33.42		3	2	1		
24.08	8.8	1	4	4	1	22.5	15.1
28.36	31.93	1	4	4	1	2.3	2.1
6.27	5.59	1	4	4	1	185.1	149.8
			1				
5.88	19.76	1	4	4	1	150.5	137.4
10.64	12.12	1	4	4	1	61.2	96.6
19.05	13.92	1	4	4	1	232.8	192.6

4.24	7.21	1	3	4	1	3.7	4.1
15.19	39.87	1	4	4	1	10.2	9.1
	48.55			2	1		
26.95	33.62	1	4	4	1	16.9	8.6
15.99	18.4	1	4	4	1	27.6	43.9
13.28	21.38	1	4	4	1	13.1	12.4
14.41	30.14	1	4	4	1	32	23.8
5.58	7.81	1	4	4	1	47.9	50.4
			1	1	1		
14.81	21.86	1	4	4	1	34.4	26
28.21	30.8	1	4	4	1	25.1	19.7
			1	1			
41.4	31.19	1	4	4	1	10.7	3
29.55	13.15	1	4	4	1	9.7	5.1
40.88	66.98	1	3	4	1	2.6	
57.22	24.5	1	3	4	1	3.1	2.3
2.9	7.44	1	4	4	1	595.7	574.3
9.13	9.89	1	4	4	1	120.2	113
6.98	7.15	1	4	4	1	131.2	129.2
8.51	23.22	1	4	4	1	48.5	54.5
11.2	7.92	1	4	4	1	122.8	130.2
11.86	8.07	1	4	4	1	72.7	75.1
24.57	18.86	1	4	4	1	16.9	22.6
17.66	14.46	1	4	4	1	115.2	105.9
6.09	7.52	1	4	4	1	157.4	151.3
9.08	8.79	1	4	4	1	110.3	101.9
18.68	14.04	1	4	4	1	202.1	278.2
22.82	6.44	1	3	3	1	3.4	2.3
25.22	18.39	1	4	4	1	29.5	22.4
34.51	52.54	1	3	4	1	3.2	
38.17	10	1	4	4	1	27.3	15.3
28.66	21.46	1	4	4	1	3.4	3.3
	13.25	1		2		2.4	
4.83			2	1	1		

50.46	30.66	1	4	4	1	1.9	2.1
10.65	15.83	1	4	4	1	64.2	55.4
16.48	17.98	1	4	4	1	2.1	11.1
30.89	20.9		3	2	1		2.4
7.78	11.29	1	4	4	1	27.7	34.8
39.47	34.29	1	4	4	1	19.8	16.7
5.87	4.22	1	4	4	1	82.7	91
1.64	4.06	1	4	4	1	1384.2	1377.1
0.87	10.82	1	4	4	1	141.9	129.8
14.16	38.1	1	4	4	1	15.2	13.9
70.68	48.96		3	3	1		
12.06	10.29	1	4	4	1	129.9	130.8
9.57	9.51	1	4	4	1	53.5	56.2
15.08	5.8	1	4	4	1	68	62.2
18.66	13.46	1	4	4	1	25.1	30.9
15.94	9.96	1	4	4	1	63.1	56.3
33.94	13.83	1	4	4	1	3.1	5.1
22.92	11.29	1	4	4	1	113.4	93
		1				1.9	
22.58	7.91	1	4	4	1	58.1	38.5
24.91			2		1		3
53.12	60.4	1	4	4	1	2.1	2.4
30.49	17.94	1	4	4	1	23.2	13.9
29	49.17	1	4	4	1	3.6	5.3
7.18	5.26	1	4	4	1	455.2	404.4
3.29	5.87	1	4	4	1	257.6	242.9
24.91	38.81	1	4	4	1	19.5	24.5
12.93	5.46	1	4	4	1	45.7	35.7
22.01	39.42	1	4	4	1	9.2	13.5
5.03	13.71	1	4	4	1	92.8	94.2
19.57	22.67	1	4	4	1	39.9	33.9
19.16	10.34	1	4	4	1	15.6	11.5
14.79	81.59	1	2	3	1	10.5	
			1				
66.4	56.15		3	4	1		6.5
77.42	33.1	1	3	4	1	3.2	2

29.73	38.55		3	3	1		2.1
14.37	15.89	1	4	4	1	26.3	27.3
8.84	3.7	1	4	4	1	83.5	80.3
28.72	36.48		3	4	1		
4.49	13.07	1	4	4	1	10.9	10.6
76.87	15.34	1	2	4	1	7.3	2.3
9.8	9.17	1	4	4	1	16.4	20.9
1.96	25.48		2	3	1		
59.46	15.81	1	3	3	1	3.6	
5.27	7.38	1	4	4	1	807.5	726.9
8.25	7.87	1	4	4	1	41.5	40.6
	0.76		1	2			
	15.86	1	1	4		2.1	
	6.83			2			
8.54	16.86	1	4	4	1	30.2	37.7
15.71	10.1	1	4	4	1	50.3	60.7
20.05	55.97	1	4	4	1	9.9	12.1
18.92	19.08	1	4	4	1	20.4	15.6
35.83	29.61	1	4	4	1	11.5	12.6
71.4	28.92	1	4	4	1	3.4	5.1
51.7	19.01	1	4	4	1	6.7	14.1
33.07	14.65	1	4	4	1	10.2	11.4
11.27	7.1	1	4	4	1	167.9	158.3
17.17	4.05	1	4	4	1	101.4	110.3
19.92	4.47	1	4	4	1	152.8	149.6
16.77	8.86	1	4	4	1	67	61.5
23.93	44.51	1	4	4	1	2.1	3
5.24	10.44	1	4	4	1	221.4	212.3
24.26	6.64	1	4	4	1	19.3	15.1
		1		1	1	2.9	
5.97	7.28	1	4	4	1	395.3	428.3
10.79	26.43	1	4	4	1	20.8	30.1
40.92	29.03	1	4	4	1	7.5	10
5.97	5.01	1	4	4	1	41.5	53.9
26.69			2		1		3.9
9.44	8.52	1	4	4	1	2429.4	2299.2
5.61	10.43	1	4	4	1	115.3	112.7
16.23	11.86	1	4	4	1	60.2	64.8
16.64	18.57	1	4	4	1	84.4	70.7
5.33	11.44	1	4	4	1	55.8	46.6

23.25	4.29	1	4	4	1	1224.4	2003.1
8.18	17.46	1	4	4	1	25.8	29.1
47.61	7.81	1	3	3		3.1	2.1
3.84	5.92	1	4	4	1	350.4	347.7
25.85	46.12	1	4	4	1	3.4	2.4
6.42	20.42	1	4	4	1	20.9	24.5
44.78	9.27	1	4	4	1	30.2	16.5
23.2	10.12	1	4	4	1	40.1	38.8
53.87	14.07	1	4	4	1	17.7	9.8
12.6	3.03	1	4	4	1	83.2	76.3
	36.53	1	1	2	1	2.3	
	16.1		1	2	1		
			1	1			
18.05	30.92		4	4	1		2.4
7.65	18.4	1	4	4	1	208	220.7
18.16	32.2	1	4	4	1	104.1	87.1
6.93	5.7	1	4	4	1	473.7	420.9
8.7	24.94	1	4	4	1	23.2	23.5
21.21			3	1	1		3.8
21	49.05		4	4			2.4
6.35	6.07	1	4	4	1	657.3	647.7
20.11			3	1			2.9
47.23	33		4	4	1		5.6
10.56	9.91	1	4	4	1	171.6	177.5
38.39	16.85	1	4	4	1	10.7	14.5
10.09	22.08	1	4	4	1	25.1	30.1
73.5	48.15	1	3	3		2.4	
25.35	30.66		2	2	1		2
3.74	1.83	1	4	4	1	305.5	296.5
12.41	4.7	1	4	4	1	210.6	210.5
	10.97		1	3	1		
60.02	53.84	1	4	4	1	3.1	3.2
50.77	34.52	1	3	3	1	2.8	
7.92	11.79	1	4	4	1	57.1	53.8
18.74	13.82	1	4	4	1	105.8	146.3
5.12	9.09	1	4	4	1	319.9	345.7
35.78	8.43		3	3	1		2.3
32.24	26.66	1	4	4	1	11.2	8.9
23.32	33.37	1	4	4	1	14.3	19.7
4.3	3.62	1	4	4	1	442	499.2
2.16	11.02	1	4	4	1	219.3	212.8
				1			
4.34	5.37	1	4	4	1	128.5	123.7
19.92	13.69	1	4	4	1	23	16.8
		1				2.6	

39.01	30.61	1	4	4	1	6.2	5.8
2.82	1.13	1	4	4	1	371.5	397.1
75.44	52.81	1	4	4	1	7	8.2
			1				
44.67	46.86		3	3			5.3
28.68	28.41		3	4	1		3.9
4.03	6.44	1	4	4	1	1345.3	1172.2
6.65	5.37	1	4	4	1	132.2	128.7
11.74	7.43	1	4	4	1	200.5	244.9
36.92	33		4	2	1		2.3
19.59	12.23	1	4	4	1	54.7	41.5
3.15	5.62	1	4	4	1	126.2	132.4
21.6	19.77	1	4	4	1	95.4	95
7.48	19.15	1	4	4	1	106.7	102.1
30.31	35.72		4	4	1		2.7
	16.1	1	1	2	1	1.9	
24.51	35.24	1	4	4	1	9.6	16.4
13.92	20.85	1	4	4	1	83.9	80.9
79.08	50.97	1	4	4	1	6.2	9.4
7.06	9.61	1	4	4	1	21.4	28.2
17.5	36.52	1	4	4	1	8.4	8.9
22.58	8.99	1	4	4	1	29.5	33.9
70.21	38.21		2	2			5.5
12.51	32.08		4	4	1		2
6.91	14.68	1	4	4	1	120.9	142.5
					1		
11.47	18.36	1	4	4	1	47.4	58.2
15.77	31.35	1	3	4	1	2.4	
4.88	3.43	1	4	4	1	125.4	129.8
3.94	10.5	1	4	4	1	131.4	134.2
12.58	13.44	1	4	4	1	131.4	113
	15.96	1	1	4	1	2.9	3.6
33.14	43.08	1	3	4	1	3.1	
2.65	3.92	1	4	4	1	99.9	92.7
3.09	6.24	1	4	4	1	529.2	522
50.25	32.23	1	4	3	1	4.7	5.5
5.19	4.38	1	4	4	1	421.9	404.2

23.25	18.8	1	4	4	1	36.3	25.3
3.1	11.71	1	4	4	1	138.5	139.8
25.66			3	1	1		5
13.79	19.46	1	4	4	1	19.3	26.8
			1	1			
20.63	14.97	1	4	4	1	35.5	31.3
	25.69			2	1		
	10.31		1	2	1		
12.03	17.62	1	4	4	1	20.1	16.2
10.63			3				2.6
38.36	19.38	1	4	2	1	4.7	3.3
38.18	35.68	1	3	4	1	2.9	4.8
8.63	7.87	1	4	4	1	138.5	146.9
10.06	12.85	1	4	4	1	43.6	55.9
8.26	14.6	1	4	4	1	50.4	51.9
		1		1	1	2.3	
35.99	14.21	1	4	4	1	18.3	6.2
18.18	9.64	1	4	4	1	8.4	20
	8.71			2	1		
2.55	6.37	1	4	4	1	209.6	204.6
11.08	12.03	1	4	4	1	89.1	98.7
2.57	12.17	1	4	4	1	72.8	70
41.72	38.6	1	4	4	1	2.8	1.8
12.93	11.01	1	4	4	1	115.5	118.1
32.79	45.4	1	4	4	1	7.6	9.4
	28.2			2			
13.88	25.24	1	4	4	1	372.8	315.8
19.69	32.67	1	4	4	1	26	23
8.03	5.22	1	4	4	1	127.5	124.6
46.37	27.72	1	4	4	1	4.4	4.1
29.87	18.77	1	4	4	1	26.9	63.8
19.38	49.01	1	4	4	1	3.6	7
28.59	4.6	1	4	4	1	83.1	54.5
13.17	7.91	1	4	4	1	181.7	125.5
	21.07			2			

	20.59			2			
51.37	11.24	1	3	4	1	12.7	
7.47	18.25	1	4	4	1	55.2	40.4
			1				2.3
51.69	15.07	1	4	4	1	15.2	25.9
17.9	40.79	1	4	4	1	41.2	24.5
27.65	12.02	1	4	4	1	48.8	84.5
8.45	14.01	1	4	4	1	240.2	261.4
15.55	15.04	1	4	4	1	28.9	35.3
11.1	6.29	1	4	4	1	139.3	140.1
23.12	6.85	1	4	4	1	3310.9	5714.1
18.23	13.1	1	4	4	1	47.9	36
51.58	25.3	1	4	4	1	11.4	15.4
13.98	8.39	1	4	4	1	37.8	49.1
32.27	14.68	1	4	4	1	7.5	7.7
15.42	42.83		2	4	1		
7.25	5.48	1	4	4	1	208.5	222
				1	1		
12.42	15.01	1	4	4	1	6.2	11.5
12.52	13.58	1	4	4	1	47.4	49.2
5.57	4.15	1	4	4	1	213	201.9
60.29	49.44	1	4	4	1	2.4	2.7
16.05	15.36	1	4	4	1	14	15.6
18.04	33.1		2	4	1		
65.87	52.13	1	3	4	1	4.4	2.7
20.44	17.01	1	4	4	1	2.9	7
20.06	12.77	1	4	4	1	30.5	24.8
7.19	15	1	4	4	1	55	62.4
21.69	25.14	1	4	4	1	29.5	35.9
3.64	8.48	1	4	4	1	358.7	317.1

31.25	13.27	1	4	4	1	33.7	23.3
24.55	7.76	1	4	4	1	37.6	33.2
8.73	8.65	1	4	4	1	45.9	31.8
	14.05			2	1		
13.31	8.89	1	4	4	1	60.8	67.4
3.78	9.65	1	4	4	1	156.1	154.2
4.94	16.29	1	4	4	1	95.7	102.5
31.94	17.13	1	4	4	1	5.7	4.8
28.82	8.24	1	4	4	1	18	23.2
9.43	25.12		3	4	1		
7.49	2.94	1	4	4	1	376.2	363.3
12.17	31.72	1	4	4	1	22.4	27.1
5.54	11.78	1	4	4	1	217.7	204.6
26.25	11.39	1	4	4	1	23.8	19.2
7.31			2	1	1		
30.3	23.39	1	4	4	1	6.2	6.7
56.07	49.57	1	4	4	1	1.9	6.1
14.81	16.6	1	4	4	1	20.4	17
32.02	22.43	1	4	4	1	25.5	21.5
2.28	3.3	1	4	4	1	142.9	135.2
21.88	8.1	1	3	4	1	2.8	3
6.52	7.54	1	4	4	1	123.4	126.3
11.08	4.8	1	4	4	1	89.5	88.7
8.64	16.57	1	4	4	1	25.5	18.6
15.45	9.51	1	4	4	1	91.2	98.9
35.64	11.48	1	4	4	1	35.9	17.3
16.59	12.19	1	4	4	1	7.8	24.5
54.71	39.94	1	2	4	1	1.9	
	68.36		1	3	1		
	20.51		1	3			
13.15	8.17	1	4	4	1	37.5	45.9
13.75	4.93	1	4	4	1	268.8	252.5
14.93	8.18	1	4	4	1	97.3	83.1
49.16	46.58	1	4	4	1	17.2	14.7
22.8	8.11	1	4	4	1	117	138.1
28.13	14.2	1	4	4	1	14.3	11.1
20.96	6.87	1	4	4	1	196.9	232.3
16.07	11.45	1	4	4	1	196.4	219.3
16.76	8.47	1	4	4	1	251.1	241.7
14.41	12.04	1	4	4	1	153.8	159.5
31.88	15.59	1	4	4	1	11.2	9.7
16.34	8.86	1	4	4	1	259.1	271.4
4.3	14.85	1	4	4	1	146.5	157.3
16.05	13.73	1	4	4	1	107.6	155.4

37.81	40.41	1	4	4	1	2.8	1.8
30.56	17.97		3	4			2.9
	38.39			3	1		
25.53	40.41	1	4	4	1	6.7	10.3
13.01	17.99	1	4	4	1	5.7	8.5
29.42	33.86	1	4	4	1	14.6	11.1
2.99	7.13	1	4	4	1	550.2	560.6
4.56	11.87	1	4	4	1	62	58.6
3.83	12.17	1	4	4	1	208.6	167.2
			1				
22.36	24.68	1	4	4	1	16.4	15.4
19.75	17.55	1	4	4	1	87.8	86
36.08	31.6	1	4	4	1	35.2	20.1
6.58	12.93	1	4	4	1	147.3	134
11	12.68	1	4	4	1	31.3	26.5
29.02	27.98	1	4	4	1	19.8	30.4
54.57	19.8		4	4	1		2
20.58	25.4	1	3	4	1	9.6	
61.37	53.35	1	4	4	1	23.8	30.1
36.47	18.4	1	4	4	1	18.3	12.1
15.54	7.34	1	4	4	1	227.9	213.5
5.4	6.59	1	4	4	1	1122.6	1044.1
	34.23		1	2			2.1
56.31	1.2		3	2	1		4.4
30.38	6.81		4	2			2.3
65.86	10.8	1	2	3	1	2.4	4.1
19.48	93.85		3	4	1		2
3.85	5.71	1	4	4	1	266.5	276.5
5.94	8.21	1	4	4	1	139.8	171.4
4.1	10.88	1	4	4	1	135.5	148.6
7.72	6.28	1	4	4	1	3156.4	3120.2
10.93	14.26	1	4	4	1	67.6	109
26.12	49.33	1	4	4	1	5.8	3.3
4.22	3.19	1	4	4	1	236	217.5
5.27	9.33	1	4	4	1	67.8	64.1
8.5	6.31	1	4	4	1	113.9	101.3
12.39	20.55	1	4	4	1	105.9	96.5

11.74	14.97	1	4	4	1	49.2	38.2
43.22	15.3	1	4	4	1	3.6	2.3
39.16	21.27	1	3	4	1	2.6	6.4
44.44	26.64	1	4	4	1	5.4	2.1
21.53	48.05	1	4	4	1	4.2	3.6
0.13	5.08	1	4	4	1	449.7	492.3
54.32	21.34	1	4	4	1	5.7	10.1
16.23	16.57	1	4	4	1	42.5	37
9.55	16.25	1	4	4	1	131.7	121.8
7.53	35.73		2	4	1		
18.58	28.4	1	3	4	1	7.8	5.5
37.75	63.41		3	4	1		2.4
29.16	23.43	1	4	4	1	10.9	9.4
		1	1	1	1	3.1	
38.75	55.97		3	4	1		
41.82	53.45		4	4	1		3
15.78	7.29	1	4	4	1	186.7	180.7
18.5	42.41	1	4	4	1	5	4.4
	39.88		1	2	1		
17.78	35.48	1	4	4	1	15.1	13.6
41.87	9.81	1	4	4	1	10.4	4.5
	49.67			3			
44.54	18.29	1	4	4	1	34.6	24.2
53.77	7.44	1	4	3	1	5.2	3
90.48	57.94		3	4	1		2.6
29.61	65.83		3	4	1		
22.28	19.32	1	4	4	1	59.4	55
26.41	43.53		2	4	1		2.4
48.22	9.58	1	4	4	1	11	13
44.86	19.76	1	4	4	1	7.1	7.9
33.36	43.1	1	4	4	1	10.2	5.6
46.78	8.07	1	4	4	1	13.1	5.3
21.82	11.14		2	3	1		
48.56	11.41	1	4	4	1	14.8	4.5
	67.79		1	2	1		
19.19	30.68	1	3	4		4.2	2.4
20.67	37.64		3	3	1		
49.21	13.45	1	4	4	1	2.1	7.6
10.36	6.68	1	4	4	1	205	194.5
13.04	38.72	1	2	4	1	2.1	2.1

7.53	27.24		2	3	1		
11.92	13.23	1	4	4	1	24.7	26.5
15.87	19.75	1	4	4	1	18.3	16.1
4.99	3.63	1	4	4	1	81.8	82.5
26.68	53.98	1	4	4	1	7.9	8.5
15.64	41.86		4	4	1		4.8
65.92	28.85	1	4	4	1	13.6	33.5
46.41	39.18	1	4	4	1	2.3	6.2
13.63	15.75	1	4	4	1	24.7	24.5
6.19	21.47	1	4	4	1	1020.2	799.2
			1	1			
8.46	9.31	1	4	4	1	61.5	60.4
39.88	51.74	1	4	4	1	5.4	11.7
32.09	7.31		3	2	1		2
12.47	11.39	1	4	4	1	38.6	35.6
10.31	25.29	1	4	4	1	7.1	10.6
20.83	18.58	1	4	4	1	27.7	26.4
			1	1			
21.2	15.71	1	4	4	1	13.8	10.1
24.71	22.28	1	2	3		2.1	
		1		1		2.6	
				1			
29.69	67.77	1	3	4	1	4.9	
2.09	8.87	1	4	4	1	131.1	134.8
20.66	13.98	1	4	4	1	32.8	36
12.84	22.93	1	4	4	1	36.5	37.6
	21.83		1	4	1		
26.25	17.36	1	4	4	1	23.7	17.1
32.5	50.99	1	4	4	1	8.9	4.4
26.91	23.24	1	4	4	1	8.6	6.2
	42.5	1	1	3	1	2.1	
3.56	11.68	1	4	4	1	243.3	196.7
11.44	7.11	1	4	4	1	101.5	96.2
5.8	13.93	1	4	4	1	70.6	84.7
7.72	90.89		3	2	1		
			1				
47.46	9.66	1	2	3	1	2.1	
25.23	18	1	3	3	1	2.3	
24.05			2	1	1		
3.21	5.01	1	4	4	1	148.8	150.5
33.62	16.69	1	4	4	1	13.8	5.9
14.75	34.13		2	4	1		2.1
80.98	33.74	1	2	3	1	2.8	

	35.63	1	1	4	1	2.1	
63.06	23.65	1	4	4	1	27.1	17.7
36.65	37.41	1	4	4	1	6	7.6
14.43	8.67	1	4	4	1	1643.8	2087.2
7.86	7.47	1	4	4	1	658	565.8
7.4	14.02	1	4	4	1	287.9	329.1
10.83	18.76	1	4	4	1	63.8	57.4
10.38	5.33	1	4	4	1	56.6	61.5
	54.32		1	2			
16.56	50.23	1	4	4	1	6.3	16.8
3.77	5.87	1	4	4	1	206.8	187.2
12.74	19.27	1	4	4	1	16.5	13.2
4.81	8.79	1	4	4	1	111.8	101.5
22.64	5.79	1	4	4	1	84.5	66.3
54.22	28.88	1	4	4	1	14.1	7.1
17.13	15.61	1	4	4	1	34.4	52.7
12.42	14.79	1	4	4	1	31.5	26.7
3.98	4.5	1	4	4	1	357.2	346.7
	19.72		1	3			
10.61	9.32	1	4	4	1	369.7	375.3
17.69	19.27	1	4	4	1	400.2	378.6
24.33	32.92	1	4	4	1	9.4	18.8
18.99	41.65	1	4	4	1	5.8	10.8
14.26	15.44	1	4	4	1	9.4	11.1
3.94	4.74	1	4	4	1	96.2	115.7
27.91	35.57	1	4	4	1	32.6	23.2
8.15	13.14	1	4	4	1	39.3	36.2
13.72	11.11	1	4	4	1	128.6	101.3
28.22	24.91	1	3	4	1	5.7	
				1	1		
3.5	6.74		2	2			2.4
54.49	23.59	1	4	4	1	5	2
4.64	4	1	4	4	1	5334.1	4727.9
85.33	13.79	1	3	3		2.3	2.1
6	8.82	1	4	4	1	237.2	280
11.59	4.23	1	4	4	1	65.9	68
6.42	2.68	1	4	4	1	362.2	391.9

18.93	13.81	1	4	4	1	10.2	7
	66.48		1	2			
46.73	26.87	1	4	3	1	7.3	2.6
17.6	67.45		2	3	1		
7.78	7.67	1	4	4	1	281.8	259.4
21.6	5.37	1	4	4	1	12	13.8
24.99	45.11	1	4	4	1	5.4	4.1
11.73	32.08		3	2	1		3
6.99	19.16	1	4	4	1	32.6	47.3
36.05	11.17	1	4	4	1	30.5	22.6
20.96	19.57	1	4	4	1	13.8	17.4
24.41	50.12	1	4	4	1	3.4	2.9
3.86	13.64	1	4	4	1	29.4	31.3
5.84	22.8	1	4	4	1	16.5	24.7
	41.07	1	1	3	1	2.8	
9.79	2.76	1	4	4	1	243	208.2
42.46	41.31	1	3	4	1	2.8	
10.74	14.74	1	4	4	1	93	85.3
2.68	4.25	1	4	4	1	325.7	322.9
23.78	15.26	1	4	4	1	45.6	43.2
2.95	4.57	1	4	4	1	274.5	291.5
15.84	9.59	1	4	4	1	61.5	53.8
27.48	17.08	1	4	4	1	30.2	64.2
3.69	14.94	1	4	4	1	192.6	181
12.77	43.48	1	4	4	1	14.1	25.3
21.26	44.07	1	4	4	1	18.3	20.9
15.18	42.53	1	4	3	1	3.1	2.4
8.97	5.9	1	4	4	1	788.9	893.8
8.97	8.07	1	4	4	1	122.3	143.4
9.02	7.96	1	4	4	1	17	22.3
30.1	28.59	1	4	4	1	14.4	7.1
16.4	38.22	1	4	4	1	24.7	29.1
41.21	29.17	1	4	3	1	3.6	4.7
		1	1			2.1	
19.61	18.54		3	3	1		2.1
	36.52			2			
35.05	34.45	1	4	4	1	2.6	9.7
3.42	12.66	1	4	4	1	392.9	347.6
33.42	26.66	1	4	4	1	2.1	11.8
77.7	7.08		4	4	1		2.6

5.47	1.29	1	4	4	1	239.3	223.4
27.45	23.13	1	4	4	1	7.1	22.1
	57.12		1	2	1		
58.49	18.78	1	3	4	1	3.7	1.8
47.7	30.25		4	4	1		2.4
24.61	3.64	1	4	4	1	36.8	21.8
12.54	21.36	1	4	4	1	9.7	25.6
13.76	12.82	1	4	4	1	20	28
6.9	12.13	1	4	4	1	109	131.5
17.21	14.37	1	4	4	1	28.2	25.1
28.53	19.93		2	4	1		
	45.15	1		2	1	2.9	
10.64	5.54	1	4	4	1	164.5	161.6
50.62	48.8	1	4	2	1	5.2	4.8
			1	1			
	7.68			2	1		
			1		1		
17.39	14.24	1	4	4	1	15.1	22.3
11.8	3.28	1	4	4	1	125.9	99
	5.27			2	1		
9.62	5.87	1	4	4	1	90.8	64.7
6.02	10.35	1	4	4	1	365.6	284.1
18.05	7.73	1	4	4	1	41.9	44.8
9.77	6.63	1	4	4	1	268.5	304.6
56.28	36.58	1	4	4	1	7.1	6.8
13.55	24.68	1	3	3	1	4.1	
18.63	11.98	1	4	4	1	84	83.1
16.28	6.31	1	4	4	1	64.6	58.9
78.54	30.76	1	4	4	1	4.4	3.3
	21.25		1	2	1		2.1
42.41	13.21	1	4	4	1	4.7	4.5
13.03	19.01	1	4	4	1	30.7	23.9
14.23		1	4	1		12.2	7.9

				1	1			
					1			
	38.41				3			
22.94	28.92		1	4	4	1	2.3	5
40.16	18.7		1	3	4	1	2.9	2.4
33.06	28.78		1	4	4	1	5.4	8.5
3.91	10.58		1	4	4	1	194.3	190.7
31.11	23.13		1	4	4	1	26.1	15.4
28.46	15.39		1	4	4	1	24.8	23
34.16	28.97		1	4	4	1	4.2	3.6
19.35	12.72		1	4	4	1	102.7	99.2
17.47	20.11		1	4	4	1	712.9	675.6
7.27	18.55		1	4	4	1	72.5	66.3

Abundances (Normalized): F6: 128N, Sample,	Abundances (Normalized): F6: 129N, Sample,	Abundances (Normalized): F6: 130N, Sample,	Abundances (Normalized): F6: 127C, Sample,	Abundances (Normalized): F6: 128C, Sample,	Abundances (Normalized): F6: 129C, Sample,	Abundances (Normalized): F6: 130C, Sample,	Abundances (Normalized): F6: 131, Sample,	Abundances Count: F6: 126, Sample, wt, pool
28	36.5	24.7	37.6	41.7	32.3	34.8	44.4	6
75.7	72.6	99.6	123	133.1	135.5	144.1	145.4	8
132.2	131.7	129	97.3	104	98.2	108.7	108.4	7
2	1.9	1.8		3.1	2.4	5	4.2	
100.8	91.4	98.6	105.5	115.5	100.7	93.5	98	6
			1.6	1.6	5.8	5.5	1.9	
57.7	66.4	54.8	131.6	128.8	147.7	171.3	135	8
48.8	52.7	47.2	53.2	56.7	36.6	53	57	3
153.3	151.6	140.3	135.5	122.6	127.3	123.7	114.1	6
117.1	123.2	146.5	145.9	153.8	152.6	147.8	141.8	7
15.6	15.6	22.1	18.6	19.9	26.6	19.1	21	1
38.5	34.8	30.7	51.3	57.8	51.4	46.7	40.4	7
1696.3	1579.5	1488.3	1407.1	1475.2	1386.3	1588.5	1598.7	27
34.2	37.1	33.1	86.8	116.5	91.4	110.2	98.7	2
40.3	35.3	37.4	26.7	34	34.8	32.1	28.9	1
19.5	27.3	27.9	19.5	24.9	22.8	18.5	13	2
20.2	13.9	28.5	82.7	58.6	77.2	85.4	86.4	3
33.9	34.1	49.5	69.6	55.3	67.1	84.2	58.7	5
40.2	31	42.9	27.8	26.2	18.9	21.4	27.4	4
43.1	43.1	43.1	80.9	63	70.9	82.5	63	5
120.8	133.5	130.2	127.2	132.8	123.1	154.1	149.6	9
95.9	107.3	83.2	76.8	75.9	72.3	91.7	91.4	7
85.4	83.2	61.9	67.1	92.6	76.2	89.5	92.7	9
60.7	77.7	93.9	84.4	117.4	66.1	106.5	96.9	8
680.3	705.3	668.5	641.5	668.7	585	667.8	697.4	13
602.3	531	499.2	472.6	356.3	515.2	525.4	511.3	17
		1.6			1.8			
		1.6		2			1.5	
84.4	95.3	122.8	115.4	117.1	111	94.8	115.1	4

6.8	12.9	9.2	12.6	11.7	14.8	12.9	11.4	2
222.1	224	299.8	300.1	330	280.9	244.3	275.2	9
12.4	12.1	6.8	11.8	15.5	6.8	6.8	18.4	4
2.7	4.2	1.6	2.4	2.6	2.6	3.1		1
91.2	99.7	81.7	92.5	70.8	84.2	92.4	88	1
22.3	27	30.6	32.6	30.5	34.1	29.1	31.6	1
99.2	97.4	88.2	70.7	81.6	75.4	67.5	73.3	8
432	406.7	376.2	208.2	201.1	213.9	238.9	243.8	9
211	205.7	197.9	153.4	157.9	138.8	147.6	152.6	7
114.1	140.8	133.1	69.6	90.9	73.3	83.8	83.9	4
74	91.1	96.7	232.3	244.8	209.7	266.8	234.1	8
12.6	15.6	24.4	36.4	43.7	38.3	41.9	48.4	3
13.4	9.3	23.3	29.2	34.5	19.2	28	26	2
6.1	7.7	9.6	11.8	20.6	8.2	21	19.4	2
162.7	172.9	223.9	314.1	386.2	290.5	383.7	354.3	9
29.8	40.2	56.3	79.2	89.1	62.5	78.2	79.7	6
				5.1	1.6		2.5	
45.5	66.6	83.4	140.1	180.1	134.7	167	158.8	6
6.6	7.1	5.2	7.3	6.8	10.1	6.8	10.7	1
17	13.3	21.7	20.3	26.2	18.4	20.9	17.5	2
4.2		1.9	2.4	5	2.1	2.9		
233.8	214.3	199.2	190.3	188.9	196.7	158	164	3
1629.3	1552.8	1405.3	1281.4	1149.1	1329.1	1217	1180.2	3
297.2	332.4	307.7	189.9	201.1	186.7	206.2	197	7
105.8	105.6	92.5	79.3	94.1	76.2	94.1	91.9	11
36.5	49.7	64	82.1	72.2	75.8	41.2	67.7	2
62.9	71	82.1	94.1	96.5	100.1	75.1	94.5	4
4	2.6	2.2	3.4	3.2			4	1
2	2	3.3	3	5.2	3.8		4.1	1
8.8	10.1	9.6	12.5	12.4	19	10.3	6.7	1
3.3	4.7	4.1	8.1	13.8	16.2	18.2	9.9	2
37.6	55.9	45.1	51	48.3	55.2	50.9	45.3	9
210.3	212.9	221.9	238.1	225.4	221.6	271.8	267.7	8
30.3	32.4	35.1	42.9	40.2	35.9	42.6	41.6	6
50.2	42.2	53.9	70.3	61.7	56.2	73.1	65.4	3
247.2	265.3	279.9	322.6	347.8	276.8	375.8	333.4	14
2.4		2.1	4.3	6.7	2.5	9.5	8.6	1
2.8		4.1	4.5			5	2.2	
95.9	105.7	123.7	136.9	154.2	117.7	161	136	6
180.1	170.3	178.1	298.4	299	327.7	318.7	299.2	7

29	36.3	40.7	44.6	46.6	49.1	51.7	50.8	4
2.4	6.4	7	7.6	7.9	7	2	4	2
26.3	25.4	31.1	47.8	43.8	49.1	49.4	46.5	5
120.5	118.5	132.5	165.4	177.4	163.5	192.4	173.1	7
2.3	1.5	4.5	3.8	9.3	4.4	11.7	10.4	1
	1.8			1.7			1.6	
15.3	21.7	18.7	24.5	26.1	20.5	34.1	37.2	2
19.2	16.3	27.2	23.2	36.3	21.7	22.8	22.2	5
35.1	49.7	52.5	171.9	229.6	161.8	192.8	177.3	3
28.4	38.8	34.4	113.7	141.1	107.5	137.5	132	5
218	210.7	269	359.8	415	310.5	386.2	362.6	4
23.5	26.7	23.8	32	35	28.9	32.8	38.1	1
5	1.9	3.2	4.1	8.2	9.3	8.6	8.8	1
			3		2	2.4		1
	1.5							
304.5	299.6	308.5	284.5	281.4	308.1	299	287	7
235.5	241.7	227.2	274	285.7	288.1	327	301.9	9
141	140.5	118.9	126.1	131.4	128.2	147.2	144.9	4
760.7	683.9	668.4	559.5	600.4	542.9	613.7	604.3	16
17	18.1	11.8	14.4	18.1	14.6	15.5	13.6	1
39.9	34.4	39.8	39.5	48.8	42.1	53.4	47.3	2
165.3	200.4	183.9	223.5	224	203.8	240.1	230.3	7
39.7	39.3	42.3	53.5	58.1	44.2	58.9	45.8	1
6.8	9.6	8.8	10.2	7.2	9.4	10.3	8.8	2
12.9	9.7	12.8	14	8.6	20.7	11.9	17.8	2
131.7	138	115.9	95.2	98.7	96.7	96	116.2	10
23.9	21.4	26.3	40.6	40.6	35.7	36.4	42	2
134.2	155.2	133.1	131.7	122.3	137.5	160.8	141	11
	5.7	3.6	2.9	5.3	5.5	10	8.5	2
5.9	7.4	13.6	13.8	16.1	17.5	8.7	13.8	2
2		1.9						
197.5	198.2	182.5	144.6	142.6	172.2	143.8	154.8	9
14.4	17.9	15.5	10.4	9.2	15.2	6.7	17.1	2
405.9	361.7	341	299.5	295.6	332	325.3	322.8	10
31.8	30.7	54.9	88.5	67.5	69	38.3	71	5
40.6	35.2	63.6	63.4	64.8	45.3	51.4	54.2	4
			2					
14.1	10.2	13	10.9	11.4	5.8	4	8	4
6.4	10.8	9.4	6.2	1.6	10.3	4.2	2.3	2
424.6	286.1	268.6	251.6	198.3	157.2	149.7	256.5	8
367.3	360.6	328.1	291.4	295.1	293.4	232.7	241.9	8
193.8	180.7	175.3	145.1	133	119.5	136.7	132	6
16.1	20.7	12.5	4.5	8.4	12.6	11.7	7.4	1
72	67.1	54.2	47.7	33.6	46.1	33.1	34.8	3
326.7	312.3	261.4	218.1	224.8	244.4	205	211.8	5
19.9	33.9	23.3	21.6	25.9	24.5	28.1	22.8	3

26	33.4	31.6	13.8	21.5	24.8	30.7	28.1	4
19.2	11	23.5	32.6	32.1	32.8	20	39.6	5
5.9	8.8	13.5	11.1	11.8	16.2	6.7	11.5	2
2	2.8	2.4	1.8	2.5	3	2.7	4.2	
13.2	12.4	6.8	11.5	15.9	11.2	13	20.6	2
	2.3	2.9		2.1	2.4		1.8	1
32.8	28.1	29.6	33	27.1	19.9	30.5	27.9	1
		2.4			2.5			
2.4	4.3	2.9	3.5	3.4	3.8		2.3	
13.3	5.1	12.8	44.3	38.6	56.7	55.4	37.5	2
2	4.7	2.1	1.8	3.1		2.8	1.7	1
19.2	17.7	11.9	11.7	10.7	5.2	13.3	12.8	6
19	34.4	28.3	33.3	27.8	26	30.3	34.5	6
51.6	44.5	47.7	29.4	40.4	41.7	44.7	47.2	11
27.7	32.1	37.8	23.6	23.5	25.9	19.6	31.1	3
3.8	3.8	2.3	2.9	2.5		3.2	2.6	1
35.8	30.4	29.4	17.8	20.5	12.2	13.4	13.4	3
			2	1.4	2.9	3.2		
7.1		11.6	9	7.6	6.3	5.5	6.7	1
90.2	78.4	102	141.7	124.4	119.9	116.8	112.4	10
582.7	548.4	676.6	794.1	688.3	682.3	626.2	643.7	9
436.1	440.1	517.7	597.4	522.8	518.4	493.9	526.5	9
212.9	185.8	272.8	292.6	262.2	260.6	232.2	242.7	6
5.4	11.1	11.7	4.3	3.4	3.5	5.4	3.5	1
25.9	20.7	23	25.4	22.4	17.7	18.7	17.4	2
107.5	136.1	130.4	84.4	81.9	80.2	72.2	89.2	6
16.8	17	18.1	19	24.1	19	19.8	17.9	1
18	19.6	20.2	11.1	14.5	14.8	5	14	1
25.9	29.3	32.9	14	13.4	14.8	17.7	12.1	2
61	75.5	56.3	41.7	32.9	32.7	37.1	41.9	3
14.4	12.5	9.1	9.8	7.1	9.4	9.2	10.3	4
				4.5				
9.6	3.8	9.3	8	9.9	2.4	9.2	11.9	1
6.4	4.1	4.4	2.4	8	2	7.2	2.1	1
	1.8	1.5			1.6			
342.4	336.2	368	308.3	325.4	251.1	304.5	288.9	4
5.7		7.6	2	3.6	2	2.5	4.2	
43.1	39.2	39.1	38.9	42.1	44.2	57.9	45	7
30	29.1	25.1	16.8	23.5	27.5	23	26.8	2

2.1							1.6	
42.6	61.1	66.2	119.6	117.8	131	69.8	108.7	8
351.5	332.1	289.3	217.9	301	325.7	227.8	243.7	7
2.8				2.3	4.7		3.5	
243.8	298.6	284.7	227.7	295.7	229.3	266.2	271.3	53
11.6	22.2	22.9	53.6	52	55.8	22.9	45.6	3
69.2	95.5	82.2	153.1	164.2	187	110.5	135.7	7
15.3	24.2	17.8	14.7	14.2	13.4	10.4	21.4	6
115.3	158.3	162.1	296.9	286.4	274.6	166.5	227.8	4
60.7	88	98	185.9	183.6	175.6	116.4	150.7	5
99.3	137.1	167.5	319.1	327.7	297.8	173.2	268.5	8
62.9	82.4	98.1	132.7	146.1	140.7	87.6	114.9	2
31.8	40.3	44.7	63.2	74.1	70.6	49.1	69.3	3
				2.5				
2.4	8.2	3.3	4.1	3	4.4	3.3	7.4	1
4	1.8		2.1	4.1	1.8	4.2		
375.5	398.7	360.6	442.8	452.6	439.6	482.4	441.6	12
11	11.9	10.7	11.9	10.4	17.1	11.2	11.1	1
8.8	16.8	20.5	27.8	33.1	27.5	13.5	30.1	1
641	651.6	980.9	1088.4	1184.4	1062.7	784.9	979	9
12.4	13.3	13.6	17.8	21.9	16.5	18.5	20.8	1
315.3	271.5	262.1	321.6	304.4	347.7	318.7	329.2	11
51.6	65.9	79	95.8	101.7	98.9	71	99.5	4
52.2	60.3	61.3	48.4	53	53.5	49.5	48	3
168.6	199.1	179.5	140.9	165.9	147.2	161.9	171.4	6
	1.5			1.6				1
57.8	70.4	85.9	72.8	94.7	60.3	63.6	77.9	7
14.4	37	25.8	11.7	31.1	7.7	7.5	20.6	4
5.4		4.8	3.1	1.4		1.7	5	
625.7	662.6	893.4	710.9	870.6	578.3	672.4	727.3	6
2.7				2.5	2			
9.1	9.4	14.1	10.4	12.8	8.9	10.8	12.7	1
26	17.1	33.9	33.2	20.6	13.4	51.7	59.7	4
8.8	8.8	15.9	5.9	21.1	8.7	6.8	15	1
321.4	344.5	424	504.7	464.8	510.8	366.5	464.3	9
17.5	15.8	26.9	30.8	13.3	10.6	28.8	23.5	3
47.7	40.7	40.9	27.4	35.3	35.3	29.1	36.1	8
9.2	15.6	16.7	6.9	4.9	7	8.6	5.8	2
1.8		1.6		1.5				

			3.7	2.1		4		
3.1		2.2						
293.8	297	255.8	205.5	220.8	216.4	247.7	260	17
38.3	32.7	38	36.4	30.1	21.1	30	23.4	5
74.8	79.6	63.6	37.2	45.7	35.9	43.4	47.7	5
				4.7	1.6	2.4	2.3	2
								1
2.5			3.1	3.9	2.4	3.6	3.8	1
316.3	280.2	271.8	233.3	224.1	220.3	254.6	240.7	8
3.8	8.4	4.5	3.8	6.3	10.1	11.1	3.1	1
33.2	44.9	47.9	43.4	37.2	30.5	52.2	57.2	8
2.3			3.9	3.2			2.9	1
			2.1					1
3.4	5.2	6.2	6.9	10.4	7.7	5.8	11	1
13.9	16.5	14.3	16.5	20.5	15.8	11.2	18.4	5
12.7	8.7	9.1	9.4	11.4	11.9	13	10.8	1
60.1	65.3	74.2	57.2	55.7	45.1	61.9	59.6	3
2.5	9.7	10.2	7.7	9.2	8.9	6.8	10.4	1
2.1		3.6	5.1	3.9	4.7	2.5	4	1
					2.6			
		3.2	2	6	4	1.9	4.3	
165.5	182	159.6	114.3	123.2	126.8	129.2	111.3	4
5	3.8	7.9	5.2	11.5	6.8	10.6	6.2	2
				1.9		2.4		
51.2	35.8	40.9	26.9	22.8	27.2	29.9	26.5	3
4.5	8.7	12.5	10.1	12.6	11.3	11.4	16.6	1
128	146.9	154.2	131.2	176.1	147.9	153.3	136.1	13
885	882.6	812.2	699.5	659.1	775.5	703.7	681.9	11
86.6	104.3	89.8	75.4	63.8	81.2	68.7	59	9
76.1	106.4	84.4	72.1	58.8	71.1	71.4	60.9	9
4.8	2.7	7.3	5.5	4.6	10.1	2.4	7.8	1

82.3	97.1	136.7	78.5	107.8	88.2	77.9	108.1	10
86.7	93.5	124.2	115.1	119.2	88	103	98.4	7
150.4	142	173.2	155.5	162	138	148.5	151.5	9
4.7	5.7	6.4	2.1	7.5		4		2
		2.1		1.3				
42.4	56.9	91.1	79.6	87.5	63.7	70.2	71.3	7
			2.2					
66.3	64.5	65.9	58.5	49.6	65.9	62.1	45.8	2
1.8			2.8				1.7	
128.7	128.4	130.7	88.1	97.4	89.5	76.2	100.1	9
2	6.6	8.5	9.3	7.2	8	16.7	17.2	2
43.3	54.5	58.8	60.3	60.3	56.8	58.4	71	6
17.1	21.6	19.6	17.6	28.1	19.5	20.5	20.3	6
39	50.4	35.8	35.7	39.4	37.3	36.6	39.5	8
67.6	68.2	57.4	58.7	70.7	60.1	54.9	64.4	7
13.7	16.2	25.3	36.7	25.9	19.4	41.2	37.3	7
2.4						2.5	1.5	
188	213.1	178.9	139	130.1	150.3	151.7	147.5	5
17.3	15.7	21.2	19.8	14.7	15.5	21	15.4	1
16.3	15.9	15.5	11.8	12.8	11.4	14.6	10.5	2
2	4.8	1.8		7.3			2.6	1
24.6	23.2	21.9	18	11.2	19.9	22.8	21.1	2
44.1	39.7	40.5	50.7	41.8	45	55.2	54	4
26.9	30.9	33.6	37.2	39.4	29.3	38.3	36.3	1
89.2	92	100	88.2	95.7	95	99.5	102.3	7
266.3	268.5	256.8	213.2	213.1	232.9	207	219.6	18
2.3	1.8		3.9	2.7	5.7	3.5	6.6	2
70.2	57.8	76.9	117.1	111.8	91.4	101.4	87.4	6
86.8	86.2	64.5	61.6	62.4	95.8	95.1	75.7	11
16.4	18.6	27.1	34.1	30.1	22.5	27.5	28.9	2
1616	1505	1549.1	1438.2	1380.4	1273.4	1501.7	1355.9	8
5.2	3.8	3.4	2.2	7.7	2.3	1.7	3.2	2
14.6	16.5	18.3	29.9	29.1	26	22	24.8	1
232.2	250.1	303	463.8	408.8	396.2	323	404.8	4
10.2	4.5	5.3	13.1	11	13.2	7.9	11.5	1
85.6	84.4	85.4	82.6	50.2	59.1	96.2	104.3	7
8.8	12.5	17.7	18.1	5.7	6.7	16.6	19.2	2
9.6	10.2	6.9	19.1	15.3	13.6	18.9	14.3	3
2537.5	2506.8	2385.9	2032.3	2166.5	2070.3	2132.5	1885.6	8
494.1	430.7	336.3	380.8	230.6	408.4	362.9	299.2	3
126.3	155	136.4	104.6	116.6	123.1	128.4	107.9	12

3.1	2	1.6		4.5	1.8	2.3	1.6	1
				1.8	2.6	2.8		1
107.2	110.6	127.8	155.5	164.7	163.3	173	160.6	7
97.3	93.6	89.5	50.6	49.9	49.4	55.2	53	7
10.6	14	12.6	12.1	8.6	12.8	11.7	6.2	1
184.2	205.5	184	155.9	159	162	152.4	174.3	10
2.8	10.2	10.1	59.8	70.4	66.7	80.1	83.7	1
			1.7					
19.9	33.3	35.5	17.6	33.5	29	21.6	25.6	4
202.4	186.8	249.8	217.9	224.3	216.4	167.3	224.2	9
		2.8	2	1.9	1.8	2	1.6	
7.1	12.9	14.9	7.7	13.3	7.7	10.3	7.9	2
				1.7	1.9			1
8.8	3.8	4	3.1	3.5	4.5	3.2	2.9	1
5.1	4.7	11.2	10.6	11.7	7.4	12.7	11.6	1
5.2	10.5	7.1	4.7	7	4	3.7	4.5	1
8.6	9.8	13.5	9.6	11.6	6.4	2.5	10.8	1
41.7	41.5	38.1	31.9	33.6	36.2	24	27.6	3
							5.6	
72.6	71.3	65.2	49.8	54.3	58.4	43.4	66.7	8
2	4.2	6.3		5.4	4.4		1.5	
		1.8				2.7		
		2.1		2.6			2.1	
2.1	5	5.7	8.9	7.2	3.9	5.2	3.8	1
25.9	22.3	28.3	27	27.5	27.9	18.7	18.4	1
72	83	107.7	118.4	100.7	108.6	81.2	85.6	4
140.2	157.3	129.6	102.9	102.2	123.1	123.7	127.8	11
20.2	31.2	39	42.1	20	15.2	32.7	63.8	7
19	21.8	34.9	19	24.1	16.7	28.5	19.6	3
12.6	10.7	14.8	11.7	17	13.1	17.7	14.2	3
16.5	13.4	31.3	24.3	42.2	39	36.7	38.9	6
		2.5	3.5	4				2
		1.7	1.4				1.5	
55	38.6	52.5	50.1	39.4	34.2	53.7	62	8
61.4	49.2	45.1	58.2	38	58.8	63.2	51.5	3
2		3.3	6	10.9	5	8.8	11.1	1
33.1	45.9	38.4	42.9	41.5	25.4	49.1	43.3	7

271.7	244.5	217	268.5	215.8	255.7	288.9	268.2	8
48.8	34.3	39.3	43.5	30.9	44.2	55.4	36.2	3
						1.9		
51.9	79.2	112.6	102.2	100.4	137.9	88.8	99.2	4
2		1.7	4.2	2.8	2.6	2.7	2.2	
10	7.5	9.4	14.3	17.7	11.7	8.2	13.5	3
125.5	81.6	75.8	88.2	81.1	61.7	57	93.2	2
10.5	17.7	10.2	12.2	13.4	5.7	8.2	8.8	4
69	82.1	59	47.3	57.1	52.2	62.3	63	7
2.7	2.4	2.3		3.2	1.5	2.9	2.1	
121.5	127.5	99.9	100.7	100.3	98	94.1	106.7	7
6.6	10.7	4.6	2	2.9	1.8	5.9	8.3	2
2.7	4.2	3.6			1.9		2.1	1
	1.9							
114.1	116.4	113.7	97.4	100.7	98	114	99.9	4
337.9	323.4	284.6	264.9	260.4	270.6	294.9	265.4	4
	5.2	2.2	2.1					
286.4	263.5	265.7	221	212.3	205.9	225.9	230	7
10.9	14.4	6.6	10.7	11.2	12.2	1.7	9.6	
8.1	10.3	9.5	7.1	5.7	7.2	9.8	10.8	2
3.8	9.6	6.1	3.4	9	7.3	5.6	2.6	2
7.1	8.3	8.1	22.8	19.4	15.5	12.2	18.7	3
1.6				2.4		2.3		1
6.9	12	10.5	17	28.6	22.9	16.5	24.2	3
84.7	79.5	86.3	56	76.1	54	81.4	65	4
64.5	56.5	64.3	49.4	55.4	45.5	47.5	47.6	3
24.8	32.1	31.1	33.6	48.9	42.7	49.7	38.5	2
292.6	322	272.2	208.7	204.9	224	213.1	238	7
4	4.6	4.2	10	3.3	4.7	9	10.5	1
		1.8	3.5	2.1	2.1	2.5		1
8.8	8.9	12.4	9.8	21.5	16.6	10.6	18	1
2.3	4	3.9					2.2	
141.9	143.7	129.2	126	106.8	112.5	127.6	117	9
35.8	40.3	34.1	21.5	24.5	36.1	31.6	40.2	6
52.9	64	76.9	65.8	85.9	79.7	74.7	77.4	7
5.7	5.1	6	4.9		5.9	2.7	9.4	1
				3		2.5	4.5	1
405.4	411.8	401.6	386.7	457.2	407.1	424.8	411.8	5
969.4	968.8	938.2	878.6	885.3	888.8	958.4	857.6	8
31.3	32.7	45.2	58.7	45.2	48.4	55.6	59.5	6

		4.6	11	4.6	8.7	5	8.9	
44.6	53.7	62.7	108.7	115.5	107.6	104.3	105.7	7
51.3	39.3	49.3	76.3	67.5	68.3	62.3	65.1	4
6.6	4.7	1.6	6	5.1	5.2	12.2	12	
		1.8	1.6	3.5	4.1	8.4	2.2	
220.4	215.7	223.2	200.3	191.9	208.7	177.3	202.3	8
16.3	14.3	16.4	19.9	16.7	28.5	13.8	22.6	2
5.9	19	8.9	9.4	9.1	4.4	8.4	12.9	4
							1.8	
21.8	19.1	15.9	19	29.3	34.9	34.8	40.1	1
							1.7	1
2			2.8	1.5	4.8	2.1	2.5	
6.1	1.7	2.4	5.2	3.6	1.9	3.1	2.9	1
	2.7	3.9	5.2	8.4	8.7	4.2	2.9	
5.4	7.5	7.2	10.9	10.4	8.2	6.2	11.3	1
32.8	36.3	58.6	37.9	56.2	69.1	27.5	59.4	6
360.5	161.2	240.4	570.4	398	315.4	284.7	348.1	8
64.5	82	84.7	68.2	80	67.7	59.3	68.2	7
	1.9							
							1.4	
1778.5	1825.4	1742.2	1921	1891.1	1923.5	2037.5	2004.4	9
	1.9	1.8		1.7			1.9	
453.3	447.7	448.1	326.1	339.3	341.1	297	284.4	9
148.7	173.2	152.4	112.5	135	140.7	113	126.6	8
3	7.9	8.1	3.8	6.4	6.8	6.2	7.8	
36.6	42.9	47.1	66.1	64.2	71	55.4	60.3	8
		2.3	4.1	7.1	3.5	3.9	1.8	1
2.8	2.8			5.9	5.7	5.2	1.7	
26.2	32.7	50.8	43.9	53.7	44	51	45.6	6
105.4	118.2	149.5	142.5	162.1	140.8	120.7	150.3	5
3027.7	3141.6	3008.4	2468.7	2486.8	2430.6	2371.7	2291.7	8
2.7	8	7.7	2.4	7.6	5.4	6.6	6.1	2
779.9	778.4	706.5	637.5	566.5	693.7	605.7	569.8	9
24.3	33.9	17.9	18	16.5	32.4	13.4	19.8	4
7.2	4.3	8.5	14.2	14.7	9.9	6.6	11.3	
12.4	9.7	16.5	10.9	10.3	13.7	7.2	13.6	4

5	4.1	1.9	5.5	8.4	7	1.7	4.5	2
5.2	4	7.2	11.1	1.9	4	3.5	7.2	1
2.4	4.5	3.6	7.7	6.3	4.1	2.5	4.5	
	1.9		2	2.3				
	3.8	2.2	4.2	3.7	3.8	4.7	4.3	1
	2.2		4.5	2.7	1.9	2.8		1
	1.7			1.9				
42	26.4	57.9	64.6	48.7	51.8	59.1	52.2	6
181.5	186.5	185.4	209.1	209.3	222.2	249.4	192.1	5
204.9	198.3	207.9	262.8	286.3	311.7	303.2	265.6	2
5.1	1.9	4.1	5.9	4.1	2.4	5.2	1.8	
3.7	2.7	3	3	3.5	3.5	4.6	3.5	1
62.4	71	74	53.4	52	62.3	58.1	53.8	2
415	424.7	399.9	327.2	328.5	328.8	331.2	319.3	6
86.8	79.5	101.9	129.6	110.5	127.6	84.1	114.4	8
158.4	140.9	159.5	182.5	162.4	187.3	150	144	9
14.6	5	9.9	15.3	15.1	12.9	11.1	13	1
333.9	333.6	302.8	262.4	265.1	293.2	278	298.2	12
13.2	14.3	10.1	11.3	11.7	11.2	11	14.2	1
33	35.3	34.9	23.7	26.8	24.6	31.9	28.8	5
20.1	13.8	17.1	8.9	8.1	8.8	8	12.2	2
299.1	305.5	307.6	184.2	236	178.6	221	209	14
88.5	98.5	97.7	64.4	80.1	68.4	72.4	56.5	4
	4.8	3.7	4.7	6		2	4.8	
41.3	38	39.7	41.9	48	38.2	45	52.1	8
4.1	6.9		17.6	10.2	12.6	7.6	9.9	2
48.1	56.8	47.9	40.8	41.4	41.7	51.3	53.1	5
126.3	109.2	105.6	94.5	90.3	100.6	102.3	96.3	5
22.2	10.8	21.7	51.8	44.6	53.7	52.6	46.6	1
	3.2	2.4	3.1	2.6	2.8	3.6	2.4	1
								1
2	2.7	1.6		2.9	2	2.1	2.3	1
99.6	96.8	107.5	96.5	100.1	110.6	90.7	103	5
14.1	15.6	26.5	35.9	33.1	18.1	17.4	28.5	4
19.4	18.2	22.4	21.6	19.2	21.7	15.1	15.9	6
21.9	27	18.5	58.3	58	100.9	60.8	69.2	6
56.6	69.1	59.3	42.2	49	45.6	36.2	48.6	5
26.6	27.3	38.3	34.5	32	21.6	44.9	51.6	7
89.8	94.8	104.8	100.9	90.3	74.5	123.1	122.8	6
567.7	601.4	561.7	476.8	526.4	495.4	619.9	592.8	15
633.8	618.6	539	478.3	447.9	483.2	581.6	505.2	6

53	43.6	49.2	34.5	46.2	38.3	27.5	35.2	6
				1.7	1.8			1
				1.6				
				3.5				
			3.7	1.6	5.5	8.6	2.7	
27.9	26.9	32.1	146.8	153.5	133.4	179.8	159.6	6
			7.7	10.8	8.9	12.2	11.1	
1.7			5.4	6.4	3.8	11.9	7.7	1
	3.6	2.4	89.4	84.1	110.5	134.9	108.7	
				3.1		2.3	8.2	
1.8	3.6	3.8	34.6	37	27.5	29.2	29.1	1
			10.1	4.2		13.7	19.8	
			3.5	5.9	3.8	5.6	7.7	
		2.2	1.8	3.4	2.3	5.8	5.6	
			2.9	1.4		2		
21.8	13.5	36.1	112.3	137.2	125.4	152.1	118.6	4
	6.4	1.7	10.2	17.1	10.3	18.5	14.7	1
			2.5	5.2	4.7	2	4.7	
					1.6		1.7	
2.4		1.8	22.4	28.1	22.6	32.9	27.2	
3.3	2.7	3.3	1.8	3.3		2.4	7.1	
2129.5	1959.9	1547.5	1224	1351.6	1701.8	1204.2	1190.5	8
77.8	74.1	119.2	121.5	159.4	113.8	121.2	132.6	9
102.3	107.1	144.5	185.5	220.1	178.7	189.1	194.4	9
159.8	174.9	149.5	143.9	139.3	174.3	164.3	159.5	12
141.2	165	170.4	154.7	179.2	159.5	205.3	190.9	25
16.5	12	16.1	48.9	42.4	42.2	83.6	69.5	3
32.1	28.1	30.6	37.1	40.4	36.8	45.1	40.7	1
5	8	6.3	37.4	27.5	42.1	45.8	42.9	2
179.6	183.8	183.7	185	201.1	187.3	215.9	189.6	8
53.6	71.3	80.3	111.3	130.6	111	124.7	115.4	7
2.1	1.8	1.7	2.2	2		3.7	1.6	1
	1.8							
89.2	71.9	73.7	69.5	52	72.5	76.9	62.5	5
211.5	200.2	218.2	190.9	199.5	182.1	218.1	189.1	6
89.4	87.9	96.7	69.3	70.1	80.6	83.8	82.4	7
5.8	1.8	1.4	5.2	5.8		5.2	1.9	2
42.6	29.2	35.5	22.5	36.9	41.4	33.2	34.7	6
137.9	146	123	89.7	81.9	99.7	95.2	94.9	12

4.4	2.7	3.9	2	1.5	2.8		2.5	
5.4	6.9	7.5	2.6	8.8	4.4	7.8	8.6	1
21.1	16.6	10.9	20.6	11.8	5.2	11	6.7	2
	4.7	2.3						1
42.6	31.4	27.4					1.7	2
120.8	120.9	122	61.1	66.7	59.2	61.1	65.2	10
139.6	149.9	151.5	115.8	122.3	97.2	125.9	114.9	9
156.6	145.1	138.2	94.6	116.2	93.5	101.1	98.8	7
41.7	46.4	49.1	32.8	45.7	32.3	30.5	37.7	4
9.9	8.8	10.1	15.9	11	11.6	12.2	9.2	2
128.1	117.5	126.1	122.6	82	73.8	132	159.3	8
59.4	78.1	65	67.4	67.6	60.6	61.2	66.5	2
89.7	84.7	63.9	73.9	59.6	83.5	69.6	63.5	2
83.3	88.1	112.4	132.3	148.8	133.2	139	137.6	6
137.2	154.2	152.9	180.2	209.7	200	211.6	213	5
193.6	194.4	242.6	308.5	318.8	301.4	308.8	308.9	9
3.5	3.3	3	7.9	9.8	3.6	7.8	7.4	1
16.7	13.5	17.3	29.4	33.2	29.7	34.8	29.5	1
	2.2						1.9	
1907.5	1985.9	1899.7	3036.9	3260.3	3186	2914.4	2750.3	8
289.8	259.7	216.8	302	221.7	312	304.8	266.6	12
514.8	497.5	462.6	357.7	358.4	387.8	385.5	368	15
260.5	252.9	324.8	278	269.7	289.6	240.5	277.5	6
53.5	60.3	62.8	53.6	64.3	70.3	48.7	56.2	2
			2.1	3.4	3.4		3	
232.5	243.1	295.9	269.3	264.4	280.3	197.4	256	2
173	183.5	165.8	114.2	104.3	111.1	130	124.1	4
101.7	119.4	125.4	90.5	67	65	111	120.7	8
26.3	28.3	43.9	50.7	47	27	71.6	77.5	5
	2		6.6	6.5		4.4	4.8	1
30	27.9	26.5	49	43.7	45.8	39.5	42.8	3
37.8	28.8	44.8	43.3	52.2	42.7	59.2	48.8	4
36.8	32.7	43.1	49.4	47.8	41.2	38.3	46	2
563.4	540.6	482.3	403	355.8	398.6	409.2	391.7	3
3.1								1
88.1	86.9	60.4	61.9	67.5	76.8	71.8	73.9	9
4.7	4.3	5.8	3.3	1.7	3.8	3.2	5.1	3
7.5	14	8.4	3.9	10.6	5.4	10.3	13	3
57	61.9	63.4	42.1	59.4	62	65.6	73.8	10
7.2	7.4	8.4	7.9	5.5	8.7	5.8	8	2
147.2	149.3	153.7	99.9	126.5	82.7	112.4	105.2	17
24.6	34.3	31.9	16.1	30.7	14.5	23.7	24.7	5
25.9	39.9	40.5	33.6	39.1	34.7	43.5	41.9	4
21.4	28.3	37.3	32.9	47.3	40.2	27.9	31.9	2

66.2	76.8	76.6	153.2	178.1	143.8	157.9	149.7	7
324	315.8	351.3	209.5	204.5	182.8	209.7	215.8	9
135.1	146.3	130	98.1	101.5	98.3	103.2	100	7
	1.8			2.7	2.4	4.3	2.5	1
3.7	3.2	7.6	9.7	8.7	4.4	9.4	8.9	1
4.8	12	10.5	5.4	13.5	12.4	15	15.1	1
445.4	438.1	442	390.6	362.5	351.9	448.5	413.6	16
347.7	361.7	349.2	282.2	285	274.4	289.5	299.9	10
		2.8	3.3	7.2	2.8	4.6	3.5	
77.8	90.8	107.9	115.1	128.7	106.2	105	111.2	6
605.2	520.1	533	337.6	327.2	323.3	414.7	335.5	9
27.7	29.6	37.3	55.5	52.4	51.2	43.4	43.8	8
8.1	6	17.1	16.8	12.6	8.8	4.7	13.5	3
24.8	28.4	36.5	27.8	31.5	29.8	29.7	30	5
5			1.7	5.6	2.6	4.7	3.5	2
7.2	5.1	6.6	5.6	7.9	9.1	11	7.1	3
114.9	105.9	90.5	60.2	43.9	57.8	63.3	62.8	5
			2.1		2.3			
12.9	17.6	16.5	2.9	14.5	9.8	11.4	14.7	3
36.5	36.7	31.9	22.5	33.8	30.3	32.4	39.2	6
24.3	20.8	26.6	15.6	20.4	27.9	18.6	29.3	5
93.8	75	76.4	67.8	67.2	67.4	84.2	76.9	6
5.4	1.7	4.8	6.4	1.9	4.1	2.4	1.6	1
					1.6	3.2	3.2	
9.3	10.1	6.6	8.3	5.8	9.8	4.4	8.7	1
				2	2		2.5	
	3.7						1.7	
113.3	132.5	125.5	195.2	189.1	166.8	167.8	170	7
41.7	33.7	51	60.4	66.6	63.5	61.6	59.7	5
24	24.4	41.7	45.9	54	46.6	52.2	53.4	5
			1.6	1.5		1.7		
13.7	15.3	24.2	10.6	12.7	25	21	16.4	5
64.4	82.9	80.1	115.4	97.4	120.4	96.4	101.9	8
4.2	2.4	6.9	9.3	16.6	15.2	6.6	16.4	1
10.3	12.6	3	3.9	7.8	9.2	9.5	3.7	1
12.6	19.8	21.2	23.6	33.8	25.4	27.6	23.3	1
224.5	222	212.5	194.8	195.8	197.3	194.3	210.8	3
1740.3	1727.4	1651.5	1548.8	1586.9	1566.3	1644.6	1536.5	9
64.1	48.6	85.4	70.8	76.8	60.8	86.6	67.8	7
14	18.9	27.4	35.5	39.5	48.6	36.3	37	4

2.4	1.9	5.8	2.5	2.6	2.3	3.2		1
4	4.2	2.5	3	8.7	2.6	4.3	9.2	2
231.1	238.5	211.5	189.7	205	218.8	223.8	239.5	8
1043.7	1113.9	1335	1655.8	1508.8	1586.6	1216.2	1402.5	9
37.9	46.9	51.9	74.6	78.6	70.5	56.6	76.2	5
37.9	42.3	46.1	57.8	53.6	52	44.2	47.8	4
30.6	39	46.9	56.6	49.3	42.7	34.7	44	2
15	13.1	15.9	14.9	20	12.1	23.2	21	2
14.6	14.3	23.4	21.1	22.6	25.5	30	26.7	3
20.4	18.7	28.3	15.7	24.7	26.1	19.8	30.1	4
385.9	418.6	394.8	379.1	406.8	367.3	434.8	403.8	17
51.2	55.7	62.3	84.4	77.4	77.3	62.4	76.4	6
457.4	498.3	452.5	430.2	421.2	425.1	447.7	424.8	7
80.2	82	71	52.8	59.1	37.8	55	62.2	5
231	241.6	202.6	178.5	170.7	180.2	172.9	181.1	7
107.4	101.4	112.9	167.9	152.4	158.8	127.8	145	11
3.3			3.7	3	2.8		1.8	1
7.5	6.2	6.4	2.4	1.4	3.9	1.9	4.8	
201.4	206.5	187.7	184.3	212	215.9	210.9	206.3	6
3.4		2.4		3.6	3.3	2.4	3.3	
			2.1			2		
16.4	24.5	27.5	27.9	25.2	17.8	20.1	20.6	2
	2.7	1.6	2.2		4.3	1.9	4.2	1
			2	4.2	3.6		5.4	
14.3	12.6	19.7	27.8	20.5	15.6	38.7	78.9	6
7.5	16.8	22.2	16.1	15.5	4.7	18.1	33.3	4
13.9	19.5	31.8	31.9	15.1	15.5	46.6	100.3	6
5.5	8	21.7	23.5	15.5	17.8	19.8	62.7	3
3.5	4.1	7.5	3.9	3.2	4.7	5.1	10.8	1
9.2	7.3	4.5	6.3	6.9		1.9	4.5	1
292.1	281.9	281.7	277.1	300.9	260.1	289.1	273	8
55.6	45.3	42.7	52.8	44.2	53.3	45.9	53.7	6
31.5	44.8	36	40.4	41.2	39.6	48.7	49.7	2
302.5	305.1	297.9	258.5	226.2	249.1	249.5	253.8	6
			3.7	5.2	6.9	13.4	11.6	
5	9.8	12	37.1	34.7	34.2	43.4	35.2	1
2.4	4.7		3.8	3.1	3.3	4.2		1
5.5		5.4	2.5	5.7	7.2	2.1	4.8	
2.3		2.3		1.3				

3								
7.5				4.5		5.1	8.8	
	1.8		2.6	1.7				
	1.5		2	1.7			1.6	
17	17.7	16.6	13.2	15.8	14.5	16.7	16.9	1
2.1	2.2			2		4	2.3	1
35.4	34.8	32.7	41.7	36.7	38.8	31.6	39.2	1
3.7	4.2	3.3	3.3	3.5	3.4	5.1	3.5	1
5.8	10.5	11	4.6	9.2	10.4	14.7	11.9	1
14.6	14.3	22.9	20.1	17.1	14.7	16.3	15.6	3
42.3	48.5	53.9	57.2	54.9	50.3	47.3	50	5
	1.9	2.8	1.8	1.7	7	7.2	11	1
	2	1.8						
64.2	98.1	112.8	130	136	145.7	128.3	128.5	5
13.7	10.8	8.8	9.4	10.3	5.5	8.2	9.5	2
8.9	8.3	8.3	11.8	13.9	17	8.3	11.8	1
2		1.9		3.6				
		2.4		2.5		3.2		
18.7	27.4	30.3	40.4	44.5	36.5	33.5	38.6	2
3.3	2.4				2.6	2.4	1.8	1
5.2	2.8	1.4	6.4	6.7	7	11.5	4.7	1
			2.2	2.2			2.3	
45	49.6	66.4	65	50.1	41	83.4	88.7	6
72.8	79.6	84.6	93.2	69.7	54.3	122	190.1	8
42.3	43.7	45.9	41.8	67.9	45.1	49.3	52.2	2
358	351.8	332.4	279.3	288.8	322.9	263.4	262.3	9
42.6	48.5	59.4	45.2	37.5	26.5	67.4	65.1	7
10.2	9.2	8.6	18.6	13	15.2	5	10.6	1
11.6	9.3	11.1	13.4	11.1	15.1	13.1	11.3	1
71.7	71.8	63.4	73.1	86.9	73	69.2	80.8	4
112.4	128.1	109.8	86	100.3	106.7	101.1	112.5	7
2.8	2.2			3.4	2	2.1		
2.1		3.6						
164.2	187.7	165.4	105.4	138.5	113.3	122	123	12
60.8	69.1	59.8	42.3	53.9	50.9	44.2	50.9	8
	2.6	1.9			2	3.9	1.7	
288.5	301	271.5	263.2	251.4	252.9	298.4	294	9
20.2	18.5	28.8	32.9	33.3	25.9	36.3	43.2	3
15	17.2	14.2	14.9	12.6	17	13.8	16.3	1
118	140.8	189.1	218.7	226.7	207.9	175.3	199.3	9
9.5	8.8	22.6	16.5	13.8	13.1	19.3	28.1	3
116.7	121.3	123.4	104.9	118.2	101.1	96.8	108.7	9
208.8	221.3	197.3	204.1	169.6	200.4	194.2	186	6
23.5	22.3	19.1	13.4	15.1	13.8	12.6	15.3	3
8.3	12.8	10	9.8	14.1	13.2	13.4	14.8	3

53	59.8	63.9	74.2	68.1	66.1	60.8	64.5	2
119.7	134.6	147.6	170	191.3	169.2	180.9	189.8	13
91.1	103.3	83.6	83.8	83.7	92.3	112	99.7	5
51.3	38.8	31.5	57.3	35.8	64.5	64.3	39.4	6
3.5	6	8.5	7.3	7.9	11.4	7.6	8.8	1
21.9	15.2	28.8	28.4	25	26.9	28.9	34.9	3
	6.4	4	5.1	5.1	4	3.2	3.9	2
210.7	208.3	181.3	113.3	100.9	122.6	112.8	98.9	6
611	568.3	572.5	492.9	444.7	454.4	521.5	510.3	9
99	82.8	64.5	131	100	134	130	107	7
68.7	67.3	78.7	70.9	68	75.5	73.8	63.6	8
7.4	4.5	2.5	2.9	5.5	2.8	5	5.7	2
	4.3	6.1	3.9			2	7.1	2
7.8	7.8	4.2	6.8	6.3	14.2	3.9	4.2	2
4309.4	4149.4	3861.3	3693.6	3104.4	4027.8	3657.5	3316.2	9
24	20.8	20.6	24.8	23.2	19.6	22.9	24.1	1
65.1	85.3	89.9	108.7	114.7	111.7	88	110.3	8
20.2	27.2	33.5	47.7	37.8	39.7	36.2	38.9	6
76.1	92.1	99.3	121	112.3	120.5	76.9	103.5	3
28.6	24.6	25.2	38.9	39.4	33.8	31.7	35.2	3
31.8	47.3	49.8	71.6	66.4	72.4	58.4	59.4	2
7.4	8.8	6.4	6.8	6.2	7.4	7.8	11.6	1
382.3	532.9	777.8	583.7	633.7	895.7	563	646.4	7
52.5	64.2	50.2	45.9	45.9	41.9	39.4	45.2	4
185.9	189.9	181.8	136.6	148.1	140.5	147.2	139.2	9
74.7	89.8	71.2	48	63	54	79.1	77.8	9
24.9	27.7	23.4	30.2	36.3	35.2	25.8	25.1	3
	2.4		2	1.5			1.6	1
56.3	45	46	44.7	48.2	50.2	60.3	47.3	7
18.7	25.9	35.8	29.2	36.2	32.3	25.3	31.4	3
9.6	6	7.8	6	9.8	9.8	6.3	7.9	1
9.9	9.8	15	19.1	16.8	17.3	20.9	16.6	2
2.3		3	14.4	9.5	8	11.8	10.8	
6.8	3.8	9.3	11.8	6.6	8.7	10	9.5	2
2.4		3		5.2	5.4			
32.5	48.3	52.3	47.7	49.1	50	55	59.9	5
20.9	25.1	36	35.9	39.4	29.4	34.8	33.1	2
3.7	2.9	3.8	8.4	8.1	3.5	4.6	5.8	1
2	2.4		3.8	1.7	1.8			
				1.6				1

764.1	726	668.4	13.2	1.7	2.9	5.2	9.9	9
8.9	12.6	18.7	19.4	18.6	17.7	17.9	17	3
180.8	203.6	188.4	205	187.2	195.7	229.8	222.4	7
1.8	5	4.4	2	1.2	1.8			1
1.7								
105.2	97.7	92.1	85.2	64.9	80.6	83.8	82.4	9
318.4	307.9	289.5	387.9	353.6	403.4	423	421.7	14
148.2	129.3	123.5	101.5	98.1	108.1	104.5	89.2	5
119.2	104.8	105.1	75.5	98	92.8	93.3	95.7	4
25.7	31.5	25.7	25.7	41.4	42.4	40	37	7
1.7	5.4		2	1.3		2.4	2.5	
134.8	158.4	143.1	18.4	6.2	6.3	12.3	7.8	2
610.9	584.8	526.7	355.3	320.6	382.4	340.8	341.8	9
908.8	911.7	812.9	742.5	663.9	807.6	753	783.7	7
4		1.8	2				2.4	
35.5	34.1	20.2	14.7	15.6	19.5	14.9	7	4
56.9	68.7	75.2	36.8	46.3	46.3	49.4	48.1	7
4.2	13	6.3	3.3	6.6	4.1	5.9	7.9	2
7.6	9.6	4.5	8.5	7.9	7.3	3.9	7.1	1
10.6	9.2	10.5	7.5	10.7	15	6.4	7.5	1
20.4	19.3	18.7	18.4	14.7	14.2	5.5	9.7	4
58.4	64.5	45.9	56.8	47.8	42.4	54.2	54.4	5
101.7	95.3	106.9	105.3	97.6	105.3	142.5	118.6	5
	1.8		2		4			
7.5	6.5	3.8	2	5.2	5.7	4.8	4.2	
	1.8							
8.8	5.9	10.1	14.8	15.4	13.6	16.1	14.3	2
16.4	21.9	19.3	16	15.9	10.3	17.1	7	3
2.5	7.8	2.6	8.8	5.3	8.4	5	1.5	1
1.8	2.7	3.8	5	5		5.6	4.1	1
2.7	3.2		1.7	2	1.9	4.4	1.8	
114.9	153.7	182	164.5	176.6	197.6	122.1	172.1	9
254.3	278.4	261.9	214.5	208.5	197.7	196.6	198.8	9
59.5	65.8	70.5	84	79.7	79.9	81.8	81.6	7
95.6	82.8	78	71.2	64.8	68.4	78.6	66.6	4
129	108.5	147.8	135.5	148.8	147.8	148.4	146.3	7
45.3	39.7	58.2	56.8	64.9	52.2	50.8	61.9	4
24.5	17.5	22.2	21.6	22.6	17.6	29.9	23.4	1
4.5	4.2	7.6	3.8	5.2	5	4.6	7.2	2
	7.7	4.5	12.1	9.4	7.3	4.8	2.7	2
82.9	71.7	78	67.4	71.6	63.9	57.3	62.3	9

57.7	53.2	65.9	48	57.9	49.5	53	55.5	4
		1.6						
28	43.5	54.5	38.7	36.3	40.7	24.8	40.8	5
55.3	68.9	65.5	60.4	65.1	68.4	58.9	81.6	7
28.9	34.6	32	33.3	30.6	41.1	34.4	33.9	2
42.4	34.2	39.9	42.5	37.7	37	36.7	36.3	1
182	163.8	250.5	249.6	265.7	283.2	215.3	241.3	8
5.9	7.5	4	5.6	3.1	1.9	4.3	6.2	3
605.1	595.2	561.6	490.8	486.2	456.6	537.5	503.2	14
112	115	140.7	155.2	184.2	179.5	147.8	160.4	2
481.8	506	484.8	579.1	524.6	580	624.3	572.3	7
6.5	12.9	6.1	7.3	8.2	10.7	12.3	12.8	2
127.7	134.6	125.5	117.2	134.4	111	127	106	2
86.4	88.6	74	56.6	52.2	63.5	64.8	54.7	3
	4	3	2.1	3.1		2.1	2.1	1
17.1	14.2	17.8	9.8	20.9	10.4	18.5	13.4	3
13	13.6	8.1	14	10.2	11.8	5.6	12.1	2
20.9	18.6	18.8	19.3	16.3	16.1	25.7	17.6	2
	1.8			1.6		2	1.8	
5.2	3.7	7	3.9	1.3	4	2	3.9	1
	3.6	2.9	3.1	2.9	2.4	6	2.4	1
114	120.7	104.3	96.9	101.8	86.7	110.2	113.3	8
7.2	5	7.3	9.3	6.2	11.9	6.2	11	1
11.5	13.8	11.9	14.2	10.8	12.2	9.6	11.2	3
		2.2		1.5		2.8		
				1.4				
4	4.1		2.8		2.3		7.8	
17.4	14.8	12.4	11.9	13.4	10.7	10.8	11.3	4
9.3	8.3	13.1	22.5	31.1	18.6	20.2	34.1	6
6.8	9.3	11.5	12.8	10.9	14.2	8.6	12.6	2
15.7	18.5	19.7	19.5	17.9	22.9	17.8	21.9	2
24.3	33.2	35.5	82.2	101.5	70	108.5	97.7	8
2.8	1.9	8.1	7.5	9.8	7.7	6.7	5.8	1

14.3	12.8	14.4	18	19.1	20.1	11.4	17.1	1
95.2	91.6	81.3	69.9	74.6	70.8	71.6	78.7	9
936.3	960.4	855.4	745.9	741.2	826.9	727.3	739	11
116.1	130.2	123	88.1	99.1	99	99.9	105.2	6
223.2	218.6	187.8	166.6	181	168.9	167.1	181.3	19
12.3	15.9	10	1.8	13.6	7.9	7.1	10.8	1
6.1	12.5	13.8	11.5	7.3	3.1	12.7	33.9	4
8.9	8.4	9.4	8	12.4	7	4.6	16.1	2
6.6	4.3	4.6	7.7	10.3	8.2	7.5	13.5	1
2.7	2.6	4.5	3.3	2.4	3.9	3.3		1
5.8	7.9	16.9	25.3	32.8	31.3	28.3	33.2	2
47.2	58.8	74.4	92.7	88.6	82.5	87.8	84.8	4
33.5	25.8	26.1	26.6	16.2	28.2	22.4	20.7	3
95.9	102	96.1	102.1	94.7	107.1	126.4	100.7	7
399.1	385	529	638.7	681.9	616.3	622.6	616.5	9
27.4	21.8	25.1	26.1	37.9	28.8	42.2	28.9	3
24.3	30.9	35.8	29.2	35.7	37.2	32.4	30	5
1894.9	1824.5	2424.2	3127	3150.4	2653.7	2972.9	2839.3	9
129.1	142.1	145.7	95.7	125.9	105.2	116.8	122.9	3
3.7	8.2	8.4	6.2	3.9	6.3	6.2	11.8	1
12.7	11.7	4.7	4.5	6	7.5	7.4	12.4	1
767.3	743.1	686.4	749	683.9	755.8	843.1	812.9	8
285.9	284.8	267.8	277.4	253.6	252.5	285.1	246.8	9
249.4	228.6	207.3	229.8	206.3	207.3	230.2	217.3	17
8.2	1.8	4.8		3.8	4.8	2.1	9.2	3
3.1	4.3	1.8	7.9	7.8	2	3.3	7.1	1
		1.7					2.7	
523.2	494.3	442.6	388.2	342.2	407.3	367.9	351.8	7
38.9	37.6	54.3	63.3	64.1	76.8	66.2	76.7	3
185.1	222.6	235.3	257.9	257.1	272.3	225.8	249.3	2
				1.5				1
51.5	61.5	58.9	85.2	91.7	78.1	82.9	94	5
			3.8		1.9	1.7	2.6	2
	1.7							
29.4	34.8	35.5	32.2	39.6	43	33.9	22.7	4
			2	1.3			1.7	
54.5	40.2	40.4	37.1	37.8	45.3	42.2	23.1	6
64.1	60.5	59.7	65.3	60.8	58.3	57.2	56.2	3
7.4	11	11.6	6.6	5.7	10.8	7.4	8.1	2
				1.6			1.5	

106.8	133.9	199.3	150.8	148.3	215.9	126.7	151.8	7
								1
241.4	227.7	241.6	139.3	132.8	129	148.6	155.6	6
27.3	33.8	25	22.7	22.4	20	25.4	25.9	6
3.7	4.5	6.1	7.6	8.5	9.2	6.7	6.7	2
16.4	5.2	18.5	19.4	13.9	20.7	11.1	17.9	1
99.2	109.9	131.2	140.7	168.7	135.5	136.1	139.8	9
3.7		3.2	4.2	6.2	3.1	2		2
24.9	23.5	23.3	30.4	20.7	29.5	30	29	2
9.9	9.8	17.4	21	14.4	20.5	12.9	17.9	1
37.8	38.4	60.7	76.8	96.1	76.3	89.2	95	8
80.5	95.8	105.1	143.4	158.7	128.7	134.7	154.6	7
330.5	330.1	447.8	467.2	516.8	452.2	372.3	467	9
57.7	74.6	79.1	87.3	112	87.2	79.8	78	3
12.9	15.6	20.1	17.8	19.5	20.1	19.1	21.6	1
64.2	78.4	108.3	143	154.4	121.2	130.7	141.1	7
2.3	8.5	7.8	9	13.4	6	7.5	13.9	1
198.4	237.1	247.7	382.8	405	334.2	359.8	384.3	7
144.7	171.7	182.3	255	281.7	233.7	240.4	260.9	4
31.7	29.1	41.3	45.2	46.4	43	36.7	44.9	1
60.1	65.4	83.4	77.2	93.2	78.6	74.2	85.3	8
81.9	75.9	88.7	162.2	175.4	152.1	151.6	161.1	8
4.5	4.1	8.3	10.5	9.8	4.9	4.4	7.2	1
13	10.7	14.8	46	39.1	45.3	58.7	52.3	1
19.1	17.7	19.4	23.6	21.3	18	13.9	19.9	2
30.8	27.5	43	17	31.9	21.6	23	24.2	7
6.9	7.9	7.2	8.4	7.4	10.3	9	12.7	1
12.4	15.3	16.5	21.6	22.6	18.6	21.4	16.8	4
54.9	68.1	59.7	51.3	51.4	32.6	52	50.4	8
159.5	136.1	161.7	162.4	179.6	159.6	190.7	179.7	6
209.1	160.8	220.7	175.9	181.6	138	202.1	176.5	6
793.3	822	834.6	721.8	719.3	655	799.5	772.3	17
73.7	59.1	74.6	68	48.2	40.3	52.6	49.4	9
160.5	153.9	181.4	169.5	173.5	154.2	171.8	159.8	7
8.1	10.1	6.3	9.6	7.7	6.9	16.9	12.7	
90.1	79.1	90.7	82.3	96.1	76.7	105.1	96.8	6
17.7	19.9	20.3	18.4	13.9	16	21.2	21	1
7.6	10.7	11.1	13.6	11	7.9	4.7	12.3	2
			2	1.7				
				1.3				1
2.5								
10.3	17.2	10.8	15.9	22.5	14.1	17.8	13.8	3
360.4	369.4	338.9	316.6	317.1	298	298.6	322.6	15
14.7	14.7	10.2	17.2	19.2	15.2	16.7	22.2	4

38.9	29.8	27.7	15.9	30	23	30.9	40.7	8
10	14.9	15.2	12.6	19.6	11.6	19.8	20.4	5
15.7	20.2	19.7	23.5	22.8	19	26	20	2
115.1	131	126.3	124.1	111	124.1	111.8	107.8	2
55.3	59.2	68.9	60	64	58.4	57.7	58.6	8
		2.2		1.5		3.5		
860.4	869.8	831.3	719	698.8	756.9	698.9	705.6	9
11.5	14.8	16.6	14.2	13.6	10.7	15.4	19.5	3
28.6	37.2	39	54.5	54	41.7	72.4	54.7	8
	2			2.3	2.3		2.4	
115.6	134.2	121.6	96.1	89.5	101.7	117	98.1	7
2.4	5	1.9	2	8.8	8.8	7.6	5.6	1
49.4	51.7	48.3	33.4	28.5	27.4	41.2	28.5	6
233.5	228.8	216.5	182.5	165.6	184.4	222	194.9	8
7.2	3.2	14.1	8.8	8.5	4	4.8	8.3	3
	6.8	2.5	6	4.1	5.5	7.4	6.1	
6.6	11.7	14	16.8	7.5	7.8	5.6	11.8	2
123.2	126.6	124.2	159.8	143.7	151	146	145.1	2
38.8	38.5	30.5	42.3	44.2	42.7	56.6	43.3	1
	1.5			1.5				
	1.8							
41.9	53.6	41.5	37.9	34.7	38.6	38.3	24.9	4
	4.2	1.9		1.4		1.9	3.1	
37.1	40	31	23.1	17.3	30.2	33.6	26.1	5
	2.2	3.4			2.4		3.1	
2.5	4.3	1.8	2.9	1.6	2.9	2.7	1.4	1
379.3	370.2	369.3	343.7	364.2	362.6	431.7	371.5	7
390.1	381.6	341.2	302.7	284.8	323.4	337.5	321.9	8
96.7	106	102.3	77.3	86.8	92.1	85.3	84.8	1
413.3	400.6	381.9	323.1	350.3	345.4	390	382.8	6
325.7	314.3	317.7	258.8	260.5	255.4	292.9	282.4	10
26.3	33.8	36.3	43	62.6	42.1	59.2	58.4	6
222.2	196.8	175	145.8	134.1	153.3	144.1	144.3	4
8.6	8.3	14.3	11.3	11.6	13.4	12.1	13.9	3

2				2.8				
431.3	419.2	652.5	691.8	648.7	591	410.9	560.3	3
109.5	113	109.7	90.2	76.9	110.2	87.3	96.3	8
71.3	80.4	73.3	47.5	51	43.9	62.5	61	9
5.9	5	6.2	3.5	7.9		4.3	2.1	2
362.7	342.1	333.8	310.8	343.4	314.5	335.9	316	14
66.5	76.4	94.4	41.3	41.9	46.6	38.7	34.5	5
9.6	18	16.2	11.8	14.4	14.1	19.6	17.1	5
11.2	6	8.1	9.3	11.3	8.9	7	7.1	2
71.9	72.4	62.9	65.4	65.2	63.9	70.7	64.1	3
						3.5		
55.7	62.1	44.6	26.5	17.9	22	23.2	26.9	3
			2.5				1.9	
63.5	62.9	64.3	89.5	75.3	74.4	85.4	77.6	3
66.6	71	62.7	54.1	60.2	63.2	66.4	62.7	3
4.7		2.8	3.3	5.9	3.8	4.4	9.7	
57.8	52.2	65.9	73.1	83.3	74	76.5	75.5	4
122.5	119.6	105.6	77.1	99.3	92	108.2	94.4	7
55.3	39.2	52.4	35.5	34.9	33.1	41.5	40.7	3
5	4.1	6.9	5.6	3.5	7.9	6.3	5.4	2
168.6	145.1	143	122.7	121.2	111	136.3	147.3	12
238.5	234.5	234.8	186.5	184.7	203.8	193.9	193.1	10
1412.4	1516.6	1415.3	1032.1	1090.6	1000.9	1023.8	986.5	5
326.7	321.1	294	326	343.3	327.7	343.6	345	14
94.5	91.2	75.2	78.4	70	77.7	88.7	91.1	8
24.5	24.6	37.4	39.6	47.9	43.2	41.5	40.1	2
				1.5			1.6	
184.7	178.9	191.7	172.8	195.5	180.4	212.9	213.9	9
12.2	8.9	5	6.7	9.6	5.2	7.2	2.3	1
76.1	87.4	103.8	125.1	143.6	118.8	129.1	132.2	6
	3.1	4.4	3.4	1.9	2		1.5	1
	2.3	3	1.6	2.1	2.1	2.1	2.3	
76.8	62.9	61.2	53.9	64	62	81.4	79.1	7
22.2	22.2	21	14.3	19.2	24.1	16.6	21.7	4
125.3	145.9	116.7	98.2	73.9	97.9	99.5	88.3	3
24.9	35.3	36.3	50.6	51.2	48.9	49.1	47.4	3
					3	2.8	1.9	
3.3	4.7	6.1	4.7	5.6	9.2	6.2	5.3	2

29.1	33.2	31.9	15.7	17.7	22.1	14.7	27.6	4
12.3	9.1	10.2	2.1	6.3	2.4	10.4	10.8	2
74.4	81.8	86.3	45.6	65.5	51.4	37.8	43.7	8
19.9	15.4	9.7	5.5	14.9	10.1	4.4	1.8	3
2.1				1.8	1.5	1.9		
90.2	106.5	96.3	81.9	71.8	82.5	75.5	90	9
23.9	24	21.8	30.3	27.2	30.5	23.6	27.1	3
178.9	170.9	170	151.4	136.8	147.9	157.9	137.9	5
6.2	6.6	3.3		1.9	2.4		2.2	2
		1.6			2.1		1.9	1
7.4	8.5	3.4	3.7	5.8	1.6	1.9	5.5	1
10.2	19.1	18.7	5.6	11.9	10.9	15.8	15.4	6
443.7	450	427.4	370.6	380	372.4	371.8	357.9	8
8.1	4.2	4.7	5.9	3.2	6	7.4	7	2
102.3	116.3	116.7	190.1	194.2	157.1	174.2	163.1	5
19.8	19.5	36.5	59.5	53.9	54.9	38.8	57.9	4
52.6	64.3	58.6	67.5	100.2	85.8	78.3	77.1	4
383	397.2	392.8	314.5	278.3	325.9	316.3	311.7	9
60	52.4	50.4	50.5	42.8	49.4	56.8	48.3	1
19.4	16.3	17.5	33	42.7	48.8	50	49.6	4
13.9	7.3	9.3	8.8	12.3	14.3	12.1	9	2
194.8	217.8	183.1	175.1	188.7	180	196.9	160.4	5
30	35.3	42.5	58.7	59.6	49.5	65.5	67.3	2
87	88.5	126.5	156	181.3	133.7	180.8	175.9	6
1.8	2.8			1.8	2	7.4	8.3	
31.4	42	42.4	82.2	86.9	60.8	82.2	79.6	2
12.7	14.2	23.4	31.6	40.4	29.4	39	35.6	2
10.3	13.6	14.4	25.8	31.4	20.5	24.2	25.6	1
5.9	2	2.3	5.8	4		4.4	8	2
5.2	4.1	1.7	1.8	8.5		7	9.8	1
	2.3	1.5						
	3.3	1.8		3.1	2.4	1.7	2.2	
64.2	51.3	45.9	78.7	75.4	97.7	87.6	100	8
776.7	734.4	697.9	592.8	547.1	619.8	520	572.9	7
147.9	157.5	142.5	147.9	162.1	155.1	147.8	150	8
							1.7	
344.1	367.2	330.3	292.9	345.1	283.6	362.8	342.3	7

529.3	498.2	466.4	427.5	414.6	433.4	508.7	466.4	9
11.3	11.2	18.6	10	6.1	10.8	11.5	13.1	3
204.5	201.3	201.4	194.1	183.9	188.3	199.9	197.3	6
433.4	436.4	413.3	365.9	414.5	367.9	438.8	411.3	18
3.5	6.2	4.7	5.4	6.6	7	5.2	4.1	1
3.1	4	3.9	8.1	7.4	5	2.1	3.7	1
			2					
60.8	71.7	45.4	43.7	53.1	46.8	49.8	57.4	13
	2.2		1.7	2.8	2.3	2.1		
2.8	7.7	1.9	3.4	2.2	2.1	8.6	3.7	1
6.5	3.4	6.2	4.7	4.3	5.5	2.8	6.2	1
3.1	5.2	2.4	5.1	3.1		2	3.1	
31.3	30.4	29.7	20.6	20.8	22	22.8	17.4	6
25.9	30.7	32.6	47.7	51	40.7	38	38.1	2
6.8	7.3	6.1	2.8	12.8	6.7	10.8	12.8	1
13.6	11.7	17	17.7	26.2	21.4	18.9	23.2	5
	2.9	1.9	3.5	7.1	3.6	4.7	2.6	
9.2	6	3.9	8.4	5.9	3.6	5.9	3.7	4
128.9	130.7	230.7	143.5	187.3	226.1	154.9	171.6	4
214.4	207.6	293.5	212.4	291.3	294.1	255.1	242.9	5
98.4	105.1	161.3	102.8	133	157.2	108.9	126	3
30.3	31.5	39.6	35.7	41.1	26.5	43.4	33.6	7
65.5	77.3	110.8	125.2	75.6	48.1	148	140.9	5
56	36.9	49.8	56.8	63	47.3	78.9	45.9	4
			2.5	1.6	2.1	3.7	2.9	
4.4	2.3	9.5	8.8	7.4	8.5	8.7	8.9	1
124.2	133.8	128.3	103.3	101	97.4	125.3	104	4
132.8	162.6	158	157.7	208.2	150.3	165	175.4	9
35.6	28.8	33.6	29.9	24.1	20.4	31.3	20.2	5
							1.4	
23.9	25.8	27.1	22.8	29.1	31.2	37.9	36.8	1

11	16.3	28.5	39.2	42.4	41.1	38.6	37.6	4
		1.5	1.6	2.1				
562.9	462.3	493.4	477.8	466.5	432.5	425.3	412.6	17
15.1	18.4	17.8	13.9	17.2	23.1	15.7	19.1	1
108.5	83.9	97.2	98.6	109.3	106.1	112.4	123.6	14
32.1	29.7	27.6	22.3	27.4	27.4	26.8	29.1	5
162.8	152.2	141	123	120.4	129.6	131.9	120	3
855.4	829.9	772.6	687.4	597	671.3	671.3	650.1	2
				1.3				
52.2	63.4	56.4	51.8	53	43	58.4	46.7	1
58.7	63.8	56.2	66.3	66.2	64.1	68.7	57.2	3
55.3	54.6	59.5	75.8	71.3	69	72.4	70.3	3
84.9	95	73	69.1	66.3	76.2	71.5	70.7	3
1.7				2.3	1.5		3.3	
391.1	453.8	416.4	442.3	429.8	490.2	488.4	485.8	7
	1.8	1.7	3	2.4				
64.1	65.9	59.6	47.3	62.9	72.8	73.3	56	2
4.7	3.2	3.6		2.6		3.7	3.9	
571.3	605.2	683.3	681.3	681.7	663.4	540.8	624.4	6
33	46.6	56.4	44.7	49.4	48.3	43.5	47	2
16.8	28.6	32.6	48.8	30.6	38.1	27.5	42.6	3
177.1	149.1	213.6	207	189	216.3	182.7	199.9	4
3.5	2.3	6.9	6	4.2	9.7	3.9	6.1	1
		2.9		1.6				
21.9	24.2	24.7	21.8	27.7	27.4	25.3	26.4	3
13.9	21.2	19	20.7	19	20.5	15.7	20.2	4
10.3	5.2	7.2	11.5	8.5	17.6	11.9	12	2
82.7	63.1	45.7	24	14.1	27.2	19	19	7
47.2	57.4	46.1	36.7	50.1	38.7	31.1	39.3	11
246.8	211.8	217.2	214.3	207.2	208.7	200.5	175.4	7
38.2	44.6	33.4	33.6	44.8	52.7	44.6	34	6
219	237.6	228.2	189	199.4	228.1	203.7	208.7	7
199.7	226.6	216.2	227.2	225.3	236.9	241.9	249.2	6
3.3	4.7	2.3	4.6	4.8	2.9	2	6.4	1
2.8								
54.3	67.1	79.5	95	58.2	49.1	95.3	122	4
281.6	319.4	408.3	445	277.1	232.9	523.2	601.7	9
2.5			3.8	1.4	4.4	2	2.7	1
592.5	612.7	571.3	567.1	593.9	596.3	703.2	671	17
17.8	29.1	30.3	43.1	50.2	44.7	32.3	39.5	1
161.8	169	145.5	177.1	153.2	173.7	175.4	153	9
14.7	15.9	26	27.5	36.6	30.2	20.4	29.1	4
2.7		1.7	3.7	5.2	6.3	1.7		

110.5	122.1	136.8	147.9	131	140.8	142.8	123.7	6
			2.2	2.6	2.3		2.3	1
13.4	9.2	13.6	23.9	19.3	19.7	22.6	13.9	1
10.6	11	12.3	9.2	12.6	9.6	13.1	13.7	1
18	17.1	13.3	16	13	20.2	15.5	18.7	3
102.4	99.7	96.5	92.2	91.4	107.8	106.6	101.1	5
157.1	156.9	178.9	209.9	188.8	200.2	222	201.3	7
17.4	13.4	10.1	27.4	31.8	27.3	25.8	39.5	5
21.1	22.6	23.3	13.4	15	17.3	17	12.9	6
173.1	152.3	150.5	116.1	129.7	136.9	126.3	131.3	10
			1.8	1.9				
13.9	7	9.2	18.5	20.4	18.2	21.3	17.9	2
	2	1.5		4.7	5.3	1.9	3.2	
4.1	3.1	4.6	5.8	5.9		2.3	4.6	2
20.7	22.4	19.1	22	23.1	35.2	33.1	26.4	4
138.8	121	120.6	91.4	90.3	101.4	97.9	104	6
40.6	47.6	41.2	24	23.3	24.9	23.4	31.1	6
14.6	18.4	15.6	6.4	14.1	11.8	10.8	9.1	4
		1.9	1.7					
3.4	4.7	10	9.3	4	3	4.6	7.7	1
2.8	3.3	2.8	4.2	3.5	4.3	4.2	2.3	1
181.9	169	161.2	141.3	131.1	148.7	129.5	129.7	5
22.8	28.7	15.4	20.4	21.4	16.5	20.6	17.8	2
83.3	86.1	59.5	43.1	59.5	58.4	59.5	54.1	3
52.3	59.7	57.8	55.6	49.8	56.1	61.6	67.3	3
12.2	21	19.4	17.8	18.7	25.9	33.5	32.3	4
20.8	19.3	20.4	15.5	18.9	23.5	13.8	23.5	4
21.9	14.2	19.3	16	13.8	21.6	18.5	20.7	3
2.4	4.8	8.7	8.5	5.3	4.8	11.8	2.3	2
33.2	39.5	47.9	46.8	25.1	29.4	45.9	59	2
	2.2			1.4		3.9	1.6	
25.9	33.4	44.9	51.4	41.2	38.5	45.5	51	3
110.2	100.9	106.6	76.7	95.8	104.5	60	73.1	9
193.8	194.5	173.4	188.6	191	217.3	240.8	243.5	5
43.7	54.3	39.3	46.7	56.5	47.6	50	42.3	6
60.8	47.4	50.4	21.8	54.5	28.5	32.8	27.9	7
66.2	58.5	94.5	93.1	96	114.6	67.5	91.7	4
15.8	19	27.1	28.8	26.5	28.8	22.5	26	2
		4.1		1.2	2.3	4.2	3.4	
5364.7	5121.3	4844.2	4167.4	3741.6	4462.8	4125.5	4011.6	9

54	43	45.1	34.2	29.2	34.9	30.4	32.1	2
129.1	125.6	111.9	106.7	103.8	110.5	109	114.3	5
2								
25.2	20.5	27.5	19	17.6	22.2	22.4	21.2	2
116.5	126.3	139.1	106.2	96.3	74	92.7	67	4
37.6	38.8	34.5	27.4	33.1	35.6	28.8	28.8	3
29.1	30.9	25.5	62.3	58.3	50.9	47.1	53.9	5
13.4	14.3	23.6	22.3	24	15.1	18.3	21.4	2
98.6	115.3	86.1	83.6	73.3	67.9	82.8	75.3	3
68.7	69.1	63.4	48.6	61.5	46.1	43.5	54.1	4
2.1	1.8	3.2						
13.7	14.8	21.8	12.8	20.8	13.3	23	14.5	4
					1.5			
2.3	2.3	2.4		2.7	1.5	2.4	4.3	1
							1.5	
1.8	6.2		2.2	2.6			4	
			2		2.1			
5615.1	5161.6	4949.6	5334.1	5308.2	5513.6	4953.5	5281.1	17
57.7	48.1	48.3	115	88.3	151.3	134.7	125.6	3
49.4	52.3	42.5	56.5	59.8	50.3	52.8	59.2	2
179.1	187.5	173.6	192.2	201.2	193.3	204.8	192.1	11
16.5	14.7	7.7	16.9	18.5	8.7	15.9	17.9	2
							1.6	
6.1	6	17.5	15.7	19.4	14.1	8.6	18.5	2
		1.8		3.5	1.9	5	2.3	
3.5	4.5	7.8	2	6.5	3.8	8.2	3.2	1
4.2	9.8	8.9	2.9	5	4	2.9	3.8	2
76.5	81.8	67.4	77.5	87	75.7	88.1	91.1	4
11.9	9.4	13.1	8.4	8.8	6.2	4.6	8.2	2
	1.5	2.3			1.9	2		
96.2	155.6	151.1	232.2	237.1	245.2	173.3	212.5	8
13.7	25.3	23	41.8	41.8	43.9	30	39.5	3
83.7	78.1	79.6	63.1	66.4	61.2	61.7	61.1	2
26.9	20	26.8	29	28.8	30.3	34.4	34.3	4
122.1	127.4	163.2	184.2	196.7	163.3	224.8	211.7	9
	2	1.9	1.7					
43	29.1	45.9	47.8	41.9	38	48.2	48.8	3

58.6	51.9	57	53.4	62.3	61.8	70.8	70.3	6
	2.4	1.5	1.6	2.5	2.4	6.4	4.5	
278.1	284.8	318	381.7	370.9	352.4	334.3	342.6	6
72.7	77.5	91.1	115.4	120.8	119.8	108.6	118.5	3
72.4	71.3	70.2	65.2	69.7	67.4	57.3	56.1	7
8.8	5.7	5.5	2.1	4	1.9	2.3	3.5	2
439.2	478.5	457.4	425.6	411.9	414.3	446.2	416.1	15
5.7	7.9	9.1	4.2	11.4	2		3.2	
19.8	19.4	24.7	26.1	38.1	31.8	25	24.4	6
	2.8		1.8					
20.7	23.7	24.4	21.2	27.9	27.2	29.6	21.4	5
92.6	79.3	89.1	85.5	93.4	92.9	107	100.1	9
3.5	14.5	13.3	13.4	13.5	11.9	12.1	10.6	1
92.4	92.3	95.9	73.5	108.6	68	82.1	75.1	6
16.3	20.8	14.8	19	19	15.7	21.3	19.8	1
260.4	305.8	286.5	216.2	323.1	219.8	279.9	276.8	4
61.5	55	54.3	46	54.9	41.2	52.1	37.2	2
111.2	135.7	116.7	78.7	83.3	72.5	76.9	71	4
555.6	568.8	542.2	308.6	350.9	315.7	325.5	332.1	6
3.3	4.2	2.1	4.9	6	4.1	2.4	5.6	1
68.5	79.5	76.1	67.5	70.1	74.4	84	75	4
102.8	102.9	107.3	98.6	92.4	85.8	102.7	112.8	9
1348.4	1421.4	1361.9	1388.9	1359.3	1321.8	1389.4	1100.1	11
54.6	62.5	58.7	60.6	60.9	61.7	72.7	57.1	3
6.4	6.6	7.8	7.7	4.9	6.2	4.8	5	
9.2	4.2	11.2	7.6	15.6	7.8	4	9.6	
33.9	32.8	33.8	47.1	47.5	39.6	32.4	45	3
195.2	181.2	168.2	139.7	115.9	145.8	145.2	141.6	6
	1.8							
20.8	17.3	11.8	10.1	13.6	15.1	15.8	17.1	5
13.9	23.7	14.7	9.4	20.6	18	19.3	16.9	4
8.5	15.6	9.3	14.3	17.9	15.6	26.5	20.2	2
1.8	1.9	1.8	6.2	1.3	4.4	5.4	5.7	
1.7	1.5	3.1	2.4	2.2	2.9	4.7	4.3	

47	56.1	59.2	35.8	53.1	46.8	64	46.5	10
269.2	261.7	323.7	387.9	394.7	352.1	319.3	347.7	8
141.7	146.3	131.9	96.5	116.4	139.4	117	122.1	13
11.7	12.2	15.4	8.3	17.9	11.4	14.1	13.2	3
39	26.3	22.8	33.7	21.8	32.6	25.7	28.7	3
3.1		3.1					2.3	1
184.2	195.4	255.2	288	280.5	270.7	238.1	280	5
19.2	12.2	13.9	15.5	16.3	9.2	9.1	14.8	5
	1.8			2.5		1.9		
8.1	3.7	8.6	10.5	8.2	11.4	15.3	10.6	1
3.4	2.7	3.8	2.2		5.3	2		
4	9.2	4.2	8.8	9.2	8.7	9	8.3	1
3.3	1.9	6.2	3.9	4.1	4.7	4.7	8.6	
7.4	6.2	4.2	5.6	9.8	7.7	3.2	6.9	2
638.6	574.7	536.2	500.9	521.2	513.5	510.8	520.7	8
28.3	33.4	25.8	30.8	24.7	29.8	34.3	40.2	6
278.8	278.7	278	272.5	265.1	250.3	277.3	285.8	16
3.4	3.4	1.6	3.1	3.2	4	4.2	6.4	1
4.8	8	7.2	10.1	8.2	10.4	11.9	13.6	1
	2.6	4.6	3.7	5.7	4.3	3.5	3.8	1
5.5	8.9	10.1	20.1	21.8	13.3	12.6	16.6	1
4.2	4.3	3.3	4.9	11.4	8.2	5.2	8.2	1
19.5	23	18.1	16.6	16	18.7	20.1	20.2	1
30.7	65.7	75.4	114	148.2	115.9	152.7	150.3	7
				2.9				
38.5	31.5	45.1	73.5	72.3	73.8	93.2	70.7	1
1093.8	1100.3	1602.5	1596.4	1783.5	1521.7	1475.2	1485.4	9
72.6	93.1	89.5	76.7	81	79.8	90.1	79.6	9
71.7	99.6	87.6	74.3	87.3	64.7	76.5	84.2	11
9.2	6	6	6.3	14	1.8	15.5	22.3	4
737.6	694.7	663.2	593	516.1	601.1	538.7	515.9	8
6.1	5.2	12.4	10.4	3.6	4.5	10.3	11.6	3
	1.8			2		1.9		
10.2	4.5	4.2	4.2	3.8	4.9	4.8	3.3	1
249.9	253	237.8	248.5	250.6	271.1	255.9	255.2	9
2			5.9				2.1	
				1.3				
2	2	2.4	5.6			3.5	5.5	
18	16.5	25.2	37.2	36.9	31	37.8	40	5
3.3	2.2	1.7	2.2	4.9	5.2	4.4	3.8	1
157.1	142.6	165	184.3	162.1	172.3	180.1	153	5
	1.8							
119.8	125.8	131.6	165.4	197.9	120.3	174.4	177.6	6
76.7	84.6	95	102.1	128.3	98.4	110.3	99.5	13
165.3	224	258.1	351.6	368	275.4	292.6	323.5	7

	3.8	3.8	3.4	4	3.9	3.6	3.7	1
11.3	10.2	7.9	6.4	10.6	6.4	4	12.2	2
			2		4		1.6	
15	11.4	16.2	15.3	17	12.3	7.1	14.6	2
57.4	44.8	40.4	27.9	41.5	30.7	30.7	28	5
14.1	15.7	11.7	9.2	11.8	12.3	15.5	9.6	1
33.8	30.2	31.5	35.9	41.1	46	68.7	44.2	4
50.4	55.7	55.3	54.1	60	53.2	62.4	65.7	6
		1.9		2.8			2.6	
31.1	22.1	29.6	43.3	26.5	32.3	41.2	32.2	4
30	40.4	35	23.7	39.9	34.4	20.4	25.2	5
		1.7				2.1		
10	9.4	9.1	8.3	8.2	4.5	5	8	1
7.1	9.1	10.5	12.3	12.6	9.4	10.7	13.2	4
9.2	8.3	3.8	6.2	3.1	9.7	1.9	7.9	1
2.5		6	6.6	9.4	7.5	5.2	10.2	1
568.9	549.4	539.9	412.4	402.8	347.4	396.8	367.5	7
116.1	134.7	111.1	217.2	172.7	210.7	196.5	199.1	7
131.1	133.8	150	147.1	165.9	141.4	146.6	159.4	9
56.6	66.1	59.8	31.6	43.1	38.5	54.8	51.7	7
120.8	111	144.2	127.5	145.9	126.3	145.3	141.1	6
62.2	62.4	77.7	71.1	86.4	78.3	77.1	84	4
13	21	24.2	16.9	26.1	22.6	19.3	22.3	2
81.5	94.8	123.8	147	190.7	143.8	182.1	184.9	11
164.9	157.3	142.7	217	207.5	217.2	246	233.4	7
118.7	121.9	104	118.8	108.4	108.1	129.6	123.1	7
210.3	210.2	181.4	165.4	222.2	230.1	216.1	200.5	5
3.5	2.7			2.1	2.4	2.3	3.1	1
37.5	23.5	32.9	26	21.2	25.8	17.3	31.6	5
2.5	4.2	2.3	8.3	2.7	4.1	3.6	4.7	1
15.1	16.6	30.4	30.9	32.6	29	25.7	24.3	2
2.4	4.7	3.1	1.8	2.5	2.3	3.1	2.7	1
					2.3	1.9		1
2.3	2.4			1.8			1.8	

3.7	5.6	7.7	5.1	5.7	4.5	2.5	4.6	1
71	61.7	59.5	56.8	53.9	53.9	73.5	77.2	4
14.1	13.4	9.9	7.6	11.3	11.2	11.5	17.1	1
3.4		1.8		1.4	1.9		1.6	
30.6	36.9	33.6	30.5	26.1	25.3	31.7	33.7	7
11.5	28.3	27.5	19.4	35.1	34.2	18.2	25.4	4
87.4	86.3	79	79.6	83.3	85.3	77.8	75.7	5
1384	1390.3	1340.1	1239.8	1224.7	1209.4	1323.1	1282.6	9
131.8	129.8	131.7	172.9	201.6	157.7	192	179.8	7
15.4	19.4	16.9	14.3	21	20.4	8	14.7	2
2	7.8	3.2	6.4	6.2		2.1	3.1	
155.4	123.3	120.2	97.8	97.6	90	114.4	106.9	8
70.7	62.5	61.6	55.6	59	47	52.5	67	8
63.9	53.9	77.4	67.8	75.8	75.7	77.3	64.2	5
46.3	48.5	44.8	41.8	35.4	31.7	31.9	38.4	7
65.6	70.7	82.7	77.7	71	77.7	62.5	69.1	4
9.6	12.5	11.8	12.6	10.5	10.8	9	7.4	1
70	77.8	116.5	125.8	125.2	133.5	101.8	113.8	6
								1
46.5	50.9	65.6	83	85.3	71	78.6	86.3	7
2.1							2.2	
4.4	7.5	9.5	4.3	11	2.4	7	6.4	1
27.4	31.4	27.4	16.1	16.6	22.4	22.4	17.2	4
7.5	4.3	4.1	2.6	7.5	3	5.1	3.1	1
428.9	479.8	440.4	401	454.2	431.6	441.7	438.8	15
261.1	257.2	248.2	225.1	259	241.3	236.5	236.5	7
16	30.4	24	11.3	26.8	21.7	32.3	27.5	4
47	48.2	42.9	39.9	44.7	43.1	45	41.2	2
9.1	11.9	8.5	9.2	12.7	7.2	4.8	7.2	3
92.2	84.2	87.7	81.5	96.1	79.4	105.7	88.5	6
54.6	43.2	42.1	29.9	35.5	38.7	22.4	33	6
10.7	12.6	16.3	18.7	15.4	16.1	15	18.5	1
3.1		2.5	3.5	9.4	1.8		2.3	1
	1.8							
	1.7	3.1	6	11	2.1	6.7	4.7	
	7.7	2.5	11.4	15.5	14.1	6.6	13.8	1

2.1		3.4	5.8	2.5		4.7	4.2	
21.1	29.8	28.1	37.6	35.2	40.7	27.6	28.8	2
83.3	97.4	84	77.5	84	80.9	78.2	67.1	3
2.4	3.4	4.4	5.5	5	6.9	2.5	4.8	
10.7	10.3	11.5	16.3	20	19.1	15.1	13.2	1
		7.7	9.6	9.5	11.2	7.6	12.2	3
17	18.5	17.2	23.5	19.4	19.7	22.1	20.6	6
2.1		2.1		6.1	4	4	2.2	
4.8	2	1.7		1.7	2.3	2.3	1.9	1
686	776	709	775	801.7	738.8	877.8	893.9	9
34.4	34.4	35.2	44.6	39.3	45.9	47.3	49.6	2
	1.8				1.8	1.7		
		2.1	2	2.3	2.6	1.9		1
				1.8	1.6			
43.1	45.8	39.9	31.3	43.7	35.6	30.8	43.8	7
61.7	67.9	46	37.8	47.3	43.9	39.8	35.5	3
11.7	16.2	10.3	7.2	8.3	16.2	4.4	7.1	3
16	17.9	23	22.5	25.9	25.3	16.5	20.9	1
6.1	8.7	6.3	8.4	8	6.4	4	7.7	3
2.1	2	8.9	18.4	13.4	8.9	16.6	12.6	1
4.4	22.1	17.8	34.5	28.9	35.6	45.4	50.1	3
11	20.7	19.6	54.9	41.4	40.3	44.9	55.6	4
145	151.4	186	273.3	319.9	281.7	301.7	318.7	9
73.7	94.3	106.7	174.2	184.3	177.4	190.7	176.2	7
131.7	152.5	205.6	308.1	320.1	304.4	335.9	317.8	8
44.7	60.8	67.8	116.8	121.9	103.4	127.9	122.4	9
3.8	2.3	4	2.5	7.4	3.8	5.5	3.9	1
194.3	219.5	203.7	169.9	162.4	148.4	190.4	164.5	3
24.5	16.8	24.3	17.2	18.1	17.1	15.4	19.9	2
				3.2			4.1	1
416	420.9	373.9	293.6	311.7	277.5	263.3	268	9
28.6	23.9	25.2	12.7	17.5	13.7	22.4	23.2	4
8.9	4.2	4.9	9.7	6.2	4.9	7.9	8.7	2
55.2	58.8	50.9	48.4	45.7	49.3	44.2	43.2	3
2.7							1.8	
2738.2	2442.9	2218	2382.8	2026.8	2483	2297.7	2194.6	8
99.3	101.6	103.5	111	104.2	108.6	131	121.3	2
59.3	70.1	85.6	75.4	87.2	68.8	68	74.5	5
62.8	69.9	91.3	72.9	88.8	83.7	57	78	5
48.2	47.6	52.5	50.5	54.8	48.3	62.3	51	5

1504.1	1306.7	1219.6	1154	1181.5	1175.7	1074.9	1202.4	14
30.6	29.6	25.2	59.4	43.2	65.7	52.6	58.2	2
	5.5	3.2	2	2	2.3			1
371.6	378.9	375.5	288	304.8	293	328.4	295.6	17
2.4	3.4	4	4.6	5.4	7.4	2	1.7	1
22.5	21	22.2	24.1	24.3	22.8	34.4	28.4	3
24.8	42.9	47.7	47.3	59.3	55.7	54.9	50.2	8
22.5	35.8	39.4	45.1	51.9	43	52.8	51.8	6
9.6	20	28.8	25.4	36.1	31.8	31.3	40.2	5
71.3	64.8	87.1	97.3	101	96	94	103.5	5
		2.5	2.9	1.7			2.2	1
		1.5		1.4	1.8		4.2	
		1.9		3.1				
2.5	3.6	2.9	1.6	2.2	2.4	3.3	3.1	
183	201.5	206	195.5	266.8	175.5	224.8	225.2	7
122.9	101.1	83.4	89	47.5	113.1	95.3	89.2	6
496.7	455.4	446.5	422.2	383.7	440.1	411.1	399.9	8
21.1	19.5	19.7	23.2	33.6	20.9	20.6	32.1	3
2.8	2.6		2				2.7	
2.7	2.6	1.6	4.5	1.7	2	4.7		
688.8	683	598.4	405.1	366.8	423.2	388.4	432.8	18
2.4	1.9			1.6				
3.5	1.9	6.5	5	7.5	4.7	9.2	7.8	
179.9	162.5	208.6	171.3	187.2	168.7	146.6	171.7	8
17.3	8.9	23.8	12.6	15.3	18.2	13.4	22.6	3
31.4	25.4	32	26	30.2	36.5	43.1	40	2
2	6.1	1.8		7	4.4	2.5		1
2.8			4.2	2.7			1.7	
294.1	315.9	291.2	266.5	267.1	258.4	258.6	287.2	13
232.2	236.2	281.5	273.1	298.3	274.4	269.7	270.7	23
		2.1		3.5	3.6	4.3	1.8	
4.7	12.5	12	6.6	10	8	19.8	18.2	1
4.2	1.7	2.2	2.5	4.7		2.9	3.5	1
60.4	57.9	50.4	43.5	44.7	49.3	56.1	56.9	4
94.6	115.9	137.6	295.2	362.9	288.2	377.4	357.6	8
335.4	318.1	308.5	334.1	328.8	351.1	399.3	371.1	13
4		2.2	6	5.1		5.5	4.1	
6.9	11.6	14.8	3.9	6.6	6	4	5.3	2
12.7	13.4	12.6	9.4	9.3	13.7	5.9	11	4
505.7	491.3	458.4	440.3	437.1	471.1	439.1	389.7	6
223.8	221	220.8	183.1	171.8	164.8	210.5	182.6	9
					1.8			
115.3	116.3	125.7	171.2	168.7	152.8	157.9	161.4	8
13.4	17.9	21.9	30.3	35.8	32.7	41.4	40.4	4
								1

14.3	9.8	15.4	12.2	23.4	22.6	14.9	15.1	2
409.6	425	407	350.1	351.3	345.3	354.9	353.5	9
2	1.9	3.6	1.8	9.2	6.3	5.6	7.4	2
	1.4							
4.4		1.9	2.1	4.6	2.3			
	2.2	3.4	3	2.4	4.4	2.7	2.2	
1244.7	1131.8	1165.3	1057.5	910	959.7	1008.3	910.6	6
135.5	123.3	143.8	128.1	128.9	115.1	128.7	119	5
269.6	207.9	269.4	270.2	293.8	252.8	296.4	245.2	4
1.8	3.2	4.2	3.5	2.2			2.7	
57.1	67.9	54.7	39.7	45.2	51.9	41.2	50.4	9
135.5	133	125.8	149.3	148.9	143.7	163.5	164.9	9
133.2	98.1	81.6	97.8	67.3	102.8	76.2	84.7	7
121.6	109.8	107.5	97.7	69.4	111.9	102.2	103.9	8
5.1	6.1	5.3	5.2	7.2	3	4.3	7	
		1.9		1.9	2.4		1.6	1
21.9	16.6	11.9	19.4	13.4	20	8.6	12.9	2
76.4	77.8	101.5	88.2	82.7	104.5	61.9	90	9
3.1	2.4	15	4.7	10.4	12.6	4.4	10.4	1
32	33.2	30.2	34.6	30.1	29.9	27.6	37.2	6
10	13.1	12.3	4.5	8.2	7.5	11.5	7.9	3
28.9	42.9	48.2	45.7	44.4	50.2	40.3	43.5	7
		1.8		1.3	2.3			
1.7	1.9	2.3	5.2	2.3	4.8	5.2	5.5	
131.5	140.3	155.4	169.9	220.3	158.8	181.1	202.2	7
							4	
57.8	61.5	73.1	96.1	134.3	90.2	115.7	120.9	7
2.7	2	2.8	2.6	2.9	1.8	3.9	4.5	1
128.4	133.5	118.9	92	91.2	98.2	92.3	82.3	8
131.8	142.2	142.3	86.8	110.7	97	105.8	118.8	15
142.3	152	129.6	111.4	80.6	105.3	102.6	109.7	7
			2.5	3.5	3.6	3.3	2.9	1
3.7	1.9	2.5	1.8	3.9	4.8	2.3	2.7	1
90.8	92.2	87.4	92	86.8	83.7	87.4	78.1	5
533.1	505.6	497.8	532.4	501.2	482.7	555.3	488.1	8
6.5	2.3	2.5		2.6	3.9	5.1	6.7	2
447.8	405.3	404.5	378.3	342.7	359.6	373.2	364.8	5

32.8	18.2	27.4	34	26.7	24.3	36.2	32.7	4
140	132.5	132.7	96.7	118.1	105.2	126	138.9	7
3.4	3.2				2.1		3.5	
32.5	24.4	24.9	32	38.7	42	51.2	35.3	5
	1.5			1.6				
32.4	38.8	48.3	56.2	52.6	48	39.2	49.4	6
			2.4		1.6		1.7	
2.1				3.2	2.8		2.1	
20.7	18.9	21.4	13.8	14.6	13.3	19.1	19.6	2
3	2.4							
3.3	6.1	6.9		5.3	4		4.7	2
2.1		4.1	5.4	2.1	4	3.6	2.2	1
146	170.5	141.6	116.1	115.5	135.4	128.7	135.3	7
52.6	47.6	44.6	38.3	30.4	35.3	41.4	43.4	2
54.7	50.5	44.8	42.5	39.5	46.1	54.9	50	3
					1.8		1.8	1
13.3	16.2	11.1	19.4	22.1	18.9	15.5	17.7	6
17.7	15.6	23.7	26.6	22.7	25.4	28.7	15.8	2
				4	4.5		3.7	
195.2	203.4	195.3	192.4	198.7	191.9	171.1	170.6	4
76.2	91.4	96	182.5	208.7	187.7	155.1	181.3	7
70.6	67.6	67	62.7	72.7	53.9	65.2	70	7
6.1	5	4.5	3.3	5.8	2.9	6.4	3.9	1
150.4	156.1	159	108.4	120.6	105.6	92	118.3	16
7.1	9.3	14.9	11	19.6	10.9	6.6	15.1	3
			4.2	2.8				
389.8	347.9	281.1	359.3	212.4	399.5	380.6	355.7	9
24.3	22.6	33.4	62.7	42.5	44.7	83.6	92.5	4
113.3	135.3	116.5	116.1	131.8	122.7	125.2	130.4	4
9.5	4.3	4.5	4.2	7	3.9	5.1	4.3	1
48.7	31.6	39.9	60	52.2	38.2	57.6	56.2	7
6.2	4.8	7.8	5.5	16.1	7.5	15.8	7.3	1
62.8	64.9	100.1	99.8	93.5	96.3	89.5	100.4	9
138.3	140.5	170.3	178.5	166.4	148.9	175.2	160.7	9
				2.7	3.6			

				1.5	2			
4.5	6.9	12.5	13.8	12.8	14.8	16.6	12.4	4
42.4	46.7	47.2	42.6	47.4	49.4	64.1	51.2	4
8.3	18.1	10.1	42.5	35.2	34.2	29.6	35.2	5
18.7	27.2	28.8	31.9	17.8	14.1	34	29.2	1
64.5	44.3	54.7	84.8	71.6	69.6	64.3	79.7	6
245.8	221.9	219.6	309.8	325.6	307.7	407.6	364.6	9
24.2	33.2	31.2	45.1	44.4	42.5	31.9	28.3	2
115.1	126.9	109.3	93.2	103	104.2	92.7	104.1	8
4381.6	3789.7	3437.8	2931.5	3028.3	3125.3	2658.6	2946.2	20
49.2	49.1	57.1	68.6	90.4	73.4	70.8	76.1	9
7.1	8.5	21.9	9.8	17.1	18.2	17.9	15.3	4
63.2	68.6	65.2	77.1	89.5	94.1	85.2	90.2	7
8.5	10.5	15.2	15.2	18.7	19.1	14.2	16.3	2
	3.3	4.1	4.7	11	4.7	8	7.4	
191.9	203.2	223.3	265.1	273.2	263.3	240	251.3	8
					2.3		2.2	
8.8	10.3	9.2	11	9.5	7.8	8.6	9.6	1
55.9	45.3	60	87.8	76.9	69.4	94.4	78.8	8
193.9	195.1	218.4	210.9	219.1	210.9	198.1	199.6	6
3.1	1.9	6.9	4.7	3.7	10.7	5.9	9.1	1
18	22.6	20.9	16.5	19.7	22.4	16.3	33.9	3
3.1		2.4	3.1	1.4	2	2.7	1.6	
1.7	6.1		2	1.4	4.5	2.5	5.1	1
5.5	4.2	6.2	3	2.9	2	2.8	7.1	1
19.7	30.1	31.2	50.9	41.9	40.7	38.3	38.9	1
62.1	53.4	57.7	48.4	46.8	37.7	54.8	40.4	2
27.2	37.9	46.7	40.6	53	36.6	29.1	39.3	5
332.5	345.8	326.2	232.6	244	279	270	274.9	9

20.4	33.4	40.2	30.8	37.8	29.2	28.8	39.4	7
25.7	46.7	35.7	47.6	46.6	42	40.6	49.8	7
31.8	31.5	37.5	32.5	39	35.7	32.8	38.9	2
			2	2.4			1.7	
62	54.6	75	76.4	92.9	78.4	84.1	82.6	2
164.8	166.6	156.6	165.3	137.1	168.6	169.5	167.7	8
95.3	103.2	93.7	137.6	129.8	148.8	185.2	148.3	9
5.7	9.7	6.4	16.4	13.3	11.8	11.4	15.4	2
13	26.1	27.1	40.2	37.2	38.1	44.6	44.2	3
2.3	1.9	1.9	2.9	3.6	2.6	4.6	2.1	
352.6	377.4	315.8	275.3	262	280.8	275.9	289.8	7
34.5	27.2	28.1	30.9	24.3	16.7	16.2	16.8	4
185.6	204.7	211.5	215.5	187.3	204.1	246.9	204.3	12
23.1	30.6	17.2	29.9	24.2	30.9	31.3	30.6	2
2.1	1.9				2.3		2.3	
10	14.2	9.7	9.8	7.7	6	10.3	8.6	2
2.1	9.6	11.4	3.1	8.9	9.4	13.8	8.9	1
19.5	21.2	24.2	24.4	17.6	26.5	23.4	23.6	1
22.3	40.9	35.1	26.1	39.8	40	46.3	47.8	8
142.9	140.2	140.2	126	134.4	124.9	128.3	111.1	7
	2.2	2.1	3.5	3	3	3.1	3.1	1
108.8	124.1	119.6	86.4	100	92.9	85	100.5	6
115.8	107.1	100.6	88.5	84.8	84.6	93.6	82.1	3
20.8	23	20.3	18.1	17.9	12.3	16.5	20.2	7
69.6	96.9	96.7	105.8	120.4	104.3	96	95.1	5
28.3	31.5	43.3	35.3	40.7	45.1	36.3	39.5	3
17.1	24.2	25.1	21.2	24.8	28.7	24.8	27.5	3
	7.8	3.4	2.4	6.9	4.8	4.6	7.5	1
		4	2	5.5	1.8		5.8	
	2.4			2.7	1.9	2.8		
37.1	46.2	51.4	69.7	77	84	72.6	83.1	5
232.7	237.9	310	383.4	424.3	399	382.2	422.4	9
80.8	91.4	110.9	148.9	163	181.6	168.5	183.5	8
20.2	26.5	44.7	14.2	34.1	38.1	53.8	50.2	5
83.7	104.7	136.9	279.3	311.7	256.8	275.9	295.8	9
7.6	11.5	15.5	26.6	33.8	28.5	24.4	26.9	5
150.4	194.9	247.1	458.3	511.4	449	440.4	494	14
164.6	168.6	221.5	390.9	437.9	329.7	392.6	424.2	8
200.6	222	294.4	427.2	498	411.1	451	461.9	9
145.8	150.1	197.4	253.5	328.5	262.1	274.7	272.6	7
17	10.8	18.8	29.1	21.6	21.2	22.6	21.8	2
214.9	253.2	319	465.8	531.6	433.1	459.6	498.1	8
143.4	150.8	144.6	165.7	126.9	163.4	183.5	178.7	8
142	144.8	105	116	144.4	161	153.9	135.4	4

1.7	1.7	3.3	2.1	2	4.5	2.9	6.1	1
	1.8	1.7	2.6	2	2.4	1.7		
				3.7	2.1	1.9	1.7	
11.6	10.8	17.2	15.2	27.2	11.8	14.1	19.3	1
11.3	11.1	11.2	10.2	11.4	14.3	15	10.6	1
7.1	14.7	13.9	13	21.6	9.7	17.8	11.5	4
526.2	551.2	561.2	711.5	695.2	674.5	791.6	729.9	9
59.4	64.8	61.9	52	49.2	54.9	64.3	65.7	4
169.6	169.9	181.8	242.3	212.8	234	182.8	207.5	9
		2.3						
24.3	17.5	24.1	27.7	25.1	21.4	15	21.5	2
73.4	74	109.6	121.7	108.8	112.2	78.9	110.3	9
22.6	22.8	40.9	53.5	51.1	33.2	27.2	45.6	7
130.1	134.6	150.5	170.4	153.5	180.6	133.5	149.6	8
25.5	23.1	30	25	33.8	31.8	29.1	33	2
23.1	23	14.3	18.2	16.7	16.3	8.8	18.7	2
2.1	5.4	6	7.1	6.1	4.4	5.4	8.7	
4.7	6.1	7.1	5.4	4.2	6.4	3.6	5.9	2
50.2	12.1	17.7	15.9	13.5	5.7	5.4	26.3	6
25.9	25.1	33.2	22.7	20.2	17.3	14.7	19.1	5
220.4	199.1	279.6	280.5	312.7	264.5	300	316.5	9
1163.6	1132.4	1051.8	1047.1	951.5	1072.7	1114	1083	8
			2	1.2				
	1.7	1.9	1.6	1.6			1.8	
4	2.6	4.2	2.4			2.1		
		1.5	4.2	3.4	4		3.9	1
2		1.4	8.1	1.5	1.8	2.1	1.8	
276.9	279.7	256.9	269.9	258.2	271.4	295.4	252.6	9
186.6	162.9	167.7	178.9	209.2	213.1	214.1	224.7	26
157.7	148.1	160.4	176.2	164.4	167.7	207	180	6
3497.1	3278.8	2912.8	2415	2216.8	2550.2	2279.2	2102	11
109.3	88.6	92.3	76.9	97.1	86.5	107.3	115.7	5
4.8	2.6	3.7	9.4	8.3	4.4	2.9	8.3	1
200.1	220.4	211.5	195.3	208.7	208.7	201	201.2	4
69.2	68	61.7	52.7	45.9	51.5	43.3	48.2	3
83.3	98.8	93.1	76.6	84	78.1	87.6	91.6	9
127.7	123.8	110.3	82.6	52.6	86.5	81	91.8	8

47.2	36.3	40.6	30	35.8	34.2	42.9	39.2	3
5	4	1.9	3.7	2.8	2.9	3.7	5.6	1
5.1	10.6		3.3	4.6	3.9	2.8	4	1
4	4.7	1.8	2.1	2.8	4	3.3	2.9	1
4.4	2.6	3.4	3.7	7.2	4.9	11	3.3	1
490.9	491.9	491.2	437.3	466.2	464.9	419.4	446.3	12
8.3	1.8	11.6	60	69.9	57.2	89.9	79	2
39.6	41.7	52.7	62.7	75.5	57.1	82.1	74.8	10
101.3	100	103.5	142.2	143	115.3	172.2	161	12
	1.8	1.6	5.4	6.1	2.5	3.9	5.7	
4.1		6	14.6	19.9	10.1	13.3	14.4	3
	4	1.9	4.2	11.6	6.5	2.5	2.2	
13	15.8	19.3	10.7	19.3	15.6	14.5	13.1	3
		2.1				3.1	2.1	1
2.8	1.8	4	3.4	9.4	3.8	3.9	7.2	
2.5	6	5.8	4.9	15.5	5.8	10.6	11.6	
137.6	181.2	204.1	346.6	365	305.9	344.6	356.4	8
2.8	3.6	3.3	8.4	7.8	4.7	3.1	3.4	1
	1.7			1.5		2.7	1.9	
13.4	19.4	15.7	13.6	19.1	13.2	7.5	18.6	5
4.8	4.1	9.2	11.4	11.5	9.7	9.6	10.5	1
			5.2	3.6		1.7		
30.4	34.9	62.6	49.8	66.2	62.6	44.7	54.4	4
6.8	6.1	1.8	5.8	5.7	5		5.7	2
1.7		9.1	1.8	9.3	4.3	7.2	3.9	
5.5	9.2	5.8	8.8	12.8	3.6	2.9	2.3	
53.3	47.3	76.9	76.4	95.7	62.3	67.9	91.5	8
3.5			4.7	1.7	2.5	2.8	1.5	
8.6	3.1	9.5	11	11.3	12.2	9.6	9.1	1
7.4	2	6.4	7.9	8.9	5.9	6.2	10.4	2
5	9.9	8.9	3.8	10.7	13.4	9.8	4.3	1
12	19.6	13.3	11.8	14.2	13.3	13.9	16.6	4
2.3	1.7		2.5	2.4		2	2.1	
11.2	13.3	18.5	16	18.4	14.8	14.3	18.4	1
	1.8				1.5	4.3	3.2	
	3.6	3	10.2	5.5	5.9	6.6		2
2.3	2.4	1.6	2.1	4		2.3	5.1	
6.5	10.7	18.2	22.7	17.7	24.1	23.7	22.2	1
197.9	189.3	235.6	349.2	344.7	308.6	309.7	331.3	9
	2.6		3.1	5.8	2.4	5	2.9	1

	1.8	1.6	4.5	3.1		2.7	1.8	
26.9	29.2	34.1	54.1	58.5	45.4	44.9	51	6
19.7	19.6	23.7	40.1	44	31.5	28.8	40.4	6
89.8	92.6	86.1	130.8	124.4	119.8	124.4	130.4	6
9.1	4.6	7.7	3.9	11.4	4.4	5.8	4.7	3
4.8	3.8	3.6	3.8	7.8	3.3	4.6	7.9	
13.2	10.7	10.2	11.4	23.4	17.8	16.1	16	4
3.1	3.4	2.2	3.9	3.6	2	1.7	6.4	1
32	31	25.2	24	31.2	29.9	35.5	30.9	4
745.7	698.2	792.5	764.1	599	518.6	835.4	840.1	8
	1.7		2.1					
69.2	61.9	56.6	56.9	67.3	55.9	64.9	60.7	2
6.8	7.8	16.1	4.2	8.5	6.3	2.1	9.7	2
	1.5	2.9		1.7	1.9		1.8	
38.3	42.7	47.2	38.8	48.5	47.8	50.9	54.2	5
10.5	11.4	8.8	11.5	19.1	12.8	18.7	23.1	3
37.9	26.9	38.8	27.8	31.8	21.2	32.9	41.5	3
	2.7				2.4			
12.7	10.7	7.5	8.7	10.4	11.7	8.4	11.4	1
2.1		1.5		2.9	2	2		1
			2.2					1
				1.2				
4.4	2.4	4.2	2.1	1.3	6.8	4.4	4.1	2
138	141.4	136.2	108.4	126.9	121.3	134.2	129.7	13
57.3	59.4	51.7	37.5	44.6	52.9	46.2	50.1	6
29.3	37.5	39.8	45.7	55.8	50.5	31.3	44.6	7
	1.5		4.1	4.5	6.4	4.4	2.9	
17.7	14.9	26.3	19.4	17.6	15.8	12.7	23.3	2
2.3	4.1	2.5	6.8	9.7	1.9	8.3	6.4	3
5.4	9.8	8	7.9	8.6	4.9	6.6	8.3	2
		3	4.2	1.9		2.4	3.3	1
187.4	195	182.2	216	182.4	205.6	242	192.6	12
81.6	88.6	106.5	172	169.2	148.8	153.5	165.5	5
96.5	87.4	92.2	50.2	67.2	69.6	61.5	54.6	8
2.4	2.3	2.1	1.8			8.4	1.8	
	1.9							
4.1	2		2.5	3	2.6		4.9	1
6.4	4.5	4	6.6	5.9		4.6	4	1
2.3		1.6				2.1	2.2	
158.1	149.5	158.9	135.2	123.4	131.1	121.6	130.1	6
12.3	13.3	14.7	10.7	13.1	15.2	11	13.7	1
		1.7	4.1	5.4	4.1	2.1	7.5	
	5.5	1.5	5.9	5.9	10.2		1.7	1

		4.4	2.8	3.9	3.1	5.9	3.2	1
9.5	9.9	33.2	19.7	28.5	18.6	17.7	34.4	7
3.5	9.3	6.2	11.7	8.4	5.7	14.2	8.3	2
1837.5	1727.4	1467.7	1332.5	1143.7	1398.4	1240.5	1306.1	12
661.5	645.2	576.5	538.6	468.4	559.5	530.6	520.9	16
311	281.2	286.2	246.4	301	250.3	215.2	229.1	4
64.2	56.4	49.2	59.4	43	66.7	50.8	46.4	3
79.2	72.7	69.8	61.1	66.4	59.5	65.5	67.4	11
	1.9		2			4.4		
11.2	13.8	13.9	4.3	6.7	14.7	11.5	10.5	1
203.4	201.4	194	193.2	188.2	204.6	214.4	196.8	4
14.7	16.6	12.5	11.1	8.7	10.8	13.9	6.1	4
101.6	110.2	98.8	85.1	89.5	94.5	104.2	93.9	10
53.6	59.9	88.5	88.6	96.8	87.5	84.8	90.9	9
12	10.5	23.7	16.9	19.1	22.1	10.4	23.2	3
63.9	69.6	47.8	36.6	53.2	50.8	47.9	52.3	7
23.8	26.1	31.8	20.1	20.9	22.8	15.8	26.8	7
379.6	365.8	354.2	330	334.8	336.1	363.8	371.7	15
		1.8	2.5	2.8		1.9		
435.1	399.5	337.5	326.1	287.5	342	283.4	271.2	9
351.3	326.5	481.3	540.5	498.1	508.4	337.7	425.7	6
11.7	12	12.6	12.2	15.6	21.6	10.4	14.5	2
7.8	9.1	7	2	5.6	4.9	6.6	3.4	2
14	10.7	13.9	10.4	10.2	8.4	12.3	12.3	3
118.7	120.4	110	106.6	106.1	116.5	114	109.4	10
16.3	20.8	31.5	32.4	38.1	34.7	14.3	36.1	6
30.3	31.2	31.6	50.2	58.6	49.8	42.5	42	2
102.8	99.4	130.8	137.5	147.4	140.3	113	111	5
3.5	2.4	4.4	8.5	7	5	5.4	4.6	1
					2.1		1.5	
2.5			1.7			1.9		
6.5	9.6	10.8	7.7	8.9	11.2	6.4	2.6	2
5188.1	5255.2	5093.9	5850.1	5675.5	5311.9	5634.8	5233.5	8
	2	8.1	2.2	2.9		2.8		1
251.6	277.1	250.6	273.1	289	263.6	321.3	280.3	8
65.8	59.9	52.1	58.2	56.7	60	54.2	54.6	2
445.5	406.7	388.2	330.5	333.4	350.9	340.3	363.4	15

9.9	10.8	10.8	13.1	11.1	12.4	15.4	33.7	3
2.1				1.4		3.9		
3	4.2	6.9	6.7	11		7.6	5.9	3
	1.8	2.3		1.6	2.9	6.3	3.7	
288	266.6	238.4	235.7	203.2	230.8	243.5	218.2	7
20.9	17.5	23	28.2	28.5	26.4	25.4	28.8	2
4.7	3.4	2.5	7.5	3.6	9.1	12.5	9.8	1
2.4		2.6		3.4		2.1	2.3	
44.8	39.9	45.1	38.3	39.9	27.8	45	39.2	7
18.5	37.5	40	37.1	48.8	44.1	45.1	41.6	5
16.7	25.9	22	42.7	42.1	42.5	27.3	45.7	3
4.5	3.2	2.8	3.5	8.3	4.8	2.8	7.4	1
34.4	33.5	33	35.3	42.9	45.3	34.6	36.9	2
27.2	27.4	24.7	32.1	24.7	19.7	21	29	4
	2.8		4.6	4.2	1.9		4.2	1
232	260.9	220.5	256.4	246	242.8	241.3	237.7	12
5.9	2.7	3.4	4.7	2.2	2.1	4.4	2.9	1
109.8	103.7	95.7	170.2	136.4	196.2	178.8	159.3	7
325.2	322.7	306.6	231.5	248.6	239.8	225.5	240.3	14
28	32.3	47	42.7	56.2	55.1	42.6	47.5	2
297.7	308.5	288.8	248.3	259.2	241.1	267.3	299.2	12
43.8	46.3	61.9	40.2	34.3	41.2	43.1	41.2	6
50.6	36.5	37.7	34	23.9	26.3	33.2	30.6	3
179.8	168.2	170.5	107.6	95.9	86.7	122.4	92.5	9
32.1	29	24.4	34.7	15.4	15.2	19.6	23.3	3
20.4	12.6	17.4	6.6	10.1	2.9	7.8	5.9	2
2.3	1.8	1.8		3.7	5.5	2.3	3.3	1
818.9	733.2	756.8	578.9	542.2	502.5	557	548.3	22
139.9	118.9	124.6	104	85.3	95.4	94	85.3	2
20.7	17.9	20.1	15.9	17.1	15.7	14.1	20	1
13.7	12.2	15.7	9.7	6.3	7.7	12.2	13.4	3
30.3	26.1	20.5	7.3	13.6	9.4	5.6	7	4
2.7	2	2.3	3.9	3.3	2.1		1.7	1
2.3								1
2.7		1.8		3	2.4	3.5	2.1	
				1.5		2.5		
5.5	4.8	9.6	2.4	4.6	3.4	2.3	3.4	1
348.8	359.9	331.1	313.8	273.5	259.1	341.4	301.3	8
4.8	10.1	8.9	9.8	17.7	11.2	14.9	16.7	1
4.4	8.4	16.5	9.4	9.4	9.6	10.8	8.7	

234.4	238.2	210.6	189.2	184.3	184.1	187.1	179.5	9
11.2	19.3	15.9	7.6	11.2	12.6	13.5	8.2	2
2.1				4.1		1.7	2.1	
	7.8	6.8	10.7	7.6	11.1	8.2	13.2	1
3	6.4	6.5	8.9	12.8	7.7	6.6	11.4	
39.6	37.1	30.6	43	45.4	46.8	44.1	37.2	4
24.6	27.9	20.5	22	37.7	29.8	30.5	24.4	3
21.8	23.1	28.8	16.3	15.5	16.8	20.5	21.2	1
138.6	143.6	122.3	132	127.7	161	125.3	112.2	6
38.2	35.7	32.6	32.2	35.6	25.9	27.9	43.4	7
2		3	37.9	43.5	59.8	45.9	67.9	
			4.5	2.3			2.4	1
203	173.5	165.6	177.1	179.3	190.7	199.3	209.2	17
1.7	3.7	6.9	1.7	3.5			4.1	2
		1.7				2.1		
			1.7	1.9			1.7	
	2.4						1.6	
15.4	20.7	23.5	16.4	19.8	14.2	18.5	18.6	4
100.8	97.1	123.6	96.1	102.4	100.4	95.9	79.4	5
				1.4	1.5		1.7	
78.1	81.2	75.9	65.5	72.4	70	75.4	68.3	4
319.5	313.2	326.9	292.6	276.5	279.8	343.1	289.7	5
31.5	31.8	41.3	41.4	46.9	39.3	44.5	34.7	1
256.4	273.7	243.8	222.2	214.1	194.3	226.3	221.1	9
12	2.4	12.4	29.9	19.6	24.9	11.5	25.1	3
3.3	3.4	2.6	5	3	4.4		2.6	1
69.2	66.4	98.6	125.2	143.4	108.2	118.2	128	9
46.4	66.4	67.5	129.1	126	142.7	124.7	125.7	6
2.4	4.5	11.9	13.6	18.2	9.7	10	11	2
				1.3	1.8		3.2	
3.5	4.3	8.5	10.7	10.1	9.8	13	12	1
25	24.6	31.3	49.6	50.1	41.5	32.5	53.3	2
6.9	6.1	5.7		1.7				4

	2.7		2.2					
				1.6				
				1.8	3.5	2		
4.7	5.5	7.6	19.8	19.7	21.6	34	21.5	1
	3.4	5.4	25.6	26	18	28.7	29.6	1
5.4	11.2	12.3	24.1	27.4	15.3	16.1	21.8	2
199.2	199.2	183.6	158.6	131.4	141.7	166.2	157.7	9
17.5	14.7	27.3	113.9	87.9	131.9	154.7	128.5	4
23.8	29.2	41	164.5	135.2	187.7	192.3	163.6	4
5.2	4.8	8	25.6	17.1	34.7	23.3	21.7	1
88.5	91.6	131.9	434.4	391.2	497.6	519.1	441.1	8
513	755.4	773.1	1688.7	1580.7	1667.2	1050.7	1401.6	9
56.6	64	59	123.9	91.8	145.2	133.6	116.2	3

Abundances Count: F6: 127N, Sample, wt, single	Abundances Count: F6: 128N, Sample, wt, single	Abundances Count: F6: 129N, Sample, wt, single	Abundances Count: F6: 130N, Sample, wt, single	Abundances Count: F6: 127C, Sample, ko, single	Abundances Count: F6: 128C, Sample, ko, single	Abundances Count: F6: 129C, Sample, ko, single	Abundances Count: F6: 130C, Sample, ko, single	Abundances Count: F6: 131, Sample, ko, pool
9	8	10	7	9	12	10	8	12
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7	7	7	7	7	7	7	7	7
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6	6	6	6	6	6	6	6	6
				1	1	3	2	1
7	9	8	8	9	9	9	9	9
3	3	3	3	3	3	3	3	3
6	6	6	6	6	6	6	6	6
7	7	7	7	7	7	7	7	7
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5	7	7	7	7	7	7	7	7
29	29	29	29	27	29	29	29	29
2	2	2	2	2	2	2	2	2
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3	3	3	3	3	3	3	3	2
3	3	3	3	3	3	3	3	3
6	6	6	6	6	6	6	6	6
5	5	5	5	5	5	4	5	5
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7	7	7	7	7	7	7	7	7
8	8	9	8	9	9	9	9	9
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13	13	13	13	13	13	13	13	13
17	17	17	17	17	17	17	17	17
			1			1		
			1		1			1
4	4	4	4	4	4	4	4	4

5	3	5	3	5	6	6	5	5
9	9	9	9	9	9	9	9	9
2	4	4	2	5	5	3	3	6
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1	1	1	1	1	1	1	1	1
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9	9	9	9	9	9	9	9	9
7	7	7	7	7	7	7	7	7
4	4	4	4	4	4	4	4	4
8	8	8	8	8	8	8	8	8
5	5	6	7	7	8	8	8	8
1	2	2	2	2	2	2	2	2
3	2	3	3	3	3	2	3	3
9	9	9	9	9	9	9	9	9
8	5	8	9	9	9	8	8	9
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6	6	6	6	6	6	6	6	6
1	2	2	2	3	2	3	2	3
2	2	1	2	2	2	2	2	2
	2		1	1	2	1	1	
3	3	3	3	3	3	3	3	3
3	3	3	3	3	3	3	3	3
7	7	7	7	7	7	7	7	7
11	10	11	10	9	14	9	9	11
2	2	2	2	2	2	2	2	2
4	4	4	4	4	4	4	4	4
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1	1	1	1	1	2	1		2
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	1	2	2	2	2	2	2	2
7	9	9	9	11	10	10	10	10
8	8	8	8	8	8	8	8	8
6	5	5	5	5	5	6	7	6
3	3	3	3	3	3	3	3	3
15	16	16	16	16	16	16	16	16
	1		1	2	3	1	4	4
	1		1	2			2	1
5	6	7	7	7	9	7	9	9
7	7	7	7	7	7	7	7	7

4	4	4	5	4	6	6	5	5
1	1	2	3	3	3	3	1	2
5	5	5	5	5	5	5	5	5
7	7	7	7	7	7	7	7	7
1	1	1	2	2	4	2	3	4
		1			1			1
3	3	3	4	3	3	2	3	3
5	5	5	7	6	8	7	6	6
3	3	3	3	3	3	3	3	3
5	5	5	5	5	5	5	5	5
4	4	4	4	4	4	4	4	4
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	1	1	1	1	1	1	1	1
1				1		1	1	
		1						
7	7	7	7	7	7	7	7	7
9	10	9	9	9	10	10	10	10
4	4	4	4	4	4	4	4	4
16	16	16	16	16	16	16	16	16
1	1	1	1	1	1	1	1	1
2	2	2	2	2	2	2	2	2
7	7	7	7	7	7	7	7	7
1	1	1	1	1	1	1	1	1
2	2	3	3	3	3	3	3	3
2	5	4	5	5	4	7	5	6
10	9	10	10	11	10	9	10	10
2	2	2	2	2	2	2	2	2
10	11	11	11	11	12	11	12	12
1		2	2	1	2	2	3	3
2	2	2	2	2	2	2	1	2
1	1		1					
9	9	9	9	9	9	9	9	9
2	2	2	2	2	2	2	2	2
9	10	10	11	9	10	10	11	10
5	5	5	5	5	5	5	5	5
4	4	4	4	4	4	4	4	4
				1				
2	5	4	5	5	6	2	2	3
3	2	5	4	3	1	5	2	1
8	8	8	8	8	8	8	8	8
8	8	8	8	8	8	8	8	8
6	6	6	6	6	6	6	6	6
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3	3	3	3	3	3	3	3	3
5	5	5	5	5	5	5	5	5
4	3	4	3	3	5	4	4	3

4	4	4	4	4	4	4	4	4
5	5	4	6	7	7	7	6	6
1	2	3	3	2	3	3	2	2
1	1	1	1	1	1	1	1	2
4	4	4	3	5	4	3	4	4
1		1	1		1	1		1
1	1	1	1	1	1	1	1	1
			1			1		
1	1	2	1	2	2	2		1
3	5	2	5	9	9	9	9	9
1	1	2	1	1	2		1	1
6	7	7	6	5	6	2	5	5
6	5	7	8	7	7	7	7	8
10	14	14	13	9	14	13	13	14
7	6	9	10	6	8	7	6	9
2	1	1	1	1	1		1	1
2	3	3	3	2	3	3	3	3
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1	2		2	2	2	2	2	2
10	10	10	9	10	10	9	9	10
9	9	9	9	9	9	9	9	9
9	9	9	9	9	9	9	9	9
6	6	6	6	6	6	6	6	6
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2	2	2	2	2	2	2	2	1
3	3	3	3	3	3	3	3	3
4	4	4	4	3	3	3	3	4
					2			
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3	2	2	2	1	4	1	3	1
		1	1			1		
4	4	4	4	4	4	4	4	4
	2		3	1	2	1	1	2
6	7	6	7	8	8	8	7	7
2	2	2	2	2	2	2	2	2

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8	9	8	9	9	9	9	8	9
7	7	7	7	7	7	7	7	7
	1				1	2		2
56	61	78	75	61	95	62	65	77
2	2	3	2	2	4	3	3	4
7	8	8	8	8	8	8	8	8
6	4	3	5	5	4	5	3	6
4	4	4	4	4	4	4	4	4
5	5	5	5	5	5	5	5	5
8	8	9	9	10	10	10	10	10
2	2	2	2	2	2	2	2	2
3	3	3	3	3	3	3	3	3
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	1	1		1	2	1	2	
12	12	12	12	12	12	12	12	12
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6	4	7	8	8	8	6	5	8
9	9	9	9	9	9	9	9	9
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12	13	10	11	11	12	11	11	14
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6	6	6	6	6	6	6	6	6
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9	9	9	9	9	9	9	9	9
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6	8	8	8	7	7	7	8	8
2	2	2	2	2	2	2	2	2
	1		1		1			

				2	1		2	
	1		1					
16	17	17	17	16	17	17	17	17
6	8	9	8	7	8	5	7	7
5	5	5	5	5	5	5	5	5
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5	8	10	9	8	8	8	9	9
	1			2	2			1
				1				
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4	4	5	4	5	5	5	4	4
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3	3	3	3	3	3	3	3	3
3	1	3	2	2	3	3	2	3
1	1		2	2	2	2	1	2
						1		
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4	4	4	4	4	4	4	4	4
1	2	2	3	2	4	2	3	2
1					1		1	
3	3	3	3	3	3	3	3	3
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18	16	16	17	18	19	17	19	18
11	11	11	11	11	11	11	11	11
9	9	9	9	9	9	9	9	9
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1	2	1	3	2	3	3	1	3

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7	7	7	7	7	7	7	7	7
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			1		1			
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				1				
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	1			1				1
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2	1	3	4	2	3	3	5	5
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9	8	7	10	8	9	8	8	9
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3	6	6	7	5	6	4	6	5
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4	4	4	4	4	4	4	4	4
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7	7	7	7	6	7	7	7	7
18	18	18	18	18	18	18	18	18
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6	6	6	6	6	6	6	6	6
10	10	12	11	10	11	13	13	12
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8	8	8	8	8	8	8	8	8
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1	1	1	1	1	1	1	1	1
4	4	4	4	4	4	4	4	4
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7	7	7	7	7	7	7	7	7
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2	3	2	2	4	3	3	4	3
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3	3	3	3	3	3	3	3	3
12	12	12	12	12	12	12	12	12

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2	2	2	2	2	2	2	2	2
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2	3	4	3	4	5	2	1	4
3	3	3	3	3	3	3	3	3
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1			1				1	
			1		2			1
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4	4	4	4	4	4	4	4	4
11	12	12	12	12	12	12	12	12
5	5	8	8	7	8	4	8	9
4	3	5	4	3	4	3	4	4
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7	5	5	7	7	7	7	6	7
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			1	1				1
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3	3	3	3	3	3	3	3	3
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7	7	8	8	7	8	6	7	6

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Quan Info	XCorr Sequest HT	Confidence Sequest HT	Percolator q-Value Sequest HT	Percolator PEP Sequest HT
No Quan Va	1.358633	High	0.002754	0.0519
Unique	5.01532	High	0	2.14E-08
Unique	1.88558	High	0.000432	0.006361
No Quan Va	1.42676	High	0.000961	0.01788
Unique	2.392193	High	0.000112	0.0026
Unique	1.139306	High	0.002121	0.03683
No Quan Va	2.111808	High	0	0.001321
Unique	2.510377	High	0.000112	0.003526
Unique	3.108305	High	0	4.91E-05
Unique	3.991532	High	0	1.42E-05
No Quan Va	2.864865	High	0.000112	0.001847
Unique	2.188016	High	0.000664	0.0104
Unique	2.210287	High	0.000432	0.006944
Unique	2.321025	High	0.001803	0.03032
Unique	1.783096	High	0.002267	0.04305
No Quan Va	3.667816	High	0	1.61E-07
Unique	2.876528	High	0.001547	0.02598
Unique	3.088577	High	0.000112	0.003186
No Quan Va	1.581505	High	0.004127	0.06778
No Quan Va	2.32583	High	0.001004	0.01943
Unique	2.301754	High	0.002391	0.04525
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Unique	3.19945	High	0	1.88E-06
Unique	2.008555	High	0.002121	0.03692
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No Quan Va	0.998209	High	0.000664	0.01053
No Quan Va	1.599411	High	0.002154	0.03823
No Quan Va	3.550296	High	0	1.96E-05
No Quan Va	2.467245	High	0.000432	0.006813
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Unique	2.171406	High	0.000664	0.009567
Unique	2.557202	High	0	0.001174
No Quan Va	3.851927	High	0	0.000112
No Quan Va	3.899326	High	0	1.96E-06
No Quan Va	1.772276	High	0.005472	0.08673
Unique	2.950279	High	0.000885	0.01728
Unique	3.009464	High	0	6.62E-05
Unique	3.188384	High	0	0.000076
Unique	2.316688	High	0	0.00096
Unique	3.762105	High	0	3.33E-05
Unique	3.968333	High	0	1.81E-07
Unique	2.421703	High	0	0.000333
Unique	1.554965	High	0.000112	0.002073
Unique	2.4725	High	0.000112	0.001929
No Quan Va	4.866184	High	0	3.11E-07

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Unique	2.9805	High	0	7.82E-05
Unique	2.961591	High	0	7.69E-05
Unique	2.800314	High	0	1.26E-05
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No Quan Va	2.264418	High	0	0.001583
No Quan Va	0.773062	High	0.002808	0.05301
Unique	1.799453	High	0.001004	0.02004
Unique	2.388811	High	0.002323	0.04451
Unique	3.019292	High	0	0.000189
Unique	2.158429	High	0	0.00052
Unique	1.537856	High	0.001547	0.02579
Unique	1.676221	High	0.003226	0.05887
Unique	2.608452	High	0	0.000465
Unique	3.028191	High	0	0.000067
Unique	3.091471	High	0	0.001092
No Quan Va	2.660981	High	0	0.001252
Unique	2.534723	High	0.000112	0.002156
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Unique	3.224686	High	0	1.49E-05
Unique	2.60631	High	0	5.29E-05
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Unique	2.817278	High	0	0.000265
No Quan Va	2.120475	High	0.000112	0.004583
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No Quan Va	1.433875	High	0.001676	0.02698
Unique	2.123642	High	0.003529	0.06101
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No Quan Va	2.309663	High	0	0.001147
Unique	3.053843	High	0.002267	0.04323
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No Quan Va	2.326843	High	0.001004	0.01989
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Unique	1.81476	High	0.000112	0.002179
Unique	1.690821	High	0.007839	0.1161
No Quan Va	2.476222	High	0.000664	0.01078
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Unique	2.817113	High	0	6.55E-05
Unique	3.729548	High	0	2.17E-06
Unique	3.576117	High	0	1.41E-05
Unique	4.219652	High	0	1.02E-05
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Unique	3.414362	High	0	8.4E-07
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Unique	4.38373	High	0	9.16E-07
Unique	3.150739	High	0	2.97E-05

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Unique	3.334532	High	0	7.04E-06
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Unique	1.624354	High	0.002267	0.04118
Unique	1.875188	High	0.002754	0.05049
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Unique	5.920742	High	0	6.17E-08
Unique	2.538604	High	0	0.00071
Unique	4.754027	High	0	5.18E-07
Unique	2.286996	High	0	0.00101
Unique	2.594015	High	0.000664	0.01115
Unique	1.621677	High	0.00075	0.01317
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Unique	3.237602	High	0	2.62E-05
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Unique	2.446383	High	0.00053	0.007495
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Unique	2.118555	High	0.000836	0.01363
Unique	2.585668	High	0	0.000449
Unique	2.69335	High	0	0.000522
Unique	5.09385	High	0	6.48E-09
Unique	2.938684	High	0	5.16E-06
Unique	4.078972	High	0	4.61E-07
Unique	3.632328	High	0	7.06E-08
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Unique	2.013857	High	0.003763	0.06544
Unique	4.222917	High	0	2.12E-06

Unique	5.270833	High	0	1.24E-10
Unique	3.934191	High	0	5.01E-06
Unique	4.023864	High	0	3.58E-08
No Quan Va	1.79566	High	0.000885	0.01681
No Quan Va	3.819099	High	0	2.01E-07
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Unique	3.470082	High	0	1.77E-05
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Unique	2.184522	High	0.001948	0.03222
Unique	1.206411	High	0.002519	0.04684
No Quan Va	2.02456	High	0.001004	0.02191
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Unique	2.931081	High	0	0.000129
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Unique	2.518122	High	0	0.000204
Unique	3.094743	High	0.000112	0.002649
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No Quan Va	0.737016	High	0.001993	0.03401
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No Quan Va	2.847999	High	0	8.21E-05
Unique	3.322406	High	0	3.44E-05
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Unique	3.230747	High	0	1.34E-05
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Unique	1.489683	High	0.001743	0.0299
Unique	2.468466	High	0.008998	0.1233
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Unique	3.280153	High	0.000112	0.002105
Unique	2.359934	High	0.000885	0.01757
No Quan Va	2.94393	High	0	0.000382
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Unique	5.413143	High	0	2.33E-09
Unique	2.89727	High	0	8.17E-05
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Unique	5.087126	High	0	9.73E-08
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Unique	2.281466	High	0	5.22E-05
Unique	2.299789	High	0.001004	0.02102
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Unique	2.270283	High	0.000333	0.005966

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Unique	2.93891	High	0	2.98E-06
Unique	2.78422	High	0	0.000442
No Quan Va	3.443438	High	0	7.04E-06
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Unique	3.356647	High	0	2.63E-05
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Unique	3.189828	High	0	0.00021
Unique	3.78887	High	0	1.37E-05
Unique	3.561288	High	0	2.61E-06
Unique	4.470419	High	0	1.08E-08
Unique	4.422313	High	0	8.97E-10
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Unique	3.259339	High	0	8.39E-05
Unique	3.438246	High	0	7.31E-06
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Unique	3.396219	High	0	8.42E-07
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Unique	2.22873	High	0.001676	0.02843
Unique	2.510059	High	0.000961	0.01807
Unique	3.138278	High	0	0.000757
Unique	3.356718	High	0	0.000988
Unique	3.714866	High	0	1.24E-05
Unique	1.410829	High	0.001087	0.02293
Unique	2.554886	High	0.001803	0.03144
Unique	1.017239	High	0.002154	0.03882
Unique	1.829256	High	0.003226	0.05785
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No Quan Va	1.524049	High	0.001475	0.02481
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Unique	3.003642	High	0	8.05E-06
Unique	2.288945	High	0.001004	0.02043
Unique	4.867053	High	0	3.94E-05
Unique	2.177484	High	0	0.00156

Unique	3.366405	High	0	4.89E-05
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Unique	3.813864	High	0	0.000267
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No Quan Va	5.066315	High	0	9.84E-10
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Unique	1.627332	High	0.001004	0.01944
No Quan Va	1.8131	High	0.000333	0.006138
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Unique	2.882874	High	0	2.16E-05
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Unique	1.513063	High	0.002754	0.04906
No Quan Va	3.351038	High	0	0.000303
Unique	3.138901	High	0	0.000963
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Unique	1.241668	High	0.000112	0.003372
Unique	1.223173	High	0.002154	0.03939
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No Quan Va	2.021221	High	0	0.00097
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No Quan Va	2.955548	High	0	0.000461
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Unique	1.454835	High	0.002267	0.04283
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Unique	3.118934	High	0	0.000258
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Unique	3.173172	High	0	0.000112
Unique	2.99032	High	0	4.74E-05
Unique	3.771272	High	0	3.2E-07
Unique	2.502642	High	0	6.75E-05
Unique	2.302615	High	0.000608	0.008321
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Unique	1.978525	High	0.001163	0.02308
Unique	1.078765	High	0.002519	0.04677
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Unique	2.772209	High	0	0.00026
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Unique	2.682039	High	0	3.91E-05
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Unique	2.281569	High	0.000664	0.01133
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Unique	3.984359	High	0	3.3E-07
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Unique	2.391041	High	0	0.000761
Unique	5.379077	High	0	1.71E-10
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Unique	2.743719	High	0	0.000428
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Unique	3.229013	High	0	0.000558
Unique	3.432854	High	0	0.000012
No Quan Va	3.161779	High	0.001803	0.03074
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Unique	3.840363	High	0	1.12E-07
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Unique	3.516083	High	0	5.33E-06
Unique	2.183385	High	0.000885	0.01404
Unique	2.97092	High	0.000112	0.002156
Unique	3.3455	High	0	1.41E-05

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No Quan Va	2.432774	High	0.000112	0.002052
Unique	2.680751	High	0	0.001782
No Quan Va	1.830518	High	0	0.000625
Unique	2.613675	High	0	0.000451
No Quan Va	1.358648	High	0.001993	0.0345
No Quan Va	1.532138	High	0.000961	0.01868
Unique	3.16171	High	0	0.000034
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Unique	1.753078	High	0.000961	0.01855
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Unique	3.045815	High	0	0.001486
Unique	3.500758	High	0	0.000264
Unique	2.556795	High	0.000112	0.005243
Unique	1.843048	High	0.000885	0.01691
No Quan Va	1.444488	High	0.002267	0.04284
Unique	1.628073	High	0.002754	0.05168
Unique	3.948515	High	0	1.78E-06
Unique	3.00839	High	0	0.000203
Unique	1.992509	High	0	0.001492
Unique	4.561214	High	0	5.17E-05
Unique	1.351896	High	0.002121	0.03564
No Quan Va	4.814847	High	0	2.72E-09
No Quan Va	1.075258	High	0.00299	0.05566
Unique	3.152954	High	0	0.000183
No Quan Va	2.581017	High	0	0.000169
Unique	2.179003	High	0	6.64E-05
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No Quan Va	1.878728	High	0.004774	0.07961
Unique	1.218761	High	0.001004	0.02131
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Unique	1.445316	High	0.00299	0.05592
Unique	3.627319	High	0	5.58E-07
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Unique	3.801466	High	0	4.77E-07
Unique	2.841866	High	0.000112	0.003111
No Quan Va	2.624027	High	0.000112	0.002243
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Unique	2.168755	High	0	0.001182
Unique	2.242007	High	0.000112	0.003682
Unique	0.901336	High	0.002808	0.05365
Unique	1.954758	High	0.000112	0.002566
Unique	2.930069	High	0	7.42E-05
Unique	2.356122	High	0.001004	0.02044
Unique	1.872222	High	0	0.001227
Unique	4.942809	High	0	8.75E-10

Unique	3.266178	High	0	2.23E-05
Unique	2.228203	High	0.000432	0.006233
Unique	2.106548	High	0.001004	0.01955
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Unique	2.886967	High	0.003641	0.0631
Unique	4.463651	High	0	4.02E-08
Unique	5.598207	High	0	1.55E-10
Unique	1.800569	High	0.00053	0.007536
Unique	5.059475	High	0	2.03E-08
Unique	1.838724	High	0.003763	0.06514
No Quan V	1.499745	High	0.00075	0.01316
Unique	1.381891	High	0.001948	0.03235
Unique	0.929915	High	0.002754	0.05207
Unique	2.592963	High	0	0.001436
Unique	3.829278	High	0	0.000216
No Quan V	3.804406	High	0	3.67E-06
Unique	3.105445	High	0	0.001392
No Quan V	0.829355	High	0.006385	0.0982
Unique	2.99481	High	0.000112	0.002593
No Quan V	2.171604	High	0	0.000181
Unique	3.000193	High	0	7.72E-05
Unique	5.209968	High	0	9.03E-09
Unique	2.568275	High	0	0.000285
Unique	3.263608	High	0	1.62E-06
No Quan V	1.78068	High	0	0.001282
Unique	1.191063	High	0.001803	0.03013
No Quan V	1.220309	High	0.002718	0.0477
Unique	1.342364	High	0.003641	0.06403
No Quan V	1.676999	High	0	0.001326
No Quan V	3.201375	High	0	7.78E-05
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Unique	2.386526	High	0.000112	0.004124
Unique	2.111505	High	0.004336	0.07199
Unique	2.347953	High	0.00627	0.09655
No Quan V	2.028648	High	0	0.00054
Unique	2.05468	High	0.000112	0.005851
Unique	1.107997	High	0.001993	0.03357
Unique	2.291763	High	0	0.000891
Unique	1.816267	High	0.000608	0.007697
Unique	3.745831	High	0	0.00001
Unique	4.811501	High	0	8.71E-10
Unique	2.799495	High	0	0.000529
Unique	2.020324	High	0	0.001422
No Quan V	3.589781	High	0	1.05E-05
Unique	1.70644	High	0.000112	0.00505
No Quan V	1.499994	High	0.003226	0.05773
Unique	3.843816	High	0	6.57E-06
Unique	4.810089	High	0	6.49E-09
Unique	2.292863	High	0.000112	0.002148
No Quan V	2.928176	High	0	0.000342

Unique	2.781928	High	0	3.36E-05
Unique	2.552662	High	0.000112	0.004428
Unique	2.524906	High	0.000112	0.003662
Unique	1.579792	High	0.000608	0.008997
Unique	1.473582	High	0.000333	0.006122
No Quan Va	0.706635	High	0.002267	0.04304
No Quan Va	2.993513	High	0	0.00015
No Quan Va	3.151409	High	0	8.13E-05
Unique	2.508965	High	0.000112	0.001862
Unique	2.67421	High	0	1.73E-05
No Quan Va	1.440787	High	0.000836	0.01336
Unique	3.36838	High	0	3.12E-06
Unique	3.154061	High	0	6.23E-05
Unique	3.229587	High	0	6.51E-06
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Unique	1.524574	High	0.000885	0.01668
Unique	1.611335	High	0	0.001787
No Quan Va	2.422031	High	0.000112	0.003164
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Unique	2.354411	High	0	0.000894
No Quan Va	2.399345	High	0	0.00074
No Quan Va	1.631054	High	0.00053	0.007427
No Quan Va	2.815097	High	0	0.000063
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Unique	2.482791	High	0.002154	0.03852
Unique	3.176085	High	0	0.000486
Unique	0.959684	High	0.001004	0.02059
Unique	1.531541	High	0	0.001489
No Quan Va	2.0055	High	0	0.000285
No Quan Va	2.724493	High	0.00053	0.007019
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No Quan Va	1.826341	High	0.000333	0.006067
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Unique	2.346883	High	0.000112	0.00457
Unique	2.169798	High	0	0.000895
Unique	3.471404	High	0	0.000137
Unique	1.874032	High	0.000664	0.01192
Unique	3.649224	High	0	1.27E-06
No Quan Va	2.613387	High	0.000112	0.004924
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Unique	3.535129	High	0	1.79E-08
Unique	2.323403	High	0.002154	0.03865
Unique	2.112422	High	0.000112	0.004682
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Unique	4.278385	High	0	4.23E-07
No Quan Va	1.520169	High	0.000432	0.006301
No Quan Va	1.130149	High	0.002154	0.03985
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Unique	0.987652	High	0.005514	0.08688
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Unique	2.775156	High	0.000112	0.003532
No Quan Va	1.284437	High	0.002808	0.05298
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No Quan Va	3.201704	High	0	4.96E-06
No Quan Va	0.738001	High	0.002121	0.03624
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Unique	2.074011	High	0.000112	0.002976
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Unique	1.883807	High	0.000836	0.01349
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Unique	4.77827	High	0	7.17E-08
No Quan Va	3.76609	High	0	2.42E-06
Unique	3.924945	High	0	3.23E-05
Unique	1.50822	High	0.002121	0.03625
No Quan Va	1.638727	High	0.001993	0.03388
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Unique	2.466669	High	0.000112	0.002062
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Unique	1.675826	High	0.002267	0.04182
No Quan Va	2.585179	High	0	0.001119
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Unique	1.453922	High	0.000112	0.004769
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Unique	2.504779	High	0	0.000232
Unique	7.588603	High	0	0
Unique	2.136509	High	0.001004	0.02109
Unique	2.02911	High	0.001676	0.02773
Unique	2.628455	High	0	6.85E-05
Unique	2.55461	High	0	3.44E-05
No Quan Va	2.438212	High	0	0.000353
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No Quan Va	3.877452	High	0	8.94E-07
Unique	3.005561	High	0	1.99E-05
Unique	3.969709	High	0	2.76E-07
Unique	3.213709	High	0	3.56E-05
Unique	2.732216	High	0	4.16E-05
Unique	3.184689	High	0	5.65E-05
Unique	2.838144	High	0	0.001191
Unique	2.537365	High	0.000333	0.005937
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Unique	3.742114	High	0	2.64E-05
No Quan Va	1.88028	High	0.002267	0.04193
No Quan Va	2.288293	High	0.00075	0.01322
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Unique	0.490334	High	0.002718	0.04806
Unique	3.04662	High	0	1.03E-05
Unique	1.621974	High	0.000112	0.003078
No Quan Va	2.870977	High	0.000664	0.01107
No Quan Va	2.404033	High	0.000112	0.004732
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Unique	2.762643	High	0	0.000888
Unique	4.771692	High	0	1.88E-07
Unique	4.132795	High	0	3.48E-07
Unique	2.305888	High	0	0.001126
Unique	5.06225	High	0	5.08E-10
Unique	2.861953	High	0	1.11E-06
Unique	5.532806	High	0	1.56E-09
Unique	4.518605	High	0	1.98E-06
Unique	3.58786	High	0	0.000179
Unique	2.51543	High	0	7.62E-05
Unique	2.503722	High	0	0.00013
No Quan Va	2.442639	High	0.000112	0.001875
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No Quan Va	2.112024	High	0	0.000953
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Unique	2.513958	High	0	0.000371
Unique	4.604001	High	0	3.68E-09
Unique	4.481606	High	0	1.43E-07
No Quan Va	3.621368	High	0	6.61E-06
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Unique	2.788211	High	0	0.000357
Unique	1.955089	High	0	0.00165
Unique	2.028857	High	0.000608	0.008423
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Unique	0.831196	High	0.009141	0.1256
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No Quan Va	1.700824	High	0	0.000376
Unique	2.347442	High	0	0.000158
No Quan Va	2.454403	High	0.000112	0.002637
No Quan Va	1.523246	High	0.000664	0.01191
No Quan Va	0.737668	High	0.002323	0.04492
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Unique	3.731622	High	0	1.1E-09
Unique	3.637588	High	0	3.33E-05
Unique	1.637154	High	0.000885	0.0159
Unique	3.445937	High	0	9.41E-06
Unique	3.924536	High	0	7.39E-07

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Unique	4.291688	High	0	3.91E-06
Unique	2.081204	High	0.000112	0.002879
No Quan Va	0.912745	High	0.001993	0.03318
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Unique	1.820152	High	0.000885	0.01621
Unique	2.606345	High	0	1.94E-05
No Quan Va	1.196482	High	0.001993	0.03468
No Quan Va	1.136517	High	0.00075	0.01313
No Quan Va	3.096358	High	0.000112	0.002158
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Unique	3.428077	High	0	3.87E-05
Unique	2.330969	High	0	0.000984
No Quan Va	0.738001	High	0.002808	0.05307
Unique	2.507203	High	0.001676	0.02818
Unique	2.990079	High	0	0.000629
Unique	4.289038	High	0	2.95E-08
Unique	3.087724	High	0	0.000666
Unique	2.28662	High	0	0.000275
Unique	3.81483	High	0	1.78E-07
Unique	1.902792	High	0.001475	0.02445
Unique	1.288092	High	0.001803	0.03133
Unique	1.542693	High	0.001004	0.02183
Unique	2.617777	High	0.000112	0.003747
Unique	3.41552	High	0	0.000903
No Quan Va	2.654708	High	0	0.000133
Unique	3.580657	High	0.000112	0.002088
Unique	1.783014	High	0.000112	0.002343
Unique	1.651569	High	0.006325	0.09776
Unique	1.909115	High	0.000608	0.0083
Unique	3.352835	High	0.004388	0.07409
Unique	3.956156	High	0	1.67E-05
Unique	4.238794	High	0	3.53E-06
Unique	2.757022	High	0	0.000603
Unique	3.328078	High	0	7.08E-06
Unique	2.273174	High	0.000112	0.004077
Unique	2.547808	High	0.001004	0.01929
Unique	1.697168	High	0.002154	0.03944
Unique	1.676203	High	0	0.001321
Unique	2.398952	High	0	7.89E-05
Unique	3.041129	High	0	4.67E-06
Unique	2.922745	High	0	0.000733
No Quan Va	1.394263	High	0.000112	0.004655
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Unique	1.550734	High	0.000664	0.0111
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Unique	2.119766	High	0.000608	0.008702
No Quan Va	4.88722	High	0	5.7E-09
Unique	2.06226	High	0.000112	0.002194
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No Quan Va	1.973201	High	0.00075	0.0132
No Quan Va	1.869679	High	0	0.000664
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No Quan Va	3.14268	High	0	3.07E-05
Unique	2.120543	High	0.000112	0.001902
Unique	1.986395	High	0.000112	0.002868
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No Quan Va	2.374452	High	0	2.25E-05
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No Quan Va	2.782249	High	0	0.000138
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Unique	2.975529	High	0	0.0003
Unique	1.94907	High	0.000961	0.01806
No Quan Va	2.927987	High	0	1.58E-06
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No Quan Va	0.954091	High	0.00075	0.01296
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Unique	2.862114	High	0	0.000176
Unique	1.877195	High	0	0.000841
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Unique	2.477294	High	0.000112	0.004376
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Unique	3.456398	High	0	3.54E-07
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Unique	1.535438	High	0.000112	0.005217
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Unique	2.885767	High	0	9.21E-05
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Unique	3.112264	High	0	1.86E-05
No Quan Va	1.478277	High	0.000112	0.002495
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No Quan Va	1.932791	High	0.000112	0.002464
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Unique	1.285824	High	0.007102	0.1074
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Unique	2.52209	High	0	0.000207
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Unique	1.960356	High	0.000885	0.01486
Unique	1.787786	High	0.001993	0.03245
Unique	2.168416	High	0.005959	0.09284
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Unique	2.319916	High	0.000664	0.01172
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Unique	2.500937	High	0	0.000659
Unique	1.94723	High	0.000664	0.01234
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Unique	1.653334	High	0.001676	0.02691
Unique	1.870684	High	0.002519	0.04645
Unique	2.552906	High	0.000112	0.002473
Unique	3.653687	High	0	2.39E-06
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Unique	3.235739	High	0	3.12E-05
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No Quan Va	1.992925	High	0.000112	0.005908
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Unique	2.629879	High	0	0.000392
Unique	1.521111	High	0.001004	0.02007
Unique	1.701296	High	0	0.001207
No Quan Va	1.756178	High	0	0.001042
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Unique	1.644314	High	0.000608	0.007726
Unique	1.522465	High	0	0.001704
Unique	2.166934	High	0.000608	0.008896
No Quan Va	1.746313	High	0.003415	0.05994
Unique	1.855334	High	0.000112	0.001967
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Unique	3.585179	High	0	1.39E-07
No Quan Va	2.298721	High	0	0.00035
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Unique	4.098411	High	0	2.4E-08
Unique	4.024823	High	0	2.75E-08
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Unique	1.371745	High	0.000608	0.008897
Unique	2.357697	High	0.000885	0.01475
Unique	3.678263	High	0	0.000031
Unique	2.807477	High	0	7.67E-05
Unique	2.811972	High	0	0.001091
No Quan Va	2.549112	High	0	0.000124
Unique	2.494081	High	0	0.000347
Unique	2.190404	High	0.003529	0.06213
No Quan Va	2.101861	High	0.007839	0.1152
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Unique	3.658553	High	0	1.28E-06
Unique	2.386064	High	0	0.000345
Unique	4.32934	High	0	2.36E-07

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Unique	1.235214	High	0.001993	0.03358
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Unique	2.283746	High	0.000885	0.01549
No Quan Va	2.784673	High	0.000112	0.003049
Unique	1.752383	High	0.000112	0.001847
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Unique	1.114628	High	0.002718	0.04803
Unique	1.940658	High	0.002871	0.05409
Unique	3.199285	High	0	0.000118
Unique	2.032538	High	0.000112	0.002183
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Unique	2.587276	High	0	0.001453
Unique	2.4387	High	0.000112	0.003246
Unique	1.529434	High	0.000885	0.01725
Unique	1.433788	High	0.000608	0.009228
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Unique	1.361981	High	0.000885	0.01696
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Unique	1.116173	High	0.002154	0.03999
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Unique	2.552418	High	0.000112	0.00575
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Unique	2.361809	High	0.000112	0.004742
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Unique	2.131194	High	0.000112	0.005074
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No Quan Va	1.403292	High	0.000432	0.006395
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Unique	2.112958	High	0	0.0008
Unique	3.886803	High	0	5.57E-06
Unique	3.830365	High	0	0.000014
No Quan Va	1.905677	High	0.003529	0.06201
No Quan Va	0.9019	High	0.001676	0.02674
Unique	3.732575	High	0	1.82E-06
Unique	4.77449	High	0	2.51E-08
Unique	1.81842	High	0.001676	0.02754
Unique	2.407066	High	0.002154	0.03787
No Quan Va	2.474829	High	0	0.000148
Unique	2.882444	High	0	0.000041
Unique	3.932202	High	0	6.97E-06
Unique	4.46783	High	0	1.36E-06
Unique	4.20814	High	0.000112	0.003244
Unique	2.950588	High	0	0.000722
Unique	2.358957	High	0.000112	0.002503
No Quan Va	2.285924	High	0.00075	0.01303

Unique	1.44388	High	0.000961	0.01785
Unique	4.222513	High	0	7.63E-05
Unique	2.126565	High	0.000961	0.01868
No Quan Va	3.39145	High	0	0.000039
Unique	2.740061	High	0	0.000564
Unique	5.421901	High	0	1.51E-08
Unique	2.902095	High	0	0.000513
Unique	2.235322	High	0	0.001116
No Quan Va	3.167397	High	0	1.36E-05
Unique	2.30967	High	0.00053	0.007492
Unique	2.998206	High	0.000112	0.002296
Unique	3.033293	High	0	2.14E-06
Unique	4.151942	High	0	1.05E-05
Unique	1.546936	High	0.001004	0.02154
Unique	0.775682	High	0.009189	0.1263
Unique	1.989395	High	0.000112	0.002949
No Quan Va	1.674045	High	0.003052	0.05666
No Quan Va	2.799657	High	0.000112	0.001952
No Quan Va	0.982168	High	0.007839	0.1158
Unique	3.778276	High	0	6.06E-05
Unique	2.859613	High	0	5.96E-06
Unique	3.418001	High	0	2.61E-06
Unique	2.992681	High	0	5.19E-06
Unique	2.72742	High	0.000112	0.00263
Unique	1.951123	High	0.000664	0.01002
Unique	2.052404	High	0.002154	0.0379
Unique	2.648444	High	0.000112	0.002212
Unique	1.759189	High	0.000885	0.01424
No Quan Va	2.047317	High	0.003415	0.06
Unique	3.084448	High	0	5.17E-06
Unique	5.399519	High	0	5.6E-07
Unique	6.056657	High	0	0
No Quan Va	3.161873	High	0	0.000018
No Quan Va	2.695668	High	0	3.88E-05
Unique	1.748395	High	0.002121	0.03678
Unique	1.678995	High	0	0.001547
Unique	4.845436	High	0	5.68E-07
Unique	4.430326	High	0	3.18E-06
No Quan Va	3.127399	High	0	1.53E-06
Unique	2.362764	High	0	0.000391
Unique	3.429148	High	0	0.000143
Unique	4.047452	High	0	9.41E-09
No Quan Va	2.159488	High	0	0.000807
Unique	3.011594	High	0	1.79E-05
Unique	2.29535	High	0	0.001559
Unique	2.066084	High	0.000608	0.008837
Unique	2.071394	High	0.001004	0.01953
Unique	1.384057	High	0.001676	0.02808
Unique	1.505736	High	0.001948	0.03214
Unique	1.28332	High	0.003415	0.06031
No Quan Va	3.695652	High	0	4.43E-07
Unique	1.809982	High	0.000112	0.003549

Unique	2.287591	High	0.001676	0.02773
Unique	2.454822	High	0	0.00084
No Quan Va	3.332303	High	0	9.55E-05
No Quan Va	2.643029	High	0	2.51E-05
Unique	2.476347	High	0	0.001647
Unique	2.280858	High	0.000112	0.003611
Unique	0.741501	High	0.002267	0.04073
Unique	2.413274	High	0.000112	0.005742
Unique	3.597516	High	0	5.55E-05
Unique	1.826101	High	0.000664	0.01246
Unique	1.814253	High	0.001246	0.02375
Unique	1.555995	High	0.002121	0.03631
Unique	2.646413	High	0	7.35E-05
Unique	1.719916	High	0.001993	0.03239
No Quan Va	2.185289	High	0	0.001349
Unique	2.930921	High	0	0.000232
Unique	2.925744	High	0.002154	0.03861
Unique	4.641337	High	0	9.68E-10
Unique	4.042952	High	0	2.67E-06
Unique	3.661372	High	0	2.04E-06
Unique	2.350263	High	0	0.000371
Unique	3.541071	High	0	8.02E-06
Unique	2.137836	High	0.000112	0.00203
Unique	3.717665	High	0	2.35E-07
Unique	2.239845	High	0.004388	0.074
Unique	3.404255	High	0	1.95E-07
No Quan Va	1.70754	High	0.002267	0.04221
No Quan Va	2.544368	High	0	0.001491
No Quan Va	1.731231	High	0	0.00141
Unique	1.32718	High	0.00053	0.007252
No Quan Va	2.395466	High	0	0.000134
Unique	4.892745	High	0	3.09E-08
Unique	0.944249	High	0.001743	0.02902
Unique	1.804746	High	0.000885	0.01426
No Quan Va	0.985835	High	0.002754	0.05003
Unique	3.22058	High	0	1.04E-05
Unique	2.475796	High	0	0.000135
No Quan Va	2.036184	High	0	0.000592
Unique	1.624675	High	0.000885	0.01496
Unique	1.038001	High	0.003641	0.06321
No Quan Va	3.540652	High	0	1.11E-06
Unique	2.364097	High	0.000885	0.01563
Unique	4.135983	High	0	2.43E-08
Unique	3.42077	High	0	0.000184
Unique	3.173475	High	0	2.35E-05
Unique	2.209618	High	0.000432	0.006639
Unique	1.80727	High	0.002267	0.04329
Unique	1.65122	High	0.000664	0.01258
Unique	1.462127	High	0.000885	0.01397
No Quan Va	2.965432	High	0	3.97E-05
Unique	2.603513	High	0	2.04E-05
Unique	4.237358	High	0	1.6E-07

No Quan Va	1.618055	High	0.000608	0.008805
Unique	2.148206	High	0.002754	0.05011
No Quan Va	0.682106	High	0.001993	0.0339
Unique	0.72711	High	0.003052	0.05622
Unique	3.205005	High	0	1.18E-05
Unique	5.340086	High	0	1.67E-09
Unique	2.821009	High	0	7.38E-05
Unique	3.189543	High	0	0.000153
Unique	2.738169	High	0.000112	0.002643
No Quan Va	1.697797	High	0.000112	0.004043
No Quan Va	0.775764	High	0.001004	0.02096
No Quan Va	1.918372	High	0	0.001226
Unique	2.28705	High	0	0.001007
No Quan Va	1.94878	High	0.001676	0.02725
No Quan Va	1.458973	High	0.000608	0.008505
Unique	5.008239	High	0	1.35E-09
Unique	2.771852	High	0.000112	0.002202
No Quan Va	1.448333	High	0.002154	0.03992
No Quan Va	3.070242	High	0	0.000054
Unique	2.87648	High	0	0.000295
No Quan Va	1.65701	High	0.000112	0.003474
Unique	2.192417	High	0.000112	0.002247
Unique	1.582864	High	0.004336	0.07234
No Quan Va	1.139818	High	0.001993	0.03289
Unique	2.147965	High	0.000112	0.003842
Unique	1.847783	High	0.000112	0.00414
No Quan Va	2.002505	High	0.000885	0.01743
Unique	2.73113	High	0	0.001486
Unique	1.993023	High	0.000885	0.01564
No Quan Va	2.490157	High	0	0.000364
No Quan Va	1.826301	High	0.000112	0.00305
No Quan Va	1.27633	High	0.001475	0.02499
Unique	3.777987	High	0.000112	0.002284
Unique	2.276347	High	0.000112	0.003021
No Quan Va	2.583237	High	0	9.14E-05
Unique	2.419741	High	0	0.00176
Unique	1.479523	High	0.003052	0.05654
No Quan Va	2.065585	High	0.000664	0.01237
Unique	2.652869	High	0	0.000145
Unique	1.804163	High	0.000112	0.003796
Unique	3.884857	High	0	1.39E-08
No Quan Va	4.391893	High	0	3.82E-08
Unique	2.068749	High	0.000112	0.004069
Unique	2.067508	High	0	0.000916
Unique	2.165731	High	0	0.001054
Unique	2.088937	High	0.000112	0.00577
Unique	3.028792	High	0	3.49E-05
Unique	3.594141	High	0	2.54E-07
Unique	4.587969	High	0	1.22E-09
No Quan Va	3.062669	High	0	3.9E-06
Unique	2.357447	High	0	0.001138
Unique	1.396083	High	0.001743	0.02957

Unique	2.43622	High	0.000885	0.01582
Unique	4.037475	High	0	1.26E-06
Unique	4.673926	High	0	9.91E-08
Unique	2.069037	High	0.003703	0.06484
Unique	5.904279	High	0	0
Unique	3.703137	High	0	1.27E-05
Unique	2.783339	High	0.000112	0.002531
No Quan Vɛ	2.343191	High	0.000885	0.01433
Unique	2.508835	High	0	0.000237
Unique	2.281074	High	0.000112	0.005547
Unique	1.428884	High	0.000961	0.01783
Unique	2.758011	High	0	4.69E-05
Unique	4.128028	High	0	7.02E-07
Unique	3.463769	High	0.000112	0.002769
Unique	4.810902	High	0	7.07E-05
Unique	2.844717	High	0.000112	0.004414
Unique	2.412008	High	0.002226	0.04053
Unique	2.022502	High	0.000112	0.005346
Unique	2.68523	High	0.002154	0.03895
No Quan Vɛ	4.661415	High	0.003703	0.06455
Unique	2.069049	High	0.002061	0.03551
Unique	3.947593	High	0	1.85E-06
Unique	3.718339	High	0	3.34E-06
Unique	2.934887	High	0.002754	0.05061
Unique	4.078112	High	0	0.000133
Unique	2.681169	High	0.000112	0.002019
Unique	2.419179	High	0	0.000298
No Quan Vɛ	3.017803	High	0	0.000561
Unique	2.418206	High	0	0.00034
Unique	1.691189	High	0.001004	0.01903
No Quan Vɛ	2.810734	High	0	0.000313
Unique	3.403942	High	0	5.1E-06
Unique	2.226915	High	0.000885	0.01667
No Quan Vɛ	2.442109	High	0.000112	0.002022
No Quan Vɛ	2.659862	High	0.004232	0.07036
Unique	2.265673	High	0.002267	0.04145
Unique	3.228951	High	0	5.42E-06
Unique	2.866343	High	0	0.000206
Unique	1.858312	High	0.000112	0.004723
No Quan Vɛ	1.325873	High	0.003893	0.06578
No Quan Vɛ	1.440365	High	0.002121	0.03663
Unique	2.121312	High	0	0.001085
Unique	5.08625	High	0	9.12E-07
Unique	1.018108	High	0.001803	0.03012
No Quan Vɛ	2.273573	High	0.000112	0.002982
No Quan Vɛ	1.992628	High	0.000112	0.001999
No Quan Vɛ	2.663467	High	0.000664	0.00985
Unique	3.063891	High	0	7.46E-05
Unique	2.738516	High	0	0.000385
Unique	1.954489	High	0.003415	0.06046
No Quan Vɛ	2.075176	High	0.000608	0.009098
Unique	0.98693	High	0.002267	0.04306

Unique	2.408309	High	0.000664	0.0117
No Quan Va	1.572121	High	0.00075	0.01307
No Quan Va	4.963787	High	0	4.66E-09
No Quan Va	2.576017	High	0.000664	0.01177
Unique	0.736769	High	0.006641	0.1016
No Quan Va	3.006358	High	0	0.000355
No Quan Va	1.461329	High	0.000112	0.004511
Unique	3.347937	High	0	0.001771
Unique	2.446136	High	0.000664	0.01197
No Quan Va	2.625528	High	0	3.21E-06
No Quan Va	2.089295	High	0	0.000998
Unique	5.517143	High	0	0
Unique	2.633585	High	0	0.00045
Unique	4.713281	High	0	2.62E-07
Unique	2.786495	High	0	0.000121
Unique	1.688729	High	0.003641	0.06453
Unique	3.487984	High	0	5.09E-05
Unique	2.692649	High	0	0.000144
Unique	2.438263	High	0	0.00136
Unique	3.340503	High	0	0.000154
Unique	3.059921	High	0	0.000518
Unique	2.997806	High	0	0.000188
Unique	2.95474	High	0	0.00052
Unique	2.443661	High	0	0.00013
Unique	2.789517	High	0.001803	0.03125
Unique	1.451585	High	0.000664	0.01111
Unique	2.250687	High	0.002267	0.04199
Unique	3.653714	High	0	2.18E-05
Unique	2.027303	High	0.000608	0.007975
Unique	2.107999	High	0.000664	0.01176
Unique	2.8048	High	0	0.001083
No Quan Va	0.966925	High	0.001246	0.02381
Unique	1.972861	High	0.003641	0.0636
Unique	3.641216	High	0	2.47E-06
Unique	2.445848	High	0	4.25E-05
Unique	2.740907	High	0	0.001738
Unique	3.97592	High	0	1.13E-07
Unique	2.854091	High	0	5.26E-06
Unique	2.689009	High	0	7.39E-05
Unique	3.995338	High	0	2.64E-06
Unique	3.95888	High	0	1.5E-06
Unique	2.280905	High	0.000112	0.005441
Unique	1.491041	High	0.000664	0.01068
Unique	2.346864	High	0.000885	0.01603
Unique	2.223017	High	0.000885	0.01693
Unique	1.503872	High	0.002121	0.0357
Unique	1.173473	High	0.000432	0.006636
Unique	1.324029	High	0.000664	0.009893
Unique	0.824206	High	0.002267	0.04327
Unique	3.450578	High	0	2.36E-05
Unique	3.226916	High	0	5.13E-07
Unique	3.822438	High	0	2.48E-07

No Quan Va	1.222497	High	0.000885	0.01419
No Quan Va	1.203365	High	0.001004	0.0192
No Quan Va	1.174417	High	0.001405	0.02422
Unique	1.938172	High	0.001004	0.02098
Unique	2.489068	High	0	0.000138
Unique	2.363593	High	0.000885	0.0174
Unique	2.305468	High	0.000112	0.005711
Unique	3.86917	High	0	1.81E-06
Unique	4.179415	High	0	1.22E-08
Unique	3.205905	High	0.000112	0.004201
No Quan Va	1.734665	High	0.001004	0.01935
Unique	2.106764	High	0	0.001683
Unique	5.158538	High	0	2.03E-09
Unique	1.054989	High	0.003226	0.058
Unique	3.434422	High	0	0.000142
No Quan Va	1.030287	High	0.003529	0.06201
No Quan Va	1.122833	High	0.002808	0.05282
Unique	1.621958	High	0.000112	0.0056
Unique	3.108797	High	0	0.00038
No Quan Va	1.279012	High	0.000885	0.01562
Unique	3.213444	High	0	0.000184
No Quan Va	2.553889	High	0.000432	0.006322
No Quan Va	2.04158	High	0.001475	0.02438
No Quan Va	1.851724	High	0.000885	0.01734
No Quan Va	1.928646	High	0.000885	0.0169
No Quan Va	1.512721	High	0.003415	0.0604
No Quan Va	1.548338	High	0.001993	0.03445
Unique	2.815934	High	0	0.000136
Unique	3.471466	High	0.000112	0.002422
Unique	4.172219	High	0	2.52E-08
No Quan Va	0.785575	High	0.003226	0.05821
No Quan Va	1.139755	High	0.000112	0.005706
Unique	4.51232	High	0	2.84E-08
Unique	4.798236	High	0	1.26E-08
Unique	2.025475	High	0.000112	0.005065
Unique	1.224044	High	0.002754	0.0495
No Quan Va	2.317987	High	0.000112	0.002634
Unique	1.895439	High	0.003703	0.06478
Unique	0.947873	High	0.000885	0.01655
Unique	5.140139	High	0	2.42E-10
Unique	2.144026	High	0.000112	0.002083
Unique	1.05753	High	0.003763	0.06519
No Quan Va	2.308912	High	0.000112	0.003053
Unique	2.656063	High	0.003529	0.06116
Unique	2.890917	High	0	0.000356
Unique	1.81437	High	0.003115	0.05719
Unique	2.309697	High	0.002808	0.05384
No Quan Va	1.639544	High	0.000112	0.005213
Unique	3.954934	High	0	9.57E-07
Unique	3.237788	High	0	3.14E-05
Unique	3.572409	High	0	4.83E-09
Unique	3.472281	High	0.000112	0.001839

Unique	1.453161	High	0.001993	0.03468
Unique	2.443858	High	0	0.00016
Unique	4.400049	High	0	4.44E-07
Unique	3.140488	High	0	2.72E-06
Unique	1.119002	High	0.001993	0.03372
No Quan V	1.553907	High	0.003226	0.05926
No Quan V	0.691851	High	0.001405	0.02403
No Quan V	1.992158	High	0	0.00167
Unique	3.653133	High	0	3.15E-05
Unique	2.204429	High	0	0.001278
Unique	5.302172	High	0	0
Unique	4.113532	High	0	7.65E-08
Unique	2.423891	High	0	0.001215
Unique	2.924129	High	0	0.001166
No Quan V	1.938213	High	0.000112	0.004134
Unique	2.160969	High	0.000608	0.007691
Unique	1.268963	High	0.001405	0.02397
Unique	3.271071	High	0.002519	0.04638
Unique	2.010692	High	0.007058	0.1058
No Quan V	2.824663	High	0	0.000317
No Quan V	1.662531	High	0.000664	0.01239
Unique	3.213396	High	0	1.66E-06
Unique	1.560786	High	0.002519	0.0463
Unique	3.614298	High	0	0.000241
No Quan V	1.819793	High	0.000112	0.00237
Unique	1.435269	High	0.003226	0.05783
Unique	1.301467	High	0.001163	0.02309
No Quan V	2.08897	High	0.000112	0.003187
Unique	2.638543	High	0.000664	0.01127
No Quan V	2.705548	High	0.000112	0.004363
Unique	4.01795	High	0	6.37E-05
Unique	2.163413	High	0.000112	0.003374
Unique	4.882312	High	0	8.67E-05
Unique	2.414342	High	0.000608	0.008807
Unique	1.482855	High	0.002323	0.04402
Unique	0.730002	High	0.001004	0.0214
Unique	3.027139	High	0	0.000269
No Quan V	3.408326	High	0	6.2E-06
Unique	3.894107	High	0	3.63E-05
No Quan V	1.82875	High	0.000112	0.004811
Unique	2.272989	High	0.000664	0.01029
Unique	1.504528	High	0.001676	0.02733
No Quan V	1.507664	High	0.00075	0.01287
Unique	3.318497	High	0	1.05E-06
Unique	6.690676	High	0	0
Unique	3.775431	High	0	1.13E-05
No Quan V	1.068129	High	0.000885	0.0149
Unique	1.764433	High	0.00299	0.0555
Unique	2.209072	High	0.001004	0.02092
Unique	0.946983	High	0.002267	0.04209
No Quan V	1.668979	High	0.002267	0.04302
Unique	1.00547	High	0.002808	0.05283

No Quan Va	0.93626	High	0.002267	0.04099
No Quan Va	2.957751	High	0.000432	0.006773
No Quan Va	2.291569	High	0	0.00064
Unique	1.674901	High	0.001004	0.02257
Unique	5.757622	High	0	9.62E-10
Unique	2.968789	High	0	0.000416
Unique	3.530771	High	0	1.25E-05
Unique	3.47939	High	0	7.17E-08
No Quan Va	2.300804	High	0.000961	0.01804
No Quan Va	2.648217	High	0	0.000175
Unique	2.389236	High	0	0.000962
Unique	1.780843	High	0.004175	0.06946
Unique	3.835195	High	0	4.54E-08
Unique	3.676224	High	0	3.12E-07
No Quan Va	2.214768	High	0	0.000397
Unique	1.920708	High	0.000885	0.01518
Unique	2.451419	High	0	0.000253
Unique	3.275704	High	0	8.99E-06
Unique	3.24607	High	0	0.000001
No Quan Va	3.886267	High	0	1.45E-06
Unique	2.220306	High	0	0.001221
Unique	2.328432	High	0.000664	0.01177
No Quan Va	2.077476	High	0.001004	0.01924
Unique	1.675809	High	0.001993	0.03439
No Quan Va	1.16844	High	0.002808	0.05343
Unique	2.571941	High	0	0.001496
No Quan Va	1.717323	High	0.000112	0.004873
No Quan Va	0.891049	High	0.002754	0.05174
Unique	3.083811	High	0	1.44E-05
Unique	2.838997	High	0	1.97E-05
Unique	3.353224	High	0	3.69E-06
Unique	1.385428	High	0.000836	0.01382
Unique	2.168438	High	0.00627	0.09699
Unique	4.037047	High	0	2.09E-06
Unique	3.609676	High	0	0.000157
Unique	3.158778	High	0	1.34E-06
Unique	2.428745	High	0.00053	0.007199
Unique	1.711799	High	0.000664	0.01198
Unique	1.726197	High	0.001163	0.02306
No Quan Va	1.447949	High	0.000961	0.01797
No Quan Va	1.925525	High	0	0.001361
Unique	3.450104	High	0	9.02E-06
Unique	3.296001	High	0	4.29E-05
Unique	3.409451	High	0	2.04E-05
No Quan Va	0.486835	High	0.003289	0.05978
Unique	1.535903	High	0.000664	0.009878
No Quan Va	2.029855	High	0.000885	0.01669
Unique	2.648769	High	0	0.000374
Unique	4.54729	High	0	4.3E-06
Unique	3.272604	High	0	0.000435
Unique	1.345089	High	0.007839	0.1157
Unique	2.812567	High	0	0.001791

Unique	3.355228	High	0	0.000025
No Quan Va	1.826952	High	0.000112	0.003907
No Quan Va	2.465937	High	0.004948	0.08168
Unique	3.106756	High	0	0.000359
Unique	4.092752	High	0	1.25E-08
Unique	3.554244	High	0	3.18E-06
Unique	1.73612	High	0	0.00123
Unique	2.021029	High	0.000112	0.003907
No Quan Va	2.682514	High	0.000112	0.002593
Unique	1.945385	High	0.000608	0.009096
No Quan Va	2.503184	High	0	0.000025
Unique	4.129906	High	0	1.06E-07
No Quan Va	0.801744	High	0.005959	0.09065
No Quan Va	3.946042	High	0	6.37E-05
No Quan Va	2.560884	High	0	0.000493
Unique	0.910127	High	0.003529	0.06165
No Quan Va	1.577502	High	0.000836	0.01358
Unique	2.581554	High	0	0.000575
Unique	2.488177	High	0	0.000187
Unique	1.51317	High	0.002808	0.05275
Unique	4.756581	High	0	5.42E-09
Unique	2.184575	High	0.000664	0.01257
No Quan Va	3.079165	High	0	8.63E-07
Unique	2.795091	High	0	0.000208
Unique	4.095577	High	0	1.61E-06
Unique	1.894023	High	0.000608	0.009207
No Quan Va	2.550805	High	0	0.000223
Unique	3.004078	High	0	3.26E-05
No Quan Va	1.769726	High	0.001743	0.02917
No Quan Va	1.712163	High	0.001004	0.0203
No Quan Va	1.920799	High	0	0.000267
Unique	2.883917	High	0	0.000755
Unique	3.15853	High	0	0.000122
Unique	3.748958	High	0	0.00017
No Quan Va	1.329316	High	0.00053	0.007059
No Quan Va	1.195021	High	0.000664	0.0101
No Quan Va	2.329552	High	0.000112	0.005462
No Quan Va	2.403885	High	0.002154	0.03775
No Quan Va	2.948585	High	0	0.001486
Unique	3.520399	High	0	0.000025
Unique	3.053094	High	0.000608	0.008187
Unique	1.504886	High	0.000664	0.0124
Unique	1.212257	High	0.003641	0.06385
Unique	1.662629	High	0.002931	0.05492
Unique	6.722911	High	0	2.54E-09
Unique	6.316185	High	0	8.58E-07
Unique	2.898107	High	0	3.28E-05
Unique	3.610794	High	0	1.37E-07
No Quan Va	2.868517	High	0	9.83E-06
No Quan Va	2.460564	High	0.000112	0.002216
No Quan Va	4.382322	High	0	2.36E-05
Unique	2.333224	High	0.000885	0.0169

No Quan V	1.871672	High	0.000664	0.01003
No Quan V	1.54119	High	0.000608	0.008202
Unique	1.82697	High	0.000664	0.01096
No Quan V	2.03621	High	0.000112	0.002395
No Quan V	2.410296	High	0.000885	0.01572
Unique	0.963192	High	0.002718	0.04897
Unique	3.252309	High	0.001004	0.01925
No Quan V	1.664049	High	0.00075	0.01272
No Quan V	1.664049	High	0.000664	0.01245
Unique	1.510532	High	0.001676	0.02762
Unique	5.12914	High	0	8.72E-08
Unique	3.680835	High	0	5.14E-05
Unique	2.763782	High	0	0.000356
Unique	4.396065	High	0	0
Unique	0.892363	High	0.004388	0.07462
Unique	3.020201	High	0	0.000227
Unique	2.136023	High	0.000885	0.01613
Unique	1.849543	High	0.008376	0.1203
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Unique	0.45405	High	0.003529	0.0624
Unique	3.270038	High	0	0.00092
Unique	1.409704	High	0.000112	0.005393
Unique	2.203317	High	0.001948	0.03196
Unique	1.311514	High	0.002154	0.04022
Unique	1.896763	High	0.007686	0.1142
Unique	1.655352	High	0.003052	0.05624
Unique	2.009329	High	0.000608	0.008375
Unique	2.647463	High	0.001004	0.01894
Unique	1.494686	High	0.001743	0.02953
Unique	1.315492	High	0.001676	0.02764
Unique	2.420214	High	0.005808	0.08985
No Quan V	1.046417	High	0.002931	0.05467
Unique	2.686888	High	0.000112	0.002001
Unique	2.595928	High	0	2.29E-05
Unique	3.540589	High	0	1.93E-08
Unique	3.590703	High	0	6.28E-05
Unique	5.172562	High	0	0
Unique	2.676687	High	0	0.000575
Unique	2.275362	High	0.006753	0.1024
Unique	2.56833	High	0	0.000532
No Quan V	1.903452	High	0	0.000688
Unique	2.860938	High	0.000112	0.004149
Unique	1.46661	High	0.000885	0.01417
Unique	3.210492	High	0	5.68E-05
Unique	2.342857	High	0.002457	0.04588
Unique	1.875623	High	0.000885	0.01624
No Quan V	2.968906	High	0	0.000105
Unique	3.789894	High	0	0.000117
Unique	2.183867	High	0.002061	0.03532
Unique	3.328573	High	0	0.000973
Unique	3.298205	High	0	8.18E-06
Unique	1.975115	High	0	9.81E-05

Unique	2.407847	High	0.000112	0.001848
Unique	1.715776	High	0.000664	0.01152
Unique	1.617001	High	0.000112	0.002625
No Quan Va	1.919958	High	0.00053	0.007588
No Quan Va	3.362043	High	0	7.29E-06
Unique	1.716676	High	0.002121	0.03626
Unique	2.023901	High	0.000664	0.01196
Unique	2.383116	High	0.000112	0.001892
No Quan Va	1.274754	High	0.001004	0.02067
Unique	5.447109	High	0	0
Unique	1.479718	High	0.000664	0.01023
Unique	3.551679	High	0	3.62E-05
Unique	3.333683	High	0	1.64E-05
No Quan Va	3.481169	High	0	4.42E-06
No Quan Va	3.969851	High	0	0.000083
Unique	3.890944	High	0	7.47E-06
Unique	2.006403	High	0.000112	0.00255
Unique	4.500051	High	0	5.38E-07
Unique	1.246653	High	0.009445	0.1286
Unique	2.432618	High	0.000112	0.002187
Unique	1.883266	High	0.000608	0.009029
Unique	3.014296	High	0	7.06E-06
Unique	2.897711	High	0.000664	0.01033
No Quan Va	3.059032	High	0	1.94E-05
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Unique	2.483077	High	0.00053	0.007517
Unique	1.362291	High	0.003529	0.06231
Unique	2.236848	High	0	0.001048
Unique	2.33045	High	0.000112	0.00421
Unique	2.029775	High	0.001004	0.02213
Unique	1.519725	High	0.000432	0.006908
Unique	5.219239	High	0	2.67E-07
No Quan Va	1.410835	High	0.001743	0.02981
Unique	2.874902	High	0.000112	0.002403
Unique	2.897978	High	0	3.27E-05
Unique	1.667765	High	0.000112	0.004016
No Quan Va	2.253892	High	0	0.001646
Unique	4.072362	High	0	2.01E-05
No Quan Va	2.632953	High	0	0.000114
Unique	2.03541	High	0.00053	0.007508
Unique	1.898715	High	0.000961	0.01872
Unique	3.739426	High	0	0.000249
No Quan Va	2.732418	High	0	0.000576
Unique	2.460922	High	0.000112	0.002169
Unique	3.434354	High	0	0.000228
Unique	2.704934	High	0	8.75E-05
Unique	2.462488	High	0	0.000833
Unique	1.574931	High	0.00961	0.1296
No Quan Va	2.063689	High	0	0.000772
Unique	2.050306	High	0.000432	0.006807
No Quan Va	4.1099	High	0	0.000122
Unique	3.890587	High	0	9.41E-05

Unique	2.06167	High	0	0.00088
No Quan Va	2.519496	High	0.000112	0.00219
No Quan Va	2.58363	High	0.000112	0.004222
Unique	2.16852	High	0.005307	0.08447
Unique	0.930361	High	0.001676	0.02717
No Quan Va	2.830679	High	0	0.001006
Unique	3.567085	High	0	1.21E-05
Unique	2.67394	High	0.001743	0.02935
Unique	1.755082	High	0.000961	0.01794
Unique	3.175302	High	0	4.86E-05
Unique	1.851465	High	0.001877	0.0316
No Quan Va	1.585565	High	0.00075	0.01298
Unique	3.192798	High	0	0.00045
Unique	2.371832	High	0	0.000599
No Quan Va	1.560293	High	0.006017	0.09349
No Quan Va	1.655524	High	0.001475	0.02534
No Quan Va	1.459665	High	0.000664	0.01097
Unique	2.175076	High	0	0.001618
No Quan Va	2.520223	High	0	0.000644
Unique	2.638485	High	0	0.001445
Unique	2.022505	High	0	0.00119
Unique	1.924544	High	0.000112	0.004846
Unique	1.706127	High	0.000664	0.01033
Unique	1.738576	High	0.001475	0.02481
Unique	3.069207	High	0	1.75E-05
Unique	2.961457	High	0.000432	0.00627
Unique	3.044142	High	0	0.00017
Unique	2.139565	High	0.002754	0.0513
No Quan Va	0.968337	High	0.001803	0.03029
Unique	3.440487	High	0	1.56E-07
Unique	2.825194	High	0	0.000183
No Quan Va	4.364038	High	0	1.44E-07
Unique	1.797728	High	0.000112	0.004758
Unique	2.26917	High	0.000112	0.003441
No Quan Va	1.663046	High	0.007431	0.1107
Unique	1.175579	High	0.002323	0.0449
No Quan Va	0.770784	High	0.002931	0.05472
No Quan Va	1.189467	High	0.00053	0.006995
Unique	2.652288	High	0	0.001498
Unique	3.596908	High	0	0.000054
Unique	2.510565	High	0.001676	0.02807
Unique	2.84787	High	0.004774	0.08041
Unique	4.450434	High	0	9.17E-06
Unique	2.409788	High	0.000112	0.002947
Unique	1.873242	High	0.001676	0.02646
No Quan Va	2.526477	High	0.001626	0.02618
No Quan Va	4.18292	High	0	3.8E-08
Unique	3.164139	High	0	0.000215
Unique	1.815799	High	0	0.001761
Unique	2.893772	High	0	0.00131
Unique	1.351554	High	0.000664	0.01106
Unique	1.862486	High	0.001087	0.02293

No Quan Va	3.596585	High	0	2.8E-06
Unique	3.223402	High	0	4.42E-05
Unique	1.675994	High	0.000112	0.003325
No Quan Va	1.904311	High	0.000112	0.003165
No Quan Va	0.489168	High	0.002323	0.04417
No Quan Va	3.379919	High	0	3.13E-05
Unique	1.969323	High	0.000432	0.006398
Unique	2.176613	High	0.002323	0.04397
Unique	4.893954	High	0	6.84E-06
No Quan Va	2.66189	High	0.000112	0.004011
No Quan Va	2.912311	High	0.001676	0.02768
No Quan Va	5.169384	High	0	3.35E-09
No Quan Va	0.984654	High	0.000112	0.004845
Unique	1.806395	High	0.000664	0.009987
Unique	2.982399	High	0	0.001301
Unique	2.553059	High	0	3.74E-05
Unique	3.001443	High	0	0.001056
Unique	3.898751	High	0	1.49E-05
Unique	3.499307	High	0	2.08E-05
Unique	1.905228	High	0	0.001745
Unique	2.553821	High	0.000112	0.002261
Unique	4.831007	High	0	1.42E-08
Unique	2.793872	High	0	9.81E-05
Unique	5.244509	High	0	1.21E-09
Unique	2.74074	High	0	0.000207
Unique	3.051918	High	0	0.000659
Unique	2.673979	High	0.000112	0.005101
No Quan Va	1.252679	High	0.00075	0.01276
Unique	1.752617	High	0.00299	0.05588
No Quan Va	1.092012	High	0.003529	0.0618
No Quan Va	2.687865	High	0	0.000026
Unique	2.585638	High	0.000112	0.002366
No Quan Va	1.604673	High	0.000432	0.006171
No Quan Va	1.228783	High	0.003226	0.05844
Unique	3.436804	High	0	2.23E-05
No Quan Va	2.816428	High	0.000432	0.006252
Unique	3.413808	High	0	1.37E-05
Unique	2.040649	High	0.003529	0.06113
Unique	2.426062	High	0	0.000111
Unique	2.043777	High	0	0.000392
No Quan Va	0.691462	High	0.002808	0.05339
Unique	2.490487	High	0.000112	0.001994
Unique	2.678574	High	0.001004	0.0215
Unique	1.986736	High	0.00053	0.007468
No Quan Va	2.289296	High	0	0.000553
Unique	3.714336	High	0	2.7E-07
No Quan Va	1.968668	High	0.001803	0.03005
Unique	2.339618	High	0	0.001815
No Quan Va	1.27598	High	0.001004	0.02283
Unique	2.171309	High	0	0.001632
Unique	1.636131	High	0.000664	0.01093
Unique	2.557483	High	0	6.25E-05

Unique	2.24893	High	0.000112	0.005177
Unique	2.626336	High	0	0.000678
Unique	3.567631	High	0	1.97E-06
Unique	2.622971	High	0	3.45E-06
Unique	2.332735	High	0.000112	0.003299
Unique	0.949991	High	0.001803	0.03001
Unique	2.446689	High	0.002154	0.03757
Unique	1.582365	High	0.002154	0.03722
Unique	3.825344	High	0	2.63E-07
Unique	2.906821	High	0.000112	0.005556
Unique	3.775262	High	0	0.000159
No Quan Va	1.28882	High	0.004336	0.07314
Unique	1.402694	High	0.002267	0.04124
Unique	3.302451	High	0	9.66E-05
No Quan Va	2.812022	High	0.000112	0.001976
Unique	1.717894	High	0.000664	0.009515
Unique	3.82215	High	0	0.000319
Unique	1.853642	High	0.000608	0.008041
Unique	3.614842	High	0	2.58E-07
Unique	2.458848	High	0	0.001135
Unique	2.188022	High	0.000112	0.005592
Unique	1.572227	High	0.000432	0.006319
Unique	1.419318	High	0.001803	0.03076
Unique	1.29131	High	0.004291	0.07108
Unique	2.222448	High	0	0.00172
Unique	3.072625	High	0	9.74E-06
Unique	2.537191	High	0	0.000786
Unique	3.338351	High	0	4.22E-05
Unique	3.263982	High	0	0.000263
Unique	2.178272	High	0.000432	0.006189
No Quan Va	1.29226	High	0.00299	0.05601
Unique	3.586566	High	0	1.89E-06
Unique	1.666251	High	0.000112	0.002642
Unique	4.564441	High	0	1.27E-09
Unique	1.675315	High	0.001993	0.03497
No Quan Va	0.742334	High	0.001803	0.03084
Unique	1.138721	High	0.002808	0.05383
Unique	1.872713	High	0.002457	0.04567
Unique	3.103386	High	0	9.63E-05
Unique	5.036059	High	0	5.35E-09
Unique	2.340853	High	0	0.000709
Unique	2.274727	High	0	0.000182
Unique	3.755102	High	0	1.17E-07
Unique	1.711298	High	0	0.000603
Unique	3.245067	High	0.000608	0.008217
Unique	2.111383	High	0	0.000697
No Quan Va	2.036499	High	0	0.001452
No Quan Va	1.45482	High	0.000608	0.007859
No Quan Va	1.14604	High	0.000885	0.01745
Unique	6.383596	High	0	3.95E-09
Unique	2.718704	High	0.000112	0.001953
Unique	4.693049	High	0	2.26E-06

Unique	2.113909	High	0.000432	0.006393
No Quan Va	1.435058	High	0.000885	0.01585
Unique	2.922752	High	0	1.45E-05
Unique	1.288824	High	0.000664	0.01011
No Quan Va	0.496	High	0.002931	0.05488
No Quan Va	1.608535	High	0.000112	0.005235
No Quan Va	3.056603	High	0.000333	0.00607
Unique	2.125494	High	0.004232	0.07076
No Quan Va	2.086172	High	0.006063	0.09486
Unique	2.041448	High	0.000112	0.003137
No Quan Va	1.277952	High	0.002267	0.04143
No Quan Va	0.247167	High	0.002267	0.0435
Unique	1.874883	High	0.00075	0.01293
Unique	5.023273	High	0	1.28E-09
Unique	4.501827	High	0	1.7E-07
Unique	0.616078	High	0.001676	0.0267
Unique	2.321486	High	0	0.000811
No Quan Va	1.217644	High	0.002121	0.0368
Unique	2.882251	High	0	0.001618
Unique	2.047248	High	0	0.001117
Unique	0.967492	High	0.002267	0.04192
Unique	2.887902	High	0	0.000331
No Quan Va	4.298595	High	0	2.47E-07
Unique	4.528701	High	0	1.41E-07
Unique	3.552681	High	0	3.08E-07
No Quan Va	1.246885	High	0.002754	0.05114
Unique	2.995527	High	0.000608	0.008184
Unique	2.499638	High	0.003529	0.06065
No Quan Va	1.628018	High	0.00627	0.09717
Unique	2.891694	High	0	0.001612
Unique	3.727537	High	0	9.64E-06
Unique	2.356767	High	0.000112	0.002404
Unique	2.531926	High	0.000664	0.01111
Unique	1.571818	High	0.003529	0.06246
Unique	3.171705	High	0	1.46E-06
No Quan Va	2.789451	High	0	0.000702
Unique	2.511282	High	0	0.000755
Unique	2.175287	High	0.00053	0.007495
No Quan Va	1.913608	High	0.002931	0.05524
Unique	2.283479	High	0.004127	0.06739
No Quan Va	1.625355	High	0.002121	0.03678
Unique	3.341933	High	0	5.96E-05
Unique	5.842911	High	0	1.01E-09
No Quan Va	4.003956	High	0	7.58E-06
Unique	1.140994	High	0.004948	0.08196
Unique	2.030761	High	0.000664	0.01127
No Quan Va	3.449676	High	0	7.2E-06
No Quan Va	2.28046	High	0	0.000228
Unique	1.247859	High	0.000664	0.01046
Unique	1.730704	High	0.001004	0.0195
No Quan Va	1.893013	High	0.000885	0.01727
Unique	2.122194	High	0	0.000451

Unique	2.387018	High	0	2.07E-05
No Quan Va	3.151085	High	0	1.5E-06
Unique	2.293487	High	0.000432	0.00633
Unique	2.226851	High	0.002154	0.03989
Unique	0.985976	High	0.003226	0.0581
No Quan Va	3.40773	High	0	0.000762
No Quan Va	2.538007	High	0	7.48E-07
No Quan Va	2.746655	High	0.000112	0.00264
Unique	2.78874	High	0	8.31E-06
Unique	2.252712	High	0	0.001818
Unique	2.197662	High	0.000885	0.01482
No Quan Va	1.275101	High	0.001993	0.03311
No Quan Va	1.562415	High	0.002808	0.05303
Unique	4.297229	High	0	7.86E-07
No Quan Va	1.381075	High	0.002519	0.04657
Unique	2.393741	High	0.001993	0.03469
Unique	2.404967	High	0.000432	0.006572
Unique	2.143238	High	0	0.000779
No Quan Va	1.306386	High	0.001004	0.02182
Unique	3.915908	High	0	2.53E-06
No Quan Va	2.831829	High	0	0.000109
No Quan Va	0.486001	High	0.003529	0.06175
Unique	4.529736	High	0	4.3E-07
Unique	2.994877	High	0	2.38E-05
Unique	3.133798	High	0	2.5E-06
Unique	2.465016	High	0	0.001656
Unique	3.17642	High	0	2.58E-05
Unique	2.773123	High	0	0.000307
Unique	2.082511	High	0	0.000494
No Quan Va	1.038383	High	0.002267	0.0411
Unique	2.230711	High	0.000112	0.00487
Unique	1.287118	High	0.001004	0.02285
No Quan Va	2.092566	High	0.000112	0.004978
Unique	3.593031	High	0	2.25E-06
Unique	4.714977	High	0	3.15E-08
Unique	4.730193	High	0	2.08E-05
Unique	3.678712	High	0	3.98E-07
Unique	4.216315	High	0	1.61E-07
Unique	3.184991	High	0	0.000109
Unique	1.944493	High	0.000112	0.001838
Unique	2.404659	High	0.005124	0.08309
Unique	1.825752	High	0.000664	0.009778
No Quan Va	6.316733	High	0	6.8E-09
No Quan Va	5.081685	High	0	1.59E-06
Unique	2.526753	High	0.000112	0.001917
No Quan Va	1.284716	High	0.000885	0.01659
Unique	4.101639	High	0	1.53E-06
Unique	1.564815	High	0.002754	0.04915
Unique	1.46139	High	0.000112	0.00581
No Quan Va	0.992391	High	0.007839	0.116
Unique	2.438242	High	0.000112	0.004713
Unique	1.330359	High	0.000608	0.008766

Unique	1.927824	High	0.000608	0.009442
Unique	2.098264	High	0.000608	0.009355
Unique	1.684514	High	0.003641	0.06315
Unique	3.091095	High	0	6.87E-07
Unique	1.783275	High	0.000112	0.003953
Unique	1.608436	High	0.004336	0.07203
Unique	3.144249	High	0	1.44E-05
Unique	1.47567	High	0.000961	0.01799
No Quan Va	3.105422	High	0	0.000175
Unique	2.101802	High	0.000112	0.005419
Unique	2.635347	High	0.000836	0.01355
Unique	1.597317	High	0.003052	0.05647
No Quan Va	2.224816	High	0.000112	0.001967
Unique	1.315047	High	0.000112	0.005606
Unique	1.377707	High	0.000885	0.01638
Unique	1.490875	High	0.009445	0.1289
Unique	2.309758	High	0.001547	0.02594
Unique	2.36182	High	0	0.00052
Unique	2.445673	High	0	0.001625
No Quan Va	3.197433	High	0	4.52E-05
No Quan Va	1.37759	High	0.001993	0.03447
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Unique	3.968571	High	0	8.66E-07
Unique	5.210555	High	0	6.17E-08
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Unique	5.225122	High	0	4.18E-06
Unique	4.80385	High	0	4.73E-08
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Unique	1.610499	High	0.003226	0.05764
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No Quan Va	1.845104	High	0.001676	0.02865
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Unique	1.497453	High	0.000664	0.0103
No Quan Va	1.251385	High	0.003226	0.05909
No Quan Va	1.321028	High	0.003289	0.05959
No Quan Va	2.681774	High	0	0.000025
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Unique	3.233493	High	0	2.59E-05
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Unique	2.908916	High	0.000112	0.00221
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Unique	2.248271	High	0.000664	0.01072
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No Quan Va	1.630948	High	0.000664	0.0123
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Unique	3.492544	High	0	0.000482
Unique	2.675647	High	0	0.000162
Unique	2.968015	High	0	0.000559
Unique	2.750357	High	0	0.000759
Unique	1.9526	High	0.000112	0.003879
Unique	1.584003	High	0.000664	0.009559
Unique	0.976652	High	0.001004	0.0216
Unique	1.036001	High	0.003182	0.0574
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Unique	2.836277	High	0	0.000422
Unique	4.210067	High	0	0
Unique	1.983801	High	0	0.001538
Unique	1.124962	High	0.000885	0.01591
Unique	1.720139	High	0.007891	0.1167
No Quan Va	3.013167	High	0.000112	0.004325
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Unique	2.030953	High	0.000112	0.00184
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Unique	2.02033	High	0	0.000154
Unique	2.352701	High	0.000112	0.001927
No Quan Va	2.142961	High	0.00053	0.007555
Unique	1.82084	High	0.000112	0.002625
Unique	0.734292	High	0.003958	0.0658
Unique	3.304345	High	0	0.000696
Unique	4.463354	High	0	1.44E-06
Unique	1.442542	High	0.000664	0.01177
Unique	2.232286	High	0.000961	0.01836
Unique	1.219555	High	0.002267	0.04319
Unique	2.001673	High	0.002226	0.04029
No Quan Va	2.356733	High	0	0.00089
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Unique	2.828629	High	0	0.000667
Unique	4.806998	High	0	1.21E-07
No Quan Va	2.925797	High	0	0.001709
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Unique	2.156937	High	0.006426	0.09974
Unique	2.810583	High	0	0.001113
No Quan Va	3.562556	High	0	0.000145
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Unique	3.410197	High	0	7.44E-06
Unique	2.330394	High	0.000333	0.00603
Unique	1.428814	High	0.001004	0.01937
No Quan Va	2.356576	High	0.000112	0.002277

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Unique	2.837145	High	0.000112	0.005092
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No Quan V	0.956521	High	0.002154	0.03881
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No Quan V	3.14963	High	0	2.54E-05
Unique	1.340828	High	0.000608	0.008576
No Quan V	0.786547	High	0.002808	0.05289
Unique	2.332228	High	0	0.001083
No Quan V	4.463002	High	0	1.3E-07
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No Quan V	1.748951	High	0.000885	0.01495
Unique	2.179513	High	0.00075	0.01272
Unique	1.569478	High	0.007058	0.1057
Unique	2.670249	High	0	0.001663
Unique	3.081402	High	0	7.86E-06
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Unique	1.871972	High	0.000112	0.003193
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Unique	1.306835	High	0.003226	0.05832
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Unique	5.012742	High	0	2.64E-08
Unique	2.220111	High	0.000112	0.003321
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No Quan V	1.006129	High	0.006794	0.1034
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Unique	1.274906	High	0.002267	0.04148
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Unique	3.333093	High	0	6.45E-06
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Unique	1.907056	High	0.000112	0.002288
Unique	3.34652	High	0	2.41E-06
Unique	3.737031	High	0	4.18E-06
Unique	2.803536	High	0.000112	0.002008
Unique	1.831538	High	0.001004	0.01941
Unique	2.07557	High	0.003182	0.05738
Unique	3.029206	High	0	0.000223
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Unique	1.62837	High	0.000112	0.002498
No Quan V	1.803167	High	0.000432	0.006374
No Quan V	1.768413	High	0.000664	0.009607
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Unique	2.323883	High	0.000608	0.007742
No Quan Va	1.316596	High	0.001877	0.0317
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Unique	3.902052	High	0	7.29E-08
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No Quan Va	2.305178	High	0.000112	0.002875
No Quan Va	1.738277	High	0.000112	0.004602
No Quan Va	1.836671	High	0.000608	0.007741
Unique	1.998415	High	0.000112	0.004315
No Quan Va	0.953473	High	0.001004	0.02191
No Quan Va	0.738501	High	0.002154	0.03884
Unique	1.817341	High	0.001743	0.02941
No Quan Va	4.029298	High	0	3.21E-05
Unique	2.881693	High	0	6.68E-06
Unique	1.430929	High	0.002718	0.04748
Unique	3.780002	High	0	1.01E-07
Unique	3.183326	High	0	0.00057
Unique	3.320844	High	0	7.26E-07
Unique	3.575792	High	0	1.36E-05
No Quan Va	2.285957	High	0	0.00102
Unique	2.694112	High	0.001743	0.02929
No Quan Va	2.094866	High	0	0.000724
No Quan Va	1.031376	High	0.002754	0.04903
Unique	2.707333	High	0	0.000291
No Quan Va	2.653231	High	0.002154	0.0402
Unique	2.085517	High	0.000112	0.004471
Unique	2.512901	High	0	6.06E-05
Unique	2.840736	High	0	0.00014
Unique	4.660475	High	0	3.09E-07
No Quan Va	2.677984	High	0.000112	0.003435
Unique	2.650541	High	0	7.91E-05
Unique	2.093992	High	0.002061	0.03555
Unique	2.394617	High	0.001475	0.02441
No Quan Va	1.288688	High	0.001743	0.02912
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Unique	1.764318	High	0.000664	0.01017
No Quan Va	1.265564	High	0.001004	0.01978
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No Quan Va	1.719489	High	0.002754	0.05209
Unique	2.043232	High	0.000112	0.002973
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Unique	2.105148	High	0.000961	0.0187
Unique	3.016699	High	0.006794	0.104
Unique	3.643105	High	0	4.27E-06
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Unique	2.822069	High	0	6.57E-05
No Quan Va	3.559331	High	0	1.04E-06
Unique	2.898613	High	0	8.28E-05
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Unique	2.857637	High	0	4.05E-05

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No Quan Va	0.743667	High	0.00299	0.05603
No Quan Va	2.471443	High	0.000112	0.003371
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Unique	2.558475	High	0.000664	0.01084
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No Quan Va	0.492334	High	0.003703	0.06462
Unique	1.934603	High	0.002226	0.04044
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Unique	4.7308	High	0	3.89E-06
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Unique	1.098538	High	0.003226	0.05766
No Quan Va	2.051554	High	0.006017	0.09352
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Unique	4.081665	High	0	9.54E-08
Unique	3.736354	High	0	9.67E-05
No Quan Va	1.97111	High	0	0.001406
Unique	4.049646	High	0	7.88E-08
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Unique	3.265519	High	0	3.45E-05
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Unique	1.936079	High	0.002323	0.04412
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No Quan Va	2.696876	High	0.000112	0.003066
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Unique	3.409902	High	0	6.98E-06

Unique	3.462445	High	0	2.14E-05
Unique	2.493572	High	0	0.000978
Unique	2.620159	High	0.001993	0.03309
Unique	1.260027	High	0.003641	0.06418
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Unique	2.669484	High	0	0.000262
Unique	3.263666	High	0	1.43E-05
Unique	1.600748	High	0.002718	0.0475
Unique	2.496997	High	0.000885	0.01701
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Unique	3.638056	High	0	3.73E-05
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Unique	2.184583	High	0	6.28E-05
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No Quan Va	0.935573	High	0.003641	0.0629
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Unique	2.844799	High	0	5.63E-06
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Unique	2.120385	High	0.003529	0.06206
Unique	3.475235	High	0	5.17E-05
Unique	2.451899	High	0	0.000452
No Quan Va	2.449045	High	0	0.000752
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Unique	2.703627	High	0	0.00016
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Unique	2.846365	High	0	5.13E-05
Unique	2.471616	High	0	1.23E-05
Unique	3.512486	High	0	9.32E-05
Unique	3.956004	High	0.000112	0.004148
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Unique	3.936658	High	0	1.18E-05
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Unique	2.792702	High	0	0.000381
Unique	3.094939	High	0	7.92E-05
Unique	2.613259	High	0.000112	0.003094
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Unique	1.927484	High	0.001475	0.02467
Unique	2.208777	High	0.002154	0.03767

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Unique	5.461223	High	0	2.85E-08
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Unique	2.293966	High	0	0.000175
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Unique	3.152235	High	0	0.000778
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Unique	2.815866	High	0.000112	0.004373
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Unique	2.576232	High	0	0.000823
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Unique	2.534389	High	0.000112	0.005737
Unique	2.548279	High	0	4.02E-05
Unique	2.592743	High	0	0.000282
Unique	3.987815	High	0	4.68E-07
Unique	3.278437	High	0	5.64E-06
No Quan V	2.408798	High	0.000112	0.00237
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No Quan V	2.188876	High	0.000112	0.005116
Unique	1.254076	High	0.002267	0.04112
No Quan V	0.734668	High	0.002154	0.03857
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Unique	3.359052	High	0	0.001412
No Quan V	1.221254	High	0.002808	0.0538
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No Quan V	1.39938	High	0.000608	0.008524
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Unique	1.524184	High	0.001803	0.03077
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No Quan V	1.114465	High	0.000664	0.009932
No Quan V	2.867887	High	0.000112	0.003539
Unique	3.090104	High	0	0.000653
Unique	1.828742	High	0.002154	0.04006
No Quan V	2.479181	High	0	0.000888
No Quan V	0.495834	High	0.001676	0.02697
No Quan V	1.661389	High	0.000664	0.01134
Unique	2.585166	High	0	0.000294
No Quan V	1.966058	High	0	0.000703
Unique	2.232614	High	0.000432	0.006525

Unique	1.855466	High	0.001993	0.03249
Unique	2.858503	High	0	0.001443
Unique	2.117475	High	0.001676	0.02783
Unique	1.886955	High	0.000885	0.01752
Unique	1.541854	High	0.003641	0.06327
Unique	3.886025	High	0	0.000426
No Quan V	2.302477	High	0	9.29E-05
No Quan V	1.081767	High	0.005472	0.08682
Unique	3.487014	High	0	0.000289
Unique	3.162985	High	0	0.001344
Unique	2.729007	High	0	0.000447
No Quan V	2.725606	High	0	2.27E-05
No Quan V	4.217031	High	0	1.09E-07
Unique	2.537551	High	0	0.000105
Unique	2.962329	High	0	2.86E-06
Unique	2.772193	High	0	0.000252
Unique	2.724697	High	0	0.000988
Unique	2.118988	High	0	0.000353
Unique	2.009592	High	0.000608	0.009017
Unique	1.710037	High	0.000608	0.008946
Unique	2.061155	High	0.001004	0.01997
Unique	1.539162	High	0.002154	0.03722
Unique	1.389199	High	0.002519	0.04701
No Quan V	0.597798	High	0.002154	0.0388
No Quan V	2.157824	High	0	0.0002
Unique	4.633369	High	0	3.19E-07
No Quan V	3.789074	High	0	2.79E-06
No Quan V	1.190967	High	0.000112	0.005063
Unique	1.838751	High	0.000885	0.01678
No Quan V	2.210806	High	0.001547	0.02563
Unique	3.885832	High	0	4.78E-08
Unique	4.286937	High	0	2.95E-07
No Quan V	2.838276	High	0	0.000217
Unique	3.698024	High	0	9.27E-08
Unique	2.765217	High	0	4.58E-05
Unique	3.073739	High	0	4.5E-06
Unique	1.942806	High	0.001743	0.02982
Unique	1.403951	High	0.001004	0.02227
Unique	1.943875	High	0.001475	0.0252
Unique	0.853279	High	0.005472	0.08504
Unique	1.544647	High	0.003226	0.05921
No Quan V	1.473955	High	0.002121	0.03617
Unique	3.795233	High	0	6.2E-06
No Quan V	2.682864	High	0	0.000561
Unique	1.404686	High	0.000112	0.004068
Unique	1.871118	High	0.003052	0.05654
Unique	2.213784	High	0	0.001748
Unique	3.28943	High	0	1.41E-06
Unique	2.850574	High	0	9.88E-06
Unique	4.923717	High	0	3.15E-08
Unique	2.981237	High	0.000112	0.004149
Unique	1.625169	High	0.000112	0.002013

Unique	1.472654	High	0.001743	0.02894
Unique	3.176493	High	0	6.86E-05
Unique	3.524676	High	0	4.33E-08
Unique	2.44259	High	0.000112	0.001881
Unique	3.853118	High	0	1.29E-06
Unique	1.651351	High	0.000885	0.01749
Unique	1.954425	High	0.000961	0.0178
No Quan Va	1.719058	High	0.000608	0.009273
No Quan Va	1.894155	High	0.000112	0.005518
Unique	2.96549	High	0	2.45E-05
No Quan Va	2.007094	High	0.000432	0.006383
No Quan Va	1.725166	High	0.000608	0.00913
Unique	3.939589	High	0	2.33E-07
Unique	3.72171	High	0	6.04E-06
No Quan Va	1.664884	High	0.000432	0.006415
No Quan Va	1.622648	High	0.003115	0.05722
Unique	2.465401	High	0	0.000121
Unique	2.087552	High	0.001743	0.02921
Unique	4.162873	High	0	2.14E-07
No Quan Va	1.31546	High	0.001004	0.01934
Unique	3.187799	High	0	1.03E-05
Unique	4.08557	High	0	1.21E-05
Unique	2.691414	High	0	0.000597
Unique	4.878937	High	0	8.18E-08
Unique	0.735002	High	0.000432	0.006739
Unique	1.582166	High	0.002754	0.05145
Unique	2.297597	High	0	0.000222
Unique	1.510047	High	0.000608	0.008956
Unique	0.911155	High	0.002754	0.04969
Unique	1.755296	High	0.004611	0.0778
Unique	1.732652	High	0.000664	0.01041
Unique	3.75002	High	0	4.27E-06
Unique	2.731292	High	0	0.001567
Unique	3.76387	High	0	1.88E-06
Unique	4.006247	High	0	2.75E-05
Unique	2.462611	High	0	0.000718
Unique	2.112326	High	0.004611	0.07808
No Quan Va	2.942446	High	0	3.53E-05
Unique	2.309142	High	0	0.000369
Unique	3.766691	High	0	5.31E-07
Unique	2.717319	High	0	0.00134
Unique	3.408123	High	0	0.000163
No Quan Va	1.224743	High	0.000885	0.0149
Unique	2.149315	High	0	0.001134
Unique	2.177335	High	0	0.000331
Unique	1.971068	High	0	0.001275
Unique	4.404878	High	0	7E-09
Unique	1.87669	High	0.000112	0.001837
Unique	1.89518	High	0.000112	0.002275
Unique	1.566845	High	0.000885	0.01566
Unique	2.577068	High	0	0.000198
Unique	2.198305	High	0	0.001423

No Quan Va	1.769527	High	0.000112	0.005048
Unique	0.98978	High	0.001676	0.02795
No Quan Va	2.406508	High	0	0.001663
Unique	4.052941	High	0	1.65E-06
Unique	2.622397	High	0	0.000129
No Quan Va	2.012197	High	0.000432	0.006281
No Quan Va	0.496334	High	0.002808	0.05351
Unique	4.493508	High	0	2.85E-06
Unique	3.212804	High	0	7.02E-05
Unique	3.01132	High	0.00075	0.0131
Unique	5.576428	High	0	2.13E-10
Unique	4.94549	High	0	7E-09
Unique	1.499064	High	0.001163	0.0236
Unique	1.939355	High	0.00075	0.01281
Unique	1.968296	High	0.001993	0.03404
No Quan Va	2.0991	High	0.000112	0.002694
Unique	1.322925	High	0.002718	0.04764
No Quan Va	1.116567	High	0.008271	0.119
Unique	3.219621	High	0	2.61E-06
Unique	3.440243	High	0	0.000827
Unique	1.907832	High	0.000885	0.01482
Unique	4.283935	High	0	1.12E-06
No Quan Va	0.739334	High	0.002519	0.04635
Unique	3.904227	High	0	3.43E-06
Unique	3.938593	High	0	0.00029
No Quan Va	2.837501	High	0	0.000497
No Quan Va	2.561405	High	0	0.000122
Unique	0.98551	High	0.001475	0.02475
Unique	2.104157	High	0.003641	0.06278
Unique	2.722222	High	0.00053	0.007343
Unique	2.237643	High	0	0.000518
Unique	2.74523	High	0.000885	0.01509
Unique	2.04758	High	0	0.000749
No Quan Va	3.893746	High	0	9.04E-05
Unique	4.122842	High	0	3.25E-09
No Quan Va	2.621943	High	0	0.000903
Unique	1.970963	High	0	0.000216
No Quan Va	2.144667	High	0	0.000555
Unique	3.492874	High	0	0.000014
Unique	4.045678	High	0	1.24E-09
Unique	2.341013	High	0	0.000984
Unique	1.7358	High	0	0.001688
Unique	1.487874	High	0.000432	0.006643
Unique	2.494097	High	0.000664	0.009614
No Quan Va	2.087932	High	0.002871	0.05395
Unique	2.899678	High	0	0.001462
Unique	4.058377	High	0	7.82E-08
No Quan Va	0.740781	High	0.002589	0.04725
No Quan Va	3.002623	High	0.000112	0.001961
Unique	5.662776	High	0	4.67E-08
Unique	4.19762	High	0	2.29E-07
Unique	4.432527	High	0	1.95E-08

Unique	2.201144	High	0.002323	0.04386
No Quan V	1.944187	High	0.000112	0.005186
No Quan V	1.425776	High	0.001004	0.01943
Unique	2.294932	High	0	0.000112
Unique	3.528348	High	0	8.11E-07
Unique	4.962149	High	0	4.63E-08
Unique	2.832727	High	0	0.000161
No Quan V	2.946701	High	0	0.000187
Unique	2.228733	High	0.000112	0.002104
No Quan V	1.634068	High	0.002519	0.04695
Unique	1.514337	High	0.000664	0.009635
Unique	1.821324	High	0.00053	0.007135
No Quan V	0.248333	High	0.001803	0.03012
Unique	5.334461	High	0	3.1E-08
No Quan V	2.938816	High	0	0.000297
Unique	2.481074	High	0	0.0002
Unique	1.552598	High	0.00053	0.007238
No Quan V	1.244721	High	0.001948	0.032
Unique	1.399444	High	0.002931	0.05507
Unique	1.692046	High	0.000608	0.009283
Unique	3.525673	High	0	2.37E-05
Unique	2.651692	High	0	0.001109
Unique	4.991268	High	0	2.49E-09
Unique	2.913866	High	0	1.24E-05
Unique	3.632109	High	0	2.46E-05
Unique	3.216762	High	0	4.93E-05
Unique	2.021729	High	0.004024	0.0659
No Quan V	1.113539	High	0.003226	0.05782
Unique	3.81787	High	0	7.72E-07
No Quan V	2.87232	High	0	0.000201
No Quan V	2.506977	High	0	0.000302
Unique	4.321384	High	0	5.91E-07
Unique	2.763154	High	0	0.000555
Unique	4.294761	High	0	9.1E-06
Unique	3.728048	High	0	2.53E-06
Unique	3.865364	High	0	0.000123
Unique	2.73841	High	0	2.31E-05
Unique	5.613854	High	0	0
Unique	3.720455	High	0	4.61E-07
Unique	2.71196	High	0	5.83E-05
Unique	1.912635	High	0.001004	0.02145
Unique	1.702899	High	0.000885	0.01489
No Quan V	1.101462	High	0.001676	0.02723
Unique	1.365579	High	0.001676	0.02695
Unique	0.892901	High	0.002323	0.04368
Unique	0.966795	High	0.002267	0.04169
Unique	2.515674	High	0	9.86E-06
Unique	3.812146	High	0	2.19E-05
Unique	3.091235	High	0	2.86E-05
No Quan V	1.68679	High	0.000961	0.01868
Unique	1.96617	High	0.000112	0.003265
Unique	4.214488	High	0	5.19E-07

Unique	3.393055	High	0	1.06E-05
Unique	1.578099	High	0.000885	0.01535
Unique	1.588701	High	0	0.000518
No Quan Va	1.756216	High	0.001004	0.02191
No Quan Va	1.921898	High	0.000112	0.005596
No Quan Va	2.250256	High	0.004388	0.07391
Unique	2.81114	High	0	9.49E-06
No Quan Va	4.123194	High	0	1.65E-05
Unique	1.814052	High	0.007589	0.1124
Unique	3.073149	High	0	0.000299
Unique	2.476698	High	0	0.001792
No Quan Va	0.742334	High	0.000836	0.01369
Unique	2.096061	High	0.002121	0.03581
Unique	2.197886	High	0.000112	0.003358
No Quan Va	2.307015	High	0.000112	0.004536
No Quan Va	2.125431	High	0.000112	0.001934
Unique	2.068229	High	0	0.001485
Unique	3.047498	High	0.000112	0.002866
Unique	1.372976	High	0.000885	0.0162
No Quan Va	0.784552	High	0.003415	0.0602
Unique	5.447382	High	0	5.07E-05
Unique	2.818926	High	0	0.000603
Unique	1.320487	High	0.00075	0.01305
No Quan Va	3.242995	High	0	1.51E-05
Unique	1.202082	High	0.005929	0.09007
No Quan Va	1.021983	High	0.003415	0.06026
Unique	3.446865	High	0	1.43E-07
No Quan Va	3.58254	High	0	4.79E-05
Unique	3.448437	High	0	0.000288
Unique	2.531407	High	0.000112	0.005716
No Quan Va	2.187596	High	0.00053	0.007418
Unique	1.268663	High	0.001004	0.02103
No Quan Va	0.738834	High	0.002323	0.04385
Unique	2.359845	High	0.001676	0.02648
Unique	2.45186	High	0.001993	0.03336
No Quan Va	1.435548	High	0.002931	0.05482
Unique	1.991361	High	0.002754	0.05148
Unique	3.047503	High	0	0.000837
Unique	2.424553	High	0	0.000119
Unique	1.478803	High	0.002267	0.04225
Unique	4.208537	High	0	1.26E-05
Unique	2.482766	High	0	0.001802
Unique	6.031785	High	0	0
Unique	3.706865	High	0	2.75E-05
No Quan Va	2.878489	High	0	0.00062
Unique	1.995516	High	0.001948	0.0321
Unique	1.949171	High	0.002323	0.04467
No Quan Va	0.757892	High	0.006641	0.1016
No Quan Va	0.743001	High	0.003641	0.06312
Unique	4.65929	High	0	2.19E-08
No Quan Va	1.848469	High	0.001877	0.03182
No Quan Va	2.124533	High	0.001004	0.02227

Unique	3.056015	High	0	3.35E-05
Unique	2.619942	High	0.000333	0.006059
No Quan Va	1.225729	High	0.002267	0.04258
Unique	2.872479	High	0	7.87E-06
No Quan Va	5.1175	High	0	6.48E-08
No Quan Va	2.683678	High	0	0.000197
Unique	3.136281	High	0	3.71E-05
Unique	3.568662	High	0	0.000107
Unique	3.026508	High	0	7.47E-05
Not Unique	3.195796	High	0	0.000956
No Quan Va	1.737607	High	0	0.00056
Unique	1.794872	High	0.00627	0.09725
Unique	1.72475	High	0.003763	0.06537
Unique	1.572543	High	0.001676	0.02844
Not Unique	3.240401	High	0	9.42E-07
Not Unique	3.449977	High	0	3.64E-06
Not Unique	1.797642	High	0.003226	0.0589

Master Protein Accessions	[Product Description]	[# TM Domains]	[SignalP Scores]	[Protein Length]	Confidence	Annotated Sequence	Modifications	Modifications in Master Proteins
TGGT1_228	inner meml	1	NN Sum: 2,	1596	High	[L].SGIIKTL\	2xTMT6plex [N-Term; I	
TGGT1_240	putative rh	1	N/A	553	High	[L].DSLIPGF	2xTMT6plex [N-Term; I	
TGGT1_241	hypothetica	0	NN Sum: 4,	474	High	[L].AEGKPG	1xAcetyl [N	TGGT1_241
TGGT1_356	cAMP-depe	0	NN Sum: 4,	306	High	[A].APVQG	1xTMT6plex [N-Term]	
TGGT1_319	microneme	0	NN Sum: 4,	383	High	[G].GDCSCE	2xTMT6plex [N-Term; I	
TGGT1_263	CMGC kina	0	N/A	539	High	[M].APPRP	1xTMT6plex [N-Term]	
TGGT1_309	putative pe	0	N/A	402	High	[L].SGDLPFI	1xTMT6plex [N-Term]	
TGGT1_208	protease in	0	NN Sum: 4,	318	High	[A].DTTEQF	3xTMT6plex [N-Term; I	
TGGT1_319	microneme	0	NN Sum: 4,	383	High	[F].AVTETH	3xTMT6plex [N-Term; I	
TGGT1_270	hypothetica	0	N/A	300	High	[M].ALSASF	1xAcetyl [N	TGGT1_270
TGGT1_255	apical mem	1	N/A	569	High	[T].ALQCTA	3xTMT6plex [N-Term; I	
TGGT1_232	protein pho	0	N/A	145	High	[-].MQVIGK	1xAcetyl [N	TGGT1_232
TGGT1_319	CBF/Mak21	0	N/A	674	High	[M].SVKDA	1xAcetyl [N	TGGT1_319
TGGT1_269	rhoptry me	1	NN Sum: 4,	1291	High	[F].VDSTSG	1xAcetyl [N	TGGT1_269
TGGT1_258	hypothetica	0	N/A	408	High	[M].TDNAC	2xTMT6plex [N-Term; I	
TGGT1_305	programme	0	N/A	482	High	[M].GSKSEF	1xAcetyl [N	TGGT1_305
TGGT1_209	formate/ni	6	N/A	412	High	[M].VVTASI	1xTMT6plex [N-Term]	
TGGT1_240	hypothetica	0	N/A	553	High	[-].MIKSLSC	1xAcetyl [N	TGGT1_240
TGGT1_290	CS domain-	0	NN Sum: 2,	377	High	[A].ASVAPS	2xTMT6plex [N-Term; I	
TGGT1_293	Yip1 domai	5	N/A	588	High	[Q].GDFLSL	1xTMT6plex [N-Term]	
TGGT1_310	hypothetica	3	N/A	224	High	[A].ASAKAT	3xTMT6plex [N-Term; I	
TGGT1_312	serine/thre	0	N/A	548	High	[M].AEGEG	1xTMT6plex [N-Term]	
TGGT1_278	myosin F	0	N/A	1953	High	[L].GASAVG	2xTMT6plex [N-Term; I	
TGGT1_268	zinc finger (	0	N/A	449	High	[S].SIVASAA	1xTMT6plex [N-Term]	
TGGT1_209	actin ACT1	0	N/A	376	High	[V].DNGSGI	2xTMT6plex [N-Term; I	
TGGT1_288	dense gran	1	NN Sum: 4,	436	High	[V].AAGNEI	2xTMT6plex [N-Term; I	
TGGT1_290	putative cla	0	N/A	1731	High	[E].SLELVRF	1xTMT6plex [N-Term]	
TGGT1_230	hypothetica	0	N/A	142	High	[A].EVVYAT	2xTMT6plex [N-Term; I	
TGGT1_308	rhoptry pro	0	NN Sum: 4,	549	High	[E].EVADM:	1xTMT6plex [N-Term]	
TGGT1_411	actin	0	N/A	287	High	[SC].YVGDE	2xTMT6plex [N-Term; I	
TGGT1_221	acetyl-CoA	1	NN Sum: 3,	2614	High	[S].GGVHEY	2xTMT6plex [N-Term; I	
TGGT1_311	rhoptry nec	0	NN Sum: 3,	1699	High	[Q].AAQTD.	3xTMT6plex [N-Term; I	
TGGT1_312	heat shock	0	N/A	195	High	[A].SSKAPG	2xTMT6plex [N-Term; I	
TGGT1_232	hypothetica	0	N/A	208	High	[T].EKETLLT	2xTMT6plex [N-Term; I	
TGGT1_297	hypothetica	1	NN Sum: 4,	519	High	[L].NLPDVE	2xTMT6plex [N-Term; I	
TGGT1_316	superoxide	0	NN Sum: 4,	287	High	[A].FTLPPLF	1xTMT6plex [N-Term]	
TGGT1_258	hypothetica	1	N/A	557	High	[E].EKTKGQ	3xTMT6plex [N-Term; I	
TGGT1_264	acyl carrier	1	NN Sum: 4,	183	High	[A].ADEASS	1xTMT6plex [N-Term]	
TGGT1_249	hypothetica	0	N/A	838	High	[S].SSLPGGI	2xTMT6plex [N-Term; I	
TGGT1_247	hypothetica	0	N/A	2303	High	[A].GAGAAI	3xTMT6plex [N-Term; I	
TGGT1_311	rhoptry nec	0	NN Sum: 3,	1699	High	[A].GQAAQ	3xTMT6plex [N-Term; I	
TGGT1_313	hypothetica	0	N/A	2799	High	[S].ESNAQP	1xTMT6plex [N-Term]	
TGGT1_233	SAG-relate	0	NN Sum: 1,	336	High	[A].SDPPLV.	1xTMT6plex [N-Term];	
TGGT1_324	heat shock	0	N/A	185	High	[H].ERPTGF	1xTMT6plex [N-Term]	
TGGT1_313	hypothetica	0	N/A	2799	High	[L].GDTPHC	1xTMT6plex [N-Term]	

TGGT1_31	dense gran	0	NN Sum: 4,	345	High	[S].FGSHLA	1xTMT6plex [N-Term];
TGGT1_27	SAG-relate	0	N/A	374	High	[A].AKAQG	1xAcetyl [NTGGT1_27
TGGT1_26	putative pr	8	NN Sum: 3,	473	High	[C].ILPEVQ	1xTMT6plex [N-Term]
TGGT1_27	hypothetica	0	N/A	1174	High	[L].SPAPES	1xTMT6plex [N-Term]
TGGT1_20	actin ACT1	0	N/A	376	High	[L].VVDNG	2xTMT6plex [N-Term;
TGGT1_32	heat shock	0	N/A	185	High	[A].EIQAPA	1xTMT6plex [N-Term]
TGGT1_22	rhoptry ne	0	NN Sum: 4,	984	High	[L].GPTVSD	1xTMT6plex [N-Term]
TGGT1_411	actin	0	N/A	287	High	[T].EAPLNP	2xTMT6plex [N-Term;
TGGT1_31	hypothetica	1	N/A	131	High	[A].SLTPGG	1xTMT6plex [N-Term]
TGGT1_36	rhoptry pro	1	NN Sum: 4,	561	High	[L].LNSHTE	1xTMT6plex [N-Term]
TGGT1_20	dense gran	2	NN Sum: 4,	236	High	[K].GTDDH	2xTMT6plex [N-Term;
TGGT1_29	Yip1 domai	5	N/A	588	High	[Q].TPEAPA	1xTMT6plex [N-Term]
TGGT1_22	alveolin do	0	N/A	444	High	[A].GSEVTP	1xTMT6plex [N-Term]
TGGT1_20	dense gran	2	NN Sum: 4,	236	High	[V].DSKGT	3xTMT6plex [N-Term;
TGGT1_26	RNA recog	0	N/A	430	High	[A].GAPAY	1xTMT6plex [N-Term]
TGGT1_31	dense gran	0	NN Sum: 4,	345	High	[F].VFTPSS	1xTMT6plex [N-Term]
TGGT1_20	subtilisin SU	0	NN Sum: 4,	795	High	[L].SHHGEY	2xTMT6plex [N-Term;
TGGT1_28	microtubul	0	N/A	357	High	[-].MELPLD	1xAcetyl [NTGGT1_28
TGGT1_30	rhoptry pro	0	NN Sum: 4,	549	High	[A].DETHQ	1xTMT6plex [N-Term]
TGGT1_29	dense gran	1	NN Sum: 4,	219	High	[A].DDAFID	2xTMT6plex [N-Term;
TGGT1_24	hypothetica	4	NN Sum: 4,	378	High	[Q].SPSAPC	1xTMT6plex [N-Term]
TGGT1_29	ribosomal	0	N/A	195	High	[L].DVDNLV	1xTMT6plex [N-Term]
TGGT1_31	isocitrate d	0	NN Sum: 2,	621	High	[F].NLEGKI	2xTMT6plex [N-Term;
TGGT1_21	multi-pass	6	N/A	389	High	[M].GGAAP	1xTMT6plex [N-Term]
TGGT1_20	dense gran	2	NN Sum: 4,	236	High	[M].DKASV	2xTMT6plex [N-Term;
TGGT1_26	putative el	0	NN Sum: 0,	552	High	[C].DDFIPE	1xTMT6plex [N-Term]
TGGT1_27	dense gran	2	N/A	223	High	[A].EGDVD	2xTMT6plex [N-Term;
TGGT1_32	heat shock	0	N/A	185	High	[A].EHEVVL	1xTMT6plex [N-Term]
TGGT1_311	rhoptry ne	0	NN Sum: 3,	1699	High	[G].SPAADL	1xTMT6plex [N-Term]
TGGT1_20	actin ACT1	0	N/A	376	High	[A].EDSSDI	2xTMT6plex [N-Term;
TGGT1_22	alveolin do	0	N/A	444	High	[T].EQGFD	1xTMT6plex [N-Term]
TGGT1_30	rhoptry pro	0	NN Sum: 4,	549	High	[A].EEVAD	1xTMT6plex [N-Term]
TGGT1_20	subtilisin SU	0	NN Sum: 4,	795	High	[K].GAWDII	1xTMT6plex [N-Term]
TGGT1_28	dense gran	1	NN Sum: 4,	436	High	[A].ATVAA	2xTMT6plex [N-Term;
TGGT1_30	rhoptry pro	0	NN Sum: 4,	549	High	[A].DGAGV	1xTMT6plex [N-Term]
TGGT1_201	hypothetica	2	NN Sum: 4,	108	High	[A].SHGTTF	1xTMT6plex [N-Term]
TGGT1_231	alveolin do	0	N/A	609	High	[L].QQLHGT	1xTMT6plex [N-Term]
TGGT1_26	enolase 2	0	N/A	475	High	[K].MVAIKD	1xAcetyl [NTGGT1_26
TGGT1_23	hypothetica	0	N/A	4118	High	[S].NVAPFA	1xTMT6plex [N-Term]
TGGT1_21	hypothetica	1	NN Sum: 1,	1249	High	[F].SSTEDE	1xTMT6plex [N-Term]
TGGT1_321	hypothetica	0	N/A	372	High	[Q].GEENEE	1xTMT6plex [N-Term]
TGGT1_20	subtilisin SU	0	NN Sum: 4,	795	High	[A].WDIITT	1xTMT6plex [N-Term]
TGGT1_20	dense gran	2	NN Sum: 4,	236	High	[T].SMDKA	2xTMT6plex [N-Term;
TGGT1_31	dense gran	0	NN Sum: 4,	345	High	[Y].TAQVVF	1xTMT6plex [N-Term]
TGGT1_22	transporter	12	N/A	589	High	[Q].GLDSRF	3xTMT6plex [N-Term;
TGGT1_29	hypothetica	0	NN Sum: 4,	312	High	[L].GPSLPSF	1xTMT6plex [N-Term]
TGGT1_21	hypothetica	0	N/A	138	High	[M].SPPTA	1xTMT6plex [N-Term];
TGGT1_31	dense gran	0	NN Sum: 4,	345	High	[A].QVVPG	1xTMT6plex [N-Term]
TGGT1_25	hypothetica	1	N/A	151	High	[-].MVDTN	1xAcetyl [NTGGT1_25
TGGT1_22	putative ca	1	NN Sum: 1,	335	High	[Y].DLNAD	2xTMT6plex [N-Term;
TGGT1_201	microneme	1	NN Sum: 3,	769	High	[W].SIVDAL	1xTMT6plex [N-Term]
TGGT1_28	dense gran	1	NN Sum: 4,	436	High	[R].AATVA	2xTMT6plex [N-Term;

TGGT1_28	putative el	0	N/A	448	High	[V].NMEPS	2xTMT6plex [N-Term;
TGGT1_24	hypothetic	1	NN Sum: 3,	256	High	[Y].ATLNTP	2xTMT6plex [N-Term;
TGGT1_24	hypothetic	4	NN Sum: 4,	378	High	[A].VTSPAA	1xTMT6plex [N-Term]
TGGT1_28	dense gran	1	NN Sum: 4,	436	High	[A].TVAAG	2xTMT6plex [N-Term;
TGGT1_31	heat shock	0	N/A	195	High	[L].GAPASA	1xTMT6plex [N-Term]
TGGT1_22	EF-1 guani	0	N/A	328	High	[K].MVVPD	1xAcetyl [NTGGT1_22
TGGT1_25	Sad1 / UNC	0	N/A	796	High	[E].QAQQL	1xTMT6plex [N-Term]
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[D].AIDAES	1xTMT6plex [K8]
TGGT1_20	subtilisin S	0	NN Sum: 4,	795	High	[T].SFLSHH	2xTMT6plex [N-Term;
TGGT1_22	dense gran	0	NN Sum: 4,	185	High	[G].VVNQG	2xTMT6plex [N-Term;
TGGT1_20	hypothetic	0	N/A	793	High	[S].EAGLED	1xTMT6plex [N-Term]
TGGT1_20	subtilisin S	0	NN Sum: 4,	795	High	[K].YADDDI	1xTMT6plex [N-Term]
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[T].SGVQE	2xTMT6plex [N-Term;
TGGT1_20	subtilisin S	0	NN Sum: 4,	795	High	[T].YNLIKEI	2xTMT6plex [N-Term;
TGGT1_23	hypothetic	2	N/A	175	High	[SA].FLSEE	1xTMT6plex [N-Term]
TGGT1_24	hypothetic	0	N/A	844	High	[A].GSEAIA	1xTMT6plex [N-Term]
TGGT1_36	rhoptry pr	1	NN Sum: 4,	561	High	[N].SHTETP	1xTMT6plex [N-Term]
TGGT1_41	actin	0	N/A	287	High	[L].TEAPLN	2xTMT6plex [N-Term;
TGGT1_22	dense gran	0	NN Sum: 4,	185	High	[P].VDVPFS	2xTMT6plex [N-Term;
TGGT1_41	actin	0	N/A	287	High	[G].MGQKD	3xTMT6plex [N-Term;
TGGT1_20	hypothetic	0	N/A	2072	High	[L].DLPHYP	1xTMT6plex [N-Term]
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[L].LDAIDA	2xTMT6plex [N-Term;
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[L].DAIDAE	2xTMT6plex [N-Term;
TGGT1_41	actin	0	N/A	287	High	[M].GQKDS	3xTMT6plex [N-Term;
TGGT1_41	actin	0	N/A	287	High	[D].GQVITI	1xTMT6plex [N-Term]
TGGT1_36	rhoptry pr	1	NN Sum: 4,	561	High	[L].NSHTET	1xTMT6plex [N-Term]
TGGT1_31	dense gran	0	NN Sum: 4,	345	High	[S].FGSHLA	1xTMT6plex [N-Term]
TGGT1_21	EF hand do	7	N/A	3700	High	[S].SLLDLD	1xTMT6plex [N-Term]
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[A].ESDKVD	2xTMT6plex [N-Term;
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[Q].EATAP	2xTMT6plex [N-Term;
TGGT1_32	SAG-relate	1	NN Sum: 1,	398	High	[A].DNLLEG	1xTMT6plex [N-Term]
TGGT1_22	dense gran	2	NN Sum: 3,	222	High	[E].ATAPGA	2xTMT6plex [N-Term;

Contaminant	spike-in std	Qvality PEP	Qvality q-value	# Protein Groups	# Proteins	# PSMs	Positions in Master Proteins	# Missed Cleavages
FALSE	FALSE	0.109568	0.001981	1	1	3	TGGT1_228	1
FALSE	FALSE	0.11706	0.002459	1	1	9	TGGT1_240	1
FALSE	FALSE	0.165139	0.005258	1	1	2	TGGT1_241	1
FALSE	FALSE	0.000025	0	1	1	10	TGGT1_356	0
FALSE	FALSE	0.103781	0.001981	1	1	4	TGGT1_319	1
FALSE	FALSE	2.32E-05	0	1	1	9	TGGT1_263	0
FALSE	FALSE	0.165139	0.005258	1	1	6	TGGT1_309	0
FALSE	FALSE	0.050148	0.000606	1	1	6	TGGT1_208	2
FALSE	FALSE	0.005387	0	1	1	2	TGGT1_319	1
FALSE	FALSE	0.06821	0.001557	1	1	3	TGGT1_270	1
FALSE	FALSE	0.029956	0.000606	1	1	3	TGGT1_255	2
FALSE	FALSE	0.022337	0	1	1	6	TGGT1_232	1
FALSE	FALSE	0.001841	0	1	1	4	TGGT1_319	2
FALSE	FALSE	0.00324	0	1	1	3	TGGT1_269	2
FALSE	FALSE	0.000131	0	1	1	3	TGGT1_258	1
FALSE	FALSE	0.192005	0.005483	1	1	6	TGGT1_305	1
FALSE	FALSE	0.134318	0.002851	1	1	4	TGGT1_209	0
FALSE	FALSE	0.043768	0.000606	1	1	6	TGGT1_240	1
FALSE	FALSE	7.28E-05	0	1	1	6	TGGT1_290	1
FALSE	FALSE	0.054673	0.000606	1	1	4	TGGT1_293	0
FALSE	FALSE	0.151216	0.004951	1	1	2	TGGT1_310	2
FALSE	FALSE	0.000104	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.00013	0	1	1	3	TGGT1_278	1
FALSE	FALSE	0.001554	0	1	1	12	TGGT1_268	0
FALSE	FALSE	0.000492	0	1	1	5	TGGT1_209	1
FALSE	FALSE	4.06E-05	0	1	1	9	TGGT1_288	1
FALSE	FALSE	0.059962	0.001175	1	1	4	TGGT1_290	0
FALSE	FALSE	0.061833	0.001175	1	1	9	TGGT1_230	1
FALSE	FALSE	0.015344	0	1	1	9	TGGT1_308	0
FALSE	FALSE	0.203315	0.00584	2	2	3	TGGT1_411	1
FALSE	FALSE	0.043229	0.000606	1	1	1	TGGT1_221	1
FALSE	FALSE	0.154821	0.004951	1	1	1	TGGT1_311	2
FALSE	FALSE	0.016133	0	1	1	5	TGGT1_312	1
FALSE	FALSE	0.017832	0	1	1	5	TGGT1_232	1
FALSE	FALSE	0.09652	0.001557	1	1	8	TGGT1_297	1
FALSE	FALSE	0.000237	0	1	1	9	TGGT1_316	0
FALSE	FALSE	0.066967	0.001557	1	1	2	TGGT1_258	2
FALSE	FALSE	0.074764	0.001557	1	1	6	TGGT1_264	0
FALSE	FALSE	0.071196	0.001557	1	1	8	TGGT1_249	1
FALSE	FALSE	0.086013	0.001557	1	1	4	TGGT1_247	1
FALSE	FALSE	3.14E-05	0	1	1	2	TGGT1_311	2
FALSE	FALSE	0.003605	0	1	1	9	TGGT1_313	0
FALSE	FALSE	0.000079	0	1	1	16	TGGT1_233	0
FALSE	FALSE	0.164176	0.004951	1	1	1	TGGT1_324	0
FALSE	FALSE	0.024686	0	1	1	8	TGGT1_313	0

FALSE	FALSE	0.076146	0.001557	1	1	5	TGGT1_310	0
FALSE	FALSE	0.056732	0.000606	1	1	4	TGGT1_273	2
FALSE	FALSE	0.145091	0.004951	1	1	4	TGGT1_269	0
FALSE	FALSE	0.00688	0	1	1	4	TGGT1_276	0
FALSE	FALSE	7.12E-06	0	1	1	10	TGGT1_209	1
FALSE	FALSE	0.028498	0	1	1	6	TGGT1_324	0
FALSE	FALSE	0.140023	0.004678	1	1	1	TGGT1_229	0
FALSE	FALSE	0.000153	0	2	2	9	TGGT1_411	1
FALSE	FALSE	0.079954	0.001557	1	1	2	TGGT1_316	0
FALSE	FALSE	0.003961	0	1	1	7	TGGT1_363	0
FALSE	FALSE	0.003697	0	1	1	8	TGGT1_203	1
FALSE	FALSE	0.190904	0.005483	1	1	2	TGGT1_293	0
FALSE	FALSE	0.002412	0	1	1	9	TGGT1_220	0
FALSE	FALSE	0.020983	0	1	1	2	TGGT1_203	2
FALSE	FALSE	7.01E-05	0	1	1	9	TGGT1_264	0
FALSE	FALSE	0.005664	0	1	1	7	TGGT1_310	0
FALSE	FALSE	0.21398	0.006605	1	1	1	TGGT1_204	1
FALSE	FALSE	0.11636	0.002459	1	1	5	TGGT1_286	1
FALSE	FALSE	0.000551	0	1	2	17	TGGT1_308	0
FALSE	FALSE	0.070762	0.001557	1	1	7	TGGT1_297	1
FALSE	FALSE	0.002473	0	1	1	9	TGGT1_247	0
FALSE	FALSE	0.000141	0	1	1	9	TGGT1_299	0
FALSE	FALSE	0.02138	0	1	1	2	TGGT1_313	1
FALSE	FALSE	0.000364	0	1	1	11	TGGT1_219	0
FALSE	FALSE	0.019834	0	1	1	6	TGGT1_203	1
FALSE	FALSE	0.077081	0.001557	1	1	4	TGGT1_262	0
FALSE	FALSE	0.001114	0	1	1	8	TGGT1_275	1
FALSE	FALSE	1.34E-07	0	1	1	19	TGGT1_324	0
FALSE	FALSE	0.000335	0	1	1	9	TGGT1_311	0
FALSE	FALSE	0.002074	0	1	1	4	TGGT1_209	1
FALSE	FALSE	0.060703	0.001175	1	1	3	TGGT1_220	0
FALSE	FALSE	0.006462	0	1	1	9	TGGT1_308	0
FALSE	FALSE	0.032686	0.000606	1	1	5	TGGT1_204	0
FALSE	FALSE	0.001525	0	1	1	8	TGGT1_288	1
FALSE	FALSE	0.000426	0	1	2	6	TGGT1_308	0
FALSE	FALSE	0.001414	0	1	1	9	TGGT1_201	0
FALSE	FALSE	0.006421	0	1	1	8	TGGT1_231	0
FALSE	FALSE	0.006584	0	1	1	4	TGGT1_268	1
FALSE	FALSE	0.002769	0	1	1	4	TGGT1_235	0
FALSE	FALSE	0.022477	0	1	1	5	TGGT1_218	0
FALSE	FALSE	0.002181	0	1	1	9	TGGT1_321	0
FALSE	FALSE	0.015059	0	1	1	5	TGGT1_204	0
FALSE	FALSE	0.00688	0	1	1	8	TGGT1_203	1
FALSE	FALSE	0.004903	0	1	1	8	TGGT1_310	0
FALSE	FALSE	0.151216	0.004951	1	1	1	TGGT1_226	2
FALSE	FALSE	0.022059	0	1	1	17	TGGT1_290	0
FALSE	FALSE	0.131939	0.002851	1	1	3	TGGT1_214	0
FALSE	FALSE	0.000521	0	1	1	8	TGGT1_310	0
FALSE	FALSE	0.000483	0	1	1	9	TGGT1_258	1
FALSE	FALSE	0.000917	0	1	1	2	TGGT1_229	1
FALSE	FALSE	0.201008	0.00584	1	1	2	TGGT1_201	0
FALSE	FALSE	0.000248	0	1	1	9	TGGT1_288	1

FALSE	FALSE	0.075222	0.001557	1	4	3	TGGT1_286	0
FALSE	FALSE	0.002967	0	1	1	6	TGGT1_247	0
FALSE	FALSE	0.021514	0	1	1	8	TGGT1_247	0
FALSE	FALSE	0.00039	0	1	1	3	TGGT1_288	1
FALSE	FALSE	0.0004	0	1	1	9	TGGT1_312	0
FALSE	FALSE	0.002752	0	1	1	10	TGGT1_226	2
FALSE	FALSE	0.020852	0	1	1	1	TGGT1_250	1
FALSE	FALSE	0.005593	0	1	1	8	TGGT1_227	1
FALSE	FALSE	0.00365	0	1	1	2	TGGT1_204	1
FALSE	FALSE	0.001773	0	1	1	7	TGGT1_227	0
FALSE	FALSE	0.128061	0.002851	1	1	3	TGGT1_202	0
FALSE	FALSE	0.182298	0.005483	1	1	5	TGGT1_204	0
FALSE	FALSE	9.54E-05	0	1	1	2	TGGT1_227	1
FALSE	FALSE	0.148563	0.004951	1	1	3	TGGT1_204	1
FALSE	FALSE	0.240719	0.008677	1	2	1	TGGT1_233	0
FALSE	FALSE	1.48E-05	0	1	1	8	TGGT1_240	0
FALSE	FALSE	0.001864	0	1	1	8	TGGT1_363	0
FALSE	FALSE	0.000261	0	2	2	9	TGGT1_411	1
FALSE	FALSE	0.02711	0	1	1	3	TGGT1_227	0
FALSE	FALSE	0.153009	0.004951	1	1	1	TGGT1_411	2
FALSE	FALSE	0.003605	0	1	1	9	TGGT1_206	0
FALSE	FALSE	0.007055	0	1	1	8	TGGT1_227	1
FALSE	FALSE	0.004011	0	1	1	7	TGGT1_227	1
FALSE	FALSE	0.112238	0.001981	1	1	5	TGGT1_411	2
FALSE	FALSE	0.09652	0.001557	1	1	5	TGGT1_411	0
FALSE	FALSE	0.00265	0	1	1	9	TGGT1_363	0
FALSE	FALSE	0.000598	0	1	1	9	TGGT1_310	0
FALSE	FALSE	0.022618	0	1	1	4	TGGT1_216	0
FALSE	FALSE	0.228936	0.007683	1	1	1	TGGT1_227	1
FALSE	FALSE	2.4E-06	0	1	1	7	TGGT1_227	1
FALSE	FALSE	0.007848	0	1	1	9	TGGT1_320	0
FALSE	FALSE	3.38E-05	0	1	1	14	TGGT1_227	1

Theo. MH+ [Da]	20171104_04_S65989_asp5_tmt10_tails_po.raw	20171104_05_S65989_asp5_tmt10_tails_po.raw	20171104_07_S65989_asp5_tmt10_tails_po.raw	Found in Sample: [S51] F6: 126, Sample, wt, pool	Found in Sample: [S52] F6: 127N, Sample, wt, single	Found in Sample: [S54] F6: 128N, Sample, wt, single	Found in Sample: [S56] F6: 129N, Sample, wt, single	Found in Sample: [S58] F6: 130N, Sample, wt, single
2183.332	Not Found	High	High	High	High	High	High	High
1603.994	High	High	High	High	High	High	High	High
1471.863	High	High	Not Found	High	High	High	High	High
2689.472	High	High	High	High	High	High	High	High
1791.863	High	High	High	High	High	High	High	High
2184.209	High	High	High	High	High	High	High	High
1755.948	High	High	High	High	High	High	High	High
3467.822	High	High	High	Not Found	Not Found	High	Not Found	High
3990.063	Not Found	Not Found	High	High	High	High	High	High
1858.06	Not Found	High	High	High	Not Found	High	High	High
3332.679	Not Found	High	High	High	High	High	High	High
2579.32	High	High	High	Not Found	High	High	High	High
3184.74	High	High	High	High	High	High	High	High
2658.458	Not Found	High	High	High	High	High	High	High
3054.524	High	High	Not Found	High	High	High	High	High
1953.028	High	Not Found	High	High	High	High	High	High
2220.211	High	High	High	Not Found	High	High	Not Found	High
1671.966	High	High	Not Found	High	High	High	High	High
3700.841	High	High	Not Found	High	High	High	High	High
1872.965	High	High	High	Not Found	High	Not Found	Not Found	High
4646.501	Not Found	High	High	High	High	High	High	Not Found
1893.899	High	High	High	High	High	High	High	High
2629.369	High	High	Not Found	High	High	High	Not Found	High
1630.933	High	High	High	High	High	High	High	High
2158.125	High	High	High	High	High	High	High	High
2099.176	High	High	High	High	High	High	High	High
1653.001	High	High	High	High	High	High	High	High
2242.248	High	High	High	High	High	High	High	High
1150.572	High	High	High	High	High	High	High	High
1610.89	High	Not Found	High	High	High	High	High	High
2749.421	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
3202.852	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	High
2032.028	High	High	High	High	High	High	High	High
2350.265	High	High	High	High	High	High	High	High
1742.021	High	High	High	High	High	High	High	High
2751.492	High	High	High	High	High	High	High	High
1987.263	Not Found	Not Found	High	High	High	High	High	High
1802.908	High	High	High	High	High	High	High	High
1982.023	High	High	High	High	High	High	High	High
2492.419	Not Found	High	High	High	High	High	High	High
3387.932	Not Found	High	High	High	High	High	High	High
2008.952	High	High	High	Not Found	High	Not Found	Not Found	High
1969.026	High	High	High	High	High	High	High	High
1385.753	High	Not Found	Not Found	High	High	High	High	High
1826.883	High	High	High	High	Not Found	Not Found	High	High

1663.842	High	High	High	Not Found	High	High	High	High
3376.67	High	High	High	Not Found	High	High	High	High
1366.789	Not Found	High	High	High	High	High	High	High
2152.12	High	High	High	Not Found	Not Found	High	High	High
2356.262	High	High	High	High	High	High	High	High
1255.721	High	High	High	High	High	High	High	High
1176.606	High	Not Found	Not Found	High	High	High	High	High
1567.932	High	High	High	High	High	High	High	High
2054.069	High	Not Found	High	High	High	High	High	High
2002.019	High	High	High	High	High	High	High	High
2746.408	High	High	High	High	High	High	High	High
1411.738	Not Found	Not Found	High	Not Found	High	High	High	High
2192.054	High	High	High	Not Found	High	Not Found	Not Found	High
3305.725	High	High	Not Found	High	High	High	High	High
2469.148	High	High	High	Not Found	Not Found	Not Found	High	High
2619.398	High	High	High	Not Found	High	Not Found	High	High
2845.5	High	Not Found	Not Found	High	Not Found	High	High	High
2203.106	High	High	Not Found	Not Found	Not Found	High	Not Found	High
1703.903	High	High	High	High	High	High	High	High
1622.915	High	High	High	High	High	High	High	High
1821.945	High	High	High	High	High	High	High	High
1893.039	High	High	High	High	High	High	High	High
2912.501	High	High	Not Found	Not Found	Not Found	High	High	High
2014.008	High	High	High	High	High	High	High	High
1687.974	High	High	Not Found	High	High	High	High	High
1346.679	Not Found	High	High	High	High	High	High	High
2488.308	High	High	High	High	High	High	High	High
3178.56	High	High	High	High	High	High	High	High
1973.05	High	High	High	High	High	Not Found	High	High
3138.584	High	High	High	High	High	High	High	High
1744.943	Not Found	High	High	Not Found	Not Found	Not Found	Not Found	High
1279.615	High	High	High	High	High	High	High	High
1933.964	High	High	Not Found	High	High	High	High	High
2370.329	High	High	High	High	High	High	High	High
2174.115	High	High	High	High	High	High	High	High
1476.739	High	High	High	High	High	High	High	High
1511.813	High	High	High	High	High	High	High	High
1388.813	High	Not Found	High	High	High	High	High	High
1743.949	High	High	High	High	Not Found	High	High	High
2495.127	Not Found	High	High	High	High	High	Not Found	High
1965.935	High	High	High	High	High	High	High	High
1805.905	High	High	High	High	Not Found	High	Not Found	High
1906.047	High	High	High	High	High	High	High	High
2520.425	High	High	High	Not Found	Not Found	Not Found	High	High
2502.497	High	Not Found	Not Found	High	High	High	High	High
1501.858	High	High	High	High	High	High	High	High
2174.035	High	High	Not Found	High	High	High	High	High
2348.34	High	High	High	High	High	High	Not Found	High
1946.98	High	High	High	High	High	High	High	High
3413.807	High	High	Not Found	High	Not Found	Not Found	High	Not Found
1002.615	High	Not Found	Not Found	High	High	High	High	High
2441.367	High	High	High	High	High	High	High	High

2836.478	High	High	Not Found	High	High	Not Found	High	High
2353.364	High	High	High	High	High	High	High	High
1317.685	High	High	High	High	High	High	High	High
2299.292	High	Not Found	Not Found	High	High	High	High	High
2412.272	High	High	High	Not Found	Not Found	Not Found	High	Not Found
3222.76	High	High	High	High	High	High	High	High
2639.42	High	Not Found	Not Found	High	High	High	High	High
2133.026	High	High	High	High	Not Found	Not Found	High	High
3192.684	High	High	Not Found	High	Not Found	High	High	High
2511.397	High	High	High	High	High	High	High	High
1416.753	High	High	High	High	High	High	High	High
1096.547	High	High	High	High	High	High	High	High
3770.908	High	High	Not Found	High	Not Found	High	Not Found	High
1506.941	High	Not Found	High	High	High	High	High	High
1066.573	Not Found	Not Found	High	High	High	High	High	High
2403.247	High	High	High	Not Found	Not Found	High	Not Found	High
1774.892	High	High	High	High	High	High	High	High
1668.98	High	High	High	High	High	High	High	High
1917.085	Not Found	High	High	High	High	High	High	High
2486.328	Not Found	Not Found	High	High	High	High	High	High
1910.883	High	High	High	High	High	High	High	High
2590.3	High	High	High	High	High	High	High	High
2477.216	High	High	High	High	High	High	High	High
2355.287	High	High	Not Found	High	High	High	High	High
1315.753	High	High	High	High	High	High	High	High
1888.935	High	High	High	High	High	Not Found	High	High
1647.847	High	High	High	High	High	High	High	High
1374.743	High	High	High	High	High	High	High	High
1992.003	Not Found	Not Found	High	Not Found	High	High	Not Found	High
3399.728	High	High	High	High	High	High	High	High
1408.811	High	High	High	Not Found	Not Found	High	Not Found	High
3270.685	High	High	High	Not Found	High	Not Found	High	High

Found in Sample: [S53] F6: 127C, Sample, ko, single	Found in Sample: [S55] F6: 128C, Sample, ko, single	Found in Sample: [S57] F6: 129C, Sample, ko, single	Found in Sample: [S59] F6: 130C, Sample, ko, single	Found in Sample: [S60] F6: 131, Sample, ko, pool	Found in Sample Group: wt, pool	Found in Sample Group: wt, single	Found in Sample Group: ko, single	Found in Sample Group: ko, pool
Not Found	Not Found	Not Found	Not Found	High	High	High	Not Found	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
Not Found	High	Not Found	Not Found	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	Not Found	High	High	High
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Not Found	High	High	Not Found	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	Not Found	High	High	Not Found	High	High	High
High	High	High	Not Found	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
Not Found	High	High	Not Found	Not Found	Not Found	High	High	Not Found
High	High	High	High	High	High	High	High	High
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High	High	Not Found	High	High	High	High	High	High
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High	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	Not Found	High	High	High	High	High

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High	Not Found	Not Found	High	High	Not Found	High	High	High
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High	High	High	High	High	Not Found	High	High	High
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Not Found	High	High	High	High	Not Found	High	High	High
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Not Found	High	High	High	High	Not Found	High	High	High
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High	Not Found	Not Found	High	High	Not Found	High	High	High
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High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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Not Found	High	Not Found	Not Found	High	High	High	High	High
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High	High	Not Found	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
High	High	High	High	High	Not Found	High	High	High

Abundance Ratio: (ko, pool) / (wt, pool)	Abundance Ratio: (ko, single) / (wt, single)	Abundance Ratio (log2): (ko, pool) / (wt, pool)	Abundance Ratio (log2): (ko, single) / (wt, single)	Abundances (Grouped): wt, pool	Abundances (Grouped): wt, single	Abundances (Grouped): ko, single	Abundances (Grouped): ko, pool	Abundances (Grouped) Standard Error [%]: wt, pool
0.056	0.01	-4.17	-6.64	30.8	32.3		1.7	
0.014	0.01	-6.14	-6.64	700.3	717.6	5.8	9.9	
0.052	0.073	-4.28	-3.78	150.7	148.3	10.8	7.8	
0.01	0.255	-6.64	-1.97	12.2	6.7	1.7		
0.282	0.34	-1.82	-1.56	24.7	26.5	9	7	
0.366	0.358	-1.45	-1.48	51.7	58.8	21.1	19	
1.101	0.367	0.14	-1.45	23.8	27.5	10.1	26.3	
100	0.383	6.64	-1.39		6.6	2.5	4.2	
0.324	0.383	-1.63	-1.38	18.3	17.8	6.8	5.9	
0.682	0.384	-0.55	-1.38	5.2	6.7	2.6	3.5	
0.493	0.404	-1.02	-1.31	54.7	55.4	22.4	26.9	
100	0.419	6.64	-1.25		5.7	2.4	4.8	
1.32	0.425	0.4	-1.23	2.6	7.4	3.2	3.4	
0.664	0.456	-0.59	-1.13	5.7	8.1	3.7	3.8	
0.372	0.469	-1.43	-1.09	5.8	4.6	2.1	2.2	
2.425	0.469	1.28	-1.09	2.9	5.7	2.7	7.1	
100	0.47	6.64	-1.09		4.5	2.1	5	
0.01	0.483	-6.64	-1.05	2.9	3.4	1.6		
0.469	0.487	-1.09	-1.04	11.2	10.6	5.1	5.3	
	0.489		-1.03		3.6	1.8		
1.54	0.496	0.62	-1.01	2.6	7.3	3.6	4	
1.813	0.5	0.86	-1	5.4	10.6	5.3	9.7	
3.297	1.998	1.72	1	3.1	3.6	7.2	10.2	
2.723	2.001	1.45	1	19.8	27.3	54.7	53.9	
1.948	2.002	0.96	1	77.4	82.6	165.4	150.7	
1.827	2.002	0.87	1	67	58.7	117.5	122.4	
1.755	2.002	0.81	1	23	17.5	35	40.4	
2.24	2.003	1.16	1	66.8	79	158.3	149.7	
2.159	2.004	1.11	1	196.4	193.5	387.8	424.2	
1.603	2.01	0.68	1.01	72.5	61.5	123.6	116.2	
100	2.012	6.64	1.01		3.3	6.6	2.9	
100	2.012	6.64	1.01		1.7	3.4	1.8	
0.717	2.014	-0.48	1.01	8.9	3.3	6.7	6.4	
2.506	2.016	1.33	1.01	14.8	19.8	40	37	
2.036	2.025	1.03	1.02	89.1	90.6	183.5	181.3	
0.813	2.03	-0.3	1.02	7.3	4.2	8.4	5.9	
2.106	2.032	1.07	1.02	37.8	38.4	78	79.6	
2.255	2.032	1.17	1.02	17.5	13.8	28.1	39.5	
2.155	2.033	1.11	1.02	74.8	78.9	160.3	161.1	
1.889	2.047	0.92	1.03	3.1	3.9	7.9	5.8	
10.505	2.05	3.39	1.04	2.1	10.8	22.1	22.2	
100	2.051	6.64	1.04		1.9	3.9	7.5	
4.864	2.072	2.28	1.05	16.2	12.4	25.6	78.9	
2.549	2.088	1.35	1.06	4.7	5.2	10.9	12	
0.621	2.101	-0.69	1.07	2.8	3.5	7.3	1.7	

100	2.108	6.64	1.08		4.4	9.2	11.6
100	2.11	6.64	1.08		2	4.3	5.7
2.676	2.12	1.42	1.08	14.8	18.6	39.4	39.5
100	2.128	6.64	1.09		2.1	4.6	5.5
1.911	2.177	0.93	1.12	140.5	128.4	279.4	268.5
1.947	2.183	0.96	1.13	64.6	59.8	130.6	125.7
1.476	2.184	0.56	1.13	5	3.3	7.3	7.4
1.966	2.204	0.98	1.14	712.9	679.3	1496.8	1401.6
1.834	2.213	0.88	1.15	5.4	3.7	8.1	9.8
4.074	2.22	2.03	1.15	5.4	9.3	20.7	21.8
4.814	2.224	2.27	1.15	10.1	18	40.1	48.4
100	2.228	6.64	1.16		2	4.4	5.5
100	2.23	6.64	1.16		3.3	7.3	8.9
1.803	2.234	0.85	1.16	14.4	12.4	27.7	26
100	2.238	6.64	1.16		1.8	4	3.2
100	2.241	6.64	1.16		2.8	6.2	2.2
3.614	2.244	1.85	1.17	2.4	3.4	7.5	8.8
100	2.252	6.64	1.17		2.1	4.7	2.2
2.508	2.254	1.33	1.17	196.9	206.2	464.8	494
3.564	2.26	1.83	1.18	26	25.8	58.4	92.5
2.105	2.264	1.07	1.18	16.2	10.2	23.1	34.1
2.306	2.265	1.21	1.18	15.2	15.6	35.4	35.2
100	2.278	6.64	1.19		2.3	5.1	1.8
2.062	2.293	1.04	1.2	9.1	7.6	17.5	18.7
2.331	2.297	1.22	1.2	68.1	67.7	155.5	158.8
2.464	2.304	1.3	1.2	15.2	17.5	40.3	37.6
2.115	2.325	1.08	1.22	71.1	57.1	132.7	150.3
2.503	2.33	1.32	1.22	4.4	5.5	12.9	11
0.01	2.356	-6.64	1.24	4.2	3	7	
2.081	2.384	1.06	1.25	21.9	19.3	46.1	45.6
100	2.406	6.64	1.27		1.8	4.4	2.2
2.529	2.425	1.34	1.28	117	115.9	280.9	295.8
3.203	2.45	1.68	1.29	3.2	3	7.3	10.4
7.537	2.476	2.91	1.31	6.7	14.6	36.1	50.1
1.888	2.482	0.92	1.31	14.3	11.4	28.3	26.9
2.82	2.483	1.5	1.31	47.9	58.3	144.8	135
4.827	2.51	2.27	1.33	3.4	4.7	11.9	16.4
2.127	2.518	1.09	1.33	59	48.6	122.3	125.6
1.698	2.524	0.76	1.34	2.8	3.1	7.9	4.7
3.251	2.541	1.7	1.35	3.4	3	7.7	11.1
3.52	2.553	1.82	1.35	7.1	8.4	21.5	25.1
3.52	2.579	1.82	1.37	2.4	2.2	5.8	8.6
2.401	2.635	1.26	1.4	97.5	90.4	238.4	234.1
100	2.635	6.64	1.4		1.7	4.5	5.7
1.954	2.675	0.97	1.42	23.8	18.9	50.7	46.6
3.381	2.677	1.76	1.42	105.8	123.6	330.9	357.6
1.245	2.747	0.32	1.46	2.1	2.7	7.3	2.6
1.848	2.792	0.89	1.48	7.8	5.2	14.4	14.4
3.357	2.799	1.75	1.48	14.8	15.6	43.6	49.6
1.971	2.854	0.98	1.51	2.4	2	5.8	4.8
2.644	2.863	1.4	1.52	37.3	35.4	101.2	98.7
5.441	2.897	2.44	1.53	10.2	15.7	45.4	55.6

4.259	2.936	2.09	1.55	3.2	4	11.9	13.8
4.996	3.014	2.32	1.59	6.7	9.8	29.4	33.2
2.998	3.065	1.58	1.62	32.6	29.5	90.5	97.7
3.687	3.138	1.88	1.65	3.4	4.6	14.3	12.6
100	3.168	6.64	1.66		1.5	4.8	2.9
2.331	3.283	1.22	1.72	29.7	21.2	69.5	69.2
4.885	3.416	2.29	1.77	10.7	13.8	47.3	52.3
6.985	3.465	2.8	1.79	2.1	4	14	14.7
1.612	3.493	0.69	1.8	6.2	4	14.1	9.9
5.496	3.616	2.46	1.85	12.7	15	54.3	69.5
4.844	3.617	2.28	1.85	17.8	21	76	86.4
3.154	3.829	1.66	1.94	41.9	32.6	124.9	132
3.628	4.045	1.86	2.02	2.1	1.7	6.9	7.7
4.019	4.089	2.01	2.03	44.1	46.2	189	177.3
3.285	4.144	1.72	2.05	10.7	9	37.3	35.2
100	4.171	6.64	2.06		2.6	10.9	10.8
9.453	4.188	3.24	2.07	2.3	5.7	23.8	21.5
4.296	4.481	2.1	2.16	102.7	102.8	460.6	441.1
8.538	4.598	3.09	2.2	5	8.3	38.2	42.9
5.144	4.63	2.36	2.21	4.2	5.4	25.2	21.7
5.92	5.125	2.57	2.36	6.3	9.5	48.8	37.5
4.453	5.163	2.15	2.37	35.9	29.7	153.4	159.6
7.699	5.285	2.94	2.4	15.4	24.9	131.8	118.6
6.593	5.808	2.72	2.54	24.8	29.3	169.9	163.6
4.919	6.516	2.3	2.7	26.1	18.7	122.1	128.5
10.129	6.543	3.34	2.71	2.9	3.8	24.5	29.6
13.918	8.695	3.8	3.12	5.7	8	69.2	79
30.352	9.798	4.92	3.29	2.8	7.1	69.3	83.7
100	9.914	6.64	3.31		2.7	26.5	27.2
9.972	10.123	3.32	3.34	2.9	3.2	32.1	29.1
100	18.861	6.64	4.24		2.5	46.8	67.9
100	30.739	6.64	4.94		3.4	104.7	108.7

Abundances (Grouped) Standard Error [%]: wt, single	Abundances (Grouped) Standard Error [%]: ko, single	Abundances (Grouped) Standard Error [%]: ko, pool	Abundances (Grouped) Count: wt, pool	Abundances (Grouped) Count: wt, single	Abundances (Grouped) Count: ko, single	Abundances (Grouped) Count: ko, pool	Abundances (Normalized): F6: 126, Sample, wt, pool	Abundances (Normalized): F6: 127N, Sample, wt, single
21.77			1	4		1	30.8	28
5.5	90.13		1	4	4	1	700.3	712.1
7.62	53.75		1	4	4	1	150.7	156.7
14.23			1	4	1		12.2	7.9
16.4	38.22		1	4	4	1	24.7	29.1
31.03	27.17		1	4	4	1	51.7	43.5
61.37	53.35		1	4	4	1	23.8	30.1
20.42	30.03			2	4	1		
21.26	44.07		1	4	4	1	18.3	20.9
27.3	37.82		1	3	4	1	5.2	
13.8	15.82		1	4	4	1	54.7	59.1
37.75	45.43			4	4	1		2.6
35.05	34.45		1	4	4	1	2.6	9.7
32.22	27.05		1	4	4	1	5.7	9.5
48.11	16.1		1	4	2	1	5.8	2.1
20.44	17.01		1	4	4	1	2.9	7
25.59	44.16			3	3	1		3.2
44.26	24.15		1	4	3		2.9	2.4
32.24	26.66		1	4	4	1	11.2	8.9
70.21	38.21			2	2			5.5
39.16	21.27		1	3	4	1	2.6	6.4
39.88	51.74		1	4	4	1	5.4	11.7
57.22	24.5		1	3	4	1	3.1	2.3
11.94	12.58		1	4	4	1	19.8	23.8
19.13	19.93		1	4	4	1	77.4	83.7
16.77	8.86		1	4	4	1	67	61.5
19.92	13.69		1	4	4	1	23	16.8
16.01	9.14		1	4	4	1	66.8	96.5
16.07	11.45		1	4	4	1	196.4	219.3
7.27	18.55		1	4	4	1	72.5	66.3
26.23	34.21			2	4	1		
7.53	27.24			2	3	1		
32.5	50.99		1	4	4	1	8.9	4.4
28.03	15.06		1	4	4	1	14.8	19.1
11.08	12.03		1	4	4	1	89.1	98.7
46.73	26.87		1	4	3	1	7.3	2.6
13.29	14.97		1	4	4	1	37.8	37.9
21.8	9.18		1	4	4	1	17.5	14.4
10.73	6.97		1	4	4	1	74.8	68.9
74.45	16.8		1	4	4	1	3.1	2.6
49.21	13.45		1	4	4	1	2.1	7.6
14.75	34.13			2	4	1		2.1
56.72	39.17		1	4	4	1	16.2	2.9
42.41	13.21		1	4	4	1	4.7	4.5
80.98	33.74		1	2	3	1	2.8	

41.82	53.45		4	4	1		3
17.55	49.45		4	4	1		2.6
35.16	16.06	1	4	4	1	14.8	12.3
10.8	33.42		3	2	1		
23.84	25.75	1	4	4	1	140.5	109.5
16.28	6.31	1	4	4	1	64.6	58.9
7.52	35.64	1	4	4	1	5	3.5
17.47	20.11	1	4	4	1	712.9	675.6
24.99	45.11	1	4	4	1	5.4	4.1
33.06	28.78	1	4	4	1	5.4	8.5
28.44	8.24	1	4	4	1	10.1	19.5
12.51	32.08		4	4	1		2
56.47	42.13		2	4	1		2
66.7	22.84	1	4	4	1	14.4	3.6
22.03	46.1		2	3	1		
37.75	63.41		3	4	1		2.4
45.39	31.3	1	3	4	1	2.4	
1.96	25.48		2	3	1		
20.96	6.87	1	4	4	1	196.9	232.3
19.69	32.67	1	4	4	1	26	23
20.1	24.06	1	4	4	1	16.2	10.1
51.69	15.07	1	4	4	1	15.2	25.9
7.72	90.89		3	2	1		
9.12	26.49	1	4	4	1	9.1	7
24.04	13.91	1	4	4	1	68.1	75.3
43.89	4.36	1	4	4	1	15.2	14.1
33.67	15.5	1	4	4	1	71.1	56.5
78.54	30.76	1	4	4	1	4.4	3.3
19.19	30.68	1	3	4		4.2	2.4
27.14	33.71	1	4	4	1	21.9	20.6
	65.6		1	4	1		
22.8	8.11	1	4	4	1	117	138.1
44.54	52.3	1	4	4	1	3.2	3.6
51.7	19.01	1	4	4	1	6.7	14.1
28.13	14.2	1	4	4	1	14.3	11.1
9.62	13.45	1	4	4	1	47.9	54.4
39.76	40.02	1	4	4	1	3.4	5.5
14.67	22.17	1	4	4	1	59	40.3
62.14	30.45	1	3	4	1	2.8	
30.96	34.74	1	3	4	1	3.4	3.8
56.28	36.58	1	4	4	1	7.1	6.8
10.78	52.57	1	2	4	1	2.4	
12.82	10.01	1	4	4	1	97.5	100.1
7.53	35.73		2	4	1		
28.62	8.13	1	4	4	1	23.8	21.1
18.74	13.82	1	4	4	1	105.8	146.3
54.97		1	4	1	1	2.1	2
18.58	28.4	1	3	4	1	7.8	5.5
28.93	17.74	1	4	4	1	14.8	9.1
	20.9	1	1	3	1	2.4	
5.62	14.2	1	4	4	1	37.3	37
33.07	14.65	1	4	4	1	10.2	11.4

77.42	33.1	1	3	4	1	3.2	2
49.87	11.32	1	4	4	1	6.7	8.5
19.11	19.47	1	4	4	1	32.6	25.1
71.4	28.92	1	4	4	1	3.4	5.1
	21.83		1	4	1		
20.7	30.18	1	4	4	1	29.7	17.3
18.75	17.37	1	4	4	1	10.7	16.8
81.34	31.23	1	2	4	1	2.1	
18.28	30.98	1	3	4	1	6.2	
13.75	36.43	1	4	4	1	12.7	15.4
28.57	15.91	1	4	4	1	17.8	21.4
15.04	13.49	1	4	4	1	41.9	28.9
	51.53	1	1	4	1	2.1	
16.66	15.87	1	4	4	1	44.1	47.6
32.89	11.31	1	4	4	1	10.7	9.2
19.36	25.47		2	4	1		
22.94	28.92	1	4	4	1	2.3	5
19.35	12.72	1	4	4	1	102.7	99.2
47.65	20.74	1	4	4	1	5	13.9
34.16	28.97	1	4	4	1	4.2	3.6
43.82	17.98	1	4	4	1	6.3	6.8
9.12	12.73	1	4	4	1	35.9	32
38.52	12.86	1	4	4	1	15.4	28.3
28.46	15.39	1	4	4	1	24.8	23
31.11	23.13	1	4	4	1	26.1	15.4
40.16	18.7	1	3	4	1	2.9	2.4
54.32	21.34	1	4	4	1	5.7	10.1
52.06	12.22	1	4	4	1	2.8	5.1
37.52	18.95		3	4	1		3.8
28.27	13.9	1	4	4	1	2.9	3.5
28.53	19.93		2	4	1		
27.22	22.06		3	4	1		4.2

Abundances (Normalized): F6: 128N, Sample, wt, single	Abundances (Normalized): F6: 129N, Sample, wt, single	Abundances (Normalized): F6: 130N, Sample, wt, single	Abundances (Normalized): F6: 127C, Sample, ko, single	Abundances (Normalized): F6: 128C, Sample, ko, single	Abundances (Normalized): F6: 129C, Sample, ko, single	Abundances (Normalized): F6: 130C, Sample, ko, single	Abundances (Normalized): F6: 131, Sample, ko, pool	Abundances Count: F6: 126, Sample, wt, pool
42.6	31.4	27.4					1.7	2
764.1	726	668.4	13.2	1.7	2.9	5.2	9.9	9
134.8	158.4	143.1	18.4	6.2	6.3	12.3	7.8	2
6.9	6.1	5.7		1.7				4
30.3	26.1	20.5	7.3	13.6	9.4	5.6	7	4
82.7	63.1	45.7	24	14.1	27.2	19	19	7
50.2	12.1	17.7	15.9	13.5	5.7	5.4	26.3	6
5.7		7.6	2	3.6	2	2.5	4.2	
20.4	12.6	17.4	6.6	10.1	2.9	7.8	5.9	2
8.8	5.7	5.5	2.1	4	1.9	2.3	3.5	2
55.7	62.1	44.6	26.5	17.9	22	23.2	26.9	3
7.5	6.2	6.4	2.4	1.4	3.9	1.9	4.8	
5.5	4.8	9.6	2.4	4.6	3.4	2.3	3.4	1
4.2	9.8	8.9	2.9	5	4	2.9	3.8	2
6.2	6.6	3.3		1.9	2.4		2.2	2
5.5	4.2	6.2	3	2.9	2	2.8	7.1	1
5.4		4.8	3.1	1.4		1.7	5	
1.8	5	4.4	2	1.2	1.8			1
6.9	11.6	14.8	3.9	6.6	6	4	5.3	2
		1.8		1.3	2.3			
5.1	10.6		3.3	4.6	3.9	2.8	4	1
6.8	7.8	16.1	4.2	8.5	6.3	2.1	9.7	2
2.5		6	6.6	9.4	7.5	5.2	10.2	1
29.1	30.9	25.5	62.3	58.3	50.9	47.1	53.9	5
60.7	88	98	185.9	183.6	175.6	116.4	150.7	5
44.7	60.8	67.8	116.8	121.9	103.4	127.9	122.4	9
13.4	17.9	21.9	30.3	35.8	32.7	41.4	40.4	4
66.2	76.8	76.6	153.2	178.1	143.8	157.9	149.7	7
164.6	168.6	221.5	390.9	437.9	329.7	392.6	424.2	8
56.6	64	59	123.9	91.8	145.2	133.6	116.2	3
	2.7	3.9	5.2	8.4	8.7	4.2	2.9	
	1.8	1.6	4.5	3.1		2.7	1.8	
2.3	4.1	2.5	6.8	9.7	1.9	8.3	6.4	3
14	18.9	27.4	35.5	39.5	48.6	36.3	37	4
76.2	91.4	96	182.5	208.7	187.7	155.1	181.3	7
3	4.2	6.9	6.7	11		7.6	5.9	3
31.4	42	42.4	82.2	86.9	60.8	82.2	79.6	2
17.4	13.4	10.1	27.4	31.8	27.3	25.8	39.5	5
81.9	75.9	88.7	162.2	175.4	152.1	151.6	161.1	8
2.8	1.9	8.1	7.5	9.8	7.7	6.7	5.8	1
6.5	10.7	18.2	22.7	17.7	24.1	23.7	22.2	1
		1.7	4.1	5.4	4.1	2.1	7.5	
14.3	12.6	19.7	27.8	20.5	15.6	38.7	78.9	6
3.5	4.3	8.5	10.7	10.1	9.8	13	12	1
	5.5	1.5	5.9	5.9	10.2		1.7	1

2.5	6	5.8	4.9	15.5	5.8	10.6	11.6	
1.8	1.9	1.8	6.2	1.3	4.4	5.4	5.7	
13.7	25.3	23	41.8	41.8	43.9	30	39.5	3
2	2	2.4	5.6			3.5	5.5	
99.3	137.1	167.5	319.1	327.7	297.8	173.2	268.5	8
46.4	66.4	67.5	129.1	126	142.7	124.7	125.7	6
3.5	3.3	3	7.9	9.8	3.6	7.8	7.4	1
513	755.4	773.1	1688.7	1580.7	1667.2	1050.7	1401.6	9
4.7	3.4	2.5	7.5	3.6	9.1	12.5	9.8	1
5.4	11.2	12.3	24.1	27.4	15.3	16.1	21.8	2
12.6	15.6	24.4	36.4	43.7	38.3	41.9	48.4	3
1.7	1.9	2.3	5.2	2.3	4.8	5.2	5.5	
		4.6	11	4.6	8.7	5	8.9	
13.4	9.3	23.3	29.2	34.5	19.2	28	26	2
	2	1.5		4.7	5.3	1.9	3.2	
	4	1.9	4.2	11.6	6.5	2.5	2.2	
5	1.9	3.2	4.1	8.2	9.3	8.6	8.8	1
2.1		2.1		6.1	4	4	2.2	
150.4	194.9	247.1	458.3	511.4	449	440.4	494	14
24.3	22.6	33.4	62.7	42.5	44.7	83.6	92.5	4
9.3	8.3	13.1	22.5	31.1	18.6	20.2	34.1	6
8.3	18.1	10.1	42.5	35.2	34.2	29.6	35.2	5
2.4	2.3	2.1	1.8			8.4	1.8	
7.1	8.3	8.1	22.8	19.4	15.5	12.2	18.7	3
45.5	66.6	83.4	140.1	180.1	134.7	167	158.8	6
11	16.3	28.5	39.2	42.4	41.1	38.6	37.6	4
30.7	65.7	75.4	114	148.2	115.9	152.7	150.3	7
2.4	4.5	11.9	13.6	18.2	9.7	10	11	2
	3.6	3	10.2	5.5	5.9	6.6		2
11.6	22.2	22.9	53.6	52	55.8	22.9	45.6	3
		1.8	1.6	3.5	4.1	8.4	2.2	
83.7	104.7	136.9	279.3	311.7	256.8	275.9	295.8	9
2.3	1.5	4.5	3.8	9.3	4.4	11.7	10.4	1
4.4	22.1	17.8	34.5	28.9	35.6	45.4	50.1	3
7.6	11.5	15.5	26.6	33.8	28.5	24.4	26.9	5
57.7	66.4	54.8	131.6	128.8	147.7	171.3	135	8
4.2	2.4	6.9	9.3	16.6	15.2	6.6	16.4	1
57.7	48.1	48.3	115	88.3	151.3	134.7	125.6	3
5.2	2.8	1.4	6.4	6.7	7	11.5	4.7	1
2		3.3	6	10.9	5	8.8	11.1	1
12	2.4	12.4	29.9	19.6	24.9	11.5	25.1	3
2.4		2.1	4.3	6.7	2.5	9.5	8.6	1
74	91.1	96.7	232.3	244.8	209.7	266.8	234.1	8
	1.8	1.6	5.4	6.1	2.5	3.9	5.7	
22.2	10.8	21.7	51.8	44.6	53.7	52.6	46.6	1
94.6	115.9	137.6	295.2	362.9	288.2	377.4	357.6	8
2	4.8	1.8		7.3			2.6	1
4.1		6	14.6	19.9	10.1	13.3	14.4	3
19.4	16.3	17.5	33	42.7	48.8	50	49.6	4
	2		6.6	6.5		4.4	4.8	1
34.2	37.1	33.1	86.8	116.5	91.4	110.2	98.7	2
11	20.7	19.6	54.9	41.4	40.3	44.9	55.6	4

	7.7	2.5	11.4	15.5	14.1	6.6	13.8	1
5.8	7.9	16.9	25.3	32.8	31.3	28.3	33.2	2
24.3	33.2	35.5	82.2	101.5	70	108.5	97.7	8
2.1	2	8.9	18.4	13.4	8.9	16.6	12.6	1
	1.5		4.1	4.5	6.4	4.4	2.9	
21.9	27	18.5	58.3	58	100.9	60.8	69.2	6
13	10.7	14.8	46	39.1	45.3	58.7	52.3	1
	6.4	1.7	10.2	17.1	10.3	18.5	14.7	1
3.3	4.7	4.1	8.1	13.8	16.2	18.2	9.9	2
16.5	12	16.1	48.9	42.4	42.2	83.6	69.5	3
20.2	13.9	28.5	82.7	58.6	77.2	85.4	86.4	3
28.4	38.8	34.4	113.7	141.1	107.5	137.5	132	5
1.7			5.4	6.4	3.8	11.9	7.7	1
35.1	49.7	52.5	171.9	229.6	161.8	192.8	177.3	3
5	9.8	12	37.1	34.7	34.2	43.4	35.2	1
2.3		3	14.4	9.5	8	11.8	10.8	
4.7	5.5	7.6	19.8	19.7	21.6	34	21.5	1
88.5	91.6	131.9	434.4	391.2	497.6	519.1	441.1	8
5	8	6.3	37.4	27.5	42.1	45.8	42.9	2
5.2	4.8	8	25.6	17.1	34.7	23.3	21.7	1
13.3	5.1	12.8	44.3	38.6	56.7	55.4	37.5	2
27.9	26.9	32.1	146.8	153.5	133.4	179.8	159.6	6
21.8	13.5	36.1	112.3	137.2	125.4	152.1	118.6	4
23.8	29.2	41	164.5	135.2	187.7	192.3	163.6	4
17.5	14.7	27.3	113.9	87.9	131.9	154.7	128.5	4
	3.4	5.4	25.6	26	18	28.7	29.6	1
8.3	1.8	11.6	60	69.9	57.2	89.9	79	2
2.8	10.2	10.1	59.8	70.4	66.7	80.1	83.7	1
2.4		1.8	22.4	28.1	22.6	32.9	27.2	
1.8	3.6	3.8	34.6	37	27.5	29.2	29.1	1
2		3	37.9	43.5	59.8	45.9	67.9	
	3.6	2.4	89.4	84.1	110.5	134.9	108.7	

Abundances Count: F6: 127N, Sample, wt, single	Abundances Count: F6: 128N, Sample, wt, single	Abundances Count: F6: 129N, Sample, wt, single	Abundances Count: F6: 130N, Sample, wt, single	Abundances Count: F6: 127C, Sample, ko, single	Abundances Count: F6: 128C, Sample, ko, single	Abundances Count: F6: 129C, Sample, ko, single	Abundances Count: F6: 130C, Sample, ko, single	Abundances Count: F6: 131, Sample, ko, pool
2	3	3	3					1
9	9	9	9	4	1	1	2	5
2	2	2	2	2	2	2	2	2
3	3	3	2		1			
4	4	4	4	2	3	4	2	3
7	8	7	8	7	5	6	6	7
6	6	4	6	5	5	2	2	6
	2		3	1	2	1	1	2
2	2	2	2	2	2	1	2	2
	2	2	2	1	2	1	1	2
3	3	3	3	3	3	3	3	3
1	3	2	3	1	1	2	1	2
3	2	2	4	1	2	2	1	1
2	1	3	2	1	2	2	1	2
1	2	2	1		1	1		1
2	2	2	3	1	2	1	1	3
1	2		2	1	1		1	2
1	1	2	2	1	1	1		
3	2	4	5	2	4	2	1	2
2			1		1	1		
2	2	2		1	2	1	1	2
4	3	3	7	2	5	2	1	5
1	1		2	3	3	3	2	3
8	9	8	9	10	10	9	9	10
5	5	5	5	5	5	5	5	5
8	9	9	9	9	9	9	9	9
3	4	4	4	4	4	4	4	4
8	7	8	8	8	8	8	8	8
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3	3	3	3	3	3	3	3	3
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		1	1	1	1		1	1
2	1	2	1	3	4	1	3	2
5	4	5	5	5	5	5	5	5
8	7	8	8	8	8	8	8	8
1	1	2	3	3	5		3	3
2	2	2	2	2	2	2	2	2
6	5	5	3	6	6	6	5	6
8	8	8	8	8	8	8	8	8
1	1	1	3	3	4	3	3	2
2	2	2	2	2	2	2	2	2
1			1	2	3	2	1	4
1	6	6	9	9	10	7	11	15
1	1	1	1	1	1	1	1	1
		3	1	3	4	4		1

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1	1	1	1	2	1	2	2	3
3	3	3	3	3	3	3	3	3
	1	1	1	2			1	3
8	8	9	9	10	10	10	10	10
6	6	6	6	6	6	6	6	6
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9	9	9	9	9	9	9	9	9
1	2	1	1	2	2	2	2	2
3	2	4	5	7	7	6	6	7
5	5	6	7	7	8	8	8	8
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1	2	2	2	2	2	2	2	2
		1	1		3	3	1	2
1		2	1	2	5	3	1	1
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	1		1		3	2	2	1
17	15	16	17	17	17	16	17	17
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4	3	4	5	6	6	6	5	5
7	9	8	8	9	9	9	9	9
2	2	1	3	4	6	6	3	5
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	2	1	1	3	3	3	4	2
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8	8	8	8	8	8	8	8	8
		1	1	2	3	1	2	3
1	1	1	1	1	1	1	1	1
10	9	10	11	17	16	15	16	14
1	1	1	1		3			1
2	2		3	6	7	4	5	5
4	6	6	7	9	8	8	9	9
		1		2	2		2	2
2	2	2	2	2	2	2	2	2
3	4	6	7	8	8	8	9	9

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6	6	8	8	8	8	8	8	8
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		1		2	3	3	2	1
6	7	7	6	10	9	10	9	10
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		3	1	4	5	2	5	6
	1	2	2	2	2	2	2	2
5	4	4	6	6	6	5	6	6
3	3	3	3	3	3	3	3	3
5	5	5	5	5	5	5	5	5
	1			1	1	1	1	1
3	3	3	3	3	3	3	3	3
1	1	1	1	1	1	1	1	1
	1		1	6	4	3	4	4
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3	5	2	5	9	9	9	9	9
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5	5	5	5	5	5	5	5	5
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4	3	1	5	8	9	8	9	9
2	1	3	4	4	4	4	4	4
1	1		1	1	1	1	1	1
1	1	1	1	2	4	2	2	2
	1		2	9	8	9	9	9
2		2	1	12	13	13	12	12

Quan Info	XCorr Sequest HT	Confidence Sequest HT	Percolator q-Value Sequest HT	Percolator PEP Sequest HT
Unique	1.820152	High	0.000885	0.01621
Unique	2.287591	High	0.001676	0.02773
Unique	1.719916	High	0.001993	0.03239
Unique	4.65929	High	0	2.19E-08
Unique	1.702899	High	0.000885	0.01489
Unique	3.540589	High	0	1.93E-08
Unique	1.208804	High	0.004388	0.07392
Unique	2.299789	High	0.001004	0.02102
Unique	3.865364	High	0	0.000123
Unique	1.806395	High	0.000664	0.009987
Unique	2.160969	High	0.000608	0.007691
Unique	1.701296	High	0	0.001207
Unique	3.812146	High	0	2.19E-05
Unique	3.596908	High	0	0.000054
Unique	3.676224	High	0	3.12E-07
Unique	1.936079	High	0.002323	0.04412
Unique	1.410829	High	0.001087	0.02293
Unique	2.280858	High	0.000112	0.003611
Unique	4.806998	High	0	1.21E-07
Unique	1.394312	High	0.000608	0.008343
Unique	2.117475	High	0.001676	0.02783
Unique	4.162873	High	0	2.14E-07
Unique	3.552681	High	0	3.08E-07
Unique	3.175302	High	0	4.86E-05
Unique	3.561288	High	0	2.61E-06
Unique	4.80385	High	0	4.73E-08
Unique	2.330394	High	0.000333	0.00603
Unique	2.016614	High	0.000432	0.006321
Unique	2.547707	High	0	0.000664
Not Unique	1.797642	High	0.003226	0.0589
Unique	1.884674	High	0.000112	0.003537
Unique	1.472654	High	0.001743	0.02894
Unique	2.462611	High	0	0.000718
Unique	2.638241	High	0.000112	0.002516
Unique	2.394617	High	0.001475	0.02441
Unique	3.528348	High	0	8.11E-07
Unique	2.428745	High	0.00053	0.007199
Unique	1.479718	High	0.000664	0.01023
Unique	2.027303	High	0.000608	0.007975
Unique	1.396083	High	0.001743	0.02957
Unique	4.923717	High	0	3.15E-08
Unique	2.577068	High	0	0.000198
Unique	3.585179	High	0	1.39E-07
Unique	1.995516	High	0.001948	0.0321
Unique	2.198305	High	0	0.001423

Unique	1.710037	High	0.000608	0.008946
Unique	1.636131	High	0.000664	0.01093
Unique	1.873242	High	0.001676	0.02646
Unique	2.274727	High	0	0.000182
Unique	4.470419	High	0	1.08E-08
Unique	2.482766	High	0	0.001802
Unique	1.902792	High	0.001475	0.02445
Not Unique	3.449977	High	0	3.64E-06
Unique	1.514337	High	0.000664	0.009635
Unique	3.026508	High	0	7.47E-05
Unique	3.028191	High	0	0.000067
Unique	1.274906	High	0.002267	0.04148
Unique	2.781928	High	0	3.36E-05
Unique	3.091471	High	0	0.001092
Unique	4.500051	High	0	5.38E-07
Unique	2.772193	High	0	0.000252
Unique	1.875188	High	0.002754	0.05049
Unique	1.47567	High	0.000961	0.01799
Unique	3.936658	High	0	1.18E-05
Unique	2.105148	High	0.000961	0.0187
Unique	3.028792	High	0	3.49E-05
Unique	4.157577	High	0	6.42E-06
Unique	2.149315	High	0	0.001134
Unique	3.263608	High	0	1.62E-06
Unique	2.877079	High	0	0.000998
Unique	1.82697	High	0.000664	0.01096
Unique	3.072625	High	0	9.74E-06
Unique	6.031785	High	0	0
Unique	3.28943	High	0	1.41E-06
Unique	3.356647	High	0	2.63E-05
Unique	1.473582	High	0.000333	0.006122
Unique	2.381524	High	0	0.001289
Unique	1.679038	High	0.000112	0.002241
Unique	3.070762	High	0	0.000016
Unique	3.70096	High	0	4.09E-06
Unique	3.991532	High	0	1.42E-05
Unique	2.327563	High	0	0.000162
Unique	3.044142	High	0	0.00017
Unique	2.50452	High	0	4.21E-05
Unique	1.872222	High	0	0.001227
Unique	2.424553	High	0	0.000119
Unique	2.341989	High	0	0.000643
Unique	2.608452	High	0	0.000465
Unique	2.537551	High	0	0.000105
Unique	2.02911	High	0.001676	0.02773
Unique	3.001506	High	0	0.001205
Unique	2.734792	High	0.001004	0.02216
Unique	2.962329	High	0	2.86E-06
Unique	3.353224	High	0	3.69E-06
Unique	3.328078	High	0	7.08E-06
Unique	2.301754	High	0.002391	0.04525
Unique	3.968571	High	0	8.66E-07

Unique	1.330359	High	0.000608	0.008766
Unique	2.758011	High	0	4.69E-05
Unique	2.357447	High	0	0.001138
Unique	3.628766	High	0	1.8E-06
Unique	3.76387	High	0	1.88E-06
Unique	2.732216	High	0	4.16E-05
Unique	2.8048	High	0	0.001083
Unique	2.503722	High	0	0.00013
Unique	2.817113	High	0	6.55E-05
Unique	2.648246	High	0	0.000194
Unique	1.77446	High	0.001004	0.021
Unique	1.916408	High	0.003115	0.05678
Unique	4.771692	High	0	1.88E-07
Unique	1.649817	High	0.001676	0.02704
Unique	2.190404	High	0.003529	0.06213
Unique	4.047452	High	0	9.41E-09
Unique	3.136281	High	0	3.71E-05
Not Unique	3.240401	High	0	9.42E-07
Unique	1.955089	High	0	0.00165
Unique	1.572543	High	0.001676	0.02844
Unique	2.931081	High	0	0.000129
Unique	2.553757	High	0	0.00019
Unique	2.51543	High	0	7.62E-05
Unique	1.72475	High	0.003763	0.06537
Unique	1.794872	High	0.00627	0.09725
Unique	3.568662	High	0	0.000107
Unique	3.487014	High	0	0.000289
Unique	2.23022	High	0.000112	0.002103
Unique	1.651148	High	0.003115	0.05673
Unique	5.06225	High	0	5.08E-10
Unique	3.047498	High	0.000112	0.002866
Unique	4.132795	High	0	3.48E-07

Master Protein Accessions	[Product Description]	[# TM Domains]	[SignalP Scores]
TGME49_200250	microneme protein MIC17A	0	NN Sum: 4,
TGME49_200250	microneme protein MIC17A	0	NN Sum: 4,
TGME49_200310	hypothetical protein	1	N/A
TGME49_201140	hypothetical protein	0	N/A
TGME49_201390	hypothetical protein	2	NN Sum: 4,
TGME49_201390	hypothetical protein	2	NN Sum: 4,
TGME49_201680	eukaryotic initiation factor-3 subunit 10, putative	0	N/A
TGME49_201780	microneme protein MIC2	1	NN Sum: 3,
TGME49_201780	microneme protein MIC2	1	NN Sum: 3,
TGME49_202200	hypothetical protein	0	N/A
TGME49_202370	T-complex protein 1, epsilon subunit (TCP-1-epsilon),	0	N/A
TGME49_202390	S15 sporozoite-expressed protein	0	N/A
TGME49_202500	GAPM1a	6	N/A
TGME49_202680	peptidase M16, alpha subunit, putative	0	NN Sum: 0,
TGME49_202830	Elicitor-responsive protein, putative	0	NN Sum: 3,
TGME49_203290	hypothetical protein	0	NN Sum: 1,
TGME49_203290	hypothetical protein	0	NN Sum: 1,
TGME49_203290	hypothetical protein	0	NN Sum: 1,
TGME49_203310	dense granule protein GRA7	2	NN Sum: 4,
TGME49_203310	dense granule protein GRA7	2	NN Sum: 4,
TGME49_203310	dense granule protein GRA7	2	NN Sum: 4,
TGME49_203310	dense granule protein GRA7	2	NN Sum: 4,
TGME49_203970	dolichyl-diphosphooligosaccharide--protein glycosyltr	1	N/A
TGME49_203980	hypothetical protein	0	N/A
TGME49_204400	ATPase synthase subunit alpha, putative	0	NN Sum: 0,
TGME49_204530	microneme protein MIC11	0	NN Sum: 4,
TGME49_205130	hypothetical protein	0	N/A
TGME49_205320	hypothetical protein	0	N/A
TGME49_205440	CCT chaperonin gamma subunit	0	N/A
TGME49_205470	translation elongation factor 2 family protein, putativ	0	N/A
TGME49_205580	nuclear factor NF4	0	NN Sum: 0,
TGME49_206320	hypothetical protein	2	N/A
TGME49_206670	hypothetical protein	0	N/A
TGME49_207130	SAG-related sequence SRS49A	0	NN Sum: 0,
TGME49_207130	SAG-related sequence SRS49A	0	NN Sum: 0,
TGME49_207130	SAG-related sequence SRS49A	0	NN Sum: 0,
TGME49_207160	SAG-related sequence SRS49D	1	NN Sum: 0,
TGME49_207160	SAG-related sequence SRS49D	1	NN Sum: 0,
TGME49_207160	SAG-related sequence SRS49D	1	NN Sum: 0,
TGME49_207160	SAG-related sequence SRS49D	1	NN Sum: 0,
TGME49_207210	hypothetical protein	0	N/A
TGME49_207210	hypothetical protein	0	N/A
TGME49_207210	hypothetical protein	0	N/A
TGME49_207240	hypothetical protein	0	N/A
TGME49_207390	coatomer protein complex, gamma sub-unit, putative	0	N/A
TGME49_207950	hypothetical protein	2	NN Sum: 4,
TGME49_208030	microneme protein MIC4	0	NN Sum: 4,

TGME49_208450	protease inhibitor PI2	0	NN Sum: 4,
TGME49_208560	carrier superfamily protein	1	N/A
TGME49_208730	microneme protein, putative	1	NN Sum: 3,
TGME49_208730	microneme protein, putative	1	NN Sum: 3,
TGME49_208730	microneme protein, putative	1	NN Sum: 3,
TGME49_208730	microneme protein, putative	1	NN Sum: 3,
TGME49_208750	RWD domain-containing protein	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209030	actin ACT1	0	N/A
TGME49_209140	anti-silencing protein, ASF1 family protein	0	N/A
TGME49_209150	non-proton pumping type-II NADH dehydrogenase I	0	NN Sum: 4,
TGME49_209600	hypothetical protein	0	N/A
TGME49_209755	hypothetical protein	0	NN Sum: 3,
TGME49_209755	hypothetical protein	0	NN Sum: 3,
TGME49_209755	hypothetical protein	0	NN Sum: 3,
TGME49_209820	syntaxin protein	4	NN Sum: 2,
TGME49_209985	cAMP-dependent protein kinase	0	NN Sum: 4,
TGME49_209985	cAMP-dependent protein kinase	0	NN Sum: 4,
TGME49_209985	cAMP-dependent protein kinase	0	NN Sum: 4,
TGME49_210690	ribosomal protein RPS6	0	N/A
TGME49_210730	ATP-dependent hsl protease ATP-binding subunit hslU	0	NN Sum: 1,
TGME49_210730	ATP-dependent hsl protease ATP-binding subunit hslU	0	NN Sum: 1,
TGME49_210840	arginyl-tRNA synthetase family protein	0	N/A
TGME49_211030	hypothetical protein	0	N/A
TGME49_211040	Sec61beta family protein	1	N/A
TGME49_211040	Sec61beta family protein	1	N/A
TGME49_211040	Sec61beta family protein	1	N/A
TGME49_211680	protein disulfide isomerase	0	NN Sum: 4,
TGME49_211680	protein disulfide isomerase	0	NN Sum: 4,
TGME49_212260	Sjogren's syndrome/scleroderma autoantigen 1 (Auto	0	N/A
TGME49_212290	ribosomal protein RPS19	0	N/A
TGME49_212980	hypothetical protein	1	N/A
TGME49_213280	SAG-related sequence SRS25	0	NN Sum: 4,
TGME49_213350	ribosomal protein RPS15	0	N/A
TGME49_213350	ribosomal protein RPS15	0	N/A
TGME49_213410	small nuclear ribonucleoprotein f (snrnp-f), putative	0	N/A
TGME49_213670	hypothetical protein	1	N/A
TGME49_214150	mitochondrial inner membrane translocase subunit TI	1	N/A
TGME49_214260	alpha-glucan water dikinase 1, putative	0	N/A
TGME49_214290	DJ-1 family protein	0	NN Sum: 3,
TGME49_214290	DJ-1 family protein	0	NN Sum: 3,
TGME49_214290	DJ-1 family protein	0	NN Sum: 3,
TGME49_214410	hypothetical protein	2	N/A
TGME49_214440	4'-phosphopantetheinyl transferase superfamily prote	0	N/A
TGME49_214480	replication factor a protein 3 protein	0	NN Sum: 2,
TGME49_214590	micro-fibrillar-associated protein 1	0	N/A
TGME49_214750	hypothetical protein	0	NN Sum: 0,

TGME49_214780	hydrolase, NUDIX family protein	0	NN Sum: 4,
TGME49_214780	hydrolase, NUDIX family protein	0	NN Sum: 4,
TGME49_214790	glycoprotein	0	N/A
TGME49_214790	glycoprotein	0	N/A
TGME49_214930	hypothetical protein	0	N/A
TGME49_215010	hypothetical protein	6	NN Sum: 3,
TGME49_215280	succinate dehydrogenase [ubiquinone] iron-sulfur pr	0	NN Sum: 0,
TGME49_215350	hypothetical protein	0	N/A
TGME49_215460	ribosomal protein RPS24	0	N/A
TGME49_215470	ribosomal protein RPL10A	0	N/A
TGME49_215560	histone arginine methyltransferase PRMT5	0	N/A
TGME49_215590	flavoprotein subunit of succinate dehydrogenase	0	NN Sum: 0,
TGME49_215775	rhoptry protein ROP8	1	NN Sum: 3,
TGME49_215785	rhoptry protein ROP2A	1	NN Sum: 4,
TGME49_215785	rhoptry protein ROP2A	1	NN Sum: 4,
TGME49_215910	hypothetical protein	0	NN Sum: 3,
TGME49_216140	tetratricopeptide repeat-containing protein	0	N/A
TGME49_216410	hypothetical protein	0	N/A
TGME49_216410	hypothetical protein	0	N/A
TGME49_216450	peptidase, T1 family protein	0	N/A
TGME49_216880	guanine nucleotide-binding protein	0	N/A
TGME49_216890	hypothetical protein	7	N/A
TGME49_216930	cholinephosphate cytidylyltransferase	0	N/A
TGME49_216970	coronin, putative	0	N/A
TGME49_217030	hypothetical protein	0	N/A
TGME49_217460	glutaminyl-tRNA synthetase (GlnRS)	0	NN Sum: 4,
TGME49_217570	ribosomal protein RPS27	0	N/A
TGME49_217680	hypothetical protein	0	N/A
TGME49_217680	hypothetical protein	0	N/A
TGME49_217740	3-ketoacyl-(acyl-carrier-protein) reductase	0	NN Sum: 4,
TGME49_217890	alkyl hydroperoxide reductase/ Thiol specific antioxid	0	N/A
TGME49_218240	hypothetical protein	1	NN Sum: 1,
TGME49_218520	microneme protein MIC6	1	NN Sum: 2,
TGME49_218530	proteasome-interacting thioredoxin domain-containi	0	N/A
TGME49_218530	proteasome-interacting thioredoxin domain-containi	0	N/A
TGME49_218530	proteasome-interacting thioredoxin domain-containi	0	N/A
TGME49_218780	phosphoserine aminotransferase, putative	0	N/A
TGME49_218820	alba 2	0	N/A
TGME49_218940	hypothetical protein	0	N/A
TGME49_219310	DnaK family protein	0	N/A
TGME49_219320	acid phosphatase GAP50	2	NN Sum: 1,
TGME49_219690	hypothetical protein	0	NN Sum: 3,
TGME49_219690	hypothetical protein	0	NN Sum: 3,
TGME49_219790	pre-mRNA processing factor PRP3	0	N/A
TGME49_219800	vacuolar ATP synthase subunit b, putative	0	N/A
TGME49_219850	prolyl-tRNA synthetase (ProRS)	0	NN Sum: 3,
TGME49_220100	phosphoribosylpyrophosphate synthetase	0	N/A
TGME49_220260	hypothetical protein	0	N/A
TGME49_220400	actin depolymerizing factor ADF	0	N/A
TGME49_220400	actin depolymerizing factor ADF	0	N/A
TGME49_221310	aminopeptidase N protein	0	N/A
TGME49_221470	hypothetical protein	0	N/A

TGME49_221950	splicesome-associated protein, putative	0	N/A
TGME49_222160	aldehyde dehydrogenase	0	N/A
TGME49_222160	aldehyde dehydrogenase	0	N/A
TGME49_222160	aldehyde dehydrogenase	0	N/A
TGME49_222840	Ser/Thr phosphatase family protein	0	NN Sum: 4,
TGME49_223050	ribosomal protein RPS20	0	N/A
TGME49_223110	glycolipid transfer protein GLTP	0	N/A
TGME49_223580	mediator complex subunit MED4	0	N/A
TGME49_223725	hypothetical protein	0	N/A
TGME49_223960	ubiquitin interaction motif family protein	0	N/A
TGME49_224050	AP2 domain transcription factor AP2X-4	0	N/A
TGME49_224770	SAG-related sequence SRS40D	0	NN Sum: 2,
TGME49_225080	ribosomal protein RPS18	0	N/A
TGME49_225310	ARF1-directed GTPase-activating protein, putative	0	N/A
TGME49_225930	triose-phosphate isomerase TPI-I	0	N/A
TGME49_225930	triose-phosphate isomerase TPI-I	0	N/A
TGME49_226000	ATP synthase, putative	0	NN Sum: 1,
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226072	Ser/Thr phosphatase family protein	0	N/A
TGME49_226410	EF-1 guanine nucleotide exchange domain-containing	0	N/A
TGME49_226420	peptidase family M3 protein	0	NN Sum: 2,
TGME49_226430	reticulon protein	3	N/A
TGME49_226430	reticulon protein	3	N/A
TGME49_226550	TBC domain containing protein	0	N/A
TGME49_226970	ribosomal protein RPS11	0	N/A
TGME49_226980	hypothetical protein	0	N/A
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227620	dense granule protein GRA2	0	NN Sum: 4,
TGME49_227650	microtubule-associated protein RP/EB family, putativ	0	N/A
TGME49_227920	hypothetical protein	0	NN Sum: 2,
TGME49_227960	PCI domain-containing protein	0	N/A
TGME49_228220	MYND finger domain-containing protein	0	N/A
TGME49_228290	phospholipase/carboxylesterase	0	N/A
TGME49_228300	CCDC25 protein	0	N/A
TGME49_228470	ribosomal protein RPL15	0	N/A
TGME49_229140	MaoC family domain-containing protein	0	N/A
TGME49_229250	ribosomal protein RPL28	0	N/A
TGME49_229250	ribosomal protein RPL28	0	N/A
TGME49_229420	cytochrome c, putative	0	N/A
TGME49_229480	calcium binding protein precursor, putative	1	NN Sum: 1,

TGME49_229920	hypothetical protein	1	NN Sum: 2,
TGME49_229930	p25-alpha family protein	0	N/A
TGME49_229950	26S proteasome regulatory subunit 6b, putative	0	N/A
TGME49_230080	DEAD/DEAH box helicase domain-containing protein	0	NN Sum: 0,
TGME49_230410	peroxiredoxin PRX3	0	N/A
TGME49_230420	sarco/endoplasmic reticulum Ca2+-ATPase	7	N/A
TGME49_230450	bifunctional GMP synthase/glutamine amidotransfera	0	N/A
TGME49_230480	hypothetical protein	2	N/A
TGME49_230705	hypothetical protein	1	NN Sum: 3,
TGME49_230705	hypothetical protein	1	NN Sum: 3,
TGME49_231100	hypothetical protein	1	N/A
TGME49_231440	LsmAD domain-containing protein	0	N/A
TGME49_231590	SGS domain-containing protein	0	N/A
TGME49_231910	ATP synthase F1 gamma subunit	0	NN Sum: 1,
TGME49_232410	PDI family protein	0	N/A
TGME49_232660	Hsp70 interacting protein HIP	0	N/A
TGME49_232760	protein phosphatase inhibitor IPP2	0	N/A
TGME49_233010	cell-cycle-assocaited protein kinase ERK7, putative	0	N/A
TGME49_233350	nuclear transport factor 2, putative	0	N/A
TGME49_233720	DNA-directed RNA polymerase II RPBABC8	0	N/A
TGME49_234220	hypothetical protein	1	N/A
TGME49_235470	myosin A	0	N/A
TGME49_235930	domain K- type RNA binding proteins family protein	0	N/A
TGME49_235930	domain K- type RNA binding proteins family protein	0	N/A
TGME49_235970	eukaryotic initiation factor-2 gamma, putative	0	N/A
TGME49_235970	eukaryotic initiation factor-2 gamma, putative	0	N/A
TGME49_236010	prenylcysteine oxidase	0	NN Sum: 4,
TGME49_236040	fructose-1,6-bisphosphate aldolase	1	N/A
TGME49_236040	fructose-1,6-bisphosphate aldolase	1	N/A
TGME49_236080	replication factor-a protein 1 (rpa1) subfamily protein	0	N/A
TGME49_236080	replication factor-a protein 1 (rpa1) subfamily protein	0	N/A
TGME49_236210	peptidase M16 family potein, putative	0	NN Sum: 0,
TGME49_236540	RNA recognition motif-containing protein	0	N/A
TGME49_236570	lysine decarboxylase family protein	0	N/A
TGME49_236570	lysine decarboxylase family protein	0	N/A
TGME49_236950	hypothetical protein	0	N/A
TGME49_237015	hypothetical protein	2	N/A
TGME49_237140	ethylene inducible protein, putative	0	N/A
TGME49_237250	hypothetical protein	0	NN Sum: 1,
TGME49_237880	hypothetical protein	1	NN Sum: 3,
TGME49_237880	hypothetical protein	1	NN Sum: 3,
TGME49_237880	hypothetical protein	1	NN Sum: 3,
TGME49_237880	hypothetical protein	1	NN Sum: 3,
TGME49_237880	hypothetical protein	1	NN Sum: 3,
TGME49_238010	ribosomal protein RPL23A	0	N/A
TGME49_238250	ribosomal protein RPL36	0	N/A
TGME49_239020	ABC transporter transmembrane region domain-conta	9	N/A
TGME49_239630	cytidine and deoxycytidylate deaminase zinc-binding	0	N/A
TGME49_239630	cytidine and deoxycytidylate deaminase zinc-binding	0	N/A
TGME49_239760	ribosomal protein RPL22	0	N/A
TGME49_239890	SCP family extracellular subfamily protein	1	NN Sum: 4,
TGME49_240090	rhoptry kinase family protein ROP34, putative	1	N/A

TGME49_240450	Maf family protein	0	N/A
TGME49_240500	hypothetical protein	0	N/A
TGME49_240600	chaperonin cpn60, putative	1	N/A
TGME49_242380	fatty acid elongase	7	N/A
TGME49_242660	vacuolar sorting protein 35, putative	0	N/A
TGME49_242660	vacuolar sorting protein 35, putative	0	N/A
TGME49_242730	guanylate kinase family protein	0	N/A
TGME49_242840	membrane protein	1	N/A
TGME49_243540	WD domain, G-beta repeat-containing protein	0	N/A
TGME49_243600	acetyltransferase, GNAT family protein	0	N/A
TGME49_243710	t-complex protein beta subunit	0	N/A
TGME49_243760	hypothetical protein	3	NN Sum: 2,
TGME49_243910	Cof family hydrolase subfamily protein	0	N/A
TGME49_244180	microneme-like protein	0	NN Sum: 3,
TGME49_244560	heat shock protein 90, putative	1	NN Sum: 4,
TGME49_244690	hypothetical protein	0	N/A
TGME49_245450	hypothetical protein	0	N/A
TGME49_246560	vacuolar ATP synthase subunit g, putative	0	N/A
TGME49_247220	nudix -type motif 9 isoform a family protein	0	N/A
TGME49_247220	nudix -type motif 9 isoform a family protein	0	N/A
TGME49_247440	hypothetical protein	4	NN Sum: 4,
TGME49_247460	proliferating cell nuclear antigen PCNA1	0	N/A
TGME49_247460	proliferating cell nuclear antigen PCNA1	0	N/A
TGME49_247510	fructose-bisphospatase II	0	N/A
TGME49_247510	fructose-bisphospatase II	0	N/A
TGME49_247510	fructose-bisphospatase II	0	N/A
TGME49_247520	hypothetical protein	1	NN Sum: 3,
TGME49_247520	hypothetical protein	1	NN Sum: 3,
TGME49_247520	hypothetical protein	1	NN Sum: 3,
TGME49_248250	translation initiation factor IF-2, putative	0	N/A
TGME49_248340	GTP-binding nuclear protein ran/tc4	0	N/A
TGME49_248340	GTP-binding nuclear protein ran/tc4	0	N/A
TGME49_248340	GTP-binding nuclear protein ran/tc4	0	N/A
TGME49_248370	prefoldin subunit 6, putative	0	N/A
TGME49_248390	ribosomal protein RPL26	0	N/A
TGME49_248460	ubiquitin, putative	0	N/A
TGME49_248810	nuclear factor NF7	0	N/A
TGME49_248810	nuclear factor NF7	0	N/A
TGME49_248940	hypothetical protein	0	N/A
TGME49_249670	cathepsin B	1	NN Sum: 4,
TGME49_249670	cathepsin B	1	NN Sum: 4,
TGME49_249780	hypothetical protein	0	N/A
TGME49_250710	microneme protein MIC10	1	NN Sum: 4,
TGME49_250710	microneme protein MIC10	1	NN Sum: 4,
TGME49_250710	microneme protein MIC10	1	NN Sum: 4,
TGME49_250710	microneme protein MIC10	1	NN Sum: 4,
TGME49_250710	microneme protein MIC10	1	NN Sum: 4,
TGME49_250830	SAC3/GANP family protein	0	N/A
TGME49_251540	dense granule protein GRA9	0	NN Sum: 4,
TGME49_251540	dense granule protein GRA9	0	NN Sum: 4,
TGME49_251540	dense granule protein GRA9	0	NN Sum: 4,
TGME49_251690	seryl-tRNA synthetase, cytoplasmic, putative	0	N/A

TGME49_251930	enoyl-acyl carrier reductase ENR	0	NN Sum: 4,
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete	0	NN Sum: 4,
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete	0	NN Sum: 4,
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete	0	NN Sum: 4,
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete	0	NN Sum: 4,
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete	0	NN Sum: 4,
TGME49_253420	PQ loop repeat-containing protein	6	N/A
TGME49_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,
TGME49_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,
TGME49_253900	parasite porphobilinogen synthase PBGS	0	NN Sum: 4,
TGME49_253910	hypothetical protein	0	N/A
TGME49_254010	serine carboxypeptidase s28 protein	1	NN Sum: 1,
TGME49_254010	serine carboxypeptidase s28 protein	1	NN Sum: 1,
TGME49_254060	SAG-related sequence SRS14A	1	N/A
TGME49_254520	mediator complex subunit MED11	0	N/A
TGME49_254610	Tim10/DDP family zinc finger superfamily protein	0	N/A
TGME49_254650	zinc finger protein	0	N/A
TGME49_254770	Ser/Thr phosphatase family protein	0	N/A
TGME49_255260	apical membrane antigen AMA1	1	N/A
TGME49_255340	tetratricopeptide repeat-containing protein	0	N/A
TGME49_255420	hypothetical protein	0	N/A
TGME49_255660	EF hand domain-containing protein	0	NN Sum: 3,
TGME49_255890	pyridine nucleotide-disulfide oxidoreductase domain-	0	N/A
TGME49_255900	Bax inhibitor-1, putative	6	N/A
TGME49_256050	signal recognition particle 14kd protein	0	N/A
TGME49_256760	pyruvate kinase PyK1	0	N/A
TGME49_256760	pyruvate kinase PyK1	0	N/A
TGME49_256760	pyruvate kinase PyK1	0	N/A
TGME49_256840	hypothetical protein	0	N/A
TGME49_257090	NAC domain-containing protein	0	N/A
TGME49_257380	hypothetical protein	0	NN Sum: 4,
TGME49_257530	transporter, major facilitator family protein	12	N/A
TGME49_257740	UMP-CMP kinase	0	N/A
TGME49_257750	homocysteine s-methyltransferase domain-containing	0	N/A
TGME49_257990	heat shock protein 101, putative	0	N/A
TGME49_258170	hypothetical protein	0	N/A
TGME49_258170	hypothetical protein	0	N/A
TGME49_258390	DnaJ protein, putative	0	NN Sum: 4,
TGME49_258720	Ubiquitin family protein, putative	0	N/A
TGME49_258730	hypothetical protein	1	N/A
TGME49_258870	hypothetical protein	2	N/A
TGME49_259010	vacuolar ATP synthase subunit d, putative	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A

TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259020	bradyzoite antigen BAG1	0	N/A
TGME49_259040	hypothetical protein	1	N/A
TGME49_259550	dihydropteroate synthase	0	NN Sum: 1,
TGME49_259550	dihydropteroate synthase	0	NN Sum: 1,
TGME49_259710	protein kinase	0	N/A
TGME49_260020	hypothetical protein	1	N/A
TGME49_260180	hypothetical protein	0	N/A
TGME49_260190	microneme protein MIC13	0	NN Sum: 4,
TGME49_260370	AtPH1 family protein	0	N/A
TGME49_260430	hypothetical protein	0	N/A
TGME49_260440	nuclear factor NF3	0	N/A
TGME49_260810	hypothetical protein	1	N/A
TGME49_261010	tat-binding family protein, putative	0	N/A
TGME49_261040	hypothetical protein	0	NN Sum: 4,
TGME49_261740	hypothetical protein	1	NN Sum: 2,
TGME49_261950	ATP synthase beta subunit ATP-B	0	N/A
TGME49_261950	ATP synthase beta subunit ATP-B	0	N/A
TGME49_262480	dynein light chain roadblock-type 2, putative	0	N/A
TGME49_262620	RNA recognition motif-containing protein	0	N/A
TGME49_262670	ribosomal protein RPL18A	0	N/A
TGME49_262690	ribosomal protein RPL27	0	N/A
TGME49_263090	14-3-3 protein	0	N/A
TGME49_263180	myosin D	0	N/A
TGME49_263270	glycerophosphodiester phosphodiesterase family pro	6	N/A
TGME49_263270	glycerophosphodiester phosphodiesterase family pro	6	N/A
TGME49_263270	glycerophosphodiester phosphodiesterase family pro	6	N/A
TGME49_263530	chaperonin, putative	0	N/A
TGME49_263720	HMG (high mobility group) box domain-containing pr	0	N/A
TGME49_263850	hypothetical protein	0	N/A
TGME49_264080	acyl carrier protein ACP	1	NN Sum: 4,
TGME49_264440	signal recognition particle receptor beta subunit prote	1	N/A
TGME49_264600	hypothetical protein	4	N/A
TGME49_265020	arabinogalactan protein, putative	0	N/A
TGME49_265180	hypothetical protein	0	N/A
TGME49_265220	co-chaperone GrpE protein	0	NN Sum: 1,
TGME49_266060	ribosomal protein RPSA	0	N/A
TGME49_267050	hydrolase, alpha/beta fold family protein	0	N/A
TGME49_267400	ribosomal protein RPL32	0	N/A
TGME49_267800	dynamin-related protein DRPA	0	N/A
TGME49_268300	hypothetical protein	0	N/A
TGME49_268650	chaperone clpB protein, putative	0	N/A
TGME49_268790	hypothetical protein	0	NN Sum: 0,
TGME49_268850	enolase 2	0	N/A
TGME49_268860	enolase 1	0	N/A
TGME49_268860	enolase 1	0	N/A
TGME49_269190	glyceraldehyde-3-phosphate dehydrogenase GAPDH2	1	NN Sum: 3,
TGME49_269190	glyceraldehyde-3-phosphate dehydrogenase GAPDH2	1	NN Sum: 3,
TGME49_269650	FFD and TFG box motifs protein	0	NN Sum: 0,
TGME49_269650	FFD and TFG box motifs protein	0	NN Sum: 0,
TGME49_269950	hypothetical protein	0	NN Sum: 4,
TGME49_270070	synaptobrevin family protein	1	N/A

TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
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TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270240	MAG1	1	NN Sum: 4,
TGME49_270250	dense granule protein GRA1	0	NN Sum: 4,
TGME49_270320	protein phosphatase 2C domain-containing protein	0	NN Sum: 3,
TGME49_270640	RNA recognition motif-containing protein	0	N/A
TGME49_270740	Cwf15/Cwc15 cell cycle control protein	0	N/A
TGME49_270830	small nuclear ribonucleoprotein	0	N/A
TGME49_271060	Sec1 family protein	0	N/A
TGME49_271930	hypothetical protein	0	N/A
TGME49_272630	U6 snRNA-associated Sm family protein LSm8, putativ	0	N/A
TGME49_272630	U6 snRNA-associated Sm family protein LSm8, putativ	0	N/A
TGME49_273460	eukaryotic translation initiation factor 3 subunit 6 inte	2	N/A
TGME49_273760	heat shock protein HSP70	0	N/A
TGME49_273905	hypothetical protein	2	NN Sum: 3,
TGME49_273950	replication factor C subunit 5, putative	0	N/A
TGME49_273960	chaperonin GroS protein	0	N/A
TGME49_273960	chaperonin GroS protein	0	N/A
TGME49_273980	hypothetical protein	3	NN Sum: 2,
TGME49_275440	dense granule protein GRA6	2	N/A
TGME49_275440	dense granule protein GRA6	2	N/A
TGME49_275440	dense granule protein GRA6	2	N/A
TGME49_275440	dense granule protein GRA6	2	N/A
TGME49_275810	ribosomal protein RPS10	0	N/A
TGME49_276850	hypothetical protein	0	N/A
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278080	Toxoplasma gondii family A protein	0	NN Sum: 4,
TGME49_278370	Toxoplasma gondii family A protein	1	N/A
TGME49_278530	multiprotein bridging factor type 1 family transcriptio	0	N/A
TGME49_278950	LSM domain-containing protein	0	N/A
TGME49_278990	phosphate carrier, putative	1	N/A
TGME49_279390	proliferation-associated protein 2G4, putative	0	N/A
TGME49_279400	glutaredoxin, putative	0	N/A
TGME49_280750	rudimentary enhancer, putative	0	N/A
TGME49_281520	zinc finger, C3HC4 type (RING finger) domain-containi	4	N/A
TGME49_281930	SAG-related sequence SRS39	0	NN Sum: 4,
TGME49_282180	hypothetical protein	0	N/A
TGME49_283780	glucose-6-phosphate isomerase GPI	1	NN Sum: 1,
TGME49_283780	glucose-6-phosphate isomerase GPI	1	NN Sum: 1,

TGME49_283780	glucose-6-phosphate isomerase GPI	1	NN Sum: 1,
TGME49_283780	glucose-6-phosphate isomerase GPI	1	NN Sum: 1,
TGME49_284540	ATP synthase F1, delta subunit protein	0	N/A
TGME49_285680	dihydrolipoamide acyltransferase, putative	0	N/A
TGME49_285870	SAG-related sequence SRS20A	1	NN Sum: 3,
TGME49_285870	SAG-related sequence SRS20A	1	NN Sum: 3,
TGME49_285870	SAG-related sequence SRS20A	1	NN Sum: 3,
TGME49_286090	translation initiation factor SUI1, putative	0	N/A
TGME49_286120	prolyl endopeptidase	0	NN Sum: 0,
TGME49_286120	prolyl endopeptidase	0	NN Sum: 0,
TGME49_286630	redoxin domain-containing protein	1	NN Sum: 2,
TGME49_286630	redoxin domain-containing protein	1	NN Sum: 2,
TGME49_288245	hypothetical protein	1	NN Sum: 3,
TGME49_288380	heat shock protein HSP90	0	N/A
TGME49_288380	heat shock protein HSP90	0	N/A
TGME49_288500	FAD Malate-dehydrogenase (MDH-FAD)	0	NN Sum: 0,
TGME49_288720	ribosomal protein RPL10	0	N/A
TGME49_288860	RuvB family 2 protein	0	N/A
TGME49_289300	methionyl-tRNA synthetase	0	N/A
TGME49_289360	hypothetical protein	1	NN Sum: 4,
TGME49_289690	glyceraldehyde-3-phosphate dehydrogenase GAPDH1	0	N/A
TGME49_289800	hypothetical protein	2	NN Sum: 2,
TGME49_289880	hypothetical protein	2	N/A
TGME49_289970	hypothetical protein	0	N/A
TGME49_289970	hypothetical protein	0	N/A
TGME49_290030	hypothetical protein	1	NN Sum: 0,
TGME49_290030	hypothetical protein	1	NN Sum: 0,
TGME49_290260	thioredoxin family Trp26 protein	0	N/A
TGME49_290660	RNA recognition motif-containing protein	0	N/A
TGME49_290850	WD-40 repeat protein	0	N/A
TGME49_290940	EMP/nonaspanin domain family protein	10	NN Sum: 4,
TGME49_290950	clathrin heavy chain, putative	0	N/A
TGME49_291010	hypothetical protein	0	N/A
TGME49_291180	hypothetical protein	0	N/A
TGME49_291300	RER1 protein, putative	2	N/A
TGME49_291330	RNA recognition motif-containing protein	0	N/A
TGME49_291600	gamma interferon inducible lysosomal thiol reductase	1	NN Sum: 4,
TGME49_291600	gamma interferon inducible lysosomal thiol reductase	1	NN Sum: 4,
TGME49_291680	Sec23/Sec24 trunk domain-containing protein	0	N/A
TGME49_292270	SAG-related sequence SRS36C	0	NN Sum: 3,
TGME49_292280	SAG-related sequence SRS36D	1	NN Sum: 4,
TGME49_292280	SAG-related sequence SRS36D	1	NN Sum: 4,
TGME49_293510	poly(ADP-ribose) polymerase and DNA-Ligase Zn-finge	0	NN Sum: 3,
TGME49_293580	prefoldin subunit protein	0	N/A
TGME49_293590	3-oxoacyl-acyl-carrier protein synthase I/II, putative	1	NN Sum: 4,
TGME49_293590	3-oxoacyl-acyl-carrier protein synthase I/II, putative	1	NN Sum: 4,
TGME49_293780	hypothetical protein	0	N/A
TGME49_293870	thioredoxin, putative	0	N/A
TGME49_294710	RNA recognition motif-containing protein	0	N/A
TGME49_295125	rhoptry protein ROP4	1	NN Sum: 4,
TGME49_297060	phosphoglycerate mutase PGMII	0	N/A
TGME49_297160	hypothetical protein	0	NN Sum: 4,

TGME49_297220	AMP-binding enzyme domain-containing protein	0	N/A
TGME49_297500	T-complex protein 1 eta subunit	0	N/A
TGME49_297900	hypothetical protein	0	N/A
TGME49_297970	aspartyl aminopeptidase	0	N/A
TGME49_299050	ribosomal protein RPL17	0	N/A
TGME49_300040	ubiquitin-conjugating enzyme subfamily protein	0	N/A
TGME49_300140	elongation factor 1-gamma, putative	0	N/A
TGME49_300310	26S proteasome regulatory subunit, S6a family AAA A	0	N/A
TGME49_301120	acetyl-CoA acetyltransferase	0	N/A
TGME49_301170	SAG-related sequence SRS19D	1	NN Sum: 4,
TGME49_304740	rhoptry kinase family protein ROP35	0	N/A
TGME49_304740	rhoptry kinase family protein ROP35	0	N/A
TGME49_305070	hypothetical protein	0	N/A
TGME49_305510	hypothetical protein	0	NN Sum: 3,
TGME49_305600	hypothetical protein	0	N/A
TGME49_305820	SGS domain-containing protein	0	N/A
TGME49_305850	RNA recognition motif-containing protein	0	N/A
TGME49_305850	RNA recognition motif-containing protein	0	N/A
TGME49_306020	hypothetical protein	0	N/A
TGME49_306030	glutathione s-transferase, n-terminal domain containi	0	N/A
TGME49_306380	U1 zinc finger protein	0	N/A
TGME49_306650	hypothetical protein	0	NN Sum: 2,
TGME49_306930	proteasome subunit beta type 7 precursor, putative	0	N/A
TGME49_307810	hypothetical protein	0	N/A
TGME49_307810	hypothetical protein	0	N/A
TGME49_308050	thioredoxin domain-containing protein	0	N/A
TGME49_308950	histidine acid phosphatase superfamily protein	0	NN Sum: 4,
TGME49_308970	hypothetical protein	0	NN Sum: 4,
TGME49_309010	elongation factor P, putative	0	N/A
TGME49_309160	IgA-specific metalloendopeptidase	0	NN Sum: 4,
TGME49_309160	IgA-specific metalloendopeptidase	0	NN Sum: 4,
TGME49_309210	peroxiredoxin 6, putative	0	N/A
TGME49_309210	peroxiredoxin 6, putative	0	N/A
TGME49_309210	peroxiredoxin 6, putative	0	N/A
TGME49_309210	peroxiredoxin 6, putative	0	N/A
TGME49_309560	nmda receptor glutamate-binding chain	7	N/A
TGME49_309600	hypothetical protein	0	N/A
TGME49_309600	hypothetical protein	0	N/A
TGME49_309752	succinate-Coenzyme A ligase, beta subunit, putative	0	NN Sum: 0,
TGME49_309752	succinate-Coenzyme A ligase, beta subunit, putative	0	NN Sum: 0,
TGME49_309760	hypothetical protein	0	NN Sum: 3,
TGME49_309820	ribosomal protein RPL11	0	N/A
TGME49_310030	cyclase-associated protein, putative	0	N/A
TGME49_310050	RNA recognition motif-containing protein	0	N/A
TGME49_310060	small nuclease	0	N/A
TGME49_310080	AMP-binding enzyme domain-containing protein	0	N/A
TGME49_310640	phosphorylase family protein	0	N/A
TGME49_310670	glycogen phosphorylase 1, putative	0	N/A
TGME49_310780	dense granule protein GRA4	0	NN Sum: 4,
TGME49_310780	dense granule protein GRA4	0	NN Sum: 4,
TGME49_310780	dense granule protein GRA4	0	NN Sum: 4,
TGME49_310840	hypothetical protein	2	N/A

TGME49_310850	MYND finger domain-containing protein	0	N/A
TGME49_310860	U5 snRNP-specific protein	0	NN Sum: 1,
TGME49_311310	protein phosphatase 2B catalytic subunit, calcineurin	0	N/A
TGME49_311480	hypothetical protein	0	N/A
TGME49_311720	chaperonin protein BiP	1	NN Sum: 4,
TGME49_311720	chaperonin protein BiP	1	NN Sum: 4,
TGME49_311720	chaperonin protein BiP	1	NN Sum: 4,
TGME49_312200	serine/threonine protein phosphatase	0	N/A
TGME49_312270	rhoptry protein ROP13	1	NN Sum: 4,
TGME49_312480	uracil phosphoribosyltransferase FUR1, putative	0	N/A
TGME49_312530	splicing factor, CC1 family protein	0	N/A
TGME49_312600	heat shock protein HSP21	0	N/A
TGME49_313100	signal recognition particle SRP54 protein	0	N/A
TGME49_313390	ribosomal protein RPL6	0	NN Sum: 1,
TGME49_313560	60S ribosomal protein L7a, putative	0	N/A
TGME49_314090	proteasome beta subunit	0	N/A
TGME49_314250	bradyzoite rhoptry protein BRP1	1	NN Sum: 2,
TGME49_314400	pyruvate dehydrogenase E1 component, beta subunit	0	NN Sum: 0,
TGME49_314430	serine/threonine specific protein phosphatase	0	N/A
TGME49_315110	prefoldin, alpha subunit protein	0	NN Sum: 0,
TGME49_315740	SAG-related sequence SRS54	0	N/A
TGME49_315770	cytochrome p450 superfamily protein	1	N/A
TGME49_315780	myosin regulatory light chain, putative	0	N/A
TGME49_315930	integral membrane protein, DUF56 family protein, pu	0	N/A
TGME49_315930	integral membrane protein, DUF56 family protein, pu	0	N/A
TGME49_316330	superoxide dismutase SOD2	0	NN Sum: 4,
TGME49_316330	superoxide dismutase SOD2	0	NN Sum: 4,
TGME49_316360	hypothetical protein	0	NN Sum: 0,
TGME49_317720	eukaryotic translation initiation factor 3 subunit 7, pu	0	N/A
TGME49_318170	hypothetical protein	0	N/A
TGME49_318230	phosphoglycerate kinase PGKI	0	N/A
TGME49_318230	phosphoglycerate kinase PGKI	0	N/A
TGME49_318410	TCP-1 chaperonin, putative	0	N/A
TGME49_318720	pyridoxal phosphate enzyme, YggS family protein	0	N/A
TGME49_318750	deoxyribose-phosphate aldolase	0	N/A
TGME49_319560	microneme protein MIC3	0	NN Sum: 4,
TGME49_319560	microneme protein MIC3	0	NN Sum: 4,
TGME49_319560	microneme protein MIC3	0	NN Sum: 4,
TGME49_319730	YOU2 family C2C2 zinc finger protein	0	N/A
TGME49_319850	splicing factor U2AF family SnRNP auxilary factor large	0	N/A
TGME49_320180	SAG-related sequence SRS16C	1	NN Sum: 1,
TGME49_320190	SAG-related sequence SRS16B	1	NN Sum: 2,
TGME49_320190	SAG-related sequence SRS16B	1	NN Sum: 2,
TGME49_320220	ubiquinol cytochrome c oxidoreductase, putative	0	N/A
TGME49_320490	N-acyl-phosphatidylethanolamine-hydrolyzing phosph	1	N/A
TGME49_320570	elongation factor Tu, putative	0	N/A
TGME49_321500	RNA recognition motif-containing protein	0	N/A
TGME49_321660	mannosyltransferase, putative	6	N/A
TGME49_321710	hypothetical protein	1	NN Sum: 4,

Confidence	Annotated Sequence	Modifications	Modifications in Master Proteins
High	[E].TTGYSCFEKGK.[E]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [C6	
High	[R].CPLCLVDNYDFR.[G]	2xCarbamidomethyl [C1; C4]	
High	[L].DAATPLPTAPAGTGAVFHSR.[L]	1xTMT6plex [N-Term]	
High	[M].AAVSSFSSTSAR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[A].SHGTTFQDAGAR.[A]	1xTMT6plex [N-Term]	
High	[A].SHGTTFQDAGAR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[-].MQSFQKPENALKR.[A]	2xTMT6plex [K6; K12]; 1xAcetyl [N-Ter	TGME49_2
High	[G].WSIVDALR.[K]	1xTMT6plex [N-Term]	
High	[G].GGWSIVDALR.[K]	1xAcetyl [N-Term]	TGME49_2
High	[A].LETAAFVPR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[-].MNIATDEFGNPFIILR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[M].ATPFLPLDSGLR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[-].MYFTYVVRPGEAPEGR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[S].GAALQPKAGPAPEYR.[R]	2xTMT6plex [N-Term; K7]	
High	[M].SDPNQPTHVTVTVHSAR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[P].YKAYGIPAESTDTTSGDDVEEAFR.[K]	2xTMT6plex [N-Term; K2]	
High	[G].HEPVASAPYKAYGIPAESTDTTSGDDVE	2xTMT6plex [N-Term; K10]	
High	[S].APYKAYGIPAESTDTTSGDDVEEAFR.[K]	2xTMT6plex [N-Term; K4]	
High	[A].ATASDDELMSR.[I]	1xAcetyl [N-Term]	TGME49_2
High	[R].SDAEVTDDNIYEEHTDR.[K]		
High	[A].ATASDDELMSR.[I]	1xAcetyl [N-Term]; 1xOxidation [M9]	TGME49_2
High	[R].SDAEVTDDNIYEEHTDR.[K]	1xTMT6plex [N-Term]	
High	[A].AVLPIPSAPPLR.[A]	1xTMT6plex [N-Term]	
High	[-].MQLQQAVR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[A].AGAKISPSEMSR.[L]	2xTMT6plex [N-Term; K4]	
High	[T].EDDKSAASIVR.[G]	2xTMT6plex [N-Term; K4]	
High	[N].MEKLPTIILPGGKAVDETPLSGR.[S]	2xTMT6plex [K3; K13]; 1xAcetyl [N-Ter	TGME49_2
High	[M].AAVVSEESIQKVLR.[E]	1xTMT6plex [K11]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MIRPQGPVLVLKQNTKR.[E]	2xTMT6plex [K12; K16]; 1xAcetyl [N-Ter	TGME49_2
High	[M].VNFSVEQMR.[E]	1xTMT6plex [N-Term]	
High	[M].ASTKSGALPLFWSAAELAANPR.[Q]	1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_2
High	[M].TSVAVSSHSPKPAPQSQSSVR.[S]	1xTMT6plex [K11]; 1xAcetyl [N-Term]	TGME49_2
High	[E].GGEDREEEEREVEYGTGLHEGR.[L]	1xTMT6plex [N-Term]	
High	[S].EVQSCSGSATPLFLR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].SEVQSCSGSATPLFLR.[L]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[A].SEVQSCSGSATPLFLR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[G].NQANSQSVTCESNASPLVLR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10]	
High	[N].SQSVTCESNASPLVLR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[S].QSVTCESNASPLVLR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].NSQSVTCESNASPLVLR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[M].AANTTATGTHPAQECHLKHPPEFDGG	2xTMT6plex [K18; K27]; 1xAcetyl [N-Ter	TGME49_2
High	[M].AANTTATGTHPAQECHLKHPPEFDGG	1xTMT6plex [K18]; 1xAcetyl [N-Term]; 1	TGME49_2
High	[M].AANTTATGTHPAQECHLK.[H]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].ATDSSSGLSLPPKNAELR.[E]	1xTMT6plex [K13]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MLSQFYVLSPR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[A].ADETHVVIPSHQEGR.[H]	1xAcetyl [N-Term]	TGME49_2
High	[D].ITPAGDDVSANVTSSEPAKLDLSCVHSD	3xTMT6plex [N-Term; K19; K30]; 1xCarbameth	

High	[A].SPETKVCSCPR.[N]	2xTMT6plex [N-Term; K5]; 2xCarbamidomethyl [C7	
High	[A].SAIPLSSSHLSSSLR.[R]	1xTMT6plex [N-Term]	
High	[A].AGVPKPAAPDGKAVR.[K]	3xTMT6plex [N-Term; K5; K12]	
High	[D].PTIHDEGHGAAAPSTPR.[A]		
High	[L].AKSSTDDPTIHDEGHGAAAPSTPR.[A]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[G].GKAVKVTPVAR.[K]	3xTMT6plex [N-Term; K2; K5]	
High	[M].TNHTEEQALELEALEALFTR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[A].DEEVQALVVDNGSGNVK.[A]	1xAcetyl [N-Term]	TGME49_2
High	[A].DEEVQALVVDNGSGNVKAGVAGDDA	1xTMT6plex [K17]; 1xAcetyl [N-Term]	TGME49_2
High	[R].TTFDSIMKCDVDIR.[K]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl [C9	
High	[R].VAPEEHPVLLTEAPLNPKANR.[E]	2xTMT6plex [N-Term; K18]	
High	[L].TEAPLNPKANR.[E]	2xTMT6plex [N-Term; K8]	
High	[T].EAPLNPKANR.[E]	2xTMT6plex [N-Term; K7]	
High	[SC].YVGDEAQSKR.[G]	2xTMT6plex [N-Term; K9]	
High	[M].SVVNVTNIR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[C].DSPASPSSPSSPKER.[V]	2xTMT6plex [N-Term; K13]	
High	[M].AKNTLETGDSLR.[L]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[R].EEEEELFPSLDDVLDTSPFPAR.[L]		
High	[A].GMPEITIREEEEELFPSLDDVLDTSPFPA	1xAcetyl [N-Term]	TGME49_2
High	[H].VSTAKGEEPFSSKEEER.[H]	3xTMT6plex [N-Term; K5; K13]	
High	[K].MQDLFEDLR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[P].VQGTLGPDVADTAGEPVVLQVAR.[G]	1xTMT6plex [N-Term]	
High	[A].APVQGTLGPDVADTAGEPVVLQVAR.[	1xAcetyl [N-Term]	TGME49_2
High	[A].APVQGTLGPDVADTAGEPVVLQVAR.[	1xTMT6plex [N-Term]	
High	[-].MKLNLANPQAGMQKTVEVDDEK.[K]	3xTMT6plex [N-Term; K2; K14]	
High	[V].SSHGEKGSQENSDSADDQGVR.[K]	2xTMT6plex [N-Term; K6]	
High	[M].LHSATPGVSSHGEKGSQENSDSADDQ	2xTMT6plex [N-Term; K14]	
High	[-].MQALNVQVKEAFR.[R]	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MELVSKVEDQDLLPFVGYCR.[I]	1xTMT6plex [K6]; 1xAcetyl [N-Term]; 1x	TGME49_2
High	[-].MVGTNAPSAQASSAQHVGGAR.[T]	1xAcetyl [N-Term]	TGME49_2
High	[M].VGTNAPSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[G].TNAPSAQASSAQHVGGAR.[T]	1xTMT6plex [N-Term]	
High	[A].EEEAVTVLTASNFDDTLK.[N]	1xTMT6plex [N-Term]	
High	[A].EEEAVTVLTASNFDDTLKNNEIVLVK.[F]	2xTMT6plex [N-Term; K]	
High	[M].SGLSSAAHGGMAASSLAEQR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[M].SNPAYLYETPLETR.[V]	1xAcetyl [N-Term]	TGME49_2
High	[-].MEELSHASLPR.[F]	1xAcetyl [N-Term]	TGME49_2
High	[A].EEHFAVFSTCR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10]	
High	[M].ADAGDAAANQPKRR.[T]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ADAGDAAANQPKR.[R]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ATVTPVNPKPFLTSLTGR.[Q]	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[L].AAETKVSGDSTAISPNTR.[G]	2xTMT6plex [N-Term; K5]	
High	[M].ASALDDDYLR.[T]	1xAcetyl [N-Term]	TGME49_2
High	[M].AQKGHTDAEAPDVR.[Q]	1xTMT6plex [K3]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLRR.[A]	2xTMT6plex [N-Term; K3]	
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLR.[R]	2xTMT6plex [N-Term; K3]	
High	[M].AVKVLVPVAHDSEEIEAVSIIDTLR.[R]	1xTMT6plex [K3]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AHVLISSPSTVELDEETQVFTSLQNAAL	1xAcetyl [N-Term]	TGME49_2
High	[-].MNTELLSLTDEPVILVR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[T].MYAGIGDPSGGFGAPAYEKYPR.[G]	1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SAADVHSILYR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[F].SVAPPPLYNGAAPGFR.[E]	1xTMT6plex [N-Term]	

High	[M].SLTAEEPKPAVEAR.[A]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SLTAEEPKPAVEAR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[F].SSEADSSVEAASKDLLK.[T]	2xTMT6plex [N-Term; K13]	
High	[F].SSEADSSVEAASK.[D]	1xTMT6plex [N-Term]	
High	[M].SPPTASASVASSGSSPHMDR.[L]	1xTMT6plex [N-Term]	
High	[M].ALTAVSSASSR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[A].SVAHAQTAASEAEAATKVPDFR.[T]	2xTMT6plex [N-Term; K17]	
High	[F].SSVKFMDQKR.[S]	3xTMT6plex [N-Term; K4; K9]	
High	[M].ADSGAFSLR.[F]	1xAcetyl [N-Term]	TGME49_2
High	[M].SKLSTDGLK.[K]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[M].PLHPPSNSCLTGPIYFGVGLPHAAVR.[T	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[F].TNVKKPAYR.[V]	3xTMT6plex [N-Term; K4; K5]	
High	[W].LEQEAAEDVTPLPDSHTEAQTQSPSAF	1xAcetyl [N-Term]	TGME49_2
High	[W].LEQEAAEEVTPLLNSHTETPTQSPSAFR	1xAcetyl [N-Term]	TGME49_2
High	[G].HVQQGAGVVRPR.[H]	1xTMT6plex [N-Term]	
High	[G].SSSASFSPEEESLVSHSR.[V]	1xAcetyl [N-Term]	TGME49_2
High	[M].ATASMTPDGDNGPR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[-].METLDEEKAEALLR.[E]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_2
High	[-].METLDEEKAEALLR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[M].AGTGSGYDLSVSTFSPDGR.[V]	1xAcetyl [N-Term]	TGME49_2
High	[M].SGESPLEFKGVLEGHTDCVTAISTPSLKS	2xTMT6plex [K9; K28]; 1xAcetyl [N-Ter	TGME49_2
High	[A].IVCGVEAPDGLLAAATAAGSSTPALDIF	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C3; C3	
High	[-].MEAVSSSSDGLPTKR.[K]	1xTMT6plex [K14]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ADAVDVPLIKNLYAEAWKQQYSDLR.[	2xTMT6plex [K10; K18]; 1xAcetyl [N-Ter	TGME49_2
High	[F].ASTLVQPTSSGSVHHDSMAR.[D]	1xTMT6plex [N-Term]	
High	[M].ALSPGAVLR.[I]	1xAcetyl [N-Term]	TGME49_2
High	[K].MEIDLLHPDPK.[V]	1xAcetyl [N-Term]	TGME49_2
High	[L].EMPNLLVENALEGTPHTR.[H]	1xTMT6plex [N-Term]	
High	[A].SATSPEHSTTDESETTIEKR.[G]	1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_2
High	[S].AYKLTFGGPETGEKDGR.[V]	3xTMT6plex [N-Term; K3; K14]	
High	[M].PAPMVSQPAPAFEAEAVMADGSFGK.	1xTMT6plex [N-Term]	
High	[A].WFGTNGDEDLHAGR.[S]	1xTMT6plex [N-Term]	
High	[S].EKPAACSSNPCGPEAAGTCNETNSGYIC	2xTMT6plex [N-Term; K2]; 4xCarbamidomethyl [C6	
High	[I].MEGTSLMSLIDKSKVECLNEDAQHSIR.[	2xTMT6plex [K12; K14]; 1xAcetyl [N-Ter	TGME49_2
High	[I].MEGTSLMSLIDK.[S]	1xAcetyl [N-Term]	TGME49_2
High	[I].MEGTSLMSLIDKSK.[V]	1xTMT6plex [K]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MEEADLSSLAATER.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[M].ADVAAAPAPNATSQAANSTEGDAAA	1xTMT6plex [K40]; 1xAcetyl [N-Term]	TGME49_2
High	[K].ATSMDHGMQYSSIYWETSHR.[T]	1xTMT6plex [N-Term]	
High	[M].AVIGIDLGSLNSVMATVQR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[F].TVLGVDDWSR.[N]	1xTMT6plex [N-Term]	
High	[M].AKPNDLAGLEK.[A]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AKPNDLAGLEKALNKNDK.[I]	3xTMT6plex [K2; K11; K15]; 1xAcetyl [N	TGME49_2
High	[-].MEGHQDQVGAAKLR.[E]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AAQAAKADAALAHAAAASR.[D]	1xTMT6plex [K6]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ATNSDVSVLSAEEQR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[Q].TAAPVPKTDKGR.[N]	3xTMT6plex [N-Term; K7; K10]	
High	[M].AVPAAVLSQLR.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[M].ASGMGVDENCVAR.[F]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].ASGMGVDENCVAR.[F]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[A].DTPEAQFKNAAVHEQR.[A]	2xTMT6plex [N-Term; K8]	
High	[-].MFNPNATMDWIR.[G]	1xAcetyl [N-Term]	TGME49_2

High	[M].SASLLEHLR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[M].TVKPEDIETR.[L]	2xTMT6plex [N-Term; K3]	
High	[M].TVKPEDIETR.[L]	1xTMT6plex [N-Term]	
High	[M].TVKPEDIETR.[L]	1xTMT6plex [K3]; 1xAcetyl [N-Term]	TGME49_2
High	[M].GIVKVCVR.[Q]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [C6	
High	[M].SKLMKGGLEGEEQR.[L]	2xTMT6plex [K2; K5]; 1xAcetyl [N-Term]	TGME49_2
High	[M].STAATESDLDPTKGEGLFVTLTSGFSKAI	2xTMT6plex [K13; K27]; 1xAcetyl [N-Ter	TGME49_2
High	[M].APPSAPAVAASSPSLQELYNLLR.[S]	1xTMT6plex [N-Term]	
High	[K].EEEHGEAGKVEEPLFCAEGGEEEER.[G]	1xTMT6plex [K9]; 1xAcetyl [N-Term]; 1x	TGME49_2
High	[M].VLEAVMLCIDNSAYAR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[M].AEMSSADGVHVLSGTSR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[L].DEVHTADENPHLAIDGR.[T]	1xTMT6plex [N-Term]	
High	[M].SIQVSNNQDFQHILR.[I]	1xAcetyl [N-Term]	TGME49_2
High	[R].MDAQTASFFKQLR.[D]	1xTMT6plex [K10]; 1xAcetyl [N-Term]	TGME49_2
High	[V].ATPAQAQEVHEHIR.[E]	1xTMT6plex [N-Term]	
High	[A].TPAQAQEVHEHIR.[E]	1xTMT6plex [N-Term]	
High	[F].ATAAGGANPFKNQLLLTLSSPSEAIYVR.[	2xTMT6plex [N-Term; K11]	
High	[R].NTPIEAVLFSGDFAAHYDDSESQKR.[V]	2xTMT6plex [N-Term; K24]	
High	[S].AEYPFLEEYTFSSTYGLPCVSGPTVAR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C19]	
High	[A].SATPVQVIFVVGNNDLPR.[D]	1xTMT6plex [N-Term]	
High	[S].ATPVQVIFVVGNNDLPR.[D]	1xTMT6plex [N-Term]	
High	[T].SAEYPFLEEYTFSSTYGLPCVSGPTVAR.[	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C20]	
High	[A].ASATPVQVIFVVGNNDLPR.[D]	1xTMT6plex [N-Term]	
High	[A].ESDPAGQFAWMAR.[E]	1xTMT6plex [N-Term]	
High	[M].VVPDFGNLK.[S]	1xTMT6plex [N-Term]	
High	[G].EIANGKGTDTTPAR.[L]	2xTMT6plex [N-Term; K6]	
High	[M].SKISAGSSSPTR.[E]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SKISAGSSSPTR.[E]	2xTMT6plex [N-Term; K2]	
High	[-].MIGSEEFWKTEADAPLLNR.[N]	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ATADVQTER.[A]	1xAcetyl [N-Term]	TGME49_2
High	[M].SSWEDEADEILEAEER.[R]	1xAcetyl [N-Term]	TGME49_2
High	[G].VVNQGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K14]	
High	[G].VVNQGPVDVPFSGKPLDER.[A]	1xTMT6plex [K14]; 1xAcetyl [N-Term]	TGME49_2
High	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]	1xAcetyl [N-Term]	TGME49_2
High	[A].AEFSGVVNQGPVDVPFSGKPLDER.[A]	1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_2
High	[P].VDVPFSGKPLDER.[A]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_2
High	[P].VDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K8]	
High	[V].NQGPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K12]	
High	[D].VPFSGKPLDER.[A]	1xTMT6plex [K6]	
High	[Q].GPVDVPFSGKPLDER.[A]	2xTMT6plex [N-Term; K10]	
High	[M].ALAHASSGTVR.[D]	1xAcetyl [N-Term]	TGME49_2
High	[M].APSTTPKDASTDAQSWR.[S]	2xTMT6plex [N-Term; K7]	
High	[P].SAQPSETPEAPPEEKR.[G]	1xTMT6plex [K15]; 1xAcetyl [N-Term]	TGME49_2
High	[I].PPILVELSAEVR.[E]		
High	[M].ASLQPGDGYGGEGFHR.[F]	1xAcetyl [N-Term]	TGME49_2
High	[M].VYTFTCSDPR.[Y]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[M].GAYKYLEELWK.[K]	2xTMT6plex [N-Term; K4]	
High	[-].MKPEKVIR.[D]	3xTMT6plex [N-Term; K2; K5]	
High	[M].VSSELLWQCVR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[-].MVSSELLWQCVR.[R]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].AQKPGSSNGKTVRPSR.[F]	2xTMT6plex [K3; K10]; 1xAcetyl [N-Ter	TGME49_2
High	[A].AMPKLSGEKLAELMQMDVK.[D]	3xTMT6plex [N-Term; K4; K9]	

High	[M].SGGHDEYPPELTR.[G]	1xTMT6plex [N-Term]	
High	[M].SIAGVFQSYTQGKGDMDSR.[T]	1xTMT6plex [K13]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SSAVVDHPAAEASLCPSDASGDSLHTR.	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[I].SGEIIPKPR.[C]	2xTMT6plex [N-Term; K7]	
High	[F].STADSPNGLCLVTR.[I]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C10]	
High	[-].MDLSNEKAVGALSKHR.[A]	2xTMT6plex [K7; K14]; 1xAcetyl [N-Term	TGME49_2
High	[M].ANAAGVGCDGSSAAAEFDGGR.[V]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].SCDEVIR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2]	
High	[C].EKADAGATHEPDASSETATVTSASGAHI	2xTMT6plex [N-Term; K2]	
High	[A].GATHEPDASSETATVTSASGAHR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[A].ELKSSSEEPSQQPASAAGGTDR.[F]	2xTMT6plex [N-Term; K3]	
High	[M].GKTDAQSPSSGPAGRPESGR.[K]	2xTMT6plex [N-Term; K2]	
High	[M].SVSNCAPASKAGESAASGPAHR.[T]	1xTMT6plex [K10]; 1xAcetyl [N-Term]; 1	TGME49_2
High	[F].GAGDLKIVAAR.[M]	2xTMT6plex [N-Term; K6]	
High	[M].SQPVFASPLNVEKR.[R]	1xTMT6plex [K13]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AALSPQKVAELKAFIGMCER.[D]	2xTMT6plex [K7; K12]; 1xAcetyl [N-Term	TGME49_2
High	[-].MQVIGKDQPNGSSGQPTHSALR.[R]	1xTMT6plex [K6]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SDEVDKHVLR.[K]	1xTMT6plex [K6]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MLQLNPQFDAIGK.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[M].SIPCLFEDR.[F]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[R].ENEQCYDPQHSR.[R]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[M].ASKTTSEELK.[T]	1xTMT6plex [K3]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AQEEAEDVKMDR.[R]	2xTMT6plex [N-Term; K9]	
High	[M].AQEEAEDVK.[M]	1xTMT6plex [N-Term]	
High	[M].ANATTDHLRPQDLETLDISKLTPLSPDV	1xTMT6plex [K20]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ANATTDHLRPQDLETLDISK.[L]	1xAcetyl [N-Term]	TGME49_2
High	[G].TPLQAFNSASFPR.[C]	1xTMT6plex [N-Term]	
High	[M].SGYGLPISQEVAKELAENAR.[K]	1xTMT6plex [K13]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SGYGLPISQEVAK.[E]	1xAcetyl [N-Term]	TGME49_2
High	[P].YHGTAECSEVNSSFSSR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C7]	
High	[Y].HGTAECSEVNSSFSSR.[E]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C6]	
High	[G].FFSAAPAAATAGVSPLAR.[S]	1xTMT6plex [N-Term]	
High	[G].SGGYGGGGGYSPAGPHHGSMDTANW	1xTMT6plex [N-Term]	
High	[-].MKAKMSHEALTETAR.[K]	2xTMT6plex [K2; K4]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SHEALTETAR.[K]	1xAcetyl [N-Term]	TGME49_2
High	[-].MNVLAYGTAEQR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[C].SAANDMDVAVSDGGHESAGLVEDIAQ	1xTMT6plex [K29]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MDQAATSAAASQR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[A].VLFEVPGSGR.[E]	1xTMT6plex [N-Term]	
High	[P].DQAQAAVSDKESESR.[V]	2xTMT6plex [N-Term; K10]	
High	[P].DQAQAAVSDKESESR.[V]	1xTMT6plex [N-Term]	
High	[G].APDQAQAAVSDKESESR.[V]	2xTMT6plex [N-Term; K12]	
High	[G].APDQAQAAVSDKESESR.[V]	1xTMT6plex [N-Term]	
High	[D].QAQAAVSDKESESR.[V]	1xTMT6plex [K9]	
High	[K].ASSSFKKAR.[V]	3xTMT6plex [N-Term; K6; K7]	
High	[M].SGIAVGLKR.[G]	2xTMT6plex [N-Term; K8]	
High	[M].SEAADGGPEPGKVR.[A]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].GQHGAESAPLSHAGISCR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C17]	
High	[M].GQHGAESAPLSHAGISCR.[V]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[K].FTVDCQKPVDDNIIEAKGLER.[F]	3xTMT6plex [N-Term; K7; K17]; 1xCarbamidomethy	
High	[Q].SGATFEDVTDECLTLHNKFR.[T]	2xTMT6plex [N-Term; K18]; 1xCarbamidomethyl [C	
High	[L].DSLIPGFLKR.[R]	2xTMT6plex [N-Term; K9]	

High	[M].ANNGELASFFR.[K]	1xAcetyl [N-Term]	TGME49_2
High	[M].ANIDSTAANTNR.[M]	1xAcetyl [N-Term]	TGME49_2
High	[C].FQLPAPNAFLGHSLLR.[S]	1xTMT6plex [N-Term]	
High	[M].APTIVDAPLIQLLADGYGQYR.[Q]	1xTMT6plex [N-Term]	
High	[I].MEHDQEKLLDEASAVVKEQAR.[Y]	2xTMT6plex [K7; K17]; 1xAcetyl [N-Ter	TGME49_2
High	[-].MIMEHDQEKLLDEASAVVKEQAR.[Y]	2xTMT6plex [K9; K19]; 1xAcetyl [N-Ter	TGME49_2
High	[R].MLAAAADANALSAAATKSR.[A]	1xTMT6plex [K17]; 1xAcetyl [N-Term]	TGME49_2
High	[M].GVYPPVAGGPVYWALR.[N]	1xTMT6plex [N-Term]	
High	[-].MESASPAGSGQAPGVAKSFHDGPR.[E]	1xTMT6plex [K17]; 1xAcetyl [N-Term]	TGME49_2
High	[M].STCACSCACCKQR.[D]	1xTMT6plex [K11]; 1xAcetyl [N-Term]; 5	TGME49_2
High	[-].MISEGGVPDVLQR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[M].AAFVVDGLAALSR.[F]	1xAcetyl [N-Term]	TGME49_2
High	[M].ASFCSSSCTSGPVGR.[E]	1xAcetyl [N-Term]; 2xCarbamidomethyl	TGME49_2
High	[F].TEFDIQQPPSDNSWLCR.[F]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C16]	
High	[A].TETDAAEPLTAEEAPR.[S]	1xTMT6plex [N-Term]	
High	[-].MEDSGVSAAASSCVAR.[S]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[-].MLNFIPKR.[C]	2xTMT6plex [N-Term; K7]	
High	[M].AAAKGSNALIQQLLEAEEEADTIVNK.[	1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_2
High	[A].AGNVEAALSHVDSHR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[A].EAAGNVEAALSHVDSHR.[S]	1xTMT6plex [N-Term]	
High	[C].SDGVFSVQSPSAPQHDILWDAR.[K]	1xAcetyl [N-Term]	TGME49_2
High	[-].MLEAKLQHASVLR.[R]	1xTMT6plex [K5]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MLEAKLQHASVLR.[R]	2xTMT6plex [N-Term; K5]	
High	[M].AASGHPIPELGEFIIANKEKLR.[N]	2xTMT6plex [K18; K20]; 1xAcetyl [N-Ter	TGME49_2
High	[M].AASGHPIPELGEFIIANK.[E]	1xAcetyl [N-Term]	TGME49_2
High	[M].AASGHPIPELGEFIIANKEK.[L]	1xTMT6plex [K]; 1xAcetyl [N-Term]	TGME49_2
High	[A].SDQKQGSQNPAGGKGGSGPHGGR.[R]	2xTMT6plex [K4; K14]; 1xAcetyl [N-Ter	TGME49_2
High	[F].VTASDQKQGSQNPAGGKGGSGPHGG	1xTMT6plex [K17]	
High	[Q].GGGPPARPPSPSPEEEPIFGTFVKTDSG	2xTMT6plex [N-Term; K24]	
High	[M].AAKHHPDLIMCR.[K]	1xTMT6plex [K3]; 1xAcetyl [N-Term]; 1x	TGME49_2
High	[M].AAAAAQAVPEFK.[L]	1xAcetyl [N-Term]	TGME49_2
High	[M].AAAAAQAVPEFKLILVGDGGVGK.[T]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AAAAAQAVPEFKLILVGDGGVGKTTLV	2xTMT6plex [K12; K23]; 1xAcetyl [N-Ter	TGME49_2
High	[M].SQEQLTEAMR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[-].MKFSSQVSSSR.[R]	2xTMT6plex [N-Term; K2]	
High	[-].MEPCTVTVTDFTGGR.[Q]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].TVATLFPKEEGVGFSLTTQSHGECKVR.	3xTMT6plex [N-Term; K8; K25]; 1xCarbamidomethy	
High	[M].TVATLFPK.[E]	1xTMT6plex [N-Term]	
High	[-].MELNTFR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[T].EPVPAHFDAR.[T]	1xTMT6plex [N-Term]	
High	[A].TEPVPAHFDAR.[T]	1xTMT6plex [N-Term]	
High	[M].AAASTASPPANR.[D]	1xAcetyl [N-Term]	TGME49_2
High	[H].DFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[G].EHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[S].IGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[Q].ASIGEHDFFNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[F].FNDYDQDEEYR.[K]	1xTMT6plex [N-Term]	
High	[M].APGVTQAEFQR.[E]	1xTMT6plex [N-Term]	
High	[A].SESDVALKVPEDPVPEEPR.[R]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_2
High	[A].SESDVALKVPEDPVPEEPR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[A].SESDVALKVPEDPVPEEPRR.[E]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_2
High	[M].TIDVNLLR.[A]	1xTMT6plex [N-Term]	

High	[R].AADSAAGVGAAQSAFPIDLR.[G]	1xTMT6plex [N-Term]	
High	[G].VAWGPNPIDGSKHGQFPSLR.[R]	2xTMT6plex [N-Term; K12]	
High	[G].VAWGPNPIDGSKHGQFPSLR.[R]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[G].SKHGQFPSLR.[R]	2xTMT6plex [N-Term; K2]	
High	[G].SKHGQFPSLR.[R]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[P].NPIDGSKHGQFPSLR.[R]	2xTMT6plex [N-Term; K7]	
High	[M].AKLSAAVPTASPAEGGGFLLVNPR.[C]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_2
High	[S].AQKGAVHQEPLR.[G]	2xTMT6plex [N-Term; K3]	
High	[A].AAGPTPVGKGTPGGAKGQFR.[G]	3xTMT6plex [N-Term; K9; K16]	
High	[G].AAAGPTPVGKGTPGGAKGQFR.[G]	3xTMT6plex [N-Term; K10; K17]	
High	[M].AADFPHSLDLR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[T].DDAIRPIFVYIGGEGPLSSLEVR.[Q]	1xTMT6plex [N-Term]	
High	[Q].EGWFLQPLDHGNPLVFNR.[L]	1xTMT6plex [N-Term]	
High	[G].ADSATDHPTCSAADKPVIVSITEPR.[A]	1xTMT6plex [K15]; 1xAcetyl [N-Term]; 1	TGME49_2
High	[M].ASSKPGGASKAGVDAVQEISMMAR.[E	2xTMT6plex [K4; K10]; 1xAcetyl [N-Tern	TGME49_2
High	[-].MDSDIPADKMQEMETQLAMLLEGQR.[	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SGLEKSGFGIAHDFKGR.[T]	2xTMT6plex [K5; K15]; 1xAcetyl [N-Tern	TGME49_2
High	[T].SDPLDFHWPGSR.[I]	1xTMT6plex [N-Term]	
High	[S].TSGNPFQANVEMKTFMER.[F]	2xTMT6plex [N-Term; K13]	
High	[-].MEEAAFSMVR.[H]	1xAcetyl [N-Term]	TGME49_2
High	[-].MFWCCCGSER.[D]	1xAcetyl [N-Term]; 3xCarbamidomethyl	TGME49_2
High	[A].AAAPQASASGKTAKDASPSTANLQPR.[	2xTMT6plex [K11; K14]; 1xAcetyl [N-Ter	TGME49_2
High	[M].VSLSGTLNGEEALER.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[-].MNVFEQYNQR.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[M].VLADNNVFLEELGR.[L]	1xTMT6plex [N-Term]	
High	[M].ASKQPQTLSAGAVESGR.[V]	1xTMT6plex [K3]; 1xAcetyl [N-Term]	TGME49_2
High	[R].SEEDWTAHR.[T]	1xTMT6plex [N-Term]	
High	[S].EEDWTAHR.[T]	1xTMT6plex [N-Term]	
High	[A].SLLASPASAFFR.[L]	1xTMT6plex [N-Term]	
High	[K].MEEELTPEILAAR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[T].MEEKVKTVTFTDPPHDK.[V]	2xTMT6plex [K4; K6]; 1xAcetyl [N-Term]	TGME49_2
High	[-].MESTEATMVER.[K]	1xAcetyl [N-Term]	TGME49_2
High	[M].AATNTIESGTTR.[C]	1xAcetyl [N-Term]	TGME49_2
High	[M].PHAGFTDDILLLDGGLGTHLR.[A]	1xTMT6plex [N-Term]	
High	[-].MDADSWTTLVKKAFLAGQEVCR.[E]	2xTMT6plex [K11; K12]; 1xAcetyl [N-Ter	TGME49_2
High	[M].TDNAQTTSAEAGAANPSGEHPSAGAK	2xTMT6plex [N-Term; K26]	
High	[M].TDNAQTTSAEAGAANPSGEHPSAGAK	1xTMT6plex [K26]; 1xAcetyl [N-Term]	TGME49_2
High	[A].AKQNLYSVLGVKR.[N]	3xTMT6plex [N-Term; K2; K12]	
High	[-].MIEVILNDR.[L]	1xTMT6plex [N-Term]	
High	[M].VDTNASKQPAATADR.[K]	2xTMT6plex [N-Term; K7]	
High	[R].GMDDGAFVR.[G]	1xTMT6plex [N-Term]	
High	[-].MELSFFNVDDGYLEGICR.[G]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[A].PSASHPPGACPPGCTK.[H]	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C10; C	
High	[P].SASHPPGACPPGCTKHPATATAISPSGV	2xTMT6plex [N-Term; K15]; 3xCarbamidomethyl [C	
High	[P].SASHPPGACPPGCTKHPATATAISPSGV	1xTMT6plex [K15]; 1xAcetyl [N-Term]; 3	TGME49_2
High	[A].PSASHPPGACPPGCTKHPATATAISPSG	2xTMT6plex [N-Term; K16]; 3xCarbamidomethyl [C	
High	[M].APSASHPPGACPPGCTKHPATATAISP	2xTMT6plex [N-Term; K17]; 3xCarbamidomethyl [C	
High	[M].APSASHPPGACPPGCTKHPATATAISP	2xTMT6plex [N-Term; K17]; 3xCarbamidomethyl [C	
High	[A].PSASHPPGACPPGCTKHPATATAISPSG	2xTMT6plex [N-Term; K16]; 3xCarbamidomethyl [C	
High	[G].ACPPGCTKHPATATAISPSGVCPMR.[A	2xTMT6plex [N-Term; K8]; 3xCarbamidomethyl [C2	
High	[M].APSASHPPGACPPGCTK.[H]	1xTMT6plex [N-Term]; 2xCarbamidomethyl [C11; C	
High	[A].LTANEMMEDITWRPR.[V]	1xTMT6plex [N-Term]	

High	[A].FHPAGPHSHFSCYDDLR.[N]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C12]	
High	[P].SASHPPGACPPGCTKHPATATAISPSGV	2xTMT6plex [N-Term; K15]; 3xCarbamidomethyl [C	
High	[S].SEGGVWEFLSGVCGR.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C13]	
High	[M].TANSHFLQKMR.[E]	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[M].TANSHFLQKMR.[E]	2xTMT6plex [N-Term; K9]	
High	[S].AAGGAYYWAR.[D]	1xTMT6plex [N-Term]	
High	[M].VVVVDGELLPDSDPR.[A]	1xTMT6plex [N-Term]	
High	[M].AFAGAAAPLGVKGR.[S]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[S].EETDIVGGR.[I]	1xTMT6plex [N-Term]	
High	[-].MNAFQSPSLDITISR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[-].MHQVSLVPSR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[-].MFYGVVVKPGQTVTLSPEDGGEVLHLS	2xTMT6plex [K8; K35]; 1xAcetyl [N-Ter	TGME49_2
High	[-].MEPSQMQEHHPPPGPVAAEEALR.[C]	1xAcetyl [N-Term]	TGME49_2
High	[M].SALAGPLRPPCATEGEDGPSSGLQTYY	1xTMT6plex [K30]; 1xAcetyl [N-Term]; 1	TGME49_2
High	[A].SGAAAFTSEGENHEAQHLSSDLFPPYKK	2xTMT6plex [K27; K28]; 1xAcetyl [N-Ter	TGME49_2
High	[R].DGEGEGSEKGPQPSPSGKPLQR.[R]	2xTMT6plex [K9; K18]	
High	[S].SAAPNPGKKPASAAPPAGTNHGR.[I]	3xTMT6plex [N-Term; K8; K9]	
High	[S].AAPNPGKKPASAAPPAGTNHGR.[I]	3xTMT6plex [N-Term; K7; K8]	
High	[M].SEVEETLNR.[I]	1xAcetyl [N-Term]	TGME49_2
High	[M].PADEQQQQLPR.[E]	1xTMT6plex [N-Term]	
High	[-].MKADPTLQQKISQYQVVGR.[K]	3xTMT6plex [N-Term; K2; K10]	
High	[M].VKLLKSGR.[V]	3xTMT6plex [N-Term; K2; K5]	
High	[M].AEEIKNLR.[D]	1xTMT6plex [K5]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AAKPEQDCKTAAALIR.[A]	2xTMT6plex [K3; K9]; 1xAcetyl [N-Term]	TGME49_2
High	[L].HPWLPEKPLLIGHR.[G]	2xTMT6plex [N-Term; K7]	
High	[R].ANLHPWLPEKPLLIGHR.[G]	2xTMT6plex [N-Term; K10]	
High	[N].LHPWLPEKPLLIGHR.[G]	2xTMT6plex [N-Term; K8]	
High	[M].AANAASKFIPLLDR.[V]	1xTMT6plex [K7]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AKDAAAGEEKK.[R]	3xTMT6plex [N-Term; K2; K10]	
High	[M].SYNPSYGGQFQGLNAAR.[G]	1xAcetyl [N-Term]	TGME49_2
High	[F].AADEASSDDRPLLER.[V]	1xTMT6plex [N-Term]	
High	[M].AASSPENSAGAAGTQR.[Q]	1xTMT6plex [N-Term]	
High	[M].ADILQENFQDLVHSPGGGR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[M].AVNPVLAQDASTKETFPLPVPGEVFFL	2xTMT6plex [K13; K28]; 1xAcetyl [N-Ter	TGME49_2
High	[-].MDAVMVVHQLQR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[L].STASAGPSNAAPESGGVSEGDSSR.[G]	1xTMT6plex [N-Term]	
High	[M].AADKQAKLSLQEDSIAK.[M]	2xTMT6plex [K4; K7]; 1xAcetyl [N-Term]	TGME49_2
High	[M].PQTNIPSWHFANEKGR.[F]	2xTMT6plex [N-Term; K14]	
High	[M].APVSTVKR.[S]	2xTMT6plex [N-Term; K7]	
High	[-].MEELIPVVNR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[M].CYEVKCTHCGKR.[T]	3xTMT6plex [N-Term; K5; K11]; 3xCarbamidomethy	
High	[A].AANTPGFSLKGDDYTDR.[A]	2xTMT6plex [N-Term; K10]	
High	[C].SIWRPQGTPEVGSLGHDAADTAAAEA	1xAcetyl [N-Term]	TGME49_2
High	[M].VAIKDITAR.[Q]	2xTMT6plex [N-Term; K4]	
High	[M].VVIKDIVAR.[E]	2xTMT6plex [N-Term; K4]	
High	[-].MVVIKDIVAR.[E]	1xTMT6plex [K5]; 1xAcetyl [N-Term]	TGME49_2
High	[F].GLLGSSSEKASAPIR.[L]	2xTMT6plex [N-Term; K9]	
High	[F].GLLGSSSEK.[A]	1xTMT6plex [N-Term]	
High	[Q].YALNEEDILHAR.[D]	1xTMT6plex [N-Term]	
High	[M].AAAPLGSATAAGSDAAGTPDVGPGAE	1xAcetyl [N-Term]	TGME49_2
High	[G].APANLSPAAHR.[A]	1xTMT6plex [N-Term]	
High	[M].CDITFVSR.[A]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2

High	[P].ELPEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[E].LPEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[Q].RVPELPEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[E].VESFDEVGTGAR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[D].IHPDQVVYILR.[V]	1xTMT6plex [N-Term]	
High	[R].VPELPEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[P].EVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[I].HPDQVVYILR.[V]	1xTMT6plex [N-Term]	
High	[Q].RVPELPEVESFDEVGTGAR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[L].PEVESFDEVGTGAR.[R]	1xTMT6plex [N-Term]	
High	[A].AEGGDNQSSAVSDR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[A].GESAADLSTSIDDDDFDSSSGVAVPSLT	1xAcetyl [N-Term]	TGME49_2
High	[M].ATGCSLLIR.[N]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[M].TTAHRPTWHQALGGEHQGGNR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[N].MDEKIVALNPNR.[D]	1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AGMCTDLVSLVSQHIR.[A]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[-].MENPPQIPVYR.[T]	1xAcetyl [N-Term]	TGME49_2
High	[M].AQVLQTLVDQK.[V]	1xAcetyl [N-Term]	TGME49_2
High	[M].AQVLQTLVDQKVEIVTVDGR.[V]	1xTMT6plex [K11]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SGEGQVADAGSLPVEKR.[E]	1xTMT6plex [K16]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ADSPAVGIDLGTTYSCVGVWKNDAVE	1xTMT6plex [K21]; 1xAcetyl [N-Term]; 1	TGME49_2
High	[M].ANSGINWPGLYR.[W]	1xAcetyl [N-Term]	TGME49_2
High	[-].MLWVDKHAPR.[E]	2xTMT6plex [N-Term; K6]	
High	[R].SASNFSFEGEDIR.[G]	1xTMT6plex [N-Term]	
High	[R].SASNFSFEGEDIRGPIKPLR.[G]	2xTMT6plex [N-Term; K17]	
High	[G].ESTGEAVTAVATR.[E]	1xTMT6plex [N-Term]	
High	[S].LGGVAVAADSGGVR.[Q]	1xTMT6plex [N-Term]	
High	[S].LGGVAVAADSGGVR.[Q]	1xAcetyl [N-Term]	TGME49_2
High	[R].GEGGEDDRRPLHPGSVNEFDF.[-]		
High	[S].SVQEPQAKVPSKR.[T]	3xTMT6plex [N-Term; K8; K12]	
High	[M].TVPGMKFSLIPKANR.[K]	3xTMT6plex [N-Term; K6; K12]	
High	[M].ATEHSHAEQSKGLMER.[A]	1xTMT6plex [K11]; 1xAcetyl [N-Term]	TGME49_2
High	[S].AAPDFTVTIPKEGLPADR.[Q]	2xTMT6plex [N-Term; K11]	
High	[A].APDFTVTIPKEGLPADR.[Q]	2xTMT6plex [N-Term; K10]	
High	[S].DAVSTQTYGDAYAFVNGKCDFR.[E]	2xTMT6plex [N-Term; K18]; 1xCarbamidomethyl [C	
High	[T].SAAPDFTVTIPKEGLPADR.[Q]	2xTMT6plex [N-Term; K12]	
High	[S].TQTYGDAYAFVNGKCDFR.[E]	2xTMT6plex [N-Term; K14]; 1xCarbamidomethyl [C	
High	[R].DSEVAATGPGEHLHVEQDRR.[K]		
High	[T].QTYGDAYAFVNGKCDFR.[E]	2xTMT6plex [N-Term; K13]; 1xCarbamidomethyl [C	
High	[G].LTSAAPDFTVTIPKEGLPADR.[Q]	2xTMT6plex [N-Term; K14]	
High	[A].SETNHLTPEADFTATIPKSGLER.[N]	1xTMT6plex [K18]; 1xAcetyl [N-Term]	TGME49_2
High	[M].SFQDWTPVSWNKTGQR.[Q]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[M].VLPLTLLR.[A]	1xTMT6plex [N-Term]	
High	[M].SSLSVAAASPLAAAKSQWDAR.[L]	1xTMT6plex [K15]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ADATGSEVETEVVQDLSNPDVVTKYR.	1xTMT6plex [K24]; 1xAcetyl [N-Term]	TGME49_2
High	[M].AETLASEAHVAEWADR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[M].SHTILLVQFSDR.[K]	1xAcetyl [N-Term]	TGME49_2
High	[-].MEAAEAEAIALQIQR.[D]	1xAcetyl [N-Term]	TGME49_2
High	[G].TPATSNTCVLAEPGADLSVENHTR.[V]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[F].SGGAAKPSWHVAR.[E]	2xTMT6plex [N-Term; K6]	
High	[M].APTQLEQCASHGKLLQEKK.[K]	3xTMT6plex [N-Term; K13; K18]; 1xCarbamidometh	
High	[M].APTQLEQCASHGK.[L]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	

High	[M].APTQLEQCASHGKLLQEK.[K]	2xTMT6plex [N-Term; K]; 1xCarbamidomethyl [C8]	
High	[G].AFDGNREDLDDFLHR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[F].STAAAEDSGASQTLEGR.[Y]	1xTMT6plex [N-Term]	
High	[S].SAAGPTEHVIKVPSLGDSITEGGLLEWR.	2xTMT6plex [N-Term; K11]	
High	[A].IAGADPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K8]; 1xCarbamidomethyl [C9	
High	[D].PEKCDQDGSLLNLR.[V]	1xTMT6plex [K3]; 1xCarbamidomethyl [C4]	
High	[G].ADPEKCDQDGSLLNLR.[V]	2xTMT6plex [N-Term; K5]; 1xCarbamidomethyl [C6	
High	[M].SLDIQNFGVSDPFANDTSQAGGAGGS	1xAcetyl [N-Term]	TGME49_2
High	[M].VAAGVSHGNR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[M].VAAGVSHGNR.[S]	1xTMT6plex [N-Term]	
High	[R].DDAEDDPFVASDVASVLKYLR.[D]	1xTMT6plex [K18]	
High	[K].AASALGSR.[S]	1xTMT6plex [N-Term]	
High	[-].MFALQDAEQLQLQR.[M]	1xAcetyl [N-Term]	TGME49_2
High	[R].QSVASSPFLEALR.[K]		
High	[RWQ].ELISNASDALDKIR.[LY]	1xTMT6plex [K12]	
High	[A].AAPTATAADTKPASATPLQKPGSSTGG	3xTMT6plex [N-Term; K11; K20]	
High	[R].GVPDAKIR.[I]	2xTMT6plex [N-Term; K6]	
High	[M].AAAAPAVGGGIR.[V]	1xAcetyl [N-Term]	TGME49_2
High	[M].TGSSPKSAASSTPLR.[L]	2xTMT6plex [N-Term; K6]	
High	[A].VTPPAVSPQTSLWISSGLVGGSDKAVR.	2xTMT6plex [N-Term; K24]	
High	[M].VCKLGINGFGR.[I]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C2	
High	[A].FQAVIELAPGQKR.[C]	2xTMT6plex [N-Term; K12]	
High	[S].ASLVGEQWNASESVPGTVDR.[E]	1xAcetyl [N-Term]	TGME49_2
High	[Q].NKPSTNVSVDR.[Q]	2xTMT6plex [N-Term; K2]	
High	[R].HRPAEVGSVTPAIAAAKKSTANR.[L]	3xTMT6plex [N-Term; K17; K18]	
High	[A].AAPAAEAAKTLER.[N]	2xTMT6plex [N-Term; K9]	
High	[N].AAAPAAEAAKTLER.[N]	2xTMT6plex [N-Term; K10]	
High	[M].PGVHGPQCGCVHEIDLKGAQFLLPYIN	2xTMT6plex [N-Term; K17]; 2xCarbamidomethyl [C	
High	[-].MEEKTTTAPPESFR.[V]	1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_2
High	[M].ATNLEIDSADVIR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[A].YVPGIAPTDYTR.[G]	1xTMT6plex [N-Term]	
High	[M].AQQFPIQLHSVVNLADQGVSASSFR.[	1xAcetyl [N-Term]	TGME49_2
High	[M].THADVSACPAR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C8]	
High	[-].MLEALVER.[L]	1xTMT6plex [N-Term]	
High	[-].MMASTSAQEDLVSAPFSSR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[M].TQSMLDMSLDDIVAAHR.[E]	1xTMT6plex [N-Term]	
High	[K].DSQYNWLLCPVPTDNMFR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[K].DSQYNWLLCPVPTDNMFR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]; 1x	
High	[-].MDVHEHEAATGCR.[F]	1xAcetyl [N-Term]; 1xCarbamidomethyl	TGME49_2
High	[A].TGQSIVLSCTR.[S]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C9]	
High	[K].GQKEQANTTATLPTCR.[V]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C1	
High	[K].GQKEQANTTATLPTCR.[V]	1xTMT6plex [K3]; 1xAcetyl [N-Term]; 1x	TGME49_2
High	[M].PAKEIVFHCEYAPSGR.[A]	2xTMT6plex [N-Term; K3]; 1xCarbamidomethyl [C9	
High	[M].ALAAASSASASSDQKR.[E]	1xTMT6plex [K15]; 1xAcetyl [N-Term]	TGME49_2
High	[R].SSTETCGVKGRPR.[V]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [C6	
High	[R].SSTETCGVKGR.[P]	2xTMT6plex [N-Term; K9]; 1xCarbamidomethyl [C6	
High	[M].VDVDGELVKVEETR.[R]	1xTMT6plex [K9]; 1xAcetyl [N-Term]	TGME49_2
High	[M].PVHHVTTEAQFK.[S]	1xTMT6plex [N-Term]	
High	[-].MLGGASGLGAAPTR.[A]	1xAcetyl [N-Term]	TGME49_2
High	[W].LEQEGVELR.[S]	1xAcetyl [N-Term]	TGME49_2
High	[M].AKAKYTLVLIR.[H]	2xTMT6plex [K2; K4]; 1xAcetyl [N-Term]	TGME49_2
High	[L].SSSQPLTAPSTPTKASR.[S]	2xTMT6plex [N-Term; K14]	

High	[M].ALLFDPSDMPPTGR.[L]	1xAcetyl [N-Term]	TGME49_2
High	[M].SHLLNAPIILLKDGVDTSQGR.[G]	1xTMT6plex [K12]; 1xAcetyl [N-Term]	TGME49_2
High	[A].HGPSDSPATKQPQVQR.[K]	2xTMT6plex [N-Term; K10]	
High	[N].MLGTSSAVAAALLEGGR.[R]	1xAcetyl [N-Term]	TGME49_2
High	[M].VKYAKEPSNENK.[C]	3xTMT6plex [N-Term; K2; K5]	
High	[M].AGSTISNHQVSSNR.[K]	1xAcetyl [N-Term]	TGME49_3
High	[-].MKLLTPKDDVR.[G]	3xTMT6plex [N-Term; K2; K7]	
High	[-].MDSAAVWSDESEDVATAELAGLSASDL	1xAcetyl [N-Term]	TGME49_3
High	[M].ASTQVASLHAQPLLR.[R]	1xAcetyl [N-Term]	TGME49_3
High	[A].VPDKFLEGLQTR.[S]	2xTMT6plex [N-Term; K4]	
High	[A].TVAAPQVETGPLLSVR.[A]	1xAcetyl [N-Term]	TGME49_3
High	[A].TVAAPQVETGPLLSVR.[A]	1xTMT6plex [N-Term]	
High	[-].METSLSAASASPGSHFEQTLQGDLAAIQ	1xAcetyl [N-Term]	TGME49_3
High	[M].AVAKLDGKTLPALR.[L]	2xTMT6plex [K4; K8]; 1xAcetyl [N-Term]	TGME49_3
High	[-].MDDLVALQR.[Q]	1xAcetyl [N-Term]	TGME49_3
High	[M].AATEQKRPQETSISR.[E]	1xTMT6plex [K6]; 1xAcetyl [N-Term]	TGME49_3
High	[G].HCPPTLAFVPR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C2]	
High	[L].GHCPPTLAFVPR.[D]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C3]	
High	[VM].AAGPLSER.[AN]	1xAcetyl [N-Term]	TGME49_3
High	[-].MKLAHHIYR.[D]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_3
High	[M].PKYYCEYCDIYLTHSSPAGR.[R]	2xTMT6plex [N-Term; K2]; 2xCarbamidomethyl [C5	
High	[S].AAPAAAPKSR.[E]	2xTMT6plex [N-Term; K8]	
High	[G].TTICGVVCKDGVVLGADTR.[A]	2xTMT6plex [N-Term; K9]; 2xCarbamidomethyl [C4	
High	[-].MWSIFAPEALTSTSEPATKPAGGATR.[	1xTMT6plex [K19]; 1xAcetyl [N-Term]	TGME49_3
High	[G].SKQGQYDTVIR.[N]	2xTMT6plex [N-Term; K2]	
High	[M].AISSALIQQR.[V]	1xAcetyl [N-Term]	TGME49_3
High	[G].SVDNGGLDDPNASR.[M]	1xAcetyl [N-Term]	TGME49_3
High	[G].LVGKQESGCHISLR.[Q]	2xTMT6plex [N-Term; K4]; 1xCarbamidomethyl [C9	
High	[F].ATVGVGDIR.[Q]	1xTMT6plex [N-Term]	
High	[A].INSTEPAPYEDAFEVLGR.[T]	1xTMT6plex [N-Term]	
High	[A].INSTEPAPYEDAFEVLGR.[T]	1xAcetyl [N-Term]	TGME49_3
High	[T].MLVLGSTFPDVHADASGVPGDK.[I]	1xAcetyl [N-Term]	TGME49_3
High	[T].MLVLGSTFPDVHADASGVPGDK.[I]	1xTMT6plex [N-Term]	
High	[T].MLVLGSTFPDVHADASGVPGDKIK.[L]	1xTMT6plex [K]; 1xAcetyl [N-Term]	TGME49_3
High	[T].MLVLGSTFPDVHADASGVPGDKIK.[L]	2xTMT6plex [N-Term; K]	
High	[-].MDTKSENSIATGVGPTPVGR.[V]	1xTMT6plex [K4]; 1xAcetyl [N-Term]	TGME49_3
High	[E].RDDGTQSKEDEAEGGTQR.[G]	2xTMT6plex [N-Term; K8]	
High	[G].ERDDGTQSKEDEAEGGTQR.[G]	2xTMT6plex [N-Term; K9]	
High	[F].LNLHEYQSMR.[I]	1xTMT6plex [N-Term]	
High	[F].LNLHEYQSMR.[I]	1xTMT6plex [N-Term]; 1xOxidation [M9]	
High	[S].TIFGGASLKGR.[N]	2xTMT6plex [N-Term; K9]	
High	[M].VKKGEENPMR.[K]	3xTMT6plex [N-Term; K2; K3]	
High	[M].AKTGAEQLELHGDTWR.[V]	1xTMT6plex [K2]; 1xAcetyl [N-Term]	TGME49_3
High	[-].MYHIPVAAPLGVYGTPAVPVPYSPAPYG	1xAcetyl [N-Term]	TGME49_3
High	[E].MEGMMEAPAR.[F]	1xAcetyl [N-Term]	TGME49_3
High	[M].ALQYAYPVDSPRPGESAIWR.[C]	1xAcetyl [N-Term]	TGME49_3
High	[M].SELKGKNIFLTPDGR.[T]	2xTMT6plex [K4; K6]; 1xAcetyl [N-Term]	TGME49_3
High	[M].ANAADENVFANDSSYHWEMR.[R]	1xAcetyl [N-Term]	TGME49_3
High	[G].SYLADMAGLTGR.[E]	1xAcetyl [N-Term]	TGME49_3
High	[C].SFGSYLADMAGLTGR.[E]	1xAcetyl [N-Term]	TGME49_3
High	[C].SFGSYLADMAGLTGR.[E]	1xTMT6plex [N-Term]	
High	[A].METSESLAAALAEADDPLSPAAVKEACF	1xTMT6plex [K24]; 1xAcetyl [N-Term]; 1	TGME49_3

High	[M].SLDDVVHKKFTFVFVPADINDPVEER.[	2xTMT6plex [K8; K9]; 1xAcetyl [N-Term]	TGME49_3
High	[M].ALVAANAAGAALSVAPADAPSALAQN	1xAcetyl [N-Term]	TGME49_3
High	[-].MEPLADPLHDR.[V]	1xAcetyl [N-Term]	TGME49_3
High	[M].ALSDLYCLAYAPIQSTCLDSIGDEDCSPE	1xTMT6plex [K33]; 1xAcetyl [N-Term]; 3	TGME49_3
High	[A].SDAEEGKVKDVVIGIDLGTTYSCVGVYR.	3xTMT6plex [N-Term; K7; K9]; 1xCarbamidomethyl	
High	[A].SDAEEGKVK.[D]	2xTMT6plex [N-Term; K7]	
High	[SN].GDTHLGGEDFDQR.[V]	1xTMT6plex [N-Term]	
High	[M].AEGEGVSGEAATSQDTR.[A]	1xTMT6plex [N-Term]	
High	[F].TEGTNETNPPTSRPPGWKYEGSDLQR.[	1xTMT6plex [K18]; 1xAcetyl [N-Term]	TGME49_3
High	[M].AQVPASGKLLVDPR.[Y]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_3
High	[M].GDLDFDEVEKLLDSR.[D]	1xTMT6plex [K10]; 1xAcetyl [N-Term]	TGME49_3
High	[M].ASPTSASSKAPGTESEACGHR.[H]	1xTMT6plex [K9]; 1xAcetyl [N-Term]; 1x	TGME49_3
High	[M].VLAELGEQISGALR.[R]	1xTMT6plex [N-Term]	
High	[M].APTAAALAKKR.[L]	3xTMT6plex [N-Term; K9; K10]	
High	[M].ANEDGETAASKMTYLSPIASPLLDGKSL	2xTMT6plex [K11; K26]; 1xAcetyl [N-Ter	TGME49_3
High	[-].MDAYNGSAVVAMAGKDCVGIASDTR.[	1xTMT6plex [K15]; 1xAcetyl [N-Term]; 1	TGME49_3
High	[R].GPKFTLQDMKK.[A]	3xTMT6plex [N-Term; K3; K10]	
High	[N].VGGSAIDFTVACR.[T]	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C12]	
High	[M].AGTSIFQGSSWAR.[I]	1xAcetyl [N-Term]	TGME49_3
High	[M].AAIAAGAASQAPR.[S]	1xAcetyl [N-Term]	TGME49_3
High	[A].EGQTSTTLACAEDAQHSKISCTCTPGTV	3xTMT6plex [N-Term; K18; K30]; 3xCarbamidometh	
High	[M].SELSTPSDLLR.[Y]	1xAcetyl [N-Term]	TGME49_3
High	[M].SNVVRPIKLQEQHLR.[L]	1xTMT6plex [K8]; 1xAcetyl [N-Term]	TGME49_3
High	[M].GKLVVPSDISLLEEKQTVGR.[R]	2xTMT6plex [K2; K15]; 1xAcetyl [N-Term	TGME49_3
High	[M].GKLVVPSDISLLEEKQTVGR.[R]	3xTMT6plex [N-Term; K2; K15]	
High	[F].STNACAFTLPPLPYAEDALAPHISAETLR.	1xTMT6plex [N-Term]; 1xCarbamidomethyl [C5]	
High	[A].FTLPPLPYAEDALAPHISAETLR.[F]	1xTMT6plex [N-Term]	
High	[M].AAFSAALAATR.[S]	1xAcetyl [N-Term]	TGME49_3
High	[-].MEQASEERPHFEHIANPGSLFGCHPQSA	1xTMT6plex [K37]; 1xAcetyl [N-Term]; 2	TGME49_3
High	[F].AHDAGSLFSFR.[S]	1xTMT6plex [N-Term]	
High	[-].MLANKLGIQDVGAQLTGKSVLIR.[V]	2xTMT6plex [K5; K18]; 1xAcetyl [N-Term	TGME49_3
High	[-].MLANKLGIQDVGAQLTGK.[S]	1xTMT6plex [K5]; 1xAcetyl [N-Term]	TGME49_3
High	[M].VSIVNAKADVLR.[S]	1xTMT6plex [K7]; 1xAcetyl [N-Term]	TGME49_3
High	[M].AFDASSLDLLIR.[E]	1xAcetyl [N-Term]	TGME49_3
High	[M].ATEQIYKQFTSR.[T]	1xTMT6plex [K7]; 1xAcetyl [N-Term]	TGME49_3
High	[Q].SPSKQETQLCAISSEGKPCR.[N]	3xTMT6plex [N-Term; K4; K17]; 2xCarbamidomethy	
High	[S].EKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K2; K8]; 1xCarbamidomethyl	
High	[L].SEKMNIVFKCPSGYHPR.[Y]	3xTMT6plex [N-Term; K3; K9]; 1xCarbamidomethyl	
High	[M].AFGSSSSSER.[Y]	1xTMT6plex [N-Term]	
High	[M].GMEDGREPYSSR.[G]	1xTMT6plex [N-Term]	
High	[A].DNLLEGLLHR.[T]	1xTMT6plex [N-Term]	
High	[A].DSLHEGLQSLSLKSQVGVSSK.[V]	2xTMT6plex [N-Term; K13]	
High	[A].DSLHEGLQSLSLK.[S]	1xTMT6plex [N-Term]	
High	[F].SVHSHNIRPDKHELPASEVPLYYNR.[F]	2xTMT6plex [N-Term; K11]	
High	[L].LTANVYEEAR.[S]	1xTMT6plex [N-Term]	
High	[M].SGFVFNPNASVFVPGGVSSAPPPPPPA	1xAcetyl [N-Term]	TGME49_3
High	[-].MEGAIPQAGEMENGATVGAPVSGVPR.	1xAcetyl [N-Term]	TGME49_3
High	[M].VSVEGELAR.[E]	1xTMT6plex [N-Term]	
High	[A].APMQGTLGPDVPENIGEPPVLPSSSSD	1xAcetyl [N-Term]	TGME49_3

Contaminant	spike-in std	host cell	Qvality PEP	Qvality q-value	# Protein Groups	# Proteins	# PSMs	Positions in Master Proteins
FALSE	FALSE	FALSE	0.001505	0	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.074218	0.003633	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.00077	0	1	1	7	TGME49_2
FALSE	FALSE	FALSE	0.06273	0.002722	1	1	2	TGME49_2
FALSE	FALSE	FALSE	0.019284	0	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.011198	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.054436	0.002015	1	1	6	TGME49_2
FALSE	FALSE	FALSE	0.01889	0	1	1	8	TGME49_2
FALSE	FALSE	FALSE	0.059434	0.002402	1	1	8	TGME49_2
FALSE	FALSE	FALSE	0.058242	0.002015	1	1	1	TGME49_2
FALSE	FALSE	FALSE	0.001623	0	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.036211	0.001288	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.007407	0	1	1	10	TGME49_2
FALSE	FALSE	FALSE	0.0047	0	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.000314	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.001484	0	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.000994	0	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.036709	0.001288	1	1	2	TGME49_2
FALSE	FALSE	FALSE	0.015055	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.014748	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.035721	0.001288	1	1	22	TGME49_2
FALSE	FALSE	FALSE	0.141954	0.005566	1	1	1	TGME49_2
FALSE	FALSE	FALSE	0.127914	0.004816	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.126252	0.004816	1	1	6	TGME49_2
FALSE	FALSE	FALSE	0.044116	0.001288	1	1	7	TGME49_2
FALSE	FALSE	FALSE	0.007256	0	1	1	7	TGME49_2
FALSE	FALSE	FALSE	0.021821	0	1	1	2	TGME49_2
FALSE	FALSE	FALSE	0.062309	0.002722	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.000803	0	1	1	7	TGME49_2
FALSE	FALSE	FALSE	0.003085	0	1	1	8	TGME49_2
FALSE	FALSE	FALSE	1.51E-05	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.000714	0	1	1	8	TGME49_2
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FALSE	FALSE	FALSE	0.007107	0	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.001536	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.000675	0	1	1	18	TGME49_2
FALSE	FALSE	FALSE	5.39E-05	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	5.94E-05	0	1	1	16	TGME49_2
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FALSE	FALSE	FALSE	0.155376	0.005777	1	1	3	TGME49_2
FALSE	FALSE	FALSE	0.023694	0	1	1	8	TGME49_2
FALSE	FALSE	FALSE	0.000266	0	1	1	11	TGME49_2
FALSE	FALSE	FALSE	0.11441	0.003917	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.000541	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.004038	0	1	1	8	TGME49_2
FALSE	FALSE	FALSE	0.005284	0	1	2	7	TGME49_2
FALSE	FALSE	FALSE	0.145677	0.005566	1	2	1	TGME49_2
FALSE	FALSE	FALSE	0.002981	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.017757	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.026441	0.00048	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.028509	0.00048	1	1	3	TGME49_2
FALSE	FALSE	FALSE	0.191615	0.008044	1	1	1	TGME49_2
FALSE	FALSE	FALSE	0.033823	0.001288	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.000414	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.100902	0.003917	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.06273	0.002722	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.169931	0.006543	1	1	2	TGME49_2

FALSE	FALSE	FALSE	0.152407	0.005777	1	1	4	TGME49_2
FALSE	FALSE	FALSE	0.002309	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	4.13E-06	0	1	1	5	TGME49_2
FALSE	FALSE	FALSE	0.000549	0	1	1	9	TGME49_2
FALSE	FALSE	FALSE	0.032244	0.000942	1	1	3	TGME49_2
FALSE	FALSE	FALSE	0.106396	0.003917	1	1	4	TGME49_3
FALSE	FALSE	FALSE	0.007614	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.042352	0.001288	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.06189	0.002722	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.034997	0.001288	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.010526	0	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.062309	0.002722	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.009825	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.161472	0.006543	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.19771	0.00846	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.02555	0	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.006107	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.013393	0	1	1	8	TGME49_3
FALSE	FALSE	TRUE	0.148528	0.005777	1	2	2	TGME49_3
FALSE	FALSE	FALSE	0.115927	0.003917	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.003591	0	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.068469	0.00344	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.046579	0.00168	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.025726	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.038241	0.001288	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.059034	0.002402	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.191615	0.008044	1	2	7	TGME49_3
FALSE	FALSE	FALSE	1.67E-06	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.132158	0.005097	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.000116	0	1	1	14	TGME49_3
FALSE	FALSE	FALSE	0.112912	0.003917	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.020234	0	1	1	14	TGME49_3
FALSE	FALSE	FALSE	0.000293	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.025726	0	1	1	18	TGME49_3
FALSE	FALSE	FALSE	0.000714	0	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.004864	0	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.010894	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.154381	0.005777	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.00282	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.210403	0.009782	1	1	3	TGME49_3
FALSE	FALSE	FALSE	2.23E-05	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.000759	0	1	1	8	TGME49_3
FALSE	FALSE	FALSE	0.000088	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.062309	0.002722	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.037467	0.001288	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.038241	0.001288	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.038241	0.001288	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.003717	0	1	1	18	TGME49_3
FALSE	FALSE	FALSE	0.007773	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.001929	0	1	1	14	TGME49_3
FALSE	FALSE	FALSE	0.129596	0.004816	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.157385	0.00607	1	1	1	TGME49_3

FALSE	FALSE	FALSE	0.001612	0	1	1	4	TGME49_3
FALSE	FALSE	FALSE	0.159417	0.006341	1	1	4	TGME49_3
FALSE	FALSE	FALSE	0.013862	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.044719	0.001288	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.000307	0	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.004208	0	1	1	9	TGME49_3
FALSE	FALSE	TRUE	0.158398	0.006341	2	2	5	TGME49_3
FALSE	FALSE	FALSE	0.122183	0.003917	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.07081	0.003633	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.12708	0.004816	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.003193	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.000168	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.051917	0.002015	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.000061	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.01788	0	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.023532	0	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.014151	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.011671	0	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.097607	0.003917	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.000386	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.201446	0.00846	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.025202	0	1	1	9	TGME49_3
FALSE	FALSE	FALSE	0.00586	0	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.001983	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.002725	0	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.000808	0	1	1	8	TGME49_3
FALSE	FALSE	FALSE	0.001385	0	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.048515	0.00168	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.040936	0.001288	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.016464	0	1	1	8	TGME49_3
FALSE	FALSE	FALSE	0.000111	0	1	1	14	TGME49_3
FALSE	FALSE	FALSE	0.059837	0.002402	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.098913	0.003917	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.00326	0	1	1	8	TGME49_3
FALSE	FALSE	FALSE	0.014647	0	1	1	15	TGME49_3
FALSE	FALSE	FALSE	1.86E-06	0	1	2	7	TGME49_3
FALSE	FALSE	FALSE	0.001424	0	1	1	8	TGME49_3
FALSE	FALSE	FALSE	0.069864	0.003633	1	1	2	TGME49_3
FALSE	FALSE	FALSE	0.023211	0	1	1	5	TGME49_3
FALSE	FALSE	FALSE	0.001515	0	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.031374	0.00048	1	1	7	TGME49_3
FALSE	FALSE	FALSE	0.000749	0	1	1	3	TGME49_3
FALSE	FALSE	FALSE	0.071287	0.003633	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.004122	0	1	1	12	TGME49_3
FALSE	FALSE	FALSE	0.004296	0	1	1	6	TGME49_3
FALSE	FALSE	FALSE	0.128752	0.004816	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.015582	0	1	1	12	TGME49_3
FALSE	FALSE	FALSE	0.09696	0.003917	1	1	1	TGME49_3
FALSE	FALSE	FALSE	0.122987	0.003917	1	2	7	TGME49_3

# Missed Cleavages	Theo. MH+ [Da]	20171104_03_S65988_asp3_tmt10_tails_po.raw	20171104_08_S65988_asp3_tmt10_tails_po.raw	20171104_09_S65988_asp3_tmt10_tails_po.raw	Sample: [S41] F5: 126, Sample, wt, pool	Sample: [S42] F5: 127N, Sample, wt, single	Sample: [S44] F5: 128N, Sample, wt, single	Sample: [S46] F5: 129N, Sample, wt, single
1	1735.909	High	High	High	High	High	High	High
0	1571.698	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2166.15	High	High	High	High	High	High	High
0	1212.586	High	Not Found	High	Not Found	Not Found	High	High
0	1476.739	High	High	High	High	High	High	High
0	1289.587	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2077.163	High	High	High	High	High	High	High
0	1188.694	High	High	High	High	High	High	High
0	1115.584	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1045.568	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1892.957	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1328.721	High	High	High	Not Found	Not Found	High	Not Found
0	1913.921	Not Found	High	High	Not Found	Not Found	High	Not Found
1	1984.138	High	High	High	High	High	High	High
0	1887.931	High	High	High	Not Found	Not Found	Not Found	High
1	3080.51	High	High	High	High	High	High	High
1	3868.892	High	High	High	High	High	Not Found	High
1	3248.6	Not Found	High	High	High	High	High	High
0	1237.537	High	High	High	High	Not Found	High	High
0	2008.837	High	High	High	Not Found	Not Found	High	Not Found
0	1253.531	High	High	High	High	High	High	High
0	2238	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	1459.92	High	High	High	High	High	High	High
0	1015.535	High	High	High	High	High	High	High
1	1691.951	High	High	High	High	High	High	High
1	1648.927	High	High	High	High	High	High	High
2	2922.674	High	Not Found	Not Found	High	High	High	High
1	1800.043	High	High	High	High	High	High	High
2	2478.511	High	High	High	High	High	High	High
0	1338.704	High	High	High	High	High	High	High
1	2529.366	High	High	High	High	High	High	Not Found
0	2408.273	High	High	High	High	High	High	High
2	2762.282	High	Not Found	Not Found	Not Found	High	Not Found	High
0	1880.974	Not Found	High	High	High	High	High	High
0	1780.853	High	High	High	High	High	High	High
0	1968.006	High	High	High	High	High	High	High
0	2404.209	High	High	High	High	High	High	High
0	1977.027	High	High	High	High	High	High	High
0	1889.995	High	Not Found	High	High	Not Found	High	High
0	2091.07	High	High	Not Found	High	High	High	High
2	4996.456	Not Found	High	High	High	High	High	High
1	3143.517	High	High	High	High	High	High	High
0	1949.913	High	High	High	Not Found	Not Found	Not Found	High
1	2114.129	High	High	High	High	High	High	High
0	1382.714	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1716.83	High	High	High	High	High	High	High
2	4115.128	Not Found	High	Not Found	High	Not Found	High	High

1	1778.929	High	High	High	High	High	High	High
0	1770.991	High	High	High	High	High	High	High
1	2121.311	High	High	High	High	High	High	High
0	1713.83	High	High	High	High	High	High	High
1	2689.302	High	High	High	High	Not Found	Not Found	Not Found
2	1813.199	High	High	High	High	High	High	High
0	2357.162	High	High	High	Not Found	High	Not Found	Not Found
0	1814.877	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2953.47	High	High	High	High	High	High	High
1	2159.124	High	High	Not Found	High	High	High	High
1	2753.571	High	High	High	High	High	High	High
1	1668.98	Not Found	High	High	High	High	High	High
1	1567.932	High	High	High	High	High	High	High
1	1610.89	High	High	High	High	High	High	High
0	1043.584	High	High	High	High	High	High	High
1	1987.05	High	High	High	High	High	High	High
1	1575.854	High	High	High	High	High	High	High
0	2535.177	High	High	High	Not Found	Not Found	Not Found	Not Found
1	3474.662	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2597.403	High	Not Found	High	High	High	High	High
0	1208.562	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	2521.382	High	Not Found	High	Not Found	Not Found	High	Not Found
0	2502.32	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2689.472	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
2	3146.716	High	High	High	High	High	High	High
1	2648.255	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1	3410.657	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1	1804.994	High	High	High	High	High	High	High
1	2669.352	High	High	High	High	High	High	Not Found
0	2038.972	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2095.084	High	High	High	High	High	High	High
0	1938.994	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	2211.123	High	High	High	High	Not Found	High	High
1	3349.814	High	High	High	High	Not Found	Not Found	Not Found
0	1929.908	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
0	1695.822	High	High	High	High	High	High	High
0	1311.636	Not Found	Not Found	High	High	High	High	Not Found
0	1611.779	High	High	High	High	High	High	High
2	1711.904	High	High	High	High	High	High	High
1	1555.803	High	High	High	High	High	High	High
0	2170.243	High	High	Not Found	High	High	High	Not Found
1	2263.229	High	Not Found	Not Found	High	High	High	High
0	1180.548	Not Found	High	High	Not Found	High	High	High
1	1765.903	High	High	High	High	High	High	High
2	3317.92	High	High	High	High	High	High	High
1	3161.819	High	High	High	High	High	High	High
1	2974.666	High	High	High	High	High	High	Not Found
0	3407.769	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1985.062	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2575.249	High	High	High	High	High	High	High
0	1273.654	High	High	High	High	High	High	High
0	1843.006	High	Not Found	Not Found	High	High	Not Found	High

0	1768.964	High	High	High	High	High	High	High
0	1539.801	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
1	2195.181	Not Found	High	High	High	High	High	High
0	1496.728	High	High	High	High	High	High	High
0	2158.04	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1091.569	High	High	High	High	High	High	High
1	2715.447	High	High	High	High	High	High	High
2	1913.125	High	High	High	High	High	High	High
0	965.4687	High	High	High	Not Found	Not Found	High	Not Found
1	1219.71	High	Not Found	High	High	High	High	High
0	2986.592	High	High	High	High	High	High	High
1	1764.11	High	High	High	High	High	High	High
0	3096.439	High	High	High	Not Found	Not Found	Not Found	Not Found
0	3124.507	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1532.897	High	High	High	High	High	High	High
0	1964.883	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1431.617	Not Found	High	High	High	Not Found	Not Found	High
1	1918.999	High	High	High	High	High	High	High
1	1689.836	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1915.867	High	High	High	Not Found	Not Found	Not Found	Not Found
2	4391.28	High	Not Found	Not Found	High	High	High	Not Found
0	3626.912	High	High	High	Not Found	Not Found	Not Found	High
1	1835.937	High	High	High	High	High	High	High
2	3406.841	High	High	High	High	High	High	High
0	2297.151	High	High	High	High	High	High	High
0	925.5465	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1349.677	High	High	High	High	High	High	High
0	2250.175	Not Found	High	Not Found	High	High	Not Found	High
1	2477.184	High	High	High	High	High	High	High
2	2513.397	High	Not Found	Not Found	High	High	High	High
0	2734.342	High	High	High	High	High	High	High
0	1803.861	High	High	High	High	Not Found	High	High
0	3616.629	High	High	High	Not Found	Not Found	Not Found	Not Found
2	3591.822	High	High	High	High	High	High	High
0	1366.659	High	High	High	Not Found	Not Found	High	Not Found
1	1810.949	Not Found	High	High	High	High	High	High
0	1564.716	High	High	High	High	High	High	High
1	4888.401	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	2616.181	High	High	High	High	High	High	High
0	1986.069	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1376.737	High	High	High	High	High	High	High
0	1426.81	Not Found	High	High	High	High	High	High
2	2668.56	High	High	Not Found	High	High	High	High
1	1810.943	High	High	High	High	High	High	High
1	2007.093	High	High	High	High	High	High	High
0	1647.782	High	High	High	High	Not Found	Not Found	Not Found
2	1928.19	Not Found	High	High	High	High	High	High
0	1166.689	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1423.594	High	High	High	High	High	High	High
0	1407.599	High	High	High	High	High	High	High
1	2299.22	High	High	High	High	High	High	High
0	1537.693	High	High	High	Not Found	Not Found	Not Found	Not Found

0	1067.584	High	High	Not Found	High	High	Not Found	Not Found
0	1645.953	High	High	High	High	High	High	High
0	1416.79	High	High	High	High	High	High	High
0	1458.8	High	High	High	High	High	High	High
1	1388.881	Not Found	High	Not Found	High	High	High	High
2	2062.137	High	High	High	High	High	High	High
2	3486.837	High	Not Found	High	High	High	High	High
0	2581.419	High	High	High	Not Found	Not Found	Not Found	Not Found
1	3117.379	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
0	2054.061	High	High	High	High	Not Found	Not Found	Not Found
0	1745.812	High	High	High	Not Found	Not Found	Not Found	High
0	2118.041	High	High	High	High	High	High	High
0	1840.93	High	High	High	High	Not Found	Not Found	Not Found
1	1813.947	High	High	High	High	High	High	High
0	1815.966	Not Found	High	Not Found	High	High	High	High
0	1744.929	Not Found	High	High	High	High	High	High
1	3347.873	High	High	High	Not Found	Not Found	High	High
1	3255.632	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	3270.587	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2155.207	High	High	High	High	Not Found	Not Found	High
0	2068.175	High	High	High	High	Not Found	High	Not Found
0	3357.619	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	2226.244	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1694.816	High	High	High	High	High	High	High
0	1217.709	High	High	Not Found	High	High	High	High
1	1889.049	High	High	High	High	High	High	High
1	1448.791	High	High	High	High	High	High	High
1	1635.943	High	High	High	High	High	High	High
1	2478.254	High	High	High	High	High	High	High
0	1032.496	High	High	High	High	High	High	High
0	1949.825	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2511.397	High	High	High	High	High	High	High
0	2324.245	High	High	High	High	High	High	High
0	2586.283	High	High	High	High	Not Found	Not Found	High
0	2815.446	High	High	High	High	High	High	High
0	1729.932	High	High	High	High	High	High	High
0	1917.085	Not Found	High	Not Found	High	High	High	High
0	2313.26	Not Found	Not Found	High	High	Not Found	High	High
0	1473.826	High	High	High	High	High	High	High
0	2071.159	Not Found	High	Not Found	High	High	High	High
0	1111.585	High	High	High	High	High	High	High
1	2277.188	High	High	Not Found	High	High	High	High
1	2024.013	Not Found	High	High	High	High	High	Not Found
0	1322.768	Not Found	High	High	High	Not Found	Not Found	Not Found
0	1689.762	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1474.72	High	High	High	High	High	High	High
1	1858.051	High	Not Found	Not Found	High	High	High	High
1	1688.086	Not Found	High	High	High	High	High	High
0	1605.862	High	High	High	High	High	High	High
0	1549.75	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2170.246	Not Found	Not Found	High	High	High	High	High
2	2806.585	Not Found	High	High	High	High	High	High

0	1686.828	High	High	High	High	High	High	High
1	2318.128	High	High	High	High	High	High	High
0	2779.259	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1454.91	High	High	Not Found	High	High	High	High
0	1719.89	High	High	High	High	High	High	High
2	2256.253	High	High	High	High	High	High	High
0	1981.83	High	Not Found	Not Found	High	High	High	High
0	1107.567	High	High	High	High	High	High	High
1	3212.582	High	High	High	High	High	High	High
0	2282.028	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2690.363	High	High	High	High	High	High	High
1	2400.263	High	High	High	High	High	High	High
1	2383.162	High	High	High	High	Not Found	High	High
1	1528.958	High	High	High	High	High	High	High
1	1843.028	Not Found	High	Not Found	High	High	High	High
2	2719.504	High	Not Found	High	High	High	High	High
1	2579.32	Not Found	High	High	High	Not Found	Not Found	High
1	1468.796	High	High	High	High	High	High	High
0	1516.783	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1178.551	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1791.792	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
1	1364.747	High	High	High	High	High	High	High
1	1878.963	High	High	High	High	High	High	High
0	1247.632	High	High	High	High	High	High	High
1	3687.975	Not Found	High	Not Found	High	High	High	High
0	2280.147	High	Not Found	High	Not Found	High	High	High
0	1664.896	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2403.272	High	High	High	High	High	High	High
0	1390.721	Not Found	High	Not Found	Not Found	Not Found	High	High
0	2146.966	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1983.903	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	1934.07	High	High	High	High	High	High	High
0	3260.513	High	High	High	Not Found	Not Found	High	High
2	2204.193	High	Not Found	High	High	High	High	High
0	1156.559	High	High	High	High	High	High	High
0	1394.673	High	High	High	High	High	High	High
1	3408.629	High	High	High	High	High	High	High
0	1349.611	High	High	High	Not Found	High	High	High
0	1289.742	High	High	High	High	High	High	High
1	2079.072	High	Not Found	High	High	High	High	High
1	1849.909	High	High	High	High	Not Found	High	Not Found
1	2247.162	High	High	Not Found	High	High	High	High
1	2017.999	High	High	High	High	Not Found	Not Found	Not Found
1	1734.882	High	Not Found	High	High	Not Found	Not Found	Not Found
2	1669.036	Not Found	High	High	High	High	High	High
1	1358.888	High	High	High	High	High	High	High
1	1640.844	Not Found	Not Found	High	High	High	High	High
0	2064.024	High	High	High	High	High	High	High
0	1876.872	High	High	Not Found	Not Found	High	Not Found	Not Found
1	3134.712	Not Found	High	Not Found	High	High	High	High
1	2798.418	Not Found	Not Found	High	High	High	High	Not Found
1	1603.994	Not Found	High	High	High	High	High	High

0	1267.607	High	High	High	Not Found	High	Not Found	High
0	1289.608	High	Not Found	High	Not Found	High	Not Found	Not Found
0	2010.149	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	2503.376	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2926.534	High	Not Found	Not Found	High	High	High	High
2	3170.659	High	High	High	High	High	High	High
1	2075.112	Not Found	High	High	High	High	High	High
0	1931.074	Not Found	High	Not Found	High	Not Found	Not Found	Not Found
1	2612.272	Not Found	Not Found	High	High	Not Found	Not Found	Not Found
1	1919.785	High	High	High	High	High	High	High
0	1442.731	High	High	High	High	High	High	High
0	1331.732	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1601.668	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2322.102	Not Found	High	Not Found	Not Found	Not Found	Not Found	High
0	1929.96	High	High	High	High	High	High	High
0	1639.705	High	High	High	High	High	High	High
1	1476.912	Not Found	Not Found	High	High	High	High	High
1	2997.594	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1604.778	High	High	High	Not Found	High	High	High
0	1992.01	High	High	High	High	High	High	High
0	2454.168	High	High	High	High	Not Found	High	High
1	1767.015	High	High	High	High	High	High	High
1	1954.167	High	High	High	High	High	High	High
2	2890.655	High	High	High	High	High	High	High
0	1906.007	High	High	High	Not Found	Not Found	High	Not Found
1	2392.307	High	Not Found	High	High	Not Found	High	High
2	2664.36	High	High	High	High	High	High	High
2	2664.34	Not Found	High	Not Found	High	High	High	High
1	3580.88	High	Not Found	Not Found	High	High	High	Not Found
1	1719.898	High	Not Found	High	High	High	High	High
0	1215.637	High	High	High	High	High	High	High
1	2453.397	High	High	High	High	High	High	Not Found
2	3224.902	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	1234.573	High	High	Not Found	Not Found	High	High	High
1	1701.936	High	High	High	High	High	High	High
0	1712.762	High	Not Found	High	High	High	Not Found	High
2	3665.993	Not Found	High	Not Found	High	High	High	High
0	1105.682	High	High	Not Found	High	High	High	High
0	952.4557	Not Found	Not Found	High	Not Found	High	Not Found	Not Found
0	1367.727	High	High	High	High	High	High	High
0	1468.775	Not Found	Not Found	High	High	High	High	High
0	1155.575	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
0	1984.84	High	High	High	High	High	High	High
0	2250.941	High	High	High	High	High	High	High
0	2421.047	High	High	High	High	High	High	High
0	2579.116	High	High	High	High	High	High	High
0	1722.744	Not Found	Not Found	High	High	High	Not Found	Not Found
0	1432.775	High	High	High	High	High	High	High
1	2364.213	High	High	High	High	High	High	High
1	2135.05	High	High	High	High	High	High	High
2	2520.314	High	High	Not Found	High	Not Found	High	Not Found
0	1172.72	High	High	High	High	High	High	High

0	2117.119	High	High	High	High	High	Not Found	High
1	2621.435	High	High	Not Found	High	High	High	High
1	2434.283	High	High	High	High	High	High	High
1	1614.948	High	High	High	High	High	High	High
1	1427.796	High	High	High	High	High	High	High
1	2111.176	High	High	High	High	High	High	High
1	2594.45	High	High	High	High	High	High	High
1	1792.059	Not Found	High	Not Found	High	High	High	High
2	2541.487	High	Not Found	High	High	High	High	High
2	2612.524	High	High	Not Found	High	High	High	High
0	1283.638	High	High	High	High	High	High	High
0	2732.482	High	High	High	High	High	High	Not Found
0	2368.24	High	High	High	High	High	High	High
0	2909.451	High	High	High	High	High	High	High
1	2848.506	High	High	High	High	High	High	High
1	3151.498	High	High	High	High	High	High	High
2	2306.266	High	High	High	High	High	High	High
0	1642.818	High	High	High	High	High	High	High
1	2545.294	Not Found	High	High	High	High	High	High
0	1212.539	High	High	High	Not Found	Not Found	High	High
0	1434.506	High	High	Not Found	High	High	Not Found	High
2	2996.617	High	High	High	High	High	High	High
0	1616.813	High	High	High	High	Not Found	High	High
0	1370.616	High	High	High	High	High	High	High
0	1817.996	High	High	High	High	High	High	High
1	1958.05	High	High	High	High	High	High	High
0	1359.649	High	High	High	High	High	High	High
0	1272.617	High	High	High	High	High	High	High
0	1495.847	High	High	High	High	High	High	High
0	1543.767	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2502.331	Not Found	High	High	High	High	High	High
0	1325.571	Not Found	High	High	High	High	High	High
0	1263.618	High	High	High	High	High	High	High
0	2447.324	High	High	High	High	High	High	High
2	3026.584	High	Not Found	High	High	Not Found	Not Found	High
1	3054.524	High	High	High	High	High	Not Found	Not Found
1	2867.372	High	High	High	High	Not Found	High	Not Found
2	2163.358	High	Not Found	Not Found	High	High	High	High
0	1331.755	High	High	High	High	High	High	High
1	2003.092	High	High	High	High	High	High	High
0	1196.593	Not Found	High	High	High	High	High	High
0	2206.978	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	1849.889	Not Found	High	Not Found	High	High	Not Found	High
1	3715.833	High	High	High	High	High	High	High
1	3528.681	High	High	High	High	Not Found	High	Not Found
1	3812.886	High	High	High	High	High	High	High
1	3899.918	High	High	High	High	Not Found	High	Not Found
1	3883.923	High	High	High	High	High	High	High
1	3828.881	High	High	High	High	High	High	High
1	3082.546	High	High	High	High	Not Found	Not Found	Not Found
0	1920.926	High	High	High	High	Not Found	High	High
0	2092.052	Not Found	High	High	High	Not Found	High	High

0	2272.056	High	High	High	High	High	High	High
1	3731.828	High	Not Found	High	High	Not Found	Not Found	Not Found
0	1868.916	High	High	High	Not Found	Not Found	Not Found	Not Found
1	1603.858	High	High	High	High	High	High	High
1	1791.01	High	Not Found	Not Found	High	High	High	High
0	1314.679	High	Not Found	High	High	High	High	High
0	1839.006	High	Not Found	Not Found	High	High	High	High
1	1556.911	High	High	High	High	High	High	High
0	1204.637	High	High	High	High	High	High	High
0	1721.853	High	High	High	Not Found	Not Found	High	Not Found
0	1195.625	Not Found	High	Not Found	High	High	High	High
1	4713.424	High	High	High	High	High	High	High
0	2580.197	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
1	4190.066	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
2	3916.962	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1	2695.405	Not Found	High	High	High	High	Not Found	High
1	2841.605	Not Found	High	Not Found	High	High	High	High
1	2754.573	High	High	Not Found	High	High	High	High
0	1118.532	High	High	High	High	High	High	High
0	1538.812	High	High	High	High	High	High	High
2	2877.659	High	High	High	High	High	High	High
2	1588.088	High	High	High	High	High	High	High
1	1243.721	High	High	High	High	High	High	High
1	2243.258	High	High	High	High	High	High	High
0	2151.296	High	High	High	High	High	High	High
0	2449.46	High	High	High	High	High	High	High
0	2264.38	High	High	High	High	High	High	High
1	1758.011	High	High	High	High	High	High	High
2	1805.074	Not Found	High	High	High	High	High	High
0	1871.867	High	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1873.945	High	High	High	High	High	High	High
0	1703.851	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	2095.02	High	High	High	Not Found	High	Not Found	Not Found
2	3671.061	High	High	High	High	Not Found	High	Not Found
0	1468.74	High	High	High	High	High	High	High
0	2407.117	High	High	High	High	Not Found	Not Found	Not Found
2	2316.317	Not Found	Not Found	High	High	Not Found	Not Found	Not Found
1	2340.261	High	Not Found	High	High	High	High	High
1	1315.846	High	High	Not Found	High	High	High	High
0	1241.656	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2285.192	High	Not Found	Not Found	High	High	High	High
1	2286.177	Not Found	High	High	High	High	High	High
0	2876.392	High	High	High	Not Found	Not Found	High	Not Found
1	1444.925	High	High	High	High	High	High	High
1	1470.977	High	High	High	High	High	High	High
1	1414.865	High	High	High	High	High	High	High
1	1931.133	High	High	High	High	High	High	High
0	1106.625	High	Not Found	Not Found	High	High	High	High
0	1672.886	Not Found	Not Found	High	High	Not Found	High	Not Found
0	3010.475	High	High	High	Not Found	High	High	Not Found
0	1333.754	High	High	High	High	High	High	High
0	1039.488	High	High	High	High	Not Found	Not Found	Not Found

0	1963.981	High	High	High	High	High	High	High
0	1834.938	High	High	High	High	High	High	High
1	2316.203	High	High	High	High	High	High	High
0	1308.607	High	High	High	High	High	High	High
0	1581.931	High	High	High	High	High	High	High
0	2160.102	High	High	High	High	High	High	High
0	1624.802	High	High	High	High	High	High	High
0	1468.847	High	High	High	High	High	High	High
1	2129.051	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	1721.854	High	Not Found	High	High	Not Found	High	High
0	1434.609	High	High	High	Not Found	Not Found	Not Found	Not Found
0	3679.637	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1032.551	High	High	High	Not Found	Not Found	Not Found	High
0	2353.129	High	High	High	High	High	High	High
1	1670.91	High	High	High	High	High	High	High
0	1828.904	High	High	Not Found	Not Found	High	Not Found	Not Found
0	1385.688	High	Not Found	High	High	Not Found	High	High
0	1284.716	High	High	High	High	Not Found	High	High
1	2482.408	High	High	High	High	Not Found	Not Found	High
1	1971.034	High	High	High	High	High	High	High
1	3976.955	High	High	High	High	Not Found	High	High
0	1389.691	High	High	High	High	High	High	High
1	1710.988	High	High	High	High	High	High	High
0	1687.812	High	High	High	High	High	High	High
1	2678.467	High	High	High	High	High	High	High
0	1520.812	Not Found	Not Found	High	High	High	High	High
0	1457.827	High	High	Not Found	High	High	High	High
0	1270.675	Not Found	High	Not Found	Not Found	Not Found	High	High
1	2330.043	High	High	High	Not Found	High	High	High
2	2141.301	Not Found	Not Found	High	High	High	High	High
2	2346.43	High	High	High	High	High	High	High
1	2082.024	Not Found	High	High	High	High	High	High
1	2356.328	High	High	High	High	High	High	High
1	2285.291	High	High	High	High	High	High	High
1	2943.435	High	High	High	High	High	High	High
1	2443.36	High	Not Found	High	High	High	High	High
1	2571.27	High	High	High	High	High	High	High
1	2203.049	High	High	High	High	High	High	High
1	2470.223	High	High	Not Found	High	High	High	High
1	2657.491	High	High	High	High	High	High	High
1	2785.421	Not Found	Not Found	High	Not Found	Not Found	High	Not Found
1	2208.104	High	High	Not Found	High	High	High	High
0	1153.787	Not Found	High	High	High	High	High	High
1	2358.261	Not Found	High	High	High	High	High	High
1	3093.543	High	High	High	High	High	High	Not Found
0	1797.84	High	High	High	Not Found	Not Found	Not Found	High
0	1457.775	High	High	High	High	High	High	High
0	1685.853	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	2769.367	High	High	High	Not Found	High	Not Found	Not Found
0	1782.018	High	High	High	High	High	High	High
2	2853.622	Not Found	High	Not Found	High	High	High	High
0	1655.837	High	High	High	High	High	High	High

1	2496.364	High	High	High	High	High	High	High
1	1861.846	High	High	High	High	High	High	High
0	1879.919	High	High	High	High	High	High	High
1	3377.847	Not Found	High	High	High	Not Found	High	Not Found
1	2530.334	Not Found	High	High	High	High	High	High
1	1873.964	Not Found	Not Found	High	High	High	High	High
1	2289.191	High	High	High	High	High	High	High
0	3511.684	High	High	High	Not Found	Not Found	High	Not Found
0	1009.517	High	High	High	High	Not Found	Not Found	Not Found
0	1196.67	High	High	High	High	High	High	High
1	2554.287	High	High	High	High	High	High	Not Found
0	961.5628	High	High	Not Found	High	High	High	High
0	1732.869	High	High	High	Not Found	Not Found	Not Found	High
0	1404.748	High	Not Found	High	Not Found	High	Not Found	High
1	1773.991	High	High	High	High	High	High	High
0	4113.185	Not Found	High	High	High	Not Found	High	Not Found
1	1313.831	High	High	High	High	High	High	High
0	1052.585	High	High	High	High	High	High	High
1	1905.081	High	High	Not Found	High	High	High	High
1	3167.783	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1	1678.983	High	High	High	High	High	High	High
1	1915.153	High	High	Not Found	High	High	High	High
0	2144.025	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	1674.954	High	Not Found	Not Found	High	High	High	High
2	3019.773	High	Not Found	Not Found	High	High	High	High
1	1757.032	High	High	High	High	High	High	High
1	1828.069	High	High	Not Found	High	High	High	High
1	4046.151	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1	1894.942	High	High	High	High	High	High	High
0	1458.743	High	High	High	High	High	High	High
0	1581.847	Not Found	High	High	High	High	High	High
0	2741.401	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1413.711	High	High	Not Found	High	Not Found	High	Not Found
0	1189.681	Not Found	High	High	High	High	High	High
0	2056.931	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
0	2132.068	High	High	High	High	High	High	High
0	2485.184	High	High	High	High	High	High	High
0	2501.179	High	High	High	High	High	Not Found	Not Found
0	1554.642	High	High	High	High	High	High	Not Found
0	1450.789	High	High	High	High	High	High	High
1	2234.196	High	High	High	High	High	High	High
1	2047.044	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found
1	2319.232	High	High	High	High	High	High	High
1	1791.94	High	High	High	High	High	High	High
1	1893.038	High	High	High	High	High	High	High
1	1639.884	High	Not Found	High	High	High	High	High
1	1858.996	High	Not Found	Not Found	High	High	Not Found	Not Found
0	1622.885	High	High	High	High	High	High	High
0	1300.668	High	High	High	High	High	High	High
0	1114.574	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
2	1776.151	High	High	High	High	High	High	High
1	2174.218	Not Found	High	High	High	High	High	High

0	1558.757	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2518.419	High	High	High	High	High	High	High
1	2191.198	High	High	High	High	High	High	High
0	1645.858	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2094.216	High	High	High	High	High	High	High
0	1499.72	High	High	High	Not Found	Not Found	Not Found	Not Found
2	2003.229	High	High	High	High	High	High	High
0	2938.326	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	1633.902	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
1	1861.095	High	High	High	High	High	High	High
0	1679.933	High	High	High	Not Found	High	High	High
0	1867.085	High	Not Found	High	Not Found	High	Not Found	High
0	3045.458	Not Found	High	High	Not Found	Not Found	High	Not Found
2	1953.226	Not Found	High	High	High	High	High	High
0	1102.556	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
1	1973.061	High	High	High	High	High	High	High
0	1523.835	High	High	High	High	High	High	High
0	1580.857	High	High	High	High	High	High	High
0	842.4367	Not Found	High	Not Found	High	High	High	High
1	1439.814	Not Found	High	Not Found	High	High	High	High
1	2938.427	High	High	High	High	High	High	High
1	1397.863	High	High	High	High	High	High	High
1	2479.341	Not Found	High	High	High	High	High	High
0	2948.503	High	High	High	High	High	High	High
1	1753.001	High	High	High	High	High	High	High
0	1128.637	High	High	Not Found	High	High	Not Found	High
0	1458.646	High	High	High	Not Found	Not Found	Not Found	Not Found
1	2042.158	High	High	High	High	High	High	High
0	1116.657	Not Found	Not Found	High	High	High	High	High
0	2237.129	High	High	High	High	High	High	High
0	2049.976	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
0	2255.101	High	High	High	Not Found	Not Found	Not Found	Not Found
0	2442.254	High	High	Not Found	High	High	High	High
1	2725.443	High	High	High	High	High	High	High
1	2912.596	High	Not Found	Not Found	High	High	High	High
1	2288.175	High	High	High	High	Not Found	High	High
2	2437.196	High	High	High	High	High	High	High
2	2566.238	High	High	Not Found	High	High	High	High
0	1519.789	High	High	High	High	High	High	High
0	1535.784	High	High	Not Found	High	High	High	High
1	1564.958	High	High	High	High	High	High	High
2	1875.109	High	High	High	High	High	High	High
1	2083.077	High	High	High	High	High	High	High
0	3943.999	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1164.485	High	High	High	High	High	High	High
0	2318.156	High	High	High	High	Not Found	Not Found	High
2	2175.254	High	High	Not Found	High	High	High	High
0	2368.989	High	High	High	Not Found	High	Not Found	Not Found
0	1296.625	High	High	High	Not Found	High	Not Found	Not Found
0	1587.747	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1774.9	High	High	High	Not Found	Not Found	Not Found	Not Found
1	3321.618	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found

2	3516.878	High	High	High	High	Not Found	Not Found	Not Found
0	2574.363	Not Found	High	High	Not Found	High	Not Found	Not Found
0	1335.636	High	High	High	Not Found	High	High	High
1	4372.124	High	High	High	High	Not Found	Not Found	Not Found
2	3717.998	High	High	High	High	High	High	High
1	1420.805	High	High	High	High	High	High	High
0	1675.787	High	High	Not Found	High	High	High	High
0	1893.899	High	High	Not Found	Not Found	Not Found	Not Found	Not Found
1	3188.545	High	Not Found	Not Found	High	Not Found	Not Found	Not Found
1	1722.011	High	High	High	High	High	High	High
1	2022.023	High	High	High	High	High	High	High
1	2359.115	High	High	Not Found	High	High	High	High
0	1684.98	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
2	1785.168	High	High	High	High	High	High	High
2	3535.872	Not Found	Not Found	High	High	Not Found	Not Found	High
1	2830.337	High	High	High	High	High	High	High
2	1980.192	High	High	High	High	High	High	High
0	1581.826	Not Found	High	High	High	High	High	High
0	1409.681	High	High	Not Found	High	Not Found	High	Not Found
0	1196.638	High	High	High	High	High	High	Not Found
2	4111.046	Not Found	High	Not Found	Not Found	High	High	High
0	1259.648	High	High	High	High	Not Found	High	High
1	2088.224	Not Found	High	High	High	High	High	High
2	2668.565	High	High	High	High	High	High	High
2	2855.717	High	Not Found	Not Found	High	High	High	High
0	3355.719	High	High	High	High	Not Found	High	Not Found
0	2751.492	High	High	High	High	High	High	Not Found
0	1091.584	High	High	High	High	Not Found	Not Found	Not Found
1	4807.204	Not Found	High	High	Not Found	Not Found	Not Found	Not Found
0	1436.748	High	High	High	High	High	High	High
2	2925.732	High	High	High	High	High	High	High
1	2128.2	High	High	High	High	High	High	Not Found
1	1555.937	Not Found	High	Not Found	High	High	High	High
0	1362.726	High	High	High	Not Found	Not Found	Not Found	High
1	1742.927	High	High	High	High	High	High	High
1	2950.569	High	High	High	High	High	High	High
2	2650.456	High	High	High	High	High	High	High
2	2737.489	High	High	Not Found	High	High	High	High
0	1243.612	High	High	Not Found	High	High	High	High
1	1612.759	High	High	High	High	High	High	High
0	1408.811	High	High	High	Not Found	High	High	High
1	2657.487	Not Found	High	High	High	High	High	High
0	1655.917	Not Found	Not Found	High	High	High	Not Found	High
1	3416.823	High	High	High	High	High	High	High
0	1394.748	High	High	High	High	High	High	High
0	3290.612	Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found
0	2567.223	High	High	High	Not Found	Not Found	Not Found	Not Found
0	1188.679	High	Not Found	Not Found	High	High	High	High
0	3198.599	High	High	High	Not Found	Not Found	Not Found	Not Found

Sample: [S48] F5: 130N, Sample, wt, single	Sample: [S43] F5: 127C, Sample, ko, single	Sample: [S45] F5: 128C, Sample, ko, single	Sample: [S47] F5: 129C, Sample, ko, single	Sample: [S49] F5: 130C, Sample, ko, single	Sample: [S50] F5: 131, Sample, ko, pool	Found in Sample Group: wt, pool	Found in Sample Group: wt, single	Found in Sample Group: ko, single
High	High	High	High	High	High	High	High	High
High	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	Not Found	High	High
High	High	High	High	High	High	High	High	High
Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
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Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
High	High	High	Not Found	Not Found	High	Not Found	High	High
High	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
High	High	High	High	High	High	High	High	High
Not Found	Not Found	High	High	High	Not Found	Not Found	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
High	High	High	High	High	High	High	High	High
Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
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Not Found	High	High	High	High	Not Found	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	Not Found	High	High
High	High	High	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High

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Not Found	High	High	High	High	Not Found	High	Not Found	High
High	High	High	High	High	High	High	High	High
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Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High
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High	High	High	High	High	High	High	High	High
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High	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
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High	High	High	High	High	High	High	High	High
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Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High
High	High	High	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
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Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
High	High	High	High	High	High	High	High	High
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Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High
Not Found	High	High	High	High	Not Found	High	High	High
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High	High	High	High	High	High	High	High	High
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High	High	High	High	High	Not Found	High	High	High
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High	High	High	Not Found	Not Found	Not Found	Not Found	High	High
Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
Not Found	Not Found	Not Found	High	Not Found	Not Found	Not Found	High	High
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Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
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Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found
High	Not Found	High	Not Found	Not Found	Not Found	Not Found	High	High
Not Found	Not Found	High	Not Found	Not Found	Not Found	Not Found	Not Found	High
High	High	High	High	High	Not Found	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	Not Found	High	High	High
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Not Found	Not Found	Not Found	Not Found	Not Found	Not Found	High	Not Found	Not Found
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High	High	High	High	High	Not Found	High	High	High
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Found in Sample Group: ko, pool	Abundance Ratio: (ko, pool) / (wt, pool)	e Ratio: (ko, single) / (wt, single)	e Ratio (log2): (ko, pool) / (wt, pool)	e Ratio (log2): (ko, single) / (wt,	Abundances (Grouped): wt, pool	Abundances (Grouped): wt, single	Abundances (Grouped): ko, single	Abundances (Grouped): ko, pool
High	0.771	1.867	-0.37	0.9	102	55	102.7	78.7
Not Found								
High	0.291	1.664	-1.78	0.73	9.5	6.5	10.8	2.8
High								
High	0.463	1.203	-1.11	0.27	10.2	12.1	14.6	4.7
Not Found								
High	0.211	1.852	-2.24	0.89	102.8	48.9	90.6	21.7
High	0.408	1.977	-1.29	0.98	718.3	346.2	684.6	292.9
Not Found								
Not Found								
Not Found								
High								
Not Found								
High	0.433	1.457	-1.21	0.54	171.9	103.8	151.3	74.4
Not Found								
High	0.494	1.666	-1.02	0.74	33.5	20	33.3	16.6
Not Found	0.01	2.298	-6.64	1.2	4.9	2.8	6.5	
High	0.23	1.661	-2.12	0.73	31.8	16.6	27.6	7.3
High								
Not Found								
High								
Not Found								
High	0.332	2.201	-1.59	1.14	27.4	9.3	20.4	9.1
High								
High	0.474	1.509	-1.08	0.59	274.6	163.4	246.6	130.2
High	0.534	2.856	-0.9	1.51	987.4	383.9	1096.5	527.6
High	0.61	3.07	-0.71	1.62	12.9	5	15.2	7.9
High	0.404	2.812	-1.31	1.49	55.7	21.8	61.2	22.5
High	0.346	1.714	-1.53	0.78	187.2	94.4	161.9	64.7
High	0.244	2.505	-2.03	1.32	769.9	261.5	654.9	188.2
Not Found	0.01	3.035	-6.64	1.6	7.5	1.9	5.8	
High	0.265	2.479	-1.92	1.31	29.8	10.9	26.9	7.9
High		100		6.64			2.1	
High	0.152	4.34	-2.71	2.12	18.1	4.8	20.6	2.8
High								
High	0.213	2.811	-2.23	1.49	322.5	107.3	301.6	68.8
Not Found	0.01	2.906	-6.64	1.54	16.4	3.2	9.2	
High	0.601	2.753	-0.73	1.46	98.7	43.1	118.6	59.4
Not Found	0.01	2.406	-6.64	1.27	3.6	2.8	6.7	
High	2.744	2.233	1.46	1.16	2.6	2.9	6.5	7.1
High	0.388	3.342	-1.37	1.74	57.4	18.7	62.3	22.3
High	0.244	5.02	-2.03	2.33	32.3	6.5	32.4	7.9
Not Found								
High	0.774	1.599	-0.37	0.68	41	28.4	45.4	31.8
High								
High								
Not Found	0.01	3.535	-6.64	1.82	7.6	2.2	7.9	

High	0.658	2.388	-0.6	1.26	664.2	328.9	785.5	436.9
High	0.384	1.659	-1.38	0.73	33.9	19.6	32.4	13
High	0.538	2.479	-0.9	1.31	271.5	117.7	291.9	146
Not Found								
Not Found	0.01	100	-6.64	6.64	91.1		97.4	
High	0.494	2.602	-1.02	1.38	1172.4	475.6	1237.4	579.7
Not Found								
Not Found								
High	0.357	1.979	-1.49	0.98	166.4	72.6	143.7	59.4
High	0.334	1.606	-1.58	0.68	29	17.4	28	9.7
High	0.49	1.654	-1.03	0.73	6	2.9	4.7	3
High	1.049	0.826	0.07	-0.28	59.4	70.5	58.2	62.3
High	0.962	0.646	-0.06	-0.63	477	631.1	407.4	459
High	1.086	0.615	0.12	-0.7	269	396	243.6	292.1
High								
High	0.148	2.323	-2.76	1.22	161.6	56.9	132.3	23.9
High	0.393	1.919	-1.35	0.94	343.6	163.9	314.5	134.9
Not Found								
Not Found								
High	0.56	2.439	-0.84	1.29	50.4	26.9	65.7	28.2
Not Found								
Not Found		1.974		0.98		2.2	4.3	
Not Found								
Not Found								
High	0.01	9.216	-6.64	3.2	22.7	2.8	25.4	
Not Found	0.01		-6.64		1.7			
Not Found		100		6.64			1.8	
High	0.307	2.655	-1.7	1.41	73.8	26.6	70.6	22.7
High	0.113	5.352	-3.14	2.42	27.8	5.3	28.6	3.2
Not Found								
High	0.076	3.775	-3.71	1.92	54.3	14.4	54.4	4.1
High	100	100	6.64	6.64			2	2.8
High	0.299	6.166	-1.74	2.62	19.1	3.9	24.3	5.7
Not Found	0.01	100	-6.64	6.64	2.1		2.1	
Not Found								
High								
Not Found								
High	0.315	1.658	-1.67	0.73	73.2	38.6	64.1	23.1
High	0.203	5.301	-2.3	2.41	77.8	15.6	82.5	15.8
High	0.435	2.807	-1.2	1.49	744.7	272.5	764.8	323.9
High	0.813	1.942	-0.3	0.96	8	5.8	11.2	6.5
Not Found	0.01	2.556	-6.64	1.35	15.4	5.5	14.1	
Not Found								
High	0.242	1.695	-2.05	0.76	97	47.9	81.2	23.5
High	0.166	2.551	-2.59	1.35	19	9.4	24	3.2
High	0.266	1.859	-1.91	0.89	43.7	22.2	41.4	11.6
High	0.32	1.288	-1.64	0.37	9.2	5.4	7	3
Not Found								
Not Found								
High	0.309	2.882	-1.7	1.53	24.3	10.6	30.4	7.5
High								
High	0.728	1.43	-0.46	0.52	4.1	2.5	3.5	3

High	0.751	2.582	-0.41	1.37	17.9	10.1	26.2	13.4
Not Found								
High	0.508	3.617	-0.98	1.85	30.3	8.7	31.6	15.4
High	0.276	4.708	-1.85	2.23	13.6	2.8	13	3.7
High	100	0.687	6.64	-0.54		2.2	1.5	3
High								
High	0.246	2.934	-2.02	1.55	44.1	17.1	50.1	10.8
High	0.642	2.468	-0.64	1.3	1194.7	573.5	1415.6	767.3
Not Found								
High	0.346	1.68	-1.53	0.75	50.2	25.9	43.5	17.4
High	0.01	0.605	-6.64	-0.73	2.3	3.1	1.9	
High	0.461	2.107	-1.12	1.08	1225.1	594.6	1252.9	564.3
Not Found								
Not Found								
High	0.498	2.092	-1.01	1.07	161.3	73	152.8	80.3
Not Found								
Not Found								
High	0.434	2.618	-1.2	1.39	47.7	20.8	54.3	20.7
Not Found								
Not Found								
Not Found	0.01	1.524	-6.64	0.61	8.6	3.2	4.8	
Not Found		0.01		-6.64		1.9		
High	0.705	1.415	-0.5	0.5	19.6	13.3	18.8	13.8
High	0.261	3.112	-1.94	1.64	42.3	18.7	58.2	11
High	0.666	1.156	-0.59	0.21	21.3	19.6	22.7	14.2
Not Found								
High								
Not Found	0.01	0.491	-6.64	-1.03	2.2	4	1.9	
High	0.307	0.934	-1.7	-0.1	9	9.9	9.2	2.8
High	0.135	2.035	-2.89	1.02	27.7	13.1	26.6	3.7
Not Found	0.01	2.131	-6.64	1.09	3.3	3.1	6.5	
High	1.029	1.196	0.04	0.26	3.5	5.7	6.8	3.6
Not Found		100		6.64			2.4	
High	0.227	2.417	-2.14	1.27	45.1	22.6	54.6	10.3
Not Found								
Not Found	0.01	2.949	-6.64	1.56	5.4	2.4	7	
High								
Not Found								
High	1.977	1.969	0.98	0.98	2.1	2.2	4.3	4.1
Not Found								
High	0.755	2.351	-0.4	1.23	171.5	81.5	191.5	129.6
High	0.439	3.833	-1.19	1.94	25.6	7.4	28.5	11.2
High	0.271	3.462	-1.88	1.79	24.8	6.9	23.8	6.7
High	0.497	1.953	-1.01	0.97	32.5	16	31.3	16.2
High	0.219	1.792	-2.19	0.84	30.7	15.3	27.4	6.7
Not Found								
High	0.524	1.575	-0.93	0.66	185.7	105.3	165.8	97.2
Not Found								
High								
Not Found								
High	0.507	1.772	-0.98	0.83	52.1	28.8	51	26.4
Not Found								

High								
High	0.379	1.717	-1.4	0.78	646	317.7	545.3	244.8
High	0.508	1.831	-0.98	0.87	179.8	95.3	174.4	91.3
High	0.454	1.772	-1.14	0.83	148	71.9	127.5	67.3
High	0.499	2.164	-1	1.11	229.9	114.5	247.8	114.8
High	0.421	2.878	-1.25	1.53	540.4	200.3	576.6	227.6
Not Found	0.01	2.923	-6.64	1.55	25.3	7.8	22.7	
Not Found								
Not Found		0.9		-0.15		2.5	2.3	
Not Found	0.01		-6.64		1.6			
Not Found								
High	0.218	2.55	-2.2	1.35	94.3	32.3	82.4	20.5
Not Found								
High	0.502	2.005	-0.99	1	383.1	190	381.1	192.3
High	0.667	1.313	-0.58	0.39	10.4	10.2	13.4	6.9
High	1.042	0.969	0.06	-0.05	36.7	35.4	34.3	38.3
Not Found		2.087		1.06		2	4.3	
Not Found		100		6.64			3	
Not Found								
High	1.412	0.945	0.5	-0.08	2.1	1.8	1.7	3
Not Found	0.01	0.336	-6.64	-1.58	2.1	7.2	2.4	
Not Found								
Not Found		0.817		-0.29		2.2	1.8	
High	0.266	3.46	-1.91	1.79	46.7	13.2	45.7	12.4
High	0.514	2.378	-0.96	1.25	65.6	27.3	64.8	33.7
High	0.267	2.142	-1.91	1.1	298.7	116.9	250.4	79.7
High	0.435	1.619	-1.2	0.7	372.6	190.7	308.7	161.9
High	0.46	1.435	-1.12	0.52	338	202.1	290.1	155.6
High	0.201	3.07	-2.31	1.62	53.9	13.4	41.3	10.8
High								
Not Found								
High	0.585	2.784	-0.77	1.48	95.1	39.7	110.4	55.6
High	3.008	0.554	1.59	-0.85	10.2	18.5	10.2	30.8
High								
High	0.385	3.727	-1.38	1.9	194.2	56.2	209.4	74.8
High	3.292	0.411	1.72	-1.28	67.5	169.6	69.7	222.3
High								
Not Found	0.01	2.384	-6.64	1.25	5.1	3	7.1	
High	0.788	1.698	-0.34	0.76	135.2	82.3	139.6	106.5
High	0.825	1.596	-0.28	0.67	16.3	11.7	18.7	13.4
High								
High	0.34	1.768	-1.56	0.82	91.2	46.9	82.9	31
High	0.558	1.842	-0.84	0.88	5.3	3	5.6	3
Not Found								
Not Found								
High	0.466	2.911	-1.1	1.54	104.6	38.6	112.4	48.7
High	0.162	3.148	-2.63	1.65	36.6	9.7	30.4	5.9
High	0.746	1.119	-0.42	0.16	429.4	366.9	410.5	320.5
High	0.6	2.949	-0.74	1.56	365.1	147.5	435	219.1
Not Found								
High	0.35	3.945	-1.51	1.98	24.8	5.5	21.6	8.7
High	0.237	3.333	-2.08	1.74	29.9	10.6	35.2	7.1

High	1.005	0.717	0.01	-0.48	38.1	51.9	37.2	38.3
High	0.599	3.85	-0.74	1.94	102	31.2	120	61.1
Not Found								
High	0.966	0.718	-0.05	-0.48	312.4	405.3	291.1	301.8
High	0.253	2.688	-1.98	1.43	88.7	28.7	77	22.5
High	0.23	1.88	-2.12	0.91	202.3	93.3	175.5	46.6
Not Found								
High	0.338	1.781	-1.56	0.83	618	294.9	525.3	208.9
High	0.412	0.849	-1.28	-0.24	8.1	4.6	3.9	3.4
Not Found								
High	0.252	2.235	-1.99	1.16	25	9	20.1	6.3
High	0.455	2.649	-1.14	1.41	294.6	127	336.5	134.1
Not Found	0.01	3.736	-6.64	1.9	12.8	2.6	9.9	
High	0.365	1.571	-1.46	0.65	662	361.3	567.8	241.4
Not Found	0.01	1.024	-6.64	0.03	4.1	3	3	
High	0.582	3.399	-0.78	1.77	90.1	31.6	107.4	52.5
Not Found	0.01	1.064	-6.64	0.09	1.7	2.2	2.3	
High	0.473	1.954	-1.08	0.97	122.6	59.2	115.6	58
Not Found								
Not Found								
Not Found		100		6.64			2.4	
High	0.113	4.968	-3.14	2.31	59.3	10.8	53.6	6.7
High	0.487	2.346	-1.04	1.23	212.2	94.2	221.1	103.4
High	0.28	4.23	-1.84	2.08	37.3	7.4	31.2	10.5
High	0.227	2.636	-2.14	1.4	16.5	3.4	9	3.7
Not Found								
Not Found		100		6.64			5.2	
High	0.405	2.404	-1.3	1.27	82.3	33	79.4	33.3
Not Found								
Not Found		100		6.64			2.2	
Not Found								
High	0.232	2.941	-2.11	1.56	99.6	33	97.1	23.1
Not Found		1.346		0.43		1.5	2.1	
High	0.556	2.014	-0.85	1.01	46.8	23.8	47.9	26
High								
High								
Not Found	0.01	1.572	-6.64	0.65	8.7	3.7	5.8	
High								
High	0.333	1.965	-1.58	0.97	508.1	224.2	440.7	169.4
High	0.396	2.548	-1.34	1.35	68.3	31.1	79.2	27
High	0.183	7.651	-2.45	2.94	20.5	1.5	11.8	3.7
High	0.362	3.632	-1.47	1.86	248.6	70.8	257.2	89.9
Not Found	0.01	100	-6.64	6.64	6		6.7	
Not Found	0.01	100	-6.64	6.64	2.2		3.7	
High	0.732	2.48	-0.45	1.31	582.5	273.4	678	426.6
High	0.609	2.486	-0.72	1.31	978.8	451.2	1121.6	595.7
High	0.951	1.547	-0.07	0.63	17.6	10	15.5	16.8
High	0.494	1.624	-1.02	0.7	41.9	16.3	26.5	20.7
Not Found								
High	0.706	3.913	-0.5	1.97	4.2	3	11.9	3
Not Found								
High	0.121	7.992	-3.05	3	256.4	30	239.4	31

Not Found								
Not Found								
Not Found		100		6.64			1.5	
Not Found		100		6.64			1.3	
Not Found	0.01	1.555	-6.64	0.64	8.4	3.9	6	
High	0.092	2.52	-3.44	1.33	38.4	11.3	28.5	3.6
Not Found	0.01	2.062	-6.64	1.04	11.2	6.8	14	
Not Found	0.01	100	-6.64	6.64	1.5		2.5	
Not Found	0.01		-6.64		2.3			
High	0.597	3.036	-0.74	1.6	113.4	45.5	138.3	67.7
High								
Not Found								
Not Found								
High	100	0.836	6.64	-0.26		1.9	1.6	4.7
High	0.269	2.083	-1.9	1.06	302.4	131.9	274.7	81.3
High								
High	0.795	1.94	-0.33	0.96	39.2	23.5	45.6	31.2
Not Found								
Not Found								
High	0.512	1.536	-0.97	0.62	12	10.6	16.3	6.1
High								
High	0.251	2.609	-1.99	1.38	62.1	21.6	56.4	15.6
High	0.371	2.112	-1.43	1.08	244.7	109.9	232	90.7
High	0.148	1.794	-2.76	0.84	134.8	61.7	110.7	19.9
High								
High	0.564	3.521	-0.83	1.82	10.8	3	10.6	6.1
High	0.477	3.031	-1.07	1.6	53.4	21.7	65.7	25.4
High								
High	0.605	3.644	-0.72	1.87	10.1	2.7	9.7	6.1
High	1.005	1.268	0.01	0.34	97.1	79.2	100.4	97.6
Not Found								
Not Found	0.01	8.761	-6.64	3.13	12	2	17.3	
Not Found		100		6.64			2.1	
Not Found								
High	0.598	2.569	-0.74	1.36	140.8	51.1	131.3	84.2
High								
Not Found	0.01	1.108	-6.64	0.15	8.9	6.4	7.1	
High	0.64	1.311	-0.64	0.39	4.3	3.5	4.6	2.8
Not Found								
High	0.54	1.926	-0.89	0.95	650.4	330.8	636.9	351.5
High	1.549	1.506	0.63	0.59	3.8	4.4	6.7	5.9
Not Found								
High	0.568	2.891	-0.82	1.53	227.1	95.6	276.4	129
High	0.66	2.117	-0.6	1.08	21.8	9.6	20.2	14.4
High	0.508	3.109	-0.98	1.64	35.7	13.1	40.6	18.1
High	0.327	4.918	-1.61	2.3	29.6	7.9	39	9.7
Not Found								
High	0.246	2.028	-2.03	1.02	114.8	47.8	97	28.2
High	0.304	2.124	-1.72	1.09	124.5	62.2	132	37.9
Not Found								
Not Found	0.01	1.46	-6.64	0.55	2	2	2.9	
High	0.371	2.057	-1.43	1.04	383.2	171	351.8	142.2

High	0.226	1.979	-2.14	0.98	12.2	5.1	10.1	2.8
High	0.289	2.434	-1.79	1.28	16.4	3.9	9.5	4.7
High	0.279	1.783	-1.84	0.83	48.8	22.3	39.7	13.6
High	0.348	1.802	-1.52	0.85	1051.9	495.4	892.9	366.3
High	0.373	1.734	-1.42	0.79	635.4	312.8	542.6	237.1
High	0.396	2.082	-1.34	1.06	57.3	32.4	67.5	22.7
High	0.73	1.274	-0.45	0.35	8.4	8.2	10.5	6.1
High	1.405	1.215	0.49	0.28	39.3	40.8	49.6	55.2
High	0.731	1.713	-0.45	0.78	76.6	48.3	82.7	56
High	0.529	2.294	-0.92	1.2	80.2	37.6	86.2	42.4
High								
Not Found	0.01	1.553	-6.64	0.64	17.6	6.7	10.4	
Not Found	0.01	3.059	-6.64	1.61	6.2	3.9	12	
Not Found	0.01	2.39	-6.64	1.26	13.1	4.5	10.6	
High	0.842	2.663	-0.25	1.41	73.8	34.8	92.8	62.1
Not Found	0.01	3.967	-6.64	1.99	18.7	4.8	19.2	
High	0.07	2.598	-3.83	1.38	42	14.6	37.9	3
High	0.254	3.295	-1.98	1.72	39.7	11.1	36.6	10.1
High	0.397	1.784	-1.33	0.84	48.2	27.3	48.6	19.1
Not Found								
High								
Not Found	0.01	3.543	-6.64	1.83	17	4.3	15.2	
High								
High								
High	0.41	3.409	-1.29	1.77	94.3	34.4	117.3	38.7
High	0.373	2.161	-1.42	1.11	803.2	354	765.2	299.6
High	0.941	1.529	-0.09	0.61	222.3	161.1	246.3	209.1
High	1.016	1.349	0.02	0.43	257.2	205.1	276.6	261.4
High	0.437	1.52	-1.2	0.6	132.3	80.1	121.8	57.8
Not Found								
High	0.442	1.904	-1.18	0.93	21.4	9.8	18.6	9.5
High								
High								
Not Found	0.01	2.509	-6.64	1.33	3.8	3.4	8.6	
Not Found	0.01	2.247	-6.64	1.17	1.8	1.8	4	
Not Found	0.01	1.647	-6.64	0.72	2.2	2.6	4.2	
Not Found	0.01	5.658	-6.64	2.5	9.4	1.5	8.7	
High	0.493	2.3	-1.02	1.2	42	19.3	44.5	20.7
High	0.552	2.44	-0.86	1.29	251.1	110.6	269.9	138.7
High	0.533	1.141	-0.91	0.19	194.3	140.2	160	103.6
High	0.421	2.185	-1.25	1.13	65.2	28.8	62.9	27.4
Not Found								
Not Found	0.01	1.694	-6.64	0.76	3.6	2.5	4.3	
High	0.494	4.337	-1.02	2.12	51.5	14.6	63.1	25.4
Not Found	0.01	2.672	-6.64	1.42	5.7	4.4	11.8	
High	0.323	2.854	-1.63	1.51	26.2	12.1	34.6	8.5
High	0.33	6.408	-1.6	2.68	8.4	3.2	20.8	2.8
High	0.349	4.039	-1.52	2.01	28.2	8.9	36.1	9.9
Not Found	0.01	3.063	-6.64	1.61	5.3	3.4	10.3	
High	1.861	100	0.9	6.64	5.3		9.2	9.9
Not Found	0.01	4.958	-6.64	2.31	17.9	1.9	9.2	
High	0.406	14.783	-1.3	3.89	8.7	2.1	31.3	3.6

High	0.497	2.151	-1.01	1.11	19.8	10.4	22.3	9.9
Not Found	0.01	100	-6.64	6.64	2.6		5.1	
Not Found		100		6.64			1.9	
High	0.323	2.127	-1.63	1.09	91.1	40.8	86.9	29.4
High	0.457	1.57	-1.13	0.65	15.5	12.9	20.2	7.1
High	0.555	2.943	-0.85	1.56	167.3	64.7	190.3	92.9
High	0.423	1.207	-1.24	0.27	6.5	4	4.9	2.8
High	0.433	1.677	-1.21	0.75	75.7	35.5	59.5	32.7
High	0.999	1.804	0	0.85	509.5	345.7	623.6	508.9
Not Found								
Not Found								
High	0.546	4.259	-0.87	2.09	56.7	17.2	73.2	31
Not Found								
Not Found		1.291		0.37		2.1	2.8	
Not Found	0.01	100	-6.64	6.64	2.8		2.2	
High	0.728	3.063	-0.46	1.61	6.8	3.9	12.1	4.9
High	0.321	2.912	-1.64	1.54	32.5	13.2	38.3	10.5
Not Found	0.01	2.057	-6.64	1.04	8.9	2.6	5.3	
High								
High	0.754	2.053	-0.41	1.04	339.1	192.1	394.3	255.6
High	0.343	2.148	-1.54	1.1	235.4	99.3	213.4	80.7
High	0.608	2.351	-0.72	1.23	2861.8	1336	3140.4	1738.7
High	0.391	2.09	-1.36	1.06	393.1	178.7	373.4	153.7
High	0.333	1.811	-1.59	0.86	212.1	101.6	184	70.6
High	0.31	1.569	-1.69	0.65	268.9	148.9	233.6	83.2
High	0.196	2.859	-2.35	1.52	123	40.3	115.3	24.1
High	0.355	1.7	-1.49	0.77	208.6	112.2	190.8	74.2
High	0.688	2.471	-0.54	1.31	647.3	298.7	738.1	445.6
High	0.621	2.401	-0.69	1.26	122.4	55.5	133.2	75.9
Not Found								
High	0.875	2.939	-0.19	1.56	86.4	39.2	115.1	75.5
Not Found								
Not Found								
Not Found	0.01	1.486	-6.64	0.57	2	1.5	2.3	
High								
Not Found	0.01	100	-6.64	6.64	3.2		2.9	
Not Found	0.01	100	-6.64	6.64	3.3		3.6	
High	0.257	3.032	-1.96	1.6	43	12.9	39	11
High	0.525	2.811	-0.93	1.49	1179.4	452.5	1272.3	619.6
Not Found								
High	1.023	2.229	0.03	1.16	66.3	42.1	93.8	67.9
High	0.383	1.534	-1.38	0.62	91.1	54.5	83.7	34.9
Not Found								
High	0.493	1.726	-1.02	0.79	3164.2	1740.5	3003.9	1558.6
High	0.409	1.998	-1.29	1	5527.6	2618.7	5231.6	2260
High	0.393	2.48	-1.35	1.31	123.6	46.8	116	48.5
High	0.438	1.829	-1.19	0.87	193.8	97.1	177.7	84.8
High	0.584	3.101	-0.78	1.63	15.5	5.9	18.1	9.1
High	1.516	0.711	0.6	-0.49	2.3	3.2	2.3	3.6
Not Found								
High	0.752	1.494	-0.41	0.58	191.5	134.1	200.3	144
Not Found								

High	1.446	0.993	0.53	-0.01	159.6	181.6	180.4	230.8
High	2.458	0.993	1.3	-0.01	6.9	9.3	9.2	17
High	0.272	2.978	-1.88	1.57	39.9	14.1	42.1	10.8
High								
Not Found	0.01	1.604	-6.64	0.68	16.3	7.6	12.2	
High	1.16	1.04	0.21	0.06	4.9	10.1	10.5	5.7
High	2.184	0.579	1.13	-0.79	80.8	144.7	83.7	176.5
High	0.432	1.493	-1.21	0.58	42	32.2	48.1	18.1
Not Found								
High	2.832	0.913	1.5	-0.13	1.6	4.6	4.2	4.5
Not Found								
Not Found								
Not Found								
High								
High	0.522	2.276	-0.94	1.19	180.4	79.3	180.5	94.1
Not Found								
High								
Not Found								
Not Found	0.01	3.25	-6.64	1.7	5.9	1.8	5.8	
High	0.61	1.675	-0.71	0.74	19.7	11.1	18.5	12
Not Found	0.01	2.868	-6.64	1.52	11	3.1	8.8	
Not Found								
High	0.224	2.038	-2.16	1.03	291.2	122.1	248.8	65.1
High	0.644	2.276	-0.64	1.19	216.4	108.7	247.3	139.3
High	0.769	2.632	-0.38	1.4	54.1	25.7	67.7	41.6
Not Found	0.01	1.258	-6.64	0.33	6.8	7.6	9.6	
High	0.336	2.094	-1.57	1.07	75.2	33.2	69.6	25.2
Not Found								
Not Found								
High	0.92	1.521	-0.12	0.6	15.6	10.4	15.8	14.4
High	0.348	2.254	-1.52	1.17	247.7	106.3	239.6	86.2
High	1.439	0.81	0.53	-0.3	30.6	41.8	33.8	44
High	0.609	3.133	-0.72	1.65	125.7	49.9	156.3	76.5
High	0.413	2.793	-1.28	1.48	34.4	12.5	35	14.2
High	0.265	3.004	-1.91	1.59	66.9	25.5	76.6	17.8
High	0.474	3.504	-1.08	1.81	59.9	20.7	72.7	28.4
High	0.82	2.946	-0.29	1.56	53.9	26.6	78.3	44.2
Not Found								
High	0.36	3.159	-1.47	1.66	65.7	18.9	59.6	23.7
High	0.665	1.998	-0.59	1	67.9	33.6	67.1	45.2
Not Found		1.335		0.42		2.5	3.3	
High	0.313	3.66	-1.68	1.87	48.6	15.4	56.3	15.2
High	0.526	2.669	-0.93	1.42	213.9	82.1	219.1	112.4
High	0.624	1.247	-0.68	0.32	16.8	10	12.5	10.5
Not Found	0.01	2.154	-6.64	1.11	27.7	10.2	21.9	
Not Found								
High								
Not Found								
Not Found		1.667		0.74		2.3	3.8	
High	0.405	1.596	-1.3	0.67	926.2	483.7	772.1	375.4
High	0.5	1.852	-1	0.89	11.8	8.5	15.8	5.9
High	0.579	5.968	-0.79	2.58	31.7	7	41.7	18.3

High	0.243	3.2	-2.04	1.68	38.1	11.1	35.6	9.3
High								
High	0.354	1.892	-1.5	0.92	11.7	8.2	15.5	4.1
High	1.267	0.993	0.34	-0.01	3	4.3	4.2	3.7
High	0.358	1.527	-1.48	0.61	116.9	65.9	100.7	41.8
High	0.604	1.757	-0.73	0.81	12.1	6.3	11	7.3
High	0.402	1.704	-1.31	0.77	184	102.7	175.1	74
Not Found								
Not Found								
High	0.158	3.113	-2.66	1.64	18.7	6.9	21.4	3
High	0.183	1.532	-2.45	0.62	17.3	6.7	10.3	3.2
High	0.455	1.846	-1.13	0.88	307.9	159.8	294.9	140.2
Not Found								
Not Found								
High	0.406	0.842	-1.3	-0.25	27.7	31.6	26.6	11.2
Not Found	0.01	1.759	-6.64	0.81	1.8	1.7	2.9	
High	0.942	1.093	-0.09	0.13	1915.5	1751.2	1914.6	1805.2
High								
High	0.476	1.82	-1.07	0.86	86.3	46.6	84.8	41
Not Found	0.01	1.279	-6.64	0.36	4.3	3.4	4.3	
High	0.401	1.406	-1.32	0.49	1217.4	717.9	1009.4	487.6
High	0.368	1.609	-1.44	0.69	53.6	30	48.4	19.7
Not Found								
High	0.412	2.375	-1.28	1.25	37.8	15.2	36.2	15.6
High	0.563	3.052	-0.83	1.61	13.3	5.1	15.6	7.5
High	0.408	1.519	-1.29	0.6	308.2	175.6	266.8	125.8
High	0.278	2.044	-1.85	1.03	103.6	45.9	93.9	28.8
Not Found								
Not Found	0.01	2.052	-6.64	1.04	6.8	3.7	7.6	
High								
High	0.188	2.904	-2.41	1.54	33.6	11.7	34.1	6.3
Not Found								
Not Found	0.01	1.865	-6.64	0.9	6.2	3.3	6.2	
High	0.412	1.682	-1.28	0.75	68.5	34.3	57.6	28.2
Not Found								
High	0.553	1.145	-0.85	0.2	6.8	6.7	7.6	3.7
High	0.311	8.491	-1.69	3.09	8.3	2.8	23.6	2.6
Not Found	0.01	1.072	-6.64	0.1	2.2	1.6	1.7	
Not Found								
High	0.333	2.489	-1.59	1.32	214	83.4	207.6	71.2
High	0.21	2.333	-2.25	1.22	196.8	72.8	169.9	41.4
Not Found		100		6.64			1.9	
High	0.638	2.865	-0.65	1.52	83.8	35.3	101.2	53.5
High	0.691	4.037	-0.53	2.01	16.3	5.8	23.5	11.2
High	0.542	2.051	-0.88	1.04	129.3	63.4	129.9	70
High	0.601	2.389	-0.73	1.26	162.4	80	191.2	97.6
Not Found								
High	0.995	1.4	-0.01	0.49	129.9	101.5	142.1	129.2
High								
Not Found								
High	0.44	1.934	-1.18	0.95	255	122.9	237.7	112.2
High	0.207	2.29	-2.27	1.2	18.1	6.9	15.8	3.7

High								
High	0.194	2.095	-2.36	1.07	134.9	52.5	110	26.2
High	0.445	1.635	-1.17	0.71	147.5	81.4	133.2	65.7
Not Found								
High	0.609	3.525	-0.72	1.82	55.1	22.6	79.8	33.5
Not Found								
High	0.344	1.647	-1.54	0.72	2862.9	1451.5	2389.9	983.9
Not Found								
Not Found								
High	11.893	0.054	3.57	-4.2	12.3	217.6	11.9	146.6
Not Found								
Not Found		1.186		0.25		2.4	2.8	
Not Found								
High	0.193	2.056	-2.38	1.04	94.1	38.2	78.6	18.1
Not Found								
High	0.505	2.17	-0.98	1.12	206	92	199.7	104.1
High	0.503	1.944	-0.99	0.96	66.3	40.3	78.2	33.3
High	0.875	1.247	-0.19	0.32	47.6	48.1	59.9	41.6
High								
High	0.588	1.288	-0.77	0.36	19.5	12.3	15.8	11.4
High	0.692	2.261	-0.53	1.18	17.4	6.3	14.2	12
High	0.578	1.469	-0.79	0.55	221.3	144.1	211.6	128
High	0.702	2.344	-0.51	1.23	52.2	25.2	59.2	36.7
Not Found	0.01	8.47	-6.64	3.08	15.8	2.5	21.1	
High	0.572	2.669	-0.8	1.42	125.1	55.7	148.7	71.6
High								
Not Found								
High	0.367	1.693	-1.45	0.76	711.5	359.1	607.9	261.2
High	0.769	2.308	-0.38	1.21	19	11.2	25.7	14.6
High	0.185	4.166	-2.43	2.06	65.1	19	79	12
Not Found								
Not Found								
High	0.404	3.903	-1.31	1.96	11.7	4.3	16.9	4.7
High	0.101	4.951	-3.31	2.31	46.8	8.6	42.5	4.7
Not Found	0.01	3.802	-6.64	1.93	11.2	3.4	12.8	
Not Found	0.01	1.293	-6.64	0.37	5.7	3.6	4.7	
High	0.349	1.036	-1.52	0.05	50.9	37.3	38.7	17.8
Not Found	0.01	0.99	-6.64	-0.01	5.5	5.6	5.5	
High	0.517	1.274	-0.95	0.35	323.6	212.7	270.9	167.3
High	0.794	1.518	-0.33	0.6	14.9	10	15.2	11.8
High	0.36	1.516	-1.47	0.6	1376.9	754.6	1143.7	495.7
High	0.472	2.49	-1.08	1.32	2107.8	875.3	2179.8	994.9
High	0.338	4.138	-1.56	2.05	68.8	19	78.7	23.3
Not Found								
High								
Not Found								
High	0.398	1.876	-1.33	0.91	195.2	94.7	177.6	77.7
High								
Not Found								
Not Found								
Not Found								
Not Found								

Not Found	0.01	100	-6.64	6.64	6.5		9.9	
Not Found								
Not Found								
High	2.172	100	1.12	6.64	1.7		1.9	3.7
High	0.452	3.224	-1.15	1.69	31.4	11.6	37.4	14.2
High	0.477	2.634	-1.07	1.4	653.6	251.9	663.3	312
High	1.831	1.265	0.87	0.34	15.4	18.4	23.3	28.2
Not Found								
Not Found	0.01	100	-6.64	6.64	2.2		1.7	
High	0.285	1.747	-1.81	0.81	55.5	21.8	38.2	15.8
High	0.24	3.812	-2.06	1.93	34.5	9.6	36.7	8.3
High	0.6	2.347	-0.74	1.23	62.5	27.7	64.9	37.5
Not Found								
High	0.498	2.305	-1.01	1.2	2028.3	874.5	2015.8	1010.1
Not Found	0.01	1.544	-6.64	0.63	2.7	2.1	3.2	
High	0.397	2.672	-1.33	1.42	15.4	7.6	20.3	6.1
High	0.529	3.207	-0.92	1.68	169.9	50.9	163.3	89.9
High	0.217	1.712	-2.2	0.78	24.5	11.4	19.5	5.3
Not Found								
High								
Not Found		0.828		-0.27		3.2	2.6	
High								
High	0.534	1.73	-0.91	0.79	32.2	22.3	38.6	17.2
High	0.226	1.62	-2.15	0.7	50.6	28.9	46.7	11.4
High	0.246	1.717	-2.02	0.78	22.4	16.1	27.6	5.5
Not Found								
High	1.12	1.495	0.16	0.58	2.5	3.1	4.6	2.8
Not Found								
Not Found		1.456		0.54		2.1	3	
High	0.349	3.549	-1.52	1.83	17.5	5.1	18	6.1
High	0.33	2.214	-1.6	1.15	243.6	116.1	257.1	80.5
Not Found	0.01	5.694	-6.64	2.51	8.7	1.9	10.7	
High	0.355	1.907	-1.49	0.93	33.9	17.8	33.9	12
Not Found								
High	0.519	1.562	-0.95	0.64	416.8	246.1	384.5	216.4
High	0.75	2.239	-0.41	1.16	108.1	56	125.4	81.1
High	0.51	4.043	-0.97	2.02	86.6	29	117.2	44.2
High	0.518	1.829	-0.95	0.87	8.4	4.7	8.6	4.3
High	0.568	2.458	-0.82	1.3	146.1	64.3	158.2	83
High	0.673	1.998	-0.57	1	115.7	57.5	114.8	77.9
High	100	0.01	6.64	-6.64		11.1		6.3
High	0.422	1.924	-1.25	0.94	20.6	8.9	17.1	8.7
Not Found								
High	0.534	1.888	-0.91	0.92	65.1	36.4	68.8	34.7
High	0.042	9.214	-4.57	3.2	145.2	14.5	133.7	6.1
Not Found								
Not Found								
Not Found								
Not Found								

es (Grouped) Standard Error [%]: wt, pool	es (Grouped) Standard Error [%]: wt, single	es (Grouped) Standard Error [%]: ko, single	es (Grouped) Standard Error [%]: ko, pool	Abundances (Grouped) Count: wt, pool	Abundances (Grouped) Count: wt, single	Abundances (Grouped) Count: ko, single	Abundances (Grouped) Count: ko, pool	es (Normalized): F5: 126, Sample,
	22.21	15.85		1	4	4	1	102
	40.26	49.28		1	4	4	1	9.5
	24.03	9.49		1	4	4	1	10.2
	19.39	21.41		1	4	4	1	102.8
	16.59	17.36		1	4	4	1	718.3
	13.27	21.45		1	4	4	1	171.9
	31.67	24.5		1	4	4	1	33.5
	51.05	45.34		1	3	4		4.9
	36.18	25.04		1	4	4	1	31.8
	14.79	41.32		1	4	4	1	27.4
	17.36	13.5		1	4	4	1	274.6
	11.96	27.97		1	4	4	1	987.4
	8.08	16.07		1	4	4	1	12.9
	16.64	18.12		1	4	4	1	55.7
	14.85	20.17		1	4	4	1	187.2
	19.11	21.14		1	4	4	1	769.9
	28.07	76.23		1	2	4		7.5
	44.24	42.59		1	4	4	1	29.8
						1		
	38.15	21.33		1	4	4	1	18.1
	22.91	17.02		1	4	4	1	322.5
	61.34	64.39		1	4	4		16.4
	5.64	21.85		1	4	4	1	98.7
	39.68	25.1		1	3	4		3.6
	42.17	33.16		1	4	4	1	2.6
	26.99	20.44		1	4	4	1	57.4
	10.52	38.46		1	4	4	1	32.3
	13.19	21.47		1	4	4	1	41
	5.16	57.05		1	3	4		7.6

15.52	20.36	1	4	4	1	664.2
18.88	40.36	1	4	4	1	33.9
5.7	15.57	1	4	4	1	271.5
	9.91	1		4		91.1
9.23	13.02	1	4	4	1	1172.4
15.53	33.24	1	4	4	1	166.4
31.8	26.11	1	4	4	1	29
27.9	34.71	1	3	4	1	6
16.29	13.38	1	4	4	1	59.4
10.69	12.38	1	4	4	1	477
8.64	12.42	1	4	4	1	269
33.36	25.38	1	4	4	1	161.6
13.18	20.95	1	4	4	1	343.6
14.26	23.18	1	4	4	1	50.4
32.55			2	1		
58.74	34.91	1	4	4		22.7
		1				1.7
				1		
15.15	47.37	1	4	4	1	73.8
14.4	12.66	1	3	4	1	27.8
58.95	30.6	1	4	4	1	54.3
				1	1	
47.22	21.71	1	3	4	1	19.1
	33.73	1		3		2.1
18.24	16.58	1	4	4	1	73.2
33.36	15.01	1	4	4	1	77.8
9.75	18.04	1	4	4	1	744.7
15.43	43.35	1	3	4	1	8
46.49	25.21	1	4	4		15.4
30.08	24.59	1	4	4	1	97
32.47	57.25	1	4	4	1	19
26.59	34.69	1	4	4	1	43.7
45.92	28.5	1	3	4	1	9.2
29.74	17.52	1	4	4	1	24.3
9.81	19.88	1	3	4	1	4.1

9.06	8.82	1	4	4	1	17.9
26.17	15.49	1	3	4	1	30.3
10.29	43.78	1	3	4	1	13.6
	11.18		1	2	1	
19.42	23.87	1	4	4	1	44.1
10.62	18.21	1	4	4	1	1194.7
21.06	16.28	1	4	4	1	50.2
59.48	27.17	1	3	3		2.3
12.45	16.76	1	4	4	1	1225.1
15.77	6.79	1	4	4	1	161.3
20.3	16.04	1	4	4	1	47.7
18.43	53.02	1	2	4		8.6
			1			
22.45	20.81	1	4	4	1	19.6
45.85	13.35	1	4	4	1	42.3
25.68	19.84	1	4	4	1	21.3
23.45	9.82	1	2	2		2.2
24.75	15.21	1	4	4	1	9
19.87	8.93	1	4	4	1	27.7
31.3	81.42	1	4	4		3.3
29.02	52.08	1	2	4	1	3.5
	26.12			3		
35.74	20.07	1	4	4	1	45.1
32.74	40.27	1	4	4		5.4
32.89	26.39	1	4	3	1	2.1
17.07	23.93	1	4	4	1	171.5
26.2	19.08	1	4	4	1	25.6
52.82	11.97	1	4	4	1	24.8
19.19	19.1	1	4	4	1	32.5
25.88	36.89	1	4	4	1	30.7
17.01	18.6	1	4	4	1	185.7
24.31	27.94	1	4	4	1	52.1

21.19	17.18	1	4	4	1	646
8.12	24.16	1	4	4	1	179.8
15.61	26.1	1	4	4	1	148
6.54	12.63	1	4	4	1	229.9
13.11	13.88	1	4	4	1	540.4
54.96	31.33	1	4	4		25.3
25.02	16.14		2	2		
		1				1.6
14.23	16.19	1	4	4	1	94.3
11.4	11.95	1	4	4	1	383.1
31.61	25.61	1	4	4	1	10.4
14.75	14.95	1	4	4	1	36.7
1.58	48.26		2	4		
	18.46			4		
	31.56	1	1	2	1	2.1
	1.4	1	1	2		2.1
			1	1		
36.12	23.47	1	4	4	1	46.7
21.47	13.56	1	4	4	1	65.6
29.9	32.81	1	4	4	1	298.7
18.85	26.8	1	4	4	1	372.6
13.68	29.03	1	4	4	1	338
43.27	24.11	1	4	4	1	53.9
23.22	26.02	1	4	4	1	95.1
25.33	52.09	1	4	4	1	10.2
23.49	21.01	1	4	4	1	194.2
13.46	6.27	1	4	4	1	67.5
27.73	53.43	1	3	4		5.1
6.2	19.64	1	4	4	1	135.2
12.54	15.09	1	4	4	1	16.3
15.21	23.57	1	4	4	1	91.2
53.09	12.87	1	2	3	1	5.3
28.21	18.92	1	4	4	1	104.6
9.75	46.12	1	4	4	1	36.6
17.55	16.7	1	4	4	1	429.4
10.22	21.72	1	4	4	1	365.1
28.63	5.19	1	4	4	1	24.8
21.04	22.66	1	4	4	1	29.9

72.71	10.73	1	4	4	1	38.1
8.4	18.87	1	4	4	1	102
12.72	11.67	1	4	4	1	312.4
41.76	22.2	1	4	4	1	88.7
17.77	24.14	1	4	4	1	202.3
16.21	26.05	1	4	4	1	618
22.97	40.13	1	3	4	1	8.1
41.52	41.45	1	4	4	1	25
7.24	12.53	1	4	4	1	294.6
28.52	32.49	1	3	4		12.8
13.84	17.99	1	4	4	1	662
16.59	15.7	1	3	4		4.1
25.65	19.99	1	4	4	1	90.1
	36.95	1	1	3		1.7
13.66	15.28	1	4	4	1	122.6
				1		
25.28	59.03	1	4	4	1	59.3
14.32	16.99	1	4	4	1	212.2
68.17	38.87	1	4	4	1	37.3
32.65	39.81	1	3	4	1	16.5
	4.9			2		
29.55	24.72	1	4	4	1	82.3
	7.18			2		
19.52	21.63	1	4	4	1	99.6
10.42	29.75		2	3		
12.25	24.3	1	4	4	1	46.8
43.05	28.41	1	4	4		8.7
16.48	24.8	1	4	4	1	508.1
22.7	14.75	1	4	4	1	68.3
	27.3	1	1	4	1	20.5
19.44	7.72	1	4	4	1	248.6
	54.15	1		3		6
	16.81	1		2		2.2
7.44	27.81	1	4	4	1	582.5
17.33	26.39	1	4	4	1	978.8
32.98	10.98	1	4	4	1	17.6
37.44	20.17	1	4	4	1	41.9
27	13.31	1	4	4	1	4.2
12.67	18.01	1	4	4	1	256.4

				1		
				1		
46.87	83.83	1	4	4		8.4
61.04	48.86	1	4	4	1	38.4
50.36	26.88	1	4	4		11.2
		1		1		1.5
		1				2.3
19.06	21.37	1	4	4	1	113.4
	11.49		1	3	1	
19.97	18.31	1	4	4	1	302.4
9.86	22.91	1	4	4	1	39.2
10.17	26.5	1	4	4	1	12
14.75	35.03	1	4	4	1	62.1
15.05	22.64	1	4	4	1	244.7
30.23	27.12	1	4	4	1	134.8
64.15	71.97	1	2	4	1	10.8
20.72	25.12	1	4	4	1	53.4
29.39	18.15	1	3	4	1	10.1
2.15	9.35	1	4	4	1	97.1
13.72	54.95	1	2	3		12
	24.31			2		
12.73	24.35	1	4	4	1	140.8
45.08	44.78	1	4	4		8.9
51.67	32.19	1	3	4	1	4.3
5.51	12.43	1	4	4	1	650.4
71.77	55.11	1	4	4	1	3.8
11.1	30.93	1	4	4	1	227.1
50.15	10	1	4	4	1	21.8
32.59	27.39	1	4	4	1	35.7
87.75	26.31	1	4	4	1	29.6
14.9	22.44	1	4	4	1	114.8
25.44	15.51	1	4	4	1	124.5
	38.38	1	1	3		2
22.72	17.97	1	4	4	1	383.2

61.19	15.41	1	3	4	1	12.2
32.05	29.35	1	3	3	1	16.4
39.65	46.9	1	4	4	1	48.8
17.32	27.03	1	4	4	1	1051.9
14.69	27.42	1	4	4	1	635.4
31.64	25.08	1	4	4	1	57.3
34.01	38.77	1	4	3	1	8.4
15.28	17.47	1	4	4	1	39.3
16.55	20.32	1	4	4	1	76.6
16.9	24.76	1	4	4	1	80.2
52.2	43.02	1	3	4		17.6
83.37	48.02	1	3	4		6.2
33.87	36.49	1	3	4		13.1
15.52	24.86	1	4	4	1	73.8
36.64	35.29	1	4	4		18.7
36.84	23.04	1	4	4	1	42
23.86	49.21	1	4	4	1	39.7
30.89	12.34	1	4	4	1	48.2
55.63	7.43	1	4	4		17
26.85	19.3	1	4	4	1	94.3
17.41	20.34	1	4	4	1	803.2
4.47	13.66	1	4	4	1	222.3
5.84	12.97	1	4	4	1	257.2
12.81	25.56	1	4	4	1	132.3
15.07	20.53	1	4	4	1	21.4
67.27	14.79	1	3	4		3.8
	2.87	1	1	2		1.8
45.9	55.86	1	2	4		2.2
	36.36	1	1	4		9.4
27.97	18.63	1	4	4	1	42
13.91	15.12	1	4	4	1	251.1
16.84	19.43	1	4	4	1	194.3
7.82	17.51	1	4	4	1	65.2
11.44	31.56	1	3	4		3.6
14.11	19.96	1	4	4	1	51.5
37.39	17.81	1	2	4		5.7
25.62	18.9	1	4	4	1	26.2
19.12	31.32	1	2	4	1	8.4
19.86	10.58	1	4	4	1	28.2
33.52	16.94	1	4	4		5.3
	33.1	1		4	1	5.3
15.25	66.09	1	2	4		17.9
22.32	58.26	1	3	4	1	8.7

36.98	22.5	1	4	4	1	19.8
	12.82	1		3		2.6
	54.39			3		
20.72	16.93	1	4	4	1	91.1
12.69	7.52	1	4	4	1	15.5
16.81	22.4	1	4	4	1	167.3
65.57	21.99	1	4	4	1	6.5
22.49	31.11	1	4	4	1	75.7
17.14	29.87	1	4	4	1	509.5
41.37	22.46	1	4	4	1	56.7
23.69	64.93		2	2		
	17.93	1		2		2.8
12.95	20.5	1	3	4	1	6.8
10.8	14.44	1	4	4	1	32.5
27.94	43.85	1	4	4		8.9
10.27	19.86	1	4	4	1	339.1
18.65	15.07	1	4	4	1	235.4
11.02	23.81	1	4	4	1	2861.8
14.93	18.37	1	4	4	1	393.1
22.23	29.67	1	4	4	1	212.1
19.31	23.82	1	4	4	1	268.9
22	28.74	1	4	4	1	123
25.39	26.83	1	4	4	1	208.6
13.5	18.52	1	4	4	1	647.3
19.72	12.97	1	4	4	1	122.4
10.42	23.61	1	4	4	1	86.4
	6.56	1	1	2		2
	61.36	1		3		3.2
	20.82	1		3		3.3
23.04	16.55	1	4	4	1	43
10.33	22.4	1	4	4	1	1179.4
13.55	36.56	1	4	4	1	66.3
8.12	24.04	1	4	4	1	91.1
14.99	12.31	1	4	4	1	3164.2
13.09	13.31	1	4	4	1	5527.6
9.84	17.69	1	4	4	1	123.6
10.84	18.57	1	4	4	1	193.8
35.04	42.15	1	4	4	1	15.5
	37.69	1	1	4	1	2.3
3.22	12.02	1	4	4	1	191.5

13.7	14.57	1	4	4	1	159.6
40.68	32.18	1	4	4	1	6.9
17.06	7.84	1	4	4	1	39.9
56.56	51.32	1	4	4		16.3
41.44	27	1	4	4	1	4.9
11.32	11.14	1	4	4	1	80.8
32.57	23.64	1	4	4	1	42
40.5	44.65	1	3	3	1	1.6
11.86	15.57	1	4	4	1	180.4
	18.58	1	1	3		5.9
39.79	44.88	1	4	4	1	19.7
64.8	49.64	1	3	4		11
23.9	24.11	1	4	4	1	291.2
3.88	20.86	1	4	4	1	216.4
25.5	19.67	1	4	4	1	54.1
25.88	42.17	1	4	4		6.8
14.44	5.1	1	4	4	1	75.2
33.77	18.06	1	4	4	1	15.6
5.99	17.6	1	4	4	1	247.7
20.13	16.81	1	4	4	1	30.6
21.76	25.24	1	4	4	1	125.7
19.52	16.33	1	4	4	1	34.4
24.66	24.38	1	4	4	1	66.9
13.2	28.28	1	4	4	1	59.9
7.56	21.76	1	4	4	1	53.9
21.91	20.03	1	4	4	1	65.7
14.3	15.4	1	4	4	1	67.9
	5.51		1	4		
18.06	24.55	1	4	4	1	48.6
8.52	14.33	1	4	4	1	213.9
37.24	29.71	1	4	4	1	16.8
37.61	45.32	1	3	4		27.7
	27.45		1	2		
18.08	19.61	1	4	4	1	926.2
42.91	25.99	1	4	4	1	11.8
42.39	30.78	1	4	4	1	31.7

29.08	54.93	1	4	4	1	38.1
18.23	24.01	1	4	4	1	11.7
	22.87	1	1	3	1	3
18.56	15.9	1	4	4	1	116.9
23.19	25.48	1	4	4	1	12.1
22.91	14.55	1	4	4	1	184
30.54	19.04	1	4	4	1	18.7
79.01	58.55	1	3	4	1	17.3
12.78	17.3	1	4	4	1	307.9
20.52	29.38	1	4	4	1	27.7
	16.01	1	1	3		1.8
6.86	11.41	1	4	4	1	1915.5
25.55	30.48	1	4	4	1	86.3
	25.12	1	1	3		4.3
22.67	23.31	1	4	4	1	1217.4
7.48	22.41	1	4	4	1	53.6
14.53	23.57	1	4	4	1	37.8
53.2	24.99	1	4	4	1	13.3
18.27	18.95	1	4	4	1	308.2
7.64	24.91	1	4	4	1	103.6
70.87	60.45	1	4	4		6.8
39.34	33.96	1	4	4	1	33.6
40.77	34.76	1	2	4		6.2
23.04	27.03	1	4	4	1	68.5
14.53	26.12	1	4	3	1	6.8
49.25	21.92	1	4	4	1	8.3
		1	1	1		2.2
19.36	14.87	1	4	4	1	214
16.3	17.6	1	4	4	1	196.8
	25.36			2		
10.08	15.77	1	4	4	1	83.8
71.33	27.1	1	4	4	1	16.3
16.55	7.3	1	4	4	1	129.3
11.39	18.17	1	4	4	1	162.4
14.07	10.73	1	4	4	1	129.9
10.75	16.98	1	4	4	1	255
34.58	15.62	1	4	4	1	18.1

12.76	31.76	1	4	4	1	134.9
12.18	22.72	1	4	4	1	147.5
19.83	11.83	1	4	4	1	55.1
20.36	22.06	1	4	4	1	2862.9
18.01	54.53	1	4	4	1	12.3
30.73	70.67		3	2		
15.57	25.89	1	4	4	1	94.1
11.57	10.82	1	4	4	1	206
4.76	8.02	1	4	4	1	66.3
16.04	9.41	1	4	4	1	47.6
17.96	5.64	1	4	4	1	19.5
26.58	16.06	1	4	4	1	17.4
9.86	18.55	1	4	4	1	221.3
18.39	23.76	1	4	4	1	52.2
53.14	34.52	1	4	4		15.8
7.74	25.33	1	4	4	1	125.1
15.45	26.64	1	4	4	1	711.5
12.8	7.1	1	4	4	1	19
36.87	23.07	1	4	4	1	65.1
2.87	54.68	1	3	4	1	11.7
34.71	34.74	1	4	4	1	46.8
31.7	42.41	1	4	4		11.2
42.18	66.6	1	3	4		5.7
40.95	26.32	1	4	4	1	50.9
41.65	44.05	1	3	4		5.5
11.07	16.7	1	4	4	1	323.6
38.09	24.15	1	4	4	1	14.9
18.85	23.51	1	4	4	1	1376.9
13.67	21.91	1	4	4	1	2107.8
23.38	20.77	1	4	4	1	68.8
16.98	20.95	1	4	4	1	195.2

	22.16	1		4		6.5
		1		1	1	1.7
41.34	18.88	1	4	4	1	31.4
10.27	15.56	1	4	4	1	653.6
30.16	15.21	1	4	4	1	15.4
	22.77	1		2		2.2
36.36	40.43	1	4	4	1	55.5
49.84	26.25	1	4	4	1	34.5
26.08	9.57	1	4	4	1	62.5
12.4	16.16	1	4	4	1	2028.3
19.56	24.98	1	2	4		2.7
64.18	25.96	1	4	4	1	15.4
28.62	18.26	1	4	4	1	169.9
30.76	18.93	1	4	4	1	24.5
20.92	8.34		3	3		
20.73	20.22	1	4	4	1	32.2
39.75	28.36	1	4	4	1	50.6
13.19	20.56	1	4	4	1	22.4
10.01	53.24	1	2	3	1	2.5
	30.78		1	4		
42.72	24.61	1	4	4	1	17.5
19.58	15.5	1	4	4	1	243.6
0.92	55.9	1	2	3		8.7
24.07	18.63	1	4	4	1	33.9
10.66	21.03	1	4	4	1	416.8
18.5	30.78	1	4	4	1	108.1
14.07	20.84	1	4	4	1	86.6
58.47	41.23	1	4	4	1	8.4
12.41	22.43	1	4	4	1	146.1
7.77	14.16	1	4	4	1	115.7
41.29			4		1	
27.01	38.55	1	4	4	1	20.6
20.57	27.14	1	4	4	1	65.1
37.61	24.5	1	4	4	1	145.2

es (Normalized): F5: 127N, Sample,	es (Normalized): F5: 128N, Sample,	es (Normalized): F5: 129N, Sample,	es (Normalized): F5: 130N, Sample,	es (Normalized): F5: 127C, Sample,	es (Normalized): F5: 128C, Sample,	es (Normalized): F5: 129C, Sample,	es (Normalized): F5: 130C, Sample,	es (Normalized): F5: 131, Sample,
40.4	59.9	50.9	68.9	100.6	109.5	81.2	119.6	78.7
3.5	9.7	5.8	6.9	13.3	17.1	6.6	6.2	2.8
10.1	16.4	10.5	11.5	13.4	16.2	13.4	15.2	4.7
56.8	57.2	42.6	39	91.1	114.4	66.9	89.9	21.7
396.1	395	305.1	288.4	643.6	828.2	547.2	719.3	292.9
114.4	111.1	106.1	83.8	176.3	180.2	113.4	135.2	74.4
13.3	28.5	18.3	19.9	39.3	41.2	24.9	27.8	16.6
4.5		1.8	2.2	6.5	10.6	4.9	3.9	
23.4	18.2	16.1	8.9	34.4	32.7	21.7	21.6	7.3
10.7	8.2	8	10.2	22.9	28.1	8.4	22.1	9.1
198.1	168.9	157	129.7	243.8	286.1	205	251.6	130.2
391	403.5	317.9	423.1	740.2	1035.2	1126.2	1484.5	527.6
5.5	4.5	5	4.9	17.2	16.6	11.8	15.2	7.9
17.4	26	20.6	23	47.3	58.8	65.1	73.7	22.5
105.6	107.5	81.9	82.8	167.9	205.1	130.6	144.1	64.7
298.2	310.4	224.8	212.5	696.7	827.9	510.2	584.8	188.2
2.3	1.5			7.1	11.6	1.9	2.7	
7.9	18	9.1	8.4	35.2	38.3	18.9	15.4	7.9
				2.1				
4.6	4.3	2.9	7.2	14.2	21.4	23.9	23	2.8
103.3	142.9	87.9	95	299.5	362.5	237.1	307.1	68.8
2.2	6.1	2.3	2.1	8.8	17.5	3.9	6.5	
41.2	40.8	44.6	45.7	89.5	116	116.4	152.6	59.4
	2.6	1.8	4	5.6	9.2	6.5	5.7	
2.9	1.3	3.2	4.3	5.5	6.9	9.3	4.3	7.1
17.6	22.9	12	22.1	49.4	63.1	57.3	79.5	22.3
5.5	6.5	7	6.8	49.4	33.7	21.3	25.2	7.9
28	31.6	23.3	30.7	46.4	57.5	33.8	43.7	31.8
	2.1	2.2	2.4	2.3	10.6	6.3	12.3	

317.3	345	265.8	387.6	599.6	772.1	780.2	990.3	436.9
18.3	15.3	24.1	20.5	43.8	42.9	26	17.1	13
123	116.9	108.5	122.5	247.5	281.5	283	355.4	146
				92.5	92.2	93	111.9	
514.3	494.5	413.1	480.5	1060.5	1153.9	1314.3	1420.9	579.7
66.5	86.9	75.8	61.2	161.7	199.7	88.9	124.4	59.4
20.6	20.4	19.5	9.1	26.2	37.9	20.4	27.4	9.7
3.7	2.6		2.2	4.7	4.2	7	3.1	3
81.5	79.1	63	58.4	65.8	63.4	48.9	54.8	62.3
685.6	678.6	620.5	539.9	478.1	407.2	363.6	380.8	459
412.4	428.5	393.5	349.4	284.3	248.7	217.5	224.1	292.1
69.7	76.7	40	41.3	125.5	180.4	102.8	120.3	23.9
185.2	178.4	139.1	152.9	345.5	380	226.8	305.6	134.9
27.4	26.5	31.6	22.3	53.8	53.8	85.6	69.7	28.2
	1.7		2.7			4.3		
2.3	1.8	1.8	5.2	17.7	31.5	18	34.6	
				1.8				
29.4	28.7	27.5	20.7	93.6	104.9	40.8	43	22.7
4.5	5.9		5.6	23.3	29.1	30.9	31	3.2
12.3	25.9	14	5.5	62.3	73.9	38.5	42.8	4.1
					2			2.8
	2.5	3.3	6	25.4	29.1	26.1	16.8	5.7
				1.3	2.5		2.6	
38.5	44.5	42.8	28.8	67.4	77.5	54.1	57.2	23.1
16.6	21.2	8.7	15.8	78.8	86.7	67.7	97	15.8
290.4	291.7	234.7	273.1	621.3	814.4	689.9	933.4	323.9
5.8	6.6		4.9	6.5	13.9	7.7	16.6	6.5
8.9	3.1	4.1	5.9	16.1	18	10.6	11.6	
60.9	59.9	35.8	35.1	89.3	105.8	65.9	64.1	23.5
8.9	8.7	13.6	6.3	28.2	41.4	11.6	14.6	3.2
28.3	26.4	16.8	17.6	37.5	62.6	33.8	31.5	11.6
7.6	2.7		5.9	8.7	7.7	7.5	4.1	3
15	8	8.8	10.5	25.8	37.5	31.5	26.9	7.5
2.3		2.8	2.4	3	3.7	3	4.5	3

9.8	9.5	9.8	11.5	24.7	27.9	23.8	28.4	13.4
	11	6.5	8.7	25.9	32.5	30.4	37.7	15.4
2.6		2.6	3.1	13.5	20.8	10.3	7.5	3.7
			2.2	1.4	1.6			3
17.9	12.5	20.4	17.6	46.8	66.9	38.7	47.8	10.8
532.1	635.2	511.4	615.4	1058.5	1478.5	1451.8	1673.8	767.3
19	31.5	24.2	28.8	46.4	51.5	35.1	40.8	17.4
	1.7	5.2	2.5	1.3	2.2	2.2		
615.1	690	526.9	546.2	1029.8	1456.4	1119.8	1405.9	564.3
58.4	69.2	82.1	82.3	160.3	162.7	141.3	146.8	80.3
16.2	26.2	19.4	21.2	48.2	57.4	46.5	65.3	20.7
2.7	3.6			8.4	3.2	2.8	4.8	
		1.9						
10.8	11.4	13.6	17.4	14.7	19.9	23.8	17	13.8
11.4	31.1	16.5	15.8	53.3	65.2	49.9	64.4	11
18.6	25.8	20.5	13.6	22.9	25.2	26.3	16.3	14.2
4.6		3.3			2.1	1.8		
9.5	13.4	8.3	8.3	8.5	9.6	7.7	11	2.8
13.3	16.4	10	12.7	26	29.4	23.8	27.4	3.7
1.9	3.4	4.1	2.8	13.4	8	1.8	2.9	
	6.9	4.5		6.5	7.5	2.3	11	3.6
				2.1		1.9	3.1	
15.1	33	24.8	17.4	48.9	66.9	42.5	60	10.3
2	2	1.9	3.5	8.8	9.5	6.5	3.3	
3.2	1.7	1.7	2.2	3.5	5.6		3.8	4.1
72	89.3	67.7	96.9	144.1	185.9	181.8	254.2	129.6
7.9	4.6	8	9.1	34.4	25.2	22.7	31.5	11.2
2.7	8.9	5.1	10.8	27.4	24.3	23	20.6	6.7
20.3	14.8	15.8	13.1	28.8	40.1	26.9	29.5	16.2
19.6	14.7	16.6	10.2	31.8	39.6	19.9	18.3	6.7
122.1	118.2	84.7	95.9	154.1	209.1	136.9	163.1	97.2
26.2	36.1	20.2	32.5	59.3	64.5	32.4	47.6	26.4

363.4	378.4	297.3	231.6	553.5	658.2	429.2	540.5	244.8
85.1	93.8	99.6	102.7	214.5	204.6	126.2	152.5	91.3
80.9	82.4	61.5	63	138.2	168.2	91.1	112.5	67.3
107.3	124.8	111.2	114.9	236.8	280.6	209.5	264.3	114.8
212.3	221.5	162.2	205.4	481.6	634.1	539.9	650.9	227.6
6.9	13.4	7.6	3.1	24.9	31.3	14.7	19.7	
		2.1	3	2	2.5			
29.3	35	27.7	37.3	85.7	96.9	64.7	82.4	20.5
191.5	220	171.4	177.2	367.5	425.3	323.3	408.2	192.3
5.8	13.3	10.2	11.7	8.4	14.2	15	16.1	6.9
33.7	39.8	28.8	39.4	39.6	32.7	37.1	27.9	38.3
	2	2.1		1.6	3.7	5.6	6.2	
				3	3.3	2.2	3.4	
		1.8			1.3	2.1		3
	7.2				2.4	2.5		
			2.2			1.8		
9.7	19.7	13.9	9.6	32.9	50.4	41.8	57.7	12.4
21.3	35	24.6	28	70.2	72.7	53.1	63.2	33.7
141	152.8	86.8	87	295.9	340.3	161.3	204	79.7
210.3	230.3	170.3	151.8	353.7	400.2	220.1	260.9	161.9
220.9	225.1	197.7	164.8	321.8	391.4	199.3	248	155.6
9.4	21	15	8.4	49.5	50.2	34.1	31.3	10.8
29.1	46.4	48.3	34.8	76.4	100.7	120.6	143.9	55.6
12.5	24	18.4	18.9	4.4	11.8	7.9	16.8	30.8
68.4	61.8	37.7	56.8	179.5	209.5	176.9	271.5	74.8
169.2	166.9	143.4	199	73.4	63.5	72.1	69.7	222.3
	3.9	2.5	2.5	2.2	9.1	10.8	6.2	
83.4	83.8	75	86.9	105.3	153.9	131.3	168	106.5
12.5	12.8	12	9.6	15	21.9	19	19	13.4
47.7	54.6	47.9	37.3	93	104.7	61.3	72.6	31
4.2	1.9			5.9	6.1	4.8		3
29.3	51.2	29.7	44.3	86.1	123.4	105.4	134.6	48.7
10.7	8.5	10.2	9.3	42.6	42	22.5	14.7	5.9
391.4	442.4	340.5	293.2	359.3	503.1	357.8	421.9	320.5
142.3	156.2	128.8	162.6	323.4	429.8	432.1	554.5	219.1
6.1	7.1	5.4	3.4	22.5	21.8	20	22.3	8.7
9.8	12.9	7.8	11.7	31.4	38.5	26.3	44.5	7.1

106.6	47	29.4	24.5	36.3	34	43	35.5	38.3
29.4	34.8	31.4	29.1	103.3	113.7	109.5	153.3	61.1
444.2	428.8	418.7	329.6	324.5	312.3	249.5	278.2	301.8
32.7	42.5	14.2	25.2	77.1	98.8	57	75.4	22.5
102.1	109	91.4	71	194.6	225	130.6	151.9	46.6
329.5	334.9	282.7	232.4	594.7	677.7	372.6	456	208.9
3.9	4	5.8		2.7	3.2	3.5	6.2	3.4
9.8	13.7	7.8	4.7	23.9	29.7	15.9	11	6.3
123.2	134.8	115.8	134.3	295.2	365.3	305.8	379.6	134.1
	3.2	1.8	3	5.7	13.1	11.5	9.3	
401.5	398.1	350.8	294.8	582.9	695.1	448	545.1	241.4
3.5	3	2.5		3.3	3.3	2.3	3.3	
33.6	32	20.6	40.1	90.4	102.4	98.2	138.8	52.5
		2.2		1.5	2.3	3.2		
58.8	66.9	62.7	48.1	122.1	136.5	95.6	108.1	58
					2.4			
7.5	10.1	11.6	14	83.7	77.4	32.9	20.4	6.7
100.7	92.8	76.1	107.4	166.8	238.6	227.1	251.8	103.4
2.3	13.8	4.7	8.7	34.2	43.4	14.5	32.5	10.5
3.6	4.4	2.2		9.6	13.5	4.9	7.9	3.7
				5	5.4			
40.2	42.6	25	24.2	85.1	102.1	55.1	75.2	33.3
				2.3	2.1			
31.1	42.5	28.1	30.4	101	125.1	78	84.5	23.1
	1.4	1.7			1.5	1.9	2.7	
26.1	22.8	20.1	26.1	58	57.7	36	39.7	26
2	5.6	4.3	2.8	7.7	6.3	3.9	5.1	
256	251.8	211.6	177.6	499.5	560.9	320.6	381.7	169.4
30.6	35.4	21.3	37	67.4	80.6	74	94.7	27
	1.5			16.4	10.6	8.9	11.3	3.7
75.7	76.1	50.5	81	238.1	270.7	242.4	277.7	89.9
				10.8	4.2	5		
						4.1	3.3	
297.5	250.3	264.8	280.8	456.3	591.3	867.5	796.7	426.6
412.7	513	359.6	519.5	791	1156.8	1036.3	1502.3	595.7
11.7	13.1	9.9	5.5	14.4	17.6	16.1	13.9	16.8
24.9	14.6	15	10.6	24.2	33.5	20.9	27.2	20.7
2	3.9	3.4	2.8	12.7	9.6	12.1	13.2	3
25.4	30	29.7	34.7	208.6	287.9	198	262.9	31

					1.5			
					1.3			
2.7	5.6	5.2	1.9	6.6	12.9	1.8	2.7	
10.4	21.1	8.5	5.2	34.3	45.4	15.8	18.5	3.6
2.5	8.7	5.8	10.2	9.5	17.6	12.3	16.4	
						2.5		
36.8	54.6	39.6	51.2	109.8	135.5	128.2	179.5	67.7
		1.9		1.4	1.7	1.7		4.7
143.9	161.9	119.4	102.2	283.2	336.3	214.5	264.7	81.3
24.9	25.6	20.5	22.9	33.7	43.9	45.6	59.1	31.2
11.4	9	11	11.1	10.9	18	15.2	21.1	6.1
20.5	26	21.6	18.4	70.9	76	38.7	40.1	15.6
113.8	131	101.8	92.8	261.3	287.4	170	209.5	90.7
69.4	79.5	62.2	35.9	122.1	148	88.6	84.3	19.9
	4.4	1.7		21.6	10.2	5.8	5	6.1
20.8	25.2	15.7	25.1	46.8	58.4	73.1	84.5	25.4
2.5	2		3.5	8	8.4	11.4	11.1	6.1
80.5	76.7	79.9	79.7	94.5	93.6	99.6	113.9	97.6
2.2	1.8			25.1	20	6.7		
				1.7	2.4			
53.4	50	42.8	58.3	90	139.9	128.1	167	84.2
4.2	8	9.8	3.8	9.3	10.4	3.9	5	
2.5		2.5	5.6	3.6	6.8	3.7	4.3	2.8
341.3	345.7	305	331.1	622.4	709.5	531.6	684.2	351.5
2.9	3.3	2.3	9.1	1.9	6.1	8	10.6	5.9
88.7	99.2	85.6	108.9	182.6	268.6	264.2	390.1	129
6.9	13.4	13.8	4.1	22.8	20.9	18.7	18.5	14.4
13.6	9.5	10.3	18.9	25.8	38.8	46.6	51.2	18.1
2	13.9	1.8	14	29.3	52.7	40.6	33.4	9.7
51.3	55.7	39.5	44.9	105.6	123.2	74.5	84.6	28.2
62.7	83.3	45.5	57.1	134.4	151.9	103.5	138.4	37.9
	2			3.6	1.6		3.6	
184	219.6	147.8	132.8	372.7	416.3	265.8	352.5	142.2

2		8.3	5	12.4	9.2	9.2	9.6	2.8
2.6	4	5.1		10.6	11.6		6.3	4.7
21.2	33.4	22.7	11.8	49.8	60.8	22.3	25.9	13.6
522.3	595.2	473.4	390.8	1055.3	1130.8	616.5	769.1	366.3
333.7	367.4	281.2	269	670.4	669.4	387.3	443.2	237.1
31.1	44	35.2	19.3	68.9	90	49.7	61.5	22.7
5.2	12	8	7.8	8.3	15.2	8		6.1
34.3	44.3	36.9	47.7	42.4	43.7	50.8	61.3	55.2
50.8	57.1	38	47.2	67	81.5	75.9	106.2	56
29.1	39.8	37.1	44.3	67	97.8	69.6	110.5	42.4
7.2	9.9		3	11.7	15.6	5	9.1	
2.3	7.7	1.8		4.7	17.9	10.5	15.1	
5.6	5	2.8		9.9	16.1	6.8	9.8	
33	41	28.3	37	74.4	87.4	82.9	126.4	62.1
2.7	7	4.4	5.2	9.5	21.7	20.3	25.2	
13.3	19.5	7.6	18	37.7	50.1	30.1	33.6	3
14.3	10.3	11.8	8	40.2	60.6	23.2	22.3	10.1
36.6	31.9	21.7	18.7	43.1	57.1	46.2	48.1	19.1
2.9	7.8	2.9	3.5	16.5	14.8	15.6	13.9	
29.1	47.5	26.8	34.2	99	116.8	104.1	149.4	38.7
401.1	413.4	299.6	302	821.4	934.7	564.9	739.8	299.6
151	162.5	162.8	168	215.5	237	238.5	294.3	209.1
220.2	207.1	191.5	201.4	244.1	272.9	262.1	327.4	261.4
86.1	85.1	84.6	64.8	139.1	156.6	90.8	100.9	57.8
8.5	11.4	8.5	10.6	21.3	21.7	13.4	18	9.5
6.1	2.3	1.9		8.1	8.7	10.2	7.2	
		1.8		4.1	3.9			
1.7			3.4	1.4	6.7	5.6	3.3	
	1.5			4.5	8.1	11.4	11	
18.6	27.1	14.6	17.1	33.7	50	42.4	51.9	20.7
110.6	118.9	89	123.8	225.2	276.8	255.3	322.2	138.7
158.5	162.3	124.6	115.5	163.6	200.5	126.1	150.1	103.6
30.7	30.4	25.9	28.2	72.4	69.6	47.8	61.8	27.4
2.7		2.2	2.7	6.1	3.9	2.8	4.3	
12.5	14.4	13.9	17.4	49.5	59.7	63.4	79.8	25.4
	5.6		3.2	12.1	11.4	9.3	14.4	
16.7	11	10.9	9.9	29	40.9	39.7	28.9	8.5
	3.7		2.8	15.8	27.9	24.7	14.7	2.8
9.8	8.2	6.9	10.9	35.7	35.5	32	41.3	9.9
3.9	4.4	1.8	3.4	8.3	12.5	10.7	9.8	
				10.2	4.7	10.3	11.5	9.9
	1.7	2.1		12.2	16.1	2.3	6.3	
	1.9	1.8	2.7	4.9	46	34.4	39.7	3.6

6.2	15.4	10.6	9.3	25	16.5	27.8	20	9.9
					5	4.5	5.8	
				1.3	1.3	3.1		
52.6	41	33.4	36.3	87	107.5	74.7	78.3	29.4
14.7	13.8	11.8	11.2	19.9	21.5	18.2	21.2	7.1
68.5	67.7	48.8	73.6	141.5	188.5	185.6	245.5	92.9
3.2	8	2.2	2.8	3.4	5.5	4.8	5.8	2.8
39.2	44.8	30.8	27.1	74	75.8	37.8	50.4	32.7
346.7	346.6	272.3	417.4	437.4	555.9	623	878.3	508.9
20.2	25.5	9.4	13.7	55.4	75.6	67.4	94.6	31
		1.8	2.5	1.5	4			
				2.5		1.9		
4		4.4	3.4	9.4	12.6	11.1	15.2	4.9
11.5	12.9	15	13.1	31.8	44	35.8	41.6	10.5
3	1.7	2.3	3.2	7.2	7.3	2.8	3.8	
199.7	205.7	162.8	200.1	294.2	374.3	434.3	474.2	255.6
103.7	123.6	87.4	82.6	195.8	235.7	177.2	244.8	80.7
1311	1425.9	1138.9	1468.2	2254.2	2981.8	3262.5	4063.1	1738.7
202.6	200.8	156.8	154.3	395.5	454.4	292.3	351.5	153.7
98.5	134.4	88.7	84.8	216.5	239.3	117.9	162.4	70.6
174.1	164.9	147.6	109	268	292.1	173.5	200.9	83.2
37.1	50.3	44.2	29.8	127.2	156.8	86.7	90.6	24.1
138.6	132.5	99.9	77.9	203	254.6	133.4	172.2	74.2
269.2	338.3	259.1	328.3	605.6	737.6	683	926.4	445.6
50.5	54.2	46.1	71.1	133.2	141.6	109.1	148.9	75.9
36.9	37.5	37	45.3	85.5	116.6	107.6	150.9	75.5
	1.5			2.4	2.2			
				2.1	1.6	4.9		
				3	3.4		4.5	
13.4	15.2	14.3	8.6	36.8	47	40.6	31.7	11
462.6	461.4	387.4	498.7	945.6	1265.7	1237	1640.7	619.6
40.2	47	34.8	46.2	60.4	88.9	84.1	141.7	67.9
51.9	61.1	53	52.1	92.7	107.6	69.7	64.6	34.9
1931.1	1995.2	1474.2	1561.6	2658.5	3379.9	2715.7	3261.6	1558.6
2867.5	2955.8	2272.7	2379	5040.3	6023.4	4379	5483.7	2260
46.9	52.8	41.7	45.7	120.4	136.8	87.7	119.2	48.5
102.2	106.7	97.1	82.5	171.4	219.9	139.7	179.7	84.8
6.8	2.8	7.4	6.3	27.3	21.2	13.9	10.1	9.1
	3.2			1.6	1.6	2.5	3.4	3.6
130.8	138.5	130	137.1	195.6	229.1	171	205.6	144

183	199.8	146	197.6	154.6	170.4	179.9	216.5	230.8
5.5	14.5	8.5	8.6	12.8	7.7	6.1	10.3	17
15	14.5	10.7	16.4	45.8	39	39.7	44	10.8
5.5	14	5.4	5.5	15.4	19	9	5.1	
9.1	12.3	14.3	4.7	12.5	9.3	7.1	13.2	5.7
155.9	151.3	120.4	151.4	74.2	79.7	96.1	85	176.5
42	40	26.7	20.2	54.9	56.5	49.3	31.7	18.1
	6.1	5.4	2.5	6.3	3.8	2.6		4.5
78.2	90.6	67.7	80.7	147.9	203.5	166.1	204.4	94.1
		1.8		4.6	6.7		6.2	
13.7	15.9	7.2	7.5	14.3	29.7	10.6	19.5	12
	5.3	1.7	2.2	5.7	14.1	4.8	10.6	
123.6	158.1	119.8	86.8	270.6	322.7	189	213.1	65.1
110	109.1	102.8	112.7	190	249.8	234.8	314.7	139.3
27.3	28.1	16.2	31.3	50.3	68.7	69.1	82.7	41.6
6.6	10.6	6.6	6.6	11	14	4.4	8.9	
33.3	40	30	29.7	67.8	74.9	67.4	68.3	25.2
10.8	12.8	12.7	5.3	16.9	19.4	13.3	13.7	14.4
111	112.5	100.6	101.1	196	253.7	216.8	291.7	86.2
31.9	52.2	42.9	40	31.3	29.3	42.1	32.5	44
35.9	60.7	47.2	55.8	122.5	142.3	147.1	213.3	76.5
9.7	14.2	14.9	11.4	29.4	35.1	32.7	42.8	14.2
33.3	27.8	19.5	21.4	57.3	68.8	79.2	101.2	17.8
20.5	22	17.1	23.5	51.5	67.3	71.2	100.7	28.4
23.9	28.7	26.4	27.3	58	80.1	75.8	99.5	44.2
19.8	24.2	14.6	17	46.2	59.8	57.3	75.2	23.7
29.4	38.3	37.1	29.5	57.6	71.5	59.8	79.7	45.2
	2.5			3.2	3.3	3.2	3.6	
18.3	13.8	12.4	17.1	40	55.2	56.3	73.8	15.2
75.4	88.9	76.8	87.3	179	236.3	210.8	250.4	112.4
15	10.3	8.5	6.2	15	15.4	12.1	7.4	10.5
9.7	14.2		6.6	28.9	32	13.4	13.4	
2.3				3.1	4.6			
546.9	561.8	450.8	375.2	831.2	950	601.1	706.1	375.4
3.3	11.4	10.7	8.7	20.4	17.4	10.7	14.7	5.9
2.7	9	7.2	9	54.3	51.1	31.3	30	18.3

8.9	10.8	8.9	15.8	60.3	40.1	27.5	14.4	9.3
9.5	8.7	8.5	6	12.2	12.4	18.6	18.8	4.1
	4.3			3.6	5.4		3.8	3.7
70.7	80.5	60	52.5	96.4	124	87.7	94.6	41.8
7.4	6.8	6.9	4.1	9.8	15.2	9	10.1	7.3
108.7	132.4	92.6	77.3	170	211.6	152.7	166	74
3.9	7.8	7	8.7	22	26.7	19.6	17.1	3
4.8	12.7		2.7	10.5	18.7	6.1	5.8	3.2
165.4	185.1	151.3	137.2	325.6	344.2	229.9	280.1	140.2
26.4	39.4	34.4	26.1	31.2	35.1	21.2	18.8	11.2
	1.7			2.5	2.8		3.4	
1724.9	1620.2	1748.9	1910.8	2111.9	1643.8	2070.2	1832.6	1805.2
57.8	54.7	32.1	41.9	90.9	118.4	59.8	70.2	41
			3.4		5	4.9	3.1	
820.6	882	641.3	527.8	1114.7	1286.5	767.6	869	487.6
32.2	31.8	28.3	27.9	47.7	61.4	34.9	49.5	19.7
13.8	18.4	15.1	13.6	25.1	35.3	38.7	45.6	15.6
3.6	9.1	3.3	4.4	12	13.2	16.5	20.7	7.5
188.6	207.1	174.9	131.8	283	328.2	210.3	245.8	125.8
47.2	50.2	44.2	42.2	99.7	124.6	74.9	76.4	28.8
7.6	2.1	2.9	2.2	5.3	14.5	5	5.7	
14	17.1	8.8	7.1	44.1	43.1	29.2	20	6.3
	4.3		2.4	8.5	3.7	5.2	7.4	
41.8	38.7	32.6	23.9	55.4	73.2	36.9	64.9	28.2
7.2	5.2	7	7.2	8.2	9.3	5.4		3.7
2	2.4	4.8	1.9	24.3	23.2	17.2	29.8	2.6
1.6				1.7				
77.4	106.4	68.8	81	182.8	239.8	179.7	228.2	71.2
82.3	80.8	71.5	56.5	160.1	212.6	143	163.8	41.4
				2.2	1.5			
34.9	40.5	33.2	32.8	77.4	108.2	107.7	111.5	53.5
2.3	11	7.3	2.7	18.4	27.3	30.5	17.8	11.2
56.7	77	53.8	66	123.4	141.2	120.9	134.3	70
81.2	92.4	74.8	71.7	163	207.1	162	232.6	97.6
86.4	97.6	101.4	120.7	147.7	137.5	123.7	159.7	129.2
125.5	140.5	113.8	111.8	219.7	266.8	189.5	274.9	112.2
10	6.1	7.3	4.3	17.1	16	12.3	17.8	3.7

51.2	62	46.1	50.9	123.8	149.5	67.5	99.4	26.2
84.4	92.8	79.5	69	145.6	168.3	98.8	119.9	65.7
20.5	22.2	18.8	29.1	78	81.9	68.3	91.1	33.5
1629.3	1754.8	1317	1104.8	2402.1	3115.8	1890.3	2151.5	983.9
234.8	261.9	201.8	171.7	19.4	12.6	3.6	11.8	146.6
2		1.9	3.2		1.4	4.3		
43.1	43.7	33.3	32.9	82.8	105.8	64.2	61.8	18.1
90.1	105.4	79.5	93.1	178.6	219.1	183.5	217.6	104.1
42.3	38.6	41.5	38.7	73.2	72.7	81.8	85.3	33.3
49	53.1	36.9	53.3	58.2	54.2	67.7	59.6	41.6
9.5	13.4	11.7	14.6	15.4	15.7	15.1	17.1	11.4
6.8	8.3	4.4	5.6	16.4	12.5	15.9	12	12
140.2	165	133.7	137.4	220.4	241.8	154.2	230.1	128
29.4	29.1	21.2	21.2	50.3	57.6	49.2	79.5	36.7
4.5	1.7	1.8	2.1	14.4	20.9	18	31.3	
56.8	51.4	53.4	61.2	103.9	132.2	172	186.5	71.6
390.1	417.7	334.5	294	701.6	779.3	423.4	527.4	261.2
9.7	10.7	13.1	11.2	23.9	25.3	25.6	28.3	14.6
10.5	27.1	16.9	21.4	62.1	85	67	102.1	12
4.2	4.4	4.4		29.2	17.8	7.5	13	4.7
4.3	9.3	11.3	9.4	50.2	57.5	23.8	38.4	4.7
2.5	4.6	3.9	2.5	18	13.9	5.2	14	
	4.9	4.1	1.9	5.6	8.7	2.1	2.4	
49.2	49.5	33.3	17.4	40	52.1	28	34.6	17.8
6.9	6.9	2.9		3.3	7	8.1	3.6	
234.6	230.5	198.8	186.8	274.3	332.8	229.1	247.4	167.3
10.4	15.2	7.6	6.8	16.9	10.8	13.7	19.2	11.8
879.4	865.1	687.8	586	1219.9	1475.9	846.6	1032.4	495.7
874.8	1009.9	719.3	897.3	1553.9	2238.6	2209.8	2716.8	994.9
15.1	25.4	18.3	17.3	59.6	82.2	74.3	98.8	23.3
101.2	111.3	92.6	73.5	178.6	227.6	138.8	165.3	77.7

				6.7	10.8	10.5	11.6	
					1.9			3.7
12.1	17.6	5.9	10.8	32.2	35	34.5	47.8	14.2
217.6	272.7	246.1	271	630.9	712.2	536	774.3	312
13.7	18.6	15.1	26.1	23.2	20.7	28.3	20.9	28.2
				1.4		1.9		
16.7	33.6	19.8	17.3	49.8	53.1	26	23.8	15.8
6.6	15.4	11.6	4.9	28	47.6	29.2	42	8.3
17.3	31.7	28.3	33.3	58.7	64.5	63	73.5	37.5
895.4	989.2	727.7	885.8	1601.2	2036.6	2027.8	2397.7	1010.1
		2.3	1.8	2.4	3.9	2.6	3.8	
4.8	5.7	14.9	5	18.8	28	16.3	18	6.1
32.4	52.7	50.5	68	172.9	151	129.8	199.4	89.9
14.3	12	6.3	13	21	24	15.8	17.3	5.3
3.9	3	2.6		2.6	2.4	2.8		
24.5	26.8	21.9	16.1	31.5	33	41.8	48.1	17.2
44.4	28.8	25	17.1	53.5	60.6	30.2	42.7	11.4
16.7	18.2	16.2	13.1	27.7	35.5	23.2	23.8	5.5
2.9	3.3			5.2	6.8	1.9		2.8
			2.1	3.2	4.2	1.9	2.7	
2.9	3.6	6.6	7.2	14.6	16.7	16.1	24.5	6.1
122.6	143	88.7	110.2	227	267.7	224.7	309	80.5
1.9	1.9			12.7	15.5	4		
24.1	14.8	16.9	15.3	35.7	40.2	25.2	34.6	12
256.8	276.3	235.5	215.7	406.6	471.6	277	382.9	216.4
56.7	65.9	41.5	59.9	83.9	111.7	130.3	175.8	81.1
24.4	31.6	33.2	26.9	89.7	114.7	115.2	149.2	44.2
5.5	8.3	2.8	2.4	7.2	4.5	10.2	12.7	4.3
61.4	69.3	54.5	72.1	112.4	154.2	168.4	197.7	83
62.7	59.6	53.5	54	98	122	105.3	134	77.9
13.8	15.1	10.5	4.9					6.3
10.8	7.7	6.1	10.9	22.3	22.5	8.9	14.6	8.7
33.2	44.8	40	27.7	80.1	88.5	58	48.5	34.7
16	18.6	16.9	6.5	157.9	164.6	97	115.5	6.1

Abundances Count: F5: 126, Sample, wt, pool	Abundances Count: F5: 127N, Sample, wt, single	Abundances Count: F5: 128N, Sample, wt, single	Abundances Count: F5: 129N, Sample, wt, single	Abundances Count: F5: 130N, Sample, wt, single	Abundances Count: F5: 127C, Sample, ko, single	Abundances Count: F5: 128C, Sample, ko, single	Abundances Count: F5: 129C, Sample, ko, single	Abundances Count: F5: 130C, Sample, ko, single
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4	1	4	2	3	6	7	3	2
4	3	5	3	3	4	5	4	4
4	4	4	4	4	4	4	4	4
8	8	8	8	8	8	8	8	8
3	3	3	3	3	3	3	3	3
3	3	3	3	3	3	3	3	2
2	2		1	1	3	2	2	1
2	2	2	2	1	2	2	2	2
3	3	3	3	3	3	3	3	3
6	6	6	6	6	6	6	6	6
7	7	7	7	7	7	7	7	7
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4	4	4	4	4	4	4	4	4
7	7	7	7	7	7	7	7	7
8	8	8	8	8	8	8	8	8
3	1	1			4	6	1	1
8	3	5	3	3	8	8	5	5
					1			
3	1	1	1	2	4	3	3	2
15	12	13	11	11	16	15	13	15
6	1	4	1	1	4	7	2	2
14	9	11	9	11	12	14	12	11
1		1	1	1	2	2	2	1
1	1	1	1	2	3	3	3	1
8	6	5	4	7	8	8	8	8
7	2	3	2	2	11	8	8	6
6	5	6	5	5	6	6	6	6
2		1	1	1	1	2	2	1

7	7	7	7	7	7	7	7	7
6	3	4	5	4	8	8	7	4
6	6	6	6	6	6	6	6	6
7					7	7	7	7
7	7	7	7	7	7	7	7	7
24	13	15	14	11	23	23	16	16
2	2	2	2	2	2	2	2	2
2	1	1		1	2	2	2	1
3	3	3	3	3	3	3	3	3
8	8	8	8	8	8	8	8	8
6	6	6	6	6	6	6	6	6
7	7	7	6	5	7	7	7	7
11	11	11	11	11	11	11	11	11
2	2	2	2	2	2	2	2	2
		1		1			2	
3	1	1	1	2	3	3	3	3
1								
					1			
9	8	8	9	7	9	9	7	8
6	2	3		2	5	6	6	5
8	5	5	5	2	9	9	7	7
						1		
6		1	2	3	9	9	9	4
1					1	1		1
9	8	7	6	6	8	8	7	7
9	5	7	3	6	9	9	9	9
16	16	16	15	16	16	16	16	16
2	2	2		2	2	2	2	2
1	1	1	1	1	1	1	1	1
7	7	7	7	6	7	7	7	5
5	3	3	4	2	6	6	4	4
8	8	7	5	6	7	12	6	7
4	4	1		2	4	5	3	1
5	5	3	3	4	5	5	5	4
1	1		1	1	1	1	1	1

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3		3	2	3	3	3	3	3
4	1		1	1	4	3	4	2
				1	1	1		
5	2	1	4	3	4	5	4	5
8	8	8	8	8	8	8	8	8
3	3	3	3	3	3	3	3	3
1		1	1	1	1	1	1	
7	7	7	7	7	7	7	7	7
8	8	8	8	8	8	8	8	8
9	4	8	6	5	8	8	8	8
1	1	1			1	1	1	1
			1					
3	3	3	3	3	3	3	3	3
10	4	10	6	6	10	10	10	9
4	5	5	5	3	5	5	4	4
1	1		1			1	1	
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2	1	2	2	1	6	4	1	1
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8	4	8	6	4	8	7	7	7
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4	4	4	4	4	4	4	4	4
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7	7	7	7	7	7	7	7	7
4	4	4	4	4	4	4	4	4
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4	3	4	2	1	4	4	4	3
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15	15	15	15	13	15	15	15	15
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1			1			1	1	
1		4				1	1	
				1			1	
4	2	4	3	2	4	4	3	2
4	4	4	4	4	4	4	4	4
7	7	7	7	7	7	7	7	7
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5	5	5	5	5	5	5	5	5
8	3	7	5	3	8	8	7	8
7	7	7	6	6	7	7	7	7
4	5	8	5	6	2	5	3	5
29	20	18	12	17	34	31	28	24
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3	3	3	3	3	3	3	3	3
2	2	1			2	2	2	
9	8	9	7	7	9	9	9	9
3	3	3	3	3	3	3	3	3
4	4	4	4	4	4	4	4	4
11	10	11	11	10	14	15	13	12
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13	7	6	5	7	12	13	13	12
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7	4	7	4	5	7	7	6	6
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5		2	1	1	3	4	5	2
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5	5	5	5	5	5	5	5	5
						1		
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6	6	6	6	6	6	6	6	6
7	1	5	2	4	8	8	5	6
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					3	3		
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					1	1		
11	6	9	9	8	11	13	10	11
		1	1			1	1	1
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3	3	3	2	3	3	3	3	3
6		1			6	4	3	3
4	4	4	4	3	4	4	4	4
3					5	2	2	
1							2	1
2	2	2	2	2	2	2	2	2
9	9	9	9	9	9	9	9	9
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2 6 3 1 1 8	1 3 1 7	2 6 3 8	2 3 2 7	1 2 3 7	2 6 3 8	1 1 2 6 4 8	1 5 3 1 8	1 6 4 8
15	13	14	1 14	12	1 15	1 16	1 15	14
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9 8 9	6 8 9	8 8 9	6 8 8	4 8 8	9 8 9	9 8 9	9 8 9	6 8 8
3 4	3	2 3	1 3	4	3 5	3 4	2 5	2 5
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9 6 9 8	7 2 4 1	7 3 4 6	8 3 4 1	7 1 6 5	9 6 9 8	10 6 9 9	11 3 9 9	10 5 9 8
4 12	4 13	4 12	4 8	4 9	4 14	4 14	4 13	4 13
1 6	6	1 6	6	6	2 6	1 6	6	1 6

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4	4	4	4	4	4	4	4	4
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8	5	5	4	3	8	8	7	4
2	2	2	2	2	2	2	2	2
4	1	1	1	1	4	3	3	3
7	6	6	6	6	8	7	6	6
16	14	16	15	13	16	16	15	16
9	9	9	9	9	9	9	9	9
7	7	7	7	7	7	7	7	7
8	8	8	8	8	8	8	8	8
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3		3		1	6	5	4	5
9	5	4	4	4	11	10	11	7
3		2		1	5	5	5	3
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3		1	1	1	2	4	4	4

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2	1	3	1	1	2	2	2	2
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10	7	9	4	4	11	11	11	10
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17	16	17	17	16	17	17	17	17
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12 6	9 5	10 5	8 4	8 2	11 6	11 6	11 6	9 6

Abundances Count: F5: 131, Sample, ko, pool	Quan Info	XCorr Sequest HT	Confidence Sequest HT	Percolator q-Value Sequest HT	Percolator PEP Sequest HT
5	Unique	3.439757	High	0	1.43E-05
	No Quan Va	1.842171	High	0.001067	0.007122
1	Unique	3.59062	High	0	3.6E-06
	No Quan Va	1.565779	High	0.000786	0.005378
1	Unique	2.420355	High	0.000465	0.003626
	No Quan Va	2.834059	High	0	0.000763
4	Unique	1.928373	High	0.002732	0.02394
8	Unique	3.056475	High	0.000605	0.004188
	No Quan Va	2.281507	High	0.001795	0.01218
	No Quan Va	2.199977	High	0.000664	0.004748
	No Quan Va	3.579776	High	0	1.24E-05
	No Quan Va	2.41265	High	0.002157	0.01479
	No Quan Va	2.763457	High	9.58E-05	0.001327
3	Unique	3.225326	High	0	7.17E-05
	No Quan Va	3.628361	High	0	8.25E-07
2	Unique	3.707042	High	0	1.07E-05
	Unique	4.674997	High	0	5.54E-06
2	Unique	2.284324	High	0.000267	0.002176
	No Quan Va	2.718221	High	0.000267	0.001917
	No Quan Va	2.748089	High	0	0.00074
	No Quan Va	1.886477	High	0.001362	0.01037
	No Quan Va	0.742501	High	0.002624	0.02179
3	Unique	1.562853	High	0.002467	0.01809
	No Quan Va	2.088018	High	0.002666	0.02296
6	Unique	2.469915	High	0.002624	0.02146
7	Unique	2.523733	High	0	0.000148
2	Unique	2.16666	High	0	0.000918
4	Unique	1.76243	High	0.000786	0.005321
6	Unique	4.413642	High	0	3.88E-06
8	Unique	3.435544	High	0	5.81E-05
	Unique	4.762944	High	0	5.45E-09
2	Unique	4.04462	High	0	3.18E-06
	Unique	1.631635	High	0.002467	0.01804
1	Unique	3.30486	High	0	0.000143
	No Quan Va	3.891703	High	0	2.26E-05
9	Unique	3.615191	High	0	3.94E-06
	Unique	5.339812	High	0	4.45E-08
7	Unique	4.920296	High	0	5.22E-08
	Unique	1.483033	High	0.002041	0.01338
2	Unique	1.285472	High	0.002041	0.01341
6	Unique	3.693238	High	0	0.00015
2	Unique	3.436746	High	0	4.73E-06
	No Quan Va	4.488818	High	0	2.61E-05
5	Unique	2.503756	High	0.000397	0.003418
	No Quan Va	2.229901	High	0	0.000406
	No Quan Va	3.63739	High	0	0.0003
	Unique	3.547709	High	0	0.000126

7	Unique	2.70794	High	0.000786	0.005381
3	Unique	3.747344	High	0	3.44E-08
6	Unique	3.290345	High	0	4.09E-06
	No Quan Va	2.667265	High	0	0.000988
	Unique	8.446517	High	0	0
7	Unique	3.056237	High	0.00412	0.04302
	No Quan Va	1.55029	High	0.000397	0.003434
	No Quan Va	3.763689	High	0	1.11E-05
11	Unique	5.750216	High	0	2.18E-10
2	Unique	1.691385	High	0.003173	0.03005
1	Not Unique	3.986645	High	0	4.99E-08
3	Not Unique	2.563497	High	0	0.000275
8	Not Unique	3.040011	High	0	2.88E-05
6	Not Unique	2.679747	High	9.58E-05	0.001346
	No Quan Va	2.758539	High	0.004303	0.04584
4	Unique	3.109324	High	0	7.01E-05
11	Unique	2.828194	High	0.00158	0.01126
	No Quan Va	2.027361	High	0	0.000611
	No Quan Va	2.944858	High	0	0.001003
2	Unique	2.519663	High	0	3.21E-05
	No Quan Va	1.61811	High	0.002041	0.01376
	Unique	2.47931	High	0	0.001009
	No Quan Va	2.582025	High	0.000187	0.001837
	No Quan Va	2.469895	High	0.000397	0.003194
	Unique	3.123907	High	0	9.76E-06
	Unique	1.698822	High	0.001837	0.01259
	Unique	2.01719	High	0.002282	0.01741
5	Unique	3.000935	High	0	0.000312
1	Unique	3.434779	High	0	0.000302
	No Quan Va	3.174097	High	0	1.62E-05
1	Unique	7.113717	High	0	0
1	Unique	1.670116	High	0.003102	0.02789
2	Unique	4.004229	High	0	8.4E-08
	Unique	2.39409	High	0	0.000908
	No Quan Va	1.423387	High	0.003641	0.03747
	No Quan Va	3.123444	High	0	5.65E-05
	No Quan Va	1.10506	High	0.003757	0.04016
5	Unique	3.291651	High	0	0.00014
4	Unique	3.197902	High	0.000327	0.003022
16	Unique	4.021817	High	0	6.23E-06
1	Unique	2.190086	High	0.002157	0.01472
	Unique	1.974172	High	0.001329	0.009355
	No Quan Va	1.780446	High	0.000905	0.005925
4	Unique	4.099261	High	0	2.23E-05
1	Unique	3.734027	High	0	1.03E-06
3	Unique	5.812408	High	0	5.55E-08
1	Unique	4.311137	High	0	1.66E-05
	No Quan Va	1.105756	High	0.000327	0.003071
	No Quan Va	1.381234	High	0.002624	0.02082
2	Unique	2.18309	High	0	0.000367
	No Quan Va	2.110217	High	0.000397	0.003179
1	Unique	1.618256	High	0.002144	0.01402

3	Unique	2.143486	High	0.001014	0.006876
	No Quan V	1.459011	High	0.001362	0.009572
3	Unique	2.87963	High	0	9.34E-06
1	Unique	2.673603	High	0	0.000021
1	Unique	4.665967	High	0	4.84E-09
	No Quan V	1.84995	High	0.003135	0.02923
2	Unique	5.650108	High	0	2.79E-10
8	Unique	2.965901	High	0	0.00011
	No Quan V	3.165097	High	0.002157	0.0157
3	Unique	2.173323	High	0.004451	0.04814
	Unique	1.952325	High	0.002467	0.01806
7	Unique	2.001125	High	0.002624	0.02105
	No Quan V	2.216067	High	0	0.000478
	No Quan V	4.066483	High	0	3.32E-06
8	Not Unique	2.79541	High	0.000267	0.001989
	No Quan V	1.546994	High	0.001414	0.01046
	No Quan V	1.727228	High	0.003675	0.039
5	Unique	3.026305	High	0	0.000287
	No Quan V	1.546325	High	0.002624	0.02199
	No Quan V	2.964871	High	0	1.59E-05
	Unique	1.589468	High	0.003102	0.02791
	Unique	2.883368	High	0	0.000082
3	Unique	2.050271	High	0.001524	0.01101
3	Unique	2.642104	High	0	1.48E-05
3	Unique	3.75616	High	0	1.94E-05
	No Quan V	2.413165	High	0.00358	0.03647
	No Quan V	2.37375	High	0.001067	0.007333
	Unique	1.438649	High	0.000905	0.005969
1	Unique	2.30451	High	0.001624	0.01171
1	Unique	2.1068	High	0	0.0002
	Unique	2.878246	High	0	0.000031
1	Unique	2.564452	High	0	0.000147
	Unique	2.077104	High	9.58E-05	0.001287
2	Unique	4.040088	High	0	6.94E-06
	No Quan V	2.01567	High	0.000327	0.002727
	Unique	1.822807	High	0.001067	0.007386
	No Quan V	3.272563	High	0	0.000112
	No Quan V	1.898749	High	0.002467	0.01846
1	Unique	3.078912	High	0	4.65E-05
	No Quan V	2.992954	High	0	0.000289
9	Unique	2.872467	High	0.001014	0.006928
2	Unique	2.230569	High	0.000187	0.001774
1	Unique	2.554655	High	0.00054	0.003948
4	Unique	2.219177	High	0.000786	0.005442
2	Unique	3.2078	High	0	5.17E-05
	No Quan V	3.31431	High	0	2.17E-05
3	Unique	3.301538	High	0	9.47E-06
	No Quan V	2.348003	High	0.000397	0.003384
	No Quan V	2.734424	High	0	0.000155
	No Quan V	3.346249	High	0	0.000171
5	Unique	5.161279	High	0	5.5E-08
	No Quan V	2.436394	High	0	0.000517

	No Quan Va	2.381594	High	0.00412	0.04336
8	Unique	2.808496	High	0.000267	0.002021
7	Unique	2.831581	High	0	0.000555
4	Unique	2.339263	High	0.002866	0.02552
2	Unique	1.495682	High	0.000664	0.004569
9	Unique	3.832266	High	0	1.05E-05
	Unique	3.584486	High	0	1.65E-06
	No Quan Va	1.162039	High	0.001014	0.006556
	Unique	1.241789	High	0.002827	0.02518
	Unique	3.188681	High	0	4.65E-05
	No Quan Va	1.485668	High	0.000327	0.002979
5	Unique	4.721132	High	0	1.48E-06
	No Quan Va	3.416358	High	0	0.000236
13	Unique	3.465892	High	0	0.000156
1	Unique	2.483754	High	0	0.000428
2	Unique	2.566098	High	0.000664	0.004527
	Unique	5.071735	High	0	4.12E-09
	Unique	2.632962	High	0	6.02E-05
	No Quan Va	2.130551	High	0	0.000223
1	Unique	3.876809	High	0	1.47E-05
	Unique	3.160377	High	0	4.51E-06
	No Quan Va	1.784499	High	0.000849	0.005525
	Unique	1.967579	High	0.001014	0.006882
2	Unique	1.526938	High	0.002384	0.01748
4	Unique	2.417861	High	0.002624	0.02093
7	Unique	2.777456	High	0	3.17E-05
8	Unique	2.728969	High	0	0.000276
5	Unique	3.187567	High	9.58E-05	0.001658
3	Unique	2.61815	High	0	0.001171
	No Quan Va	2.253606	High	0.00158	0.01122
	No Quan Va	2.097563	High	0.001267	0.009218
7	Unique	2.92223	High	0	2.49E-05
8	Unique	2.29185	High	0	0.000603
	No Quan Va	3.903287	High	0	1.79E-06
14	Unique	4.127475	High	0	1.21E-07
8	Unique	1.831623	High	0.000786	0.005022
	No Quan Va	1.797062	High	0.001362	0.009516
	Unique	1.189442	High	0.002234	0.01673
7	Unique	1.736551	High	0.002157	0.01515
1	Unique	1.28017	High	0.003334	0.03209
	No Quan Va	2.046414	High	0.000605	0.004267
3	Unique	2.220557	High	0.000605	0.004035
1	Unique	1.863821	High	0.00412	0.04278
	No Quan Va	1.720422	High	0.00358	0.03636
	No Quan Va	2.284957	High	0	0.000654
9	Unique	1.638276	High	0.002624	0.02198
2	Unique	2.316098	High	0.002994	0.02665
4	Unique	1.990252	High	0.001267	0.009144
12	Unique	3.186306	High	0	3.43E-06
	No Quan Va	2.154112	High	0	0.000431
2	Unique	2.225596	High	0.001067	0.007178
1	Unique	2.823617	High	0.000397	0.003484

9	Unique	1.967534	High	0.001624	0.01152
9	Unique	4.289836	High	0	7.45E-06
	No Quan V	1.841447	High	0.000267	0.00209
2	Unique	2.435094	High	0.008306	0.08193
4	Unique	2.446696	High	0.000327	0.002663
5	Unique	3.977051	High	0	3.24E-06
	No Quan V	1.859923	High	0.001837	0.01244
8	Unique	2.460748	High	0.006515	0.0667
1	Unique	5.816632	High	0	9.67E-07
	No Quan V	5.633773	High	0	5.63E-08
2	Unique	3.319805	High	0	0.000093
7	Unique	4.107713	High	0	5.95E-07
	Unique	2.75151	High	0.000397	0.003444
7	Unique	2.361978	High	0	0.000469
	Unique	1.699211	High	0.003544	0.03531
3	Unique	2.629181	High	9.58E-05	0.001269
	Unique	1.079037	High	0.003544	0.03559
5	Unique	3.09108	High	0.000786	0.005111
	No Quan V	1.375384	High	0.002618	0.02025
	No Quan V	1.818779	High	0.003079	0.02709
	Unique	1.174938	High	0.002282	0.01719
2	Unique	2.08945	High	0.003334	0.03185
6	Unique	3.349413	High	0	4.8E-06
3	Unique	2.238332	High	0	0.000179
1	Unique	4.355481	High	0	3.01E-07
	No Quan V	1.177102	High	0.004933	0.05122
	Unique	2.384453	High	0	0.000586
8	Unique	3.315764	High	0	0.000395
	No Quan V	2.094057	High	0.003512	0.03466
	Unique	1.803258	High	0.000465	0.003807
	No Quan V	1.864741	High	0.001267	0.009284
5	Unique	4.139167	High	0	3.03E-05
	Unique	4.057395	High	0	1.34E-06
2	Unique	4.343281	High	0	9.43E-06
	No Quan V	2.099472	High	0.002144	0.01396
	No Quan V	3.245408	High	0	6.2E-06
	Unique	5.106868	High	0	1.99E-07
	No Quan V	3.036889	High	0	1.02E-05
9	Unique	2.87569	High	0.001014	0.006498
2	Unique	4.012956	High	0	1.91E-09
1	Unique	4.680907	High	0	4.7E-09
4	Unique	5.705291	High	0	0
	Unique	3.845511	High	0	2.87E-05
	Unique	1.553386	High	0.002157	0.01544
2	Unique	2.189224	High	0.002666	0.02317
9	Unique	2.994149	High	0	0.00046
1	Unique	2.524781	High	0.000267	0.002013
3	Unique	5.014671	High	0	0
	No Quan V	2.808037	High	0	3.73E-05
1	Unique	1.582754	High	0.002596	0.01944
	No Quan V	2.334518	High	0.000267	0.002118
5	Unique	2.083363	High	0.001624	0.01171

	No Quan Va	2.611522	High	0.001165	0.00794
	No Quan Va	1.891021	High	0.000397	0.003528
	Unique	1.227569	High	0.002951	0.02607
	Unique	3.267113	High	0	2.33E-06
	Unique	1.942706	High	0	0.00058
1	Unique	3.329006	High	0	3.44E-05
	Unique	3.392662	High	0	5.8E-06
	Unique	1.132224	High	0.002666	0.02295
	Unique	1.198915	High	0.003461	0.03279
7	Unique	2.999763	High	0	0.000216
	No Quan Va	3.235787	High	0	3.55E-05
	No Quan Va	2.71013	High	0	3.97E-05
	No Quan Va	1.625802	High	0.001999	0.01328
1	Unique	0.989096	High	0.004147	0.04387
12	Unique	4.19134	High	0	9.23E-07
	No Quan Va	2.5525	High	0	0.000142
1	Unique	1.912659	High	0.003334	0.03197
	No Quan Va	1.725339	High	0.000327	0.002431
	No Quan Va	3.991536	High	0	6.35E-07
2	Unique	3.472177	High	0	1.55E-07
	No Quan Va	2.50918	High	0	0.000184
4	Unique	3.622262	High	0	0.000203
7	Unique	3.86956	High	0	1.47E-05
4	Unique	5.024486	High	0	3.66E-08
	No Quan Va	3.029281	High	0.001624	0.01187
2	Unique	2.227161	High	0.003461	0.03249
3	Unique	4.735913	High	0	1.35E-08
	No Quan Va	3.845912	High	0.001837	0.01271
1	Unique	1.315184	High	0.002618	0.02005
4	Unique	3.486466	High	0	8.98E-05
	No Quan Va	3.264484	High	0	0.000305
	Unique	2.461701	High	0.000605	0.004097
	Unique	1.665051	High	0.002732	0.02352
	No Quan Va	2.521665	High	0	0.000951
3	Unique	3.074253	High	0	0.000734
	No Quan Va	2.438306	High	0	0.000982
	Unique	4.028906	High	0	6.02E-07
1	Unique	2.062658	High	0.003102	0.02857
	No Quan Va	1.81482	High	0.00412	0.043
9	Unique	3.597894	High	0	0.00018
1	Unique	1.903391	High	0.001014	0.006754
	No Quan Va	1.581439	High	0.000605	0.004299
7	Unique	3.368668	High	0	0.00047
4	Unique	3.29424	High	0	2.07E-06
5	Unique	2.963605	High	0	3.94E-05
2	Unique	2.612561	High	0	0.000528
	No Quan Va	0.944853	High	0.003675	0.03898
4	Unique	2.339645	High	0.00054	0.003934
6	Unique	2.753109	High	0	0.000433
	No Quan Va	2.432251	High	0	0.000684
	Unique	1.240229	High	0.003334	0.03162
6	Unique	2.909466	High	0.000905	0.006036

1	Unique	4.900654	High	0	1.29E-07
1	Unique	2.489126	High	0	0.00053
4	Unique	3.657232	High	0	0.000055
9	Unique	3.558008	High	0	0.000564
7	Unique	3.837995	High	0	9.98E-05
5	Unique	3.826094	High	0	1.57E-07
2	Unique	3.427934	High	0	3.81E-05
1	Unique	2.813568	High	0	3.33E-05
2	Unique	2.75164	High	0	4.14E-07
3	Unique	3.683519	High	0	1.41E-05
	No Quan Va	1.870246	High	0.005204	0.05328
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	Unique	1.953621	High	0.000786	0.005349
	Unique	1.348258	High	0.002157	0.01478
4	Unique	1.815878	High	0.001892	0.01293
	Unique	3.388082	High	0	6.66E-05
1	Unique	3.674931	High	0	7.11E-06
3	Unique	2.214187	High	0.000664	0.004448
2	Unique	2.012974	High	0.001165	0.008256
	No Quan Va	2.40703	High	0	6.83E-05
	No Quan Va	1.755707	High	0.002157	0.01445
	Unique	2.719453	High	0	0.000201
	No Quan Va	2.135845	High	0.000267	0.001926
	No Quan Va	2.606751	High	0.000327	0.002574
7	Unique	3.352881	High	0	4.23E-06
12	Unique	4.721487	High	0	1.23E-05
9	Unique	2.633374	High	0	0.001115
7	Unique	2.265698	High	0.003641	0.03791
8	Unique	2.48504	High	0.000187	0.00178
	No Quan Va	2.765574	High	0	4.45E-05
2	Unique	2.26328	High	0.00644	0.06604
	No Quan Va	2.36099	High	0.000327	0.002718
	No Quan Va	2.229682	High	9.58E-05	0.001606
	Unique	5.375977	High	0	0
	Unique	2.872702	High	0	4.9E-06
	Unique	3.373108	High	0	3.81E-05
	Unique	4.32018	High	0	2.36E-05
1	Unique	2.077569	High	0.000905	0.006055
7	Unique	2.78508	High	0.009574	0.09167
6	Unique	2.702329	High	0	6.71E-05
3	Unique	1.839289	High	0.006889	0.06956
	No Quan Va	1.332975	High	0.001165	0.008165
	Unique	2.900733	High	0	0.000299
5	Unique	5.980645	High	0	5.05E-07
	Unique	3.470045	High	0	0.000104
3	Unique	4.202496	High	0	6.17E-06
1	Unique	4.655382	High	0	5.41E-05
2	Unique	5.405224	High	0	0.000022
	Unique	3.534119	High	0	0.000289
3	Unique	3.19684	High	0	4.13E-05
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1	Unique	2.050293	High	9.58E-05	0.001435

3	Unique	2.349629	High	0.001165	0.007972
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6	Unique	2.046736	High	0.004741	0.04927
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1	Unique	1.630309	High	0.002384	0.01768
5	Unique	2.52937	High	0.002157	0.01545
9	Unique	2.863965	High	0	0.000498
	No Quan Va	2.539365	High	0	8.71E-05
	No Quan Va	1.826531	High	0.00147	0.01083
6	Unique	3.508898	High	0	1.18E-05
	No Quan Va	0.897019	High	0.002624	0.02156
	Unique	1.516494	High	0	0.001125
	Unique	1.944991	High	0.001267	0.00881
1	Unique	3.242737	High	0	3.05E-06
2	Unique	4.461462	High	0	7.32E-05
	Unique	2.133026	High	0.000465	0.003724
	No Quan Va	2.328497	High	0.001165	0.008353
17	Unique	2.638999	High	0.000327	0.002413
5	Unique	4.663859	High	0	3E-07
8	Unique	2.423319	High	0.002866	0.0254
3	Unique	2.196693	High	0.005895	0.06097
5	Unique	2.658243	High	0	4.83E-05
11	Unique	3.711587	High	0	3.89E-05
5	Unique	4.399539	High	0	3.72E-06
12	Unique	3.935786	High	0	7.11E-06
16	Unique	3.76612	High	0	0.000251
3	Unique	2.231252	High	0.002234	0.01685
	No Quan Va	1.145913	High	0.003544	0.03527
6	Unique	4.300204	High	0	2.25E-09
	No Quan Va	1.442079	High	0.003102	0.02835
	No Quan Va	1.935902	High	0.000327	0.002505
	Unique	1.878822	High	9.58E-05	0.001555
	No Quan Va	2.96279	High	0	1.85E-05
	Unique	3.339648	High	0	3.27E-05
	Unique	1.500492	High	0.003334	0.03147
3	Unique	2.768415	High	0	4.01E-05
5	Unique	3.241336	High	0	0.000724
	No Quan Va	2.095459	High	0.002157	0.01432
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5	Unique	2.065528	High	0	0.000814
	No Quan Va	7.820833	High	0	0
9	Unique	2.997325	High	0.000465	0.00371
13	Unique	2.851456	High	0	0.000138
3	Unique	2.735598	High	0.001837	0.0127
5	Unique	2.734731	High	9.58E-05	0.001394
2	Unique	2.155756	High	0.002732	0.02388
1	Unique	2.36442	High	0	0.000053
	No Quan Va	2.04338	High	0.001067	0.007204
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	No Quan Va	2.44171	High	0.002732	0.02455

7	Unique	3.363358	High	0	2.42E-05
4	Unique	2.774506	High	0	0.000385
3	Unique	4.893584	High	0	8.06E-08
	No Quan Va	2.484776	High	0	0.000776
	Unique	3.118252	High	0	7.53E-05
2	Unique	3.12268	High	0	1.75E-05
11	Unique	2.71431	High	0	9.11E-05
5	Unique	2.982131	High	0.000327	0.002624
	No Quan Va	2.074618	High	0.003102	0.02832
1	Unique	1.70644	High	0.003512	0.03391
	No Quan Va	3.245116	High	0	5.03E-06
	No Quan Va	1.737182	High	0.000327	0.002289
	No Quan Va	2.51028	High	0.002994	0.02675
	No Quan Va	2.764068	High	0.005614	0.05716
5	Unique	2.918277	High	0.000327	0.002831
	No Quan Va	1.258053	High	0.002624	0.02179
	No Quan Va	1.463832	High	0.002732	0.02464
	No Quan Va	2.080709	High	0.000397	0.003362
	Unique	1.792327	High	0.000465	0.00379
1	Unique	3.555807	High	0	0.000233
	Unique	4.094533	High	0	2.25E-05
	No Quan Va	3.015646	High	0	6.72E-05
7	Unique	3.405024	High	0	0.000932
9	Unique	2.631367	High	0	0.000466
5	Unique	3.765919	High	0	4.64E-08
	Unique	2.408581	High	0.000664	0.004621
4	Unique	2.553957	High	0	0.001079
	No Quan Va	1.737304	High	0	0.000811
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6	Unique	2.673763	High	0	0.00029
4	Unique	3.051153	High	0	9.48E-05
10	Unique	2.606042	High	0	0.00067
3	Unique	2.832602	High	0	0.000546
4	Unique	2.142861	High	0	9.81E-05
2	Unique	4.287303	High	0	1.17E-05
3	Unique	2.627244	High	0	0.000346
	No Quan Va	3.123873	High	0	0.000247
3	Unique	1.996225	High	0.000267	0.002033
3	Unique	2.329055	High	0.000327	0.002331
	Unique	1.641446	High	0.003102	0.02776
1	Unique	3.739348	High	0	6.46E-07
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2	Unique	2.959963	High	0.000327	0.002332
	Unique	4.10298	High	0	5.58E-08
	No Quan Va	3.710934	High	0	2.58E-06
	No Quan Va	2.136297	High	0.002144	0.01417
	No Quan Va	1.588016	High	0	0.000418
	Unique	3.586023	High	0	3.85E-07
9	Unique	4.092235	High	0	4.14E-06
1	Unique	3.634842	High	0	6.79E-05
5	Unique	2.862087	High	0.001267	0.009073

2	Unique	5.264039	High	0	1.28E-08
	No Quan Va	1.932194	High	0.000465	0.003567
1	Unique	4.015126	High	0	6.69E-06
1	Unique	2.931854	High	0	0.000932
3	Unique	3.005519	High	0	0.000139
2	Unique	2.31845	High	0.000267	0.002052
7	Unique	2.559373	High	0.000397	0.003348
	No Quan Va	3.778948	High	0	1.33E-05
	No Quan Va	2.629333	High	0.000664	0.004362
1	Unique	2.121956	High	0.00147	0.01093
1	Unique	2.23682	High	0.000905	0.006174
3	Unique	2.6141	High	0.001165	0.008459
	No Quan Va	1.884811	High	0	8.48E-05
	No Quan Va	1.870633	High	0.002144	0.01412
2	Not Unique	2.021296	High	0.001165	0.007785
	Unique	1.262239	High	0.001014	0.006519
9	Unique	3.312764	High	0.000327	0.002791
	No Quan Va	2.45909	High	0	0.000516
3	Unique	2.582298	High	0.000397	0.003221
	Unique	3.417136	High	0	5.18E-05
8	Unique	2.595741	High	0	7.57E-05
1	Unique	4.027151	High	0	5.25E-07
	No Quan Va	1.034384	High	0.006968	0.06991
1	Unique	1.936586	High	0.002157	0.01566
1	Unique	2.219565	High	0.003512	0.03499
8	Unique	2.924709	High	0	0.000736
4	Unique	2.543267	High	0	0.00045
	No Quan Va	2.29199	High	0	0.000175
	Unique	1.911008	High	0.001014	0.006715
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	No Quan Va	2.673724	High	0	0.000133
	Unique	1.246553	High	0.002234	0.01704
2	Unique	2.15904	High	0.005319	0.05403
	No Quan Va	1.317485	High	0.002866	0.02543
1	Unique	2.650827	High	0	0.001053
1	Unique	3.66385	High	0	6.25E-07
	Unique	1.026639	High	0.003301	0.03113
	No Quan Va	3.542492	High	0	9.4E-06
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5	Unique	3.485898	High	0	8.72E-05
	Unique	1.342239	High	0.002666	0.02274
8	Unique	2.646088	High	0	6.14E-05
3	Unique	2.482809	High	0	0.000653
4	Unique	3.446869	High	9.58E-05	0.001265
3	Unique	2.062755	High	0.000397	0.0034
	No Quan Va	1.253875	High	0.003617	0.03687
9	Unique	2.520499	High	0.000267	0.001912
	No Quan Va	3.603085	High	0	6.21E-06
	No Quan Va	2.659144	High	0.00412	0.04342
4	Unique	2.096532	High	0.000786	0.005363
1	Unique	1.26742	High	0.003173	0.02979

	No Quan Va	0.993334	High	0.002732	0.02464
6	Unique	3.763101	High	0	2.21E-05
5	Unique	5.250795	High	0	1.12E-07
	No Quan Va	3.47972	High	0	2.07E-06
2	Unique	2.951894	High	0.000187	0.001754
	No Quan Va	1.337668	High	0.005245	0.0538
9	Unique	3.611414	High	0	0.000276
	No Quan Va	1.767509	High	0.000327	0.002785
	No Quan Va	1.892272	High	0.000786	0.005257
6	Unique	2.210525	High	0.000267	0.00201
	No Quan Va	2.394704	High	0	0.000825
	Unique	1.614007	High	0.002157	0.01481
	No Quan Va	2.259315	High	0	0.000475
3	Unique	1.910415	High	0.003079	0.02709
	No Quan Va	1.428089	High	0.003675	0.03901
6	Unique	2.83466	High	0.001524	0.01115
6	Unique	3.049407	High	0	0.000612
7	Unique	3.105816	High	0	0.00041
	No Quan Va	2.04721	High	0.002732	0.02359
1	Unique	2.301867	High	0.002157	0.01537
4	Unique	2.71916	High	0	6.61E-05
6	Unique	2.284857	High	0.002157	0.01529
3	Unique	1.948303	High	0.000397	0.003245
	Unique	2.316579	High	0	0.001209
3	Unique	2.809588	High	0.000327	0.002336
	No Quan Va	1.738335	High	0.000733	0.004861
	No Quan Va	1.545761	High	0.003641	0.038
9	Unique	5.580482	High	0	8.39E-09
1	Unique	2.271639	High	0.002552	0.01928
3	Unique	4.159215	High	0	9.09E-07
	No Quan Va	1.376311	High	0.002157	0.01463
	No Quan Va	2.161206	High	0	0.000814
1	Unique	3.210404	High	0	7.33E-07
1	Unique	2.663385	High	0	0.001211
	Unique	3.74192	High	0	3.2E-06
	Unique	3.920019	High	0	7.67E-05
3	Unique	3.064563	High	0	0.000572
	Unique	2.069032	High	0.002827	0.02515
9	Unique	2.986245	High	0	0.000314
2	Unique	1.735819	High	0.005319	0.05426
9	Unique	4.620094	High	0	1.04E-08
8	Unique	3.075098	High	0	2.24E-05
5	Unique	5.285296	High	0	1.01E-07
	No Quan Va	2.75031	High	0.000786	0.005348
	No Quan Va	2.823635	High	0.000849	0.005511
	No Quan Va	2.096933	High	0.000786	0.004996
3	Unique	3.066023	High	0.001067	0.007298
	No Quan Va	2.484386	High	0	9.71E-05
	No Quan Va	2.159666	High	0	0.000166
	No Quan Va	3.183432	High	0	1.66E-05
	No Quan Va	1.471231	High	0.002552	0.01862
	No Quan Va	1.323458	High	0.002951	0.02612

	Unique	3.139379	High	0	1.29E-05
	No Quan V	2.136796	High	0.003102	0.02886
	No Quan V	2.634175	High	0	0.00052
1	Unique	2.200027	High	0.000327	0.003055
3	Unique	3.5698	High	0	7.9E-07
9	Unique	3.480118	High	0	0.001059
5	Not Unique	1.272754	High	0.005776	0.05992
	No Quan V	1.513978	High	0.002384	0.01755
	Unique	1.034982	High	0.001014	0.006574
4	Unique	1.509063	High	0.008373	0.08312
2	Unique	3.232225	High	0	3.81E-05
5	Unique	5.834731	High	0	2.94E-07
	No Quan V	2.330343	High	0.00054	0.003931
9	Unique	4.293733	High	0	5.19E-06
	Unique	2.652438	High	0	0.000658
2	Unique	1.956475	High	0.001014	0.006417
5	Unique	2.70413	High	0	0.000447
1	Unique	2.854375	High	0	0.000325
	No Quan V	1.767833	High	0.00158	0.01134
	No Quan V	3.790569	High	0	2.71E-05
	Unique	1.829338	High	0.0038	0.04052
	No Quan V	2.615659	High	0	0.001166
3	Unique	3.444114	High	0	0.000255
2	Unique	3.321192	High	0	1.73E-05
1	Unique	3.076226	High	0	2.92E-05
	No Quan V	3.575087	High	0	1.27E-05
1	Unique	3.249046	High	0	9.54E-06
	No Quan V	2.143372	High	0.000397	0.003482
	Unique	1.672947	High	0.000327	0.002627
2	Unique	2.997832	High	0	0.001147
7	Unique	4.697728	High	0	1.48E-07
	Unique	2.571856	High	0.000849	0.005549
1	Unique	2.445189	High	0.001624	0.01168
	No Quan V	2.034967	High	0	3.94E-05
13	Unique	2.70276	High	0	0.000476
7	Unique	3.677857	High	0	1.71E-10
8	Unique	3.826567	High	0	0.00001
1	Unique	1.98553	High	0.001014	0.006714
5	Unique	2.278829	High	0.001362	0.00965
7	Unique	2.939293	High	0	3.05E-05
2	Unique	2.423365	High	0.003102	0.0288
2	Unique	3.888627	High	0	1.36E-05
	No Quan V	2.073627	High	0.001014	0.006648
8	Unique	3.091615	High	0	5.78E-05
2	Unique	2.856167	High	0	6.24E-05
	No Quan V	0.982335	High	0.002467	0.01842
	No Quan V	2.624973	High	0	0.000527
	No Quan V	2.18927	High	0.00158	0.01131
	No Quan V	2.217865	High	0.002234	0.017

Master Protein Accessions	[Product Description]	**[# TM Domains]**	**[SignalP Scores]**	Confidence	Annotated Sequence	Modifications	Modifications in Master Proteins	Contaminant
TGME49_3	SAG-relate	1	NN Sum: 4,	High	[A].VPDKFL	2xTMT6plex	[N-Term;	FALSE
TGME49_2	Ser/Thr ph	0	N/A	High	[S].ATPVQV	1xTMT6plex	[N-Term]	FALSE
TGME49_2	dense gran	0	NN Sum: 4,	High	[P].VDVPFS	1xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetic	0	N/A	High	[L].EMPNLL	1xTMT6plex	[N-Term]	FALSE
TGME49_2	ARF1-direc	0	N/A	High	[R].MDAQT	1xTMT6ple	TGME49_2	FALSE
TGME49_2	lysine deca	0	N/A	High	[-].MKAKM	2xTMT6ple	TGME49_2	FALSE
TGME49_2	SAC3/GAN	0	N/A	High	[M].APGVT	1xTMT6plex	[N-Term]	FALSE
TGME49_2	3-ketoacyl-	0	NN Sum: 4,	High	[S].AYKLTF	3xTMT6plex	[N-Term;	FALSE
TGME49_2	replication	0	N/A	High	[-].MLWVD	2xTMT6plex	[N-Term;	FALSE
TGME49_2	hypothetic	1	NN Sum: 0,	High	[N].AAAPA	2xTMT6plex	[N-Term;	FALSE
TGME49_2	3-oxoacyl-a	1	NN Sum: 4,	High	[R].SSTETC	2xTMT6plex	[N-Term;	FALSE
TGME49_2	RNA recog	0	N/A	High	[-].MEEKTT	1xTMT6ple	TGME49_2	FALSE
TGME49_2	RNA recog	0	N/A	High	[M].PADEQ	1xTMT6plex	[N-Term]	FALSE
TGME49_3	hypothetic	0	NN Sum: 3,	High	[M].AVAKLI	2xTMT6ple	TGME49_3	FALSE
TGME49_2	seryl-tRNA	0	N/A	High	[M].TIDVNL	1xTMT6plex	[N-Term]	FALSE
TGME49_2	ATP syntha	0	N/A	High	[S].AAPNPG	3xTMT6plex	[N-Term;	FALSE
TGME49_2	guanylate k	0	N/A	High	[R].MLAAA	1xTMT6ple	TGME49_2	FALSE
TGME49_2	Rhoptry kin	0	NN Sum: 4,	High	[P].NPIDGS	2xTMT6plex	[N-Term;	FALSE
TGME49_2	heat shock	1	NN Sum: 4,	High	[A].TETDAA	1xTMT6plex	[N-Term]	FALSE
TGME49_2	ATP syntha	0	NN Sum: 1,	High	[F].ATAAG	2xTMT6plex	[N-Term;	FALSE
TGME49_2	14-3-3 prot	0	N/A	High	[M].AEEIKN	1xTMT6ple	TGME49_2	FALSE
TGME49_2	rhoptry pro	1	NN Sum: 4,	High	[G].HVQQG	1xTMT6plex	[N-Term]	FALSE
TGME49_2	dense gran	2	N/A	High	[S].LGGVAV	1xTMT6plex	[N-Term]	FALSE
TGME49_2	T-complex	0	N/A	High	[M].SHLLN	1xTMT6ple	TGME49_2	FALSE
TGME49_2	flavoprotei	0	NN Sum: 0,	High	[F].TNVKKP	3xTMT6plex	[N-Term;	FALSE
TGME49_2	proliferatin	0	N/A	High	[-].MLEAKL	2xTMT6plex	[N-Term;	FALSE
TGME49_2	microneme	1	NN Sum: 4,	High	[G].EHDFF	1xTMT6plex	[N-Term]	FALSE
TGME49_2	dense gran	0	NN Sum: 4,	High	[A].SESDVA	1xTMT6ple	TGME49_2	FALSE
TGME49_2	dihydropte	0	NN Sum: 1,	High	[M].TANSH	1xTMT6ple	TGME49_2	FALSE
TGME49_2	alkyl hydro	0	N/A	High	[M].PAPMV	1xTMT6plex	[N-Term]	FALSE
TGME49_2	peptidase f	0	NN Sum: 2,	High	[G].EIANGK	2xTMT6plex	[N-Term;	FALSE
TGME49_2	ribosomal	0	N/A	High	[-].MKADP	3xTMT6plex	[N-Term;	FALSE
TGME49_2	bradyzoite	0	N/A	High	[A].FHPAG	1xTMT6plex	[N-Term];	FALSE
TGME49_2	proliferatio	0	N/A	High	[M].ADATG	1xTMT6ple	TGME49_2	FALSE
TGME49_2	pyruvate ki	0	N/A	High	[M].ASKQP	1xTMT6ple	TGME49_2	FALSE
TGME49_2	Ser/Thr ph	0	NN Sum: 4,	High	[M].GIVKV	2xTMT6plex	[N-Term;	FALSE
TGME49_3	SGS domai	0	N/A	High	[M].AATEQ	1xTMT6ple	TGME49_3	FALSE
TGME49_2	hypothetic	2	N/A	High	[R].GMDDG	1xTMT6plex	[N-Term]	FALSE
TGME49_2	dolichyl-di	1	N/A	High	[A].AVLPIP	1xTMT6plex	[N-Term]	FALSE
TGME49_3	phosphogly	0	N/A	High	[-].MLANKL	2xTMT6ple	TGME49_3	FALSE
TGME49_2	hypothetic	0	N/A	High	[M].CYEVK	3xTMT6plex	[N-Term;	FALSE
TGME49_2	SAG-relate	1	NN Sum: 0,	High	[A].NSQSV	1xTMT6plex	[N-Term];	FALSE
TGME49_2	hypothetic	1	N/A	High	[A].ELKSSS	2xTMT6plex	[N-Term;	FALSE
TGME49_3	microneme	0	NN Sum: 4,	High	[Q].SPSKQE	3xTMT6plex	[N-Term;	FALSE
TGME49_2	heat shock	0	N/A	High	[-].MDADS	2xTMT6ple	TGME49_2	FALSE

TGME49_2	ribosomal p	0	N/A	High	[M].TVPGM	3xTMT6plex [N-Term; I		FALSE
TGME49_3	U1 zinc fing	0	N/A	High	[M].PKYYCE	2xTMT6plex [N-Term; I		FALSE
TGME49_2	small nucle	0	N/A	High	[N].MDEKI	1xTMT6ple	TGME49_2	FALSE
TGME49_2	chaperonin	0	N/A	High	[R].SASNFS	1xTMT6plex [N-Term]		FALSE
TGME49_2	hypothetica	0	NN Sum: 4,	High	[L].SSSQPLT	2xTMT6plex [N-Term; I		FALSE
TGME49_2	parasite po	0	NN Sum: 4,	High	[G].AAAGP	3xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	0	NN Sum: 1,	High	[G].HEPVAS	2xTMT6plex [N-Term; I		FALSE
TGME49_2	DnaJ protei	0	NN Sum: 4,	High	[A].AKQNLY	3xTMT6plex [N-Term; I		FALSE
TGME49_3	ribosomal p	0	NN Sum: 1,	High	[M].APTAA	3xTMT6plex [N-Term; I		FALSE
TGME49_3	elongation	0	N/A	High	[F].ATVGVG	1xTMT6plex [N-Term]		FALSE
TGME49_2	non-proton	0	NN Sum: 4,	High	[C].DSPASP	2xTMT6plex [N-Term; I		FALSE
TGME49_2	SAG-relate	1	NN Sum: 4,	High	[K].GQKEQ	2xTMT6plex [N-Term; I		FALSE
TGME49_3	proteasom	0	N/A	High	[G].TTICGV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	domain K- t	0	N/A	High	[M].AQEEA	2xTMT6plex [N-Term; I		FALSE
TGME49_3	heat shock	0	N/A	High	[M].ASPTS	1xTMT6ple	TGME49_3	FALSE
TGME49_2	acid phosp	2	NN Sum: 1,	High	[F].TVLGVD	1xTMT6plex [N-Term]		FALSE
TGME49_2	ribosomal p	0	N/A	High	[M].VKLLKS	3xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	0	N/A	High	[Q].NKPSTN	2xTMT6plex [N-Term; I		FALSE
TGME49_2	EF-1 guanir	0	N/A	High	[M].VVPDF	1xTMT6plex [N-Term]		FALSE
TGME49_2	dense gran	0	NN Sum: 4,	High	[V].NQGPV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	protease in	0	NN Sum: 4,	High	[A].SPETKV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	3-oxoacyl-a	1	NN Sum: 4,	High	[R].SSTETC	2xTMT6plex [N-Term; I		FALSE
TGME49_2	SAG-relate	1	N/A	High	[G].ADSATD	1xTMT6ple	TGME49_2	FALSE
TGME49_2	HMG (high	0	N/A	High	[M].AKDAA	3xTMT6plex [N-Term; I		FALSE
TGME49_2	fructose-1,	1	N/A	High	[M].SGYGLF	1xTMT6ple	TGME49_2	FALSE
TGME49_2	SAG-relate	1	NN Sum: 0,	High	[S].QSVTCE	1xTMT6plex [N-Term];		FALSE
TGME49_2	proteasom	0	N/A	High	[I].MEGTSL	2xTMT6ple	TGME49_2	FALSE
TGME49_2	Rhoptry kin	0	NN Sum: 4,	High	[G].VAWGP	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	0	NN Sum: 3,	High	[H].VSTAKG	3xTMT6plex [N-Term; I		FALSE
TGME49_2	Ubiquitin fa	0	N/A	High	[-].MIEVILN	1xTMT6plex [N-Term]		FALSE
TGME49_3	YOU2 famil	0	N/A	High	[M].AFGSS	1xTMT6plex [N-Term]		FALSE
TGME49_2	hypothetica	0	N/A	High	[F].SSVKFM	3xTMT6plex [N-Term; I		FALSE
TGME49_2	chaperonin	0	N/A	High	[M].AANAA	1xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetica	2	N/A	High	[M].TSVAV	1xTMT6ple	TGME49_2	FALSE
TGME49_2	microneme	1	NN Sum: 3,	High	[A].AGVPKF	3xTMT6plex [N-Term; I		FALSE
TGME49_2	ribosomal p	0	N/A	High	[K].ASSSFK	3xTMT6plex [N-Term; I		FALSE
TGME49_2	enolase 1	0	N/A	High	[-].MVVIKD	1xTMT6ple	TGME49_2	FALSE
TGME49_2	ribosomal p	0	N/A	High	[M].SGIAVC	2xTMT6plex [N-Term; I		FALSE
TGME49_2	SAG-relate	0	NN Sum: 3,	High	[A].TGQSIV	1xTMT6plex [N-Term];		FALSE
TGME49_3	ribosomal p	0	N/A	High	[M].VKKGE	3xTMT6plex [N-Term; I		FALSE
TGME49_2	translation	0	N/A	High	[M].VNFSV	1xTMT6plex [N-Term]		FALSE
TGME49_2	homocyste	0	N/A	High	[M].PHAGF	1xTMT6plex [N-Term]		FALSE
TGME49_2	vacuolar so	0	N/A	High	[-].MIMEHD	2xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetica	1	NN Sum: 3,	High	[P].DQAQA	2xTMT6plex [N-Term; I		FALSE
TGME49_2	SAG-relate	0	NN Sum: 2,	High	[L].DEVHTA	1xTMT6plex [N-Term]		FALSE
TGME49_2	DJ-1 family	0	NN Sum: 3,	High	[M].AVKVL	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	1	N/A	High	[L].AAETKV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	ribosomal p	0	N/A	High	[-].MKFSSQ	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hydrolase,	0	NN Sum: 4,	High	[M].SLTAEE	1xTMT6ple	TGME49_2	FALSE
TGME49_2	zinc finger	0	N/A	High	[M].SGLEKS	2xTMT6ple	TGME49_2	FALSE
TGME49_2	microneme	1	NN Sum: 3,	High	[G].GKAVK	3xTMT6plex [N-Term; I		FALSE
TGME49_2	proliferatin	0	N/A	High	[-].MLEAKL	1xTMT6ple	TGME49_2	FALSE

TGME49_2	hypothetica	0	N/A	High	[-].METLDE	1xTMT6ple	TGME49_2	FALSE
TGME49_2	chaperonin	0	N/A	High	[R].SASNFS	2xTMT6plex [N-Term; I		FALSE
TGME49_3	chaperonin	1	NN Sum: 4,	High	[A].SDAEEG	2xTMT6plex [N-Term; I		FALSE
TGME49_2	eukaryotic	0	N/A	High	[M].ANATT	1xTMT6ple	TGME49_2	FALSE
TGME49_2	LsmAD dom	0	N/A	High	[M].GKTDA	2xTMT6plex [N-Term; I		FALSE
TGME49_2	arginyl-tRN	0	N/A	High	[-].MQALN	1xTMT6ple	TGME49_2	FALSE
TGME49_2	mediator c	0	N/A	High	[M].ASSKP	2xTMT6ple	TGME49_2	FALSE
TGME49_2	LSM domai	0	N/A	High	[M].VLPLTL	1xTMT6plex [N-Term]		FALSE
TGME49_3	hypothetica	0	N/A	High	[G].SKQGQ	2xTMT6plex [N-Term; I		FALSE
TGME49_2	bradyzoite	0	N/A	High	[P].SASHPP	1xTMT6ple	TGME49_2	FALSE
TGME49_3	proteasom	0	N/A	High	[-].MDAYN	1xTMT6ple	TGME49_3	FALSE
TGME49_2	peroxiredo	0	N/A	High	[F].STADSP	1xTMT6plex [N-Term];		FALSE
TGME49_2	SAG-relate	1	NN Sum: 0,	High	[N].SQSVTC	1xTMT6plex [N-Term];		FALSE
TGME49_2	dense gran	0	NN Sum: 4,	High	[G].VVNQG	2xTMT6plex [N-Term; I		FALSE
TGME49_2	Toxoplasma	0	NN Sum: 4,	High	[A].APDFTV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	ribosomal	0	N/A	High	[M].ADAGD	1xTMT6ple	TGME49_2	FALSE
TGME49_2	SAG-relate	0	NN Sum: 0,	High	[A].SEVQSC	1xTMT6plex [N-Term];		FALSE
TGME49_2	ribosomal	0	N/A	High	[M].APVST	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	0	N/A	High	[M].AAVVS	1xTMT6ple	TGME49_2	FALSE
TGME49_2	bradyzoite	0	N/A	High	[A].PSASHP	2xTMT6plex [N-Term; I		FALSE
TGME49_2	microneme	0	NN Sum: 4,	High	[T].EDDKSA	2xTMT6plex [N-Term; I		FALSE
TGME49_2	glyceropho	6	N/A	High	[R].ANLHPV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	poly(ADP-ri	0	NN Sum: 3,	High	[M].PAKEIV	2xTMT6plex [N-Term; I		FALSE
TGME49_2	heat shock	0	N/A	High	[M].ADSPA	1xTMT6ple	TGME49_2	FALSE
TGME49_2	ribosomal	0	N/A	High	[M].SKLMK	2xTMT6ple	TGME49_2	FALSE
TGME49_2	replication	0	NN Sum: 2,	High	[T].MYAGI	1xTMT6ple	TGME49_2	FALSE
TGME49_2	microneme	1	NN Sum: 4,	High	[H].DFFNDY	1xTMT6plex [N-Term]		FALSE
TGME49_2	EMP/nonas	10	NN Sum: 4,	High	[A].YVPGIA	1xTMT6plex [N-Term]		FALSE
TGME49_2	SAG-relate	1	NN Sum: 0,	High	[G].NQANS	1xTMT6plex [N-Term];		FALSE
TGME49_2	CCDC25 pr	0	N/A	High	[M].VYTFT	1xTMT6plex [N-Term];		FALSE
TGME49_2	ATP syntha	0	N/A	High	[S].SAAPNP	3xTMT6plex [N-Term; I		FALSE
TGME49_2	glycolipid t	0	N/A	High	[M].STAAT	2xTMT6ple	TGME49_2	FALSE
TGME49_2	succinate d	0	NN Sum: 0,	High	[A].SVAHA	2xTMT6plex [N-Term; I		FALSE
TGME49_2	acyl carrier	1	NN Sum: 4,	High	[F].AADEAS	1xTMT6plex [N-Term]		FALSE
TGME49_2	peptidase	0	NN Sum: 0,	High	[G].FFSAAP	1xTMT6plex [N-Term]		FALSE
TGME49_2	protein kin	0	N/A	High	[S].AAGGA	1xTMT6plex [N-Term]		FALSE
TGME49_2	Toxoplasma	0	NN Sum: 4,	High	[S].TQTYGD	2xTMT6plex [N-Term; I		FALSE
TGME49_2	proteasom	0	N/A	High	[I].MEGTSL	1xTMT6ple	TGME49_2	FALSE
TGME49_2	ribosomal	0	N/A	High	[M].VSSELL	1xTMT6plex [N-Term];		FALSE
TGME49_2	MAG1	1	NN Sum: 4,	High	[Q].RVPELP	1xTMT6plex [N-Term]		FALSE
TGME49_2	Toxoplasma	0	NN Sum: 4,	High	[S].DAVSTC	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	1	NN Sum: 3,	High	[A].SDQKQ	2xTMT6ple	TGME49_2	FALSE
TGME49_2	hydrolase,	0	N/A	High	[M].PQTNI	2xTMT6plex [N-Term; I		FALSE
TGME49_2	nuclear fac	0	NN Sum: 0,	High	[M].ASTKS	1xTMT6ple	TGME49_2	FALSE
TGME49_2	acetyltrans	0	N/A	High	[M].STCAC	1xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetica	0	N/A	High	[R].HRPAEV	3xTMT6plex [N-Term; I		FALSE
TGME49_2	serine carb	1	NN Sum: 1,	High	[Q].EGWFL	1xTMT6plex [N-Term]		FALSE
TGME49_2	bradyzoite	0	N/A	High	[A].PSASHP	2xTMT6plex [N-Term; I		FALSE
TGME49_2	hypothetica	1	NN Sum: 2,	High	[R].DGEGE	2xTMT6plex [K9; K18]		FALSE
TGME49_2	hypothetica	0	N/A	High	[N].MEKLP	2xTMT6ple	TGME49_2	FALSE
TGME49_2	TBC domai	0	N/A	High	[-].MIGSEE	1xTMT6ple	TGME49_2	FALSE
TGME49_2	glyceraldeh	1	NN Sum: 3,	High	[F].GLLGSS	1xTMT6plex [N-Term]		FALSE

TGME49_2	microneme	1	NN Sum: 4,	High	[S].IGEHDF	1xTMT6plex [N-Term]		FALSE
TGME49_2	coronin, pu	0	N/A	High	[M].ADAVD	2xTMT6ple	TGME49_2	FALSE
TGME49_2	prolyl endo	0	NN Sum: 0,	High	[M].VAAGV	1xTMT6plex [N-Term]		FALSE
TGME49_2	Toxoplasm	0	NN Sum: 4,	High	[S].AAPDFT	2xTMT6plex [N-Term;		FALSE
TGME49_2	ribosomal	0	N/A	High	[M].GAYKY	2xTMT6plex [N-Term;		FALSE
TGME49_2	Toxoplasm	0	NN Sum: 4,	High	[T].QTYGD	2xTMT6plex [N-Term;		FALSE
TGME49_2	glucose-6-	1	NN Sum: 1,	High	[M].APTQL	2xTMT6plex [N-Term;		FALSE
TGME49_3	bradyzoite	1	NN Sum: 2,	High	[R].GPKFTL	3xTMT6plex [N-Term;		FALSE
TGME49_3	chaperonin	1	NN Sum: 4,	High	[A].SDAEEG	3xTMT6plex [N-Term;		FALSE
TGME49_2	U6 snRNA-	0	N/A	High	[M].AQVLQ	1xTMT6ple	TGME49_2	FALSE
TGME49_2	Ser/Thr ph	0	N/A	High	[T].SDPLDF	1xTMT6plex [N-Term]		FALSE
TGME49_2	calcium bin	1	NN Sum: 1,	High	[A].AMPKL	3xTMT6plex [N-Term;		FALSE
TGME49_2	hypothetic	0	N/A	High	[M].AANTT	2xTMT6ple	TGME49_2	FALSE
TGME49_2	Hsp70 inte	0	N/A	High	[M].AALSP	2xTMT6ple	TGME49_2	FALSE
TGME49_2	signal reco	0	N/A	High	[M].VLADN	1xTMT6plex [N-Term]		FALSE
TGME49_2	Ser/Thr ph	0	N/A	High	[A].ESDPA	1xTMT6plex [N-Term]		FALSE
TGME49_2	hypothetic	0	NN Sum: 3,	High	[M].AKPND	3xTMT6ple	TGME49_2	FALSE
TGME49_2	Toxoplasm	0	NN Sum: 4,	High	[T].SAAPDF	2xTMT6plex [N-Term;		FALSE
TGME49_2	fructose-bi	0	N/A	High	[M].AASGH	1xTMT6ple	TGME49_2	FALSE
TGME49_2	ribosomal	0	N/A	High	[M].VKYAK	3xTMT6plex [N-Term;		FALSE
TGME49_2	microneme	0	NN Sum: 4,	High	[D].ITPAGD	3xTMT6plex [N-Term;		FALSE
TGME49_2	EF hand do	0	NN Sum: 3,	High	[A].AAAPQ	2xTMT6ple	TGME49_2	FALSE
TGME49_3	hypothetic	0	N/A	High	[F].AHDAG	1xTMT6plex [N-Term]		FALSE
TGME49_2	glycoprotei	0	N/A	High	[F].SSEADS	2xTMT6plex [N-Term;		FALSE
TGME49_2	hypothetic	1	NN Sum: 3,	High	[G].APDQA	2xTMT6plex [N-Term;		FALSE
TGME49_2	hypothetic	1	NN Sum: 3,	High	[Q].GGGPP	2xTMT6plex [N-Term;		FALSE
TGME49_2	multiprotei	0	N/A	High	[M].SFQDW	1xTMT6ple	TGME49_2	FALSE
TGME49_2	dense gran	0	NN Sum: 4,	High	[A].AEFSGV	1xTMT6ple	TGME49_2	FALSE
TGME49_2	SGS domai	0	N/A	High	[M].SVSNC	1xTMT6ple	TGME49_2	FALSE
TGME49_2	Sec61beta	1	N/A	High	[M].VGTNA	1xTMT6plex [N-Term]		FALSE
TGME49_3	peroxiredo	0	N/A	High	[T].MLVLGS	2xTMT6plex [N-Term;		FALSE
TGME49_3	splicing fac	0	N/A	High	[M].GDLDF	1xTMT6ple	TGME49_3	FALSE
TGME49_2	hypothetic	0	NN Sum: 3,	High	[M].AKPND	1xTMT6ple	TGME49_2	FALSE
TGME49_2	p25-alpha f	0	N/A	High	[M].SIAGVF	1xTMT6ple	TGME49_2	FALSE
TGME49_3	peroxiredo	0	N/A	High	[T].MLVLGS	1xTMT6plex [N-Term]		FALSE
TGME49_2	ribosomal	0	N/A	High	[K].FTVDCC	3xTMT6plex [N-Term;		FALSE
TGME49_2	cytochrom	0	N/A	High	[M].AQKPG	2xTMT6ple	TGME49_2	FALSE
TGME49_2	Tim10/DDP	0	N/A	High	[-].MDSDIP	1xTMT6ple	TGME49_2	FALSE
TGME49_2	prefoldin s	0	N/A	High	[M].ALAAA	1xTMT6ple	TGME49_2	FALSE
TGME49_2	bradyzoite	0	N/A	High	[M].APSAS	2xTMT6plex [N-Term;		FALSE
TGME49_3	microneme	0	NN Sum: 4,	High	[S].EKMNIV	3xTMT6plex [N-Term;		FALSE
TGME49_3	cyclase-ass	0	N/A	High	[M].AKTGA	1xTMT6ple	TGME49_3	FALSE
TGME49_3	IgA-specific	0	NN Sum: 4,	High	[A].INSTEP	1xTMT6plex [N-Term]		FALSE
TGME49_2	domain K- t	0	N/A	High	[M].AQEEA	1xTMT6plex [N-Term]		FALSE
TGME49_2	nuclear fac	0	N/A	High	[-].MFYGV	2xTMT6ple	TGME49_2	FALSE
TGME49_2	bradyzoite	0	N/A	High	[P].SASHPP	2xTMT6plex [N-Term;		FALSE
TGME49_2	SAG-relate	0	NN Sum: 0,	High	[S].EVQSCS	1xTMT6plex [N-Term];		FALSE
TGME49_2	glycoprotei	0	N/A	High	[F].SSEADS	1xTMT6plex [N-Term]		FALSE
TGME49_2	microneme	1	NN Sum: 4,	High	[Q].ASIGEH	1xTMT6plex [N-Term]		FALSE
TGME49_3	peroxiredo	0	N/A	High	[T].MLVLGS	1xTMT6ple	TGME49_3	FALSE
TGME49_2	bradyzoite	0	N/A	High	[M].APSAS	1xTMT6plex [N-Term];		FALSE
TGME49_2	myosin A	0	N/A	High	[M].ASKTTS	1xTMT6ple	TGME49_2	FALSE

TGME49_2	hypothetica	0	N/A	High	[M].AANTT	1xTMT6ple	TGME49_2	FALSE
TGME49_2	ribosomal	0	N/A	High	[M].ADAGD	1xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetica	0	N/A	High	[-].MELVSK	1xTMT6ple	TGME49_2	FALSE
TGME49_2	hypothetica	0	N/A	High	[M].TDNAC	1xTMT6ple	TGME49_2	FALSE
TGME49_3	phosphogly	0	N/A	High	[-].MLANKL	1xTMT6ple	TGME49_3	FALSE
TGME49_2	glucose-6-p	1	NN Sum: 1,	High	[M].APTQLI	1xTMT6plex [N-Term];		FALSE
TGME49_2	protein disu	0	NN Sum: 4,	High	[A].EEEAVT	1xTMT6plex [N-Term]		FALSE
TGME49_2	bradyzoite	0	N/A	High	[M].APSASI	2xTMT6plex [N-Term;		FALSE
TGME49_2	hypothetica	1	NN Sum: 3,	High	[P].DQAQA	1xTMT6plex [N-Term]		FALSE
TGME49_2	rhoptry kin	1	N/A	High	[L].DSLIPGF	2xTMT6plex [N-Term;		FALSE
TGME49_3	hypothetica	0	N/A	High	[-].MWSIFA	1xTMT6ple	TGME49_3	FALSE
TGME49_2	gamma inte	1	NN Sum: 4,	High	[K].DSQYN	1xTMT6plex [N-Term];		FALSE
TGME49_2	GTP-bindin	0	N/A	High	[M].AAAAA	1xTMT6ple	TGME49_2	FALSE
TGME49_3	N-acyl-pho	1	N/A	High	[L].LTANVY	1xTMT6plex [N-Term]		FALSE
TGME49_2	ribosomal	0	N/A	High	[-].MKLNLA	3xTMT6plex [N-Term;		FALSE
TGME49_2	bradyzoite	0	N/A	High	[A].LTANEN	1xTMT6plex [N-Term]		FALSE
TGME49_2	microneme	1	NN Sum: 3,	High	[L].AKSSTDI	1xTMT6ple	TGME49_2	FALSE

spike-in std	host cell	Qvality PEP	Qvality q-value	# Protein Groups	# Proteins	# PSMs	Positions in Master Proteins	# Missed Cleavages
FALSE	FALSE	0.034997	0.001288	1	1	6	TGME49_3	1
FALSE	FALSE	0.000468	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.060242	0.002722	1	1	8	TGME49_2	0
FALSE	FALSE	0.066651	0.003073	1	1	1	TGME49_2	0
FALSE	FALSE	0.007306	0	1	1	15	TGME49_2	1
FALSE	FALSE	0.001376	0	1	1	3	TGME49_2	2
FALSE	FALSE	0.051917	0.002015	1	1	5	TGME49_2	0
FALSE	FALSE	0.008679	0	1	1	1	TGME49_2	2
FALSE	FALSE	0.021971	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.014151	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.026441	0.00048	1	1	4	TGME49_2	1
FALSE	FALSE	0.06488	0.002722	1	1	7	TGME49_2	1
FALSE	FALSE	0.026622	0.00048	1	1	17	TGME49_2	0
FALSE	FALSE	0.161472	0.006543	1	1	3	TGME49_3	2
FALSE	FALSE	0.067101	0.003073	1	1	6	TGME49_2	0
FALSE	FALSE	0.050529	0.002015	1	1	2	TGME49_2	1
FALSE	FALSE	0.001022	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.000115	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.000336	0	1	1	17	TGME49_2	0
FALSE	FALSE	1.27E-05	0	1	1	6	TGME49_2	1
FALSE	FALSE	0.191615	0.008044	1	1	3	TGME49_2	1
FALSE	FALSE	0.022123	0	2	2	8	TGME49_2	0
FALSE	FALSE	0.008158	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.002309	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.041215	0.001288	1	1	7	TGME49_2	1
FALSE	FALSE	0.001801	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.000549	0	1	1	8	TGME49_2	0
FALSE	FALSE	0.007407	0	1	1	17	TGME49_2	1
FALSE	FALSE	0.053704	0.002015	1	1	7	TGME49_2	1
FALSE	FALSE	0.00282	0	1	1	8	TGME49_2	0
FALSE	FALSE	0.00239	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.000171	0	1	1	5	TGME49_2	2
FALSE	FALSE	0.079365	0.003633	1	1	6	TGME49_2	0
FALSE	FALSE	6.19E-05	0	1	1	8	TGME49_2	1
FALSE	FALSE	4.09E-05	0	1	1	16	TGME49_2	1
FALSE	FALSE	0.057074	0.002015	1	1	2	TGME49_2	1
FALSE	FALSE	0.02555	0	1	1	6	TGME49_3	1
FALSE	FALSE	0.195252	0.008262	1	1	3	TGME49_2	0
FALSE	FALSE	0.127914	0.004816	1	1	4	TGME49_2	0
FALSE	FALSE	0.000111	0	1	1	14	TGME49_3	2
FALSE	FALSE	0.084291	0.003857	1	1	3	TGME49_2	2
FALSE	FALSE	0.106396	0.003917	1	1	5	TGME49_2	0
FALSE	FALSE	0.003901	0	1	1	6	TGME49_2	1
FALSE	FALSE	1.86E-06	0	1	2	7	TGME49_3	1
FALSE	FALSE	0.000928	0	1	1	2	TGME49_2	2

FALSE	FALSE	0.00214	0	1	1	7	TGME49_2	2
FALSE	FALSE	0.003591	0	1	1	6	TGME49_3	1
FALSE	FALSE	0.027739	0.00048	1	1	14	TGME49_2	1
FALSE	FALSE	0.007059	0	1	1	10	TGME49_2	0
FALSE	FALSE	0.169931	0.006543	1	1	2	TGME49_2	1
FALSE	FALSE	0.000896	0	1	1	3	TGME49_2	2
FALSE	FALSE	0.000994	0	1	1	5	TGME49_2	1
FALSE	FALSE	0.067101	0.003073	1	1	1	TGME49_2	2
FALSE	FALSE	0.000061	0	1	1	9	TGME49_3	2
FALSE	FALSE	0.132158	0.005097	1	1	1	TGME49_3	0
FALSE	FALSE	0.004603	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.005284	0	1	2	7	TGME49_2	1
FALSE	FALSE	0.046579	0.00168	1	1	3	TGME49_3	1
FALSE	FALSE	0.000915	0	1	1	6	TGME49_2	1
FALSE	FALSE	0.000168	0	1	1	5	TGME49_3	1
FALSE	FALSE	0.008386	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.033593	0.000942	1	1	8	TGME49_2	2
FALSE	FALSE	0.117462	0.003917	1	1	1	TGME49_2	0
FALSE	FALSE	0.139218	0.005566	1	1	4	TGME49_2	0
FALSE	FALSE	0.122183	0.003917	1	1	2	TGME49_2	0
FALSE	FALSE	0.0057	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.028509	0.00048	1	1	3	TGME49_2	1
FALSE	FALSE	0.068469	0.00344	1	1	4	TGME49_2	0
FALSE	FALSE	0.122183	0.003917	1	1	3	TGME49_2	2
FALSE	FALSE	0.008984	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.095679	0.003917	1	1	3	TGME49_2	0
FALSE	FALSE	0.00032	0	1	1	8	TGME49_2	2
FALSE	FALSE	0.01569	0	1	1	2	TGME49_2	1
FALSE	FALSE	0.002879	0	1	1	2	TGME49_2	2
FALSE	FALSE	0.019152	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.023211	0	1	1	5	TGME49_3	0
FALSE	FALSE	0.006065	0	1	1	8	TGME49_2	2
FALSE	FALSE	0.000848	0	1	1	17	TGME49_2	1
FALSE	FALSE	0.000714	0	1	1	8	TGME49_2	0
FALSE	FALSE	0.0006	0	1	1	6	TGME49_2	1
FALSE	FALSE	0.147572	0.005566	1	1	2	TGME49_2	2
FALSE	FALSE	0.032465	0.000942	1	1	3	TGME49_2	1
FALSE	FALSE	0.014347	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.004038	0	1	1	8	TGME49_2	0
FALSE	FALSE	0.000759	0	1	1	8	TGME49_3	2
FALSE	FALSE	0.003085	0	1	1	8	TGME49_2	0
FALSE	FALSE	1.28E-06	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.00244	0	1	1	6	TGME49_2	2
FALSE	FALSE	8.01E-06	0	1	1	3	TGME49_2	1
FALSE	FALSE	0.000446	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.00036	0	1	1	6	TGME49_2	2
FALSE	FALSE	0.087155	0.003857	1	1	1	TGME49_2	1
FALSE	FALSE	0.017515	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.055551	0.002015	1	1	5	TGME49_2	0
FALSE	FALSE	0.001157	0	1	3	4	TGME49_2	2
FALSE	FALSE	0.055177	0.002015	1	1	7	TGME49_2	2
FALSE	FALSE	0.008158	0	1	1	9	TGME49_2	1

FALSE	FALSE	0.005982	0	1	1	9	TGME49_2	1
FALSE	FALSE	5.54E-05	0	1	1	5	TGME49_2	1
FALSE	FALSE	0.004208	0	1	1	9	TGME49_3	1
FALSE	FALSE	0.000171	0	1	1	2	TGME49_2	1
FALSE	FALSE	0.000259	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.011354	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.104996	0.003917	1	1	4	TGME49_2	1
FALSE	FALSE	0.050529	0.002015	1	1	2	TGME49_2	0
FALSE	FALSE	0.038241	0.001288	1	1	3	TGME49_3	1
FALSE	FALSE	0.00586	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.023532	0	1	1	7	TGME49_3	1
FALSE	FALSE	0.021821	0	1	1	8	TGME49_2	0
FALSE	FALSE	5.94E-05	0	1	1	16	TGME49_2	0
FALSE	FALSE	0.002474	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.013958	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.000734	0	1	1	18	TGME49_2	1
FALSE	FALSE	0.000675	0	1	1	18	TGME49_2	0
FALSE	FALSE	0.01889	0	1	1	5	TGME49_2	1
FALSE	FALSE	0.062309	0.002722	1	1	4	TGME49_2	1
FALSE	FALSE	0.001065	0	1	1	11	TGME49_2	1
FALSE	FALSE	0.007256	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.000714	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.002981	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.000754	0	1	1	7	TGME49_2	1
FALSE	FALSE	0.001464	0	1	1	9	TGME49_2	2
FALSE	FALSE	0.012589	0	1	1	5	TGME49_2	1
FALSE	FALSE	0.003128	0	1	1	15	TGME49_2	0
FALSE	FALSE	0.169931	0.006543	1	1	3	TGME49_2	0
FALSE	FALSE	5.39E-05	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.10293	0.003917	1	1	9	TGME49_2	0
FALSE	FALSE	0.004732	0	1	1	2	TGME49_2	1
FALSE	FALSE	0.000478	0	1	1	4	TGME49_2	2
FALSE	FALSE	2.51E-06	0	1	1	6	TGME49_2	1
FALSE	FALSE	8.88E-06	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.000967	0	1	1	18	TGME49_2	0
FALSE	FALSE	0.023532	0	1	1	3	TGME49_2	0
FALSE	FALSE	0.012079	0	1	1	6	TGME49_2	1
FALSE	FALSE	0.075727	0.003633	1	1	6	TGME49_2	1
FALSE	FALSE	0.000744	0	1	1	17	TGME49_2	0
FALSE	FALSE	7.72E-05	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.005661	0	1	1	9	TGME49_2	1
FALSE	FALSE	2.61E-05	0	1	1	5	TGME49_2	2
FALSE	FALSE	0.003306	0	1	1	4	TGME49_2	1
FALSE	FALSE	1.51E-05	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.009108	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.185686	0.007533	1	1	1	TGME49_2	2
FALSE	FALSE	0.062309	0.002722	1	1	8	TGME49_2	0
FALSE	FALSE	0.010894	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.000694	0	1	1	2	TGME49_2	1
FALSE	FALSE	0.021821	0	1	1	2	TGME49_2	2
FALSE	FALSE	0.023694	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.149489	0.005777	1	1	2	TGME49_2	0

FALSE	FALSE	0.00326	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.001801	0	1	1	10	TGME49_2	2
FALSE	FALSE	0.047216	0.00168	1	1	8	TGME49_2	0
FALSE	FALSE	0.017635	0	1	1	14	TGME49_2	1
FALSE	FALSE	0.159417	0.006341	1	1	3	TGME49_2	1
FALSE	FALSE	0.035237	0.001288	1	1	4	TGME49_2	1
FALSE	FALSE	2.54E-05	0	1	1	10	TGME49_2	1
FALSE	FALSE	0.014151	0	1	1	5	TGME49_3	2
FALSE	FALSE	0.000307	0	1	1	7	TGME49_3	2
FALSE	FALSE	0.050872	0.002015	1	1	7	TGME49_2	1
FALSE	FALSE	0.016464	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.048515	0.00168	1	1	2	TGME49_2	2
FALSE	FALSE	0.007306	0	1	1	8	TGME49_2	2
FALSE	FALSE	0.026441	0.00048	1	1	3	TGME49_2	2
FALSE	FALSE	0.000848	0	1	1	16	TGME49_2	0
FALSE	FALSE	0.125428	0.004816	1	1	4	TGME49_2	0
FALSE	FALSE	0.052269	0.002015	1	1	2	TGME49_2	2
FALSE	FALSE	0.001558	0	1	1	3	TGME49_2	1
FALSE	FALSE	0.078308	0.003633	1	1	6	TGME49_2	1
FALSE	FALSE	0.032244	0.000942	1	1	3	TGME49_2	2
FALSE	FALSE	0.006588	0	1	1	2	TGME49_2	2
FALSE	FALSE	0.008739	0	1	1	4	TGME49_2	2
FALSE	FALSE	0.016464	0	1	1	8	TGME49_3	0
FALSE	FALSE	0.001366	0	1	1	4	TGME49_2	1
FALSE	FALSE	1.87E-10	0	1	1	4	TGME49_2	1
FALSE	FALSE	0.135646	0.005566	1	1	1	TGME49_2	1
FALSE	FALSE	0.000271	0	1	1	2	TGME49_2	1
FALSE	FALSE	6.19E-05	0	1	1	41	TGME49_2	0
FALSE	FALSE	0.048187	0.00168	1	1	6	TGME49_2	1
FALSE	FALSE	1.63E-07	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.000714	0	1	1	6	TGME49_3	1
FALSE	FALSE	0.003193	0	1	1	9	TGME49_3	1
FALSE	FALSE	0.032465	0.000942	1	1	3	TGME49_2	0
FALSE	FALSE	0.00119	0	1	1	13	TGME49_2	1
FALSE	FALSE	0.000293	0	1	1	5	TGME49_3	0
FALSE	FALSE	0.133022	0.005097	1	1	1	TGME49_2	1
FALSE	FALSE	0.074218	0.003633	1	1	2	TGME49_2	1
FALSE	FALSE	0.002782	0	1	1	15	TGME49_2	1
FALSE	FALSE	0.017757	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.001266	0	1	1	5	TGME49_2	1
FALSE	FALSE	0.001424	0	1	1	8	TGME49_3	2
FALSE	FALSE	0.000088	0	1	1	9	TGME49_3	1
FALSE	FALSE	0.000116	0	1	1	14	TGME49_3	0
FALSE	FALSE	0.008158	0	1	1	8	TGME49_2	0
FALSE	FALSE	0.000797	0	1	1	11	TGME49_2	1
FALSE	FALSE	3.46E-05	0	1	1	8	TGME49_2	1
FALSE	FALSE	0.007107	0	1	1	4	TGME49_2	0
FALSE	FALSE	0.000332	0	1	1	5	TGME49_2	0
FALSE	FALSE	0.006819	0	1	1	9	TGME49_2	0
FALSE	FALSE	0.025726	0	1	1	18	TGME49_3	1
FALSE	FALSE	0.002543	0	1	1	7	TGME49_2	0
FALSE	FALSE	0.161472	0.006543	1	1	8	TGME49_2	1

FALSE	FALSE	0.000909	0	1	1	12	TGME49_2	1
FALSE	FALSE	0.023371	0	1	1	9	TGME49_2	2
FALSE	FALSE	0.001692	0	1	1	17	TGME49_2	1
FALSE	FALSE	0.001484	0	1	1	6	TGME49_2	1
FALSE	FALSE	0.059837	0.002402	1	1	7	TGME49_3	1
FALSE	FALSE	0.018252	0	1	1	8	TGME49_2	0
FALSE	FALSE	7.88E-05	0	1	1	14	TGME49_2	0
FALSE	FALSE	0.003955	0	1	1	6	TGME49_2	1
FALSE	FALSE	1.38E-05	0	1	1	9	TGME49_2	1
FALSE	FALSE	0.098913	0.003917	1	1	5	TGME49_2	1
FALSE	FALSE	0.025726	0	1	1	9	TGME49_3	0
FALSE	FALSE	0.000266	0	1	1	11	TGME49_2	0
FALSE	FALSE	0.049177	0.00168	1	1	9	TGME49_2	1
FALSE	FALSE	0.004296	0	1	1	6	TGME49_3	0
FALSE	FALSE	0.001404	0	1	1	4	TGME49_2	2
FALSE	FALSE	0.028509	0.00048	1	1	5	TGME49_2	0
FALSE	FALSE	9.65E-09	0	1	1	7	TGME49_2	1

Theo. MH+ [Da]	20171104_03_S65988_asp3_tmt10_tails_po.raw	20171104_08_S65988_asp3_tmt10_tails_po.raw	20171104_09_S65988_asp3_tmt10_tails_po.raw	Found in Sample: [S41] F5: 126, Sample, wt, pool	Found in Sample: [S42] F5: 127N, Sample, wt, single	Found in Sample: [S44] F5: 128N, Sample, wt, single	Found in Sample: [S46] F5: 129N, Sample, wt, single	Found in Sample: [S48] F5: 130N, Sample, wt, single
1861.095	High	High	High	High	High	High	High	High
2068.175	High	High	High	High	Not Found	High	Not Found	Not Found
1729.932	High	High	High	High	High	High	High	High
2250.175	Not Found	High	Not Found	High	High	Not Found	High	Not Found
1813.947	High	High	High	High	High	High	High	High
2204.193	High	Not Found	High	High	High	High	High	High
1432.775	High	High	High	High	High	High	High	High
2513.397	High	Not Found	Not Found	High	High	High	High	High
1710.988	High	High	High	High	High	High	High	High
1828.069	High	High	Not Found	High	High	High	High	High
1893.038	High	High	High	High	High	High	High	High
1894.942	High	High	High	High	High	High	High	High
1538.812	High	High	High	High	High	High	High	High
1953.226	Not Found	High	High	High	High	High	High	High
1172.72	High	High	High	High	High	High	High	High
2754.573	High	High	Not Found	High	High	High	High	High
2075.112	Not Found	High	High	High	High	High	High	High
2111.176	High	High	High	High	High	High	High	High
1929.96	High	High	High	High	High	High	High	High
3347.873	High	High	High	Not Found	Not Found	High	High	Not Found
1243.721	High	High	High	High	High	High	High	High
1532.897	High	High	High	High	High	High	High	High
1457.827	High	High	Not Found	High	High	High	High	High
2518.419	High	High	High	High	High	High	High	High
1764.11	High	High	High	High	High	High	High	High
1954.167	High	High	High	High	High	High	High	High
2250.941	High	High	High	High	High	High	High	High
2364.213	High	High	High	High	High	High	High	High
1603.858	High	High	High	High	High	High	High	High
2734.342	High	High	High	High	High	High	High	High
1889.049	High	High	High	High	High	High	High	High
2877.659	High	High	High	High	High	High	High	High
2272.056	High	High	High	High	High	High	High	High
3093.543	High	High	High	High	High	High	Not Found	High
1958.05	High	High	High	High	High	High	High	High
1388.881	Not Found	High	Not Found	High	High	High	High	High
1973.061	High	High	High	High	High	High	High	High
1196.593	Not Found	High	High	High	High	High	High	High
1459.92	High	High	High	High	High	High	High	High
2925.732	High	High	High	High	High	High	High	High
2285.192	High	Not Found	Not Found	High	High	High	High	High
2091.07	High	High	Not Found	High	High	High	High	High
2690.363	High	High	High	High	High	High	High	High
2950.569	High	High	High	High	High	High	High	High
3026.584	High	Not Found	High	High	Not Found	Not Found	High	Not Found

2346.43	High	High	High	High	High	High	High	High
2938.427	High	High	High	High	High	High	High	High
1670.91	High	High	High	High	High	High	High	High
1687.812	High	High	High	High	High	High	High	High
2174.218	Not Found	High	High	High	High	High	High	High
2612.524	High	High	Not Found	High	High	High	High	High
3868.892	High	High	High	High	High	Not Found	High	High
2163.358	High	Not Found	Not Found	High	High	High	High	High
1785.168	High	High	High	High	High	High	High	High
1116.657	Not Found	Not Found	High	High	High	High	High	High
1987.05	High	High	High	High	High	High	High	High
2234.196	High	High	High	High	High	High	High	High
2479.341	Not Found	High	High	High	High	High	High	High
1878.963	High	High	High	High	High	High	High	High
2359.115	High	High	Not Found	High	High	High	High	High
1376.737	High	High	High	High	High	High	High	High
1588.088	High	High	High	High	High	High	High	High
1674.954	High	Not Found	Not Found	High	High	High	High	High
1217.709	High	High	Not Found	High	High	High	High	High
2313.26	Not Found	Not Found	High	High	Not Found	High	High	High
1778.929	High	High	High	High	High	High	High	High
1639.884	High	Not Found	High	High	High	High	High	High
2909.451	High	High	High	High	High	High	High	Not Found
1805.074	Not Found	High	High	High	High	High	High	High
2403.272	High	High	High	High	High	High	High	High
1889.995	High	Not Found	High	High	Not Found	High	High	High
3591.822	High	High	High	High	High	High	High	High
2621.435	High	High	Not Found	High	High	High	High	Not Found
2597.403	High	Not Found	High	High	High	High	High	High
1331.755	High	High	High	High	High	High	High	High
1243.612	High	High	Not Found	High	High	High	High	High
1913.125	High	High	High	High	High	High	High	High
1758.011	High	High	High	High	High	High	High	High
2408.273	High	High	High	High	High	High	High	High
2121.311	High	High	High	High	High	High	High	High
1669.036	Not Found	High	High	High	High	High	High	High
1414.865	High	High	High	High	High	High	High	High
1358.888	High	High	High	High	High	High	High	High
1450.789	High	High	High	High	High	High	High	High
1875.109	High	High	High	High	High	High	High	High
1338.704	High	High	High	High	High	High	High	High
2447.324	High	High	High	High	High	High	High	Not Found
3170.659	High	High	High	High	High	High	High	High
2079.072	High	Not Found	High	High	High	High	High	High
2118.041	High	High	High	High	High	High	High	High
3317.92	High	High	High	High	High	High	High	High
2263.229	High	Not Found	Not Found	High	High	High	High	High
1701.936	High	High	High	High	High	High	High	High
1768.964	High	High	High	High	High	High	High	High
2306.266	High	High	High	High	High	High	High	High
1813.199	High	High	High	High	High	High	High	High
1767.015	High	High	High	High	High	High	High	High

1918.999	High	High	High	High	High	High	High	High
2678.467	High	High	High	High	High	High	High	High
1420.805	High	High	High	High	High	High	High	High
3687.975	Not Found	High	Not Found	High	High	High	High	Not Found
2400.263	High	High	High	High	High	High	High	High
1804.994	High	High	High	High	High	High	High	High
2848.506	High	High	High	High	High	High	High	High
1153.787	Not Found	High	High	High	High	High	High	High
1753.001	High	High	High	High	High	High	High	High
3528.681	High	High	High	High	Not Found	High	Not Found	High
2830.337	High	High	High	High	High	High	High	High
1719.89	High	High	High	High	High	High	High	High
1977.027	High	High	High	High	High	High	High	High
2511.397	High	High	High	High	High	High	High	High
2285.291	High	High	High	High	High	High	High	High
1555.803	High	High	High	High	High	High	High	High
1968.006	High	High	High	High	High	High	High	High
1315.846	High	High	Not Found	High	High	High	High	High
1800.043	High	High	High	High	High	High	High	High
3812.886	High	High	High	High	High	High	High	High
1648.927	High	High	High	High	High	High	High	High
2449.46	High	High	High	High	High	High	High	High
2319.232	High	High	High	High	High	High	High	High
3976.955	High	High	High	High	Not Found	High	High	High
2062.137	High	High	High	High	High	High	High	High
2575.249	High	High	High	High	High	High	High	High
1984.84	High	High	High	High	High	High	High	High
1581.847	Not Found	High	High	High	High	High	High	High
2404.209	High	High	High	High	High	High	High	High
1474.72	High	High	High	High	High	High	High	High
2841.605	Not Found	High	Not Found	High	High	High	High	High
3486.837	High	Not Found	High	High	High	High	High	High
2715.447	High	High	High	High	High	High	High	High
1873.945	High	High	High	High	High	High	High	High
1934.07	High	High	High	High	High	High	High	High
1314.679	High	Not Found	High	High	High	High	High	High
2571.27	High	High	High	High	High	High	High	High
1810.949	Not Found	High	High	High	High	High	High	High
1605.862	High	High	High	High	High	High	High	High
2316.203	High	High	High	High	High	High	High	High
2943.435	High	High	High	High	High	High	High	High
2664.36	High	High	High	High	High	High	High	High
2340.261	High	Not Found	High	High	High	High	High	High
2529.366	High	High	High	High	High	High	Not Found	Not Found
1919.785	High	High	High	High	High	High	High	High
3019.773	High	Not Found	Not Found	High	High	High	High	High
2368.24	High	High	High	High	High	High	High	Not Found
3828.881	High	High	High	High	High	High	High	High
2695.405	Not Found	High	High	High	High	Not Found	High	High
2922.674	High	Not Found	Not Found	High	High	High	High	High
2478.254	High	High	High	High	High	High	High	High
1106.625	High	Not Found	Not Found	High	High	High	High	High

2421.047	High	High	High	High	High	High	High	High
3406.841	High	High	High	High	High	High	High	High
1196.67	High	High	High	High	High	High	High	High
2356.328	High	High	High	High	High	High	High	High
1858.051	High	Not Found	Not Found	High	High	High	High	High
2470.223	High	High	Not Found	High	High	High	High	High
2496.364	High	High	High	High	High	High	High	High
1980.192	High	High	High	High	High	High	High	High
3717.998	High	High	High	High	High	High	High	High
2482.408	High	High	High	High	Not Found	Not Found	High	Not Found
1642.818	High	High	High	High	High	High	High	High
2806.585	Not Found	High	High	High	High	High	High	High
4996.456	Not Found	High	High	High	High	High	High	High
2719.504	High	Not Found	High	High	High	High	High	High
1817.996	High	High	High	High	High	High	High	High
1694.816	High	High	High	High	High	High	High	High
2668.56	High	High	Not Found	High	High	High	High	High
2443.36	High	Not Found	High	High	High	High	High	High
2392.307	High	Not Found	High	High	Not Found	High	High	Not Found
2094.216	High	High	High	High	High	High	High	High
4115.128	Not Found	High	Not Found	High	Not Found	High	High	High
2996.617	High	High	High	High	High	High	High	High
1436.748	High	High	High	High	High	High	High	High
2195.181	Not Found	High	High	High	High	High	High	High
2247.162	High	High	Not Found	High	High	High	High	High
3580.88	High	Not Found	Not Found	High	High	High	Not Found	High
2208.104	High	High	Not Found	High	High	High	High	High
2815.446	High	High	High	High	High	High	High	High
2383.162	High	High	High	High	Not Found	High	High	High
2095.084	High	High	High	High	High	High	High	High
2912.596	High	Not Found	Not Found	High	High	High	High	High
2022.023	High	High	High	High	High	High	High	High
1426.81	Not Found	High	High	High	High	High	High	High
2318.128	High	High	High	High	High	High	High	High
2442.254	High	High	Not Found	High	High	High	High	Not Found
3134.712	Not Found	High	Not Found	High	High	High	High	High
2170.246	Not Found	Not Found	High	High	High	High	High	High
3151.498	High	High	High	High	High	High	High	High
1791.94	High	High	High	High	High	High	High	High
3883.923	High	High	High	High	High	High	High	High
2650.456	High	High	High	High	High	High	High	High
2083.077	High	High	High	High	High	High	High	High
2237.129	High	High	High	High	High	High	High	High
1247.632	High	High	High	High	High	High	High	High
4713.424	High	High	High	High	High	High	High	High
3715.833	High	High	High	High	High	High	High	High
1880.974	Not Found	High	High	High	High	High	High	High
1496.728	High	High	High	High	High	High	High	High
2579.116	High	High	High	High	High	High	High	High
2725.443	High	High	High	High	High	High	High	High
1920.926	High	High	High	High	Not Found	High	High	Not Found
1364.747	High	High	High	High	High	High	High	High

3143.517	High	High	High	High	High	High	High	High
1711.904	High	High	High	High	High	High	High	High
2669.352	High	High	High	High	High	High	Not Found	High
2867.372	High	High	High	High	Not Found	High	Not Found	Not Found
2128.2	High	High	High	High	High	High	Not Found	Not Found
1655.837	High	High	High	High	High	High	High	High
2211.123	High	High	High	High	Not Found	High	High	High
3899.918	High	High	High	High	Not Found	High	Not Found	High
1849.909	High	High	High	High	Not Found	High	Not Found	Not Found
1603.994	Not Found	High	High	High	High	High	High	High
2948.503	High	High	High	High	High	High	High	High
2485.184	High	High	High	High	High	High	High	High
2453.397	High	High	High	High	High	High	Not Found	Not Found
1394.748	High	High	High	High	High	High	High	High
3146.716	High	High	High	High	High	High	High	High
2092.052	Not Found	High	High	High	Not Found	High	High	High
2689.302	High	High	High	High	Not Found	Not Found	Not Found	Not Found

Found in Sample: [S43] F5: 127C, Sample, ko, single	Found in Sample: [S45] F5: 128C, Sample, ko, single	Found in Sample: [S47] F5: 129C, Sample, ko, single	Found in Sample: [S49] F5: 130C, Sample, ko, single	Found in Sample: [S50] F5: 131, Sample, ko, pool	Found in Sample Group: wt, pool	Found in Sample Group: wt, single	Found in Sample Group: ko, single	Found in Sample Group: ko, pool
High	High	High	High	High	High	High	High	High
Not Found	High	High	Not Found	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
Not Found	High	High	Not Found	Not Found	High	High	High	Not Found
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High	High	High	High	Not Found	High	High	High	Not Found
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High	High	High	High	High	High	High	High	High
High	High	Not Found	High	Not Found	High	High	High	Not Found
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
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High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High

High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	Not Found	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	Not Found	Not Found	High	High	High	Not Found
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	High	High	High	High	High
High	High	High	High	Not Found	High	Not Found	High	Not Found

Abundance Ratio: (ko, pool) / (wt, pool)	Abundance Ratio: (ko, single) / (wt, single)	Abundance Ratio (log2): (ko, pool) / (wt, pool)	Abundance Ratio (log2): (ko, single) / (wt, single)	Abundances (Grouped): wt, pool	Abundances (Grouped): wt, single	Abundances (Grouped): ko, single	Abundances (Grouped): ko, pool	Abundances (Grouped) Standard Error [%]: wt, pool
11.893	0.054	3.57	-4.2	12.3	217.6	11.9	146.6	
0.01	0.336	-6.64	-1.58	2.1	7.2	2.4		
3.292	0.411	1.72	-1.28	67.5	169.6	69.7	222.3	
0.01	0.491	-6.64	-1.03	2.2	4	1.9		
0.502	2.005	-0.99	1	383.1	190	381.1	192.3	
0.556	2.014	-0.85	1.01	46.8	23.8	47.9	26	
0.246	2.028	-2.03	1.02	114.8	47.8	97	28.2	
0.135	2.035	-2.89	1.02	27.7	13.1	26.6	3.7	
0.224	2.038	-2.16	1.03	291.2	122.1	248.8	65.1	
0.278	2.044	-1.85	1.03	103.6	45.9	93.9	28.8	
0.542	2.051	-0.88	1.04	129.3	63.4	129.9	70	
0.01	2.052	-6.64	1.04	6.8	3.7	7.6		
0.754	2.053	-0.41	1.04	339.1	192.1	394.3	255.6	
0.193	2.056	-2.38	1.04	94.1	38.2	78.6	18.1	
0.371	2.057	-1.43	1.04	383.2	171	351.8	142.2	
0.01	2.057	-6.64	1.04	8.9	2.6	5.3		
0.01	2.062	-6.64	1.04	11.2	6.8	14		
0.396	2.082	-1.34	1.06	57.3	32.4	67.5	22.7	
0.269	2.083	-1.9	1.06	302.4	131.9	274.7	81.3	
	2.087		1.06		2	4.3		
0.391	2.09	-1.36	1.06	393.1	178.7	373.4	153.7	
0.498	2.092	-1.01	1.07	161.3	73	152.8	80.3	
0.336	2.094	-1.57	1.07	75.2	33.2	69.6	25.2	
0.194	2.095	-2.36	1.07	134.9	52.5	110	26.2	
0.461	2.107	-1.12	1.08	1225.1	594.6	1252.9	564.3	
0.371	2.112	-1.43	1.08	244.7	109.9	232	90.7	
0.66	2.117	-0.6	1.08	21.8	9.6	20.2	14.4	
0.304	2.124	-1.72	1.09	124.5	62.2	132	37.9	
0.323	2.127	-1.63	1.09	91.1	40.8	86.9	29.4	
0.01	2.131	-6.64	1.09	3.3	3.1	6.5		
0.267	2.142	-1.91	1.1	298.7	116.9	250.4	79.7	
0.343	2.148	-1.54	1.1	235.4	99.3	213.4	80.7	
0.497	2.151	-1.01	1.11	19.8	10.4	22.3	9.9	
0.01	2.154	-6.64	1.11	27.7	10.2	21.9		
0.373	2.161	-1.42	1.11	803.2	354	765.2	299.6	
0.499	2.164	-1	1.11	229.9	114.5	247.8	114.8	
0.505	2.17	-0.98	1.12	206	92	199.7	104.1	
0.421	2.185	-1.25	1.13	65.2	28.8	62.9	27.4	
0.332	2.201	-1.59	1.14	27.4	9.3	20.4	9.1	
0.33	2.214	-1.6	1.15	243.6	116.1	257.1	80.5	
1.023	2.229	0.03	1.16	66.3	42.1	93.8	67.9	
2.744	2.233	1.46	1.16	2.6	2.9	6.5	7.1	
0.252	2.235	-1.99	1.16	25	9	20.1	6.3	
0.75	2.239	-0.41	1.16	108.1	56	125.4	81.1	
0.01	2.247	-6.64	1.17	1.8	1.8	4		

0.348	2.254	-1.52	1.17	247.7	106.3	239.6	86.2
0.692	2.261	-0.53	1.18	17.4	6.3	14.2	12
0.522	2.276	-0.94	1.19	180.4	79.3	180.5	94.1
0.644	2.276	-0.64	1.19	216.4	108.7	247.3	139.3
0.207	2.29	-2.27	1.2	18.1	6.9	15.8	3.7
0.529	2.294	-0.92	1.2	80.2	37.6	86.2	42.4
0.01	2.298	-6.64	1.2	4.9	2.8	6.5	
0.493	2.3	-1.02	1.2	42	19.3	44.5	20.7
0.498	2.305	-1.01	1.2	2028.3	874.5	2015.8	1010.1
0.769	2.308	-0.38	1.21	19	11.2	25.7	14.6
0.148	2.323	-2.76	1.22	161.6	56.9	132.3	23.9
0.21	2.333	-2.25	1.22	196.8	72.8	169.9	41.4
0.702	2.344	-0.51	1.23	52.2	25.2	59.2	36.7
0.487	2.346	-1.04	1.23	212.2	94.2	221.1	103.4
0.6	2.347	-0.74	1.23	62.5	27.7	64.9	37.5
0.755	2.351	-0.4	1.23	171.5	81.5	191.5	129.6
0.608	2.351	-0.72	1.23	2861.8	1336	3140.4	1738.7
0.412	2.375	-1.28	1.25	37.8	15.2	36.2	15.6
0.514	2.378	-0.96	1.25	65.6	27.3	64.8	33.7
0.01	2.384	-6.64	1.25	5.1	3	7.1	
0.658	2.388	-0.6	1.26	664.2	328.9	785.5	436.9
0.601	2.389	-0.73	1.26	162.4	80	191.2	97.6
0.01	2.39	-6.64	1.26	13.1	4.5	10.6	
0.621	2.401	-0.69	1.26	122.4	55.5	133.2	75.9
0.405	2.404	-1.3	1.27	82.3	33	79.4	33.3
0.01	2.406	-6.64	1.27	3.6	2.8	6.7	
0.227	2.417	-2.14	1.27	45.1	22.6	54.6	10.3
0.289	2.434	-1.79	1.28	16.4	3.9	9.5	4.7
0.56	2.439	-0.84	1.29	50.4	26.9	65.7	28.2
0.552	2.44	-0.86	1.29	251.1	110.6	269.9	138.7
0.568	2.458	-0.82	1.3	146.1	64.3	158.2	83
0.642	2.468	-0.64	1.3	1194.7	573.5	1415.6	767.3
0.688	2.471	-0.54	1.31	647.3	298.7	738.1	445.6
0.265	2.479	-1.92	1.31	29.8	10.9	26.9	7.9
0.538	2.479	-0.9	1.31	271.5	117.7	291.9	146
0.732	2.48	-0.45	1.31	582.5	273.4	678	426.6
0.393	2.48	-1.35	1.31	123.6	46.8	116	48.5
0.609	2.486	-0.72	1.31	978.8	451.2	1121.6	595.7
0.333	2.489	-1.59	1.32	214	83.4	207.6	71.2
0.472	2.49	-1.08	1.32	2107.8	875.3	2179.8	994.9
0.244	2.505	-2.03	1.32	769.9	261.5	654.9	188.2
0.01	2.509	-6.64	1.33	3.8	3.4	8.6	
0.092	2.52	-3.44	1.33	38.4	11.3	28.5	3.6
0.396	2.548	-1.34	1.35	68.3	31.1	79.2	27
0.218	2.55	-2.2	1.35	94.3	32.3	82.4	20.5
0.166	2.551	-2.59	1.35	19	9.4	24	3.2
0.01	2.556	-6.64	1.35	15.4	5.5	14.1	
0.598	2.569	-0.74	1.36	140.8	51.1	131.3	84.2
0.751	2.582	-0.41	1.37	17.9	10.1	26.2	13.4
0.07	2.598	-3.83	1.38	42	14.6	37.9	3
0.494	2.602	-1.02	1.38	1172.4	475.6	1237.4	579.7
0.251	2.609	-1.99	1.38	62.1	21.6	56.4	15.6

0.434	2.618	-1.2	1.39	47.7	20.8	54.3	20.7
0.769	2.632	-0.38	1.4	54.1	25.7	67.7	41.6
0.477	2.634	-1.07	1.4	653.6	251.9	663.3	312
0.227	2.636	-2.14	1.4	16.5	3.4	9	3.7
0.455	2.649	-1.14	1.41	294.6	127	336.5	134.1
0.307	2.655	-1.7	1.41	73.8	26.6	70.6	22.7
0.842	2.663	-0.25	1.41	73.8	34.8	92.8	62.1
0.526	2.669	-0.93	1.42	213.9	82.1	219.1	112.4
0.572	2.669	-0.8	1.42	125.1	55.7	148.7	71.6
0.01	2.672	-6.64	1.42	5.7	4.4	11.8	
0.397	2.672	-1.33	1.42	15.4	7.6	20.3	6.1
0.253	2.688	-1.98	1.43	88.7	28.7	77	22.5
0.601	2.753	-0.73	1.46	98.7	43.1	118.6	59.4
0.585	2.784	-0.77	1.48	95.1	39.7	110.4	55.6
0.413	2.793	-1.28	1.48	34.4	12.5	35	14.2
0.435	2.807	-1.2	1.49	744.7	272.5	764.8	323.9
0.213	2.811	-2.23	1.49	322.5	107.3	301.6	68.8
0.525	2.811	-0.93	1.49	1179.4	452.5	1272.3	619.6
0.404	2.812	-1.31	1.49	55.7	21.8	61.2	22.5
0.323	2.854	-1.63	1.51	26.2	12.1	34.6	8.5
0.534	2.856	-0.9	1.51	987.4	383.9	1096.5	527.6
0.196	2.859	-2.35	1.52	123	40.3	115.3	24.1
0.638	2.865	-0.65	1.52	83.8	35.3	101.2	53.5
0.01	2.868	-6.64	1.52	11	3.1	8.8	
0.421	2.878	-1.25	1.53	540.4	200.3	576.6	227.6
0.309	2.882	-1.7	1.53	24.3	10.6	30.4	7.5
0.568	2.891	-0.82	1.53	227.1	95.6	276.4	129
0.188	2.904	-2.41	1.54	33.6	11.7	34.1	6.3
0.01	2.906	-6.64	1.54	16.4	3.2	9.2	
0.466	2.911	-1.1	1.54	104.6	38.6	112.4	48.7
0.321	2.912	-1.64	1.54	32.5	13.2	38.3	10.5
0.01	2.923	-6.64	1.55	25.3	7.8	22.7	
0.246	2.934	-2.02	1.55	44.1	17.1	50.1	10.8
0.875	2.939	-0.19	1.56	86.4	39.2	115.1	75.5
0.232	2.941	-2.11	1.56	99.6	33	97.1	23.1
0.555	2.943	-0.85	1.56	167.3	64.7	190.3	92.9
0.82	2.946	-0.29	1.56	53.9	26.6	78.3	44.2
0.01	2.949	-6.64	1.56	5.4	2.4	7	
0.6	2.949	-0.74	1.56	365.1	147.5	435	219.1
0.272	2.978	-1.88	1.57	39.9	14.1	42.1	10.8
0.265	3.004	-1.91	1.59	66.9	25.5	76.6	17.8
0.477	3.031	-1.07	1.6	53.4	21.7	65.7	25.4
0.257	3.032	-1.96	1.6	43	12.9	39	11
0.01	3.035	-6.64	1.6	7.5	1.9	5.8	
0.597	3.036	-0.74	1.6	113.4	45.5	138.3	67.7
0.563	3.052	-0.83	1.61	13.3	5.1	15.6	7.5
0.01	3.059	-6.64	1.61	6.2	3.9	12	
0.01	3.063	-6.64	1.61	5.3	3.4	10.3	
0.728	3.063	-0.46	1.61	6.8	3.9	12.1	4.9
0.61	3.07	-0.71	1.62	12.9	5	15.2	7.9
0.201	3.07	-2.31	1.62	53.9	13.4	41.3	10.8
0.584	3.101	-0.78	1.63	15.5	5.9	18.1	9.1

0.508	3.109	-0.98	1.64	35.7	13.1	40.6	18.1
0.261	3.112	-1.94	1.64	42.3	18.7	58.2	11
0.158	3.113	-2.66	1.64	18.7	6.9	21.4	3
0.609	3.133	-0.72	1.65	125.7	49.9	156.3	76.5
0.162	3.148	-2.63	1.65	36.6	9.7	30.4	5.9
0.36	3.159	-1.47	1.66	65.7	18.9	59.6	23.7
0.243	3.2	-2.04	1.68	38.1	11.1	35.6	9.3
0.529	3.207	-0.92	1.68	169.9	50.9	163.3	89.9
0.452	3.224	-1.15	1.69	31.4	11.6	37.4	14.2
0.01	3.25	-6.64	1.7	5.9	1.8	5.8	
0.254	3.295	-1.98	1.72	39.7	11.1	36.6	10.1
0.237	3.333	-2.08	1.74	29.9	10.6	35.2	7.1
0.388	3.342	-1.37	1.74	57.4	18.7	62.3	22.3
0.582	3.399	-0.78	1.77	90.1	31.6	107.4	52.5
0.41	3.409	-1.29	1.77	94.3	34.4	117.3	38.7
0.266	3.46	-1.91	1.79	46.7	13.2	45.7	12.4
0.271	3.462	-1.88	1.79	24.8	6.9	23.8	6.7
0.474	3.504	-1.08	1.81	59.9	20.7	72.7	28.4
0.564	3.521	-0.83	1.82	10.8	3	10.6	6.1
0.609	3.525	-0.72	1.82	55.1	22.6	79.8	33.5
0.01	3.535	-6.64	1.82	7.6	2.2	7.9	
0.01	3.543	-6.64	1.83	17	4.3	15.2	
0.349	3.549	-1.52	1.83	17.5	5.1	18	6.1
0.508	3.617	-0.98	1.85	30.3	8.7	31.6	15.4
0.362	3.632	-1.47	1.86	248.6	70.8	257.2	89.9
0.605	3.644	-0.72	1.87	10.1	2.7	9.7	6.1
0.313	3.66	-1.68	1.87	48.6	15.4	56.3	15.2
0.385	3.727	-1.38	1.9	194.2	56.2	209.4	74.8
0.01	3.736	-6.64	1.9	12.8	2.6	9.9	
0.076	3.775	-3.71	1.92	54.3	14.4	54.4	4.1
0.01	3.802	-6.64	1.93	11.2	3.4	12.8	
0.24	3.812	-2.06	1.93	34.5	9.6	36.7	8.3
0.439	3.833	-1.19	1.94	25.6	7.4	28.5	11.2
0.599	3.85	-0.74	1.94	102	31.2	120	61.1
0.404	3.903	-1.31	1.96	11.7	4.3	16.9	4.7
0.706	3.913	-0.5	1.97	4.2	3	11.9	3
0.35	3.945	-1.51	1.98	24.8	5.5	21.6	8.7
0.01	3.967	-6.64	1.99	18.7	4.8	19.2	
0.691	4.037	-0.53	2.01	16.3	5.8	23.5	11.2
0.349	4.039	-1.52	2.01	28.2	8.9	36.1	9.9
0.51	4.043	-0.97	2.02	86.6	29	117.2	44.2
0.338	4.138	-1.56	2.05	68.8	19	78.7	23.3
0.185	4.166	-2.43	2.06	65.1	19	79	12
0.28	4.23	-1.84	2.08	37.3	7.4	31.2	10.5
0.546	4.259	-0.87	2.09	56.7	17.2	73.2	31
0.494	4.337	-1.02	2.12	51.5	14.6	63.1	25.4
0.152	4.34	-2.71	2.12	18.1	4.8	20.6	2.8
0.276	4.708	-1.85	2.23	13.6	2.8	13	3.7
0.327	4.918	-1.61	2.3	29.6	7.9	39	9.7
0.101	4.951	-3.31	2.31	46.8	8.6	42.5	4.7
0.01	4.958	-6.64	2.31	17.9	1.9	9.2	
0.113	4.968	-3.14	2.31	59.3	10.8	53.6	6.7

0.244	5.02	-2.03	2.33	32.3	6.5	32.4	7.9
0.203	5.301	-2.3	2.41	77.8	15.6	82.5	15.8
0.113	5.352	-3.14	2.42	27.8	5.3	28.6	3.2
0.01	5.658	-6.64	2.5	9.4	1.5	8.7	
0.01	5.694	-6.64	2.51	8.7	1.9	10.7	
0.579	5.968	-0.79	2.58	31.7	7	41.7	18.3
0.299	6.166	-1.74	2.62	19.1	3.9	24.3	5.7
0.33	6.408	-1.6	2.68	8.4	3.2	20.8	2.8
0.183	7.651	-2.45	2.94	20.5	1.5	11.8	3.7
0.121	7.992	-3.05	3	256.4	30	239.4	31
0.01	8.47	-6.64	3.08	15.8	2.5	21.1	
0.311	8.491	-1.69	3.09	8.3	2.8	23.6	2.6
0.01	8.761	-6.64	3.13	12	2	17.3	
0.042	9.214	-4.57	3.2	145.2	14.5	133.7	6.1
0.01	9.216	-6.64	3.2	22.7	2.8	25.4	
0.406	14.783	-1.3	3.89	8.7	2.1	31.3	3.6
0.01	100	-6.64	6.64	91.1		97.4	

Abundances (Grouped) Standard Error [%]: wt, single	Abundances (Grouped) Standard Error [%]: ko, single	Abundances (Grouped) Standard Error [%]: ko, pool	Abundances (Grouped) Count: wt, pool	Abundances (Grouped) Count: wt, single	Abundances (Grouped) Count: ko, single	Abundances (Grouped) Count: ko, pool	Abundances (Normalized): F5: 126, Sample, wt, pool	Abundances (Normalized): F5: 127N, Sample, wt, single
18.01	54.53		1	4	4	1	12.3	234.8
	1.4		1	1	2		2.1	
13.46	6.27		1	4	4	1	67.5	169.2
23.45	9.82		1	2	2		2.2	4.6
11.4	11.95		1	4	4	1	383.1	191.5
12.25	24.3		1	4	4	1	46.8	26.1
14.9	22.44		1	4	4	1	114.8	51.3
19.87	8.93		1	4	4	1	27.7	13.3
23.9	24.11		1	4	4	1	291.2	123.6
7.64	24.91		1	4	4	1	103.6	47.2
16.55	7.3		1	4	4	1	129.3	56.7
70.87	60.45		1	4	4		6.8	7.6
10.27	19.86		1	4	4	1	339.1	199.7
15.57	25.89		1	4	4	1	94.1	43.1
22.72	17.97		1	4	4	1	383.2	184
27.94	43.85		1	4	4		8.9	3
50.36	26.88		1	4	4		11.2	2.5
31.64	25.08		1	4	4	1	57.3	31.1
19.97	18.31		1	4	4	1	302.4	143.9
1.58	48.26			2	4			
14.93	18.37		1	4	4	1	393.1	202.6
15.77	6.79		1	4	4	1	161.3	58.4
14.44	5.1		1	4	4	1	75.2	33.3
12.76	31.76		1	4	4	1	134.9	51.2
12.45	16.76		1	4	4	1	1225.1	615.1
15.05	22.64		1	4	4	1	244.7	113.8
50.15	10		1	4	4	1	21.8	6.9
25.44	15.51		1	4	4	1	124.5	62.7
20.72	16.93		1	4	4	1	91.1	52.6
31.3	81.42		1	4	4		3.3	1.9
29.9	32.81		1	4	4	1	298.7	141
18.65	15.07		1	4	4	1	235.4	103.7
36.98	22.5		1	4	4	1	19.8	6.2
37.61	45.32		1	3	4		27.7	9.7
17.41	20.34		1	4	4	1	803.2	401.1
6.54	12.63		1	4	4	1	229.9	107.3
11.57	10.82		1	4	4	1	206	90.1
7.82	17.51		1	4	4	1	65.2	30.7
14.79	41.32		1	4	4	1	27.4	10.7
19.58	15.5		1	4	4	1	243.6	122.6
13.55	36.56		1	4	4	1	66.3	40.2
42.17	33.16		1	4	4	1	2.6	2.9
41.52	41.45		1	4	4	1	25	9.8
18.5	30.78		1	4	4	1	108.1	56.7
	2.87		1	1	2		1.8	

5.99	17.6	1	4	4	1	247.7	111
26.58	16.06	1	4	4	1	17.4	6.8
11.86	15.57	1	4	4	1	180.4	78.2
3.88	20.86	1	4	4	1	216.4	110
34.58	15.62	1	4	4	1	18.1	10
16.9	24.76	1	4	4	1	80.2	29.1
51.05	45.34	1	3	4		4.9	4.5
27.97	18.63	1	4	4	1	42	18.6
12.4	16.16	1	4	4	1	2028.3	895.4
12.8	7.1	1	4	4	1	19	9.7
33.36	25.38	1	4	4	1	161.6	69.7
16.3	17.6	1	4	4	1	196.8	82.3
18.39	23.76	1	4	4	1	52.2	29.4
14.32	16.99	1	4	4	1	212.2	100.7
26.08	9.57	1	4	4	1	62.5	17.3
17.07	23.93	1	4	4	1	171.5	72
11.02	23.81	1	4	4	1	2861.8	1311
14.53	23.57	1	4	4	1	37.8	13.8
21.47	13.56	1	4	4	1	65.6	21.3
27.73	53.43	1	3	4		5.1	
15.52	20.36	1	4	4	1	664.2	317.3
11.39	18.17	1	4	4	1	162.4	81.2
33.87	36.49	1	3	4		13.1	5.6
19.72	12.97	1	4	4	1	122.4	50.5
29.55	24.72	1	4	4	1	82.3	40.2
39.68	25.1	1	3	4		3.6	
35.74	20.07	1	4	4	1	45.1	15.1
32.05	29.35	1	3	3	1	16.4	2.6
14.26	23.18	1	4	4	1	50.4	27.4
13.91	15.12	1	4	4	1	251.1	110.6
12.41	22.43	1	4	4	1	146.1	61.4
10.62	18.21	1	4	4	1	1194.7	532.1
13.5	18.52	1	4	4	1	647.3	269.2
44.24	42.59	1	4	4	1	29.8	7.9
5.7	15.57	1	4	4	1	271.5	123
7.44	27.81	1	4	4	1	582.5	297.5
9.84	17.69	1	4	4	1	123.6	46.9
17.33	26.39	1	4	4	1	978.8	412.7
19.36	14.87	1	4	4	1	214	77.4
13.67	21.91	1	4	4	1	2107.8	874.8
19.11	21.14	1	4	4	1	769.9	298.2
67.27	14.79	1	3	4		3.8	6.1
61.04	48.86	1	4	4	1	38.4	10.4
22.7	14.75	1	4	4	1	68.3	30.6
14.23	16.19	1	4	4	1	94.3	29.3
32.47	57.25	1	4	4	1	19	8.9
46.49	25.21	1	4	4		15.4	8.9
12.73	24.35	1	4	4	1	140.8	53.4
9.06	8.82	1	4	4	1	17.9	9.8
36.84	23.04	1	4	4	1	42	13.3
9.23	13.02	1	4	4	1	1172.4	514.3
14.75	35.03	1	4	4	1	62.1	20.5

20.3	16.04	1	4	4	1	47.7	16.2
25.5	19.67	1	4	4	1	54.1	27.3
10.27	15.56	1	4	4	1	653.6	217.6
32.65	39.81	1	3	4	1	16.5	3.6
7.24	12.53	1	4	4	1	294.6	123.2
15.15	47.37	1	4	4	1	73.8	29.4
15.52	24.86	1	4	4	1	73.8	33
8.52	14.33	1	4	4	1	213.9	75.4
7.74	25.33	1	4	4	1	125.1	56.8
37.39	17.81	1	2	4		5.7	
64.18	25.96	1	4	4	1	15.4	4.8
41.76	22.2	1	4	4	1	88.7	32.7
5.64	21.85	1	4	4	1	98.7	41.2
23.22	26.02	1	4	4	1	95.1	29.1
19.52	16.33	1	4	4	1	34.4	9.7
9.75	18.04	1	4	4	1	744.7	290.4
22.91	17.02	1	4	4	1	322.5	103.3
10.33	22.4	1	4	4	1	1179.4	462.6
16.64	18.12	1	4	4	1	55.7	17.4
25.62	18.9	1	4	4	1	26.2	16.7
11.96	27.97	1	4	4	1	987.4	391
22	28.74	1	4	4	1	123	37.1
10.08	15.77	1	4	4	1	83.8	34.9
64.8	49.64	1	3	4		11	
13.11	13.88	1	4	4	1	540.4	212.3
29.74	17.52	1	4	4	1	24.3	15
11.1	30.93	1	4	4	1	227.1	88.7
39.34	33.96	1	4	4	1	33.6	14
61.34	64.39	1	4	4		16.4	2.2
28.21	18.92	1	4	4	1	104.6	29.3
10.8	14.44	1	4	4	1	32.5	11.5
54.96	31.33	1	4	4		25.3	6.9
19.42	23.87	1	4	4	1	44.1	17.9
10.42	23.61	1	4	4	1	86.4	36.9
19.52	21.63	1	4	4	1	99.6	31.1
16.81	22.4	1	4	4	1	167.3	68.5
7.56	21.76	1	4	4	1	53.9	23.9
32.74	40.27	1	4	4		5.4	2
10.22	21.72	1	4	4	1	365.1	142.3
17.06	7.84	1	4	4	1	39.9	15
24.66	24.38	1	4	4	1	66.9	33.3
20.72	25.12	1	4	4	1	53.4	20.8
23.04	16.55	1	4	4	1	43	13.4
28.07	76.23	1	2	4		7.5	2.3
19.06	21.37	1	4	4	1	113.4	36.8
53.2	24.99	1	4	4	1	13.3	3.6
83.37	48.02	1	3	4		6.2	2.3
33.52	16.94	1	4	4		5.3	3.9
12.95	20.5	1	3	4	1	6.8	4
8.08	16.07	1	4	4	1	12.9	5.5
43.27	24.11	1	4	4	1	53.9	9.4
35.04	42.15	1	4	4	1	15.5	6.8

32.59	27.39	1	4	4	1	35.7	13.6
45.85	13.35	1	4	4	1	42.3	11.4
30.54	19.04	1	4	4	1	18.7	3.9
21.76	25.24	1	4	4	1	125.7	35.9
9.75	46.12	1	4	4	1	36.6	10.7
21.91	20.03	1	4	4	1	65.7	19.8
29.08	54.93	1	4	4	1	38.1	8.9
28.62	18.26	1	4	4	1	169.9	32.4
41.34	18.88	1	4	4	1	31.4	12.1
	18.58	1	1	3		5.9	
23.86	49.21	1	4	4	1	39.7	14.3
21.04	22.66	1	4	4	1	29.9	9.8
26.99	20.44	1	4	4	1	57.4	17.6
25.65	19.99	1	4	4	1	90.1	33.6
26.85	19.3	1	4	4	1	94.3	29.1
36.12	23.47	1	4	4	1	46.7	9.7
52.82	11.97	1	4	4	1	24.8	2.7
13.2	28.28	1	4	4	1	59.9	20.5
64.15	71.97	1	2	4	1	10.8	
19.83	11.83	1	4	4	1	55.1	20.5
5.16	57.05	1	3	4		7.6	
55.63	7.43	1	4	4		17	2.9
42.72	24.61	1	4	4	1	17.5	2.9
26.17	15.49	1	3	4	1	30.3	
19.44	7.72	1	4	4	1	248.6	75.7
29.39	18.15	1	3	4	1	10.1	2.5
18.06	24.55	1	4	4	1	48.6	18.3
23.49	21.01	1	4	4	1	194.2	68.4
28.52	32.49	1	3	4		12.8	
58.95	30.6	1	4	4	1	54.3	12.3
31.7	42.41	1	4	4		11.2	2.5
49.84	26.25	1	4	4	1	34.5	6.6
26.2	19.08	1	4	4	1	25.6	7.9
8.4	18.87	1	4	4	1	102	29.4
2.87	54.68	1	3	4	1	11.7	4.2
27	13.31	1	4	4	1	4.2	2
28.63	5.19	1	4	4	1	24.8	6.1
36.64	35.29	1	4	4		18.7	2.7
71.33	27.1	1	4	4	1	16.3	2.3
19.86	10.58	1	4	4	1	28.2	9.8
14.07	20.84	1	4	4	1	86.6	24.4
23.38	20.77	1	4	4	1	68.8	15.1
36.87	23.07	1	4	4	1	65.1	10.5
68.17	38.87	1	4	4	1	37.3	2.3
41.37	22.46	1	4	4	1	56.7	20.2
14.11	19.96	1	4	4	1	51.5	12.5
38.15	21.33	1	4	4	1	18.1	4.6
10.29	43.78	1	3	4	1	13.6	2.6
87.75	26.31	1	4	4	1	29.6	2
34.71	34.74	1	4	4	1	46.8	4.3
15.25	66.09	1	2	4		17.9	
25.28	59.03	1	4	4	1	59.3	7.5

10.52	38.46	1	4	4	1	32.3	5.5
33.36	15.01	1	4	4	1	77.8	16.6
14.4	12.66	1	3	4	1	27.8	4.5
	36.36	1	1	4		9.4	
0.92	55.9	1	2	3		8.7	1.9
42.39	30.78	1	4	4	1	31.7	2.7
47.22	21.71	1	3	4	1	19.1	
19.12	31.32	1	2	4	1	8.4	
	27.3	1	1	4	1	20.5	
12.67	18.01	1	4	4	1	256.4	25.4
53.14	34.52	1	4	4		15.8	4.5
49.25	21.92	1	4	4	1	8.3	2
13.72	54.95	1	2	3		12	2.2
37.61	24.5	1	4	4	1	145.2	16
58.74	34.91	1	4	4		22.7	2.3
22.32	58.26	1	3	4	1	8.7	
	9.91	1		4		91.1	

Abundances (Normalized): F5: 128N, Sample, wt, single	Abundances (Normalized): F5: 129N, Sample, wt, single	Abundances (Normalized): F5: 130N, Sample, wt, single	Abundances (Normalized): F5: 127C, Sample, ko, single	Abundances (Normalized): F5: 128C, Sample, ko, single	Abundances (Normalized): F5: 129C, Sample, ko, single	Abundances (Normalized): F5: 130C, Sample, ko, single	Abundances (Normalized): F5: 131, Sample, ko, pool	Abundances Count: F5: 126, Sample, wt, pool
261.9	201.8	171.7	19.4	12.6	3.6	11.8	146.6	4
7.2				2.4	2.5			1
166.9	143.4	199	73.4	63.5	72.1	69.7	222.3	8
	3.3			2.1	1.8			1
220	171.4	177.2	367.5	425.3	323.3	408.2	192.3	15
22.8	20.1	26.1	58	57.7	36	39.7	26	2
55.7	39.5	44.9	105.6	123.2	74.5	84.6	28.2	4
16.4	10	12.7	26	29.4	23.8	27.4	3.7	1
158.1	119.8	86.8	270.6	322.7	189	213.1	65.1	8
50.2	44.2	42.2	99.7	124.6	74.9	76.4	28.8	4
77	53.8	66	123.4	141.2	120.9	134.3	70	4
2.1	2.9	2.2	5.3	14.5	5	5.7		3
205.7	162.8	200.1	294.2	374.3	434.3	474.2	255.6	17
43.7	33.3	32.9	82.8	105.8	64.2	61.8	18.1	3
219.6	147.8	132.8	372.7	416.3	265.8	352.5	142.2	6
1.7	2.3	3.2	7.2	7.3	2.8	3.8		1
8.7	5.8	10.2	9.5	17.6	12.3	16.4		3
44	35.2	19.3	68.9	90	49.7	61.5	22.7	7
161.9	119.4	102.2	283.2	336.3	214.5	264.7	81.3	15
2	2.1		1.6	3.7	5.6	6.2		
200.8	156.8	154.3	395.5	454.4	292.3	351.5	153.7	3
69.2	82.1	82.3	160.3	162.7	141.3	146.8	80.3	8
40	30	29.7	67.8	74.9	67.4	68.3	25.2	5
62	46.1	50.9	123.8	149.5	67.5	99.4	26.2	9
690	526.9	546.2	1029.8	1456.4	1119.8	1405.9	564.3	7
131	101.8	92.8	261.3	287.4	170	209.5	90.7	8
13.4	13.8	4.1	22.8	20.9	18.7	18.5	14.4	6
83.3	45.5	57.1	134.4	151.9	103.5	138.4	37.9	12
41	33.4	36.3	87	107.5	74.7	78.3	29.4	7
3.4	4.1	2.8	13.4	8	1.8	2.9		2
152.8	86.8	87	295.9	340.3	161.3	204	79.7	7
123.6	87.4	82.6	195.8	235.7	177.2	244.8	80.7	5
15.4	10.6	9.3	25	16.5	27.8	20	9.9	6
14.2		6.6	28.9	32	13.4	13.4		6
413.4	299.6	302	821.4	934.7	564.9	739.8	299.6	16
124.8	111.2	114.9	236.8	280.6	209.5	264.3	114.8	2
105.4	79.5	93.1	178.6	219.1	183.5	217.6	104.1	6
30.4	25.9	28.2	72.4	69.6	47.8	61.8	27.4	3
8.2	8	10.2	22.9	28.1	8.4	22.1	9.1	3
143	88.7	110.2	227	267.7	224.7	309	80.5	13
47	34.8	46.2	60.4	88.9	84.1	141.7	67.9	3
1.3	3.2	4.3	5.5	6.9	9.3	4.3	7.1	1
13.7	7.8	4.7	23.9	29.7	15.9	11	6.3	4
65.9	41.5	59.9	83.9	111.7	130.3	175.8	81.1	7
	1.8		4.1	3.9				1

112.5	100.6	101.1	196	253.7	216.8	291.7	86.2	6
8.3	4.4	5.6	16.4	12.5	15.9	12	12	4
90.6	67.7	80.7	147.9	203.5	166.1	204.4	94.1	12
109.1	102.8	112.7	190	249.8	234.8	314.7	139.3	10
6.1	7.3	4.3	17.1	16	12.3	17.8	3.7	2
39.8	37.1	44.3	67	97.8	69.6	110.5	42.4	3
	1.8	2.2	6.5	10.6	4.9	3.9		2
27.1	14.6	17.1	33.7	50	42.4	51.9	20.7	1
989.2	727.7	885.8	1601.2	2036.6	2027.8	2397.7	1010.1	9
10.7	13.1	11.2	23.9	25.3	25.6	28.3	14.6	1
76.7	40	41.3	125.5	180.4	102.8	120.3	23.9	7
80.8	71.5	56.5	160.1	212.6	143	163.8	41.4	6
29.1	21.2	21.2	50.3	57.6	49.2	79.5	36.7	3
92.8	76.1	107.4	166.8	238.6	227.1	251.8	103.4	6
31.7	28.3	33.3	58.7	64.5	63	73.5	37.5	5
89.3	67.7	96.9	144.1	185.9	181.8	254.2	129.6	9
1425.9	1138.9	1468.2	2254.2	2981.8	3262.5	4063.1	1738.7	8
18.4	15.1	13.6	25.1	35.3	38.7	45.6	15.6	1
35	24.6	28	70.2	72.7	53.1	63.2	33.7	4
3.9	2.5	2.5	2.2	9.1	10.8	6.2		1
345	265.8	387.6	599.6	772.1	780.2	990.3	436.9	7
92.4	74.8	71.7	163	207.1	162	232.6	97.6	3
5	2.8		9.9	16.1	6.8	9.8		3
54.2	46.1	71.1	133.2	141.6	109.1	148.9	75.9	3
42.6	25	24.2	85.1	102.1	55.1	75.2	33.3	9
2.6	1.8	4	5.6	9.2	6.5	5.7		1
33	24.8	17.4	48.9	66.9	42.5	60	10.3	8
4	5.1		10.6	11.6		6.3	4.7	2
26.5	31.6	22.3	53.8	53.8	85.6	69.7	28.2	2
118.9	89	123.8	225.2	276.8	255.3	322.2	138.7	7
69.3	54.5	72.1	112.4	154.2	168.4	197.7	83	5
635.2	511.4	615.4	1058.5	1478.5	1451.8	1673.8	767.3	8
338.3	259.1	328.3	605.6	737.6	683	926.4	445.6	17
18	9.1	8.4	35.2	38.3	18.9	15.4	7.9	8
116.9	108.5	122.5	247.5	281.5	283	355.4	146	6
250.3	264.8	280.8	456.3	591.3	867.5	796.7	426.6	2
52.8	41.7	45.7	120.4	136.8	87.7	119.2	48.5	3
513	359.6	519.5	791	1156.8	1036.3	1502.3	595.7	9
106.4	68.8	81	182.8	239.8	179.7	228.2	71.2	8
1009.9	719.3	897.3	1553.9	2238.6	2209.8	2716.8	994.9	8
310.4	224.8	212.5	696.7	827.9	510.2	584.8	188.2	8
2.3	1.9		8.1	8.7	10.2	7.2		2
21.1	8.5	5.2	34.3	45.4	15.8	18.5	3.6	6
35.4	21.3	37	67.4	80.6	74	94.7	27	3
35	27.7	37.3	85.7	96.9	64.7	82.4	20.5	9
8.7	13.6	6.3	28.2	41.4	11.6	14.6	3.2	5
3.1	4.1	5.9	16.1	18	10.6	11.6		1
50	42.8	58.3	90	139.9	128.1	167	84.2	3
9.5	9.8	11.5	24.7	27.9	23.8	28.4	13.4	3
19.5	7.6	18	37.7	50.1	30.1	33.6	3	4
494.5	413.1	480.5	1060.5	1153.9	1314.3	1420.9	579.7	7
26	21.6	18.4	70.9	76	38.7	40.1	15.6	9

26.2	19.4	21.2	48.2	57.4	46.5	65.3	20.7	9
28.1	16.2	31.3	50.3	68.7	69.1	82.7	41.6	4
272.7	246.1	271	630.9	712.2	536	774.3	312	9
4.4	2.2		9.6	13.5	4.9	7.9	3.7	2
134.8	115.8	134.3	295.2	365.3	305.8	379.6	134.1	8
28.7	27.5	20.7	93.6	104.9	40.8	43	22.7	9
41	28.3	37	74.4	87.4	82.9	126.4	62.1	4
88.9	76.8	87.3	179	236.3	210.8	250.4	112.4	2
51.4	53.4	61.2	103.9	132.2	172	186.5	71.6	3
5.6		3.2	12.1	11.4	9.3	14.4		3
5.7	14.9	5	18.8	28	16.3	18	6.1	5
42.5	14.2	25.2	77.1	98.8	57	75.4	22.5	7
40.8	44.6	45.7	89.5	116	116.4	152.6	59.4	14
46.4	48.3	34.8	76.4	100.7	120.6	143.9	55.6	7
14.2	14.9	11.4	29.4	35.1	32.7	42.8	14.2	3
291.7	234.7	273.1	621.3	814.4	689.9	933.4	323.9	16
142.9	87.9	95	299.5	362.5	237.1	307.1	68.8	15
461.4	387.4	498.7	945.6	1265.7	1237	1640.7	619.6	5
26	20.6	23	47.3	58.8	65.1	73.7	22.5	4
11	10.9	9.9	29	40.9	39.7	28.9	8.5	9
403.5	317.9	423.1	740.2	1035.2	1126.2	1484.5	527.6	7
50.3	44.2	29.8	127.2	156.8	86.7	90.6	24.1	7
40.5	33.2	32.8	77.4	108.2	107.7	111.5	53.5	9
5.3	1.7	2.2	5.7	14.1	4.8	10.6		4
221.5	162.2	205.4	481.6	634.1	539.9	650.9	227.6	9
8	8.8	10.5	25.8	37.5	31.5	26.9	7.5	5
99.2	85.6	108.9	182.6	268.6	264.2	390.1	129	9
17.1	8.8	7.1	44.1	43.1	29.2	20	6.3	3
6.1	2.3	2.1	8.8	17.5	3.9	6.5		6
51.2	29.7	44.3	86.1	123.4	105.4	134.6	48.7	9
12.9	15	13.1	31.8	44	35.8	41.6	10.5	2
13.4	7.6	3.1	24.9	31.3	14.7	19.7		4
12.5	20.4	17.6	46.8	66.9	38.7	47.8	10.8	5
37.5	37	45.3	85.5	116.6	107.6	150.9	75.5	6
42.5	28.1	30.4	101	125.1	78	84.5	23.1	11
67.7	48.8	73.6	141.5	188.5	185.6	245.5	92.9	3
28.7	26.4	27.3	58	80.1	75.8	99.5	44.2	4
2	1.9	3.5	8.8	9.5	6.5	3.3		2
156.2	128.8	162.6	323.4	429.8	432.1	554.5	219.1	11
14.5	10.7	16.4	45.8	39	39.7	44	10.8	8
27.8	19.5	21.4	57.3	68.8	79.2	101.2	17.8	6
25.2	15.7	25.1	46.8	58.4	73.1	84.5	25.4	4
15.2	14.3	8.6	36.8	47	40.6	31.7	11	4
1.5			7.1	11.6	1.9	2.7		3
54.6	39.6	51.2	109.8	135.5	128.2	179.5	67.7	8
9.1	3.3	4.4	12	13.2	16.5	20.7	7.5	1
7.7	1.8		4.7	17.9	10.5	15.1		3
4.4	1.8	3.4	8.3	12.5	10.7	9.8		2
	4.4	3.4	9.4	12.6	11.1	15.2	4.9	2
4.5	5	4.9	17.2	16.6	11.8	15.2	7.9	2
21	15	8.4	49.5	50.2	34.1	31.3	10.8	8
2.8	7.4	6.3	27.3	21.2	13.9	10.1	9.1	2

9.5	10.3	18.9	25.8	38.8	46.6	51.2	18.1	9
31.1	16.5	15.8	53.3	65.2	49.9	64.4	11	10
7.8	7	8.7	22	26.7	19.6	17.1	3	6
60.7	47.2	55.8	122.5	142.3	147.1	213.3	76.5	11
8.5	10.2	9.3	42.6	42	22.5	14.7	5.9	3
24.2	14.6	17	46.2	59.8	57.3	75.2	23.7	4
10.8	8.9	15.8	60.3	40.1	27.5	14.4	9.3	6
52.7	50.5	68	172.9	151	129.8	199.4	89.9	5
17.6	5.9	10.8	32.2	35	34.5	47.8	14.2	5
	1.8		4.6	6.7		6.2		3
10.3	11.8	8	40.2	60.6	23.2	22.3	10.1	8
12.9	7.8	11.7	31.4	38.5	26.3	44.5	7.1	2
22.9	12	22.1	49.4	63.1	57.3	79.5	22.3	8
32	20.6	40.1	90.4	102.4	98.2	138.8	52.5	3
47.5	26.8	34.2	99	116.8	104.1	149.4	38.7	7
19.7	13.9	9.6	32.9	50.4	41.8	57.7	12.4	4
8.9	5.1	10.8	27.4	24.3	23	20.6	6.7	2
22	17.1	23.5	51.5	67.3	71.2	100.7	28.4	3
4.4	1.7		21.6	10.2	5.8	5	6.1	3
22.2	18.8	29.1	78	81.9	68.3	91.1	33.5	2
2.1	2.2	2.4	2.3	10.6	6.3	12.3		2
7.8	2.9	3.5	16.5	14.8	15.6	13.9		4
3.6	6.6	7.2	14.6	16.7	16.1	24.5	6.1	6
11	6.5	8.7	25.9	32.5	30.4	37.7	15.4	3
76.1	50.5	81	238.1	270.7	242.4	277.7	89.9	4
2		3.5	8	8.4	11.4	11.1	6.1	1
13.8	12.4	17.1	40	55.2	56.3	73.8	15.2	2
61.8	37.7	56.8	179.5	209.5	176.9	271.5	74.8	29
3.2	1.8	3	5.7	13.1	11.5	9.3		5
25.9	14	5.5	62.3	73.9	38.5	42.8	4.1	8
4.6	3.9	2.5	18	13.9	5.2	14		2
15.4	11.6	4.9	28	47.6	29.2	42	8.3	9
4.6	8	9.1	34.4	25.2	22.7	31.5	11.2	3
34.8	31.4	29.1	103.3	113.7	109.5	153.3	61.1	13
4.4	4.4		29.2	17.8	7.5	13	4.7	4
3.9	3.4	2.8	12.7	9.6	12.1	13.2	3	1
7.1	5.4	3.4	22.5	21.8	20	22.3	8.7	2
7	4.4	5.2	9.5	21.7	20.3	25.2		8
11	7.3	2.7	18.4	27.3	30.5	17.8	11.2	5
8.2	6.9	10.9	35.7	35.5	32	41.3	9.9	4
31.6	33.2	26.9	89.7	114.7	115.2	149.2	44.2	8
25.4	18.3	17.3	59.6	82.2	74.3	98.8	23.3	9
27.1	16.9	21.4	62.1	85	67	102.1	12	11
13.8	4.7	8.7	34.2	43.4	14.5	32.5	10.5	7
25.5	9.4	13.7	55.4	75.6	67.4	94.6	31	10
14.4	13.9	17.4	49.5	59.7	63.4	79.8	25.4	8
4.3	2.9	7.2	14.2	21.4	23.9	23	2.8	3
	2.6	3.1	13.5	20.8	10.3	7.5	3.7	4
13.9	1.8	14	29.3	52.7	40.6	33.4	9.7	8
9.3	11.3	9.4	50.2	57.5	23.8	38.4	4.7	9
1.7	2.1		12.2	16.1	2.3	6.3		6
10.1	11.6	14	83.7	77.4	32.9	20.4	6.7	8

6.5	7	6.8	49.4	33.7	21.3	25.2	7.9	7
21.2	8.7	15.8	78.8	86.7	67.7	97	15.8	9
5.9		5.6	23.3	29.1	30.9	31	3.2	6
1.5			4.5	8.1	11.4	11		3
1.9			12.7	15.5	4			3
9	7.2	9	54.3	51.1	31.3	30	18.3	7
2.5	3.3	6	25.4	29.1	26.1	16.8	5.7	6
3.7		2.8	15.8	27.9	24.7	14.7	2.8	3
1.5			16.4	10.6	8.9	11.3	3.7	6
30	29.7	34.7	208.6	287.9	198	262.9	31	5
1.7	1.8	2.1	14.4	20.9	18	31.3		6
2.4	4.8	1.9	24.3	23.2	17.2	29.8	2.6	3
1.8			25.1	20	6.7			5
18.6	16.9	6.5	157.9	164.6	97	115.5	6.1	6
1.8	1.8	5.2	17.7	31.5	18	34.6		3
1.9	1.8	2.7	4.9	46	34.4	39.7	3.6	3
			92.5	92.2	93	111.9		7

Abundances Count: F5: 127N, Sample, wt, single	Abundances Count: F5: 128N, Sample, wt, single	Abundances Count: F5: 129N, Sample, wt, single	Abundances Count: F5: 130N, Sample, wt, single	Abundances Count: F5: 127C, Sample, ko, single	Abundances Count: F5: 128C, Sample, ko, single	Abundances Count: F5: 129C, Sample, ko, single	Abundances Count: F5: 130C, Sample, ko, single	Abundances Count: F5: 131, Sample, ko, pool
6	6	6	6	6	5	1	3	6
	4				1	1		
8	8	8	8	8	8	8	8	8
1		1			1	1		
15	15	15	13	15	15	15	15	13
2	2	2	2	2	2	2	2	2
4	4	4	4	4	4	4	4	4
1	1	1	1	1	1	1	1	1
8	8	8	8	8	8	8	8	7
4	4	4	4	4	4	4	4	4
4	4	4	4	4	4	4	4	4
3	1	1	1	3	6	2	2	
17	17	17	17	17	17	17	17	17
3	3	3	3	3	3	3	3	3
6	6	6	6	6	6	6	6	6
1	1	1	1	1	1	1	1	
1	3	2	3	3	4	3	4	
6	7	7	5	7	7	7	7	5
13	14	14	12	15	16	15	14	12
	1	1		1	2	2	2	
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5	5	4	4	5	6	7	5	4
8	9	8	8	9	9	9	9	6
7	7	7	7	7	7	7	7	7
8	8	8	8	8	8	8	8	7
2	3	3	1	6	6	3	5	4
13	12	8	9	14	14	13	13	6
7	7	7	6	7	7	7	7	6
1	2	2	1	6	4	1	1	
7	7	7	7	7	7	7	7	7
5	5	5	5	5	5	5	5	5
3	6	4	3	6	6	6	5	3
4	5		2	8	8	4	4	
14	16	15	13	16	16	15	16	12
2	2	2	2	2	2	2	2	2
6	6	6	6	6	6	6	6	6
3	3	3	3	3	3	3	3	3
3	3	3	3	3	3	3	3	3
12	12	8	8	14	14	14	12	7
3	3	3	3	3	3	3	3	3
1	1	1	2	3	3	3	1	2
3	3	3	2	4	6	5	3	2
7	7	7	7	7	7	7	7	7
		1		2	1			

6	6	6	6	6	6	6	6	6
2	3	2	2	5	4	5	3	4
9	10	5	6	13	13	11	12	5
9	9	8	8	10	10	10	10	9
2	2	2	1	2	2	2	2	1
2	3	3	3	3	3	3	3	3
2		1	1	3	2	2	1	
1	1	1	1	1	1	1	1	1
9	9	9	9	9	9	9	9	9
1	1	1	1	1	1	1	1	1
7	7	6	5	7	7	7	7	4
6	6	6	6	6	6	6	6	5
3	3	3	3	3	3	3	3	3
6	6	6	6	6	6	6	6	6
3	4	4	4	5	5	4	5	5
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8	8	8	8	8	8	8	8	8
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4	4	4	4	4	4	4	4	4
	1	1	1	1	1	1	1	
7	7	7	7	7	7	7	7	7
3	3	3	3	3	3	3	3	3
2	2	1		4	4	3	3	
3	3	3	3	3	3	3	3	3
8	9	6	7	9	9	9	9	8
	1	1	1	2	2	2	1	
4	8	6	4	8	7	7	7	2
1	2	2		2	2		2	1
2	2	2	2	2	2	2	2	2
7	7	7	7	7	7	7	7	7
5	5	5	5	5	5	5	5	5
8	8	8	8	8	8	8	8	8
16	17	17	16	17	17	17	17	16
3	5	3	3	8	8	5	5	2
6	6	6	6	6	6	6	6	6
2	2	2	2	2	2	2	2	2
3	3	3	3	3	3	3	3	3
9	9	9	9	9	9	9	9	9
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8	8	8	8	8	8	8	8	8
8	8	8	8	8	8	8	8	8
3	1	1		4	4	5	2	
3	6	3	2	6	6	5	6	1
3	3	2	3	3	3	3	3	2
4	6	4	4	9	9	8	8	5
3	3	4	2	6	6	4	4	1
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3	3	3	3	3	3	3	3	3
3	3	3	3	3	3	3	3	3
3	4	3	3	4	4	4	4	1
7	7	7	7	7	7	7	7	7
6	8	6	4	9	9	9	6	4

4	8	6	5	8	8	8	8	5
4	4	3	5	5	5	5	5	5
9	9	9	9	9	9	9	9	9
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8	8	8	8	8	8	8	8	7
8	8	9	7	9	9	7	8	5
4	4	4	4	4	4	4	4	4
2	2	2	2	2	2	2	2	2
3	3	3	3	3	3	3	3	3
	3		1	6	5	4	5	
2	3	6	2	7	7	5	5	2
4	7	4	5	7	7	6	6	4
9	11	9	11	12	14	12	11	7
7	7	6	6	7	7	7	7	7
3	3	3	3	3	3	3	3	3
16	16	15	16	16	16	16	16	16
12	13	11	11	16	15	13	15	9
5	5	5	5	5	5	5	5	5
4	4	4	4	4	4	4	4	4
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	3	1	1	3	4	2	3	
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5	3	3	4	5	5	5	4	2
7	7	8	7	9	10	11	10	7
3	3	2	2	3	3	3	3	2
1	4	1	1	4	7	2	2	
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1	2	2	2	2	2	2	2	2
3	4	2	1	4	4	4	3	
2	1	4	3	4	5	4	5	2
6	6	6	5	6	6	6	6	6
6	9	9	8	11	13	10	11	5
3	3	3	3	3	3	3	3	3
4	3	3	4	6	5	5	6	3
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10	11	11	10	14	15	13	12	12
5	5	5	5	8	8	8	8	3
5	7	4	5	7	6	8	6	4
3	3	3	4	5	4	5	5	3
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7	8	7	7	8	8	8	8	7
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1	4	1		3	7	4	5	
1	2	1	1	3	3	3	2	
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3	7	5	3	8	8	7	8	3
2	1	2	2	2	2	2	2	2

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6	10	7	8	12	13	12	13	10
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		1		3	3		2	
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6	6	6	6	8	7	6	6	7
2	4	3	2	4	4	3	2	2
1	2	2	2	2	2	2	2	1
3	3	3	2	3	3	3	3	2
	2	1		3	3	2	2	2
2	2	2	2	2	2	2	2	2
	1	1	1	1	2	2	1	
1	1	1	1	4	3	3	3	
1	2	3	3	7	7	4	6	2
	3	2	3	3	3	3	3	3
4	4	4	3	4	4	4	4	4
1	1		1	1	1	1	1	1
2	2	2	2	2	2	2	2	1
20	18	12	17	34	31	28	24	14
	2	1	1	3	4	5	2	
5	5	5	2	9	9	7	7	1
1	2	2	1	3	3	2	3	
3	6	5	2	8	9	7	9	2
3	1	2	2	3	3	3	3	2
7	6	5	7	12	13	13	12	9
2	2	2		5	5	3	4	1
1	1	1	1	1	1	1	1	1
2	2	2	1	2	2	2	2	2
1	4	2	2	3	7	5	6	
1	4	3	1	6	5	6	4	3
4	3	2	4	5	4	4	4	2
6	8	8	6	8	8	8	8	8
5	7	5	6	9	9	9	9	5
4	9	7	7	13	14	12	10	3
1	5	2	4	8	8	5	6	3
7	9	4	4	11	11	11	10	6
4	5	4	3	7	7	7	7	5
1	1	1	2	4	3	3	2	1
1		1	1	4	3	4	2	1
1	6	1	5	8	9	9	8	2
2	4	5	4	9	9	7	8	1
	1	1		5	6	1	2	
3	3	5	4	8	8	8	6	2

2	3	2	2	11	8	8	6	2
5	7	3	6	9	9	9	9	4
2	3		2	5	6	6	5	1
	1			3	2	3	2	
1	1			6	7	2		
1	3	3	3	7	8	7	5	5
	1	2	3	9	9	9	4	2
	2		1	5	5	5	3	1
	1			6	4	3	3	1
4	5	5	5	5	5	5	5	5
2	1	1	1	7	8	7	8	
1	1	2	1	10	8	7	5	1
1	1			9	7	3		
5	5	4	2	6	6	6	6	2
1	1	1	2	3	3	3	3	
	1	1	1	2	4	4	4	1
				7	7	7	7	

Quan Info	XCorr Sequest HT	Confidence Sequest HT	Percolator q-Value Sequest HT	Percolator PEP Sequest HT
Unique	2.210525	High	0.000267	0.00201
Unique	3.160377	High	0	4.51E-06
Unique	1.831623	High	0.000786	0.005022
Unique	1.438649	High	0.000905	0.005969
Unique	3.465892	High	0	0.000156
Unique	4.343281	High	0	9.43E-06
Unique	2.339645	High	0.00054	0.003934
Unique	2.1068	High	0	0.0002
Unique	3.405024	High	0	0.000932
Unique	2.543267	High	0	0.00045
Unique	3.446869	High	9.58E-05	0.001265
Unique	1.911008	High	0.001014	0.006715
Unique	2.638999	High	0.000327	0.002413
Unique	1.910415	High	0.003079	0.02709
Unique	2.909466	High	0.000905	0.006036
Unique	2.133026	High	0.000465	0.003724
Unique	3.392662	High	0	5.8E-06
Unique	3.826094	High	0	1.57E-07
Unique	4.19134	High	0	9.23E-07
Unique	5.071735	High	0	4.12E-09
Unique	2.196693	High	0.005895	0.06097
Not Unique	2.79541	High	0.000267	0.001989
Unique	2.553957	High	0	0.001079
Unique	3.763101	High	0	2.21E-05
Unique	2.001125	High	0.002624	0.02105
Unique	3.86956	High	0	1.47E-05
Unique	3.29424	High	0	2.07E-06
Unique	2.753109	High	0	0.000433
Unique	2.046736	High	0.004741	0.04927
Unique	2.878246	High	0	0.000031
Unique	2.777456	High	0	3.17E-05
Unique	4.663859	High	0	3E-07
Unique	2.349629	High	0.001165	0.007972
Unique	4.10298	High	0	5.58E-08
Unique	4.721487	High	0	1.23E-05
Unique	1.495682	High	0.000664	0.004569
Unique	2.83466	High	0.001524	0.01115
Unique	1.839289	High	0.006889	0.06956
Unique	1.562853	High	0.002467	0.01809
Unique	4.697728	High	0	1.48E-07
Unique	2.338349	High	0.001267	0.00889
Unique	1.285472	High	0.002041	0.01341
Unique	3.319805	High	0	0.000093
Unique	3.677857	High	0	1.71E-10
Unique	2.872702	High	0	4.9E-06

Unique	2.673763	High	0	0.00029
Unique	2.71916	High	0	6.61E-05
Unique	2.918277	High	0.000327	0.002831
Unique	2.631367	High	0	0.000466
Unique	1.26742	High	0.003173	0.02979
Unique	3.683519	High	0	1.41E-05
Unique	4.674997	High	0	5.54E-06
Unique	2.077569	High	0.000905	0.006055
Unique	4.293733	High	0	5.19E-06
Unique	2.271639	High	0.002552	0.01928
Unique	3.109324	High	0	7.01E-05
Unique	3.485898	High	0	8.72E-05
Unique	1.948303	High	0.000397	0.003245
Unique	3.349413	High	0	4.8E-06
Unique	5.834731	High	0	2.94E-07
Unique	2.872467	High	0.001014	0.006928
Unique	2.423319	High	0.002866	0.0254
Unique	1.936586	High	0.002157	0.01566
Unique	2.417861	High	0.002624	0.02093
Unique	1.189442	High	0.002234	0.01673
Unique	2.70794	High	0.000786	0.005381
Unique	2.062755	High	0.000397	0.0034
Unique	1.348258	High	0.002157	0.01478
Unique	2.231252	High	0.002234	0.01685
Unique	3.315764	High	0	0.000395
Unique	1.483033	High	0.002041	0.01338
Unique	4.040088	High	0	6.94E-06
Unique	2.489126	High	0	0.00053
Unique	2.519663	High	0	3.21E-05
Unique	2.78508	High	0.009574	0.09167
Unique	2.278829	High	0.001362	0.00965
Unique	2.965901	High	0	0.00011
Unique	3.76612	High	0	0.000251
Unique	4.04462	High	0	3.18E-06
Unique	3.290345	High	0	4.09E-06
Unique	2.189224	High	0.002666	0.02317
Unique	2.735598	High	0.001837	0.0127
Unique	2.994149	High	0	0.00046
Unique	3.15671	High	0	5.61E-05
Unique	3.075098	High	0	2.24E-05
Unique	3.435544	High	0	5.81E-05
Unique	5.375977	High	0	0
Unique	3.329006	High	0	3.44E-05
Unique	4.012956	High	0	1.91E-09
Unique	4.721132	High	0	1.48E-06
Unique	3.734027	High	0	1.03E-06
Unique	1.974172	High	0.001329	0.009355
Unique	3.074253	High	0	0.000734
Unique	2.143486	High	0.001014	0.006876
Unique	3.674931	High	0	7.11E-06
Unique	3.056237	High	0.00412	0.04302
Unique	3.622262	High	0	0.000203

Unique	3.026305	High	0	0.000287
Unique	3.765919	High	0	4.64E-08
Unique	3.480118	High	0	0.001059
Unique	4.355481	High	0	3.01E-07
Unique	4.107713	High	0	5.95E-07
Unique	3.000935	High	0	0.000312
Unique	1.815878	High	0.001892	0.01293
Unique	2.906646	High	0.000465	0.003734
Unique	2.809588	High	0.000327	0.002336
Unique	3.470045	High	0	0.000104
Unique	1.956475	High	0.001014	0.006417
Unique	2.446696	High	0.000327	0.002663
Unique	4.920296	High	0	5.22E-08
Unique	2.92223	High	0	2.49E-05
Unique	2.832602	High	0	0.000546
Unique	4.021817	High	0	6.23E-06
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Unique	3.241336	High	0	0.000724
Unique	1.76243	High	0.000786	0.005321
Unique	4.202496	High	0	6.17E-06
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Unique	1.840681	High	0.008373	0.08276
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Unique	1.638276	High	0.002624	0.02198
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Unique	3.584486	High	0	1.65E-06
Unique	5.650108	High	0	2.79E-10
Unique	4.300204	High	0	2.25E-09
Unique	4.139167	High	0	3.03E-05
Unique	2.956552	High	0	0.001153
Unique	2.627244	High	0	0.000346
Unique	1.822807	High	0.001067	0.007386
Unique	3.186306	High	0	3.43E-06
Unique	4.893584	High	0	8.06E-08
Unique	2.142861	High	0	9.81E-05
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Unique	2.768415	High	0	4.01E-05
Unique	4.762944	High	0	5.45E-09
Unique	2.999763	High	0	0.000216
Unique	2.219565	High	0.003512	0.03499
Unique	1.953621	High	0.000786	0.005349
Unique	3.534119	High	0	0.000289
Unique	3.242737	High	0	3.05E-06
Unique	2.16666	High	0	0.000918
Unique	2.61815	High	0	0.001171
Unique	2.155756	High	0.002732	0.02388

Unique	2.963605	High	0	3.94E-05
Unique	2.642104	High	0	1.48E-05
Unique	2.121956	High	0.00147	0.01093
Unique	2.606042	High	0	0.00067
Unique	2.316098	High	0.002994	0.02665
Unique	1.996225	High	0.000267	0.002033
Unique	5.264039	High	0	1.28E-08
Unique	2.70413	High	0	0.000447
Unique	3.5698	High	0	7.9E-07
Unique	1.792327	High	0.000465	0.00379
Unique	2.214187	High	0.000664	0.004448
Unique	2.823617	High	0.000397	0.003484
Unique	3.693238	High	0	0.00015
Unique	2.629181	High	9.58E-05	0.001269
Unique	3.352881	High	0	4.23E-06
Unique	1.526938	High	0.002384	0.01748
Unique	2.554655	High	0.00054	0.003948
Unique	4.287303	High	0	1.17E-05
Unique	2.227161	High	0.003461	0.03249
Unique	2.951894	High	0.000187	0.001754
Unique	3.547709	High	0	0.000126
Unique	2.719453	High	0	0.000201
Unique	2.997832	High	0	0.001147
Unique	2.87963	High	0	9.34E-06
Unique	5.705291	High	0	0
Unique	1.315184	High	0.002618	0.02005
Unique	3.739348	High	0	6.46E-07
Unique	4.127475	High	0	1.21E-07
Unique	2.75151	High	0.000397	0.003444
Unique	7.113717	High	0	0
Unique	3.74192	High	0	3.2E-06
Unique	3.232225	High	0	3.81E-05
Unique	2.230569	High	0.000187	0.001774
Unique	4.289836	High	0	7.45E-06
Unique	3.210404	High	0	7.33E-07
Unique	1.582754	High	0.002596	0.01944
Unique	2.225596	High	0.001067	0.007178
Unique	3.388082	High	0	6.66E-05
Unique	2.482809	High	0	0.000653
Unique	5.405224	High	0	0.000022
Unique	3.826567	High	0	0.00001
Unique	5.285296	High	0	1.01E-07
Unique	4.159215	High	0	9.09E-07
Unique	2.238332	High	0	0.000179
Unique	3.508898	High	0	1.18E-05
Unique	5.980645	High	0	5.05E-07
Unique	3.30486	High	0	0.000143
Unique	2.673603	High	0	0.000021
Unique	2.612561	High	0	0.000528
Unique	2.663385	High	0	0.001211
Unique	2.695684	High	0	0.000026
Unique	2.08945	High	0.003334	0.03185

Unique	3.436746	High	0	4.73E-06
Unique	3.197902	High	0.000327	0.003022
Unique	3.434779	High	0	0.000302
Unique	4.32018	High	0	2.36E-05
Unique	2.571856	High	0.000849	0.005549
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Unique	4.680907	High	0	4.7E-09
Unique	2.083363	High	0.001624	0.01171
Unique	2.316579	High	0	0.001209
Unique	3.66385	High	0	6.25E-07
Unique	2.461701	High	0.000605	0.004097
Unique	2.856167	High	0	6.24E-05
Unique	3.123907	High	0	9.76E-06
Unique	2.050293	High	9.58E-05	0.001435
Unique	8.446517	High	0	0

Name1	**GeneID**	**Name**	**ASP5-proc**	TEXEL or new cleavage site (pos
TASP1	TGME49_241240	GRA65	**Yes**	**RRLAE (68/706)**; RELVD (83/706
TASP2	TGME49_320490	GRA66	**Yes**	**RHLLT (358/1134)**
TASP3	TGME49_247440	GRA33	**Yes**	
TASP4	TGME49_203290	GRA34	No	
TASP5	TGME49_279100	GRA67	**Yes**	RLLRD (250/435); RGLME (420/4
TASP6	TGME49_240090	WNG2	**Yes**	**RRLDS (109/553)**; RELPE (240/5
TASP7	TGME49_293510		No	RELRQ (138/392)
TASP8	TGME49_216060		No	
TASP9	TGME49_320180	SRS16C	No	RTLQQ (49/398)
TASP10	TGME49_301170	SRS19D	No	RSLQQ (49/389)
TASP11	TGME49_213280	SRS25	No	
TASP12	TGME49_224770	SRS40D	No	RILDE (49/389)
TASP13	TGME49_297160		No	
TASP14	TGME49_247520		N/A	
TASP15	TGME49_233695		N/A	
TASP16	TGME49_278080	SUSA1	No	RRLSD (453/499)
TASP17	TGME49_214870		N/A	RLLAE (139/492)
TASP18	TGME49_208730	MCP4	No	
TASP19	TGME49_209755		N/A	
TASP20	TGME49_219690		N/A	
TASP21	TGME49_308970	GRA68	No	RHLVD (4/342)
TASP22	TGME49_226420	GRA69	No	
TASP23	TGME49_201390		N/A	
TASP24	TGME49_263070		N/A	

	Disorder score (DISpro)				
Annotated Sequence	**Full lenght**	**1-50aa**	**51-100aa**	**101-150aa**	**151-200aa**
[TQVRRL].AEGKPGEKR.[D]	0.42	0.32	0.46	0.11	0.01
[AETVLESGRHL].LTANVYEEAR.[S]	0.21	0.49	0.03	0.02	0.00
[EISDASGGVA].VTSPAAEEER.[L]	0.35	0.15	0.16	0.82	0.08
Multipe (not so significant)	0.22	0.08	0.11	0.16	0.10
Multipe (not so significant)	0.24	0.49	0.65	0.52	0.02
[AERRRL].DSLIPGFLKR.[R]	0.29	0.26	0.27	0.19	0.00
[NSAVCTSSKM].PAKEIVFHCEYAPSGR.[A]	0.23	0.08	0.21	0.13	0.07
[M].VTGGIWRPDSLPLYSR.[S]	0.64	0.25	0.04	0.76	0.08
[VFFSSGQAVA].DNLLEGLLHR.[T]	0.17	0.21	0.15	0.10	0.02
[LGGIALFSTGEA].VPDKFLEGLQTR.[S]	0.14	0.25	0.13	0.09	0.04
[LLCWVPSWTAHA].EEHFAVFSTCR.[T]	0.06	0.08	0.04	0.05	0.06
[YLREGLQQRIL].DEVHTADENPHLAIDGR.[T]	0.16	0.28	0.08	0.10	0.03
[RHLLVQRRQL].SSSQPLTAPSTPTKASR.[S]	0.46	0.26	0.49	0.93	0.09
[VPQSVSSIY].ATLNTPKPESPPPVPPPR.[S]	0.67	0.52	0.76	0.67	0.33
[PGDSGLHSTCA].FLSEEGR.[HA]	0.26	0.49	0.16	0.10	0.30
[SARTSSCRFF].AHDAGSLFSFR.[S]	0.51	0.23	0.45	0.16	0.06
[RCLAGQRRGF].AISHLNPSISKGKVHYR.[V]	0.52	0.62	0.68	0.93	0.06
[RNGLGVEQSFVS].EETDIVGGR.[I]	0.56	0.76	0.98	0.98	0.06
[RILALPKEEKKH].VSTAKGEEPFSSKEEER.[H]	0.76	0.05	0.34	0.27	0.04
[M].AKPNDLAGLEK.[A]	0.37	0.08	0.18	0.56	0.55
[FNGAAGPVSG].LVGKQESGCHISLR.[Q]	0.05	0.13	0.02	0.03	0.00
[M].SFQDWTPVSWNKTGQR.[Q]	0.05	0.31	0.09	0.02	0.00
[A].SHGTTFQDAGAR.[A]	0.13				
[M].APPRPTADAGAPPATVAPAAR.[G]	0.05	0.08	0.06	0.06	0.00

SignalP Peptide	TM Domains	MolWT2	Lenght
MASGEMMHITTK	0	76287	706
	1	126220	1134
MRHQERFDLRTG	4	40181	378
MNTGCLFLPATRH	0	35956	330
MWRIWRCRLSFL	1	47693	435
	1	61666	553
MSRLKLTTGFISVI	0	43837	392
	1	84385	784
MVMMGSMQQR	1	42345	398
MARTQMTRRLG	1	40363	389
MRTSRLLCAFGAV	0	20790	191
MARSASMRQRLG	0	40836	389
MPPVLPRGGLLPA	0	60493	564
MKTETRQRSRGG	1	26535	256
	2	18913	175
MKAVALRGFWLT	0	52459	499
MTSCVRSALSRGA	0	53950	492
MVPLSRMAMVSV	1	104831	999
MKLFFKLVLAGVS	0	140480	1275
MDAGVFCLFLPSA	0	23379	208
MILRHLVDLATAG	0	38238	342
MISPVASVFSTMP	0	75363	667
MKTLHLLLFAVVA	2	11424	108
	0	59823	539

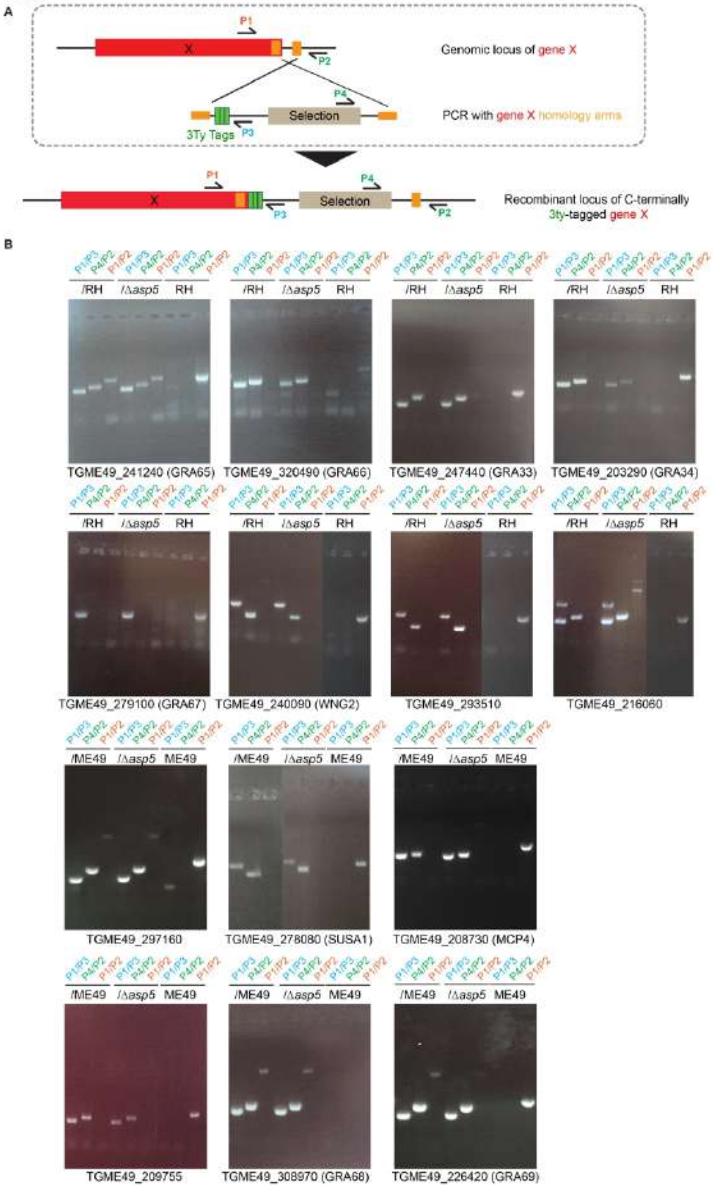
ID	Description
Tachy - Ratio 2 & SP-TM	From TAILS on tachyzoites, list of N-terminal peptides 1) fro
Brady - Ratio 2 & SP-TM	From TAILS on bradyzoites, list of N-terminal peptides 1) fro
Tachy N-term Full	Full list of N-terminal peptides from TAILS on tachyzoites
Tachy N-term Ratio 2	List of N-terminal peptides from TAILS on tachyzoites, with
Brady N-term Full	Full list of N-terminal peptides from TAILS on bradyzoites
Brady N-term Ratio 2	List of N-terminal peptides from TAILS on bradyzoites, with

m proteins with either SP or TM, **&** 2) with enrichment ratio >2 between WT and ASP-KO parasites
om proteins with either SP or TM, **&** 2) with enrichment ratio >2 between WT and ASP-KO parasites

enrichment ratio >2 between WT and ASP5-KO parasites

enrichment ratio >2 between WT and ASP5-KO parasites

S3 Fig



TGME49_241240 (GRA65)
TGME49_320490 (GRA66)
TGME49_247440 (GRA33)
TGME49_203290 (GRA34)
TGME49_279100 (GRA67)
TGME49_240090 (WNG2)
TGME49_293510
TGME49_216060
TGME49_297160
TGME49_278080 (SUSA1)
TGME49_208730 (MCP4)
TGME49_209755
TGME49_308970 (GRA68)
TGME49_226420 (GRA69)

241240	TASP1 5'	8060/p30A	875 bp
	TASP1 3'	5370/8061	1028 bp
	TASP1 C	8060/8061	1317 bp
320490	TASP2 5'	8062/p30A	939 bp
	TASP2 3'	5370/8063	1065 bp
	TASP2 C	8062/8063	1551 bp
247440	TASP3 5'	8064/p30A	838 bp
	TASP3 3'	5370/8065	1097 bp
	TASP3 C	8064/8065	1391 bp
203290	TASP4 5'	8066/p30A	879 bp
	TASP4 3'	5370/8067	1033 bp
	TASP4 C	8066/8067	1414 bp
279100	TASP5 5'	7969/p30A	1115 bp
	TASP5 3'	5370/7970	650 bp
	TASP5 C	7969/7970	1248 bp
240090	TASP6 5'	7974/p30A	1070 bp
	TASP6 3'	5370/7975	607 bp
	TASP6 C	7974/7975	1185 bp
293510	TASP7 5'	7979/p30A	1089 bp
	TASP7 3'	5370/7980	605 bp
	TASP7 C	7979/7980	1168 bp
216060	TASP8 5'	7984/p30A	1195 bp
	TASP8 3'	5370/7985	656 bp
	TASP8 C	7984/7985	1212 bp

TASP9_32018	8068/8069	624 bp
TASP10_3011	8070/8071	702 bp
TASP11_2132	7989/7990	667 bp
TASP12_2247	7997/7998	735 bp
TASP12_3604	7997/7999	735 bp

297160	TASP13 5'	8319/p30A	757 bp
	TASP13 3'	5370/8320	1058 bp
	TASP13 C	8319/8320	1295 bp
278080	TASP16 5'	8329/p30A	866 bp
	TASP16 3'	5370/8330	586 bp
	TASP16 C	8329/8330	808 bp
208730	TASP18 5'	8324/p30A	843 bp
	TASP18 3'	5370/8325	916 bp
	TASP18 C	8324/8325	1305 bp
209755	TASP19 5'	8337/p30A	778 bp
	TASP19 3'	5370/8338	989 bp
	TASP19 C	8337/8338	1051 bp
308970	TASP21 5'	8342/p30A	801 bp
	TASP21 3'	5370/8343	965 bp
	TASP21 C	8342/8343	1050 bp
226420	TASP22 5'	8347/p30A	756 bp
	TASP22 3'	5370/8348	1033 bp
	TASP22 C	8347/8348	1290 bp

Primer#	Name	Length
7929	TASP1-1	40bp
7930	TASP1-2	48bp
7931	TASP1-3	48bp
7932	TASP2-1	40bp
7933	TASP2-2	48bp
7934	TASP2-3	48bp
7935	TASP3-1	40bp
7936	TASP3-2	48bp
7937	TASP3-3	48bp
7938	TASP4-1	40bp
7939	TASP4-2	48bp
7940	TASP4-3	48bp
7941	TASP9-1	41bp
7942	TASP9-2	110bp
7943	TASP9-3	110bp
7944	TASP10-1	40bp
7945	TASP10-2	110bp
7946	TASP10-3	110bp
7965	TASP5-1	40bp
7966	TASP5-2	48bp
7967	TASP5-3	48bp
7968	TASP5-4	48bp
7969	TASP5-5	29bp
7970	TASP5-6	20bp
7971	TASP6-1	40bp
7972	TASP6-2	48bp
7973	TASP6-3	48bp
7974	TASP6-4	30bp
7975	TASP6-5	21bp
7976	TASP7-1	40bp
7977	TASP7-2	48bp
7978	TASP7-3	48bp
7979	TASP7-4	29bp
7980	TASP7-5	23bp
7981	TASP8-1	40bp
7982	TASP8-2	48bp
7983	TASP8-3	48bp
7984	TASP8-4	29bp
7985	TASP8-5	20bp
7986	TASP11-1	40bp
7987	TASP11-2	110bp
7988	TASP11-3	110bp
7989	TASP11-4	21bp
7990	TASP11-5	21bp
7991	TASP12-1	40bp
7992	TASP12-2	110bp
7993	TASP12-3	110bp
7994	TASP12-4	41bp
7995	TASP12-5	110bp
7996	TASP12-6	110bp
7997	TASP12-7	20bp

7998	TASP12-8	20bp
7999	TASP12-9	20bp
8060	TASP1-4	32bp
8061	TASP1-5	21bp
8062	TASP2-4	32bp
8063	TASP2-5	21bp
8064	TASP3-4	31bp
8065	TASP3-5	24bp
8066	TASP4-4	31bp
8067	TASP4-5	24bp
8068	TASP9-4	21bp
8069	TASP9-5	22bp
8070	TASP10-4	21bp
8071	TASP10-5	21bp
8316	TASP13-1	41bp
8317	TASP13-2	48bp
8318	TASP13-3	48bp
8319	TASP13-4	29bp
8320	TASP13-5	20bp
8321	TASP18-1	40bp
8322	TASP18-2	48bp
8323	TASP18-3	48bp
8324	TASP18-4	30bp
8325	TASP18-5	21bp
8326	TASP16-1	40bp
8327	TASP16-2	60bp
8328	TASP16-3	60bp
8329	TASP16-4	20bp
8330	TASP16-5	21bp
8331	TASP16-6	40bp
8332	TASP16-7	48bp
8333	TASP16-8	48bp
8334	TASP19-1	41bp
8335	TASP19-2	48bp
8336	TASP19-3	48bp
8337	TASP19-4	33bp
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8341	TASP21-3	48bp
8342	TASP21-4	31bp
8343	TASP21-5	21bp
8344	TASP22-1	40bp
8345	TASP22-2	48bp
8346	TASP22-3	48bp
8347	TASP22-4	32bp
8348	TASP22-5	22bp
8921	TASP19-6	40bp
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5942	ku80-1	23bp
5943	ku80-2	23bp
5950	gRNA-HX-1	40bp

5948	HX-1	22bp
5949	HX-2	23bp
6108	gRNA-BC2	40bp
6109	BC2-1	49bp
6110	BC2-2	49bp
6449	BC2-3	24bp
6450	BC2-4	24bp
8878	p21-1	51bp
8879	p21-2	51bp
8881	p21-3	22bp
8556	IST-1	40bp
8557	IST-2	48bp
8558	IST-3	48bp
8877	IST-4	40bp
8882	IST-5	21bp
8883	IST-6	21bp
2017	TgDHFR-1	23bp
2018	TgDHFR-2	26bp
4883	gRNA-Universal	20bp

Sequence (5'-3')

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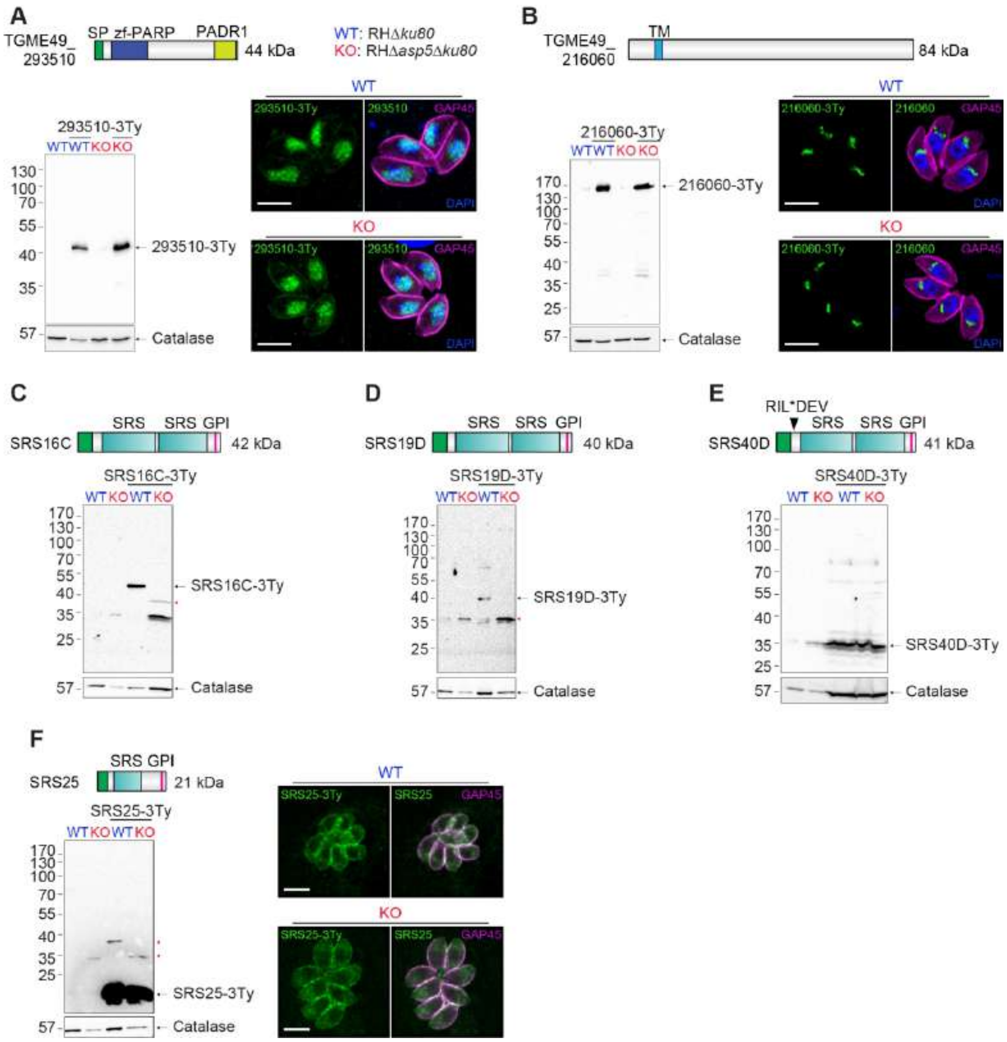
GACAGTTCGTTCCGGATTTGC
GTCTCAGTTCTAGCTCTCTGA
GTCACTTGTTGTGCCAGTTCTAC
CTTGGGGGTCATCGCGACGACCAGAC
AACTTGACATCCCCATTTAC

Comments
gRNA 27 bp downstream of the stop codon of TASP1 (TGME49_241240)
Fwd primer with TASP1 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP1 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
gRNA 93 bp downstream of the stop codon of TASP2 (TGME49_320490)
Fwd primer with TASP2 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP2 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
gRNA downstream of the stop codon of TASP3 (TGME49_247440)
Fwd primer with TASP3 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP3 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
gRNA downstream of the stop codon of TASP4 (TGME49_203290)
Fwd primer with TASP4 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP4 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
gRNA for internal Ty tagging of TASP9 (TGME49_320180)
Fwd primer with TASP9 homology (40 bp each side) for KI by insertion Ty tag (30 bp) in frame (via CRISPR/Cas
Rev primer with TASP9 homology (40 bp each side) for KI by insertion Ty tag (30 bp) in frame (via CRISPR/Cas
gRNA for internal Ty tagging of TASP10 (TGME49_301170)
Fwd primer with TASP10 homology (40 bp each side) for KI by insertion Ty tag (30 bp) in frame (via CRISPR/Ca
Rev primer with TASP10 homology (40 bp each side) for KI by insertion Ty tag (30 bp) in frame (via CRISPR/Cas
gRNA downstream of the stop codon of TASP5_TGME49_279100 (MAF1 copy)
Fwd primer with 30bp TASP5 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Fwd primer with 30bp TASP5 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Rev primer with 30bp TASP5 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Check primer Fw with KpnI site (GT1 and ME49):
Check primer Rev (GT1 and ME49):
gRNA downstream of the stop codon of TASP6_TGME49_240090 ('ROP34') (GT1 and ME49):
Fw primer with 30bp TASP6 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Cas
Rev primer with 30bp TASP6 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Check primer Fw with KpnI site (GT1 and ME49):
Check primer Rev (GT1 and ME49):
gRNA downstream of the stop codon of TASP7_TGME49_293510 (poly(ADP-ribose) polymerase and Dna-Ligas
Fw primer with 30bp TASP7 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Cas
Rev primer with 30bp TASP7 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Check primer Fw with KpnI site (GT1 and ME49)
Check primer Rev (GT1 and ME49)
gRNA downstream of the stop codon of TASP8_TGME49_216060 (GT1 and ME49)
Fw primer with 30bp TASP8 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Cas
Rev primer with 30bp TASP8 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/Ca
Check primer Fw with ApaI (GT1 and ME49)
Check primer Rev (GT1 and ME49)
gRNA before GPI anchor site of TASP11_TGME49_213280 (SRS25) (GT1 & ME49)
Fwd oligo with TASP11 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI anch
Rev primer with TASP11 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
Fwd primer to check for integration (GT1 & ME49)
Rev primer to check for integration (GT1 & ME49)
gRNA before the GPI anchor site of TASP12_TGME49_224770 (SRS40D) (ME49)
Fwd primer with TASP12 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
Rev primer with TASP12 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
gRNA before the GPI anchor site of TASP12_TGGT1_360460 (SRS40D) (GT1)
Fwd primer with TASP12 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
Rev primer with TASP12 homology (40 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
Fwd primer to check for integration (GT1 & ME49)

Rev primer to check for integration (ME49)
Rev primer to check for integration (GT1)
Fwd primer to screen for KI integration of TASP1 (with KpnI site)
Rev primer to screen for KI integration of TASP1
Fwd primer to screen for KI integration of TASP2 (with KpnI site)
Rev primer to screen for KI integration of TASP2
Fwd primer to screen for KI integration of TASP3 (with KpnI site)
Rev primer to screen for KI integration of TASP3
Fwd primer to screen for KI integration of TASP4 (with KpnI site)
Rev primer to screen for KI integration of TASP4
Fwd primer to screen for KI integration of TASP9
Rev primer to screen for KI integration of TASP9
Fwd primer to screen for KI integration of TASP10
Rev primer to screen for KI integration of TASP10
gRNA downstream of the stop codon of TASP13 (TGME49_297160 and TGGT1_297160)
Fwd primer with 30bp TASP13 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
Rev primer with 30bp TASP13 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
Fwd primer to screen for KI integration of TASP13 (with KpnI site) (GT1 & ME49)
Rev primer to screen for KI integration of TASP13 (GT1 & ME49)
gRNA downstream of the stop codon of TASP18 (TGME49_208730 and TGGT1_208730)
Fwd primer with 30bp TASP18 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
Rev primer with 30bp TASP18 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
Fwd primer to screen for KI integration of TASP18 (with KpnI site) (GT1 & ME49)
Rev primer to screen for KI integration of TASP18 (GT1 & ME49)
gRNA before the GPI anchor site (GT1 & ME49):
Fwd oligo with TASP16 homology (30 bp each side) for insertion of Ty tag (29 bp) in frame before the GPI anch
Rev primer with TASP11 homology (29 bp each side) for insertion of Ty tag (30 bp) in frame before the GPI an
Fwd primer to check for integration (GT1 & ME49)
Rev primer to check for integration (GT1 & ME49)
gRNA downstream of the stop codon of TASP16 (GT1 & ME49)
Fwd primer with 30bp TASP16 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
Rev primer with 30bp TASP16 homology for KI or KO by insertion of a 3Ty-HX/3Ty-DHFR (18 bp) (via CRISPR/C
gRNA 60 bp downstream of the stop codon of TASP19 (TGME49_209755)
Fwd primer with TASP19 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP19 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Fwd primer to screen for KI integration of TASP19 (with KpnI site)
Rev primer to screen for KI integration of TASP19
gRNA downstream of the stop codon of TASP21 (TGME49_308970)
Fwd primer with TASP21 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP21 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Fwd primer to screen for KI integration of TASP21 (with KpnI site)
Rev primer to screen for KI integration of TASP21
gRNA downstream of the stop codon of TASP22 (TGME49_226420)
Fwd primer with TASP22 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with TASP22 homology for KI or KO by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Fwd primer to screen for KI integration of TASP22 (with KpnI site)
Rev primer to screen for KI integration of TASP22
gRNA 31 bp downstream of the stop codon of TASP19 (TGME49_209755)
gRNA 46 bp downstream of the initiating ATG codon in the first exon of ku80 (TGME49_312510)
Fwd primer for sequencing, 150 bp upstream of the initiating ATG codon in the first exon of ku80 (TGME49_31
Rev primer for sequencing, 26 bp downstream after the first exon of ku80 (TGME49_312510)
gRNA in the fourth exon of hxgprt (TGME49_200320)

Fwd primer for sequencing, 733 bp downstream of the initiating ATG codon of hxgprt (TGME49_200320)
Rev primer for sequencing, 26 bp downstream of the Stop codon of hxgprt (TGME49_200320)
gRNA 87 bp downstream of the initiating ATG codon of p21 (TGME49_238440)
Fwd primer with 30 bp p21 homology for KO by insertion of a DHFR selection cassette
Rev primer with 30 bp p21 homology for KO by insertion of a DHFR selection cassette
Fwd primer to screen for KO integration of p21 (TGME49_238440)
Rev primer to screen for KO integration of p21 (TGME49_238440)
Fwd primer to amplify p21 promoter, with 30bp IST homology (TGME49_240060)
Rev primer to amplify p21 promoter, with 30bp IST homology (TGME49_240060)
Rev primer to screen for integration of p21 promoter upstream of IST-3Ty
gRNA downstream of the stop codon of IST (TGME49_240060)
Fwd primer with 30 bp IST homology for KI by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
Rev primer with 30 bp IST homology for KI by insertion of a 3Ty-HX (18 bp) (via CRISPR/Cas9)
gRNA 20 bp upstream of the initiating ATG codon of IST (TGME49_240060)
Fwd primer for screen in the 5’ of IST
Rev primer ~800 bp downstream of the intiating ATG codon of IST
Fwd primer for screen in the DHFR cassette
Rev primer for screen in the DHFR cassette
Universal Rev primer for CRISPR/Cas9

S4 Fig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KO: RHΔasp5Δku80
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WT WT KO KO
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100
70
55
40
35
57
293510-3Ty
Catalase
WT
293510-3Ty
293510 GAP45
DAPI
KO
B
TGME49_ 216060
TM
84 kDa
216060-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
216060-3Ty
Catalase
216060-3Ty
216060 GAP45
DAPI
C
SRS SRS GPI
SRS16C
42 kDa
SRS16C-3Ty
WT KO WT KO
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57
SRS16C-3Ty
Catalase
D
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SRS19D
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SRS19D-3Ty
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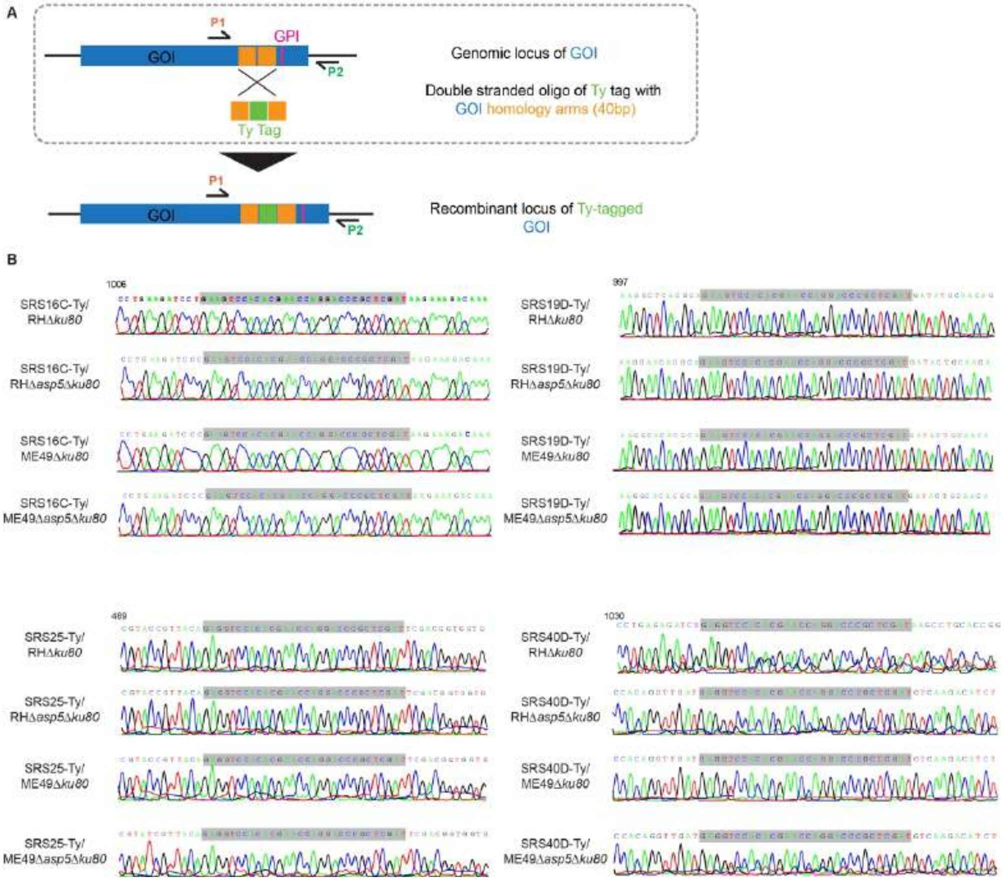
SRS25 GAP45
KO

S5 Fig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GPI
GOI
P2
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Ty Tag
P1
GOI
P2
Recombinant locus of Ty-tagged
GOI
B
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RHΔku80
SRS16C-Ty/
RHΔasp5Δku80
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ME49Δku80
SRS16C-Ty/
ME49Δasp5Δku80
997
SRS19D-Ty/
RHΔku80
SRS19D-Ty/
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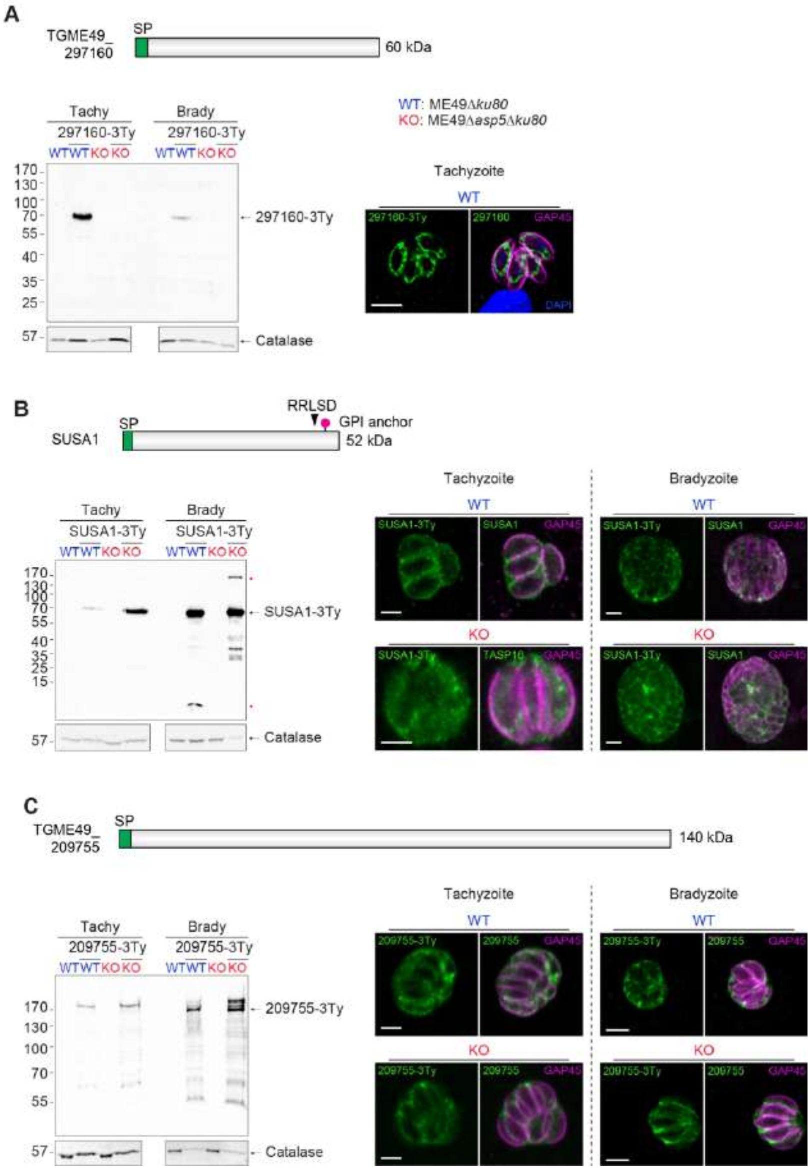
S6 Fig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100
70
55
40
35
25
← 297160-3Ty
57
← Catalase
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DAPI
B
RRLSD
SP
GPI anchor
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Brady
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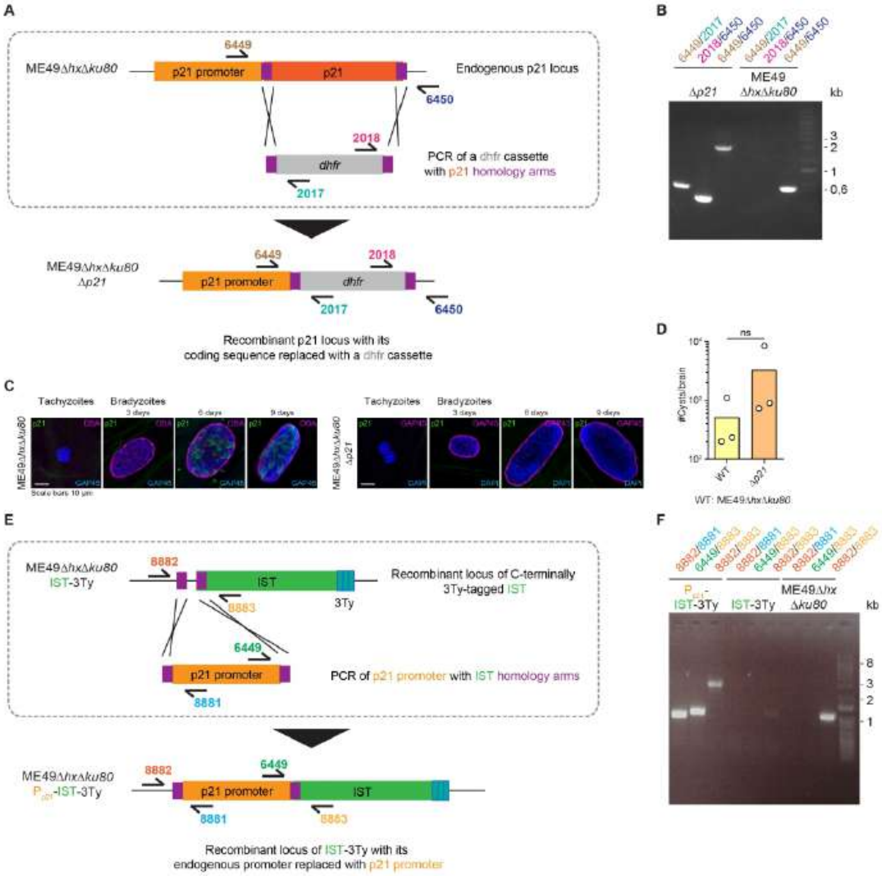
S7 Fig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p21 promoter
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Endogenous p21 locus
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ΔhxΔku80
kb
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C
Tachyzoites
Bradyzoites
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CBA
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Scale bars 10 µm
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Δp21
p21
GAP45
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D
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10³
10²
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IST-3Ty
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IST
8883
3Ty
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6449
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IST
8881
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Recombinant locus of IST-3Ty with its
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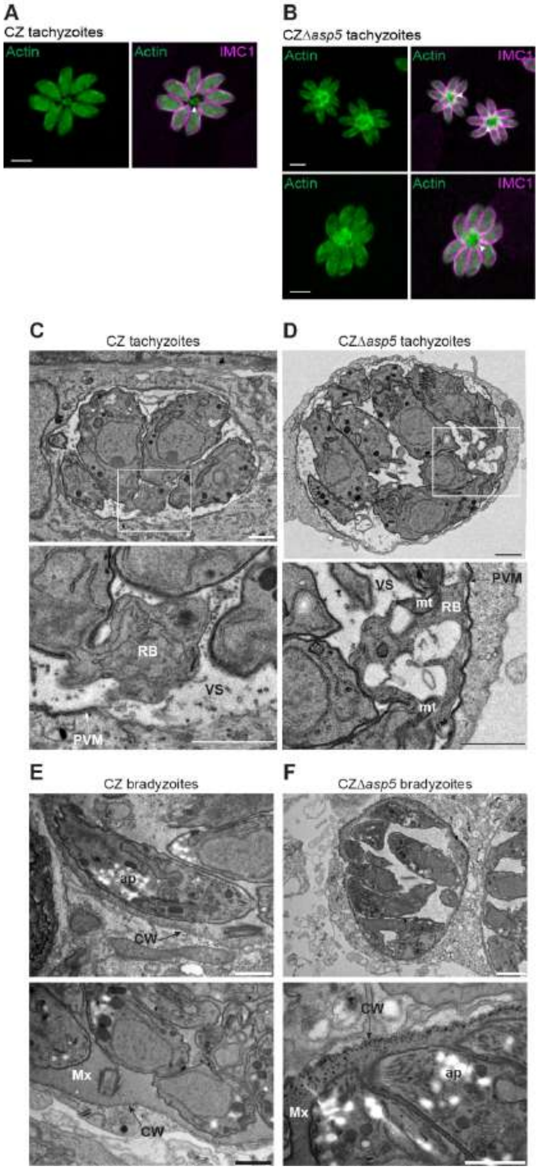
1

S8 Fig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Actin
Actin
IMC1
B
CZΔasp5 tachyzoites
Actin
Actin
IMC1
Actin
Actin
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CZ tachyzoites
RB
VS
PVM
D
CZΔasp5 tachyzoites
VS
mt
RB
PVM
mt
E
CZ bradyzoites
ap
CW
Mx
CW
F
CZΔasp5 bradyzoites
CW
ap
Mx

Supporting information

S1 Fig. Disorder profile of the protein candidates.

Disorder prediction for the indicated protein candidate was obtained with *DISpro 1.0* software. Values above 0.5 are predicted to be disordered and values below 0.5 correspond to folded domains. Below each graph, in transparency, is shown a schematic representation of domain arrangement, based on protein sequences obtained from ToxoDB with accession numbers detailed in the Table 1 and S1 Table.

S2 Fig. Cloning strategies to generate background strains

(A) Schematic representation of the strategy used to disrupt the *ku80* locus in the RHΔ*hxpgrt*Δ*asp5* background strain and related sequencing graphs to assess correct integration. (B) Schematic representation of the strategy used to disrupt the *ku80* locus in the ME49Δ*asp5* background strain and related sequencing graphs to assess correct integration. (C) Schematic representation of the strategy used to disrupt sequentially the *hxgprt* and *ku80* loci in the ME49 background strain and related sequences to show correct integration.

S3 Fig. TASPs candidates endogenous tagging strategy.

(A) Schematic representation of the strategy used to tag endogenously candidate proteins. (B) PCR analyses on the TGME49_241240 (GRA65), TGME49_320490 (GRA66), TGME49_247440 (GRA33), TGME49_203290 (GRA34), TGME49_279100 (GRA67), TGME49_240090 (WNG2), TGME49_293510, TGME49_216060, TGME49_297160, TGME49_278080 (SUSA1), TGME49_208730 (MCP4), TGME49_209755, TGME49_308970 (GRA68), TGME49_226420 (GRA69) and parental RHΔ*ku80* or ME49Δ*hxgprt*Δ*ku80* strains to assess correct integration.

S4 Fig. Localization and migration profile of TAILS candidates not matured by ASP5 in tachyzoites.

The analysis of TGME49_293510 (293510-3Ty) (A) and TGME49_216060 (216060-3Ty) (B) migration profile indicate that they are not substrates for ASP5. TGME49_293510 (293510-3Ty) (A) localize to the parasite nucleus and TGME49_216060 (216060-3Ty) (B) to the parasite Golgi apparatus. Both 293510-3Ty and 216060-3Ty localization is unchanged upon *asp5* deletion. The analysis of SRS16C-3Ty (C), SRS19D-3Ty (D), SRS40D-3Ty (E) and SRS25-3Ty (F) migration profile revealed no compelling evidence of an ASP5-dependent cleavage. Schematics of SRS proteins are based on protein sequences obtained from ToxoDB with accession numbers detailed in the Table 1 and S1 Table. Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Parasite membrane marker: α-GAP45. Scale bars: 5 µm.

S5 Fig. Endogenous tagging strategy for SAGs candidates.

(A) Schematic representation of the strategy used to tag endogenously TASPs. (B) Sequencing graphs for SRS16C-Ty, SRS19D-Ty, SRS25-Ty and SRS40D-Ty tagged in parental RHΔ*ku80*, ME49Δ*hxgprt*Δ*ku80* or RHΔ*ku80*Δ*asp5* and ME49Δ*hxgprt*Δ*ku80*Δ*asp5* to assess correct integration.

S6 Fig. Localization and migration profile of TAILS candidates not matured by ASP5 in tachyzoites and bradyzoites.

(A) TGME49_297160 (297160-3Ty) is not detectable by immunoblot or immunofluorescence in absence of ASP5. It localizes to the parasite mitochondrion in tachyzoites. (B) SUSA1-3Ty is not matured by ASP5 but a product of higher molecular weight accumulates upon *asp5* deletion in bradyzoites. It displays a diffused localization pattern in the PV space in tachyzoites and in the cyst matrix in bradyzoites, unchanged in absence of ASP5. (C) TGME49_209755 (209755-3Ty) is not matured by ASP5 and localize to the PV space and cyst matrix in tachyzoites and bradyzoites, respectively. Its localization is unchanged in parasites lacking ASP5. Schematics of candidate proteins are based on protein sequences obtained from ToxoDB with accession numbers detailed in the Table 1 and S1 Table. Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Parasite membrane marker: α-GAP45. Scale bars: 5 µm.

S7 Fig. IST knock-out and promoter replacement strategies.

(A) Schematic representation of the ME49Δ*hx*Δ*ku80*Δ*p21* recombinant locus. By CRISPR/Cas9 mediated double homologous recombination, we replaced the p21 coding sequence by a *dhfr* selection cassette. (B) PCR analyses on the Δ*p21* and parental ME49Δ*hx*Δ*ku80* strains to assess correct integration. (C) Immunofluorescence assay of PFA/GA-fixed parental ME49Δ*hx*Δ*ku80* and Δ*p21* tachyzoites and bradyzoites at 3, 6 or 9 days in differentiation conditions. CW marker: DBA lectin. Scale bars: 10 µm. (D) Cyst counts from brains of all tested ME49Δ*hxgprt*Δ*ku80*Δ*p21* and control ME49Δ*hxgprt*Δ*ku80* individuals. (E) Schematic representation of P_{p21}-IST-3Ty recombinant locus. By CRISPR/Cas9 mediated double homologous recombination, we inserted the p21 promoter upstream of IST coding sequence. Subsequently, P_{p21}-IST-3Ty is expressed only 4 to 7 days after tachyzoite conversion to bradyzoite. (F) PCR analyses on the P_{p21}-IST-3Ty, IST-3Ty and parental ME49Δ*hxgprt*Δ*ku80* strains to assess correct integration.

S8 Fig. ASP5 substrates contribute to the morphology of tachyzoites and bradyzoites residing compartments in CZ type II parasites

Immunofluorescence performed on parental (A) or CZΔ*asp5* (B) parasites infecting HFFs for 30 h revealed that ASP5 participate to residual body constriction in tachyzoites of a type II strain. Morphology of parasites was observed by staining of the inner membrane complex (α-IMC1) and the cytosol was visualized using α-actin antibody. The white arrowheads point towards the RB. Scale bars: 5 μm. Section through the residual body in CZ (C) or CZΔ*asp5* (D) parasites grown for 30 h in HFFs. Enhancement of the framed area is visible bellow each image. RB: residual body; VS: vacuolar space; mt: mitochondrion; PVM: parasitophorous vacuole membrane. (E-F) Similar to ME49 parasites, TEM analysis revealed that the absence ASP5 results in vesicles accumulation in the cyst wall of *in vitro* differentiated bradyzoites of the CZ type II strain. CW: cyst wall; Mx; cyst matrix; ap: amylopectin granules. Scale bars: 1 μm.

S1 Table. Characteristics of candidate proteins.

Accession numbers, protein sequences, dNdS ratio (Non-synonymous/Synonymous SNPs) and transcriptomics RNA-Seq data were obtained from ToxoDB (toxodb.org). For the transcriptomics RNA-Seq data, negative values indicate a lower expression in given stage compared to tachyzoites and positive values indicate a higher expression in a given stage compared to tachyzoites. Disorder prediction was obtained with *DISpro 1.0* software. Values above 0.5 are predicted to be disordered and values below 0.5 correspond to folded domains. The score was calculated for the full-length protein as well as for the 200 first aa, divided in 4 groups of 50 aa. MW: molecular weight; kDa: kilo Dalton.

S2 Table. List of peptides detected in the TAILS datasets on tachyzoites and bradyzoites.

S3 Table. Primers used in this study.

PLOS Pathogens

Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of Toxoplasma gondii

--Manuscript Draft--

Manuscript Number:	
Full Title:	Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of Toxoplasma gondii
Short Title:	Aspartyl protease 5 and its substrates during Toxoplasma encystation
Article Type:	Research Article
Section/Category:	Parasitology
Keywords:	Apicomplexa, Toxoplasma gondii, bradyzoite, cyst wall, parasitophorous vacuole, aspartyl protease 5, protein export, cyst burden
Corresponding Author:	Pierre-Mehdi Hammoudi, PhD MRC Laboratory of Molecular Biology Division of Protein and Nucleic Acid Cambridge, Cambridgeshire UNITED KINGDOM
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	Tobias Kockmann, PhD
	Dirk Bumann, PhD
	Adrian B Hehl, PhD
	Dominique Soldati-Favre, PhD
	Pierre-Mehdi Hammoudi, PhD
Abstract:	Virulence and persistence of the obligate intracellular parasite Toxoplasma gondii involve the secretion of effector proteins belonging to the family of dense granule proteins (GRAs) that act notably as modulators of the host defense mechanisms and participate in cyst wall formation. Subset of GRAs residing in the parasitophorous vacuole (PV) or exported into the host cell, undergo proteolytic cleavage in the Golgi upon the action of the aspartyl protease 5 (ASP5). In tachyzoites, ASP5 substrates play central roles in the morphology of the PV and in the export of effectors across the translocon complex MYR1/2/3. Here, we used N-terminal amine isotopic labelling of substrates to identify novel ASP5 cleavage products by comparing the N-terminome of wild-type and Δasp5 lines in tachyzoites and in bradyzoites. Validated substrates reside within the PV or PVM in an ASP5-dependent manner. Remarkably, Δasp5 bradyzoites are impaired in the formation of the cyst wall in vitro and exhibit a considerably reduced cyst burden in chronically infected animals. More specifically two-photons serial tomography of infected mouse brains revealed a comparatively reduced number and size of the cysts throughout establishment of persistence in the absence of ASP5.
Suggested Reviewers:	Manlio Di Cristina, PhD Università degli Studi di Perugia: Universita degli Studi di Perugia manlio.dicristina@unipg.it

	Toxoplasma biology and bradyzoite encystation
	Moritz Treeck, PhD The Francis Crick Institute Moritz.Treeck@crick.ac.uk Toxoplasma biology and dense granule proteins
	Eva Maria Frickel, PhD University of Birmingham e.frickel@bham.ac.uk Host-Toxoplasma Interaction
	Laura Knoll, PhD Professor, University of Wisconsin Madison ljknoll@wisc.edu Identified the PEXEL-like motifs in Tg Expert is cell biology of Tg and bradyzoite differentiation
Opposed Reviewers:	Louis M Weiss Albert Einstein College of Medicine louis.weiss@einstein.yu.edu Direct competitor
Additional Information:	
Question	**Response**
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NO authors have competing interests Enter: *The authors have declared that no competing interests exist.* **Authors with competing interests** Enter competing interest details beginning with this statement: *I have read the journal's policy and the authors of this manuscript have the following competing interests: [insert competing interests here]* * typeset This statement is required for submission and **will appear in the published article** if the submission is accepted. Please make sure it is accurate and that any funding sources listed in your Funding Information later in the submission form are also declared in your Financial Disclosure statement.	
Data Availability Authors are required to make all data underlying the findings described fully available, without restriction, and from the time of publication. PLOS allows rare exceptions to address legal and ethical concerns. See the PLOS Data Policy and FAQ for detailed information. A Data Availability Statement describing where the data can be found is required at submission. Your answers to this question constitute the Data Availability Statement and **will be published in the article**, if accepted. **Important:** Stating 'data available on request from the author' is not sufficient. If your data are only available upon request, select 'No' for the first question and explain your exceptional situation in the text box.	Yes - all data are fully available without restriction

Do the authors confirm that all data underlying the findings described in their manuscript are fully available without restriction?	
Describe where the data may be found in full sentences. If you are copying our sample text, replace any instances of XXX with the appropriate details. • If the data are **held or will be held in a public repository**, include URLs, accession numbers or DOIs. If this information will only be available after acceptance, indicate this by ticking the box below. For example: *All XXX files are available from the XXX database (accession number(s) XXX, XXX.).* • For research data submitted to Dryad, enter the following: *The data is available from Dryad repository DOI: XXX.* • If the data are all contained **within the manuscript and/or Supporting Information files**, enter the following: *All relevant data are within the manuscript and its Supporting Information files.* • If neither of these applies but you are able to provide **details of access elsewhere**, with or without limitations, please do so. For example: *Data cannot be shared publicly because of [XXX]. Data are available from the XXX Institutional Data Access / Ethics Committee (contact via XXX) for researchers who meet the criteria for access to confidential data.* *The data underlying the results presented in the study are available from (include the name of the third party and contact information or URL).* • This text is appropriate if the data are owned by a third party and authors do not have permission to share the data. * typeset	The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD034786.
Additional data availability information:	Tick here if the URLs/accession numbers/DOIs will be available only after acceptance

	of the manuscript for publication so that we can ensure their inclusion before publication.

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of Molecular
Biology

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phammoudi@mrc-lmb.cam.ac.uk

PLOS Pathogens

Cambridge, July 7th 2022

Dear Editor,

Hereby we would like to hand in the manuscript entitled “Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of *Toxoplasma gondii*” by Sunil Kumar Dogga, Matteo Lunghi, Bohumil Maco, Jiagui Li, Beatrice Claudi, Jean-Baptiste Marq, Natalia Chicherova, Tobias Kockmann, Dirk Bumann, Adrian B Hehl, Dominique Soldati-Favre and Pierre-Mehdi Hammoudi to be considered for publication as Research Article in ***PLOS Pathogens***.
This is a revised version of PPATHOGENS-D-19-02284, submitted in December 2019. During this unusually long time marked by the relocation of several authors and the COVID pandemy, we have thoroughly answered and experimentally addressed each points raised by the reviewers to strengthen our findings, taking also into account the recent literature published on the topic.

Recent studies from several laboratoires including ours, established that bradyzoites manipulate the host cell transcriptome, highlighting the contribution of effectors and questioning their translocation through the cyst wall (CW).
This study aimed at the identification of novel ASP5 substrates as candidate GRA effector proteins translocated into the host cell in stages responsible for the acute and chronic infection.
Our study not only identifies new GRA proteins and ASP5 substrates through innovative proteomics approach, but also provides a comprehensive understanding of effectors export through the CW during its maturation.

The main findings of this work are summarized as follows:

- The TAILS proteomics approach led to the identification of five new ASP5 substrates including four novel GRAs.
- Identification of the gene coding for p21, the only known late marker of bradyzoite differentiation.
- p21 promoter was used to establish that translocation of the effector IST occurs through immature CW but is progressively prevented upon CW maturation.
- ASP5 substrates participate in residual bodyconstriction in tachyzoites.
- ASP5 plays a central role in CW formation *in vitro* and *in vivo.*

Morover, two-photons serial tomography was applied at the onset and later stage of chronic infection as tool to quantify the size, number and clustering of cysts in the whole brain.

We trust that these findings enhance our understanding of the roles of ASP5 and its associated GRAs substrates during the establishment of *T. gondii* persistence and that our findings will be broadly relevant for the readership of ***PLoS Pathogens***.
Thank you in advance for your time, expertise and consideration.

Yours sincerely

Dr. Pierre-Mehdi Hammoudi

Dr. Dominique Soldati-Favre

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Dear Dr Soldati-Favre,

Thank you very much for submitting your manuscript "Importance of Aspartyl Protease 5 in cyst wall formation and cyst burden during Toxoplasma gondii chronic infection" (PPATHOGENS-D-19-02284) for consideration at PLOS Pathogens. As with all papers peer reviewed by the journal, your manuscript was reviewed by members of the editorial board and by several independent peer reviewers. The reviewers appreciated your attention to an important topic but raised substantial concerns about the paper. Based on the reports, we regret to inform you that we will not be able to accept this manuscript for publication at PLOS Pathogens at this time.

While the reviewers felt the topic is of interest, they raised substantial concerns that would require extensive revisions including a significant number of new experiments. The major weaknesses brought up by the reviewers include the lack of a well-developed, cohesive explanation for the data included (e.g. you identify a number of new cyst wall components but these do not appear to be processed by ASP5) and the lack of rigorous data to support conclusions (i.e. no 2nd markers to confirm organellar localization; no quantification of cyst wall defects; no validation of the newly defined ASP5 variant cut sites; no acknowledgement that the IST data could be explained in a number of ways). Given the high interest in the topic, however, we would possibly consider a new submission if it were improved to meet the major criticisms of the current manuscript.

The new manuscript would receive a new manuscript reference number but will likely be assigned to the previous editors. It will be their task to determine whether or not to send the manuscript to review and, if so, whether or not to include any new reviewers. We cannot promise peer review or further consideration for publication at that time.

The new submission should make reference to the previous manuscript number in the cover letter and provide a detailed response to the previous criticisms included in the cover letter.

The reviews are copied below this email, and we hope you will find them helpful if you decide to revise the manuscript for submission to this journal or elsewhere. We are sorry that we cannot be more positive on this occasion. We very much appreciate your wish to present your work in one of PLOS's Open Access publications.

Thank you for your support, and we hope that you will consider PLOS Pathogens for other submissions in the future.

Sincerely,

Kami Kim	Kasturi Haldar	Michael Malim
Section Editor	Editor-in-Chief	Editor-in-Chief
PLOS Pathogens	PLOS Pathogens	PLOS Pathogens

Reviewer #1

This article aims to explore the importance of aspartyl protease 5 in cyst wall formation and cyst burden. Some of the studies presented are interesting. However, this submission does not yet reflect a focused study that significantly advances the role of aspartyl protease 5 in mediating cyst wall formation and cyst burden. The topic of the article has high importance and is of broad interest to diverse fields, but the article falls short in originality, rigorous methodology, and substantial evidence for its conclusions. In addition, it was disappointing that the authors did not actually validate any bradyzoite specific targets of aspartyl protease 5. The presented data does not appear to support any role for bradyzoite expressed aspartyl protease 5 in cyst wall formation and cyst burden.

Reviewer #2

This is an interesting study that examines proteins processed by ASP5 and the importance of this processing to the development of the cyst wall and to the biology of T. gondii. The study uses TAILS analysis to find potential substrates taking advantage of a ASP5 KO strain that the authors have developed. The identified potential substrates were then selected for further study based on abundance and selectivity in the KO associated with the presence of a signal peptide or an N-term TM domain. Overall, this is a reasonable approach to define a "pick" list for ASP5. In total 49 tachyzoite and 74 bradyzoite proteins (found in those developmental conditions) were identified. Of these several were known ASP5 substrates, however (as expected for this type of screen) others were not known to be processed by ASP5. Of note the consensus sequence (RRL) was not present in many proteins they identified, suggesting that ASP5 may have a broader "cut site" consensus sequence than previously appreciated. No biochemistry was provided to confirm, however, that ASP5 could process these particular cut sites and no additional proteomic data was provided to demonstrate processing (in vivo in T. gondii) at any of these potential sites. The authors have also chosen to name all of the identified proteins using TASP1, TASP2, etc (as noted in the table many of these have been previously identified as GRA or other proteins).

Reviewer #3

In this manuscript by Hammoudi and colleagues, the authors use a Terminal Amine Isotopic Labeling of Substrates (TAILS) approach to conduct a comparative proteomics analysis of wild-type and Δasp5 T. gondii tachyzoites and in vitro-differentiated bradyzoites. This analysis resulted in the identification of novel ASP5 cleavage products and new GRA proteins in the parasitophorous vacuole and PVM. The role of ASP5 in cyst development was also examined. Δasp5 bradyzoites were impaired in cyst wall formation in vitro and formed fewer and smaller cysts across the brains of chronically-infected mice over time. Overall, the manuscript contributes information about new ASP5 substrates and their localization and identifies novel GRAs, but there is not a lot of follow-up on the newly identified TASPs. The study also builds on previously published findings by this group that ASP5 plays a role in cyst wall formation during induced bradyzoite differentiation.

However, as written, the manuscript seems somewhat disjointed and reads like two or three moderately developed stories that are combined into one manuscript. It first describes the use of TAILS to identify ASP5 substrates and investigates their localization and cleavage, but there is no follow-up of the newly identified tachyzoite TASPs or their functions. In addition, none of the TASPs from the TAILS bradyzoite dataset turned out to be ASP5 substrates. The rest of the manuscript focuses on the importance of ASP5 in PV formation, cyst wall development, and cyst burden in mice. All of the data are interesting, but each mini-story seems somewhat preliminary.

Reviewer #1

Major points regarding the data shown in the manuscript:

1. Figure 1: Already published studies from several labs have extensively identified and validated tachyzoite targets of aspartyl protease 5. This Figure should go into supplementary data because the new tachyzoite targets are not connected to the biology of cyst wall formation and cyst burden. The supplemental data should include specific information that comprehensively distinguishes new tachyzoite targets from previously identified targets, and clearly segregates the false-positives which are not targets of ASP5.

In this study, we are reporting the identification of novel ASP5 substrates identified using the TAILS approach and we believe that both the methodology and the newly characterized substrates are of interest and justify to keep this data in the main Figure. Nonetheless, we agree with reviewer #1 that a clear distinction has to be made among ASP5 substrates, between previously and newly identified substrates. We have therefore split Fig 1 in two, with new Fig 1 presenting newly identified GRA with the TAILS approach as ASP5 substrates, and new Fig 2 showing previously identified GRA as new substrates or as being mislocalized in the absence of ASP5.

Importantly, GRA65 (TASP1) does not co-localize with dense granule marker GRA1, but is predicted with high confidence to the dense granules by LOPIT. Overall, the nice correlation between the experimentally validated candidate proteins and the predicted allocation from the LOPIT dataset (Barylyuk K, 2020 Cell Host Microbe) strongly supports that the TAILS approach is well suited to uncover protease substrates in *T. gondii*.

2. Figure 2: In a previous PPATHOGEN article published by Hammoudi et al in 2015 regarding the deletion of aspartyl protease 5, the authors concluded that “hypermigration of dendritic cells and bradyzoite [in vitro] cyst wall formation are impaired.” In view of these previous published conclusions and using the same approach of DBA stain assessment, it is perplexing that there appears to be no visible defect in the aspartyl protease 5 deficient cyst wall as assessed by DBA staining in Figure 2.

Although the cyst wall morphology is largely impacted in ASP5 deficient parasites (as described in Hammoudi PM, 2015 PLOS pathogens), we have observed that after a prolonged time in culture, these parasites seemed to display a less striking cyst wall phenotype. Whether this is an adaptative mechanism remains uncertain. To avoid confusion, we went back to freshly frozen parasites to take new pictures of the cyst wall (presented in new Fig 3), showing a consistent morphology with what previously described. In parallel, a new ASP5-ko strain was generated to characterize the GRA69 (TASP22).

Furthermore, it was disappointing to see that the six putative identified TAILS bradyzoite genes were not cleaved by ASP5. Thus, no bradyzoite TAILS were actually identified and there is no provided evidence that any bradyzoite stage expressed protein is a target of ASP5 at this time.

The TAILS approach allowed the characterization of clear substrates in the tachyzoite stage. Among the candidate proteins, we were aiming at the identification of potential substrates specifically upregulated in bradyzoites that would contribute to cyst wall formation. While we could not spot direct substrates, we describe that the localization of MCP4 and two new GRA (GRA68 and GRA69) is altered upon ASP5 depletion. The related results are presented in new Fig 3.

3. Figure 3: This experiment looks at the translocation of IST into the host cell in the cyst stage. A published study in 2018 already reported that GRA16 and GRA24 were not translocated past the cyst wall of in vitro cysts.

The reviewer #1 refers to Krishnamurthy S, 2018 Front Cell Infect Microbiol were the authors describe that, upon conditional expression in Bradyzoites, GRA16 and GRA24 are not exported through the cyst wall. However, a recent study indicates that IST is indeed exported in Bradyzoites (Mayoral J, 2020 mBio). Moreover, two other studies presenting transcriptomics datasets from infected brains show that an extensive remodelling of host genes expression occurs during chronic infection, suggesting that at least some effector proteins are exported beyond the cyst wall (Boillat M & Hammoudi PM, 2020 Cell Reports and Seizova S, 2022 Cell Host Microbe).

Here using a WT and a P21 regulated IST, the authors looked at translocation of IST and based only on images make conclusions mentioned as “appeared more abundant”, “signal appeared weaker”, “majority of cysts rupture between 7 and 10 days”, etc. The data shown does not support these conclusions. This experiment lacks any quantification or analysis of significance.

We agree with the reviewer #1 and we have conducted an extensive quantification of the WT and P21 regulated IST nuclear translocation in Bradyzoites. The results are presented in the new Fig 4.

Two additional problems with this experiment are an apparent problem with the P21 strain which is clearly under expressing both IST as well as P21 compared with the catalase expression control (panel C), and the lack of any DBA stain on the 10 day IST cyst panel which indicates that this vacuole in fact is not a primary cyst [is it a cyst at all?] and therefore cannot be included in this analysis. 10 day cysts must represent primary 10 day cysts, not previously ruptured cysts.

IST under the control of p21 promoter is indeed under expressed, but the readout is here qualitative with the detection (or not) of IST in the nucleus. As mentioned previously, we have quantified the nuclear accumulation of WT and P21-controlled IST. We have also made the distinction between cells infected by a single vacuole or by a cluster of small-sized cysts, resulting from the rupture of a larger cyst nearby. The quantification was made from DBA positive vacuoles. To avoid confusion, we are now showing the different channels separately. The results are presented in the new Fig 4.

The method used to differentiate in vitro cysts is based on Galiza et al (2013), and it should be noted that Galiza et al only validated their method for up to 6 days of cyst development. The authors in this work show that the Galiza et al method is only useful for assessing cysts to 6 days of development in vitro, since cysts start rupturing by day 7. The Galiza method establishes a tachyzoite vacuole and then allows these tachyzoites to replicate for 24 hours prior to differentiation of the vacuole by alkaline shift. In this 24 h window, the tachyzoite stage vacuole will express and process tachyzoite stage targets of ASP5 and will also translocate GRAs into the host cell, and these host GRAs may persist for a long period of time. Because of this problem, the Galiza et al method for differentiation is clearly not adaptable to answer the question whether IST passes through the immature cyst wall. The authors need to limit the tachyzoite stage and eliminate tachyzoite replication to answer the question whether IST passes through the immature cyst wall, and correspondingly several early time points should be evaluated in a kinetic analysis using a method that allows random capture of scoreable events and the quantification of this data in an unbiased manner. Considering the authors are trying to make a statement about timing of IST in the nucleus, it is important that in Fig 3B that the time points evaluated are the same for the controls (SAG4 and DBA) as the experimental p21.

This differentiation method was already used for longer than 6-7 days in other studies (Di Cristina M, 2017 Nature Microbiol). When parasites reinvade after 6-7 days, they are expressing late bradyzoite markers, suggesting that they are fully mature bradyzoites. Unless working with in vivo purified bradyzoites, all the in vitro differentiation methods have their limitations. We believe that the alkaline pH trigger for conversion offers a convincing approximation to study bradyzoites in vitro.

4. Figure 4: Panels A-D address the tachyzoite residual body phenotype of the aspartyl protease 5 KO but this data is not linked to any cyst wall or cyst burden phenotype so perhaps this data should go into supplementary information.

The objective of this figure (new Fig 5) is to highlight the broad impact of ASP5 on the residing compartments of *T. gondii*, both in tachyzoites and bradyzoites stages. We think that the description in panels A-D of the residual body phenotype gives a clear overview of the situation in tachyzoites and should therefore remain as a main figure.

Panels E-G show EM images and the authors concluded that the ASP5 KO (and myr1 KO) “form a thinner cyst wall and accumulate electron dense vesicles on the luminal side of the cyst wall.” This conclusion is not supported by the data shown. First, there is no quantification of these potential phenotypes, and secondly while I agree the area where the wall should be does appear different, the authors provide no confirmed definition of where the cyst wall actually is represented in these images or any validated method to document that the wall is actually thinner. In addition, the EM images of the in vivo ASP5 KO in Figure 5 show a perfectly normal appearing cyst wall. If ASP5 KO makes the wall thinner, then ASP5 KO cysts should have a phenotype like the CST1 KO where the cysts are fragile. It might be interesting to look at the cyst matrix and see if there are differences (however, from the images that were shown the cyst matrix seems normal).

In fairness, EM is not optimal for quantification purposes. Although we can distinctly observe in panels E-G vesicles accumulation in the ASP5-KO and MYR1-KO, in absence of quantification, we have removed the statement “form a thinner cyst wall” that refers to in vitro cysts. Regarding the in vivo cysts images (new Fig 6, panels C-E), we only make the claim that, in addition to a reduced cyst burden, we observe vesicles accumulating in the cyst matrix of ASP5 KO.

5. Figure 5: This morphological analysis requires quantification to support any conclusions. The ASP5 KO cysts actually look remarkably normal with respect to the wall and overall features.

The quantification of the cyst wall and matrix defective morphology from EM pictures is challenging if not impossible given the very low abundancy of ASP5 KO cysts formed in vivo. Nevertheless, we saw repeatedly in ASP5 KO cysts the accumulation of vesicular material in the cyst matrix

Considering all of the data presented to this point in the article, this makes me wonder whether aspartyl protease 5 actually has any role in the cyst stage, or whether all of the phenotypes noted in this work arise from the role of ASP5 in the tachyzoite stage. Because the authors allowed the initial vacuole to remain as replicating tachyzoites for 24 h prior to alkaline shift, they may have artificially biased the in vitro cyst phenotypes observed to the tachyzoite stage biology of ASP5. Alkaline shifting immediately after vacuole formation could tighten up all of these experiments and allow a more controlled interpretation to distinguish the effects of ASP5 in the tachyzoite stage from the still to be determined potential effects of ASP5 in cysts.

We agree with the reviewer #1 that the decreased cyst burden observed in ASP5 KO infected mice can largely be attributed to the phenotypes in tachyzoites. However, recent transcriptomics datasets (Boillat M & Hammoudi PM, 2020 Cell Reports) looking at 8 weeks infected mice indicate an extensive contribution of ASP5- and MYR1-dependent effectors in the sustained remodelling of host genes over time. Regarding the reviewer's comment about the timing of the alkaline shift at 24 h, it is worth noting that for most of the phenotypes described in our study, parasites are differentiated for more than 7 days, where late bradyzoites markers are detected indicating that we are dealing with fully mature bradyzoites.

6. Figure 6: This data looks at cyst dynamics in infection by 2 photon tomography of fixed brains detected using GFP expressed under BAG1 promoter (an early bradyzoite promoter). The authors make several conclusions: "a higher cyst burden at 2 weeks compared to 5 weeks"; "predominance of tissue cysts of small volume at 2 weeks". These conclusions are not substantiated by the data. This analysis is limited by using only one marker of the cyst stage, GFP expressed in early bradyzoites. With this approach there is no confirmed way to distinguish whether the GFP+ signal originated from a bradyzoite in a cyst [cyst wall], from a bradyzoite in a vacuole [PVM], from a free bradyzoite, from a bradyzoite inside a phagocyte, from several bradyzoites inside a phagocyte, from a recent tachyzoite to bradyzoite switch, or from another bradyzoite in the CNS. The information is quite limited to just "bradyzoite" rather than "cyst" and using the term cyst here is not valid, particularly for events with volume at or under 125 cubic microns since these events could be most likely detecting just one, or maximally a few bradyzoites. Even for the larger volumes measured, another marker is still required to verify that these are intact cysts rather than degraded cysts.

We are fully aware of the limitations of the analysis presented here (new Fig 7) and we understand the reviewer's concerns. The staining with GAP45 (Fig 7A) shows that the vacuoles detected contains several parasites. As it is, the analysis allows us to conclude about the decrease in number and total volume of parasites, between 2 and 5 weeks. We have revised our statements and have used more precise terms to refer to parasites (bradyzoites rather than cysts).

7. Figure 7: Model is incorrect as presented. In PPATHOGENS Cabral et al 2016, cysts are primarily located in neuronal processes and seldomly in the cyst body so this important finding should be reflected in the model.

We thank the reviewer for his comment and we have revised our model accordingly.

8. I still have no idea what TASP stands for after reading this article, but naming new proteins should be well thought out, justified with appropriate data, and clearly explained to the readers. Being cleaved by an ASP5 substrate clearly is not a sufficient basis to rename a protein, especially since all of the targets are already named in Toxodb. The authors should rework their presentation of these genes using the format recently used by Dogga et al 2017 when the targets of ASP3 were identified in TAILS, beginning with the Toxdb gene name as the first column. Being found in a TAILS analysis and not being cleaved by ASP5 should definitely be named as a false-positive or negative, and moved to supplement charts.

We have revised the nomenclature throughout the figures and the manuscript and have either named newly identified GRA or used the classic TGME49_... identifier.

9. Given these major problems, there is substantial and not yet defined experimentation that is still necessary to support the title and conclusions of this article.

We believe that we have provided answers and complementary data to all the points raised by the reviewers. In addition to the characterization of new ASP5 substrates, our study provides an extensive overview on the contributions of ASP5 to the tachyzoite and bradyzoite stages. Furthermore, thanks to additional data, our study offers now a comprehensive understanding of protein export in cysts. We have also modified the title of our study to be better aligned with our findings.

Reviewer #2

1. Additional experiments to prove that the variant cut sites are indeed processed by ASP5 would further extend this paper (eg. in vitro assay showing cleavage or purification of processed forms of the proteins demonstrating the cut sites from proteins purified from T. gondii).

The reviewer is suggesting an interesting addition to consolidate the study however given the broad nature of the study we consider the vitro cleavage and mapping of the site beyond the scope of this paper.

Reviewer #3

1. In the IFAs used to determine TASP localization (Figures 1 and 2), all statements about the localization of the newly identified TASPs should be justified with markers showing co-localization. For example, it is stated that “TASP1 accumulates in the region of the tachyzoite Golgi in Δasp5 parasites.” However, only the 3Ty tag on the TASP and GAP45 are shown, and there are no Golgi markers used to substantiate this conclusion.

We have provided a substantial number of additional captions to describe precisely the newly identified GRA in this study and the altered localization pattern of some of the candidate proteins upon *asp5* deletion. The results are presented in the new Figures 1, 2 and 3.

2. Although all the micrographs are crisp and of high quality, some of the differences in the localization of TASPs that are described for the WT and Δasp5 line are rather subtle in the images shown, particularly for the TASPs that localize to the PV and the RB (e.g., TASP3, and

to a lesser degree TASP2). The conclusions would be strengthened if the authors quantified the localization differences of the TASPs in the WT and KO lines.

As mentioned previously, new images are now provided to better describe the changes in localization.

3. The localization and cleavage of TASPs are described, but there is little additional follow-up to explain the patterns that are observed. For example, it appears that ASP5 deficiency affects the localization of different TASPs differently, but why this may be the case is not examined. Similarly, since ASP5 is predicted to cleave the TASPs, it is unclear why the TASP2 product detected in the KO line is of lower molecular weight than the product detected in the WT line. The opposite is true for all the other tachyzoite TASPs shown.

The case of TASP2 (GRA66) is indeed puzzling but there are different possible explanations, like cleavage by an other protease because or impaired trafficking. We are indeed not exploring deeper the causes for mistargeting of the candidate proteins as the main objective was to characterize the hits obtained by the TAILS approach. The deeper characterization of some of these candidates could be the focus of follow up studies.

4. The conclusion that TgIST is only exported through an immature cyst wall and that its translocation is prevented on cyst wall maturation is not apparent from the data. This conclusion appears to be based on the fact that P(p21)-IST-3Ty was detected in the host cell nucleus at 10 days of bradyzoite differentiation, but not at 7 days. The authors note that since many cysts rupture between 7-10 days post-differentiation, the idea is that nuclear P(p21)-IST-3Ty is mostly found in smaller, less mature cysts. However, the fact that they do not detect nuclear IST signal at 4 days post-differentiation seems to conflict with this conclusion. If there is indeed a difference in bradyzoites with immature and mature cyst walls, the nuclear IST-3Ty signal should be quantified in large and small cysts at all timepoints, and if possible, including a marker of the mature cyst wall. It seems that this could even be done using the IST-3Ty line under its endogenous promoter, since they detected nuclear IST-3Ty in 10 day-differentiated bradyzoites without requiring the p21 promoter.

According to the reviewer’s comment, we have now extensively quantified the nuclear accumulation of WT and P21-controlled IST. We have made the distinction between cells infected by a single vacuole or by a cluster of small-sized cysts, resulting from the rupture of a larger cyst nearby, as they different pattern of IST accumulation in the nucleus. The quantification was made from DBA positive vacuoles. The results are presented in the new Fig 4.

5. The authors show that the ASP5-deficient parasites have a lower cyst burden in the brain during infection of mice and conclude that “the data demonstrate an important role for ASP5 in processes linked to delivery of vesicular content within cysts in vivo that result in a significant lower cyst burden in mice upon asp5 deletion.” However, they also note that there are simply fewer Δasp5 parasites entering the brain, likely due to deficient expansion of these less fit parasites in the periphery. So it is unclear that a specific role for ASP5 in bradyzoites is what contributes to the reduced cyst burden of the Δasp5 line. This may be addressed by characterizing the parasite burden in the periphery in parallel with the brain, particularly at early time-points post-infection.

The drop in cyst number is indeed mostly due to the phenotype in tachyzoites. Assessing the parasite burden in the periphery is interesting but would require a different experimental setting note trivial to be quantitative. We have toned down our conclusion, making clear in the discussion that a defect in tachyzoite not reaching the brain could contribute to the phenotype.

6. There does not appear to be any statistical analysis of the data presented in Figure 6 to demonstrate that there are differences among the groups, and the numbers of mice are not specified in the figure legend or the methods.

This analysis was done with a limited number of animals and does not allow to claim that the differences are statistically significant. As it is, the analysis allows to conclude about the decrease in number and total volume of parasites, between 2 and 5 weeks. We have revised our statements. The results are presented in new Fig 7.

Reviewer #1

A number of other issues together form a major point. Article not submitted using PPATHOGENS instructions of including line numbers.

We have formatted more carefully the articles according to PPATHOGENS guidelines.

There is no statistical analysis of any data.

We have added them when possible.

There is no consistent mention of bradyzoite or cyst developmental times.

The exhaustive alkaline differentiation protocol is detailed in the Methods and the timing corresponding to each figure is specified in the legend.

There is no mention of mice numbers or sample numbers in experiments.

The number of animals is specified in the legend for each experiment.

Why is there such high variability in ME49 cysts in vivo burdens shown in the three different cyst burden experiments? And why are the ME49 cyst numbers incredibly low?

We assume that this comment refers to the data presented in new Fig 6. The yields of cysts can indeed be quite variable between animals, although there is a clear tendency that ASP5 KO and MyoJ KO mice form less cysts than ME49 WT parasites.

References are missing in the introduction (page 5). In the methods for the TAILS analysis, it was not explained how cell lysate for bradyzoites was established in terms of (1) conditions for differentiation, (2) timing of differentiation before sample collection, and (3) sample processing and how bradyzoites were released from the cyst wall.

We have added the missing references where appropriate.

In general, the authors did not provide evidence for descriptive statements that were made regarding the TASP proteins, for example TASP1 needs to be colocalized with a Golgi marker (GRASP terminology was used in Hammoudi et al 2015) and TASP2 etc. need to be localized to the dense granules to confirm that these are actual GRA proteins.

We have provided a substantial number of additional captions to describe the newly identified GRA in this study and showed colocalization with appropriate markers. The results are presented in new Fig 1, 2 and 3.

Also, since GRA34 (TASP4) is not a direct target of ASP5 it should be moved to the supplemental and placed distinctly in the section with the false positives which are not targets of ASP5 or true TAILS. The GRA34 tachyzoite phenotype seems to be an indirect effect of ASP5 deletion, which should not be surprising to the authors. Authors statement on ROP21 in the introduction is incorrect, ROP21 is not localized to the rhoptries or to the dense granules.

We have rearranged Fig 1, which is now split in two, with new Fig 1 showing newly identified GRA cleaved by ASP5 and new Fig 2 showing previously identified GRA cleaved by ASP5 or of which localization is affected by ASP5. GRA34 is not cleaved directly by ASP5 but its localization is perturbed upon *asp5* deletion, as for a number of other GRA. We believe that this finding is relevant and could still be presented in the main figure. Regarding ROP21, based from the work of Jones and colleagues (Jones N, 2017 Cell Microbiol), the protein appears to be in the PV space, suggestive a dense granules origin.

There were numerous other minor points throughout the manuscript that were not addressed because no line numbers were provided by the authors.

Reviewer #2

1. The sue of TASP1, TASP2, etc for naming the proteins does not really add to the paper and can result in confusion in the literature. This name (TASP) does not provide any information on structure or function. Currently used name such as GRA, ROP, RON, CST, MIC, IMC, etc indicate the organelle or location of the protein. The paper could use the current ToxodB numbers for the identified proteins rather than this new nomenclature. If, however, the authors believe this new nomenclature is important then I suggest the use of a binomial naming system for proteins that already have other names, for example, TASP3(GRA33), TASP4(GRA34), TASP6(WNG2), TASP9(BSR4/SRS16C), TASP10(SRS19D), TASP11(SRS25), TASP12 (SRS40D), TASP18(MCP4), TASP16(SUSA1).

We have modified the nomenclature throughout the figures and the manuscript and have either named newly identified GRA or used the classic TGME49_... identifier.

2. Methods: The TAILS method and the mass spectrometry details are not provided. Given the importance of this method for this paper, a more detailed description of the exact methods used need to be provided. Usually this method involves labeling with stable isotopes. to allow comparison of abundance, and this labeling (presumably by cell culture is not described). The Dogga 2017 has a brief description of the method (from this group), but limited details as well. Description of the mass spectrometry settings and the analysis pathway are also needed.

The TAILS protocol used in this study is clearly explained in the methods and is the exact similar of what described in Dogga SK, 2017 eLife. Additional information can be found in Kleifeld et al., 2010 and Kleifeld et al., 2011.

3. Methods: A better description of the statistical testing and the analysis methods used to arrive at the substrates is needed

We have included more detail on the statistical testing and the methods applied.

4. Methods: The proteomic data need to be deposited (for publication). ToxodB would be the logical web based resource to deposit this data. In my opinion, the statement "data available from the authors on request" is not a reasonable deposition of data for publication

The data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD034786.

5. Page 12: I am not sure the data really prove that "IST can translocate through an immature CW, but export is prevented upon CW maturation", if you prevent secondary infection do you prevent the increase at day 10? If you change media daily, for example, to remove free organism do you see that IST continues to decrease?

The text relative to this section has been revised.

6. Figures 4 that show vesicles are very small (even the inserts). It would help to break this into 2 figures (tachyzoite and bradyzoite) and make the images (particular the inserts) larger to more clearly illustrate the vesicles and the change in CW architecture. It would help if a quantitative image analysis was done (on multiple images) to provide data on exactly how thin the CW becomes and how many more vesicles are seen. Previous work, by others, has shown that cysts with abnormal cyst walls rupture more easily. It would be useful to examine if this phenotype is present in the ASP5 knockout cysts.

The images are provided in high resolution allowing a zoom in to analyse in more details the phenotype. Although we can distinctly observe in new Fig 5, panels F and G, vesicles accumulation in the ASP5-KO and MYR1-KO, in absence of quantification, we have removed the statement “form a thinner cyst wall” about the in vitro cysts.

7. The issue of cyst number could be due to the effect of a secreted effector modifying the host cell just as easily as a change in the CW. As ASP5 is associated with processing and transport of effectors I think this needs to be part of the discussion of why fewer and smaller cysts were seen.

We have extended the discussion on this point as recommended by the reviewer.

8. The reasoning of why your observations suggest that the mode of transcellular entry is the most likely is not clear. Please expand this discussion and provide additional evidence for this statement.

We have elaborated the discussion according to the reviewer’s recommendation.

9 Some analysis, a table, of the proposed cut sites in the identified substrates (frequency, sequence, evidence that it occurs) for the « new » cut site for ASP5 should be added to the text.

Summary tables were added for clarification (Table 1 and S2 Table) and the newly identified cut sites are mentioned in the text.

Reviewer #3

1. In the legend for Figures 1 and 2, it would be helpful for the authors to specify that the red arrowheads and black arrows represent different forms of TASPs in the WT and KO lines.

The figure legends have been modified according to the reviewer’s suggestion.

2. The acronym TASP is used to name the candidates from the TAILS analysis, but the basis for the acronym is never actually defined.

We have modified the nomenclature throughout the figures and the manuscript and have either named newly identified GRA or used the classic TGME49_... identifier.

Importance of Aspartyl Protease 5 in the establishment of the intracellular niche during acute and chronic infection of *Toxoplasma gondii*

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Keywords

Apicomplexa, *Toxoplasma gondii*, bradyzoite, cyst wall, parasitophorous vacuole, aspartyl protease 5, protein export, cyst burden.

Short title

Aspartyl protease 5 and its substrates during *Toxoplasma* encystation

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Abstract

Virulence and persistence of the obligate intracellular parasite *Toxoplasma gondii* involve the secretion of effector proteins belonging to the family of dense granule proteins (GRAs) that act notably as modulators of the host defense mechanisms and participate in cyst wall formation. Subset of GRAs residing in the parasitophorous vacuole (PV) or exported into the host cell, undergo proteolytic cleavage in the Golgi upon the action of the aspartyl protease 5 (ASP5). In tachyzoites, ASP5 substrates play central roles in the morphology of the PV and in the export of effectors across the translocon complex MYR1/2/3. Here, we used N-terminal amine isotopic labelling of substrates to identify novel ASP5 cleavage products by comparing the N-terminome of wild-type and Δ*asp5* lines in tachyzoites and in bradyzoites. Validated substrates reside within the PV or PVM in an ASP5-dependent manner. Remarkably, Δ*asp5* bradyzoites are impaired in the formation of the cyst wall *in vitro* and exhibit a considerably reduced cyst burden in chronically infected animals. More specifically two-photons serial tomography of infected mouse brains revealed a comparatively reduced number and size of the cysts throughout establishment of persistence in the absence of ASP5.

Author summary

The obligate intracellular parasite *Toxoplasma gondii* replicates within a parasitophorous vacuole (PV) and co-opts host cellular functions including defense mechanisms via the secretion of effector proteins (GRAs) from the dense granules. During their intracellular traffic, a subset of GRAs residing in the PV or exported into the host cell are subjected to a proteolytic cleavage catalyzed by the Golgi aspartyl protease 5 (ASP5). In fast replicating tachyzoites, ASP5 substrates play central roles in the morphology of the PV and in the translocation of effector GRAs via the complex MYR1/2/3 across the PV membrane. In slowly dividing bradyzoites, ASP5 plays a key role in cyst wall formation and hence is an important virulence factor critical for establishment of chronic infection. Our results indicate that ASP5 substrates are not translocated across the mature cyst wall, suggesting that ASP5 might play a structural role for maintenance of the cyst wall.

Introduction

Together with *Eimeria spp*, *Sarcocystis spp*, *Besnoitia*, *Cystoisospora*, *Frenkelia*, *Neospora* and *Hammondia*, *Toxoplasma gondii* belongs to the tissue-cysts forming clade of enteric coccidians that constitute a considerable threat for human and animal health. *T. gondii* relies on felids as definitive hosts for sexual reproduction and on a broad range of warm-blooded animals to persist and ensure transmission. Most developmental stages of *T. gondii* possess a unique ability to invade almost any nucleated cell and replicate inside a parasitophorous vacuole (PV), which facilitates rapid systemic distribution of tachyzoites during the acute phase of infection. Subsequently, a potent host immune response induces differentiation of tachyzoites into bradyzoites, a slowly-replicating developmental stage enclosed within tissue cysts. Cysts are established in long-lived cells, predominantly in neurons and skeletal/smooth muscle cells. They represent a transmissible form between intermediate and definitive hosts during predation, but also between intermediate hosts, which greatly contributes to the high prevalence of *T. gondii* in animals and humans. A thick cyst wall (CW) limits detection by the immune system and protects the parasites within. The CW is elaborated from the PV membrane (PVM) and is decorated with dense granule proteins (GRAs) (1), including markers exclusively expressed during bradyzoite development (2). The CW is typically covered by highly glycosylated proteins, binding to lectins (3). While intravacuolar GRAs were shown to participate in the maturation of the cyst matrix and CW (4), the dynamic of CW formation as well as the precise molecular composition of this structure remain poorly understood.

Distinct classes of GRAs have been previously described and are associated to various functions linked to parasite-host communication and nutrient acquisition (5, 6). In the tachyzoite stage, many GRAs are restricted to the PV and participate in the elaboration of an intravacuolar network (IVN) embedding parasites and shaping the vacuole (6). In addition, several GRAs localize to the PVM, at the interface with the host cell cytosol, where they modulate host cell signaling pathways (GRA6 (7); GRA7 (8); GRA12 (9); GRA15 (10, 11); GRA60 (12)) or mediate the recruitment of host organelles to the vicinity of the PVM notably via MAF1 (13). Finally, a category of GRAs containing intrinsically disordered domains are exported beyond the PVM and reside in the host cytosol such as GRA18 (14) or are imported into the host cell nucleus i.e. GRA16 (15), GRA24 (16), GRA28 (17), IST (18, 19) and TEEGR (20, 21) to remodel the host transcriptome in favor of parasite long-term persistence. Intriguingly, GRAs are often polymorphic proteins that are associated to virulence phenotypes depending on the type of *T. gondii* strain (5). While kinases and pseudokinases discharged into the host cells by the rhoptries during invasion tend to be crucial for the virulence of type I strains (22), GRA effectors play a pivotal role in establishing persistence of type II strains (5). In the mouse model, animals infected with type I strains cannot control the acute infection and rapidly succumb to toxoplasmosis, whereas type II strains produce a chronic infection. Consequently, mice infected with type II strains are a useful model to study tissue cyst formation and chronic toxoplasmosis.

Several GRAs are proteolytically processed by the Golgi-resident aspartyl protease 5 (ASP5) that typically cleaves after an arginine-arginine-leucine (RRL) motif termed TEXEL (Toxoplasma export element) (23-25). A subset of GRAs harboring a TEXEL motif i.e. GRA19, GRA20 (25), and ROP21 (previously incorrectly assigned to rhoptries but localizing to the PV space, thus possibly originating from the dense granules (26)) are directly cleaved by ASP5 and localize to the PVM. The ASP5 substrates GRA16 (23, 24) and IST (18, 19) belong to the class of GRAs that are exported across the PVM into the host cell in a ASP5-dependent fashion. ASP5 indirectly affects the export of GRA24 and TEEGR, that do not contain a recognition motif, by processing MYR1 (20, 27). Mature MYR1 forms a complex with MYR2 and MYR3 to facilitate protein translocation across the PVM into the host cytosol (27, 28).

Recently, a proteomics method to selectively enrich N-terminally derived peptides termed Terminal Amine Isotopic Labeling of Substrates (TAILS) was used to uncover additional ASP5 substrates, all residing in the PV, i.e. LCAT, WNG1 (formerly ROP35), WNG2 (formerly ROP34), GRA44, GRA45 and GRA46 (29). Although the repertoire of ASP5 and MYR1-dependent exported effector proteins is to some extent redundant, the overlap is not complete. Indeed, a comparative analysis of the transcriptome of human foreskin fibroblasts (HFF) infected with type I Δ*asp5* or Δ*myr1* tachyzoites revealed that, in addition to a large core of genes showing similar differential regulation in both cases, ASP5 and MYR1-dependent exported effectors modulate independently the expression of a subset of genes in the infected host cell (30-32). The impact of ASP5 and MYR1 on the host transcriptome translates *in vivo* into a decreased virulence of type II tachyzoites individually deleted for these genes (25, 27, 30). However, there is little information about the contribution of ASP5 and MYR1 to protein export in bradyzoites and to persistence during the chronic stage of infection.

Here, we compared ASP5 substrates repertoires of tachyzoites and stage-converted bradyzoites *in vitro*. We used a TAILS approach for a comparative proteomic profiling of wild-type (WT) and Δ*asp5* in both developmental stages. This revealed novel PV-targeted GRAs and allowed refinement of the ASP5 cleavage signature motifs. We carried out a global analysis of GRA-related functions in tachyzoite and bradyzoite stages, by examining the translocation of GRAs across the CW upon maturation and through phenotyping of ASP5 and MYR1 mutants, including the impact on PV morphology and CW formation *in vitro*. Further, we evaluated the contribution of ASP5 on cyst formation and dissemination in brains of chronically infected mice by performing full brain imaging. This study broadens our understanding of the roles of ASP5 and MYR1 in the formation of the parasite-induced subcellular membrane bounded compartments during acute and chronic stages and outlines the dynamics of parasite dissemination in the brain.

Results

N-terminome analysis uncovered novel ASP5 substrates

In an effort to determine the repertoire of ASP5 substrates in tachyzoites and bradyzoites, we applied the Terminal Amine Isotopic Labelling of Substrates (TAILS) analysis that was successfully employed to uncover ASP3 substrates and to establish its role as broad maturase for microneme and rhoptry proteins in the endosomal-like compartment (ELC) (33). We conducted a quantitative comparison between the N-terminomes of wild-type (WT) and Δ*asp5* tachyzoites and bradyzoites. Candidate proteins identified from these datasets are presented in Table 1 with a comprehensive output in S1 and S2 Tables. 2299 and 616 N-terminal peptides were identified in the tachyzoite and *in vitro* differentiated bradyzoite samples, respectively. Normalized log2 abundance ratios (WT/Δ*asp5*) were calculated for each peptide group. Arbitrary upper and lower thresholds of <0.5 and >2 ratios were applied to identify proteins with ASP5-dependent processing. Among the labelled peptide groups, we found 133 and 225 peptides in tachyzoites and bradyzoites, respectively, with either <0.5 or >2 ratios in the absence of ASP5. The candidate list was further refined by filtering for structural features i.e. the presence of a predicted signal peptide (SP) or N-terminal transmembrane (TM) domain. This yielded 84 and 104 peptide groups, respectively, corresponding to 49 and 74 proteins, in the tachyzoite and bradyzoite lists, respectively. Previously identified and validated ASP5 substrates served as positive control to validate the results (25, 29). In addition, all protein sequences were interrogated for the presence of intrinsically disordered regions (IDR), as a potential signature for exported effector GRAs (34) (S1 Fig). Consistent with the role of ASP5 as a maturase for GRA proteins, we found several previously characterized GRAs in the list (GRA1, GRA2, GRA3, GRA4, GRA6, GRA7, GRA12, GRA17, and GRA23). Some of these GRA proteins were recently reported as ASP5 substrates (29), while others were not known to be processed by ASP5 (Table 1 and S2 Table). Importantly, the TAILS analysis also uncovered several hypothetical and uncharacterized proteins as well as proteins of the cyst wall proteome (35).

Identification of novel PV and PVM proteins processed by ASP5 in tachyzoites

We selected eight candidates from the filtered TAILS tachyzoite dataset for further investigation of ASP5-dependent cleavage and localization (Table 1). Candidate genes were epitope-tagged at the endogenous locus in WT parasites and Δ*asp5* lines (S2 and S3 Fig). To this end, we designed Cas9-targeting guides against the gene of interest for co-transfection with the PCR product of 3Ty tags linked to a DHFR selection cassette and flanked by 25-bp homology regions (S2 and S3 Fig).

Five out of the eight candidates were confirmed as ASP5 substrates: TGME49_241240 (GRA65), TGME49_320490 (GRA66), TGME49_247440 (GRA33), TGME49_279100 (GRA67) and TGME49_240090 (WNG2). GRA65 has no known domain and possesses a predicted SP and two TEXEL motifs at positions 68 (RLLAE) and 83 (RELVD) amino acids (aa), with the peptide at the RRLAE motif enriched in the TAILS tachyzoites dataset. GRA65 is detected as two products around a molecular weight (MW) of 110 kDa by Western blot (WB) (Fig 1A). In the absence of ASP5, only the upper band was detected. Immunofluorescence assays (IFA) shows weak expression in tachyzoites as a faint vesicular signal in the cytoplasm of tachyzoites and in the PV (Fig 1B). GRA65 accumulates in the region of the tachyzoite Golgi in Δ*asp5* parasites. GRA66 is a novel GRA with a MW of 126 kDa predicted to contain an N-terminal TM domain that might serve as SP and a beta lactamase superfamily domain. A tryptic peptide containing a non-canonical TEXEL motif at position 361 (RHLLT) was enriched in the TAILS bradyzoite dataset. GRA66 migrates as a major product around 120 kDa by WB, and at a lower apparent MW in Δ*asp5* (Fig 1C). Its PVM localization in WT parasites is disrupted in Δ*asp5*, where it localizes inside the PV (Fig 1D). GRA67 belongs to the *MAF1a* family (36) and is also a novel GRA. It has a predicted MW of 48 kDa and contains a SP and an internal TM domain. It migrates as multiple products from 40 to 55 kDa in SDS-PAGE and intermediate bands are detected by WB in Δ*asp5* (Fig 1E). GRA67 is detected in the PV in WT but accumulates in the parasite Golgi and endosome-like compartment (ELC) in Δ*asp5* parasites, as shown by partial co-localization with GRASP and ASP3 markers (Fig 1F).

Among all candidate genes, known dense granule proteins were selected for further validation as ASP5 substrate. GRA33 has a MW of 40 kDa and is predicted to contain a SP and three internal TM domains. GRA33 migrates as a major form around 55 kDa and is detected in the PVM in WT parasites but is concentrated inside the PV in Δ*asp5* and migrates at a higher MW (Fig 2A-B). GRA34 has a calculated MW of 36 kDa and contains a predicted SP. GRA34, does not appear to be an ASP5 substrate as its migration profile (27-30 kDa) is unchanged in absence of ASP5 (Fig 2C). However, its PV localization changes to vesicular and accumulates around the residual body (RB) in Δ*asp5* parasites (Fig 2D). WNG2 (29, 37) (formerly ROP34 (38, 39)) has a predicted MW of 62 kDa and harbors an N-terminal TM domain and a serine/threonine kinase domain. By WB, WNG2 migrates as two products around 60 kDa, with a predominance of the smaller one (Fig 2E). In absence of ASP5, we observed an accumulation of the larger product. While the protein localizes in the PV and at the PVM in WT parasites, it displays a Golgi/ELC localization pattern and seems to concentrate next to the RB in Δ*asp5* parasites (Fig 2F).

TGME49_293510 has a calculated MW of 44 kDa, contains a predicted SP, in addition to poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region domains. TGME49_293510 migrates as a single product of ~45 kDa and localizes to the parasite nucleus (S4A Fig). TGME49_216060 has a predicted size of 84 kDa with a putative N-terminal TM domain. It migrates as a single product of about 140 kDa and localizes to the parasite Golgi (S4B Fig). Both TGME49_293510 and TGME49_216060 are likely false-positive hits, which appear not to be processed by ASP5.

Of note, numerous surface antigen proteins (SAG) were identified in the tachyzoite and bradyzoite lists. SAGs are GPI-anchored and traffic through the Golgi to reach the parasite surface. Since C-terminal tagging is not possible in this case, we introduced epitope tags inside the coding sequence in transgenic lines (S5 Fig). The integration of Ty tags in the WT and Δ*asp5* parasites of type I and II strains was confirmed by sequencing the modified gene locus in the transgenic strains. Out of the four SAGs coding genes examined, only SRS25 was detectable using an anti-Ty antibody in IFA. The tagged SRS25 localized at the parasite plasma membrane and displayed no altered localization or processing in the Δ*asp5* parasites (S4C-S4F Fig). The presented data, corroborated by the co-localization with GRA1, confirms that GRA 65, 66, and 67 are novel dense granule proteins. Together with GRA33 and WNG2, all are *bona fide* substrates of ASP5.

Identification of novel components of the cyst wall

Within the TAILS analysis, six candidates were detected exclusively in the bradyzoite dataset and were further investigated. Although none was a substrate for ASP5 as evaluated by WB, five turned out to reside in the PV or PVM in tachyzoites, and in the cyst matrix or at the CW in bradyzoites. MCP4 (microneme adhesive repeat domain-containing protein 4 (2)) has a predicted MW of 105 kDa, a SP, and two sialic acid binding micronemal adhesive repeats. WB analysis revealed that MCP4 is more abundantly expressed in bradyzoites (after 1 week of *in vitro* differentiation using alkaline treatment (40)) than in tachyzoites, as previously reported (2). The tagged protein is detectable as multiple bands between 80 and 130 kDa in WB that appear unchanged in Δ*asp5* tachyzoites (Fig 3A). MCP4 is hardly detectable by IFA in tachyzoites and localizes to the dense granules in extracellular bradyzoites (Fig 3B-C). MCP4 localization to the cyst wall in WT bradyzoites remains unchanged in Δ*asp5* parasites, despite the overall different CW morphology commonly observed in Δ*asp5* (Fig 3C). GRA68 is a newly identified GRA, which contains a SP and migrates at the predicted MW of 38 kDa in tachyzoites and bradyzoites, but its expression level is reduced in bradyzoites (Fig 3D). GRA68 localizes to the dense granules in extracellular tachyzoites (Fig 3E), and is found in the PV of tachyzoites and in the cyst matrix and CW of bradyzoites (Fig 3F). GRA68 subcellular localization appears altered in Δ*asp5* bradyzoites. GRA69 is a new GRA that contains a SP, an oligopeptidase F and a peptidase family M3 domain that are typical of metalloproteases ("zincins"). GRA69 migrates as a single product at the predicted MW of 75 kDa by WB in tachyzoites and a second product of lower MW appears around 30 kDa in bradyzoites (Fig 3G). It localizes to the dense granules in extracellular parasites (Fig 3H) and to the PV in tachyzoites, in the cyst matrix and the CW in bradyzoites (Fig 3I). The localization of GRA69 is unaltered in Δ*asp5* parasites. TGME49_297160 localized to the mitochondrion (S6A Fig). SUSA1 and TGME49_209755 are two PV-resident proteins in tachyzoites and are detected in the cyst matrix in bradyzoites (S6B and S6C Fig). Overall, the analysis of the bradyzoite TAILS led to the identification of two novel GRA proteins.

Export of bradyzoite effector proteins occurs through the immature cyst wall

While secretion, export and subcellular targeting and function in the host cell have been investigated in detail for several GRAs in the tachyzoite stage, little is known about the fate of GRAs in bradyzoites. To investigate the permissiveness of the cyst wall for export to the host cell, we focused on the effector protein IST, which is exported to the host cell nucleus in tachyzoites (18, 19). We first generated an endogenously IST-3Ty tagged strain in a ME49Δ*hx*Δ*ku80* (WT) background (S7A and S7B Fig). As we aimed to express IST-3Ty selectively in mature cysts, we selected the promoter of p21 (TGME49_238440, SAG-related sequence SRS22A), a late bradyzoite marker for which a previously described antibody is available (40). TGME49_238440 was identified as the gene encoding p21 while performing a large-scale screen for a different study. The genetic deletion of TGME49_238440 led to the disappearance of p21 signal, as shown by collecting parasites as tachyzoites or as bradyzoites, at different time points after differentiation *in vitro* (Fig 4A and 4C, S7A-C Fig). We also assessed the impact of *p21* deletion *in vivo* and observed no significant effect on the cyst burden (S7D Fig). p21 localizes to the micronemes, as shown by co-localization with AMA1 (Fig 4B). p21 is expressed from day 4 following differentiation (Fig 4C) and can be considered as a late bradyzoite marker, as compared to SAG4 (Fig 4D) or DBA (Fig 4E), with an expression peaking after 7 days of differentiation (Fig 4F). Importantly, deletion of p21 does not alter appearance of early differentiation markers DBA and SAG4 (Fig 4D-E). We replaced the endogenous IST promoter with the p21 promoter to generate the line P_{p21}-IST-3Ty (S7E and S7F Fig). As anticipated, IST-3Ty under the endogenous promoter was sustainably expressed in tachyzoites and in bradyzoites differentiated *in vitro* for 4, 7 or 10 days, as observed by WB (Fig 4G). Under the p21 promoter, the IST-3Ty product was only detectable after 4 to 7 days of differentiation by WB and IFA (Fig 4G-H). We observed two scenarios for the accumulation of IST-3Ty in the host nucleus: in cells infected by a single cyst, the levels of IST-3Ty or P_{p21}-IST-3Ty in the nucleus were lower than in tachyzoites, suggesting that bradyzoites reduce or stop IST export upon CW maturation (Fig 4I-J); in cells infected with a cluster of small-sized cysts, likely resulting from the rupture of a large cyst in the vicinity, IST-3Ty was increasingly detected in the nucleus over differentiation, while P_{p21}-IST-3Ty was abundantly found in the nucleus from 4 days of differentiation (Fig 4I and 4K), indicating that newly formed cysts by fully mature bradyzoites are able to secrete IST. The increased IST-Ty signal in the host nucleus over the course of the experiment is likely explained by an accumulation of IST-Ty over time, as newly formed vacuoles have secreted less IST-Ty. Moreover, reduced expression of P_{p21}-IST-3Ty only minimally affects the analysis, as IST-positive host-cell nuclei were not assessed for their signal intensity, and were scored positive even with very faint signal.

Taken together, these data suggest that IST can translocate through an immature CW but its export is prevented upon CW maturation (Fig 4L).

ASP5 substrates participate in residual body constriction in tachyzoites and cyst wall formation in bradyzoites

Given the broad spectrum of ASP5 substrates in tachyzoites and bradyzoites, we investigated the role of ASP5 in type II ME49 and CZ strains. The CZΔ*asp5* line was generated by introducing a selection marker (DHFR) immediately after the *asp5* initiation codon, using the same strategy as for the ME49Δ*asp5* described previously (25). IFAs performed using an α-actin1 antibody on parental and Δ*asp5* parasites from both ME49 and CZ strains showed an enlarged RB with diffuse staining compared with PVs of WT parasites (Fig 5A and 5B, S8A and S8B Fig). Transmission electron microscopy (TEM) confirmed the presence of large RBs in vacuoles of ME49Δ*asp5* (Fig 5C and 5D) and CZΔ*asp5* parasites (S8C and S8D Fig). Although some GRAs have been implicated in formation of the IVN and were shown to accumulate at the basal pole and around the RB in PVs (41), the functional link between ASP5 and the RB is not clear.

TEM revealed that both ME49Δ*asp5* and CZΔ*asp5* *in vitro* differentiated bradyzoites accumulate small electron-dense vesicles on the luminal side of the CW (Fig 5E and 5F, S8E-S8F Fig). Relevantly, the ASP5 substrate MYR1 is a component of the translocation machinery for parasite effector proteins across the tachyzoite PVM (27) and presumably also the CW in bradyzoites. To address if the translocation machinery participates in CW formation, we selectively deleted *MYR1* in ME49 parasites. TEM analysis confirmed a similar phenotype to those of ME49Δ*asp5* parasites, with accumulation of vesicles and thinner CW in a ME49Δ*myr1* strain after differentiation *in vitro* (Fig 5G).

ASP5 is critical for the generation of morphologically intact tissue cysts

We previously reported that that deletion of ASP5 significantly reduces the virulence of type II parasites, as tested using a lethal dose of 10^5 ME49 parasites as inoculum in mice (25). To assess the ability of ME49Δ*asp5* parasites to form tissue cysts *in vivo*, we analyzed cyst size and number in chronically infected mice inoculated with sub-lethal doses ($5x10^2$) of ME49 (WT) or ME49Δ*asp5* parasites (Fig 6A). At 8 weeks post-inoculation with ME49Δ*asp5* parasites, a 7-8'fold lower number of brain cysts was observed compared with WT parasites, indicating either a defect in dissemination during acute infection, or an altered ability to form and develop tissue cysts (Fig 6B). We addressed this by analyzing the morphology of tissue cysts from the brain of mice chronically infected with WT or ME49Δ*asp5* parasites, fixed 8 weeks p.i. TEM also showed the accumulation of electron-dense vesicles in the matrix of ME49Δ*asp5* cysts in mice, which were absent in cysts formed by WT parasites (Fig 6C and 6D). The morphology of these cysts was comparable to those of ME49Δ*MyoJ* parasites, which also display significantly reduced cyst numbers in mice but are morphologically indistinguishable from WT cysts (42). ME49Δ*MyoJ* cysts appeared morphologically intact, similar to those formed by WT parasites (Fig 6C and 6E).

Taken together, the data demonstrate an important role for ASP5 in processes linked to delivery of vesicular content within cysts *in vivo* that result in a significant lower cyst burden in mice upon *asp5* deletion. The ASP5 substrate(s) associated to this particular function remains to be identified.

Assessment of cyst burden in mouse infected brain by 2-photon serial tomography

To investigate the impact of effector GRAs processed by ASP5 on *T. gondii* dissemination during the acute and chronic phases of the infection, we evaluated the localization of cysts at the whole brain scale with a high spatial resolution, using 2-photon serial tomography (43). Mice were infected either with ME49Δ*hx* (WT) or ME49Δ*asp5* *T. gondii* tachyzoites expressing GFP under the control of a bradyzoite specific promoter (BAG1), and the brains were analyzed at 2 or 5 weeks p.i. We first confirmed that the signal detected corresponded to *T. gondii* parasites by staining brain sections containing GFP-fluorescent structures with the parasite inner membrane complex marker GAP45 (Fig 7A and 7Ai). At first glance, we observed tissue cysts widely distributed or sometimes clustered in the brain of 2 (Fig 7B-7Bii) and 5 weeks (Fig 7C-7Cii) infected mice. An unbiased quantification of the cyst number based on fluorescence signals revealed a higher cyst burden in the brains of animals infected for 2 weeks compared to those infected for 5 weeks (Fig 7D). This decrease upon time was observed in both WT- and ME49Δ*asp5*-infected mice and was consistent with the total volume represented by the tissue cysts over the whole brain (Fig 7E). In WT-infected animals, we noticed a predominance of tissue cysts of a small volume at 2 weeks p.i., while a wide range of sizes was observed at 5 weeks p.i. (Fig 7F). The fewer cysts formed by ME49Δ*asp5* parasites at 2 weeks p.i. were slightly larger than the WT, but over time, the majority of the detected cysts tended to be of small sizes. To determine if cysts were clustered, we measured the distance between a given cyst and its closest neighbor. It appeared that a large fraction of WT cysts was highly clustered at 2 weeks p.i., and to a lesser extent at 5 weeks p.i (Fig 7G).

However, Δ*asp5* cysts were less condensed than the WT at 2 weeks p.i. and were also more distant towards each other at 5 weeks p.i.

Overall, these data underline the dynamic nature of brain colonization by *T. gondii* and indicate that at the onset of WT parasite entry, a high burden of small-sized and closely located parasites is present in the brain. Only a subfraction of this first pool of cyst successfully persist, increases in size and disseminate in the brain. This pattern is altered during infection with a Δ*asp5* strain, with a lower parasite load initially reaching the brain and mostly small-sized cysts detected at a later time point.

Discussion

Throughout its life cycle in the host, *T. gondii* is surrounded by protective and interactive interfaces. Effectors molecules released by dense granules make critical contributions to the morphology and functionality of the PVM and the PV space, as well as subverting host cellular functions during the tachyzoite stage. The export of proteins across the PVM requires a translocon machinery notably composed of MYR1 (27, 28). Through the maturation of MYR1, ASP5 mediates the transit of all known GRAs exported beyond the PVM in addition to proteolytic processing of numerous GRAs residing in the PV space (29, 44).

To determine to which extent tachyzoites and bradyzoites confined within the PVM and CW communicate with the host cell and to assess the role of ASP5 in these processes, we embarked on a TAILS analysis to identify ASP5 substrates in both stages and dissect the role of ASP5 during the transition to chronic infection. TAILS identified GRA proteins GRA33, GRA65, GRA66, GRA67 and WNG2 as ASP5 substrates (Fig 8). Strikingly, none of the previously characterized exported effectors GRA16, GRA24, GRA28, IST or TEEGR were represented in our TAILS dataset suggesting that these proteins are not as abundant as PV-resident GRAs and therefore are not detected, suggesting that the approach might lack the necessary sensitivity to uncover new members of this family of effectors.

Sequence analysis of the newly identified substrates revealed that the TEXEL motif is variable to a considerable degree. In addition to the RRL sequence, we noted the occurrence of cleavage at TEXEL-like motifs (RHLLT for GRA66, RRLDS for WNG2) as deduced from the enriched N-terminal peptides of several confirmed ASP5 substrates. This observation suggests that ASP5 does not only recognize a specific sequence of amino acids but rather a secondary/tertiary structure that could accommodate different residues, as long as they are of similar charge/polarity/hydrophobicity. Overall, vacuolar and exported GRA effectors processed by ASP5 exhibit a striking imbalance. While a large majority of the TEXEL-containing substrates are resident GRAs of the PV and/or PVM (MYR1, LCAT, WNG1, WNG2, GRA19, GRA20, GRA33, GRA34, GRA44, GRA45, GRA46, GRA65, GRA66, GRA67), the only exported effectors directly cleaved by ASP5 are GRA16 and IST. Apparent for GRA33, GRA34 and GRA66, several PV and/or PVM resident GRA accumulated around the RB in absence of ASP5. Taken together with the enlargement of the RB observed by TEM in type I and type II Δ*asp5* backgrounds, this seems to suggest a role for GRA in RB constriction, likely from the PV side.

We showed that IST also accumulates in the host cell nucleus during intracellular development of bradyzoites. However, the IST signal in the host nucleus decreases upon CW maturation, suggesting that its export beyond the PV occurs mainly early on, shortly after host cell invasion. IST was recently shown to accumulate in the host cell nucleus at the bradyzoite stage, in contrast to GRA16 and GRA24 (32, 45). Concordantly, another study showed that GRA16 export is prevented in the bradyzoite stage (46). Taken together, these data indicate that translocation across the CW in the bradyzoite stage might not be uniform for all GRAs effectors. Additionally, protein translocation seems to be dependent on the maturation state of the CW, with the export of the different GRAs being successively blocked upon CW development (Fig 8). GRAs effectors translocation during the chronic stage might also involve additional factors, such as the catalytic activity of the rhoptry protein kinase ROP17, which deletion compromise the nuclear localization of GRA16 and GRA24 in tachyzoites (47). Nevertheless, given the important changes in mRNA levels after induction of bradyzoite development (30, 32), the amount of protein exported during the early stages might be sufficient to sustainably reprogram host cellular functions. In the absence of ASP5 or MYR1, the CW fails to develop normally both in *in vitro* differentiated bradyzoites and *in vivo* purified cysts from infected mouse brains. This indicates that a functional translocation machinery is required for the formation of a morphologically mature CW. At this stage it is not clear how the accumulated vesicles in type II Δ*asp5* bradyzoites relate to MYR1 and CW formation.

The *in vivo* visualization of *T. gondii* using 2-photon serial tomography enabled us to determine that, in agreement with our previous observations (Boillat et al., 2020), the absence of ASP5 leads to fewer parasites reaching the brain, suggesting that parasite spreading, entry in the brain and subsequent cyst formation are dependent on effector GRAs. As a primary mediator of the response to infection, dendritic cells (DCs) are hijacked by *T. gondii* that increases their mobility and benefit from their ability to cross the blood brain barrier (BBB) to enter the brain. In line with previous studies showing that DCs hypermotility upon *T. gondii* infection is compromised in absence of ASP5 (25) or that GRA24 suppresses maturation of DCs (48), our findings indicate that tachyzoites are greatly dependent on ASP5-related effector GRAs to scavenge DCs functions to disseminate and ultimately enter the brain. The clustering of cysts and their relative proximity to tissue lesions indicates that parasites are readily taking advantage of a breach in the vascular epithelium to cross the BBB and colonize neighboring cells of the parenchyma to disseminate in the brain (49). This observation implies that the transcellular entry is likely the most efficient mode used by *T. gondii* to penetrate in the brain epithelium, as compared to paracellular entry or to the “Trojan horse” method (Fig 8).

Overall, this study underlines the importance of ASP5 substrates for the architecture of tachyzoites and bradyzoites residing compartments. ASP5 not only participate to parasite virulence but also plays an important role in the establishment and maintenance of a chronic infection.

Materials and Methods

Bacteria, parasite and host cell culture

The parental and derived strains of *T. gondii* tachyzoites were maintained by serial passage on confluent monolayers of human foreskin fibroblasts (HFFs) maintained in Dulbecco’s Modified Eagle’s Medium (DMEM, Gibco) supplemented with 5% fetal calf serum (FCS), 2mM glutamine and 25 mg/ml gentamicin. *E. coli* XL-10-Gold chemically competent bacteria were used for all recombinant DNA experiments.

Preparation of *T. gondii* genomic DNA

Genomic DNA (gDNA) from *T. gondii* parasites was extracted using the Wizard SV genomic DNA purification system (Promega) according to the manufacturer’s protocol.

Parasite strains, DNA vector constructs and transfections

- **TASPx-3Ty-HXGPRT (knock-in) strains**

Endogenously Ty tagged strains of candidate genes were made by amplifying the region of a plasmid encompassing the 3ty tags and the HXGPRT selection cassette using KOD DNA polymerase (Novagen, Merck) with primers having 28bp gene homology arms (as shown in

S3 Fig). Plasmids TASPx-Cas9-YFP/CRISPR for directing the integration of the 3Ty-HXGPRT fragment at the C-terminus were generated using the Q5 site directed mutagenesis kit (NEB) with primers listed in S3 Table and using the vector pSAG1::CAS9-GFP-U6::sgUPRT as template (50). The amplified 3Ty-HXGPRT PCR products were co-transfected with 20µg of their corresponding gRNA-plasmids as described before (51).

- **RHΔ*hxgprt*Δ*asp5*Δ*ku80* and ME49Δ*asp5*Δ*ku80* strain**

To generate the RHΔ*hxgprt*Δ*asp5*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gKU80(#5944) vector was used to disrupt the *ku80* locus in a RHΔ*hxgprt*Δ*asp5* background strain, previously generated (25). 48 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *ku80* gene was confirmed by sequencing of the *ku80* locus (S2 Fig), using primers listed in S3 Table.

To generate the ME49Δ*asp5*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gKU80(#5944) vector was used to disrupt the *ku80* locus in a ME49Δ*asp5* background strain, previously generated (25). 72 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *ku80* gene was confirmed by sequencing of the *ku80* locus (S2 Fig), using primers listed in S3 Table.

- **ME49Δ*hxgprt*Δ*ku80* strain**

To generate the ME49Δ*hxgprt*Δ*ku80* strain, the pSAG1-CAS9gfp-U6gHXGPRT(#5950) and pSAG1-CAS9gfp-U6gKU80(#5944) vectors were used to disrupt the *hxgprt* and *ku80* loci, respectively, in a ME49 background strain. 72 hr after transfection, parasites were cloned by FACS sorting the green fluorescent parasites into 96-well plates. Disruption of the *hxgprt* and *ku80* genes was confirmed by sequencing of the *hxgprt* and *ku80* loci (S2 Fig), using primers listed in S3 Table.

- **ME49Δ*hxgprt*Δ*ku80*Δ*p21* strain**

To generate the ME49Δ*hxgprt*Δ*ku80*Δ*p21* strain, a PCR fragment encoding the DHFR-TS selection cassette was generated using the KOD DNA polymerase with the vector p2854-DHFR (52) as template and the primers 6109/6110 that also carry 30 bp homology with the 5' and 3' ends of *p21*. To direct the insertion of the PCR product, the pSAG1-CAS9gfp-U6gP21(#6108) vector was used. The integration of the PCR product was confirmed by PCR of genomic DNA (S7A and S7B Fig) using primers listed in S3 Table.

- **IST-3Ty (knock-in) and P$_{p21}$-IST-3Ty (promoter replacement) strains**

To generate the 3Ty tagged IST strain controlled by p21 promoter (P$_{p21}$-IST-3Ty), the promoter region of p21 consisting ~1600 bp upstream of its start codon was amplified with primers 8878/8879 having 30 bp IST homology arms. The IST-Cas9-YFP/CRISPR gRNA targeting the 5' region of IST was generated similarly to the TASPx-Cas9-YFP/CRISPR with primers 8877/4883. The PCR-amplified p21 promoter region was co-transfected with 20ug of the IST-Cas9-YFP/CRISPR plasmid into IST-3Ty-KI parasites. Transfected parasites were cloned by FACS-sorting the GFP-positive parasites into 96-well plates 48 hr post-transfection. The integration of the PCR products and promoter swap was confirmed by PCR of genomic DNA (S7E and S7F Fig) using primers listed in S3 Table.

- **ME49Δ*myr1* strain**

To generate the ME49Δ*myr1* strain, a PCR fragment encoding the DHFR-TS selection cassette was targeted to the *myr1* locus using a specific double gRNA (dgRNA) vector, as previously described (30).

- **ME49Δ*hxgprt* P$_{BAG1}$-GFP strain**

To generate the ME49Δ*hxgprt* P$_{BAG1}$-GFP strain, a P$_{BAG1}$-GFP-HXGPRT construct was stably integrated in the genome of ME49Δ*hxgprt* parasites, as previously described (30).

All PCR amplifications for screening of the generated strains were performed using the GoTaq DNA polymerase (Promega). All primers used in this study are listed in S3 Table.

Parasites transfection and selection of clonal stable lines

T. gondii tachyzoites were transfected by electroporation as previously described (53). Transgenic parasites were selected with mycophenolic acid (MPA, 25 mg/mL) and xanthine (50 mg/mL) for HXGPRT selection (52), pyrimethamine (1 µg/ml) for DHFR selection (52). All stable clones were isolated by limiting dilution in 96-well plates and screened for expression of the transgenes by IFA and for genomic integration by GoTaq PCR.

Antibodies

The following primary antibodies were used in this study: monoclonal mouse α-Ty (hybridoma BB2, 1:10 IFA, 1:10 WB (54)), α-actin (hybridoma, 1:10 IFA, 1:10 WB (55)), α-SAG1 (hybridoma, 1:10 WB (56)), α-SAG4 (hybridoma, 1:10 WB (57)), α-p21 (hybridoma, 1:50 IFA, 1:10 WB (40)) and polyclonal rabbit α-catalase (1:2000 WB (58)), α-IMC1 (1:1000 IFA (59)) and α-GAP45 (1:10.000 IFA (60)). *Dolichos biflorus* Agglutinin (DBA) lectin labelled with Rhodamine was used (at 10 µg/mL; Vector) to detect the glycosylated protein CST1, as a marker of the *T. gondii* cyst wall (3). The following secondary antibodies were used in this study: α-mouse and α-rabbit HRP (Sigma) (WB), Alexa-Fluor-488-conjugated goat α-mouse and α-rabbit IgG antibodies and Alexa-Fluor-594-conjugated goat α-mouse and α-rabbit IgG antibodies (Thermofisher) (IFA).

Immunofluorescence assay

HFF monolayers were grown on coverslips and infected with *T. gondii* tachyzoites. The coverslips were subsequently fixed at the appropriate time-points with either 4% paraformaldehyde (PFA) in phosphate-buffered saline (PBS) for 10 min or 4% paraformaldehyde (PFA)/0.001% glutaraldehyde (GA) for 20 min, prior to quenching with

0.1M glycine/PBS. Fixed cells were permeabilized with 0.2% Triton/PBS and blocked with 2% BSA/0.2% Triton/PBS. Cells were then probed with primary antibodies diluted in 2%BSA/0.2%Triton/PBS for 1 hr on an orbital shaker. This is followed by 3 washes with 0.2% Triton/PBS and incubation with secondary antibodies in 2% BSA/0.2% Triton/PBS for 1 hr. After 3 more washes with 0.2% Triton/PBS, the coverslips were stained with DAPI (4',6-diamidino-2-phenylindole; 50 µg/ml in PBS) and mounted on Fluoromount G (Southern Biotech) on glass slides. Images were recorded with a LSM800 confocal microscope (Zeiss) at the Bioimaging core facility of the Faculty of Medicine, University of Geneva. Final image analysis and processing was done with ImageJ Fiji (61).

Western blotting

Freshly egressed parasites were pelleted by centrifugation at 1000g, washed once in PBS, lysed directly in SDS-loading buffer and subjected to SDS-PAGE under reducing conditions. Proteins were transferred to nitrocellulose membrane and immunoblot analysis was performed. Primary and secondary antibodies are diluted in PBS, 0.05% Tween 20 and 5% skimmed milk power, washes are performed in 0.05%Tween/PBS. Following the primary and secondary antibody incubation and washes, the membrane was incubated with a peroxidase-conjugated goat anti-mouse or anti-rabbit antibody. The bound antibodies were visualized using the ECL plus system (GE Healthcare Bio-Sciences).

Competition assay

Parasites to be assessed were mixed with GFP-expressing wild-type parasites and allowed to infect and grow on HFF monolayers. The ratios were quantified over six passages by FACS. Parasites were labeled with Hoechst prior to FACS counting of 10,000 parasites. Data are presented as mean values ± SD from three independent experiments.

In vitro bradyzoite differentiation

Tachyzoite to bradyzoite conversion *in vitro* was induced by exposing parasite cultures to pH 8.2 as described previously (62). Briefly, tachyzoites were allowed to infect HFF monolayers grown on glass coverslips inside 24-well plates. Bradyzoite differentiation was induced 24 hr post infection by replacing normal media with RPMI 1640 buffered with 50 mM HEPES to pH 8.2 and supplemented with 3% fetal bovine serum. Parasites were allowed to grow at 37°C in absence of CO_2 and alkaline media was changed daily. After the required number of days of conversion, infected HFF were fixed and analyzed.

Serial sections transmission electron microscopy on *in vitro* differentiated bradyzoites

Samples for transmission electron microscopy were processes as described previously (25). Briefly, infected HFF cells grown on round glass coverslips were fixed with 2.5% glutaraldehyde (Electron Microscopy Sciences) and 2% paraformaldehyde (Electron Microscopy Sciences) in 0.1 M phosphate buffer (PB) at pH 7.4 for 1 h at room temperature. After extensive washing with 0.1 M sodium cacodylate buffer, pH 7.4 samples were post-fixed with reduced 1% osmium tetroxide (Electron Microscopy Sciences) with 1.5% potassium ferrocyanide in 0.1 M sodium cacodylate buffer, pH 7.4 for 40 min immediately followed by 1% osmium tetroxide alone (Electron Microscopy Sciences) in 0.1 M sodium cacodylate buffer pH 7.4 for 40 min. Cells were then washed in double distilled water twice for 5 min each wash and *en block* stained with aqueous 1% uranyl acetate (Electron Microscopy Sciences) for 1 h or overnight at 4°C. After 5 min wash in double distilled water cells were dehydrated in graded ethanol series (2 × 50%, 70%, 90%, 95%, and 2 × absolute ethanol) for 3 min each wash and infiltrated with graded series of Durcupan resin (Electron Microscopy Sciences) diluted with ethanol at 1:2, 1:1, 2:1 for 30 min each, and twice with pure Durcupan for 30 min each. Cells were infiltrated with fresh Durcupan resin for additional 2 hours. For flat embedding, 1 mm thick teflon rings were placed on glass slide (3 per slide) coated with mold separating agent (Glorex), filled with fresh resin and covered with coverslip facing grown cell down and then polymerized at 65 °C oven overnight or for 24 h. The glass coverslip was removed from the cured resin disk by immersing alternately into hot (60 °C) water and liquid nitrogen until glass parted. Laser microdissection microscope (Leica Microsystems) was used to select suitable cysts and to outline their positions on the exposed resin surface. Then the selected area was cut out from the disk using a single edged razor blade and glued with superglue (Ted Pella) to a blank resin block. The cutting face was trimmed using a Leica Ultracut UCT microtome (Leica Microsystems) and a glass knife. 70 nm ultrathin serial sections were cut with a diamond knife (DiATOME) and collected onto 2 mm single slot copper grids (Synaptec, Ted Pella) coated with Formvar plastic support film.

Sections were examined using a Tecnai 20 TEM (FEI) operating at an acceleration voltage of 80 kV and equipped with a side-mounted MegaView III CCD camera (Olympus Soft-Imaging Systems) controlled by iTEM acquisition software (Olympus Soft-Imaging Systems).

Transmission electron microscopy on *in vivo* cysts

Experimental animals were intraperitoneally infected with ME49, ME49Δ*asp5* or ME49Δ*MyoJ* tachyzoites. 5 weeks post-infection, deeply anesthetized animals were fixed by cardiac perfusion (63) with 150 ml of 2.5% glutaraldehyde (Electron Microscopy Sciences) and 2% paraformaldehyde (Electron Microscopy Sciences) in 0.1 M phosphate buffer (PB) at pH 7.4 at speed of 12 ml/min for 20-30 min. After 2 h, the brain was carefully removed from the skull and kept in 0.01M PBS. Brains were embedded into 5% low melted agarose (Eurobio) in order to cut 80 µm thick vibratome coronal sections. Sections containing the cysts were then processed for electron microscopy as described previously (63, 64). Briefly, vibratome sections were extensively washed with 0.1 M sodium cacodylate buffer, pH 7.4 and post-fixed with reduced 1% osmium tetroxide (Electron Microscopy Sciences) with 1.5% potassium ferrocyanide in 0.1 M sodium cacodylate buffer, pH 7.4 for 1 h immediately followed by 1% osmium tetroxide alone (Electron Microscopy Sciences) in 0.1 M sodium cacodylate buffer pH 7.4 for 1 h. Sections were then washed in double distilled water twice for 5 min each wash and *en block* stained with aqueous 1% uranyl acetate (Electron Microscopy Sciences) for 1 h or overnight at 4°C. After 5 min wash in double distilled water cells were dehydrated in graded ethanol series (2 × 50%, 70%, 90%, 95%, and 2 × absolute ethanol) for 3 min each wash and infiltrated with graded series of Durcupan resin (Electron Microscopy Sciences) diluted with ethanol at 1:2, 1:1, 2:1 for 30 min each, and twice with pure Durcupan for 30 min each. Sections were infiltrated with fresh Durcupan resin for additional 2 h. Finally, brain vibratome sections were placed on glass slide coated with mold separating agent and overlaid with second glass slide coated with mold separating agent. This sandwich was then polymerized at 65 °C oven for 24 h. Cured sections embedded in resin were separated from glass slide using a razor blade.

Using the laser microdissection microscope (Leica Microsystems) to select suitable cysts and to outline their positions on the surface of the cured vibratome section, cutting out selected area from section and gluing with superglue to a blank resin block, trimming the cutting face and serial section ultramicrotomy as well as final ultrathin sections examination was performed in the same way as mentioned in previous section.

Mouse infection

6-weeks old B6CBAF1/J male mice (Janvier laboratories) were intraperitoneally infected with 2.10^2 parasites. The health of mice was monitored daily until they presented severe symptoms of acute toxoplasmosis (bristled hair and complete prostration with incapacity to drink or eat) and were sacrificed on that day.

Processing of the brains, tissue cysts counting and purification

Mice brains were homogenized in 1 ml PBS and syringe passaged 5-10 times through a 18G needle to break up large clumps. Then, the homogenate was sequentially syringe passaged through a 20G needle and a 23G needle (10 times each). Tissue cysts number was estimated by counting 5 fractions of 10 µl from each brain homogenate using the 10× and 20× objectives of an inverted microscope. The procedure for tissue cysts purification was adapted from Watts and colleagues (65), who modified the original Percoll gradient protocol (66). 5 ml of PBS was added to the brain homogenate and the mix was passed once through a cell strainer (Corning) prior to loading on the gradient. The gradient consisted of 4 layers of 90%, 50%, 30% and 10% Percoll diluted in 1× PBS final and supplemented with 1% PFA to avoid premature breakage of tissue cysts during the purification steps. The gradient was centrifuged at 290 × *g* for 20 min at 4°C (with low acceleration and low brake when stopping). The fractions were carefully harvested using a 22G × 2”, 0,7 × 50 mm needle.

Terminal amine isotopic labelling of substrates (TAILS) and LC-MS analysis for identification of ASP5 protease substrates

The candidate substrates were identified according to the methodology described previously (33, 67). Briefly, protein from *T. gondii* cell lysates of tachyzoites (WT and Δ*asp5*) and bradyzoites (Intracellular, WT and Δ*asp5*) was extracted by treatment with RIPA buffer (150 mM NaCl, 1% NP40, 0.5% natriumdeoxycholate, 0.1% SDS, 50 mM Tris-HCl, pH 8.0, 1 mM EDTA) for 30 min at 4°C, high-speed centrifugation for 15 min, and subsequent acetone precipitation. The acetone pellet was processed as previously described, with the only difference being no fraction of the pre-TAILS peptides were sampled for further analysis. LC-MS analysis of the purified TAILS peptides was performed as previously described (33) on an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Scientific) operated with an EASY-nLC 1000 Liquid Chromatography system (Thermo Scientific) in data dependent analysis mode (DDA).

Serial-section two-photon tomography

Anaesthetized mice were transcardially perfused with 15 ml 0.1 M phosphate buffer (pH 7.4) (PB), followed by 50 ml 4% paraformaldehyde in 0.1 M PB. Brains were removed from the skull and post-fixed them in 4% paraformaldehyde 24 hours at 4°C. The fixed brains were then stored in PBS at 4°C until imaging. The fixed brains were embedded in 4% oxidized agarose (derived from type-I agarose (Sigma-Aldrich)) and covalently cross-linked the brain to the agarose by incubation in an excess of 0.5% sodium borohydride (NaBH4, Sigma-Aldrich) in 0.05 M sodium borate buffer overnight at 4°C. Then embedded brains were applied to a TissueVision two-photon scanning microscope, which cut physical sections of the entire brain every 50 µm coronally, and acquired optical sections every 10 µm in three channels (red channel: 560-650 nm; green channel: 500–560 nm; Blue channel: 450-500 nm) by 940-nm excitation laser light (Mai Tai eHP, Spectraphysics). Each imaged section is formed from overlapping 800×800-µm 'tiles' with a resolution of 0.435 µm in x and y. The cysts were segmented and quantified with scripts available from the authors on request.

Ethics statement

All animal experiments were carried out with the authorization GE/150/16 according to the guidelines and regulations issues by the Swiss Federal Veterinary Office. No human samples were used in these experiments.

Data availability

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD034786. All other relevant data are available from the authors on request

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Conflict of interest

The authors declare no conflict of interest.

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Figure legends

Fig 1. Localization and migration profile of newly identified GRA among candidate proteins is altered upon *asp5* deletion in tachyzoites.

Subcellular localization by immunofluorescence and migration profiles of 3Ty-tagged GRA65 (A-B), GRA66 (C-D) and GRA67 (E-F) in RHΔ*ku80* (WT) and RHΔ*asp5*Δ*ku80* (KO) parasites. GRA65 (A), GRA66 (C) and GRA67 (E) all display an altered migration profile upon *asp5* deletion, as indicated by the asterisks. GRA67 (E) accumulation in the endosomal-like compartment (ELC) upon *asp5* deletion is visible thanks to the ELC markers GRASP-GFP and ASP3-myc. Parasites were fixed for 3 min in PFA alone or for 20 min in PFA/GA to visualize dense granules or PV space/PVM, respectively. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 2. Localization and migration pattern of GRA is modified by the absence of *asp5* in tachyzoites.

Subcellular localization by immunofluorescence and migration profiles of 3Ty-tagged GRA33 (A-B), GRA34 (C-D) and WNG2 (E-F) in RHΔ*ku80* (WT) and RHΔ*asp5*Δ*ku80* (KO) parasites. GRA33 (A), and WNG2 (E) both display an altered migration profile upon *asp5* deletion. Conversely, the migration profile of GRA34 in KO parasites is unchanged (C). GRA33 (B), GRA34 (D) and WNG2 (F) all display an altered migration profile upon *asp5* deletion, as indicated by the asterisks. Parasites were fixed for 3 min in PFA alone or for 20 min in PFA/GA to visualize dense granules or PV space/PVM, respectively. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 3. Characterization of novel GRA candidate proteins not processed by ASP5.

Migration profile of 3Ty-tagged (A) MCP4, (D) GRA68 and (G) GRA69 in ME49Δ*ku80* (WT) and ME49Δ*asp5*Δ*ku80* (KO) tachyzoites and bradyzoites. (B) MCP4-3Ty, (E) GRA68-3Ty and (H) GRA69-3Ty in ME49Δ*ku80* extracellular tachyzoites or bradyzoites largely colocalizes with the dense granule marker GRA1. Subcellular localization of (C) MCP4-3Ty, (F) GRA68-3Ty and (I) GRA69-3Ty in ME49Δ*ku80* and ME49Δ*asp5*Δ*ku80* intracellular tachyzoites and bradyzoites. Note that the expression of MCP4-3Ty is strongly enhanced in bradyzoites compared to tachyzoites. Schematics of TASP domain organizations are based on data from ToxoDB (for accession numbers see Table 1). Loading control in immunoblots: α-catalase. All samples for immunoblots were collected intracellularly. Scale bars: 10 µm.

Fig 4. IST export by bradyzoites is reduced upon cyst wall maturation.

(A) p21 endogenous expression in ME49Δ*hx*Δ*ku80* (WT) and ME49Δ*ku80*Δ*p21* (Δ*p21*) upon parasite differentiation under alkaline conditions was assessed by western blot. Tachyzoite marker: α-SAG1. Early bradyzoite marker: α-SAG4. Loading control: α-actin. Tz: tachyzoites; D3, D6 and D9: *in vitro* differentiated bradyzoites at 3, 6 or 9 days. All samples were collected intracellularly. (B) immunofluorescence assays (IFA) displaying the localization pattern of p21 using the IMC marker GAP45 and the microneme protein AMA1 after 10 days of differentiation. (C-E) Quantification from IFA of WT or Δ*p21* vacuoles positive for p21 (C), SAG4 (D) and DBA (E) staining upon parasite differentiation under alkaline conditions. (F) IFA of PFA/GA-fixed ME49Δ*hx*Δ*ku80* IST-3Ty tachyzoites and bradyzoites at 7 or 10 days in differentiation conditions. (G) Immunoblot showing IST-3Ty expression driven by endogenous or p21 promoter and upon parasite differentiation under alkaline conditions. Late bradyzoite marker: α-p21. Loading control: α-catalase. Tz: tachyzoites; D4, D7 and D10: *in vitro* differentiated bradyzoites at 4, 7 or 10 days. All samples were collected intracellularly. (H) P_{p21}-IST-3Ty expression kinetics was evaluated from IFA by quantification of IST-3Ty positive vacuoles in tachyzoites or in bradyzoites upon differentiation of P_{p21}-IST-3Ty parasites under alkaline conditions for 4, 7 or 10 days. (I) IFA of PFA/GA-fixed ME49Δ*hx*Δ*ku80* IST-3Ty and P_{p21}-IST-3Ty tachyzoites and bradyzoites at 7 or 10 days in differentiation conditions. Late bradyzoite marker: α-p21. Nuclei: DAPI. IMC: GAP45. Cyst wall: DBA. Asterisk: nucleus of an infected host cell. Scale bars: 10 µm. (J) Quantification from IFA of positive nuclei in infected cells with a single vacuole of tachyzoites or bradyzoites, differentiated for 0, 4, 7 or 10 days. (K) Quantification from IFA of positive nuclei in infected cells with a cluster of tachyzoites or bradyzoites vacuoles, differentiated for 0, 4, 7 or 10 days. (L) Model for IST export during tachyzoite to bradyzoite transition. Scale bars: 10 µm.

Fig 5. ASP5 substrates contributes to the organization of tachyzoite and bradyzoite PVs. Subcellular localization of *T. gondii* actin and immunofluorescence performed on ME49 WT (A) or ME49Δ*asp5* (B) parasites infecting HFFs for 30 h revealed that presence of ASP5 is required for residual body construction. Morphology of parasites was observed by staining of the inner membrane complex (α-IMC1) and the cytosol was visualized using α-actin antibody. The white arrowheads point towards the RB. Scale bars: 5 µm. Section through the residual body in ME49 (C) or ME49Δ*asp5* (D) parasites at 30 h post inoculation in HFF monolayer. Enlarged areas shown below each micrograph are indicated. RB: residual body; VS: vacuolar space; MNN: membranous nanotubular network; mt: mitochondrion; PVM: parasitophorous vacuole membrane. (E-G) TEM analysis documenting that the absence ASP5 and MYR1 results in accumulation of vesicles at the vacuolar membrane of *in vitro* differentiated bradyzoites. Enlarged areas shown below each micrograph are indicated in (E), (F) and (G). CW: cyst wall; Mx; cyst matrix; ap: amylopectin granules. Scale bars: 1 µm.

Fig 6. The absence of ASP5 reduces cyst burden *in vivo* and results in vesicles accumulation in the cyst matrix.

Survival monitoring (A) (n=10) and cyst burden (B) in C57BL/6 mice injected with sub-lethal doses of ME49 WT or ME49Δ*asp5* tachyzoites. (C-E) TEM analysis of ME49 WT (C) Δ*asp5* (D) and Δ*MyoJ* (E) cysts harvested from mice. Δ*asp5* cysts accumulates vesicles in the cyst matrix, indicated by asterisks. As a comparison for a low cyst forming strain, Δ*MyoJ* shows no vesicle accumulation. Asterisk: vesicles clusters. Scale bars: 5 µm. Below, enlarged view of the cyst wall and matrix. CW: cyst wall; Mx; cyst matrix; ap: amylopectin granules. Scale bars: 1 µm.

Fig 7. Cysts behavior in the brain assessed by 2-photon serial tomography.

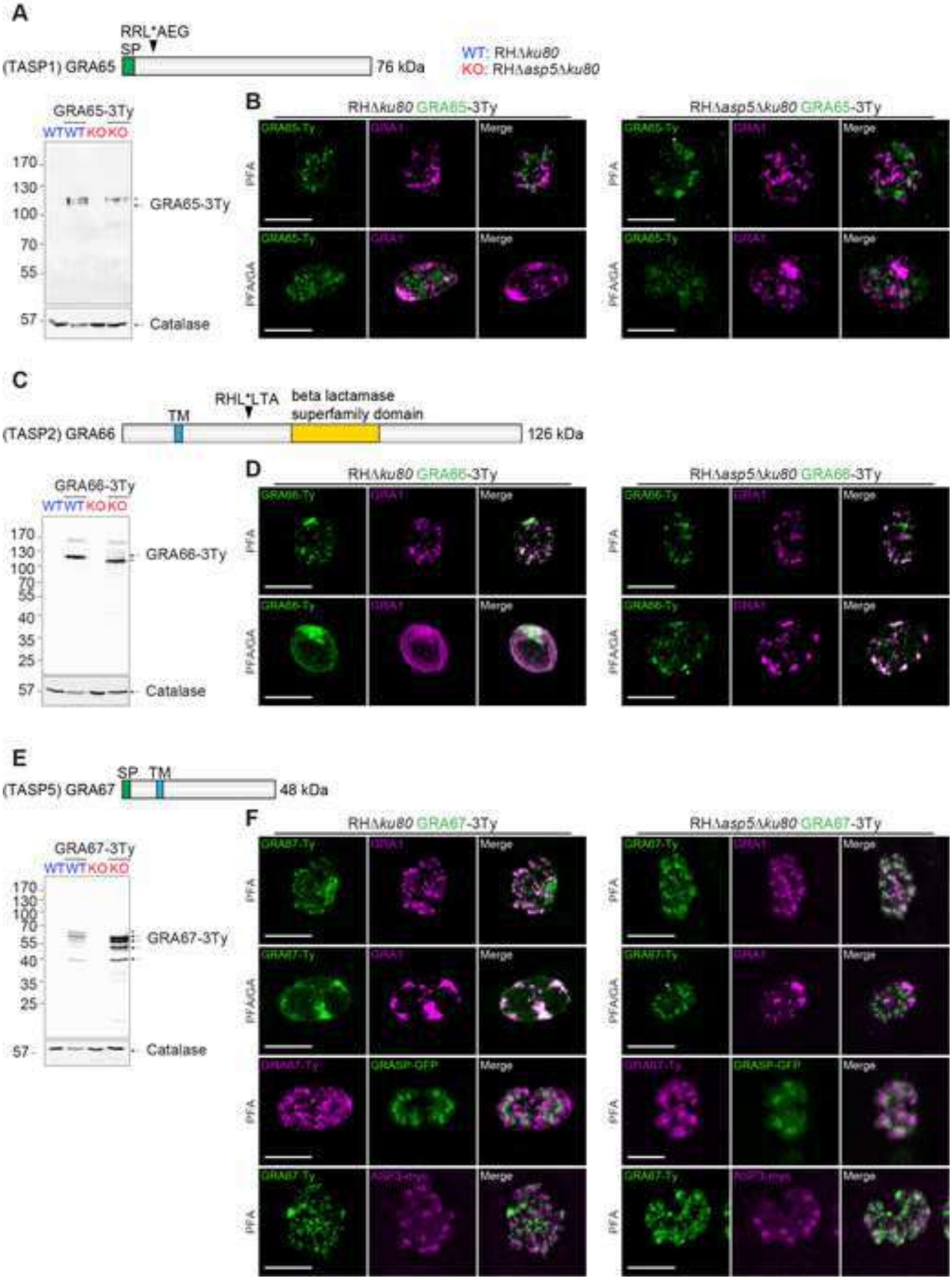
(A) Immunostaining of brain sections containing ME49Δ*hx* (WT) GFP-fluorescent structures with a parasite membrane marker (α-GAP45). (Ai) Zoom-in the framed area in (A). DAPI: DNA marker. Scale bars: 100 µm (A) and 10 µm (Ai). (B-C) Brain sections showing WT tissue cysts imaged at 2- (B) or 5-weeks (C) post-infection. (Bi-Ci) Zoom-in the framed areas in (B) and (C). (Bii-Cii) Same image as (Bi) or (Ci) taken with a shorter exposure. Scale bars: 100 µm (B and C) and 10 µm (Bi, Bii, Ci and Cii). (D) Fluorescence-based quantification of cysts number in the brain of 2- or 5-weeks-infected mice with WT or ME49Δ*hx*Δ*asp5* (KO) parasites. (E) Total volume (µm^3) represented by the detected parasites in the brain of 2- or 5-weeks-infected mice with WT or KO parasites. (F) Frequency graph showing the volume (µm^3) of the detected cysts in the brain of 2- or 5-weeks-infected mice with WT or KO parasites. (G) Distance (µm) of the nearest neighbor (cyst or single parasite) relative to each cyst or single parasite.

Fig 8. Model for ASP5 functions and targets at the tachyzoite and bradyzoite stage.
T. gondii tachyzoites multiply in circulating monocytes (A) or endothelial cells (B) within a PV. Secreted GRA proteins are targeted to the vacuolar space, the PVM, or the host cell cytosol or nucleus. ASP5 processes numerous intra- and extravacuolar GRAs: GRA33, GRA65, GRA66, GRA67, WNG2, MYR1, GRA16, GRA24, and IST. Subcellular localization of several GRA is altered as a direct or indirect (e.g. TASP4) effect of ASP5 knockout. The MYR1-2-3 translocation machinery is defective in the absence of ASP5 and the improper maturation of MYR1 is preventing translocation of GRA18, GRA28 and TEEGR to the host cell cytoplasm. (B) Three scenarios are discussed for crossing of the BBB by *T. gondii*: (1) para- or transcellular migration through epithelial cells, (2) infection of endothelial cells and creating a breach or (3) by exploitation of the trans-migration properties of immune cells (Trojan horse hypothesis). ASP5 substrates are involved in inducing hypermotility in infected dendritic cells. (C) Tissue-cysts reside predominantly in axons and dendrites of neurons or astrocytes in the CNS and in skeletal and heart muscle cells. At the onset of host cell infection by bradyzoites, IST and putatively other GRA can translocate through the immature CW. The CW likely becomes impermeable to GRA export upon maturation. This early release of effector proteins by bradyzoites triggers long-term effects on the transcriptome of infected cells and participate in the reprograming of the host cell cycle and immune signaling during the chronic stage of *T. gondii* infection. Of note, ASP5 contributes to the morphology of cysts, and its absence coincides with vesicle accumulation in the cyst matrix and at the PV membrane. PV: parasitophorous vacuole; GRA: dense granule proteins; PVM: parasitophorous vacuole membrane; BBB: blood brain barrier; CNS: central nervous system; IVN: intravacuolar network; CW: cyst wall.

Table 1. Features of candidate TASPs proteins.

Table summarizing the accession number, name, localization, fitness cost and stage expression of candidate proteins selected from the TAILS analysis. Accession numbers, protein sequences, SP, TM, dNdS ratio (Non-synonymous/Synonymous SNPs), conservation in *Eimeria* and transcriptomics RNA-Seq data were obtained from ToxoDB (toxodb.org). For the transcriptomics RNA-Seq data, negative values indicate a lower expression in bradyzoites (Bz) compared to tachyzoites and positive values indicate a higher expression in a bradyzoites compared to tachyzoites. The Localisation of Organelle Proteins by Isotopic Tagging (LOPIT) allocation and probability were obtained from proteome.shinyapps.io/toxolopittzex/. WT: Wild type; KO: Δ*asp5*; CM: Cyst Matrix; CW: Cyst wall; RB: Residual body; PV: Parasitophorous vacuole; PVM: Parasitophorous vacuole membrane; PM: Plasma membrane; ELC: Endosomal-like compartment; SP: Signal peptide; TM: Transmembrane. Additional information on TASPs candidates is available in S1 Table.

Fig 1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KO: RHΔasp5Δku80
GRA65-3Ty
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130
100
70
55
57
GRA65-3Ty
Catalase
B
RHΔku80 GRA65-3Ty
RHΔasp5Δku80 GRA65-3Ty
GRA65-Ty
GRA1
Merge
PFA
PFA/GA
C
RHL*LTA
TM
beta lactamase superfamily domain
(TASP2) GRA66
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GRA66-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
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GRA66-3Ty
Catalase
D
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RHΔasp5Δku80 GRA66-3Ty
GRA66-Ty
GRA1
Merge
PFA
PFA/GA
E
SP
TM
(TASP5) GRA67
48 kDa
GRA67-3Ty
WT WT KO KO
170
130
100
70
55
40
35
25
57
GRA67-3Ty
Catalase
F
RHΔku80 GRA67-3Ty
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GRA1
GRASP-GFP
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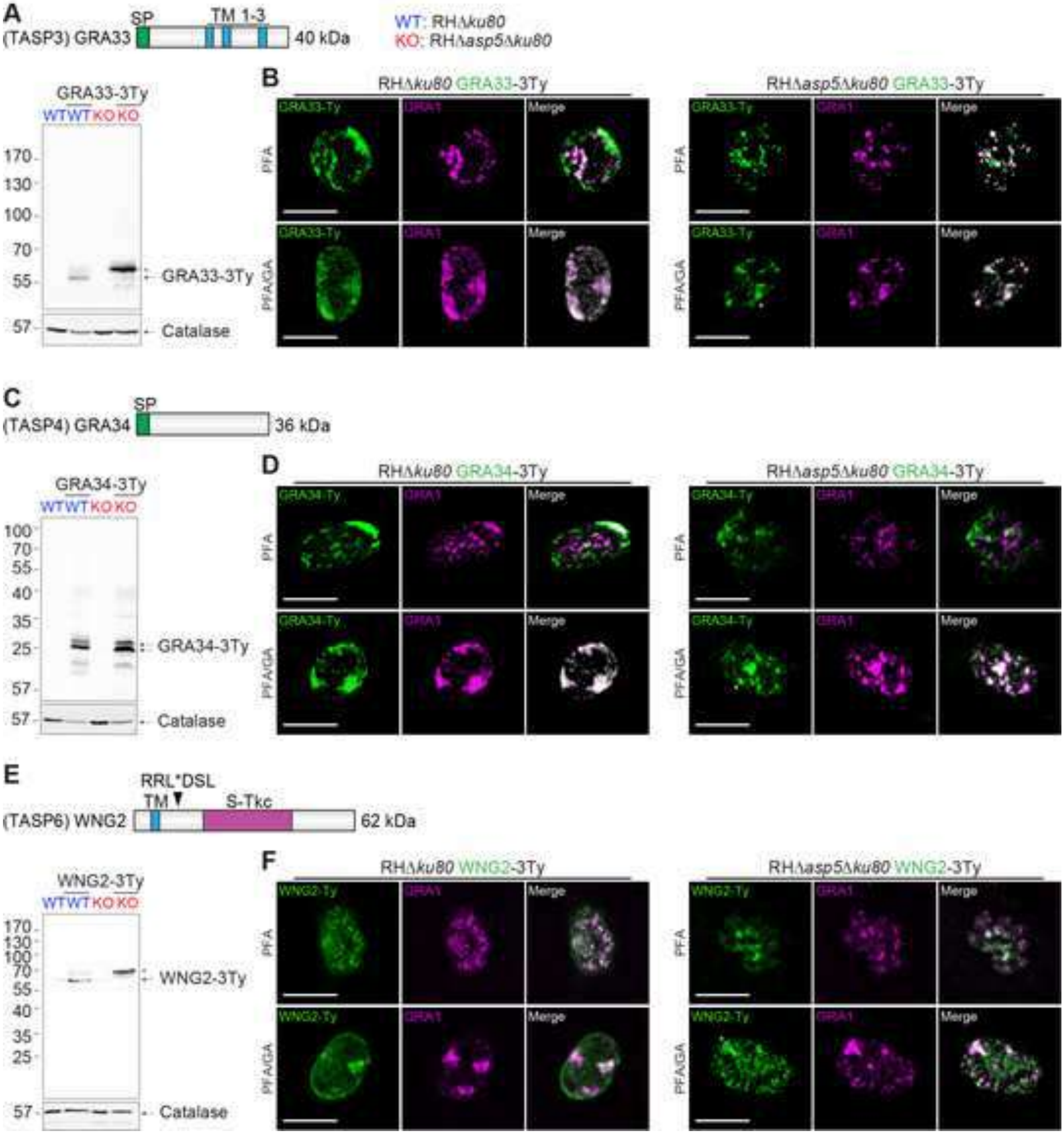
Merge
PFA
PFA/GA

Fig 2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GRA1
Merge
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PFA/GA
C
SP
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55
40
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57
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GRA34-Ty
GRA1
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PFA/GA
E
RRL*DSL
TM
S-Tkc
(TASP6) WNG2
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130
100
70
55
40
35
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WNG2-3Ty
57
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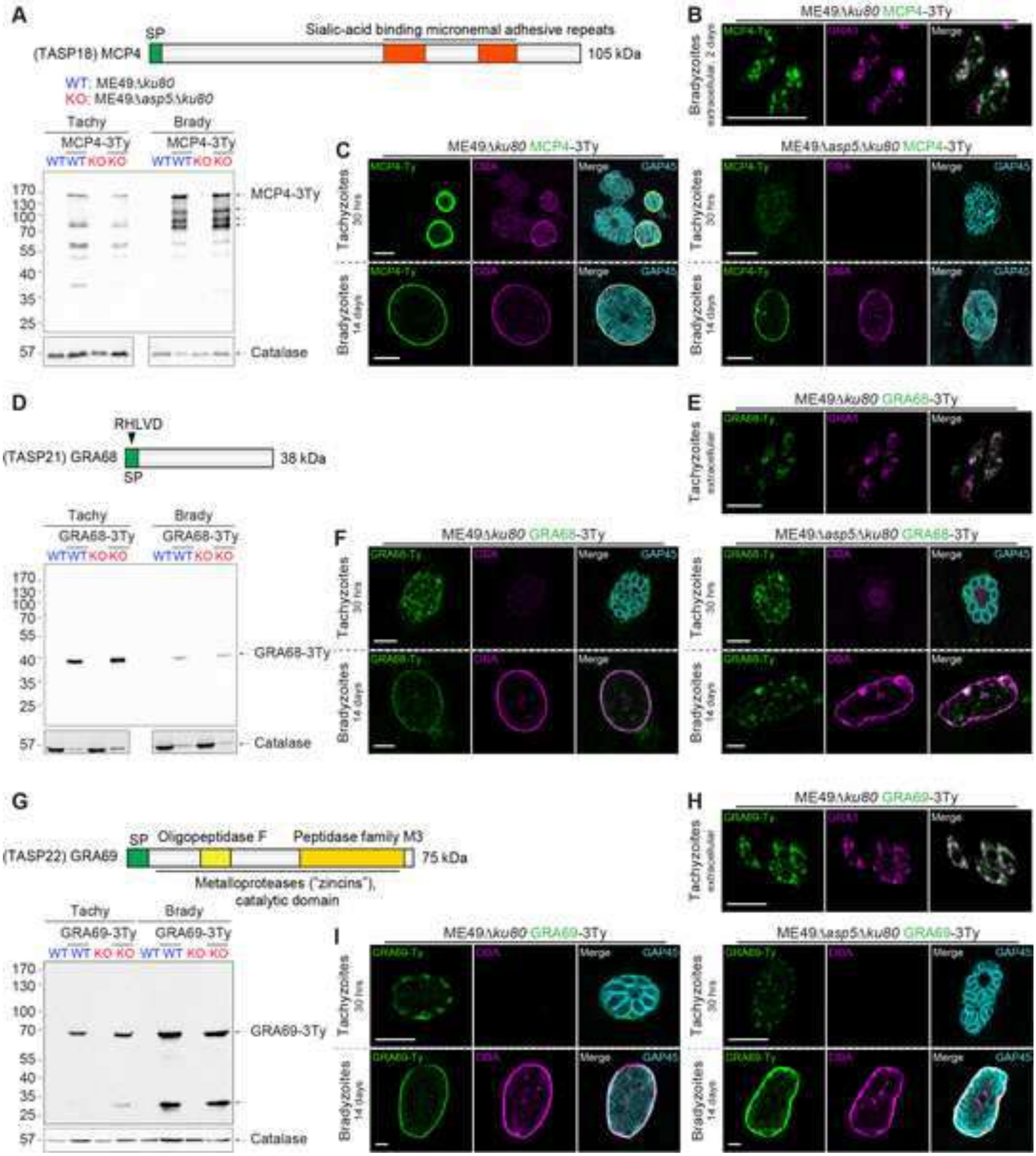
WNG2-Ty
GRA1
Merge
PFA
PFA/GA

Fig 3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MCP4-3Ty
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130
100
70
55
40
35
25
MCP4-3Ty
57
Catalase
B
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Bradyzoites extracellular, 2 days
MCP4-Ty
GRA1
Merge
C
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ME49Δasp5Δku80 MCP4-3Ty
Tachyzoites 30 hrs
Bradyzoites 14 days
MCP4-Ty
DBA
Merge
GAP45
D
RHLVD
(TASP21) GRA68
38 kDa
SP
Tachy
Brady
GRA68-3Ty
GRA68-3Ty
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WT WT KO KO
170
130
100
70
55
40
35
25
GRA68-3Ty
57
Catalase
E
ME49Δku80 GRA68-3Ty
Tachyzoites extracellular
GRA68-Ty
GRA1
Merge
F
ME49Δku80 GRA68-3Ty
ME49Δasp5Δku80 GRA68-3Ty
Tachyzoites 30 hrs
Bradyzoites 14 days
GRA68-Ty
DBA
Merge
GAP45
G
SP
Oligopeptidase F
Peptidase family M3
(TASP22) GRA69
75 kDa
Metalloproteases ("zincins"), catalytic domain
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Brady
GRA69-3Ty
GRA69-3Ty
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WT WT KO KO
170
130
100
70
55
40
35
25
GRA69-3Ty
57
Catalase
H
ME49Δku80 GRA69-3Ty
Tachyzoites extracellular
GRA69-Ty
GRA1
Merge
I
ME49Δku80 GRA69-3Ty
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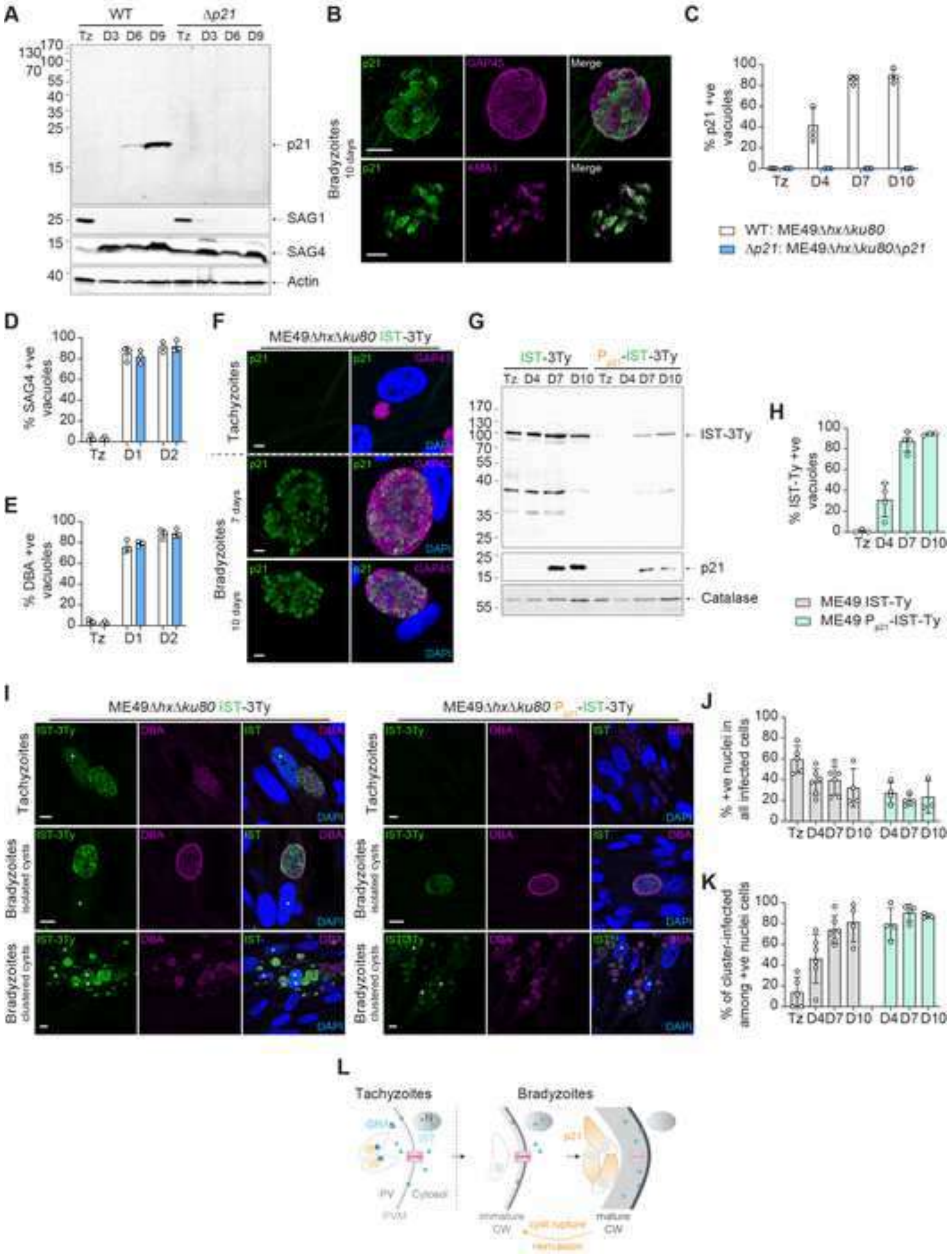
DBA
Merge
GAP45

Fig 4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p21
25
SAG1
15
SAG4
40
Actin
B
Bradyzoites 10 days
p21
GAP45
Merge
p21
AMA1
Merge
C
% p21 +ve vacuoles
100
80
60
40
20
0
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D
% SAG4 +ve vacuoles
Tz D1 D2
E
% DBA +ve vacuoles
Tz D1 D2
F
ME49ΔhxΔku80 IST-3Ty
Tachyzoites
Bradyzoites
7 days
10 days
p21
GAP45
DAPI
G
IST-3Ty
P p21-IST-3Ty
Tz D4 D7 D10 Tz D4 D7 D10
IST-3Ty
p21
Catalase
H
% IST-Ty +ve vacuoles
Tz D4 D7 D10
ME49 IST-Ty
ME49 P p21-IST-Ty
I
ME49ΔhxΔku80 IST-3Ty
ME49ΔhxΔku80 P p21-IST-3Ty
Tachyzoites
Bradyzoites isolated cysts
Bradyzoites clustered cysts
IST-3Ty
DBA
IST
DAPI
J
% +ve nuclei in all infected cells
Tz D4 D7 D10 D4 D7 D10
K
% of cluster-infected among +ve nuclei cells
Tz D4 D7 D10 D4 D7 D10
L
Tachyzoites
Bradyzoites
GRAs
N
IST
PV
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PVM
p21
immature CW
mature CW
cyst rupture
reinvasion

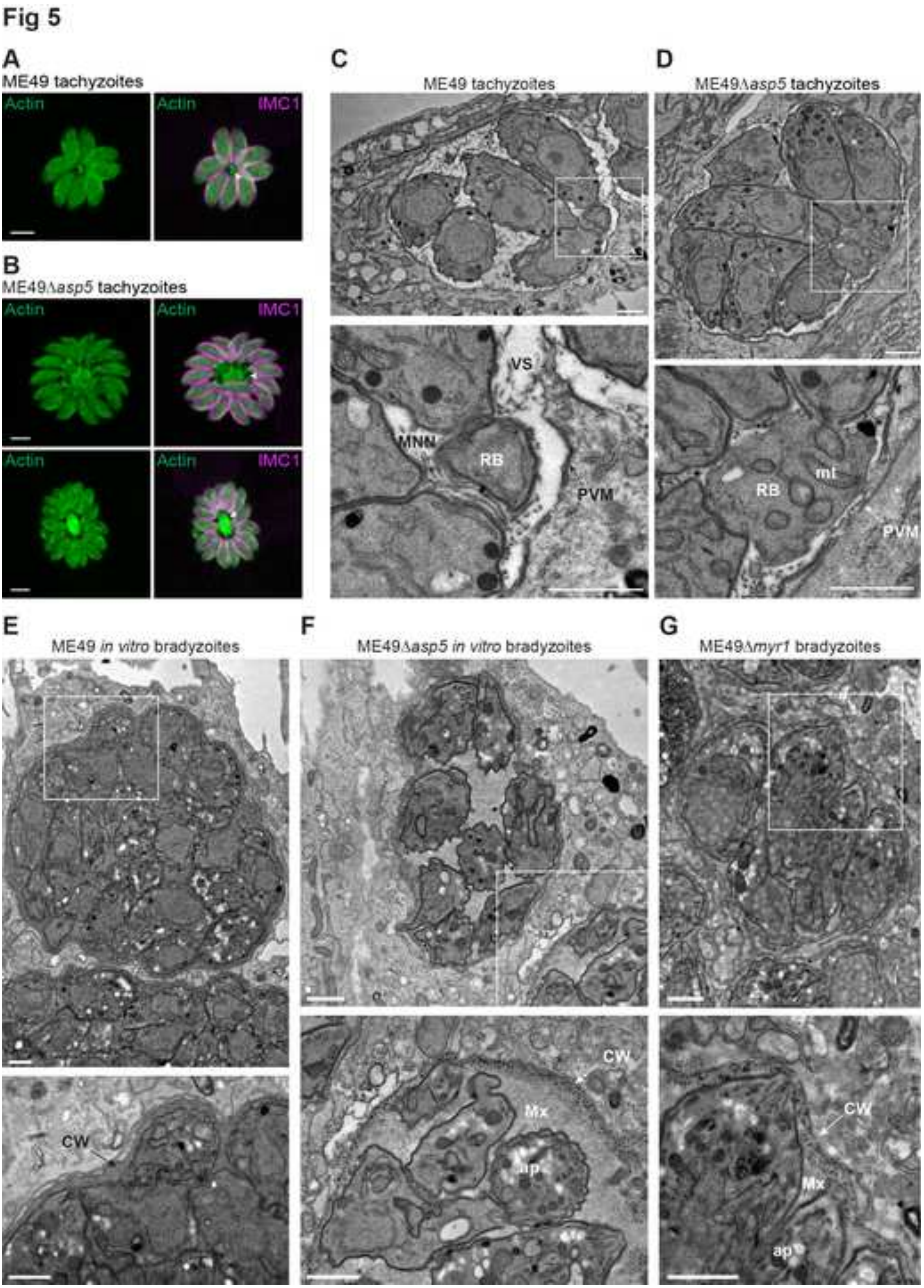
Fig 5
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Actin
Actin
IMC1
B
ME49Δasp5 tachyzoites
Actin
Actin
IMC1
Actin
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IMC1
C
ME49 tachyzoites
VS
MNN
RB
PVM
D
ME49Δasp5 tachyzoites
RB
mt
PVM
E
ME49 in vitro bradyzoites
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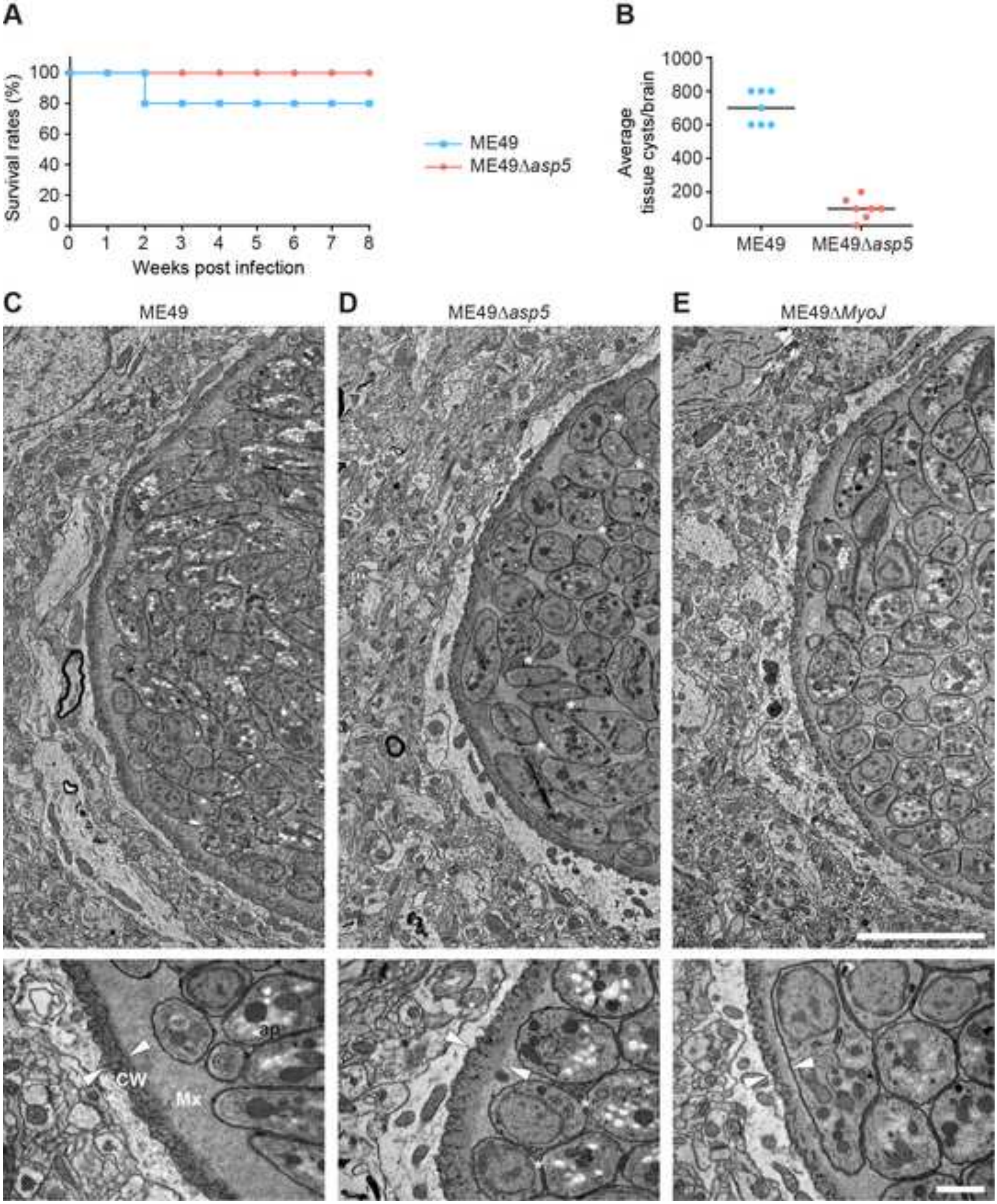
Fig 6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Survival rates (%)
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80
60
40
20
0
0
1
2
3
4
5
6
7
8
Weeks post infection
ME49
ME49Δasp5
B
Average tissue cysts/brain
1000
800
600
400
200
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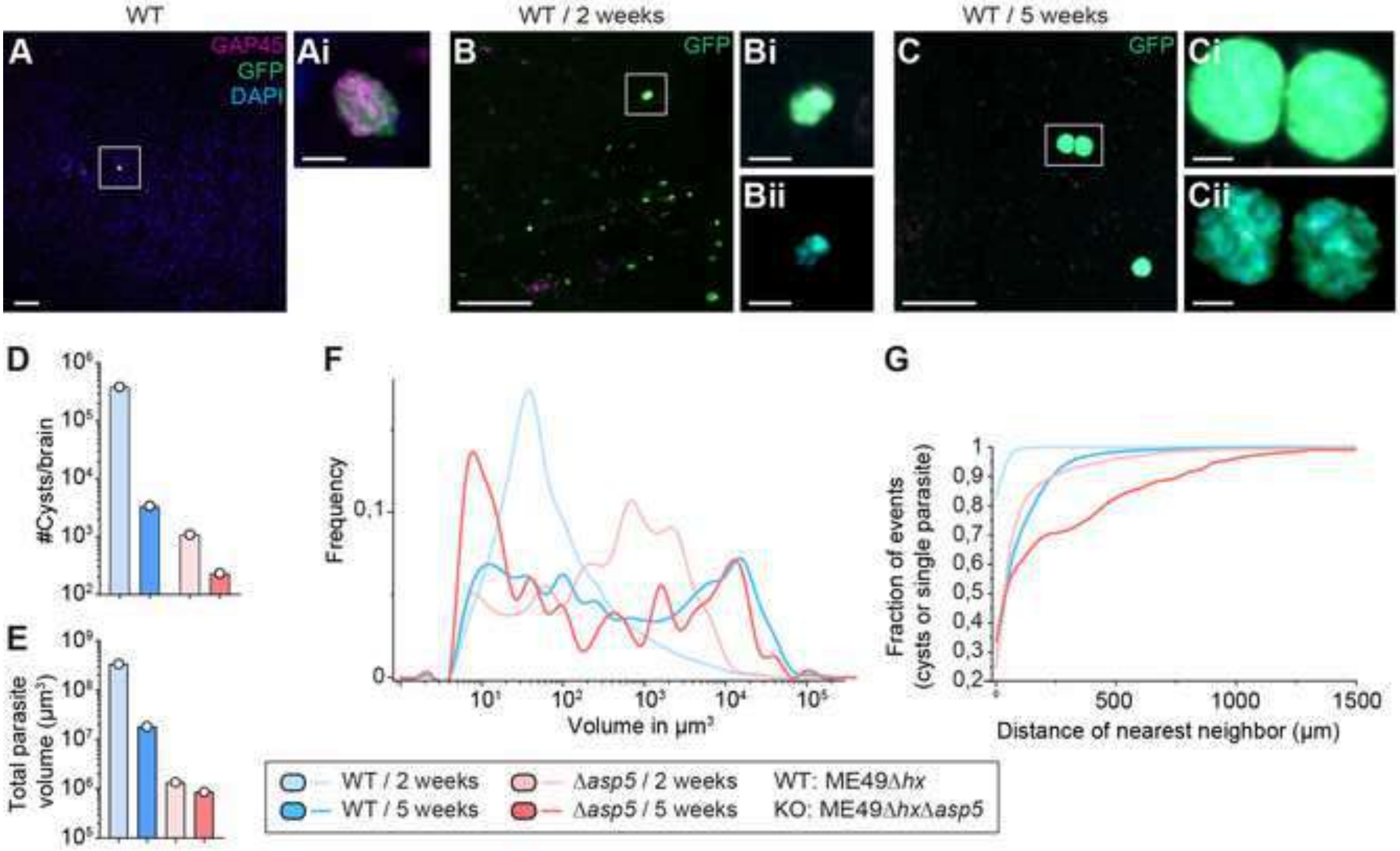
CW
Mx

Fig 7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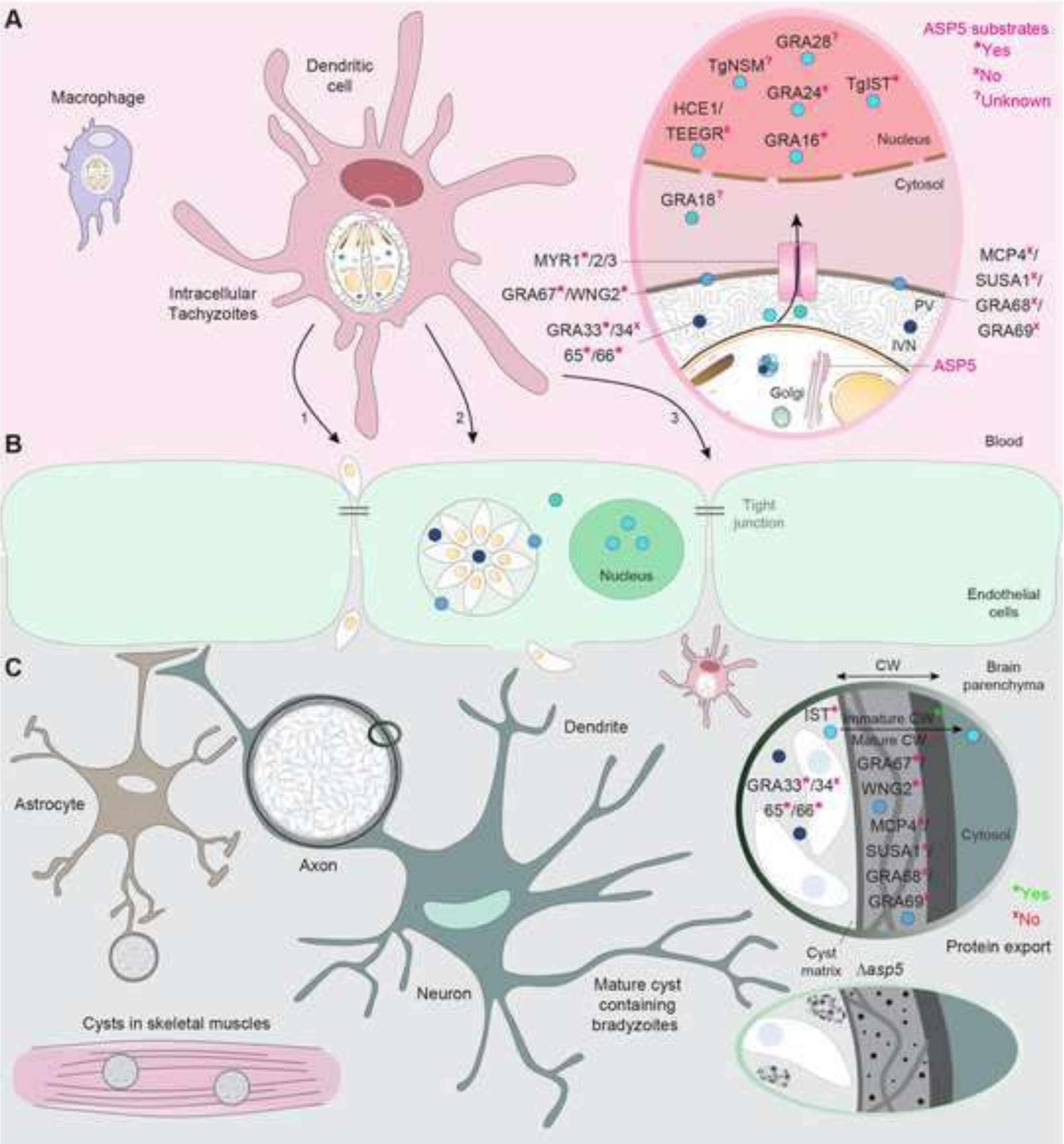
GAP45
GFP
DAPI
Ai
WT / 2 weeks
B
GFP
Bi
Bii
WT / 5 weeks
C
GFP
Ci
Cii
D
#Cysts/brain
10^6
10^5
10^4
10^3
10^2
E
Total parasite volume (µm³)
10^9
10^8
10^7
10^6
10^5
F
Frequency
0,1
0
10^1
10^2
10^3
10^4
10^5
Volume in µm³
G
Fraction of events (cysts or single parasite)
1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0
500
1000
1500
Distance of nearest neighbor (µm)
WT / 2 weeks
WT / 5 weeks
Δ*asp5* / 2 weeks
Δ*asp5* / 5 weeks
WT: ME49Δ*hx*
KO: ME49Δ*hx*Δ*asp5*

Fig 8


A
Macrophage
Dendritic cell
Intracellular Tachyzoites
ASP5 substrates
*Yes
*No
?Unknown
GRA28$^{?}$
TgNSM$^{?}$
GRA24*
TgIST*
HCE1/ TEEGR*
GRA16*
Nucleus
Cytosol
GRA18$^{?}$
MYR1*/2/3
GRA67*/WNG2*
GRA33*/34^{x}
65*/66*
MCP4^{x}/
SUSA1^{x}/
GRA68^{x}/
GRA69^{x}
PV
IVN
ASP5
Golgi
1
2
3
B
Blood
Tight junction
Nucleus
Endothelial cells
C
Astrocyte
Axon
Dendrite
Neuron
Cysts in skeletal muscles
Mature cyst containing bradyzoites
CW
Brain parenchyma
IST*
Immature CW
Mature CW
GRA67*
WNG2*
GRA33*/34*
65*/66*
MCP4*/
SUSA1*/
GRA68*/
GRA69*
Cytosol
*Yes
*No
Protein export
Cyst matrix
Δasp5

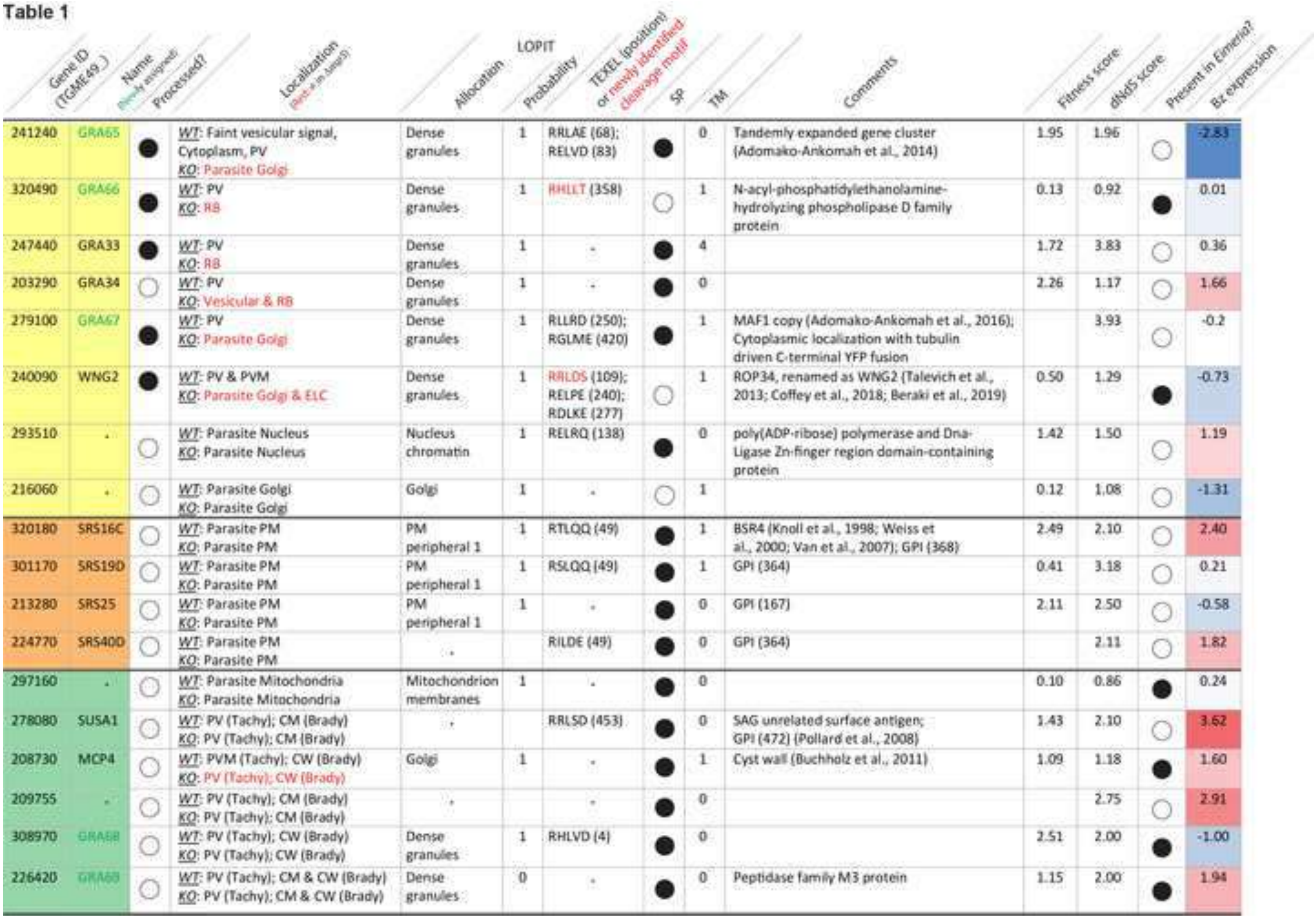


Table 1

Gene ID (TGME49_)	Name (Newly assigned)	Processed?	Localization (Red: ≠ in Δasp5)	LOPIT		TEXEL (position) or newly identified cleavage motif	SP	TM	Comments	Fitness score	dNdS score	Present in Eimeria?	Bz expression
				Allocation	Probability								
241240	GRA65	●	*WT*: Faint vesicular signal, Cytoplasm, PV *KO*: Parasite Golgi	Dense granules	1	RRLAE (68); RELVD (83)	●	0	Tandemly expanded gene cluster (Adomako-Ankomah et al., 2014)	1.95	1.96	○	-2.83
320490	GRA66	●	*WT*: PV *KO*: RB	Dense granules	1	RHLLT (358)	○	1	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein	0.13	0.92	●	0.01
247440	GRA33	●	*WT*: PV *KO*: RB	Dense granules	1	-	●	4		1.72	3.83	○	0.36
203290	GRA34	○	*WT*: PV *KO*: Vesicular & RB	Dense granules	1	-	●	0		2.26	1.17	○	1.66
279100	GRA67	●	*WT*: PV *KO*: Parasite Golgi	Dense granules	1	RLLRD (250); RGLME (420)	●	1	MAF1 copy (Adomako-Ankomah et al., 2016); Cytoplasmic localization with tubulin driven C-terminal YFP fusion		3.93	○	-0.2
240090	WNG2	●	*WT*: PV & PVM *KO*: Parasite Golgi & ELC	Dense granules	1	RRLDS (109); RELPE (240); RDLKE (277)	○	1	ROP34, renamed as WNG2 (Talevich et al., 2013; Coffey et al., 2018; Beraki et al., 2019)	0.50	1.29	●	-0.73
293510	-	○	*WT*: Parasite Nucleus *KO*: Parasite Nucleus	Nucleus chromatin	1	RELRQ (138)	●	0	poly(ADP-ribose) polymerase and Dna-Ligase Zn-finger region domain-containing protein	1.42	1.50	○	1.19
216060	-	○	*WT*: Parasite Golgi *KO*: Parasite Golgi	Golgi	1	-	○	1		0.12	1.08	○	-1.31
320180	SRS16C	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	RTLQQ (49)	●	1	BSR4 (Knoll et al., 1998; Weiss et al., 2000; Van et al., 2007); GPI (368)	2.49	2.10	○	2.40
301170	SRS19D	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	RSLQQ (49)	●	1	GPI (364)	0.41	3.18	○	0.21
213280	SRS25	○	*WT*: Parasite PM *KO*: Parasite PM	PM peripheral 1	1	-	●	0	GPI (167)	2.11	2.50	○	-0.58
224770	SRS40D	○	*WT*: Parasite PM *KO*: Parasite PM	-		RILDE (49)	●	0	GPI (364)		2.11	○	1.82
297160	-	○	*WT*: Parasite Mitochondria *KO*: Parasite Mitochondria	Mitochondrion membranes	1	-	●	0		0.10	0.86	●	0.24
278080	SUSA1	○	*WT*: PV (Tachy); CM (Brady) *KO*: PV (Tachy); CM (Brady)	-		RRLSD (453)	●	0	SAG unrelated surface antigen; GPI (472) (Pollard et al., 2008)	1.43	2.10	○	3.62
208730	MCP4	○	*WT*: PVM (Tachy); CW (Brady) *KO*: PV (Tachy); CW (Brady)	Golgi	1	-	●	1	Cyst wall (Buchholz et al., 2011)	1.09	1.18	●	1.60
209755	-	○	*WT*: PV (Tachy); CM (Brady) *KO*: PV (Tachy); CM (Brady)	-		-	●	0			2.75	○	2.91
308970	GRA68	○	*WT*: PV (Tachy); CW (Brady) *KO*: PV (Tachy); CW (Brady)	Dense granules	1	RHLVD (4)	●	0		2.51	2.00	●	-1.00
226420	GRA69	○	*WT*: PV (Tachy); CM & CW (Brady) *KO*: PV (Tachy); CM & CW (Brady)	Dense granules	0	-	●	0	Peptidase family M3 protein	1.15	2.00	●	1.94

S4 Figure

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