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Label-free proteomic analysis reveals differentially expressed *Wolbachia* proteins in *Tyrophagus putrescentiae*: Mite allergens and markers reflecting population-related proteome differences

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ABSTRACT

Tyrophagus putrescentiae is an astigmatid mite of great economic, medical and veterinary importance. The microbiome, especially intracellular bacteria, may affect allergy/allergen expression. We targeted *Wolbachia* proteins, allergen comparisons and markers in *Wolbachia*–mite interactions in three mite populations. A decoy database was constructed by proteogenomics using the *T. putrescentiae* draft genome, *Wolbachia* transcriptome assembly and current *T. putrescentiae*-related sequences in GenBank. Among thousands of mite-derived proteins, 18 *Wolbachia* proteins were reliably identified. We suggest that peroxiredoxin, bacterioferritin, ankyrin repeat domain-containing protein and DegQ family serine endoprotease indicate a higher-level bacterium–bacterium–host interaction. We produced evidence that the host–*Wolbachia* interaction is modulated through pattern recognition receptors (PRRs), mannose-binding lectins/mannose receptors, the cholinergic anti-inflammatory pathway with TNF-α, and others. We observed Tyr p 3 suppression in mites with *Wolbachia*, linking trypsin to PRR modulation. Nine out of the 12 current WHO/IUIS official allergens were reliably identified, but the remaining three allergens, Tyr p 1, 8 and 35, were detected as only trace hits. This study provides numerous markers for further *Wolbachia*–host interaction research. For accuracy, mite allergens should be considered according to abundance in species, but mite populations/strains, as well as their microbiome structure, may be key factors.

Significance: The astigmatid mites occurring in homes are significant producers of allergens that are highly dangerous to humans and domesticated animals. Mites are tightly associated with microorganisms that affect their biology and consequently allergy signatures. Mite populations were found to be infected with certain intracellular bacteria, but some populations lacked an intracellular bacterium. Our previous research showed that some populations of *Tyrophagus putrescentiae* are infected with *Wolbachia*, but some populations host additional bacteria of interest. Thus, there are not only interactions between the mites and *Wolbachia* but also likely an additional level of interaction that can be found in the interaction between different bacteria in the mites. These "higher-level" signatures and consequences that bacteria affect, including allergen production, are not understood in mites. In this study, we identified *Wolbachia*-specific proteins in mites for the first time. This study provides *Wolbachia*- and mite-derived markers that can be clues for describing "higher-level" mite-bacterium-bacterium interactions. Indeed, the microbiome contribution to allergies can potentially be derived directly from bacterial proteins, especially if they are abundant.

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1. Introduction

Many astigmatid (Acari: Astigmata) mite species infest human-created habitats. These so-called domestic mites form two groupings, house-dust mites (HDMs) and stored-product mites (SPMs) [1,2]. Astigmatid mite species greatly differ in their relative importance from medical, veterinary and economic perspectives. The cosmopolitan generalist species *Tyrophagus putrescentiae* (Schrank, 1781) combines all these properties, occurring in stored products and house dust and having great medical, veterinary, and economic importance. This species commonly infests various food products for human and animal consumption [3], and it is also common in house dust, causing allergies [4]. *T. putrescentiae* is a serious health hazard at home and in the workplace, having significant cross reactivity with other core HDMs in humans and domestic animals [4–9]. The main dangers regarding the fast reproduction and consequent spread of *T. putrescentiae* consist of foods or feeds with high protein and fat contents; a particularly notable example of the occurrence and rapid spread of *T. putrescentiae* is dry dog food [3,10–14]. Contaminated food/feed can promote further mite spread and allergen release throughout the house.

Currently, *T. putrescentiae* has 12 allergens recognized by WHO/IUIS [15] (see Table 1); however, it is relatively understudied compared to the two common pyroglyphid HDMs, *Dermatophagoides farinae* and *Dermatophagoides pteronyssinus* (36 and 31 allergens, respectively) [15]. A recent transcriptome analysis of *T. putrescentiae* indicated additional potential allergens having similarities to known and clinically confirmed allergens of other astigmatid mites, including *Dermatophagoides* spp. [16].

Table 1
The current list of *Tyrophagus putrescentiae* allergens in the WHO/IUIS database. We verified the allergens, and the expression patterns of these allergens at the protein level are shown in Fig. 3.

Allergen name in WHO/IUIS	Group designation (with respect to other mite groups)	Biochemical name	NCBI/ GenBank version	Definition in NCBI-protein	CCDs	Allergenicity reference (PubMed)	Last updated	Comments
Tyr p 1		cysteine protease	ABM53753.1	mite allergen Tyr p 1 [*Tyrophagus putrescentiae*]	Peptidase_C1A; Inhibitor_I29	32887361	2020-09-08	*
Tyr p 2		NPC2 family	CAA73221.1	group 2 allergen [*Tyrophagus putrescentiae*]	Der-p2_like	7982124	2019-09-27	
Tyr p 3		trypsin	ABZ81991.1	Tyr p 3 [*Tyrophagus putrescentiae*]	Tryp_SPc	19339798	2019-09-27	
Tyr p 7		bactericidal permeability-increasing protein	ABM53750.1	mite allergen Tyr p 7 [*Tyrophagus putrescentiae*]	Grp7_allergen s.f.	32887361	2020-09-08	**
Tyr p 8		glutathione S transferase	AGG10560.1	Tyr p 8 allergen [*Tyrophagus putrescentiae*]	GST_C_family s.f.; GST_N_Mu	23365207	2020-01-20	
Tyr p 10		tropomyosin	AAT40866.1	tropomyosin, partial [*Tyrophagus putrescentiae*]	Tropomyosin	17584167	2019-09-27	
Tyr p 13		fatty-acid binding protein	AAU11502.1	fatty acid-binding protein [*Tyrophagus putrescentiae*]	FABP_Der_p_13-like	15879018	2020-05-14	
Tyr p 20		arginine kinase	32887362	*Tyrophagus putrescentiae* arginine kinase mRNA, complete CDS		32887361	2020-09-08	***
			32887363	arginine kinase [*Tyrophagus putrescentiae*]	arginine_kinase_like			
Tyr p 28		heat shock protein	AOD75395.1	heat shock-like protein [*Tyrophagus putrescentiae*]	PTZ00009 s.f.	27496383	2019-09-27	
Tyr p 34	**Tyr p 39**	troponin C	ACL36923.1	troponin C [*Tyrophagus putrescentiae*]	PTZ00184 s.f.	19786801	2019-09-27	****
Tyr p 35	**new group (?! Tyr p 35 ~ Der f Alt a 10)**	aldehyde dehydrogenase	AOD75396.1	aldehyde dehydrogenase-like protein [*Tyrophagus putrescentiae*]	ALDH_F1AB_F2_RALDH1	27496383	2019-09-27	
Tyr p 36		profilin	AOD75399.1	profilin-like protein [*Tyrophagus putrescentiae*]	Profilin	27496383	2019-09-27	

Important notes: 1) Troponin C is denoted as Der f 39 among *D. farinae* allergens. Thus, Tyr p 34 should be renamed to Tyr p 39 to be consistent with current allergen nomenclature. 2) Tyr p 35 should functionally be an aldehyde dehydrogenase because the sequence is similar to Der f Alt a 10 (AAP35081.1). In contrast, Der f 35 (BAX34757.1; header group II allergen) has a different CCD – ML super family. Thus, Tyr p 35 and Der f 35 are functionally different allergens whose nomenclature needs to be revised. 3) In the WHO/IUIS allergen database, Tyr p 20 is identified by an mRNA sequence (MT900252) instead of a protein sequence (should be QOI58528).

Comments at www.allergen.org: * (posted: 08 Sep 2020) Sequenced originally by FT Chew in ~2008. Then, the work by Liao. It is not clear whether this is a pre-pro sequence that will be reduced in processing, and then be at 25 kDa. Based on the sequence, it should be >31 kDa. The authors did not show the sequence in their MDPI 8 Sept 2020 publication. They do not claim to have tested the aa sequence; ** (posted: 08 Sep 2020) Sequences originally by FT Chew but not published. PCR cloning by Liao, but sequences not confirmed in publication, only in submission; *** (posted: 13 Sep 2020) cDNA sequence and predicted aa sequence in submission. Not for public view until published. High identity to Der p 20 and Blo t 20. Two peptides of recombinant protein determined by LC-MS/MS; **** (posted: 07 Dec 2015) The designation of troponin C of *T. putrescentiae* was changed to Tyr p 34 (from Tyr p 24) on 7 Dec 2015 to provide a consistent number for troponin C across mites (e.g., HDMs).

Recent advances in high-throughput omics technologies have facilitated the study of mite biology and the selection of important markers, including contributions to understanding the causes of allergies. The key step is obtaining genome or transcriptome sequences to study their presence at the protein level for functional comparison to the RNA or DNA level [17–21]. However, the study at the proteome level is limited to sequences actually present in the database; thus, some proteomics studies performed on the different astigmatid mites have been able to identify only relevant portions of sequenced proteins (e.g., [22–27]). A specific and highly effective approach that combines the utilization of sequences of the transcriptome or genome is proteogenomics [28,29]. For instance, a proteogenomics approach has been recently used to analyze males and females of *D. farinae* [17]. Here, we applied the proteogenomics approach to three *T. putrescentiae* populations that differ in the various microbiomes that they harbor [16]. Astigmatid mites are tightly associated with microorganisms and bacteria, which are important components in the nutritional biology of mites [24,30–32]. In addition to the bacteria that are present in the diet and serve as a food source or facilitate digestion of food matrices for *T. putrescentiae* [24,31], there are populations of *T. putrescentiae* hosting intracellular bacteria that should impact the biology of the mite [16,33,34].

In this study, we performed a proteogenomics analysis of *T. putrescentiae* by using our draft genome (GenBank accession: JAAALH000000000; BioSample: SAMN13712654) and sought to identify proteome differences, with a particular focus on allergens and markers associated with the population-specific microbiome. In addition, we aimed to identify *Wolbachia* proteins in mites.

2. Materials and methods

2.1. Mites

In this study, three populations of *T. putrescentiae* with a known microbiome were analyzed (i.e., [16,34–36]). The three mite populations were characterized based on the presence or absence of endosymbionts into two groups, as follows: (i) Koppert (KOP) population with no endosymbionts and (ii) Phillips (PHI) and Dog (DOG) populations, both having abundant *Wolbachia*; DOG also hosts *Blattabacterium*-like bacteria, which are absent in PHI. DOG was sampled in the United States by J. Hubert in 2007; KOP was obtained from a grain-derived diet by E. van Baal in the Netherlands in 2012, and PHI was obtained from dog food by T. Phillips in Manhattan, KS, USA, in 2014. The mites were mass reared in tissue culture flasks on a wheat germ-derived diet (SPMd) composed of blended oat flakes, wheat germ, and dried yeast extract, as previously described [31]. Mites (a mixture of adults with juveniles) were sampled from approximately 28-day-old cultures when populations were in exponential growth [37,38]. Live mites were collected from flask surfaces and plugs by brushing and placed into sterile Eppendorf tubes. This method is more suitable than flotation of mites to prevent mite bodies from becoming contaminated with spent growth medium and dead mites [23,39].

2.2. nanoLC-MS/MS analysis

Two homogenization procedures were performed – one with a glass homogenizer (for the 3 × 6 dataset) and the second with beads/shards (for the 3 × 3 dataset). The latter was used due to its potential higher yield of bacterial proteins. In both methods, 6–7 mg of pure mites was used in each replicate. The mites were homogenized in 100 mM triethylammonium bicarbonate buffer (TEAB; cat. No. 17902, Fluka, Sigma-Aldrich, St. Louis, MO, USA) containing 2% *w/v* sodium deoxycholate (SDC; cat. No. 30970, BioXtra, Sigma-Aldrich). The first homogenization (for the 3 × 6 dataset) was performed using glass Potter-Elvehjem tissue grinders with a Teflon pestle (Kartell Labware division, Noviglio, Italy) with driving force. Samples were then centrifuged for 10 min at 3000 x*g* at 4 °C, and the supernatant was collected. In the second homogenization procedure (for the 3 × 3 dataset), the mites were homogenized using a mini-BeadBeater 16 grinder (BioSpec Products, Bartlesville, OK, USA). Homogenization was performed in APEX Screw-Cap Microcentrifuge Tubes (2.0 mL, cat. No. CP5912, Alpha Laboratories, UK) filled with 200 mg of 0.3 mm (cat. No. 11079103gar, BioSpec) and 200 mg of 1.0 mm (cat. No. 11079110gar, BioSpec) diameter garnet sharp particles and glass beads with diameters ranging from 2.85–3.45 mm (cat. No. R155761, Carl Roth, Germany). In the first step, the samples were homogenized for 5 min in mini-BeadBeater 16, incubated for 5 min at 95 °C and then again homogenized for 5 min. Then, the samples were centrifuged for 10 min at 3000 x*g* at 4 °C, and the supernatant was collected.

Six biological replicates per *T. putrescentiae* population were prepared using the Potter-Elvehjem homogenization method, while three biological replicates per mite population were prepared using bead homogenization. The samples were further processed, and nLC-MS/MS was applied in the same way as described elsewhere [40]. Every sample was analyzed on an Orbitrap Fusion Tribrid mass spectrometer (Thermo, Waltham MA, USA). Thus, we obtained 18 (3 × 6 – populations X biological replicates) and 9 (3 × 3 – populations X biological replicates) raw datasets that were further evaluated.

2.3. Creation of a proteomic search database

Overall, we created a search database consisting of four protein *.fasta files for the complex proteogenomic analysis of mite proteins and to ascertain the proteins of the intracellular bacterium *Wolbachia*. First, we used our mite genomic assembly with both mitochondrial and nuclear contigs (GenBank: JAAALH010000000 (nuclear genome)); the mitochondrial genome can be found in GenBank under entry CM022443. The genomic *.fasta file was translated using a six-frame translation tool, with a minimal length output of 50 amino acids (aa), in MaxQuant [41]. We received a very large sequence set consisting of a total of aa 897,136 sequences. All these sequences were further processed in OmicsBox v1.4.11 (Biobam, Valencia, Spain). Annotation was performed using the Blastp tool with an expectation e-value of $1.0E^{-3}$ against the current (10 Oct 2020) nonredundant protein sequence database version 5 (nr v5) with the Arthropoda taxonomy (NCBI: txid6656). The BLAST-identified sequences were further functionally annotated by Gene Ontology (GO) and mapped by application of the InterPro pipeline [42]. Second, we used our "*Wolbachia* endosymbiont of *Tyrophagus putrescentiae*" transcriptome assembly (TSA: GIJY01). It had 4297 proteins inferred and annotated as above but with the Bacteria taxonomy filter (NCBI:txid2). Third, we downloaded the current (24 Oct 2020) *T. putrescentiae* sequences from GenBank. Note that we appended the "gi" accession numbers to the protein sequences to facilitate comparison with earlier studies. The 331 retrieved sequences composed the third fasta file for data evaluation. In addition, we downloaded 34,694 protein sequences from the most recent (24 Oct 2020) "*Rhagoletis zephyria*" annotation (BioProject: PRJNA331175, assembly: GCF_001687245.1), and we again appended "gi" in the fasta headers. This assembly has a significant portion of *T. putrescentiae* DNA; the mite probably contaminated the fly culture and was cosequenced with the insect (see [16]).

2.4. Overall proteomic data evaluation

The raw mass spectrometry data for the two datasets (3 × 6 and 3 × 3) were analyzed and quantified with label-free quantification (LFQ) algorithms in MaxQuant v1.6.17.0 [41] with the Andromeda search engine [43]. The applied key parameters were a false discovery rate (FDR) of 0.01 for both proteins and peptides, digestion: trypsin/P, and fixed modification: MethylThio, while variable modifications were set as methionine oxidation and N-terminal protein acetylation. The two raw datasets were independently searched against a database consisting of

the four *.fasta files we created (see above). The databases and search criteria details are available along with our raw data files. The LFQ intensities were analyzed in the Perseus v1.6.14.0 environment [44]. In both datasets, hits identified as common contaminants and those identified only by site and reverse hits were removed. The datasets were then log2 transformed, and reduction to at least three and two positives of valid values was applied for the 3 × 6 and 3 × 3 datasets, respectively. Furthermore, the data were processed by two algorithms when the missing values were replaced by zero, or the missing values were replaced from a normal distribution (width 0.3; downshift = 1.8) and further *Z*-score transformed.

Proteins identified as *Wolbachia*-derived were selected and denoted in the complete list of proteins, and the relative abundance of these protein hits was illustrated as a heatmap. We also identified protein hits related to WHO/IUIS official allergens of *T. putrescentiae* [15]. Furthermore, Spearman rank correlation was applied to compare proteomes of the two populations hosting *Wolbachia* (DOG and PHI) and the *Wolbachia*-free population (KOP). Based on this analysis using *Z*-score transformed data, selected markers that were all significant at FDR = 0.01 and -log *p* value was higher than 5. The comparison of major changes in DOG vs. KOP, PHI vs. KOP and DOG vs. PHI was visualized in heatmaps.

3. Results

3.1. T. putrescentiae database created from the draft genome

The annotation process of 897,136 protein sequences retrieved from the *T. putrescentiae* draft genome provided 49,317 BLAST-identified sequences, and 27, 487 and 35,488 sequences were successfully annotated and mapped, respectively. All 49,317 BLAST-identified sequences served as one component of a database search in the LC-MS/MS data evaluation. The BLAST hit distribution was highest for five arthropod species: *D. pteronyssinus* (49,916 hits), "*R. zephyria*" (42,406), *Euroglyphus maynei* (26,668), *Sarcoptes scabiei* (25,988), and *Limulus polyphemus* (22,864). However, unique, top-scoring BLAST matches were highest for "*R. zephyria*" (21,013 hits), followed by *D. pteronyssinus* (8309 hits). See Fig. 1A for more details. Statistics on the direct GO counts of biological process (BP), cellular component (CC) and molecular function (MF) are given in Fig. S1A-C.

3.2. Wolbachia endosymbiont database created from the transcriptome assembly

Out of 4297 sequences (≥50 aa) retrieved from the *Wolbachia* of *T. putrescentiae* transcriptome assembly, 1355 returned a BLAST hit, 890 were mapped and 756 were annotated. The 1355 sequences with a BLAST hit were used in the database. The most common BLAST hits had the following taxonomies: *Wolbachia* (4005 hits), *Wolbachia pipientis* (3545) and *Wolbachia* endosymbiont of *Dactylopius coccus* (897); "*R. zephyria*" had only 77. The distribution of top-scoring BLAST matches was as follows: *Wolbachia* sp. (155 hits), *Wolbachia* (112), *W. pipientis* (98), *Wolbachia* endosymbiont of *Folsomia candida* (96), and "*R. zephyria*" (67 hits). See Fig. 1B for more details. Statistics on the direct GO counts of BP, CC and MF are given in Fig. S2A-C.

3.3. Key Wolbachia GO annotations – The importance of nitrogen metabolism

GO functional annotation of the multiple sequences indicated a wide variety of biological processes in *Wolbachia*. We can highlight that peptidoglycan biosynthetic processes and protoporphyrinogen IX biosynthetic processes (Fig. S2A) were identified [45]. Among the annotated proteins was protoporphyrinogen oxidase HemJ (GIJY01000098.1_True_3391). Furthermore, the nitrogen compound metabolic process GO: 0006807 was most important according to the number sequences (366); this process was directly linked to the organonitrogen compound metabolic process GO: 1901564 (263 sequences) and the cellular nitrogen compound metabolic process GO: 0034641 (284 sequences) (see Figs. S3 and S4).

3.4. Overall proteomic identifications

The search through the complex database provided 6860 and 4026 protein hits in the 3 × 6 and 3 × 3 datasets, respectively. After removal of trace hits (see above), the number of hits was reduced to 3641 and 2334, respectively; a full list of protein hits is shown in Tables S1 and S2. A comparison of how the histograms with LFQ intensities in the 3 × 6 and 3 × 3 datasets and counts changed after trace hit removal is shown in Figs. S5 and S6, respectively. Overall, the extraction procedure used on the 3 × 6 dataset was more efficient than the sample preparation used on the 3 × 3 dataset, which was applied in an attempt to identify more *Wolbachia*-specific proteins.

3.5. Abundance of Wolbachia proteins

Wolbachia protein hits that passed our cutoff threshold and were then verified individually are listed in Tables S1 and S2 for both datasets. In the 3 × 6 and 3 × 3 datasets, 16 and 12 *Wolbachia*-specific protein hits were reliably identified, respectively. The relative intensities of these protein hits are illustrated in Fig. 2A, B. Thus, the two different homogenization procedures gave different results to some extent. Although more *Wolbachia*-specific protein hits were identified in the 3 × 6 dataset, in the 3 × 3 dataset, two different proteins (GIJY01000081.1_False_1260 cold-shock protein and GIJY01000018.1_False_3987 transcription elongation factor GreA) were identified. We were not able report these two proteins from the 3 × 6 dataset due to the applied cutoff threshold. *Wolbachia* protein hits prior to the application of the cutoff filter can be found in Tables S3 and S4.

3.6. WHO/IUIS official T. putrescentiae allergens

The relative abundances of the 12 currently registered WHO/IUIS *T. putrescentiae* allergens (Table 1) in the three mite populations are shown in Fig. 3. Of these allergens, 9 and 8 allergens were reliably identified in the 3 × 6 (Fig. 3A) and 3 × 3 (Fig. 3B) datasets, respectively. Thus, the homogenization procedure also affected identification success for allergens. The remaining 3 allergens (aldehyde dehydrogenase aka Tyr p 35, Tyr p 8, and Tyr p 1) were found only as trace hits in the 3 × 6 dataset (Table S3). In the 3 × 3 dataset, Tyr p 8 was present as a trace hit (Table S4), while Tyr p 35 and 1 were not found as traces. Some protein hits that relate to allergen-like proteins creating important proteome differences in mite populations can also be found in Figs. 4–6 among the most statistically significant results or in the supplementary materials (Tables S1–S4).

There was an obvious difference in Tyr p 3 abundance among the three *T. putrescentiae* populations (Fig. 3). Importantly, Tyr p 3 was not detected in the DOG population, while in the KOP population, Tyr p 3 was detected in all samples of both the 3 × 6 and 3 × 3 datasets. The detection success was low in the PHI population since 2 of 6 positives were in the 3 × 6 dataset and 1 of 3 positives was in the 3 × 3 dataset.

Detection of Tyr p 36 affected sample processing for proteomic analysis because it was not detected in any sample of the 3 × 3 dataset. However, in the 3 × 6 dataset, it was detected in all three mite populations, but the fact that it was detected in 5 of 6 replicates in PHI, in 4 of 6 replicates in DOG, and only in 2 of 6 replicates in KOP indicates variation with microbiome.

For easier comparison of identity and similarity between some allergens, we provide alignments for selected sequences in supplementary materials. The alignments are provided for (i) Tyr p 35 (GenBank: AOD75396.1) and Der f Alt a 10 (GenBank: AAP35081.1) – identity 67.4% and similarity 81.4% (Fig. S7); (ii) Tyr p 34 (GenBank:

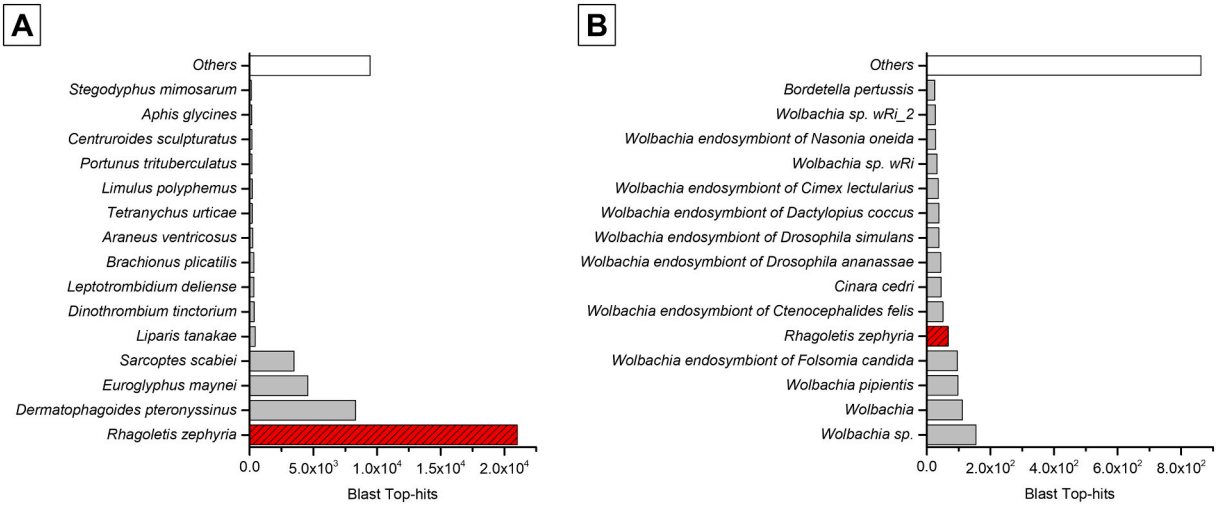


Fig. 1. The top-hit species distribution for BLAST-identified protein sequences from the A) *Tyrophagus putrescentiae* draft genome and B) *Wolbachia* endosymbiont of the *T. putrescentiae* transcriptome assembly. The taxa provided are as presented they were obtained after the Blastp search.
Only the first 15 taxa are shown. Others = 2223 taxa for *T. putrescentiae* and 307 taxa for *Wolbachia*. Our data indicate that the GenBank genome of "*Rhagoletis zephyria*" is contaminated with DNA of the mite and its *Wolbachia* endosymbiont.

ACL36923.1) and Der f 39 (GenBank: QBF67841.1) – identity 95.4% and similarity 97.4% (Fig. S8); Tyr p 3 (GenBank: ABZ81991.1) and Der f 3 (GenBank: BAA09920.1) – identity 41.4% and similarity 57.5% (Fig. S9); Tyr p 1 (GenBank: ABM53753.1), Der f 1 (GenBank: BAC53948.1) and Der p 1 (GenBank: AAB60215.1) – the percent identity for Tyr p 1 and the other two sequences is only approximately 30% and the comparison also indicates aa deletions (Fig. S10).

3.7. Candidate for Tyr p 6 allergen

We also found a predicted candidate for Tyr p 6, which had the header PREDICTED: mite allergen Der f 6-like (GenBank: XP_017489831.1); using this sequence, the protein hit was detected with a similar abundance in all three *T. putrescentiae* strains (Tables S1 and S2).

3.8. Protein hits accounting for differences in immunity among mite populations

Selection of the major differences allowed combined data evaluation through the *Z*-score normalized data and when the nondetected results were considered. The most important markers that are indicative of the differentially affected immune pathways can be found in Figs. 4–6, showing the most statistically significant markers between pairs of mite populations. We also considered qualitative differences those that were not identified in the three mite populations. This relates especially to the identification of *Wolbachia*-specific proteins (Fig. 2) and WHO/IUIS approved [15] allergens (Fig. 3). Based on these results, we were able to identify markers that relate to pathways in mites that can affect the presence of *Wolbachia* in the mite population.

A very important protein hit is trypsin allergen Tyr p 3, but results indicating similar proteins are also of high interest. The protein hit Der f 3 allergen (NODE_1869_length_12928_cov_668.109920_True_8049) was detected only in KOP. However, Der f 3-like (GenBank: XP_017493899.1; XP_017461571.1; XP_017488578.1; NODE_1763_length_13579_cov_643.766933_False_10728) and trypsin-1 (NODE_1869_length_12928_cov_668.109920_True_8601) were similar in the three populations (Tables S1–S4).

The next important markers inferred from the visual comparisons of the most significant protein hits (Figs. 4–6). Among the most significant markers can be selected C-type lectin lectoxin-Lio1, cholinesterase 1-like, lysosomal alpha-mannosidase, neprilysin/endothelin-converting enzyme, lysosomal protective protein-like, cytochrome P450s (e.g. 3A12-like and 3A11-like), cathepsins and their inhibitors/cystatin, henna-like and others. In addition, some proteins related to structure were observed among the highly significant changes.

4. Discussion

4.1. Inaccurate allergen names for Tyr p 34 (troponin C) and Tyr p 35 (Der f Alt a 10 homolog)

The WHO/IUIS official allergen database currently lists 12 allergens of *T. putrescentiae* [15]. Our revision of this allergen list revealed that in some cases, there is no agreement in *T. putrescentiae* allergen names or in those of other mite species. For the allergens Tyr p 34 (troponin C) and Tyr p 35 (aldehyde dehydrogenase), corresponding abbreviations denote different proteins, such as Der f 34 (enamine/imine deaminase; domain: TIGR00004) and Der f 35 (MD-2-related lipid recognition) [15,17,46]. Based on the *D. farinae* allergen nomenclature, the troponin C allergen "Tyr p 34" should be Tyr p 39 because Der f 39 is also troponin C, and the sequences are highly similar. The situation for Tyr p 35 is more complicated because aldehyde dehydrogenase is not among the official *D. farinae* allergens and, moreover, it is similar to Der f Alt a 10 (GenBank: AAP35081.1). Thus, a new allergen group could be created for the protein currently denoted Tyr p 35, which should then be the same for Der f Alt a 10 from *D. farinae* if it could be confirmed as an allergen. To our knowledge, to date, there is limited knowledge about Der f Alt a 10. Recombinant Der f Alt a 10 was tested by Park et al. [47], and before that study, it was identified using gel-based proteomics in 1D-E and 2D-E of affinity-purified fractions from *D. farinae* bodies, where IgE binding using human sera from allergic patients was indicated [39]. Thus, it can be suspected that the Der f Alt a 10 homolog in *T. putrescentiae* can be an allergen, which supports allergen Tyr p 35 (aldehyde dehydrogenase) placement in the WHO/IUIS database. Tyr p 35 was described as an allergen based on cDNA-produced recombinant allergen by Cui et al. [48], and our label-free proteomics analysis identified Tyr p 35 (GenBank: AOD75396.1) as only a trace hit in all three *T. putrescentiae* populations analyzed. Nevertheless, it is possible that another *T. putrescentiae* population can express this protein at a significant level or that this protein is expressed under specific conditions. This possibility may also be true for two other lowly expressed/trace-hit allergens, i.e., Tyr p 8 and Tyr p 1 (see Section 4.2 below). Overall, the expression and abundance of the allergen should be

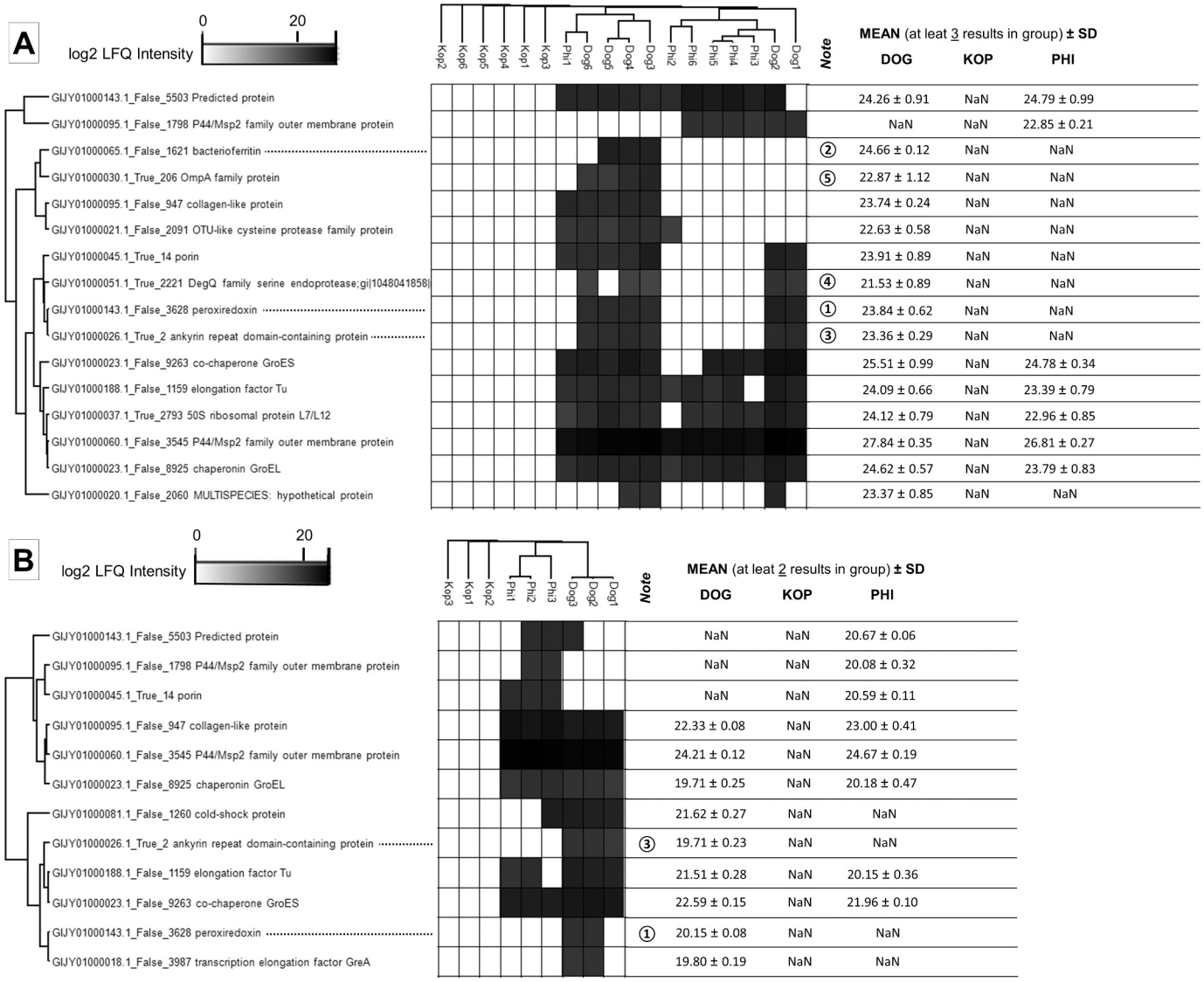


Fig. 2. Identification of *Wolbachia* proteins in three analyzed populations of *T. putrescentiae*. Overall, A) 16 and B) 12 protein hits were reliably identified in the 3 × 6 and 3 × 3 datasets, respectively. The heatmap presentations clearly show the specific identification of the *Wolbachia*-related proteins in the DOG and PHI populations infected with *Wolbachia*, as previously determined by microbiome analyses (i.e., [16,34–36]). Thus, it is correct that *Wolbachia* proteins were not detected in the KOP population. The key *Wolbachia* proteins that were detected only in the DOG population: ① peroxiredoxin; ② bacterioferritin; ③ ankyrin repeat domain-containing protein; ④ DegQ family serine endoprotease; and ⑤ OmpA family protein. These markers indicate a higher-level interaction of *Wolbachia* in the host because the DOG population and PHI populations have different microbiomes; the main difference is that the DOG population is additionally infected with *Blattabacterium*-like bacteria.

confirmed at the protein level.

4.2. *WHO/IUIS registered allergens – presence/abundance in mite populations*

In this study, 9 out of the 12 allergens currently registered by WHO/IUIS [15] were identified using state-of-the-art bottom-up gel-free proteomics. Seven mite allergens, Tyr p 7, 10, 34 (=39 based on similarity with *D. farinae*), 2, 28, 20 and 13, were consistently present in all three mite populations of *T. putrescentiae*. Two allergens, Tyr p 3 and 36, showed qualitative variation in detection across the samples and mite populations. Finally, Tyr p 1, 8 and 35 were not reliably detected; therefore, the presence of these allergens and/or the accuracy of protein sequences in mites raises doubts.

The expression of the trypsin allergen Tyr p 3 (GenBank: ABZ81991.1) can be suppressed in populations with *Wolbachia*, since it was reliably detected (in all analyses) only in the *Wolbachia*-free KOP population. Niu et al. [49] observed in *D. farinae* that Der f 3 (homologous with Tyr p 3) had an expression pattern similar to Der f 28.0201 (heat shock protein), and their expression was upregulated with increased temperature and downregulated with cold stress [49]. Therefore, Tyr p 3 can also be stress responsive. Moreover, we suggest a link between Tyr p 3 production and immune response modulation that initiates inflammatory signaling because trypsin is the major protease-activated receptor 2 (PAR2)-cleaving protease [50–52].

Tyr p 36 (GenBank: AOD75399.1) can also be affected by the microbiome since we observed its prevalence in *Wolbachia*-positive populations DOG and PHI of *T. putrescentiae*. Tyr p 36 is profilin that plays roles in cell shape changes and cell locomotion, but it also participates in modulation of the immune system. For instance, profilin of the parasite *Toxoplasma gondii* was found to modulate the host pathogen-associated molecular pattern (PAMP) of certain Toll-like receptors (TLRs) [53]. Therefore, the observed differences in the Tyr p 36 expression pattern in the 3 × 6 dataset could be associated with the

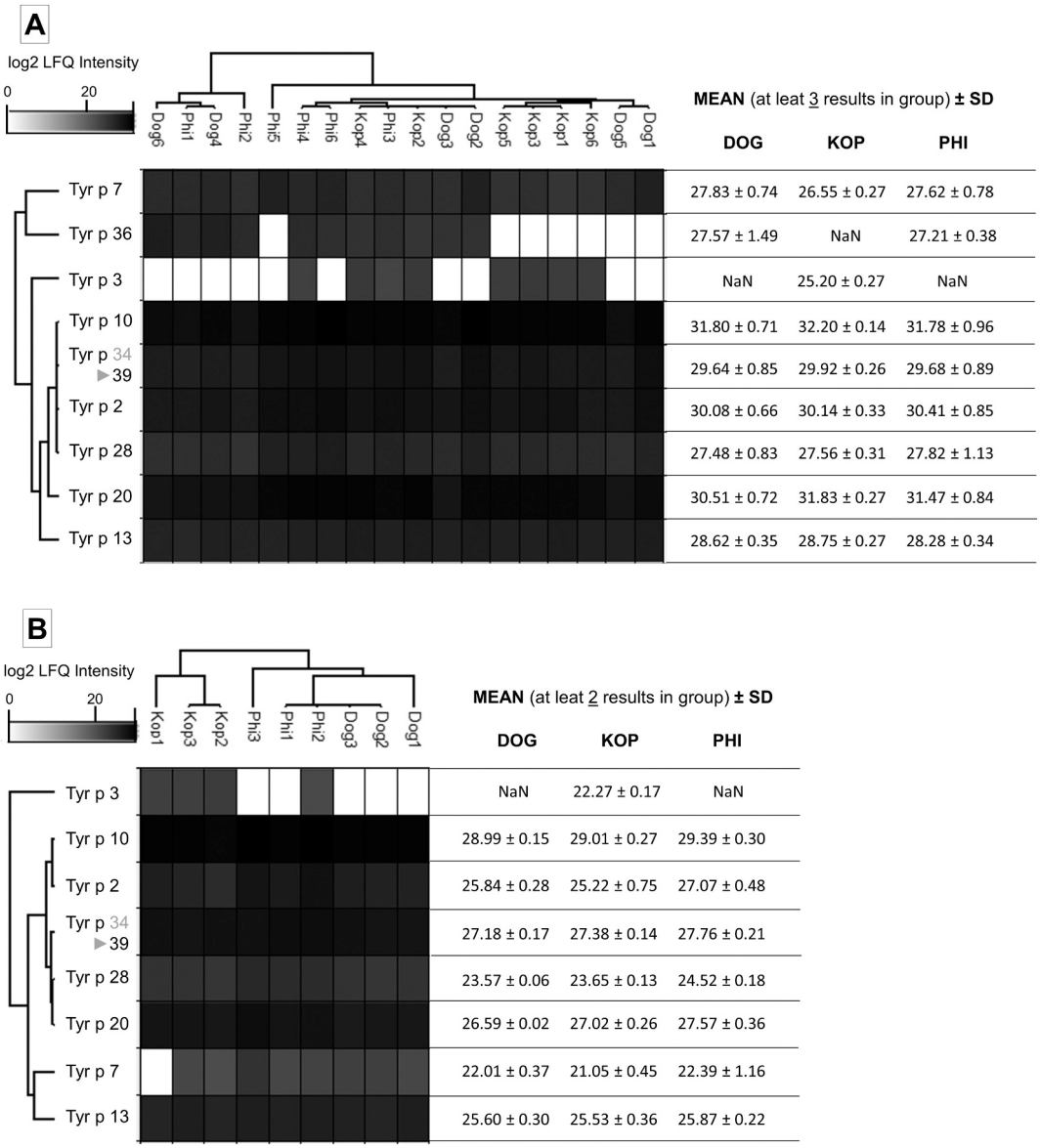


Fig. 3. The detected *T. putrescentiae* allergens are currently officially recognized by IUIS/WHO. Out of 12 WHO/IUIS [15] allergens, we identified 9 and 8 allergens in the A) 3 × 6 and B) 3 × 3 datasets, respectively. Our analysis shows that some allergens, with their exact protein sequences, may be expressed at zero- or low-abundance levels in *T. putrescentiae*.

intracellular bacterium *Wolbachia* in the host.

Although we were not able to detect Tyr p 1, 8, and 35, it is possible that these proteins are more abundant in different mites or may be induced under specific conditions. We stress the importance of knowing the baseline abundances of proteins described as allergens, as their expression may vary throughout mite development and with environmental conditions, microbiome composition and sex [16,17,49,54–56]. Understanding protein abundance in organisms and the environment is important, especially for allergens previously characterized using recombinant proteins, i.e., Tyr p 1 (GenBank: ABM53753.1; cysteine protease) [57]; Tyr p 35 (GenBank: AOD75396.1; aldehyde dehydrogenase aka Der f Alt a 10-like) [48]; and Tyr p 8 (GenBank: AGG10560.1; glutathione S transferase) [58]. Because transcripts and proteins have different durabilities, [59,60] it is necessary to consider that significant and large differences can be observed for allergens in the data at the protein and transcript levels.

One factor that characterizes the abundance of allergens/proteins in the environment is the possibility of accumulation. This phenomenon is valid, especially for mite allergens defecated via feces [23–25,61]. Here, we stress that there are differences in the expression and secretion of allergens/proteins that should be homologous in different mite species. For instance, while the trypsin allergen Der f 3 was abundant in *D. farinae* feces, Der p 3 was not identified to be same in the fecal proteome of *D. pteronyssinus* by 2D-*E*-MS/MS [23,25]. A different situation was observed for Der f 1 and Der p 1 or Der f 6 and Der p 6, which are defecated by both mites, and the pattern of isoforms was observed to be similar [23,25]. Considering these previous findings, it appears important that in this study, we found the candidate for the Tyr p 6 allergen (PREDICTED: mite allergen Der f 6-like; GenBank: XP_017489831.1) to be at similar abundances across the three mite populations of *T. putrescentiae*. Furthermore, it is apparent that we were not able to detect Tyr p 1 in the three *T. putrescentiae* populations, suggesting that the group 1 allergen should not be highly abundant in mites and feces. Therefore, it is likely that the protein sequence (GenBank: ABM53753.1) of the cysteine protease assigned as Tyr p 1 (by [57]) was not appropriately selected to be the group 1 allergen of astigmatid mites. The amino acid protein sequence was not claimed to be tested in study Yu et al. [57] (comment in WHO/IUIS [15]). Thus, whether *T. putrescentiae*

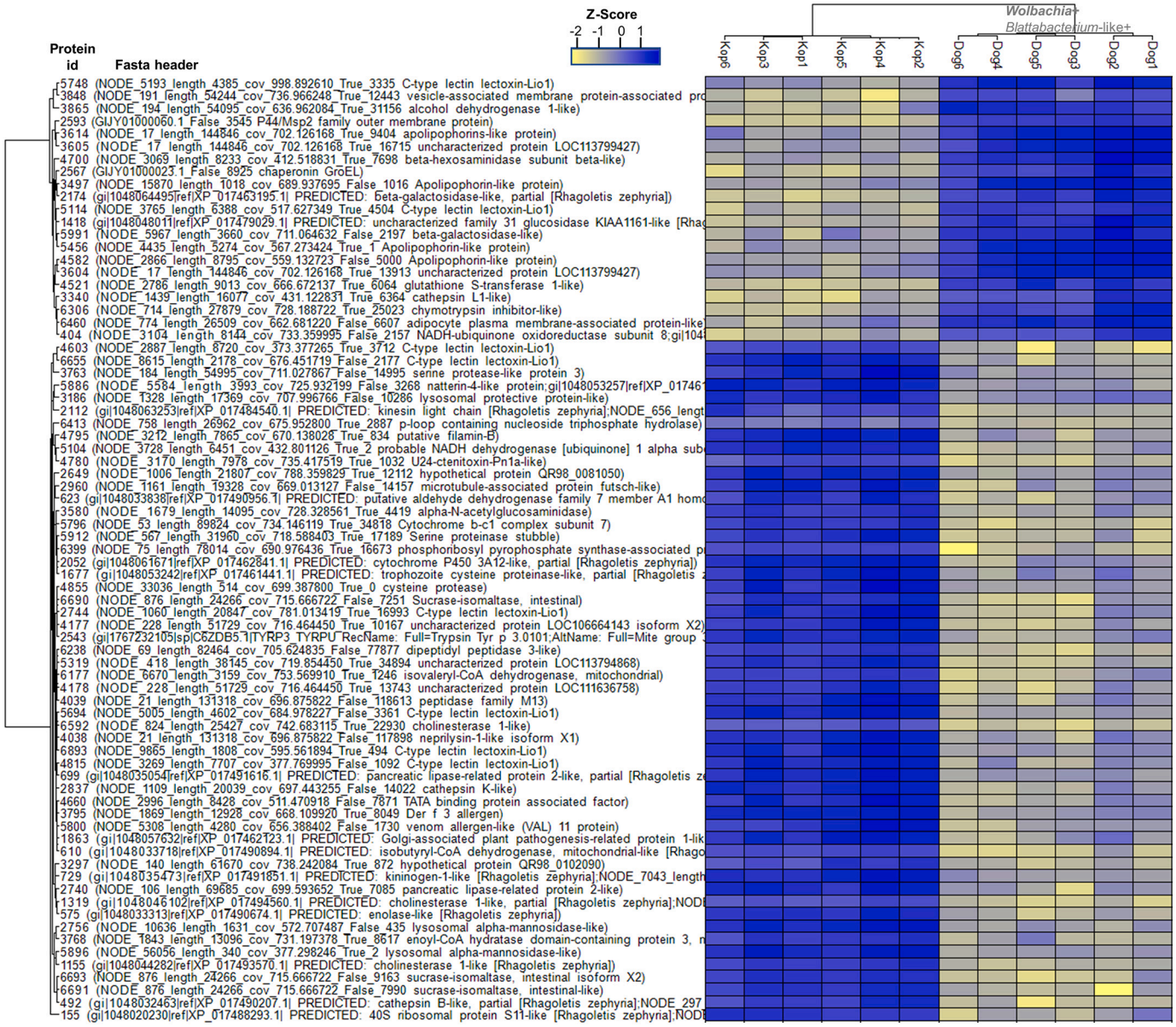


Fig. 4. Heatmap showing the *Z*-score difference in 75 markers of highest statistical significance (−log *p* value >5) between the DOG and KOP populations. The DOG population of *T. putrescentiae* is infected with *Wolbachia*, while the KOP population is not infected by that intracellular bacterium. DOG also hosts *Blattabacterium*-like.

has a homolog to the group 1 mite allergens of HDMs is disputable. Importantly, a similar sequence must not necessarily exert the same function and localization in different mites. Although more group 1 mite allergens are listed in WHO/IUIS, Der f 1 and Der p 1 are the original described members [62,63] produced by a mite family of Pyroglyphidae. Tyr p 1 should be produced by taxonomically distinct mite species that belong to family Acaridae, and the protein sequence of Tyr p 1 is relatively highly different from Der f 1 and Der p 1. Therefore, it is possible that *T. putrescentiae* Tyr p 1 is not the true homolog of group 1 mite allergens found in pyroglyphid mites. This could be confirmed in the future by analysis of the fecal proteomes of *T. putrescentiae* and/or localization studies. Previously, a fecal proteome of *T. putrescentiae* ("Laboratory" strain not included in this study) reared on dry dog food was analyzed [24], but exact proteomic identification of the disputable homolog of group 1 allergen was not possible in that study due to the limited number of sequences related to *T. putrescentiae* available at the time of analysis. However, enzymatic analysis of the *T. putrescentiae* fecal fraction in Erban et al. [24] did not support a significant portion of cathepsin B-like protease activity that should correspond to the group 1 mite allergen in gut digestive pH, although trypsin activity was high [24].

4.3. *Wolbachia* proteins in mites – clues for interactions and immune response modulation

This in-depth proteomics study enabled the proteomic identification of 18 *Wolbachia*-specific proteins that were found in one of the two or in both *Wolbachia*-infected mite populations [16,34–36]. Our identification of the 18 *Wolbachia*-specific proteins among the large array of mite-derived proteins that account for thousands of proteins shows their relatively high abundance in the mite proteome. On the other hand, the array of *Wolbachia*-specific proteins identified at the protein level was small, but for this reason, the 18 *Wolbachia* proteins appeared to be overexpressed in the host mites, but there was a difference in mite populations. Thus, the deliberate impact of these most abundant bacterial proteins on host–*Wolbachia* interactions is likely.

Identification of *Wolbachia*-specific proteins in mites enabled the use of a database that we created from a *Wolbachia* transcriptome assembly

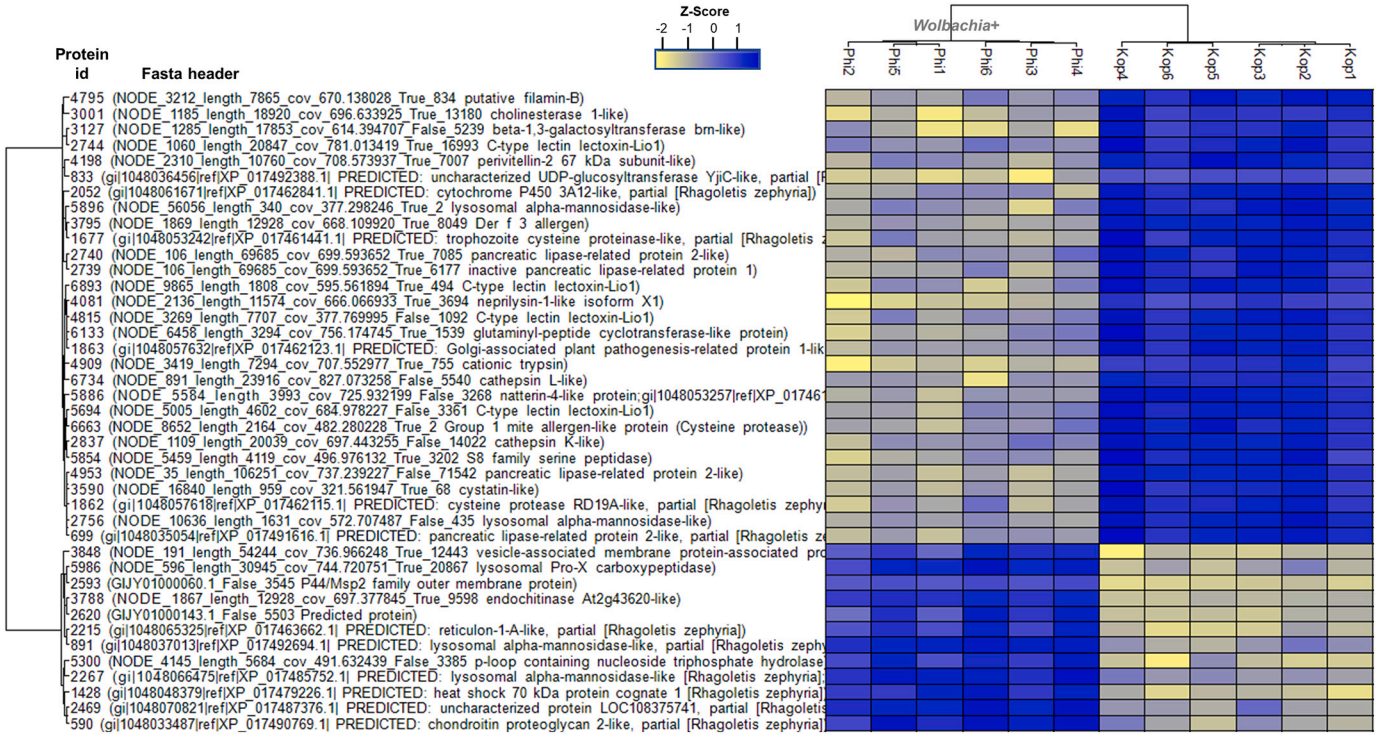


Fig. 5. Heatmap showing the Z-score difference in 41 markers of highest statistical significance (−log p value >5) between the PHI and KOP populations. The PHI population of *T. putrescentiae* is infected with *Wolbachia*, while the KOP population is not infected by that intracellular bacterium.

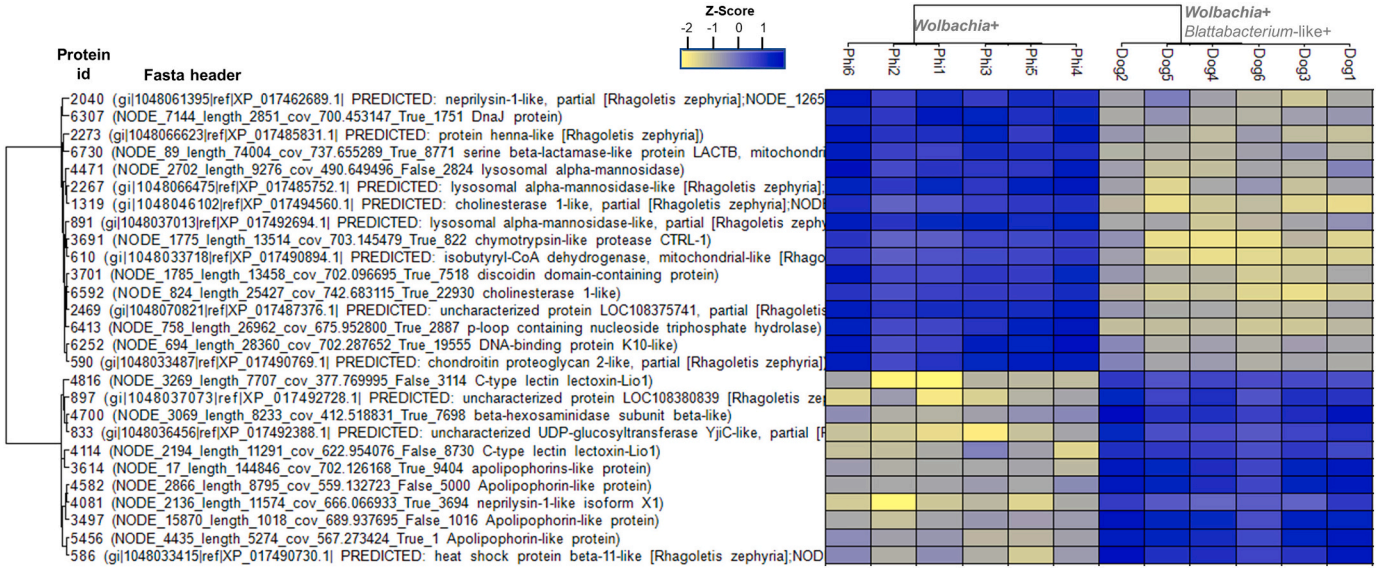


Fig. 6. Heatmap showing the Z-score difference in 27 markers of highest statistical significance (−log p value >5) between the DOG and PHI populations. Both DOG and PHI populations of *T. putrescentiae* are infected with *Wolbachia*. DOG also hosts *Blattabacterium*-like.

of *T. putrescentiae*. In addition, our GO analysis of all the retrieved sequences (1355 sequences returned a BLAST hit) indicated pathways by which *Wolbachia* can interact with the mite. Based on this analysis, *Wolbachia* can contribute to mite hosts with nitrogen metabolism and interact due to peptidoglycan biosynthetic processes. Importantly, the protoporphyrinogen IX biosynthetic process likely contributes to heme synthesis [45]. Although these *Wolbachia*-derived proteins were not identified at the protein level, they can be used in future functional studies employing transcript analysis. Indeed, heme is a key cofactor for cytochromes, hemoglobins, peroxidases, and catalases [45]. Thus, there can be a functional link of the protoporphyrinogen IX biosynthetic process, including protoporphyrinogen oxidase HemJ, to some of the 18 *Wolbachia*-specific high-abundance proteins that we identified at the protein level, i.e., bacterioferritin and peroxiredoxin (see below).

Importantly, the two *Wolbachia*-infected mite populations [16,34–36] differed in the detected *Wolbachia* proteins. Here, a higher number of proteins was detected in the DOG population than in the PHI population. This result may indicate the different levels of *Wolbachia* interaction with the host; however, the extra *Wolbachia* proteins in a population may be due to the DOG population hosts and to the absence

of *Blattabacterium*-like bacteria in the PHI population. In addition, some of the interactions may affect *Solitalea*-like bacteria, which are abundant in both DOG and PHI (see, e.g., [16]). Thus, there is strong supposition that some of the relatively high-abundance *Wolbachia*-specific proteins detected here are expressed in connection with the other bacteria in the mite, and we further discuss this possibility as the potential for higher-level, i.e., bacterium–bacterium–host, interaction. The most important *Wolbachia* proteins that we suggest are linked to the higher-level interaction are the following markers detected in only the DOG population: peroxiredoxin; bacterioferritin; ankyrin repeat domain-containing protein; DegQ family serine endoprotease; and OmpA family protein.

Peroxiredoxin is one of the key antioxidant enzymes involved in reactive oxygen species (ROS) elimination [64,65]. *Wolbachia* is likely to affect ROS levels in the host, which tries to eliminate this type of stress. This scenario is likely to be associated with AMP−/autophagy-based immunity (i.e., after a host switch), in which *Wolbachia* induces an ROS-based immune response [66]. Thus, the relatively high *Wolbachia* peroxiredoxin level may reduce the ROS-based immune response in the DOG population (a "new host" scenario). However, in a different scenario, mutually beneficial *Wolbachia*–host symbioses could take place in the PHI population, which lacks detectable peroxiredoxin. In *Aedesalbopictus* cell lines, *Wolbachia* upregulated ROS and antioxidant protein production, as well as superoxide dismutase and bacterioferritin expression [67]. We also identified *Wolbachia* bacterioferritin in the DOG population. Bacterioferritin is an important player in iron balance and modulation of Fe-mediated oxidative stress linked to the Fenton reaction [68–70]. Successful management of iron ions is also important for *Wolbachia* to modulate apoptosis and autophagy in the host [71]. *Wolbachia* was also observed in insect models to interfere with ferritin expression and upregulate bacterioferritin expression due to Fe treatment [72]; however, in our study, the mite populations were not treated with different Fe levels. Overall, our results support the supposition [66] that *Wolbachia* is able to produce its own antioxidant proteins, such as peroxiredoxin/superoxidase dismutase and bacterioferritin [67]. Because both peroxiredoxin and bacterioferritin were identified in only the DOG population, it can be suggested that the expression of these *Wolbachia* proteins could be triggered through a specific stimulus in the DOG population. Such a possible stimulus can be *Blattabacterium*-like bacterium cooccurrence in the DOG population compared to the lack of these organisms in the PHI population. Thus, whether (i) *Wolbachia* simply attempts to decrease ROS generation by the host against *Blattabacterium*-like bacteria, (ii) whether it is the result of competition between the bacteria, and (iii) whether *Wolbachia* in the DOG population infects a new host [66] emerged as open questions. We suggest that the latter appears less probable.

Another DOG-specific *Wolbachia* protein detected is an ankyrin repeat domain-containing protein. Importantly, the abundance of ankyrin domains in bacteria depends on their lifestyle since they are enriched in obligate and facultative symbioses compared to those in free-living lifestyles [73]. *Wolbachia* are bacteria with a large number of genes encoding ankyrin repeat domains [73,74]. Thus, this protein that we identified can be one of the key players in the *Wolbachia*–host interaction, especially through affecting protein-protein interactions [73]. The functions of these proteins can be diverse, such as regulation of the cell cycle, transcription and the immune response in the context of symbiosis [75]. One of the particular roles can be the modulation of reproductive functions of the host [76].

Wolbachia DegQ serine endoprotease is another protein that can play a role in the adaptation of this intracellular bacterium. According to the Conserved Domains Database (CCD) [77], these periplasmic proteins have a degP_htrA_DO domain. These proteins have trypsin and PDZ domains and function as protective and stress-responsive chaperones. They are important virulence factors for both extracellular and intracellular bacterial survival [78–80].

The OmpA family protein is an outer membrane surface-exposed porin protein. The detection of this protein aligns with the fact that OmpA is present in high copy numbers in the outer membrane of gram-negative bacteria. The OmpA function we stress is its importance for invasion, intracellular survival and host defense evasion [81]. Considering that a nonspecific outer membrane porin can participate in iron uptake [71,82], it is possible that the identified OmpA exerts that function and then may be linked to the above-discussed bacterioferritin.

4.4. Markers that can modulate immunity connected to Wolbachia

One of the important changes observed was the above-discussed variation in the trypsin allergen Tyr p 3. We observed that this protein/allergen was depleted in mite populations with *Wolbachia*. Trypsin has been reported to participate in host defense, i.e., the activation of antimicrobial peptides (AMPs) in the gut [83,84]. Interestingly, some other protein hits using the Tyr p 3/group 3-like mite allergen sequences were identified in this study. We observed a pattern similar to that of Tyr p 3 for the protein hit denoted NODE_1869_length_12928_cov_668.109920_True_8049 Der f 3 allergen, which was detected only in the KOP population lacking *Wolbachia*. Thus, additional detected protein hits/trypsin isoforms can be affected; however, some other trypsin(-like) hits that did not vary in mite strains were also detected in this study and may be of interest. Previously, we identified Tyr p 3 using 2D-*E*-MS/MS in the feces of *T. putrescentiae* [24]; however, the mite "Laboratory" (the oldest population in the laboratory of CRI) population that hosts *Cardinium* [33,85] was not included in this study. Thus, future observation of Tyr p 3 in mite fecal fractions can show whether there are differences in secretion of this protein in *T. putrescentiae* populations. Whether symbiotic bacteria affect PAR-2 [50–52], then the immune-related effect linked to the microbiome can be observed in mites but should also have significance for allergies [86–88].

The C-type lectin lectoxin-Lio1 protein isoforms were among the most promising immunity-related proteins that could be modulated by *Wolbachia*. These proteins are mannose-binding lectins (MBLs) or mannose receptors and are components of pattern recognition receptors (PRRs). MBL recognizes D-mannose, L-fucose and *N*-acetylglucosamine, which are carbohydrates found on the surface of infectious agents [89,90]. If mannose receptor is blocked, then infection and pathogen growth in the target cell should be facilitated through the effects on the immune pathways [91]. In future may be interesting study link in changes of C-type lectins and lysosomal alpha-mannosidases. Furthermore, changes in cholinesterase 1-like isoforms can be linked to modulation of the cholinergic anti-inflammatory pathway and its link to tumor necrosis factor alpha (TNF-α). Thus, we suggest that *Wolbachia* infection can affect the host immune response by affecting the nervous system [92]. There are a number of other markers that can be further studied in relation to the interaction of *Wolbachia* with the host, i.e., neprilysin/endothelin-converting enzyme [93–95], lysosomal protective protein-like [96], cytochrome P450s [97] (e.g. 3A12-like and 3A11-like), cathepsins and their inhibitors/cystatin [98], other proteases and other protein markers. Overall, the results strongly indicate modulation of lysosome function by the intracellular symbiont. We observed also significant changes in structure-related markers due to *Wolbachia* [99], e.g., downregulation of titin and filamin expression in *Wolbachia*-infected populations can be associated with the increased invasiveness of bacteria [100,101]. There may also be of importance difference in henna-like protein since protein henna isoform X2 was differentially expressed due to *Wolbachia* infection in *Nasonia vitripennis* [102]. Further, Li et al. [102] indicated that at the proteome level, various proteases and endothelin-converting enzyme were differentially expressed [102].

5. Conclusions

In this study, we performed comprehensive proteomic analysis of three *T. putrescentiae* populations that differ in hosting *Wolbachia* and

other bacteria, such as *Blattabacterium*-like bacteria. We created protein databases by utilizing a proteogenomic approach for searches that enabled the identification of thousands of mite proteins and relatively high-abundance *Wolbachia* proteins. Our analyses verified the abundance of the 12 currently recognized WHO/IUIS mite allergens based on label-free proteomics. Of them, 3 allergens were detectable as only trace hits and thus absent/lowly expressed proteins, suggesting that their allergenicity status may need revision. Furthermore, we found that two currently registered *T. putrescentiae* WHO/IUIS allergens were not correctly assigned to a mite allergen group. The abundance of the trypsin allergen Tyr p 3 was negatively affected by the presence of the mite population positivity on the intracellular bacterium *Wolbachia*, but other bacteria known to occur in the mites, such as *Blattabacterium*-like and *Solitalea*-like bacteria, may be involved factors. We suggested that *Wolbachia* suppressed Tyr p 3 levels in mites to modulate the immune response and linked trypsin protease to suppression of PAR-2 levels.

For the first time, we identified a series of *Wolbachia* proteins in the mite and confirmed evidence in different previous studies suggesting that *Wolbachia* produces its own antioxidant proteins, which can be triggered by a higher-level interaction involving additional bacterial symbionts. Furthermore, we suggest that changes in the expression of different mite C-type lectin lectoxin-Lio1 isoforms could be linked to the presence of *Wolbachia*, which can utilize the mite phagocytic machinery for cell-to-cell horizontal transmission. We also present evidence that *Wolbachia* can modulate lysosomal α-mannosidase, the cholinergic anti-inflammatory pathway with TNF-α, and other host proteins/pathways. Overall, we provided a number of markers for further research on *Wolbachia*–host and *Wolbachia*–other bacteria interactions.

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Author contributions

J.H and K.H. conceived and designed the biological study. M.N. performed the biological experiment. P.T. and K.H. performed mass spectrometry analysis. T.E. wrote the main manuscript, performed annotations, evaluated the data and prepared the figures and tables. P.K. and J.H contributed with writing main manuscript. J.H. provided grant. All authors discussed the results and commented on the manuscript.

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Availability of data and materials

The accession number for the raw nanoLC-MS/MS runs reported in this paper is MassIVE MSV000088016 (doi: 10.25345/C5R84M). Furthermore, in the dataset, we provide the entire “combined/txt” folders from MaxQuant data processing and the protein databases used for the search for download.

Declaration of Competing Interest

The authors declare that there are no competing financial interests.

Data availability

The raw data of nanoLC-MS/MS runs used in this paper along with additional details (search databases and combined/txt folders) can be accessed via MassIVE MSV000088016.

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Direct GO Counts – *T. putrescentiae* draft genome

Fig. S1A Biological Process (BP)

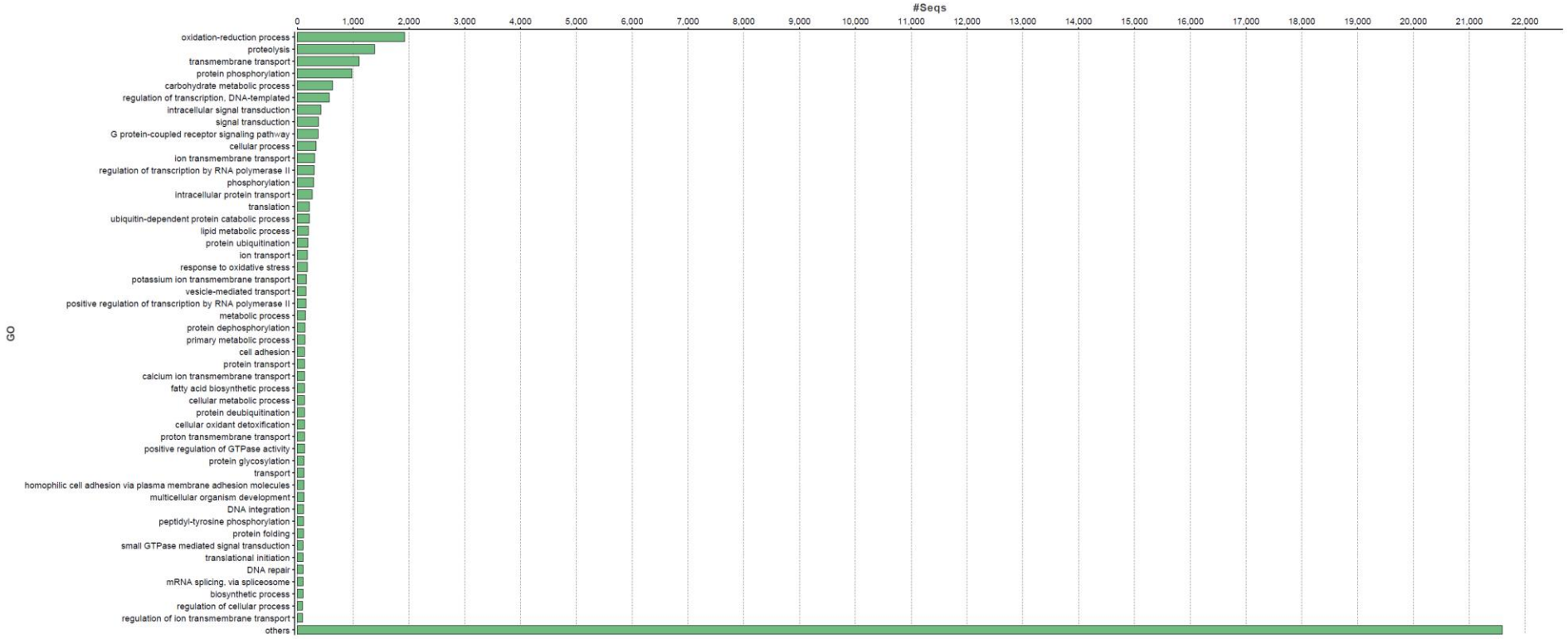


Fig. S1B Cellular Component (CC)

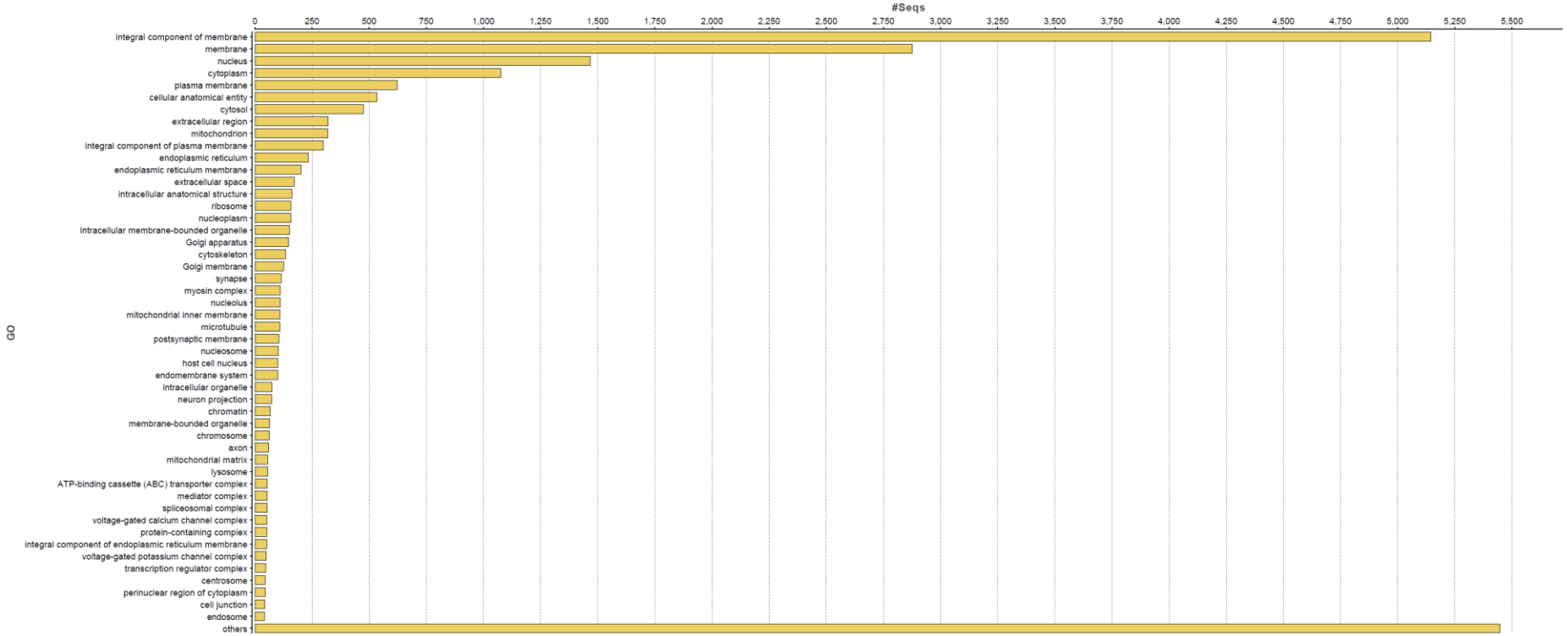
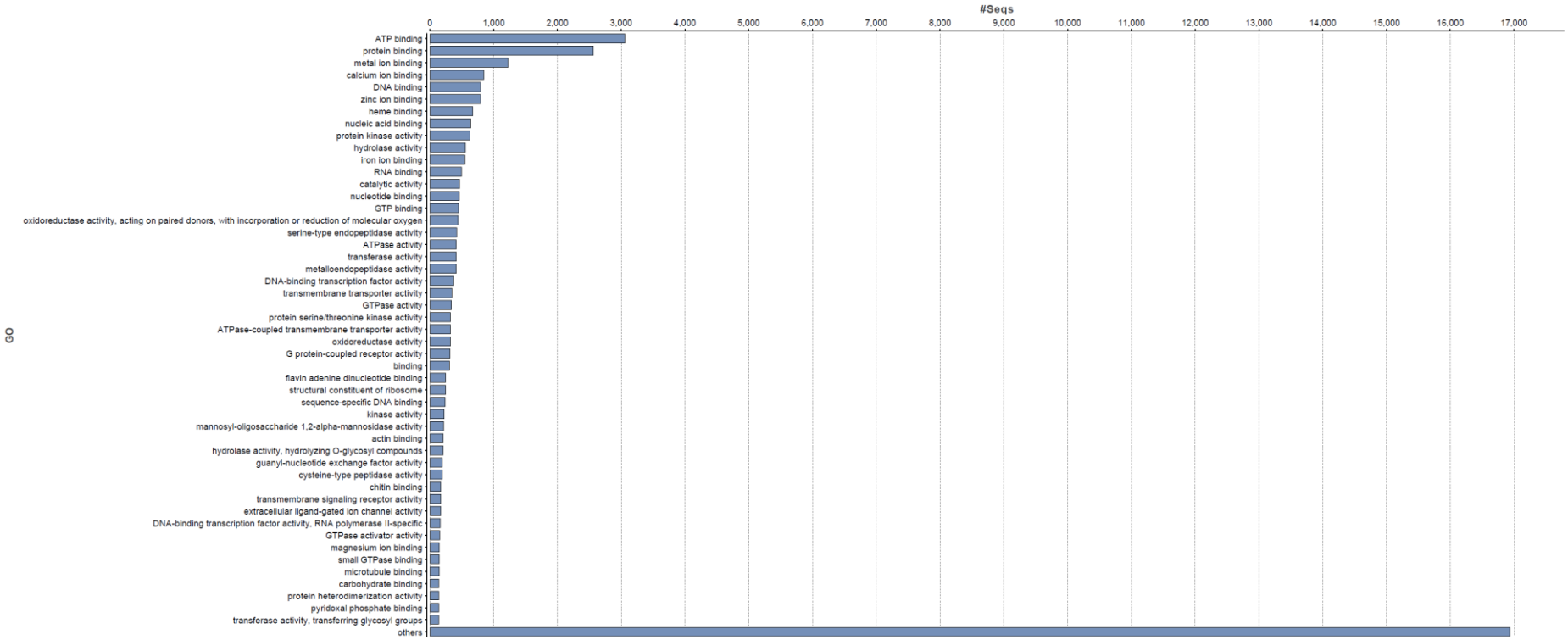


Fig. S1C Molecular Function (MF)



Direct GO Counts – *Wolbachia* transcriptome assembly

Fig. S2A Biological Process (BP)

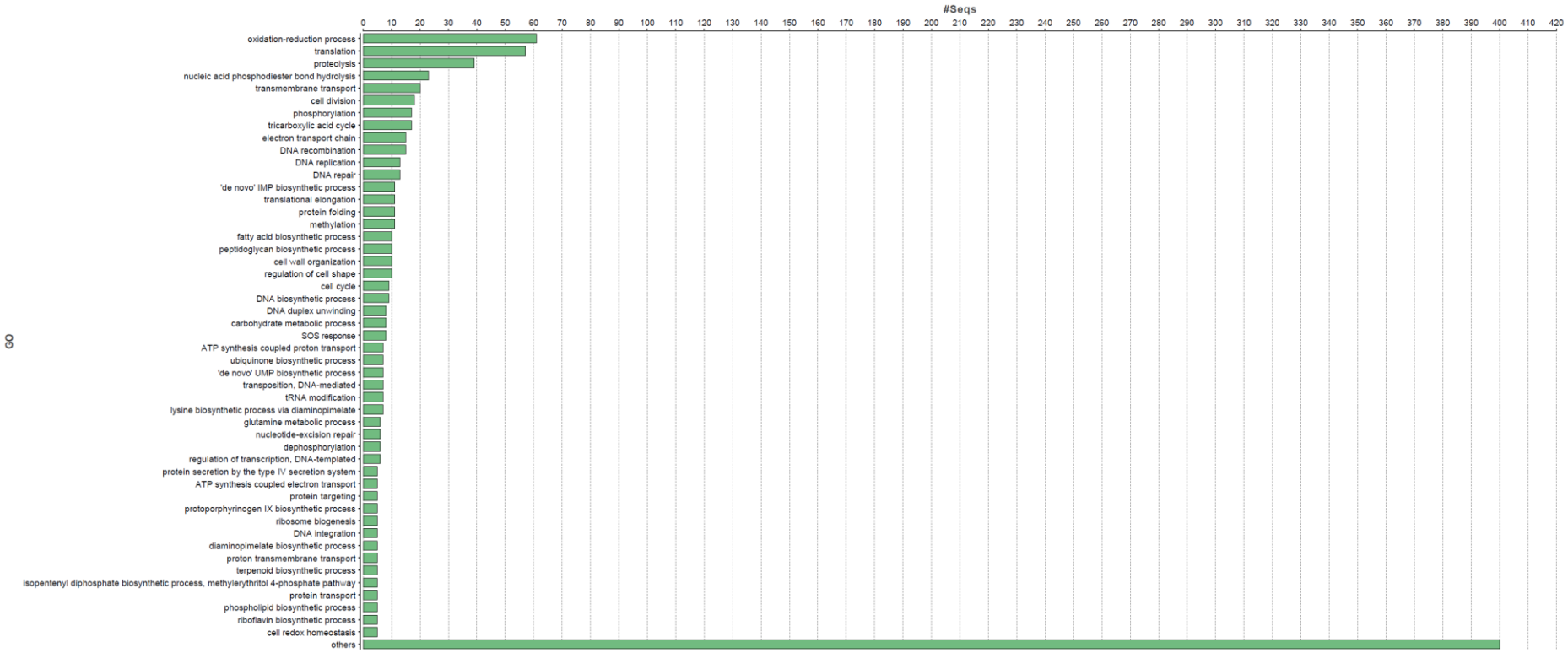


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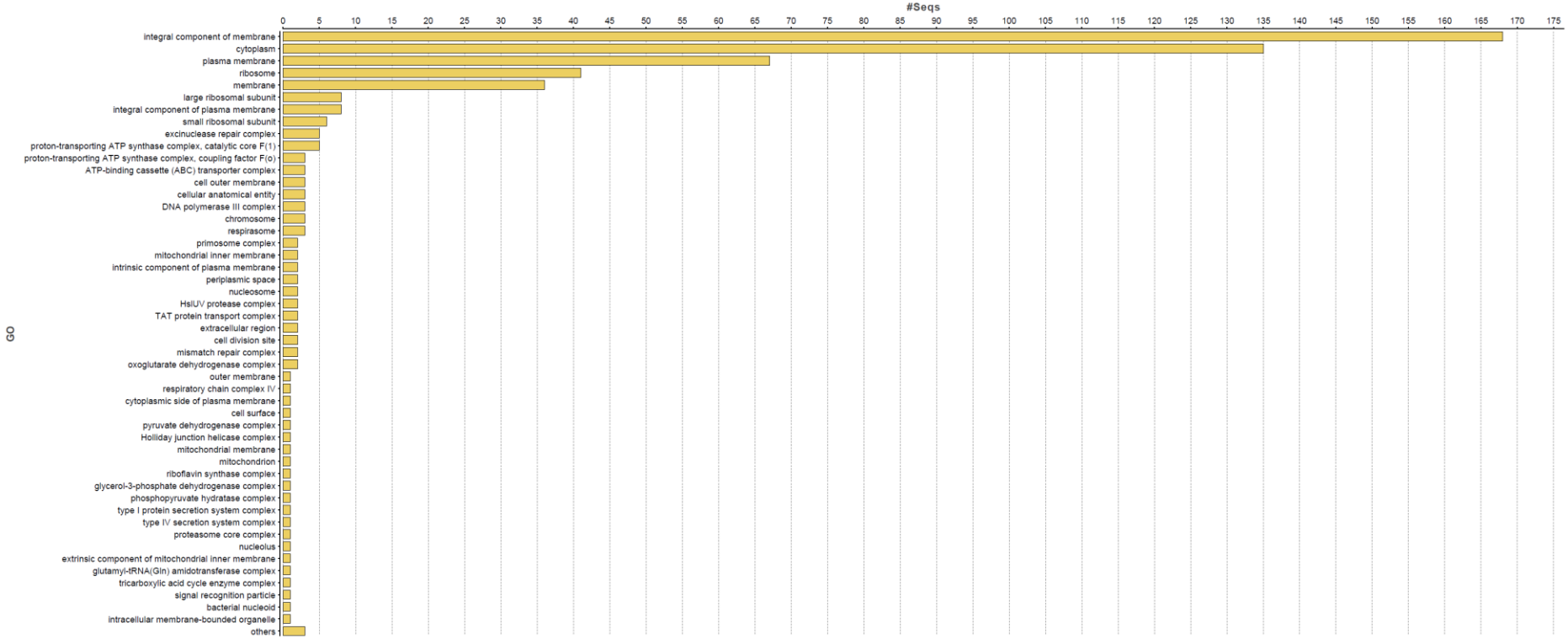


Fig. S2C Molecular Function (MF)

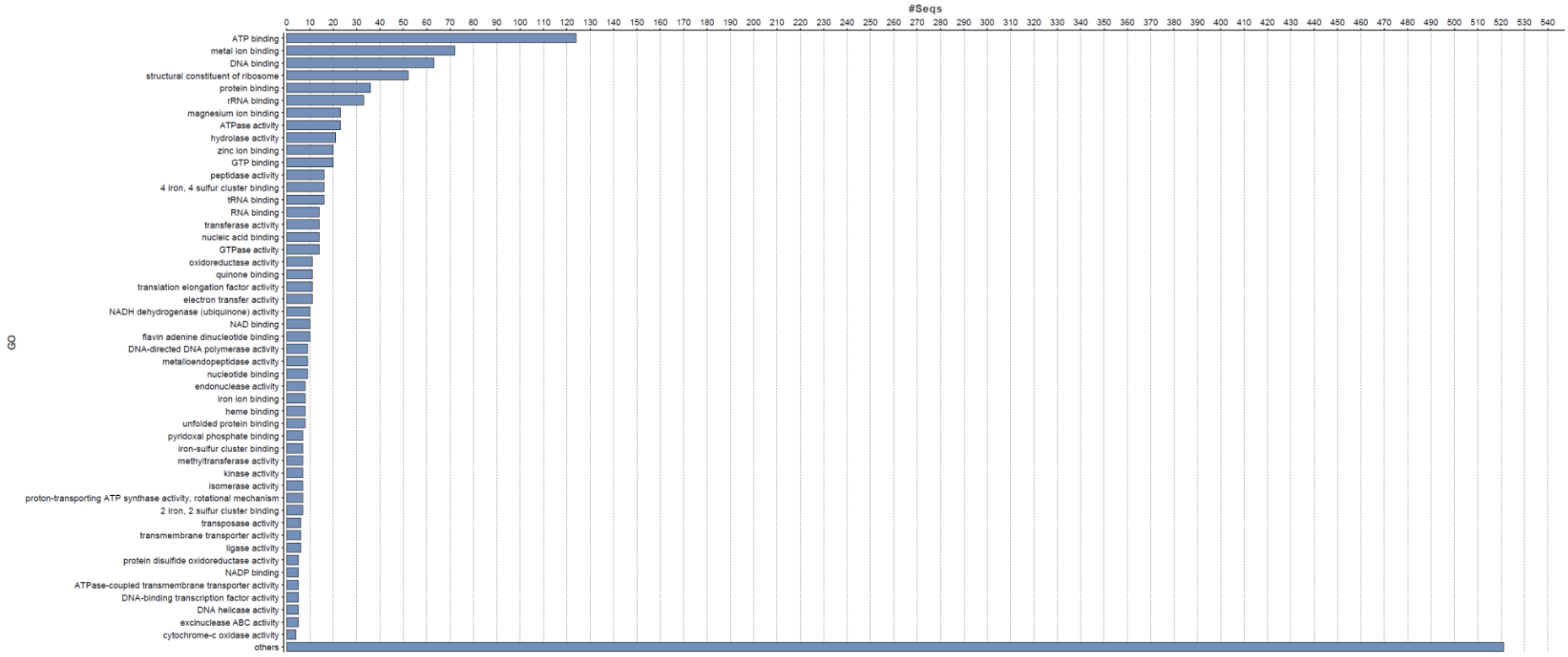


Fig. S3 The top 50 Biological Process (BP) of *Wolbachia* transcriptome assembly by number of sequences.

Nitrogen compound metabolic process (GO: 0006807) with 366 sequences, organonitrogen compound metabolic process (GO: 1901564) with 263 sequences and cellular nitrogen compound metabolic process (GO: 0034641) with 284 sequences appear highly important.

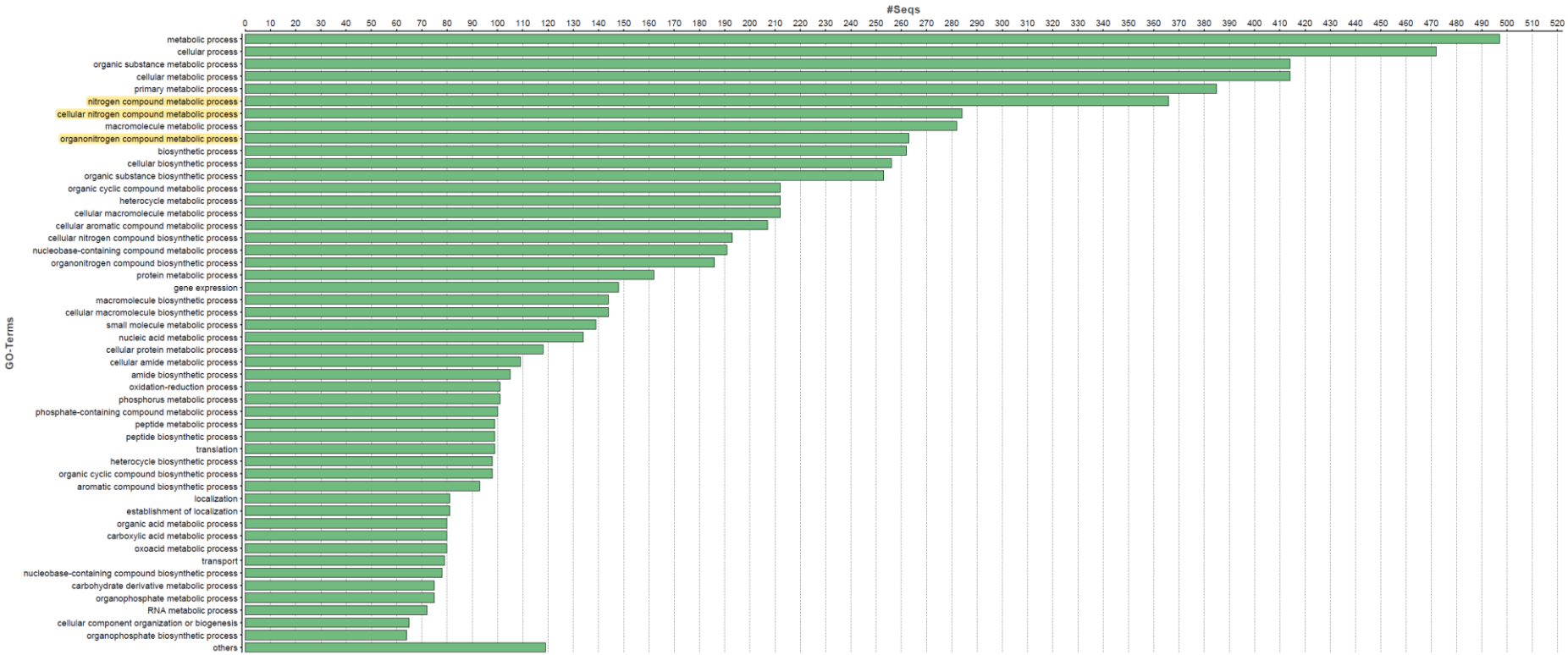
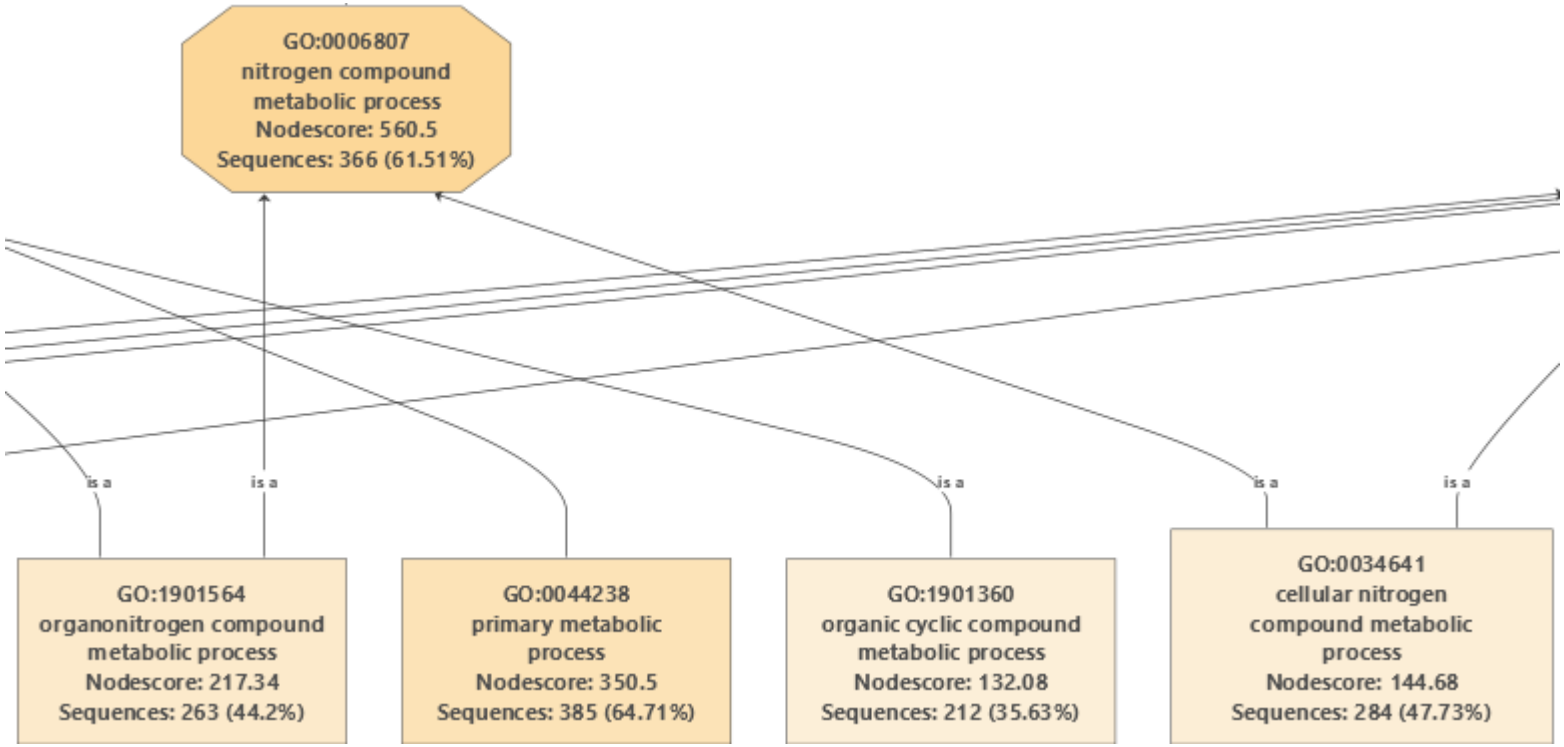


Fig. S4 Connections in BPs of *Wolbachia* transcriptome assembly.

A) SELECTION: the nitrogen compound metabolic process GO: 0006807 was most important according to the number sequences (366); this process is directly linked to the organonitrogen compound metabolic process GO: 1901564 (263 sequences) and the cellular nitrogen compound metabolic process GO: 0034641 (284 sequences)



B) – ALL connections

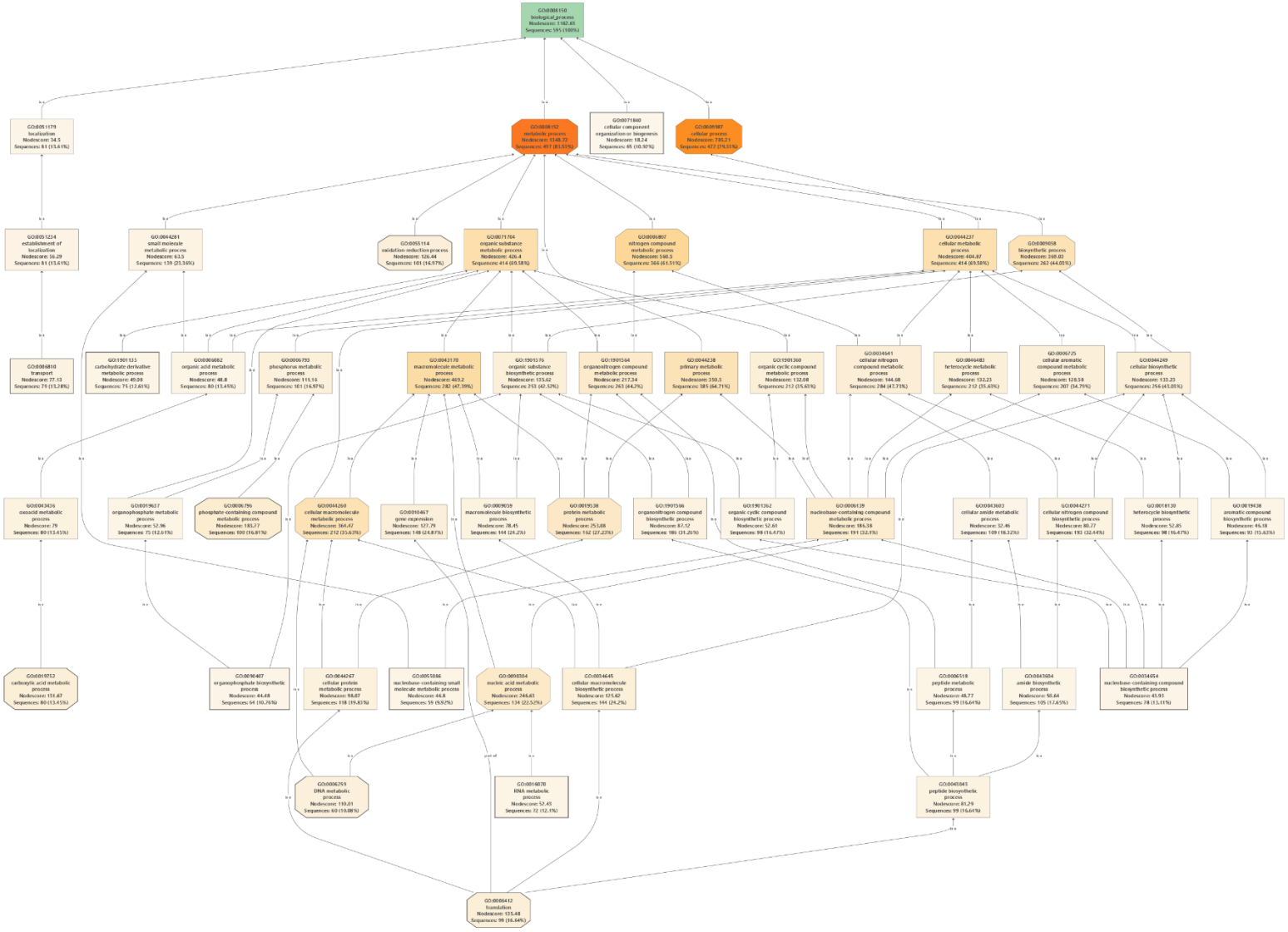


Fig. S5 Histograms showing intensities A) before and B) after the matrix (3X6 dataset) was filtered to protein hits that contained at least three valid values.

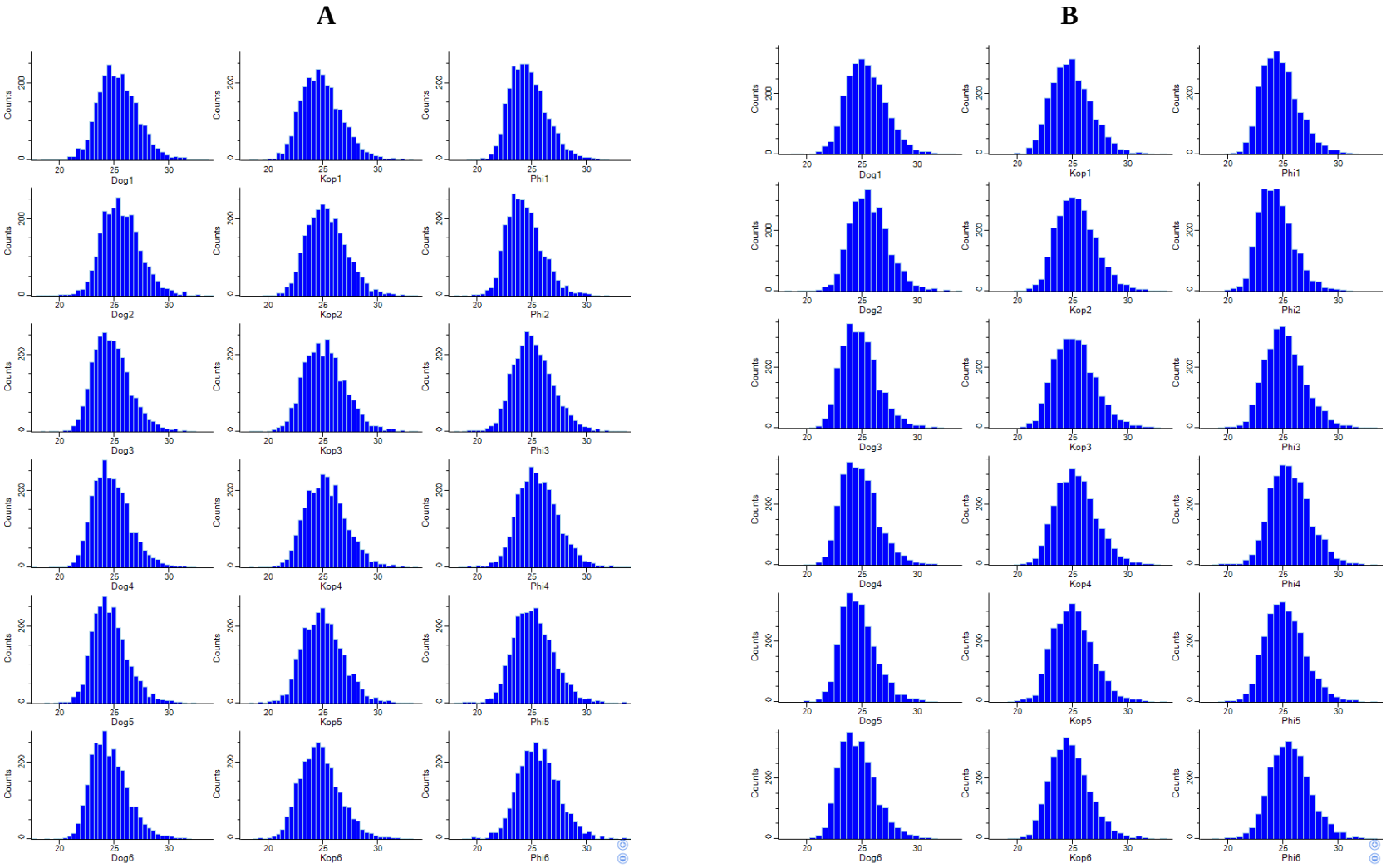
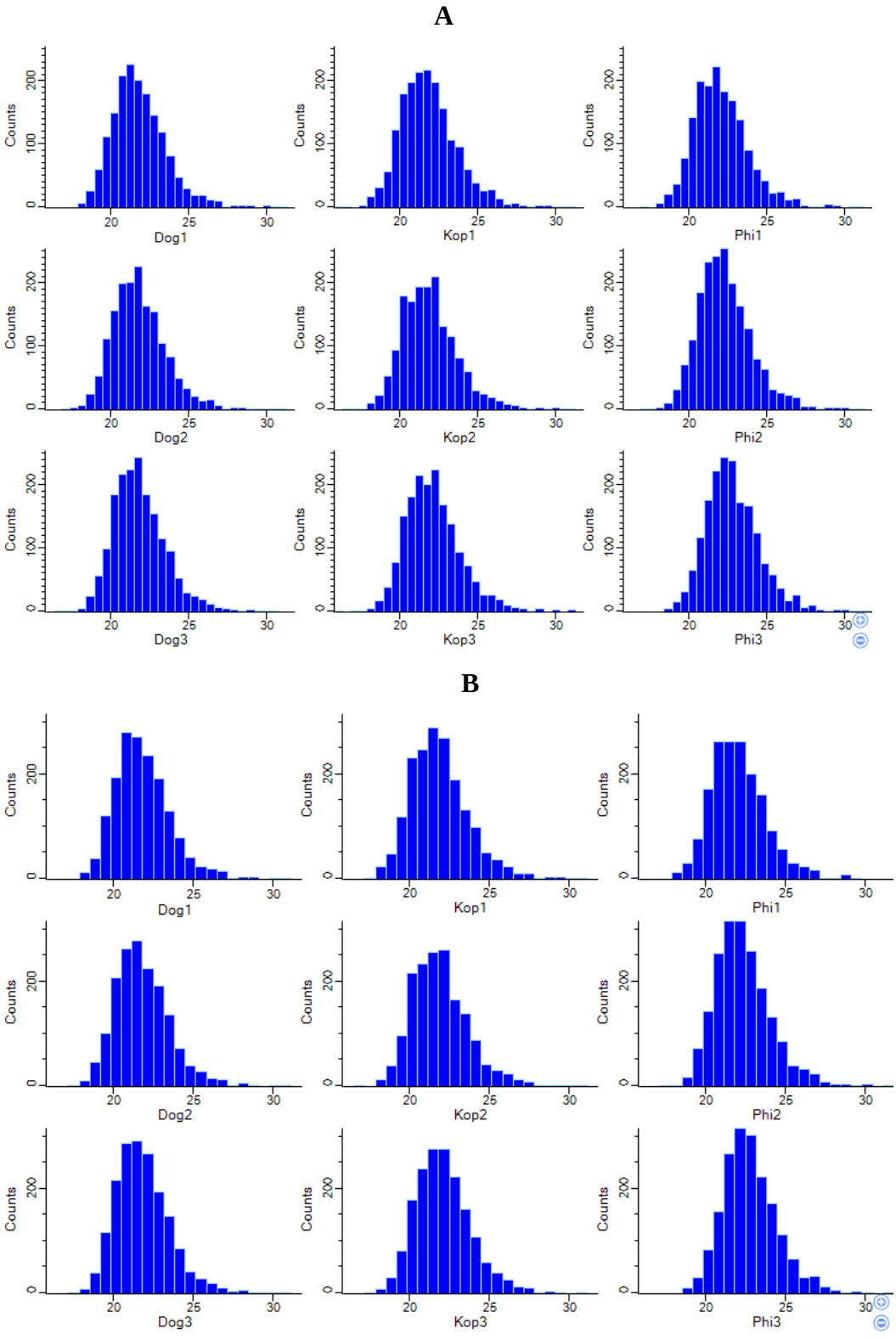


Fig. S6 Histograms showing intensities A) before and B) after the matrix (3X3 dataset) was filtered to protein hits that contained at least two valid values.



```
#=======================================
# Aligned_sequences: 2
# 1: AAP35081.1
# 2: AOD75396.1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 494
# Identity:     333/494 (67.4%)
# Similarity:   402/494 (81.4%)
# Gaps:          12/494 ( 2.4%)
# Score: 1780.0
#=======================================

AAP35081.1         1 MAQVEVKYTQIFINNEWHDSISGKTFETINPFTEEKLANVQEGDKADIDR     50
                     |:||.:|:||||||||||:|:|||||..|||.||||:|:||||||||||:
AOD75396.1         1 MSQVPIKFTQIFINNEWHNSVSGKTFPVINPATEEKIADVQEGDKADIDK     50

AAP35081.1        51 AVVAAVDAFRFDSPWRQMDASQRGHLLYRLADLIERDQDYIASLESMDNG    100
                     ||.||.:||:..|.||.||||.||.|:.:||||||.::.|::.|||:|||
AOD75396.1        51 AVTAAREAFKLGSTWRSMDASARGRLINKLADLIEIERQYLSELESLDNG    100

AAP35081.1       101 KPKTMALFDVDLAIKVFRYYAGYADKIHGKTIPADGKVFAFTRIEPVGIC    150
                     ||...|.||:|..:..||||||:||||||||||||.|.:||:|||||:|
AOD75396.1       101 KPLAEAEFDLDCTVATFRYYAGWADKIHGKTIPADGPVVSFTKIEPVGVC    150

AAP35081.1       151 GQIVPWNFPFLMASWKFGPALCAGNTVVLKPAEQTPLSALYLASLTKEGG    200
                     |||:|||:|.||.:||:.|||.|||||:||||||||||||:|.|..|.|
AOD75396.1       151 GQIIPWNYPALMLAWKWAPALAAGNTVILKPAEQTPLSALYIAKLAAEAG    200

AAP35081.1       201 FPPGVVNVVPGFGETAGAALVDNPKVDKIAFTGSTEIGKLIMRNGSHSMK    250
                     |||||:|||||:|.|||||||.:|:|||||||||||||||.:..|.::|
AOD75396.1       201 FPPGVINVVPGYGPTAGAALVAHPRVDKIAFTGSTEIGKLISKTASETLK    250

AAP35081.1       251 RITLELGGKSPLVVTENVEDIAQAARTAQDSCFLNMGQCCCAGTRTFVHE    300
                     |:|||||||||||||:| ||.:||:.|.|:||.||||||||||||:|||
AOD75396.1       251 RVTLELGGKSPLVVTESV-DIPEAAQIAHDACFANMGQCCCAGTRTYVHE    299

AAP35081.1       301 SIYDEFVKHSVEYCQSHVFGNPFDSKTAFGPQVDKIQMNRILEMIESGKQ    350
                     |||:||||||.......|.|:|||:....|||:|..|..:||::||||||:
AOD75396.1       300 SIYEEFVKHSAAIANKRVLGSPFDANVTQGPQIDAAQTAKILDLIESGKK    349

AAP35081.1       351 EGARCVAGGNRMDKRGYFVEPTVFADVTDGMRIAREEIFGPVQQILKYKT    400
                     :|||.|.||.|..::|||:||||||||.||||:||||||||||||||:
AOD75396.1       350 QGARVVTGGQRSTRKGYFIEPTVFADVTDSMRIAQEEIFGPVQQILKYKS    399

AAP35081.1       401 LDEVIERCNDTNYGLGSAILTNDINEAMKFSRSIRAGSVWINIPYMIPVS    450
                     |||||:|||.:.|||.:.|||.|||:|:|||.:::|||||:|. |...|
AOD75396.1       400 LDEVIDRCNSSAYGLAAGILTKDINQALKFSGAVQAGSVWVNC-YDHTV-    447

AAP35081.1       451 VQTPFGGFKESGVGRELGEDGLRGYGEIKTVVIMDREKKM----    490
                     |||||||||:||.||||||:||.||.|:|||.|     |:
AOD75396.1       448 VQTPFGGFKQSGHGRELGEEGLHGYCEVKTVTI-----KLAGGQ    486
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#--------------------------------------
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#=======================================
#
# Aligned_sequences: 2
# 1: QBF67841.1
# 2: ACL36923.1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 153
# Identity:     146/153 (95.4%)
# Similarity:   149/153 (97.4%)
# Gaps:           0/153 ( 0.0%)
# Score: 738.0
#
#
#=======================================

QBF67841.1         1 MSVEELTKEQVQMLRKAFDMFDREKKGHIHTNMVSTILRTLGQTFEEKDL     50
                     ||||||:||||||||||||||:|||:||||||||||||||||||.||
ACL36923.1         1 MSVEELSKEQVQMLRKAFDMFDRDKKGYIHTNMVSTILRTLGQTFEENDL     50

QBF67841.1        51 QQLITEIDADGSGELEFDEFLTLTARFLVEEDAEAMQEELREAFRMYDKE    100
                     ||||.||||||||||||||||||||||||.||||||||||||||||||
ACL36923.1        51 QQLIIEIDADGSGELEFDEFLTLTARFLVEEDTEAMQEELREAFRMYDKE    100

QBF67841.1       101 GNGYIPTSALREILRALDDKLTNDELDEMIAEIDTDGSGTVDFDEFMEMM    150
                     ||||||||||||||||||||||.||||||||||||||||||||||||||||
ACL36923.1       101 GNGYIPTSALREILRALDDKLTEDELDEMIAEIDTDGSGTVDFDEFMEMM    150

QBF67841.1       151 TGD    153
                     |||
ACL36923.1       151 TGD    153


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#---------------------------------------
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: BAA09920.1
# 2: ABZ81991.1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 292
# Identity:     121/292 (41.4%)
# Similarity:   168/292 (57.5%)
# Gaps:          40/292 (13.7%)
# Score: 587.5
#
#
#=======================================

BAA09920.1         1 MMILTIVVLLAANILATPILPS--------SPNATIVGGVKAQAGDCPYQ     42
                     |.||..:..|.:...|.|  |:        |.|..||||.:|..||.|:|
ABZ81991.1         1 MKILLFLCFLVSVAFAKP--PTIQLKSNTKSQNGFIVGGTEAVDGDAPHQ     48

BAA09920.1        43 ISLQSSSHFCGGSILDEYWILTAAHCVNGQSAKK---LSIRYNTLKHASG     89
                     :|||.:|||||||:.|.|||||||::.....   :|:|||||| :...
ABZ81991.1        49 VSLQHTSHFCGGSIISERWILTAAHCIDADDLSNPGGMSVRYNTL-NLKS     97

BAA09920.1        90 GEKIQVAEIYQHENYDSMTIDNDVALIKLKTPMTLDQTNAKPVPLPAQGS    139
                     |..::|..|..||.|.::|.|||:||::....|.|:||||....|||:|:
ABZ81991.1        98 GTLVKVKSIKVHEQYSNVTSDNDIALLETVASMNLNQTNAVAAKLPAKGN    147

BAA09920.1       140 DVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCDQLYSKAGAD    189
                     |.:.|| :.:||||.|..|..::|:.||:|.:.:.:|..|.:.|:.. .:
ABZ81991.1       148 DPQDGD-LFLSGWGTLHSGDTTIPTNLQKVTVPLTNRSVCAEAYTGI-VN    195

BAA09920.1       190 VSENMICGGDVANGGVDSCQGDSGGPVVDVATKQIVGIVSWGYGCARKGY    239
                     ::|||.|.|.:..||||||||||||..  :..|::||:||:|.||....|
ABZ81991.1       196 ITENMFCAGKMGIGGVDSCQGDSGGGA--MLNKELVGVVSFGVGCGDPKY    243

BAA09920.1       240 PGVYTRVGNFVDWIE-SKRSQ--------------------    259
                     |||||||..::|||| |.:|.
ABZ81991.1       244 PGVYTRVSQYLDWIELSAKSSATTLVAVNITLFLTLFIGAIW    285


#---------------------------------------
#---------------------------------------
```

```
CLUSTAL O(1.2.4) multiple sequence alignment


gi|121296504|gb|ABM53753.1|      MALLFYILFLFFTFIQCRHLEKVPTWEQYKVKFGKNYLTINEENFRKNNYFNSLTKIVKN   60
gi|27530349|dbj|BAC53948.1|      MKFVLAIASLLVLSTVYARPASIKTFEEFKKAFNKNYATVEEEEVARKNFLESLKYVEAN   60
gi|511953|gb|AAB60215.1|         MKIVLAIASLLALSAVYARPSSIKTFEEYKKAFNKSYATFEDEEAARKNFLESVKYVQSN   60
                                 * ::: *  *:       :  .: *:*::*  *.*.* *.::*:  ::*:::*:. :  *

gi|121296504|gb|ABM53753.1|      NGKNGVTLGLNDMSDWSDEEFFSLNSKSP--------SSVFVSARPTSTVNTSPFPKSWD   112
gi|27530349|dbj|BAC53948.1|      KGAI------NHLSDLSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSELD   114
gi|511953|gb|AAB60215.1|         GGAI------NHLSDLSLDEFKNRFLMSAEAFEHLKTQFDLNAETNACSING-NAPAEID   113
                                  *        *.:** * :** .    *         .  : :   :. :*    * . *

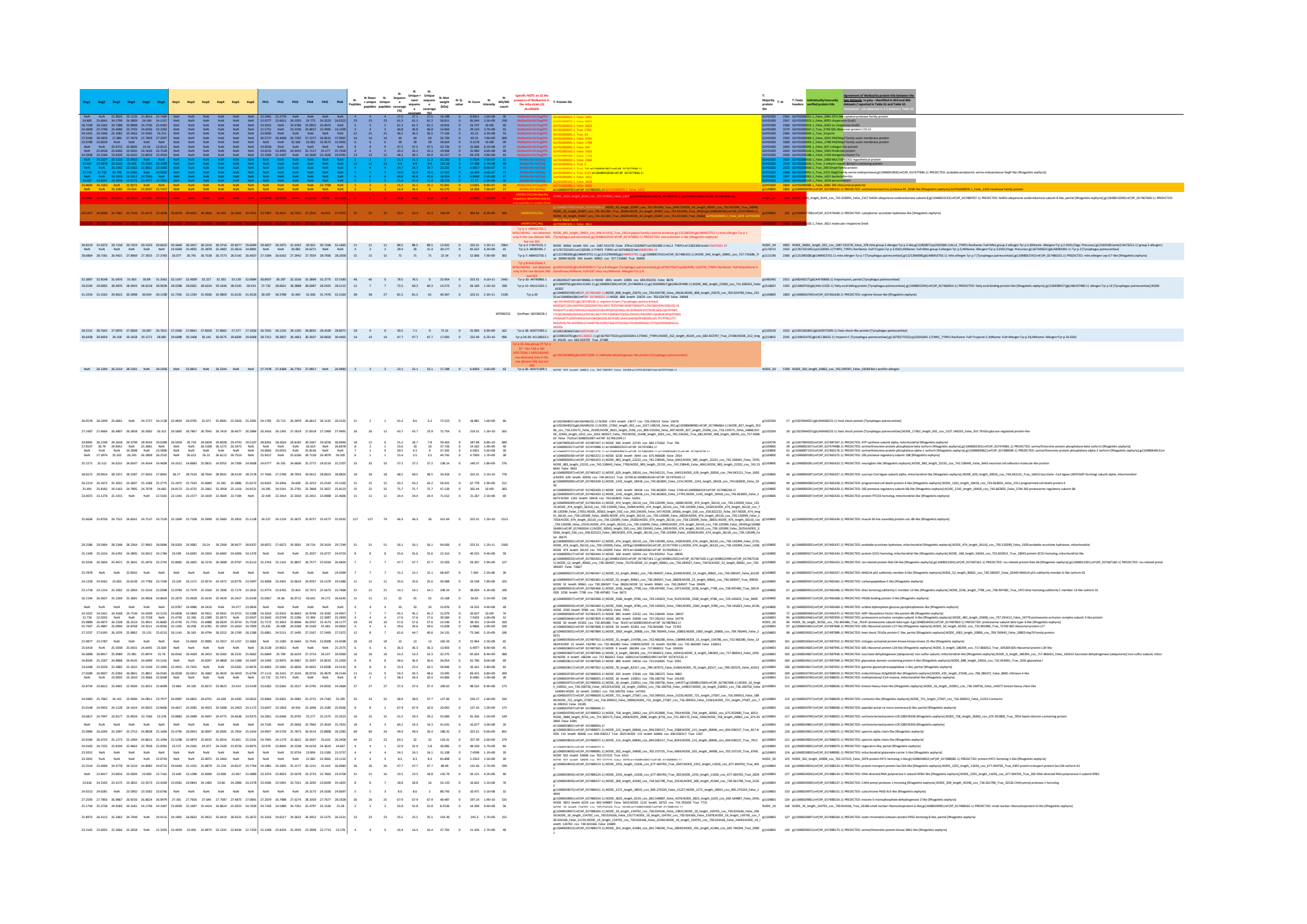
gi|121296504|gb|ABM53753.1|      WRNIIAFNSIEQQGRCSSCWAFAAATTVEAAYAHQKNKHNLHLSRQELVDCTNRTFDQHY   172
gi|27530349|dbj|BAC53948.1|      LRSLRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRN-TSLDLSEQELVDCASQ------   167
gi|511953|gb|AAB60215.1|         LRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRN-QSLDLAEQELVDCASQ------   166
                                  *.: :.. *. ** *.*****:..::.*:**   :*  .*.*:.******:.:

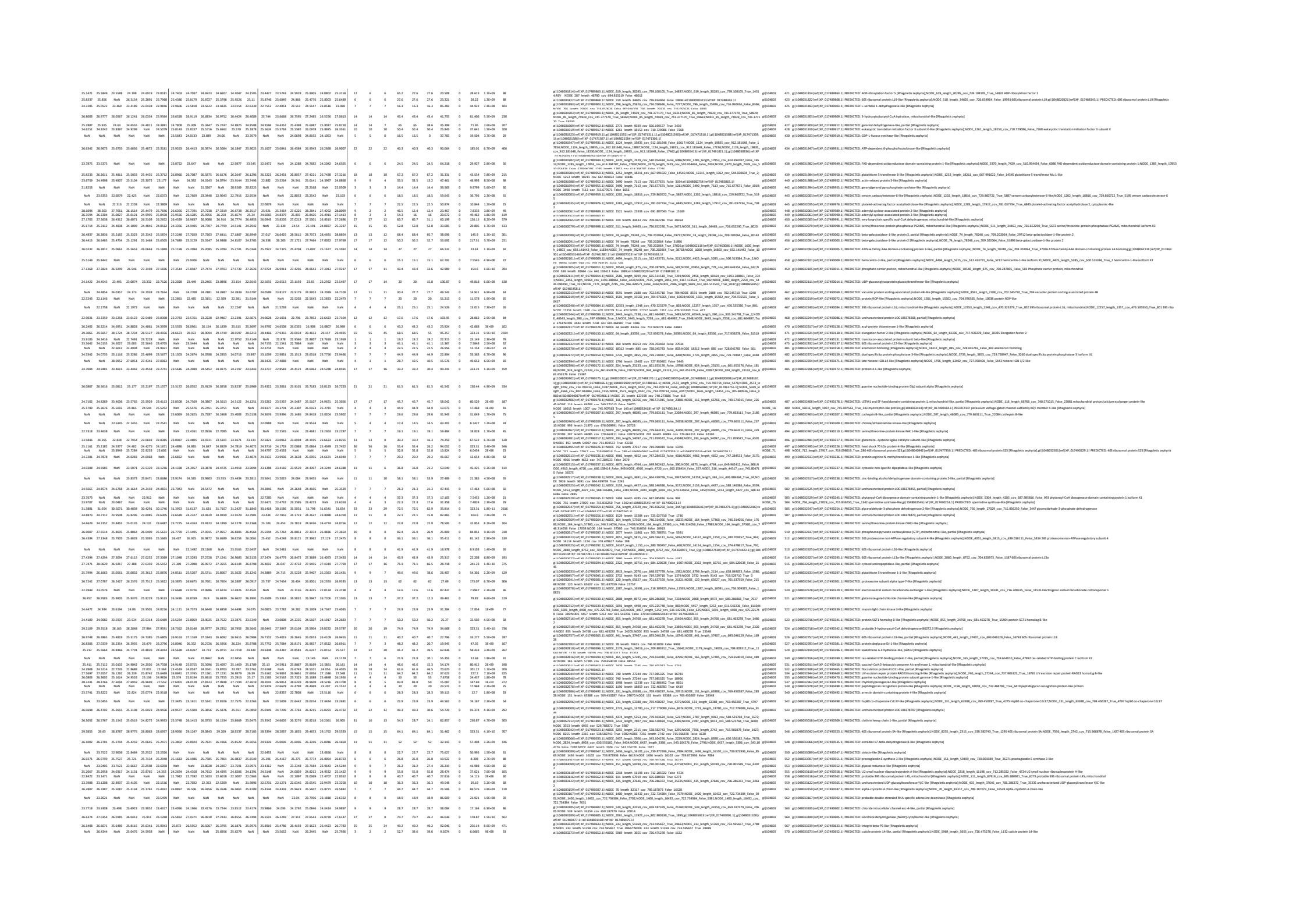
gi|121296504|gb|ABM53753.1|      LNYGCKGGWPTEAYKYIMDHGVYEDKLYHYTETFNEVCYADKVAHDKGHPVKYYISNYGR   232
gi|27530349|dbj|BAC53948.1|      --HGCHGDTIPRGIEYIQQNGVVEERSYPYVAREQQ-CR-------RPNSQHYGISNYCQ   217
gi|511953|gb|AAB60215.1|         --HGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQS-CR-------RPNAQRFGISNYCQ   216
                                   :**:*.   .. :** .:** ::  * *.   :. *        : :  :: **** :

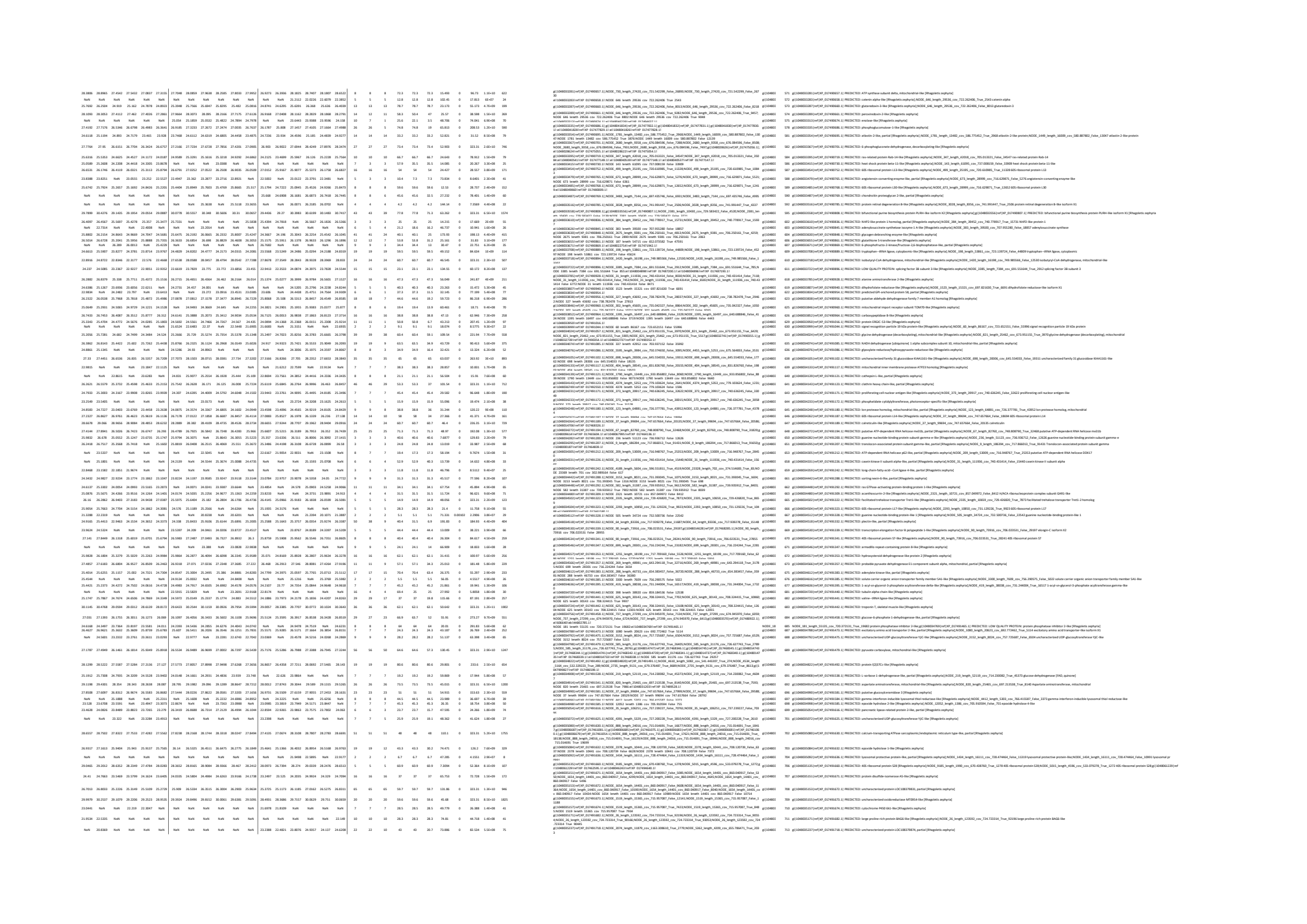
gi|121296504|gb|ABM53753.1|      LAYNDTDEAIMAMLVTYGPGTVDIHG--TSDTFRFYKGGIMRNVMPNSAYTNHIVVVVGY   290
gi|27530349|dbj|BAC53948.1|      IYPPDVKQIREAL-TQTHTAIAVIIGIKDLRAFQHYDGRTIIQHDNGYQPNYHAVNIVGY   276
gi|511953|gb|AAB60215.1|         IYPPNVNKIREAL-AQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGY   275
                                 :   :..:   *: .    . . * *     :*:.*.*  : :   .   . * * :***

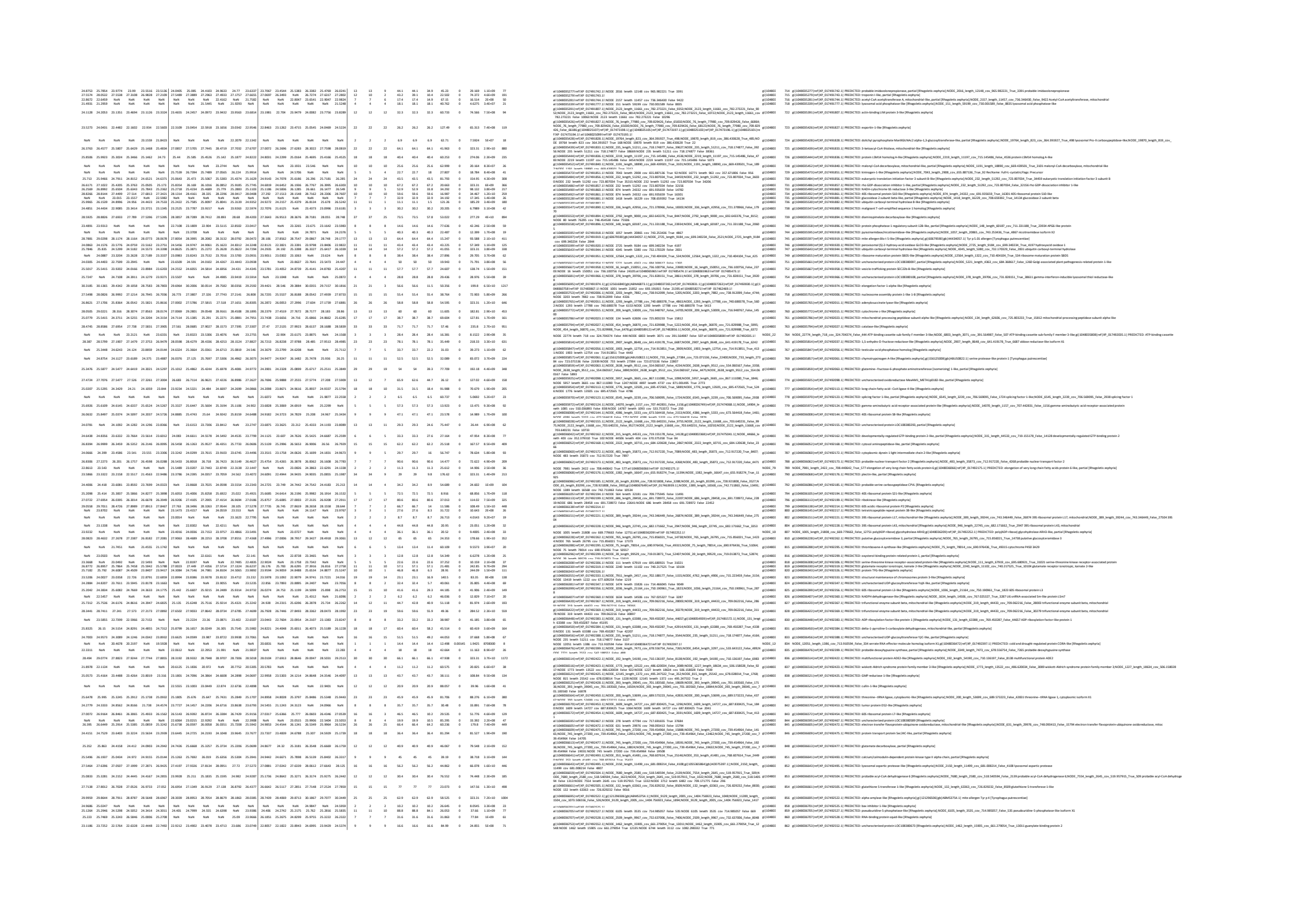
gi|121296504|gb|ABM53753.1|      GTDSSGVDYWIIRNSWGKTWGEHGYGRLERHPNLLGFNNKYNYPIL-        336
gi|27530349|dbj|BAC53948.1|      GS-TQGVDYWIVRNSWDTTWGDSGYGYFQAGNNLMMIE-QYPYVVIM        321
gi|511953|gb|AAB60215.1|         SN-AQGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIE-EYPYVVIL        320
                                 .. :.******:****...**: *** :    :*: :: :* * ::

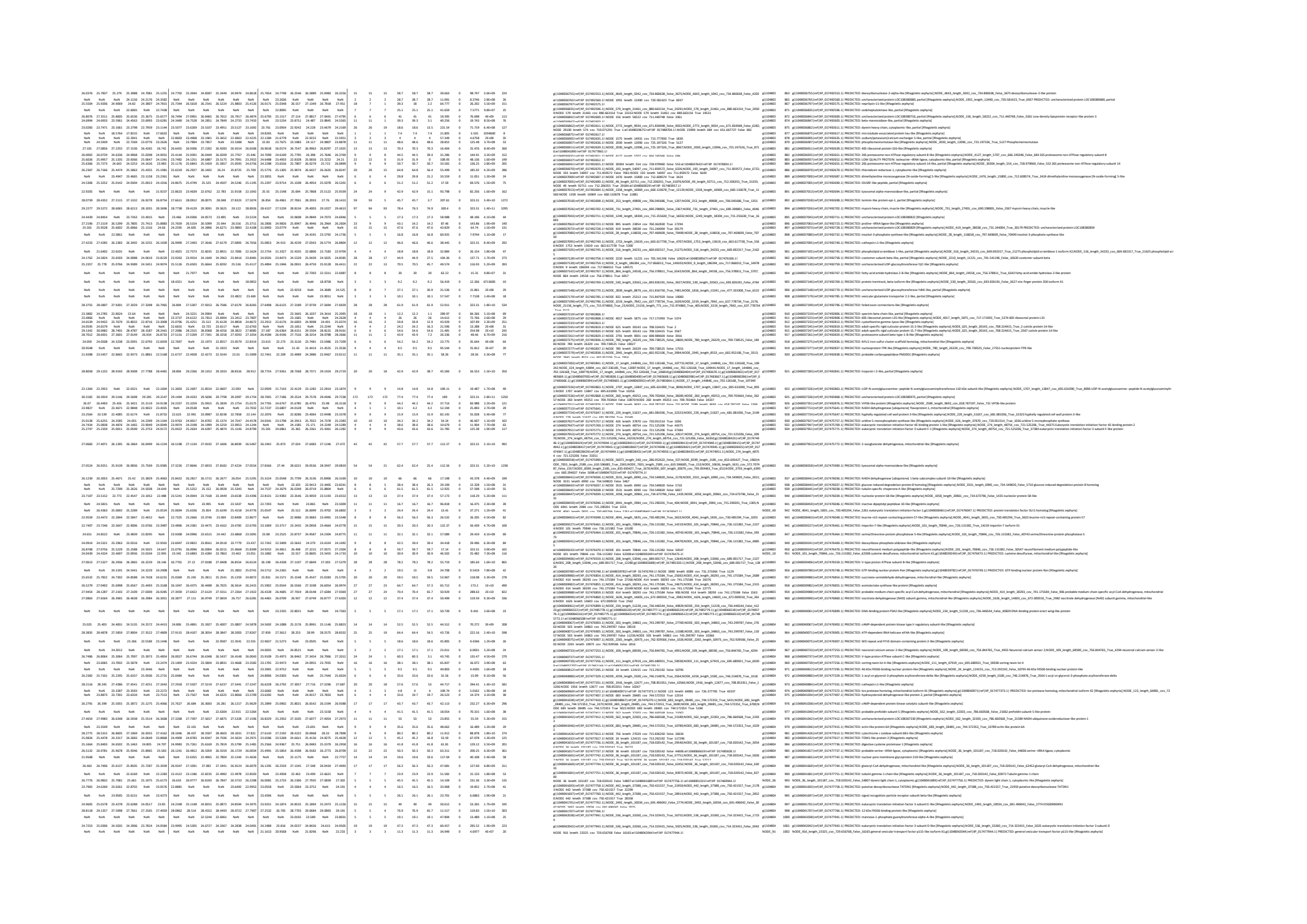
Percent Identity Matrix - created by Clustal2.1
#
#
1: gi|121296504|gb|ABM53753.1| 100.00 32.26 30.10
2: gi|27530349|dbj|BAC53948.1| 32.26 100.00 83.44
3: gi|511953|gb|AAB60215.1| 30.10 83.44 100.00
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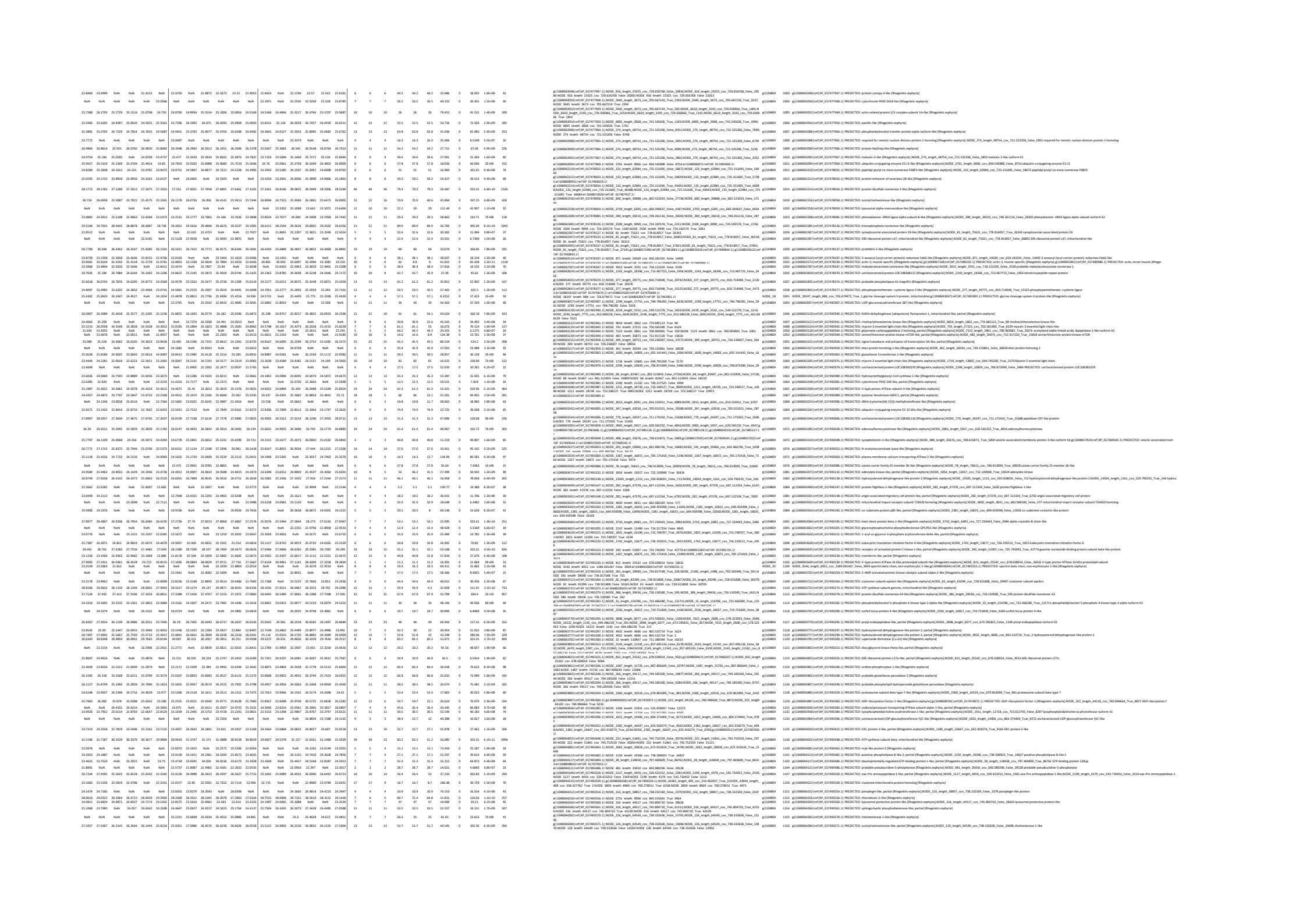


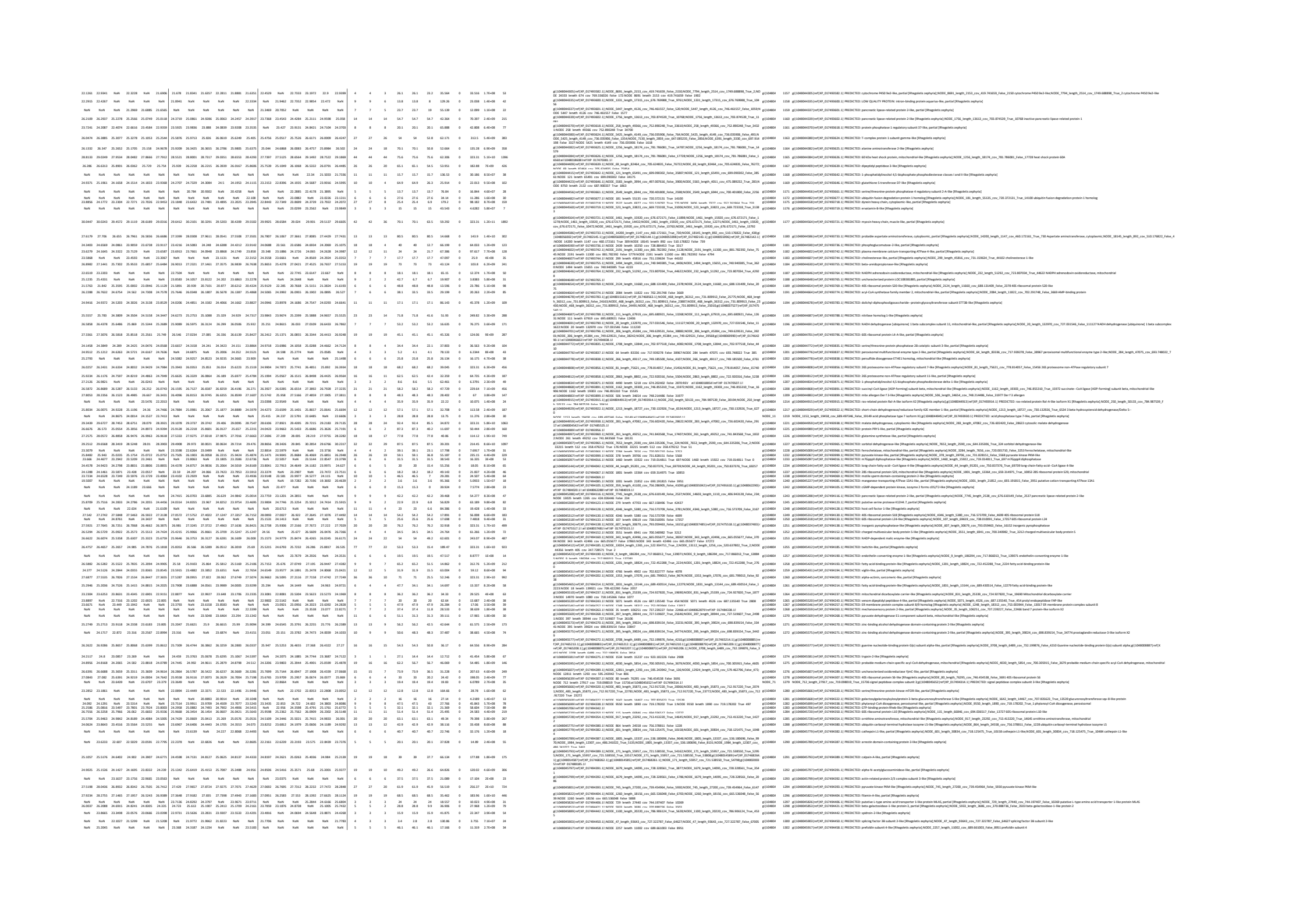


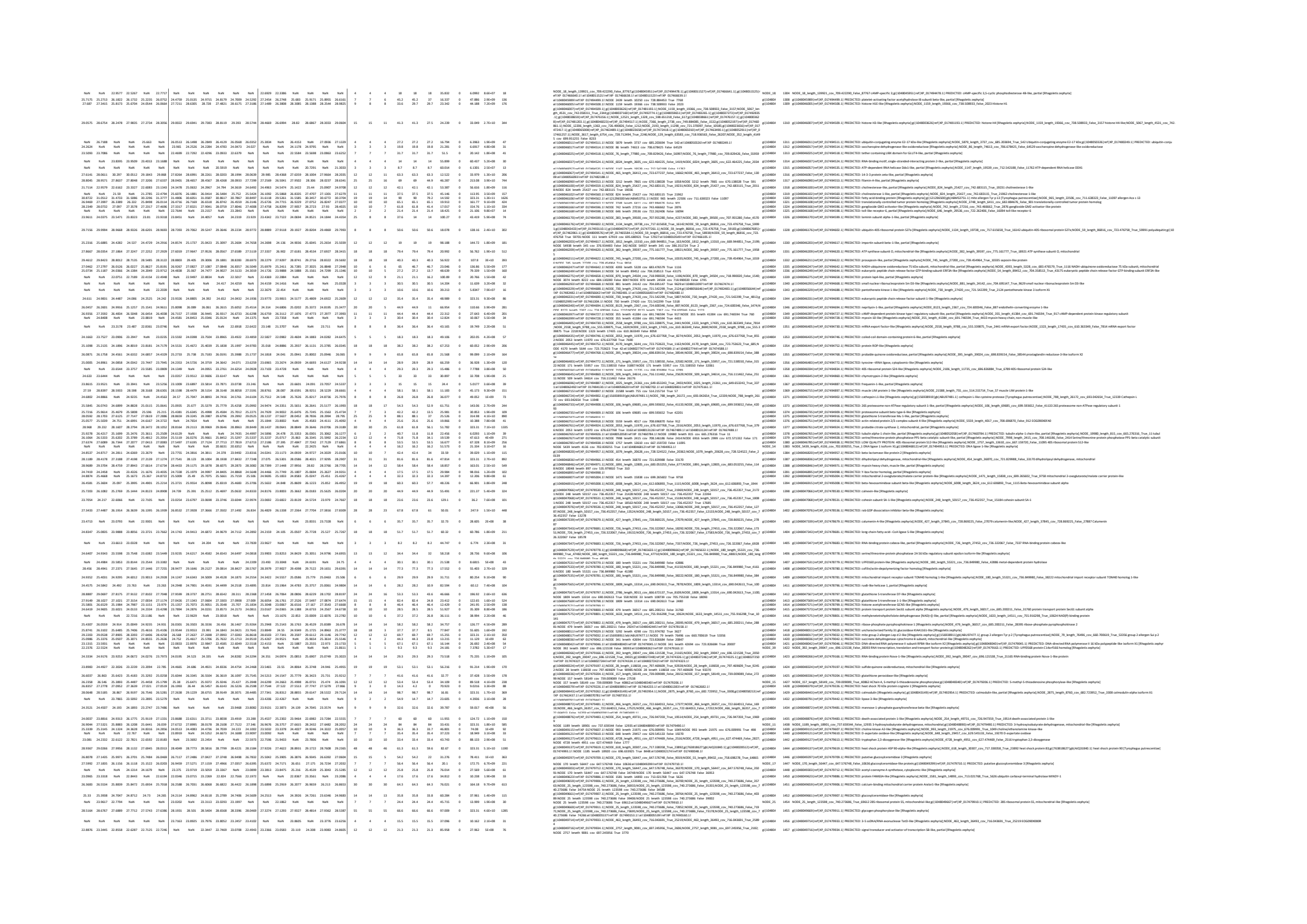


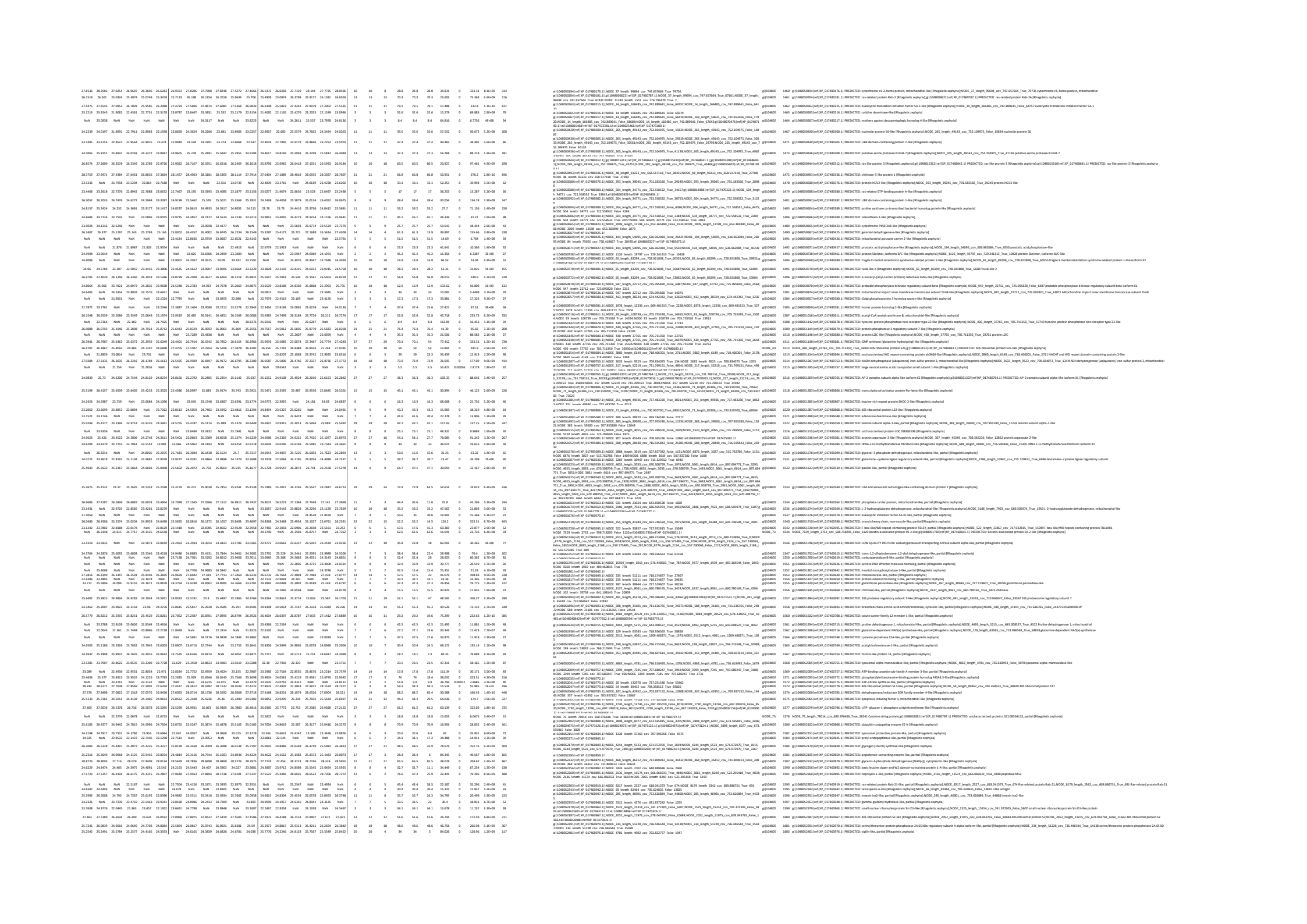


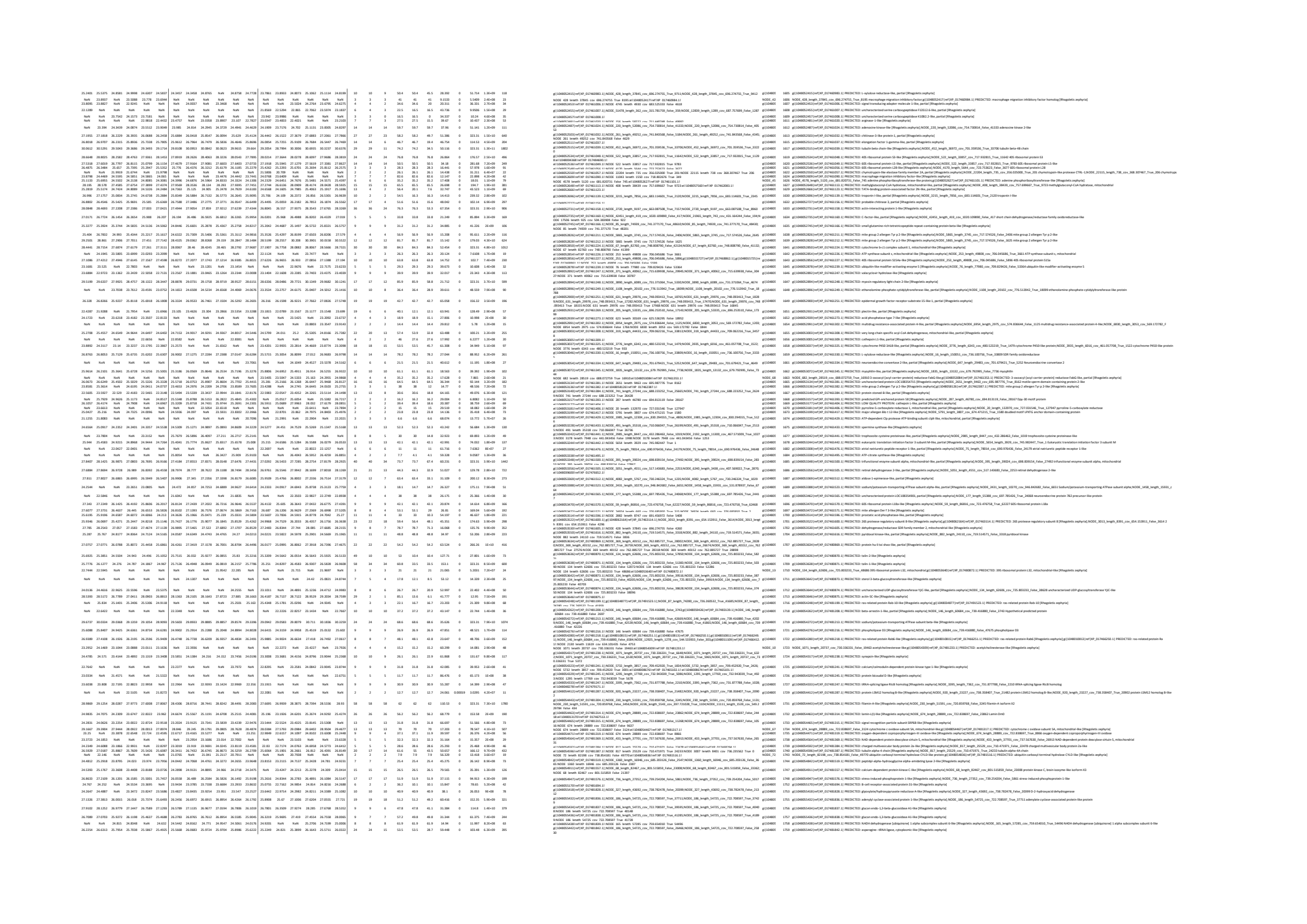


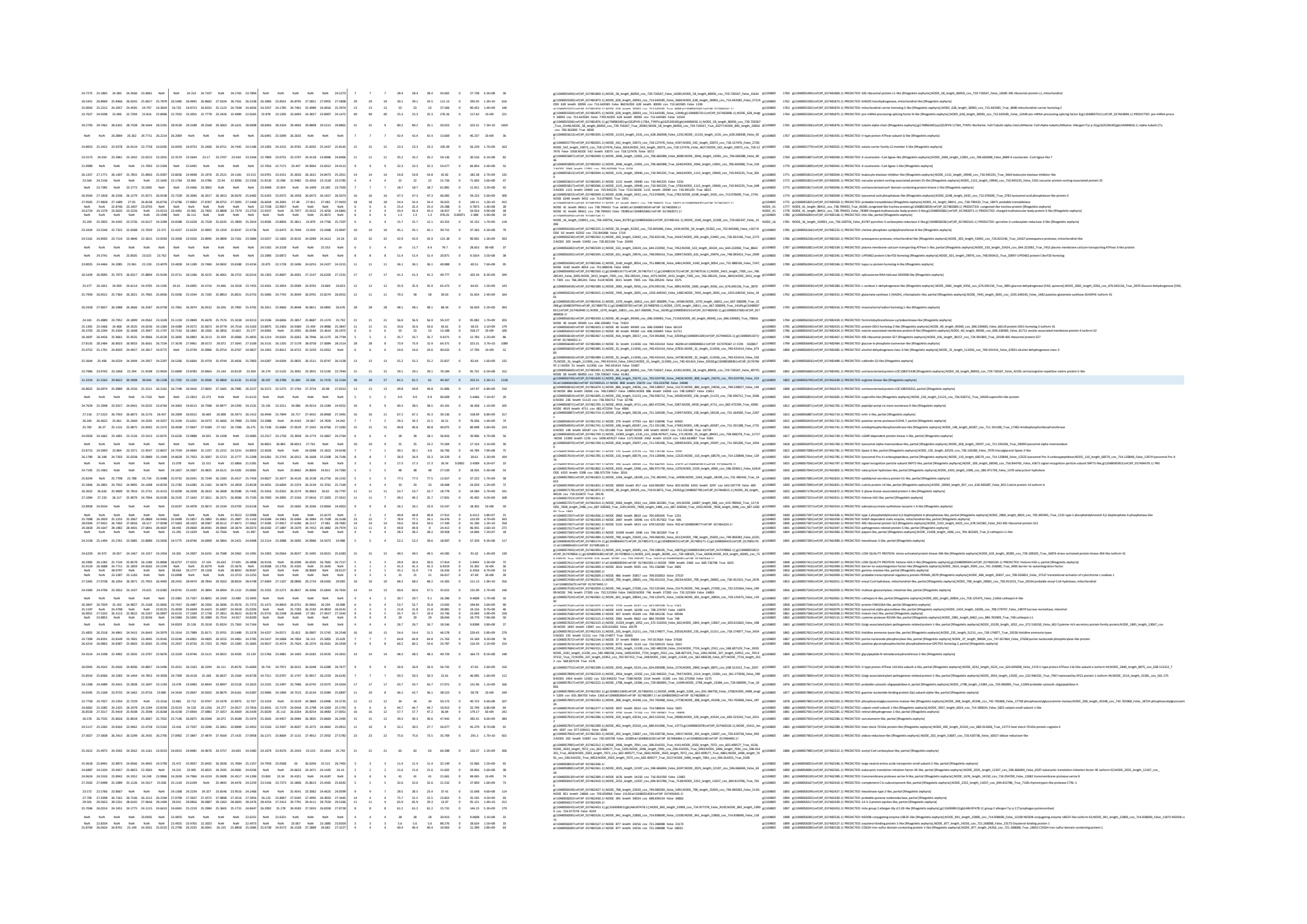


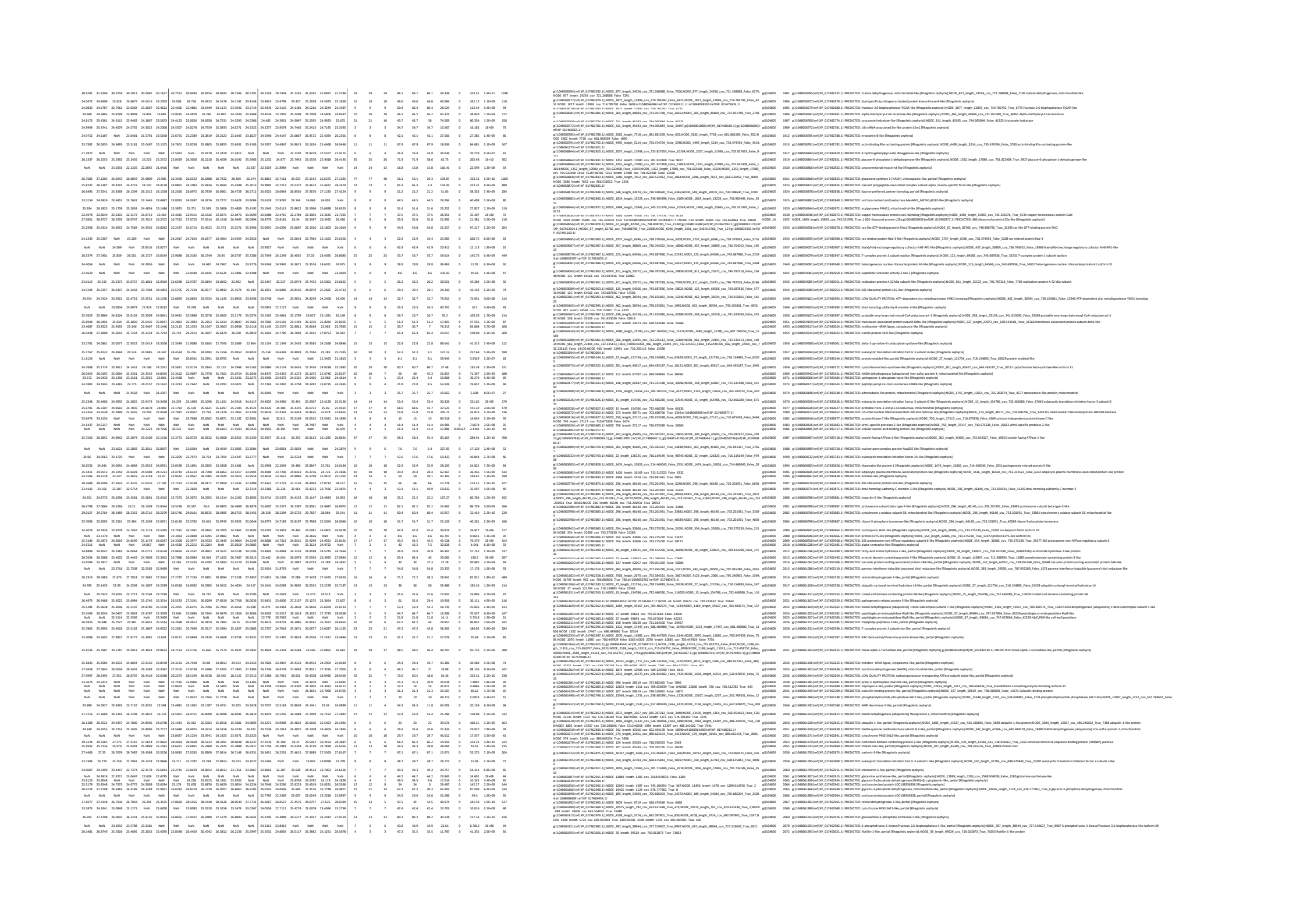


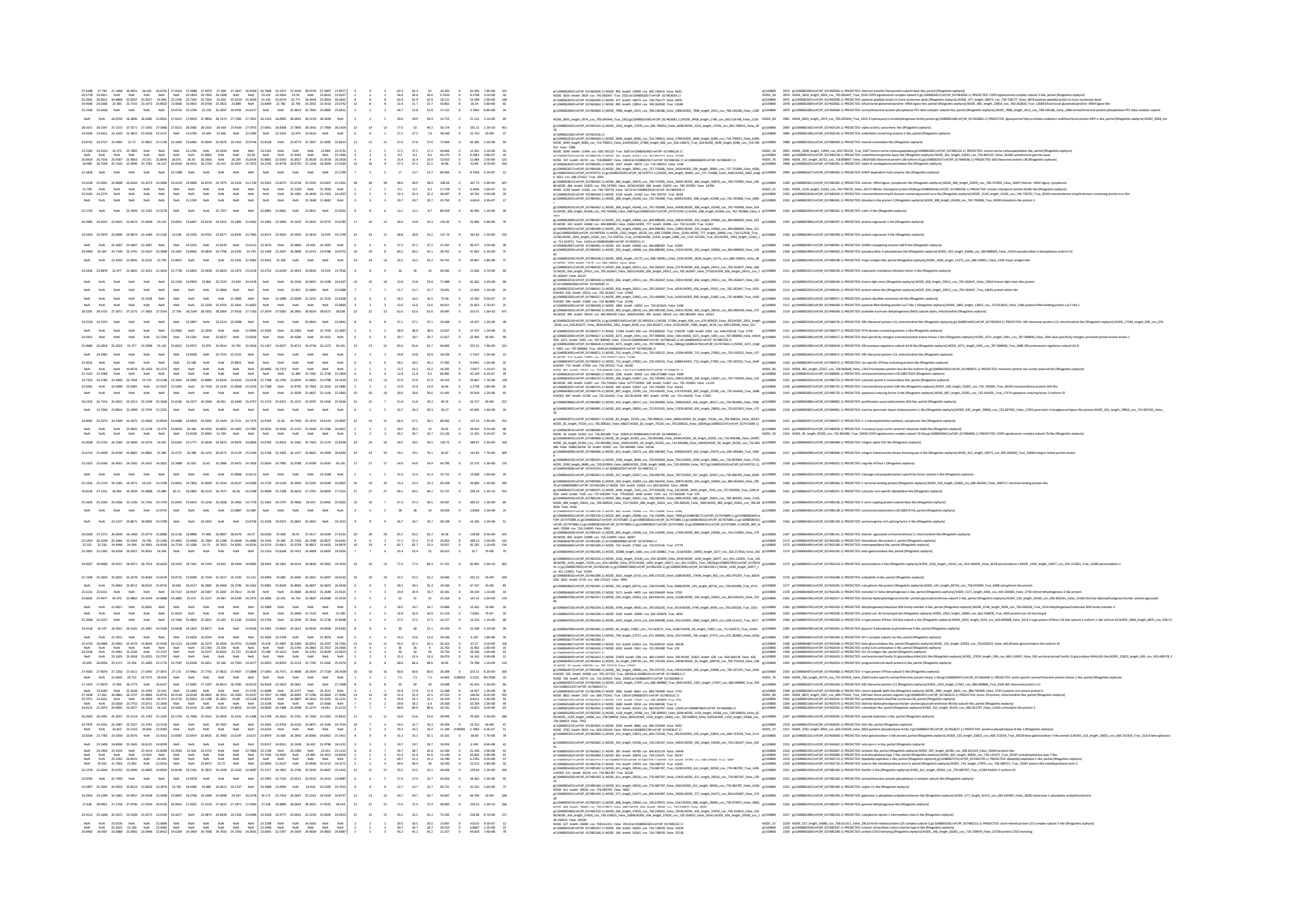


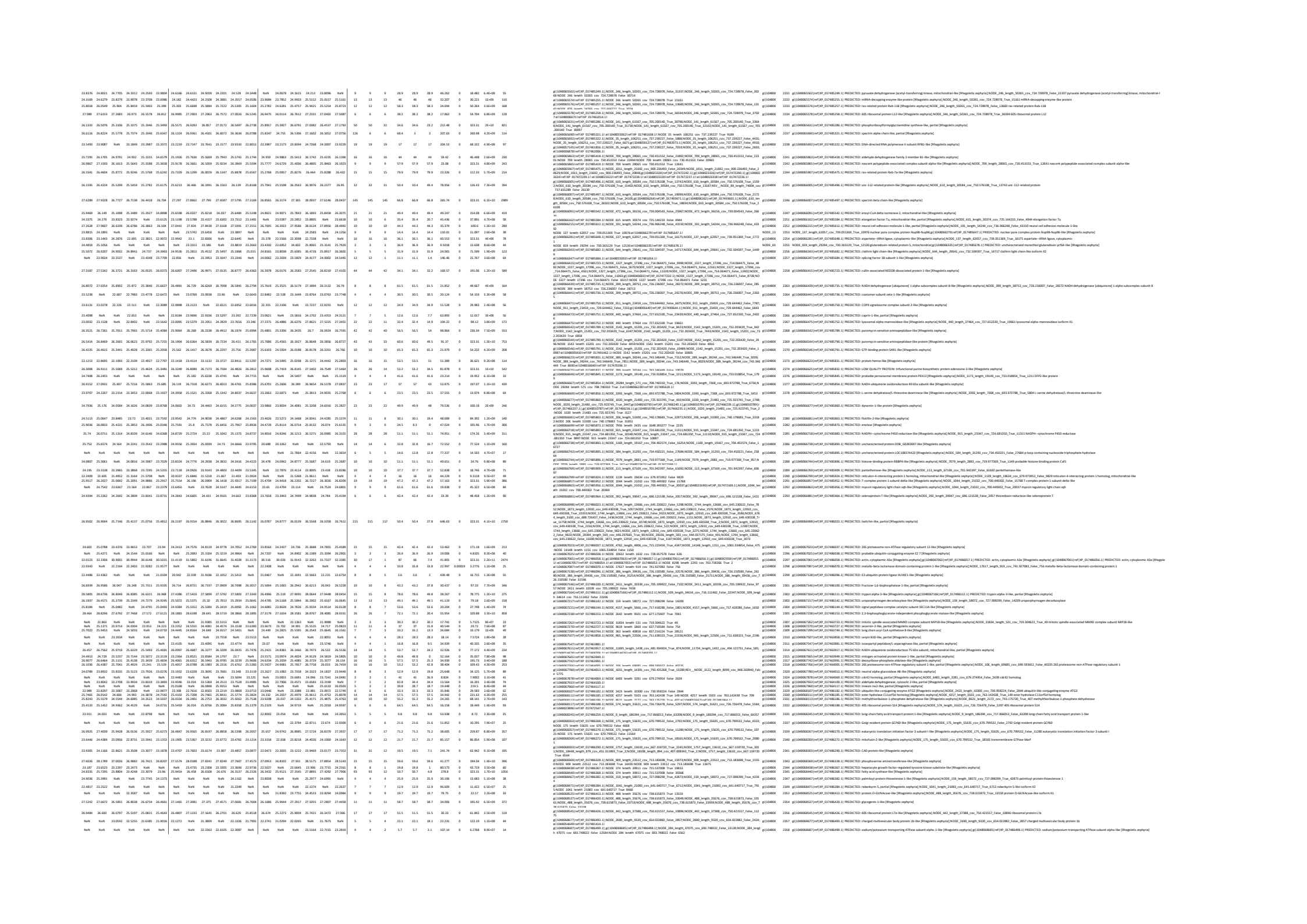


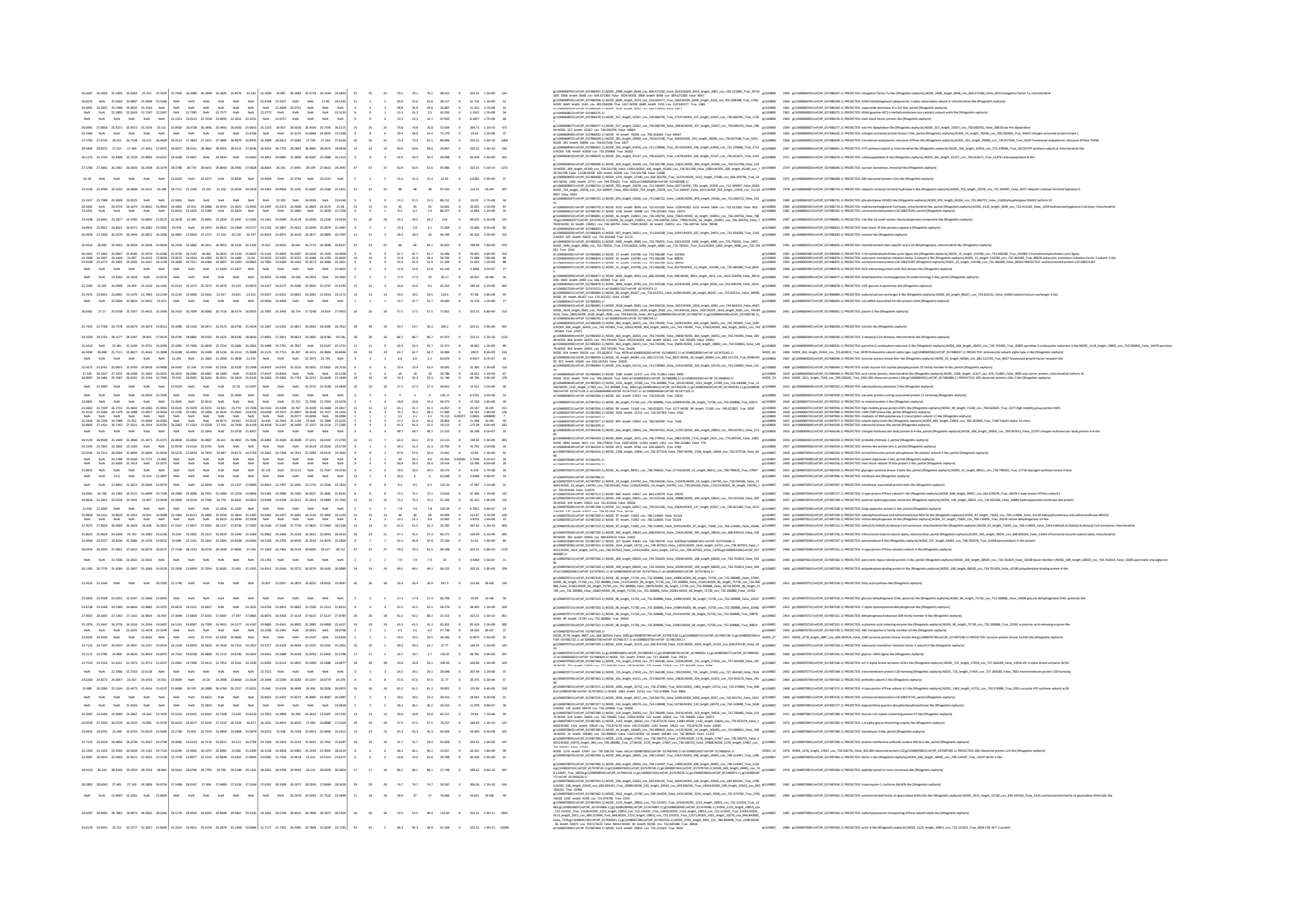


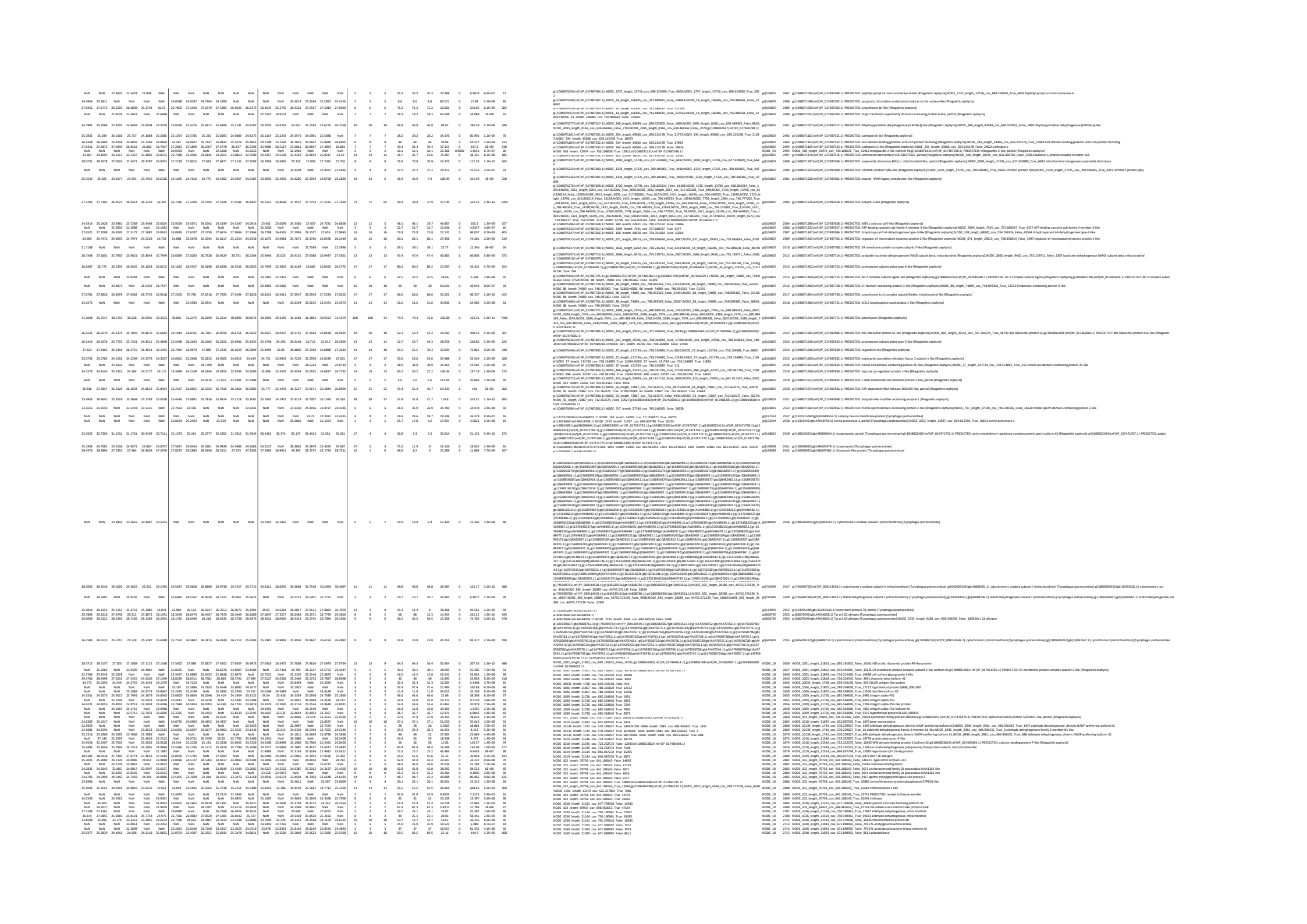


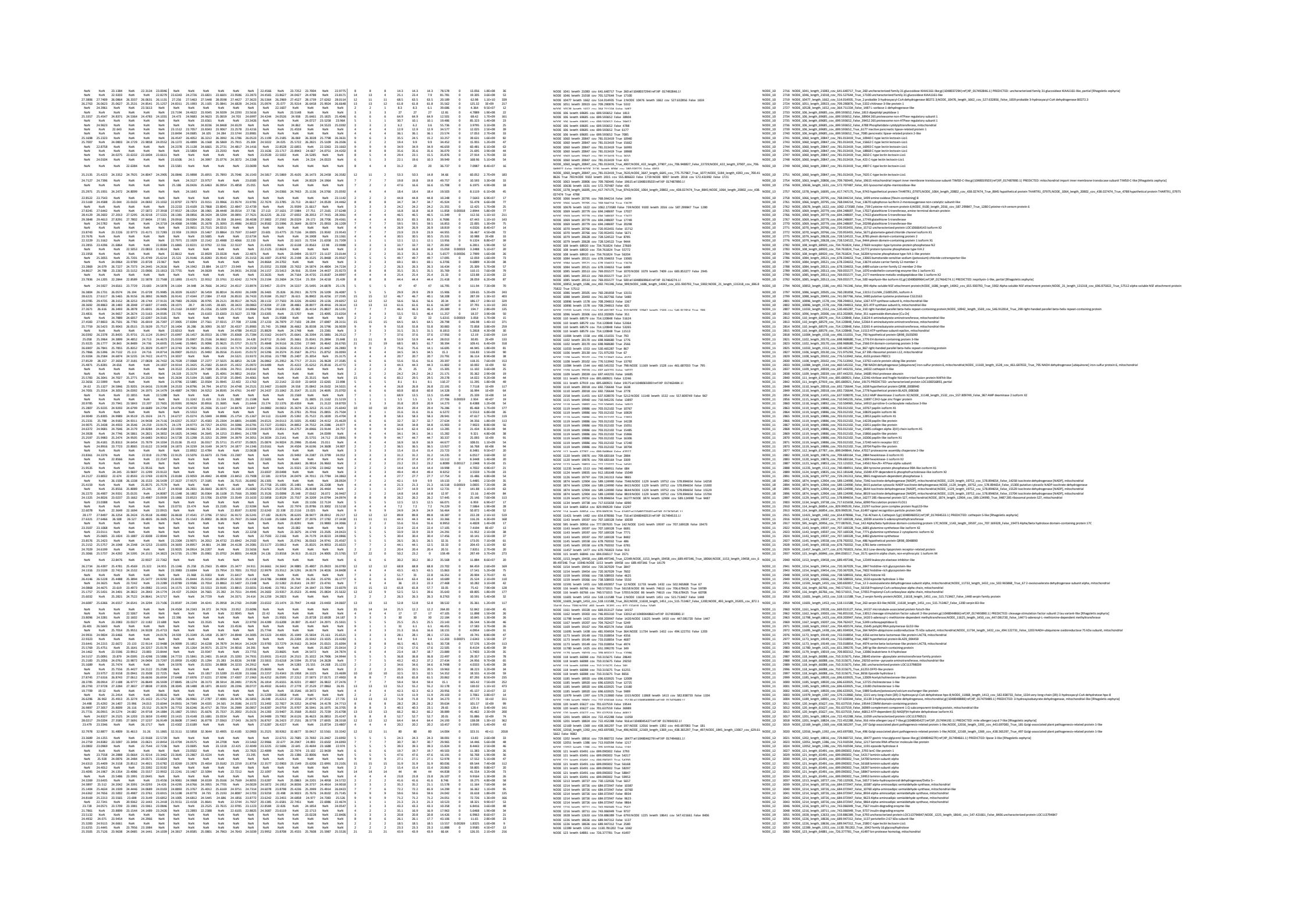


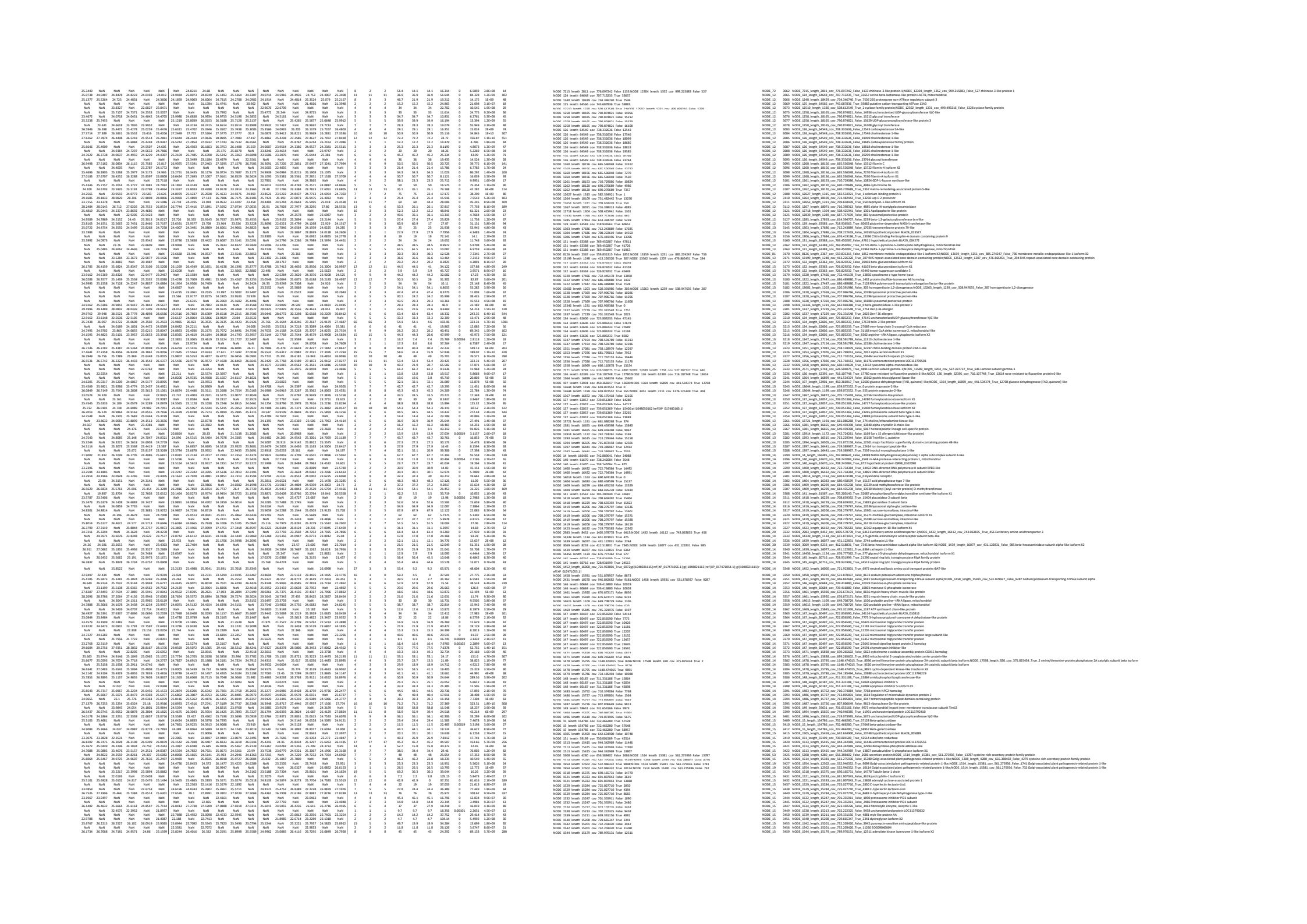


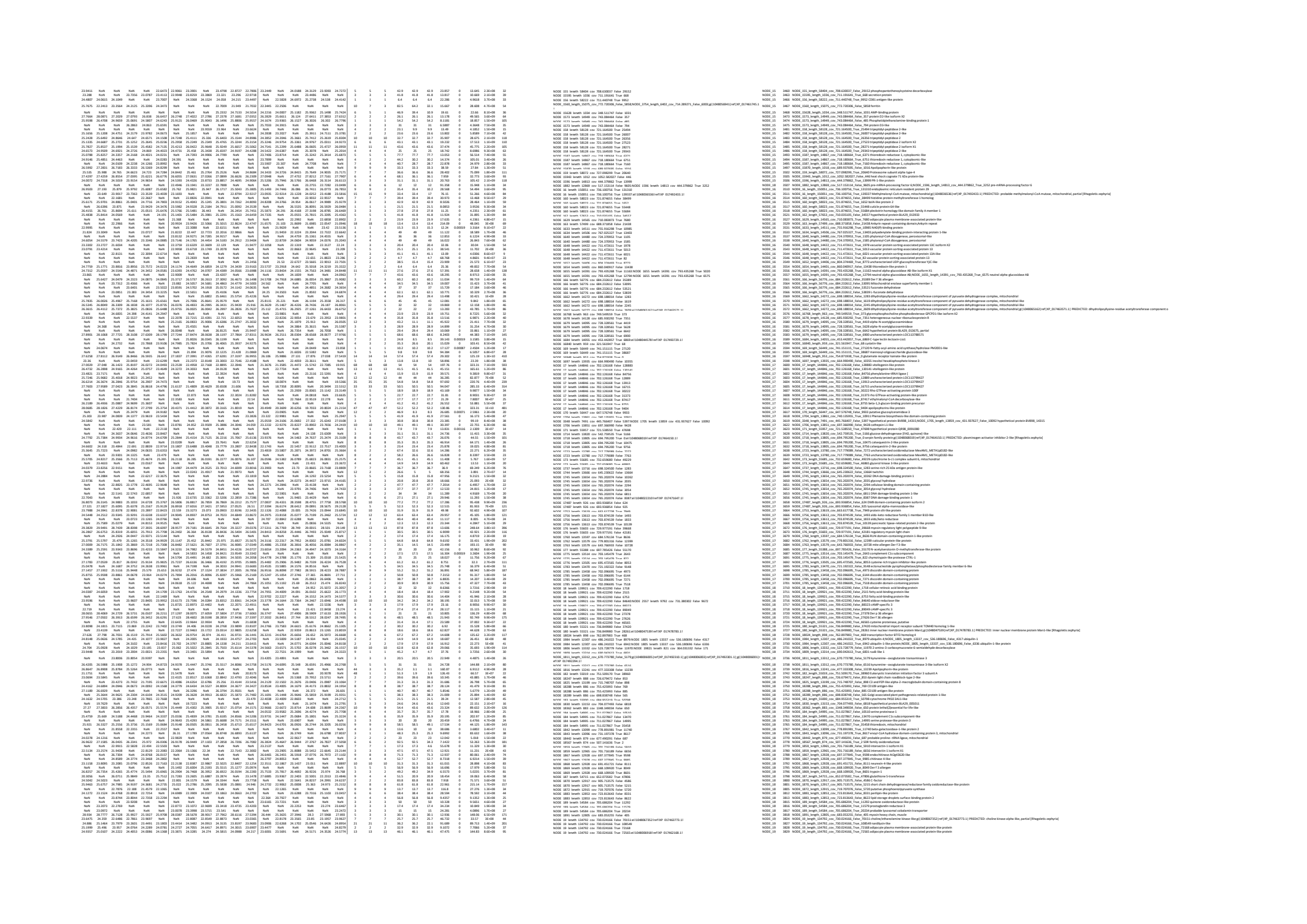


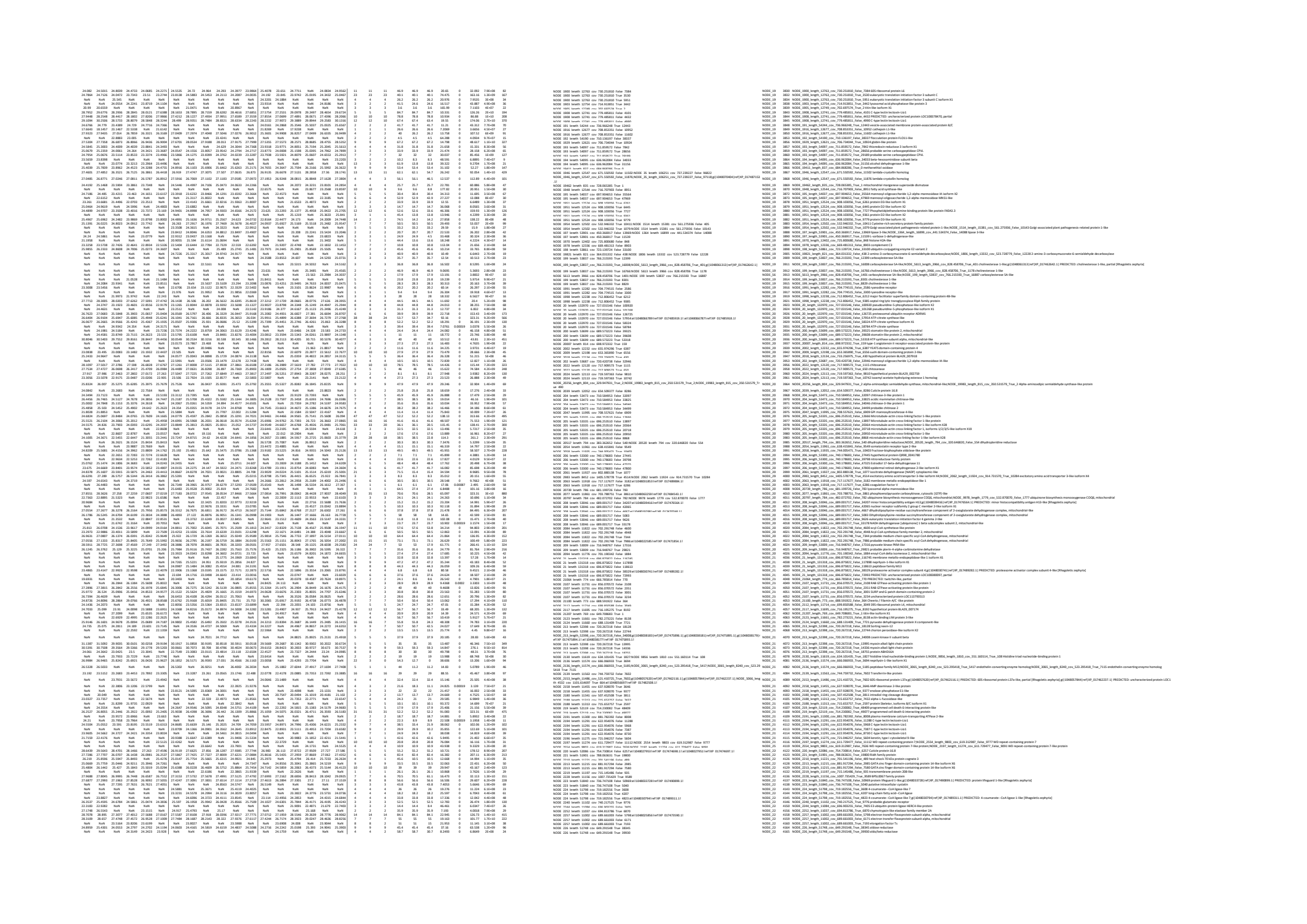




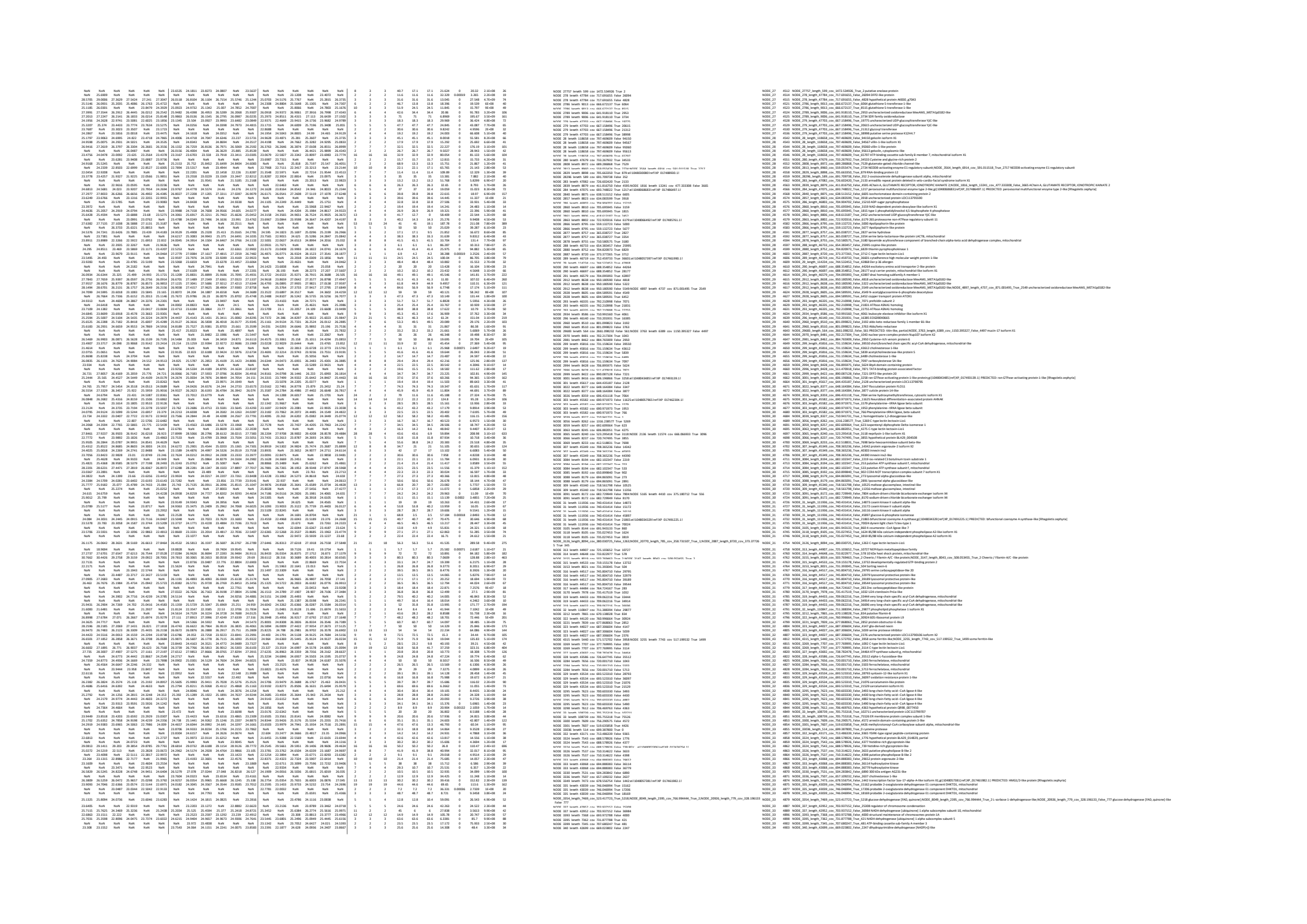


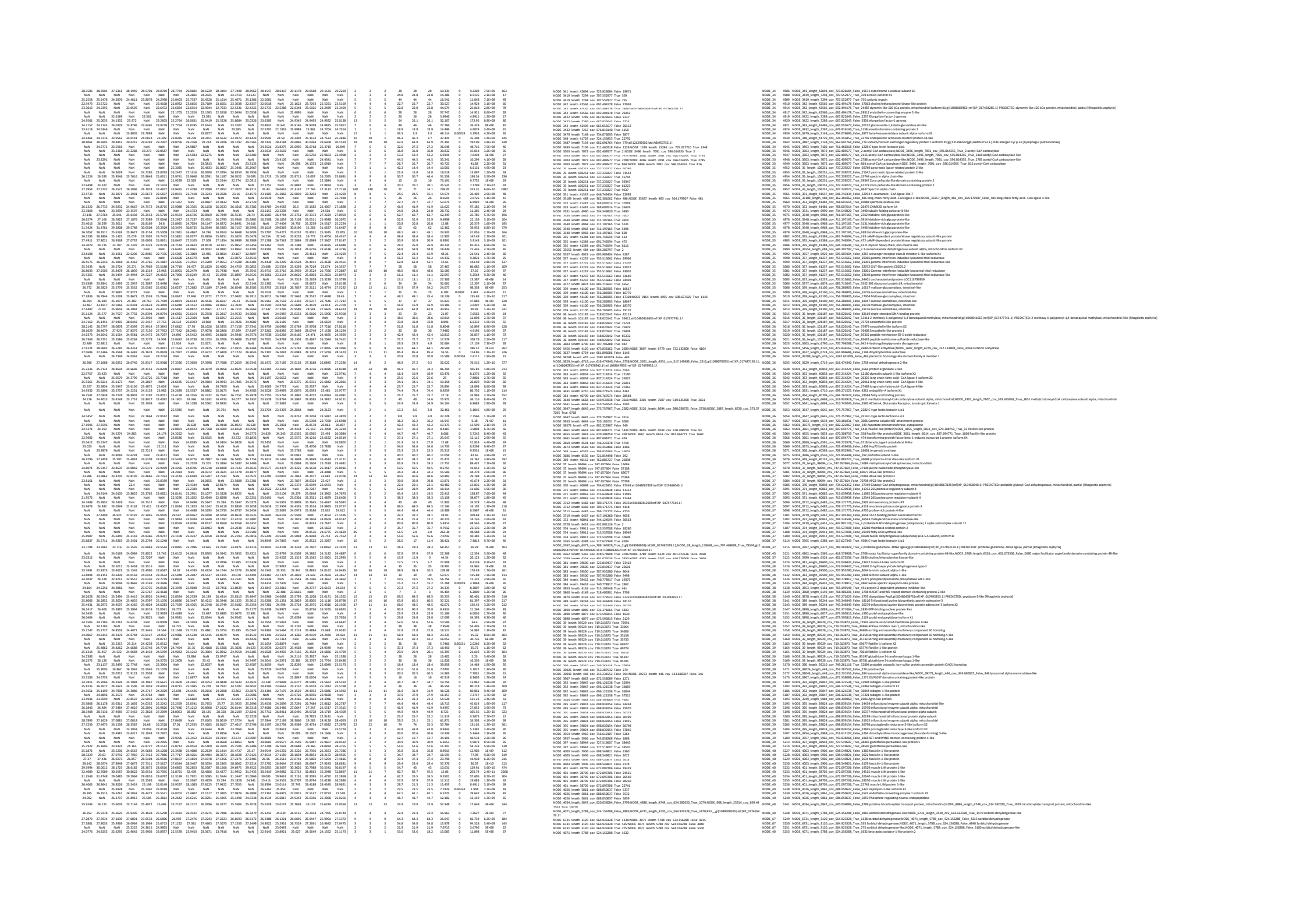


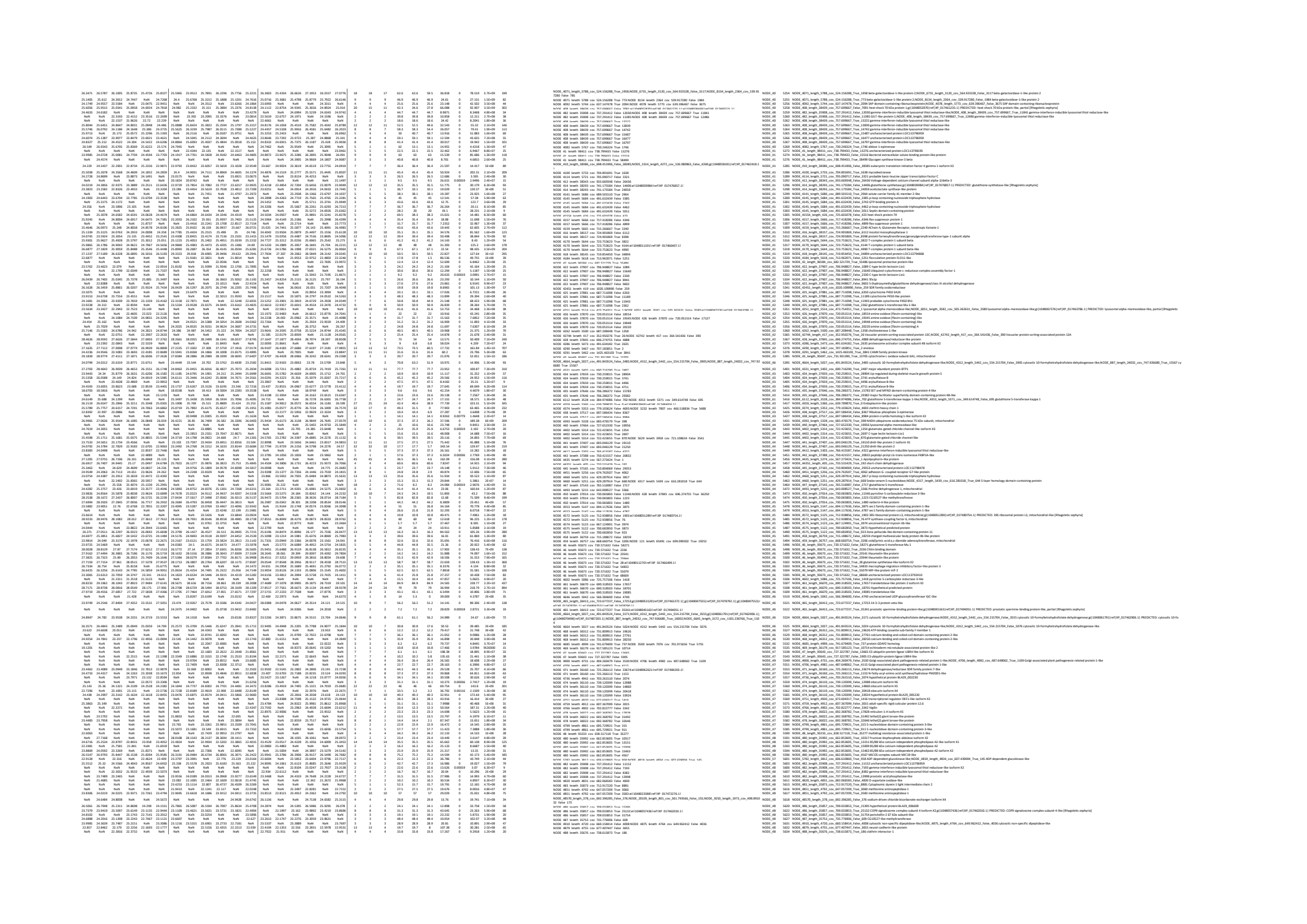


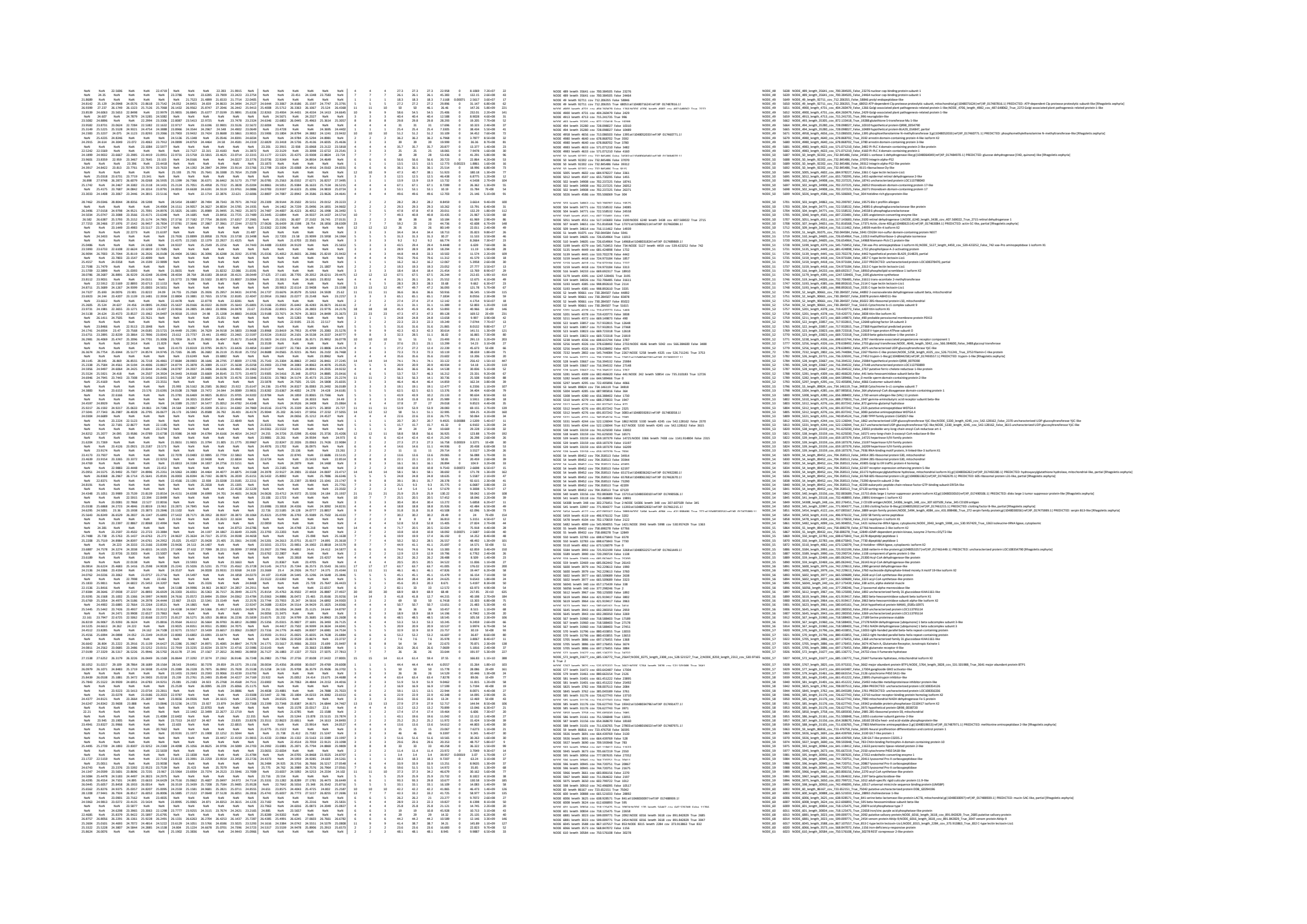


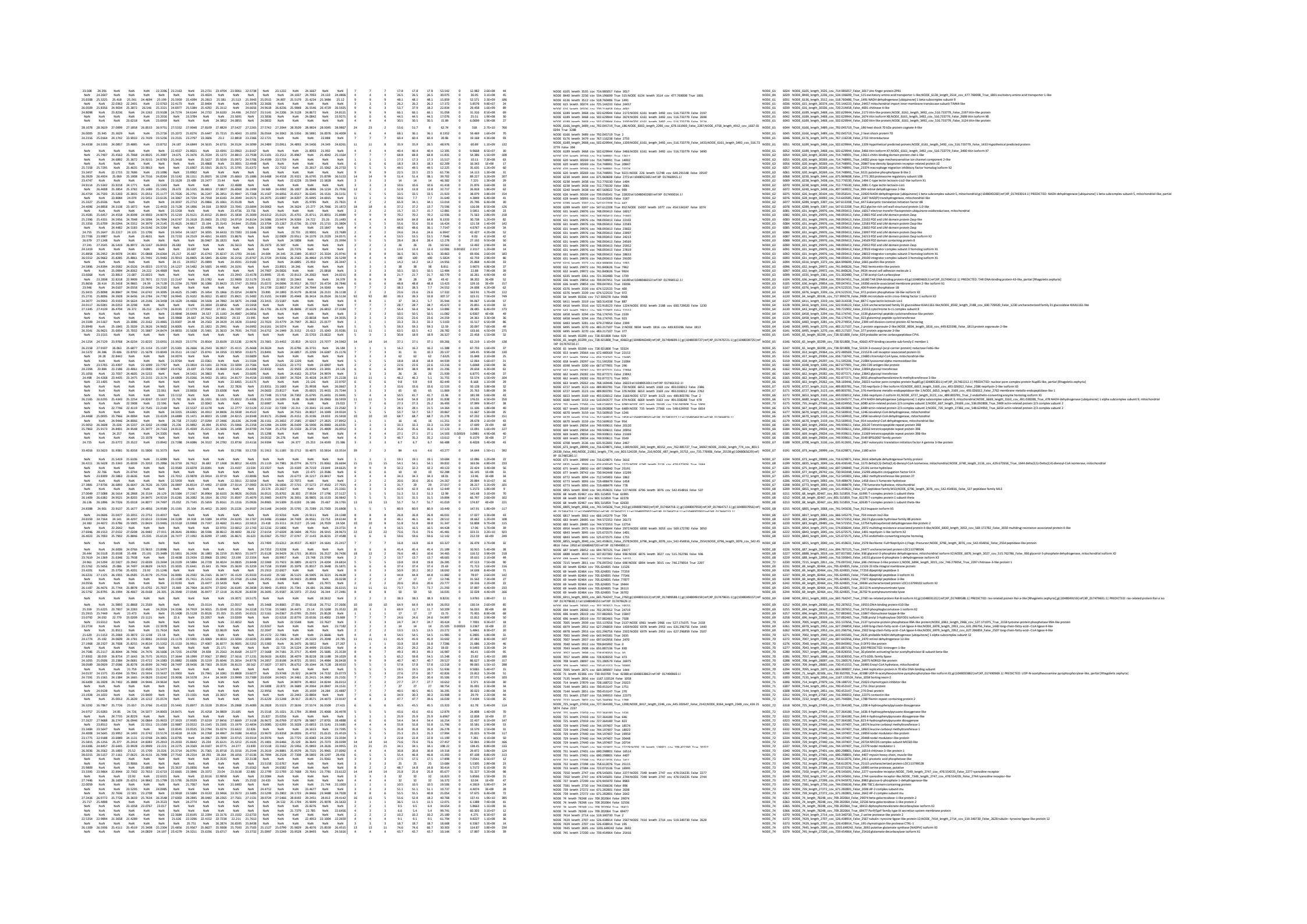


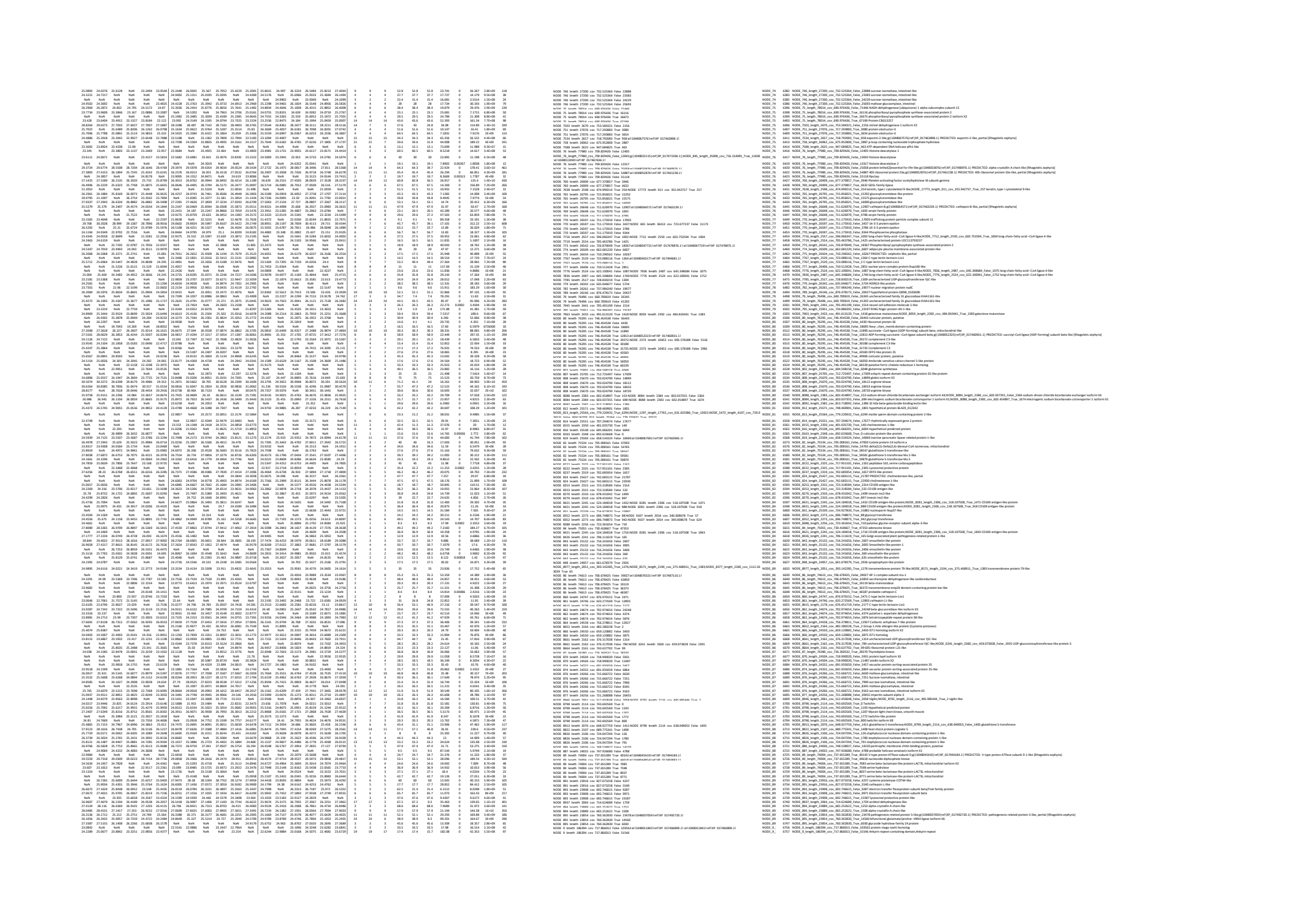


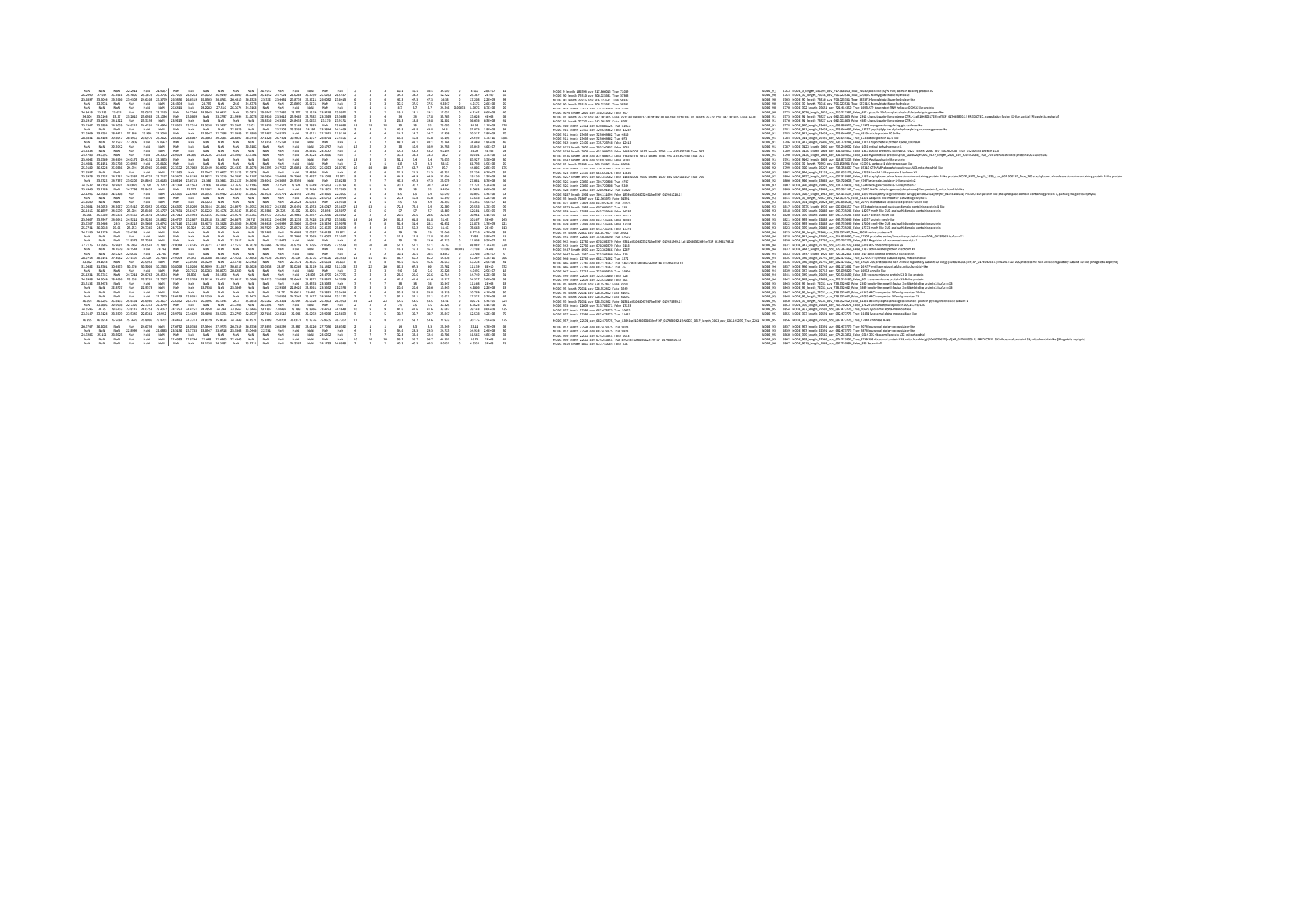






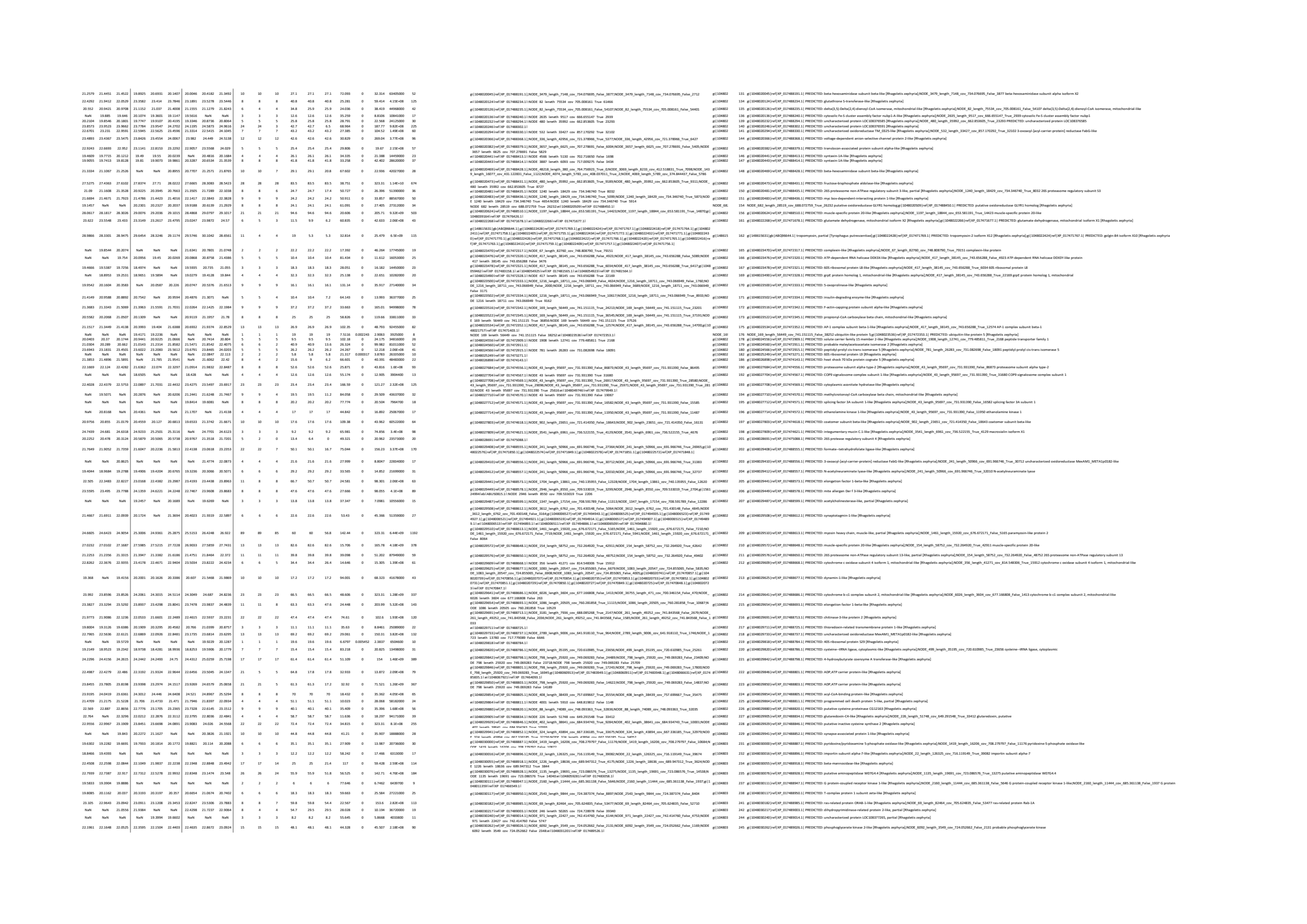


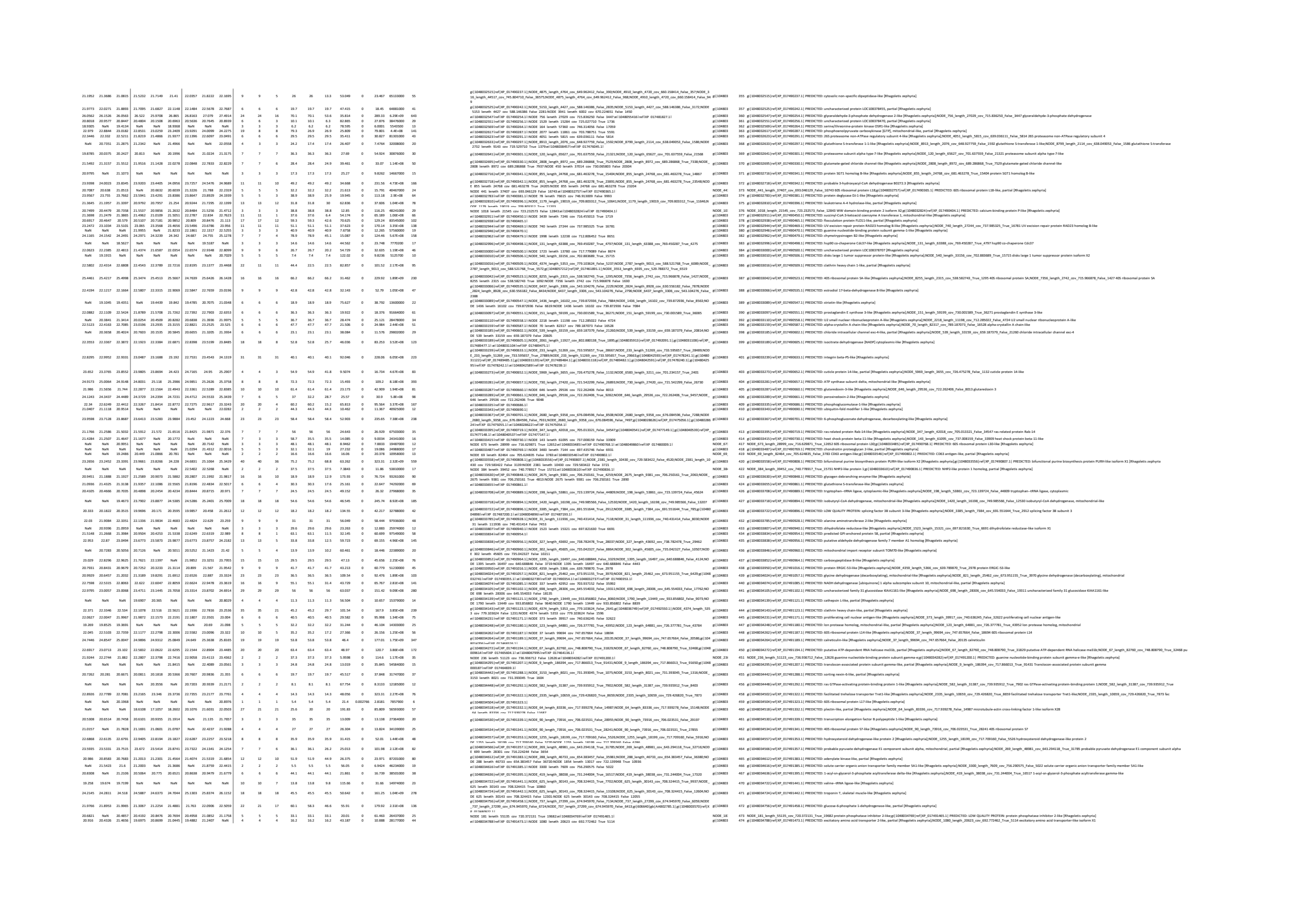


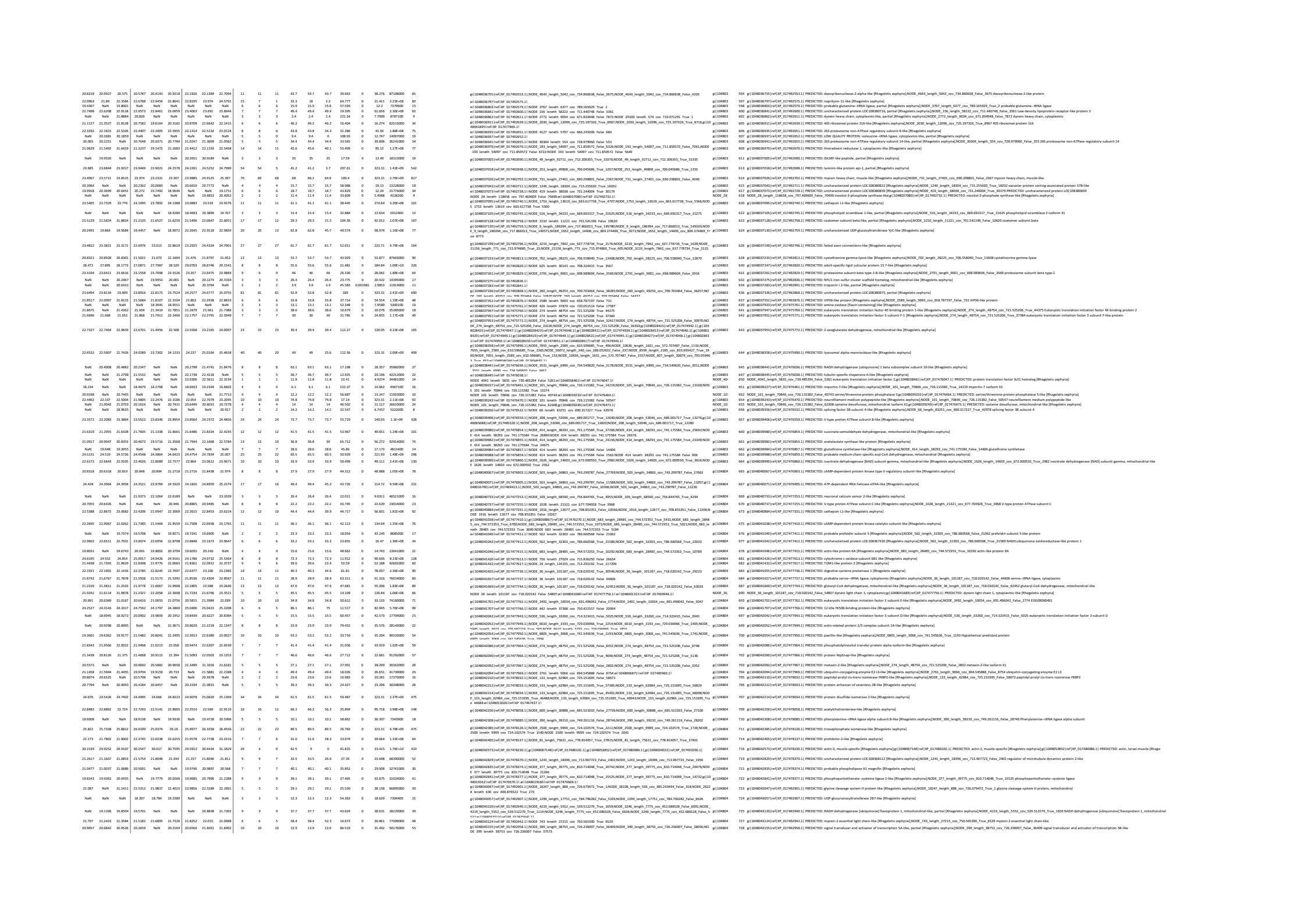


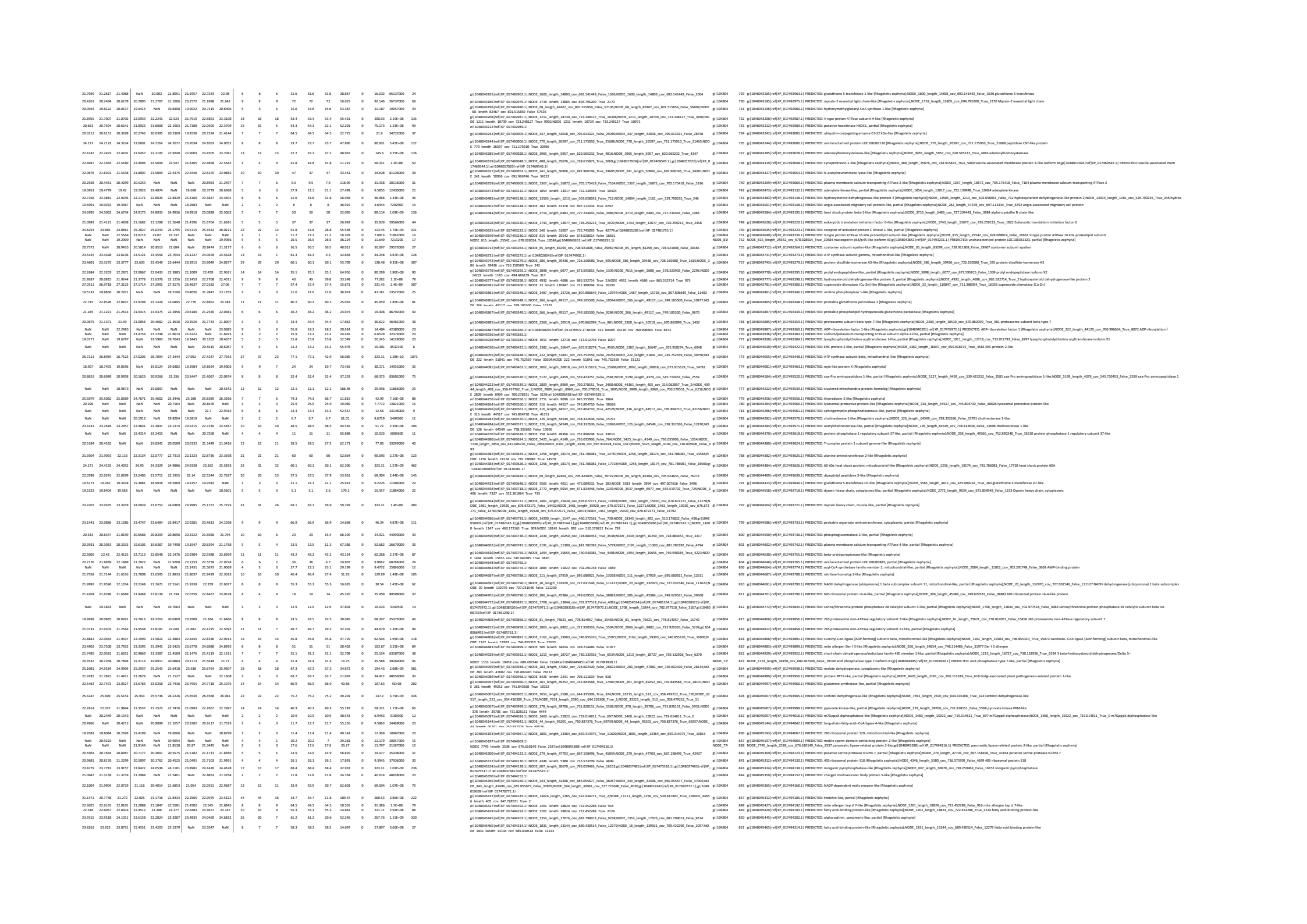
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24.3112	24.5602	NaN	NaN	23.7838	24.0339	24.7355	24.7538	24.8787	24.5793	24.9115	24.6907	23.2217	23.734	24.9421	24.9836	24.9384	24.8738	4	4	4	22.2	22.2	22.2	20.917	0	11.014	9.9E+08	84	NODE_9664_length_1859_cov_703.489468_False_1759	NODE_96	6874	NODE_9664_length_1859_cov_703.489468_False_1759 glutamate dehydrogenase, mitochondrial-like
26.6048	26.7819	25.3166	25.5232	24.8517	25.2447	26.5645	26.7979	26.695	26.7212	26.5292	26.177	25.767	24.9976	26.8818	27.7377	26.793	27.3603	4	4	4	43.3	43.3	43.3	18.232	0	25.602	2.8E+09	124	NODE_9664_length_1859_cov_703.489468_False_800	NODE_96	6875	NODE_9664_length_1859_cov_703.489468_False_800 glutamate dehydrogenase, mitochondrial
NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.4234	22.3218	24.0616	24.176	25.7138	26.9534	25.958	26.5275	4	4	4	30.2	30.2	30.2	30.309	0	87.036	6.9E+08	45	NODE_973_length_22370_cov_727.407797_True_12544	NODE_97	6883	NODE_973_length_22370_cov_727.407797_True_12544 immunogenic protein
25.5177	25.16	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.8914	NaN	NaN	NaN	NaN	NaN	5	5	1	30.4	30.4	3.9	33.836	0	22.832	3E+08	21	NODE_9744_length_1838_cov_560.980931_True_261	NODE_97	6884	NODE_9744_length_1838_cov_560.980931_True_261 retinol dehydrogenase 11-like
NaN	24.9839	NaN	23.7636	NaN	23.3333	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	4	4	4	52.4	52.4	52.4	11.935	0	16.182	3.6E+08	36	NODE_983_length_22232_cov_742.238445_False_1912	NODE_98	6888	NODE_983_length_22232_cov_742.238445_False_1912 U6 snRNA-associated Sm-like protein LSm3
NaN	NaN	22.8814	22.8776	23.4485	NaN	NaN	NaN	23.2436	NaN	NaN	22.1846	NaN	NaN	NaN	NaN	NaN	NaN	4	4	1	34.8	34.8	12.2	13.198	0	11.563	1.4E+08	23	NODE_9834_length_1816_cov_449.823396_False_631	NODE_98	6890	NODE_9834_length_1816_cov_449.823396_False_631 protein argonaute-2-like
NaN	NaN	NaN	NaN	NaN	NaN	24.1097	24.959	24.8589	25.4587	25.1224	24.6095	NaN	NaN	21.6758	NaN	NaN	20.7505	12	11	5	48.6	46.2	24.4	43.173	0	161.1	1E+09	87	NODE_9865_length_1808_cov_595.561894_True_494	NODE_98	6893	NODE_9865_length_1808_cov_595.561894_True_494 C-type lectin lectoxin-Lio1
27.1532	27.0315	25.6954	25.6997	25.5172	25.4723	25.8426	26.8585	26.5709	26.6934	26.0628	25.6515	25.5194	25.231	26.5996	27.1597	26.6954	27.2071	9	9	9	37.9	37.9	37.9	28.641	0	96.98	4.4E+09	158	NODE_99_length_71160_cov_740.022825_True_4757	NODE_99	6894	NODE_99_length_71160_cov_740.022825_True_4757 hypothetical protein QR98_0039000
25.6793	25.4626	25.167	25.4095	25.1642	25.1517	25.6039	26.0964	26.2104	25.9896	25.7173	25.7343	24.852	24.5563	25.2542	24.4606	24.2388	25.6472	11	11	11	44.7	44.7	44.7	28.687	0	31.45	2.1E+09	110	NODE_99_length_71160_cov_740.022825_True_65417	NODE_99	6895	NODE_99_length_71160_cov_740.022825_True_65417 tetratricopeptide repeat protein
NaN	24.1096	23.0545	23.2703	22.9381	22.7885	21.9248	22.8392	NaN	22.7378	22.3191	NaN	22.9747	22.9103	23.8069	23.5399	23.4081	23.6656	3	3	3	33.3	33.3	33.3	20.062	0	13.05	2.4E+08	44	NODE_992_length_22012_cov_665.666576_True_17286	NODE_99	6899	NODE_992_length_22012_cov_665.666576_True_17286 GA25341
26.8891	27.2357	26.1052	26.0532	25.9421	25.7741	26.0121	26.3388	26.265	26.3389	25.9759	25.8004	25.2369	25.0605	26.3529	26.5081	26.3031	26.6126	10	10	2	55.4	55.4	10.7	31.416	0	104.84	5.4E+09	253	NODE_9922_length_1795_cov_400.276437_False_1712	NODE_99	6901	NODE_9922_length_1795_cov_400.276437_False_1712 gastric triacylglycerol lipase-like
26.172	NaN	26.0131	25.2239	25.4449	24.9391	26.0441	26.1565	26.2958	25.9761	25.5037	25.4333	26.0451	24.618	26.1886	NaN	NaN	NaN	5	5	5	54.9	54.9	54.9	9.824	0	38.404	1.5E+09	54	NODE_995_length_21948_cov_685.502489_False_18071	NODE_99	6904	NODE_995_length_21948_cov_685.502489_False_18071 uncharacterized protein LOC113790842
25.1188	25.3544	24.1108	24.3382	23.6428	23.4499	24.8468	25.1006	25.2531	25.3508	24.9152	24.7698	23.4211	NaN	24.5408	25.3455	25.0348	25.2427	5	5	5	31.6	31.6	31.6	15.244	0	67.663	9.4E+08	115	NODE_995_length_21948_cov_685.502489_False_18511	NODE_99	6905	NODE_995_length_21948_cov_685.502489_False_18511 hypothetical protein QR98_0059340
24.8589	25.2932	23.7554	23.6264	23.8678	23.459	24.0302	24.5359	24.5091	24.8353	24.3768	24.2543	23.8133	23.9623	24.895	25.5445	25.2905	25.3478	9	9	9	60.2	60.2	60.2	23.998	0	227.32	1.4E+09	152	NODE_9958_length_1784_cov_692.514748_False_753	NODE_99	6907	NODE_9958_length_1784_cov_692.514748_False_753 probable 3-hydroxyacyl-CoA dehydrogenase B0272.3

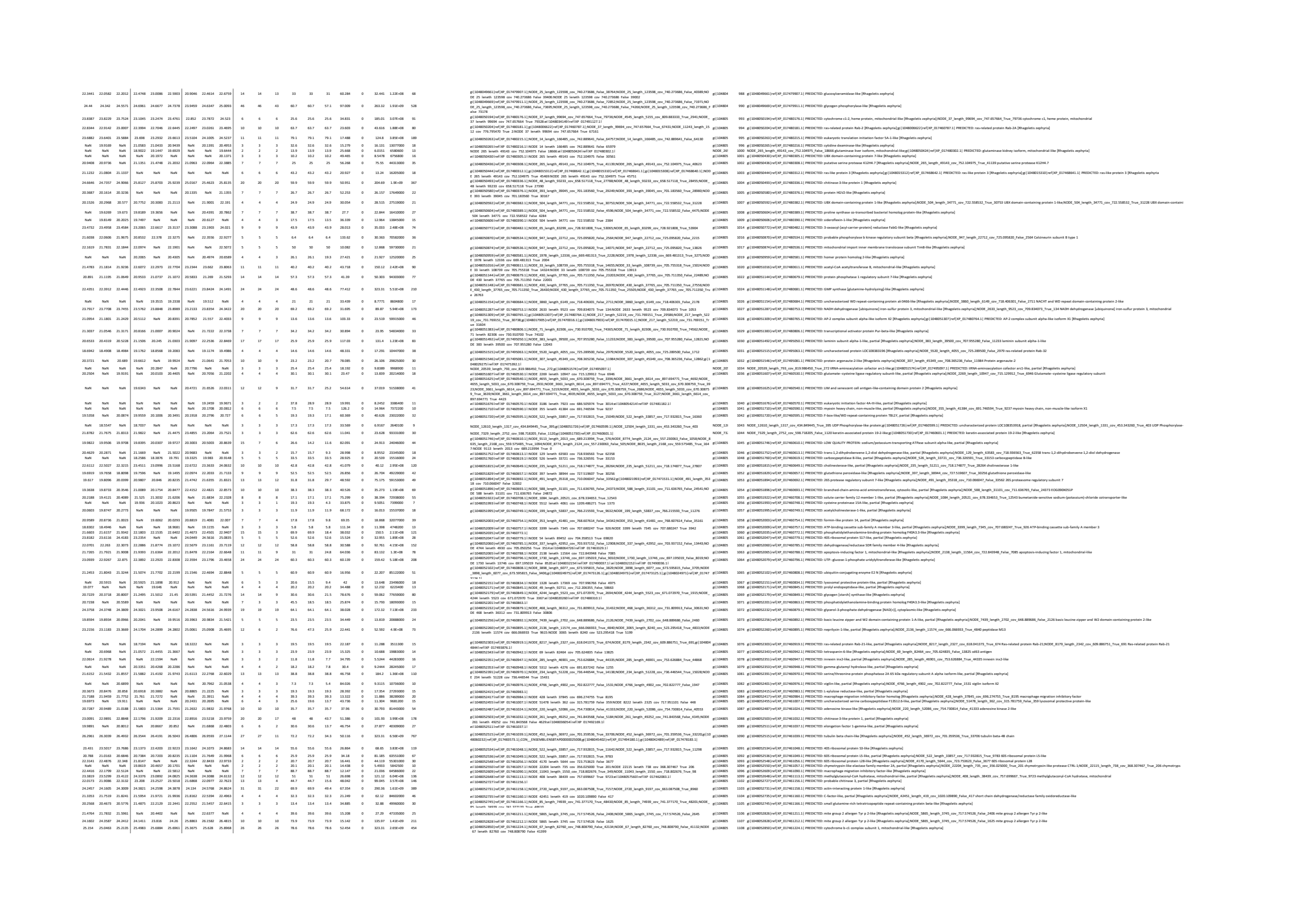
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<tr><td colspan="20"></td><td>Tyr p 7: ABM53750.1</td><td>gi|121296508|gb|ABM53755.1|;gi|121296498|gb|ABM53750.1|;gi|1048067242|ref|XP_017486155.1|;NODE_594_length_30961_cov_727.715686_True_29994;NODE_594_length_30961_cov_727.715686_True_30400</td><td colspan="5"></td></tr>
<tr><td>21.593</td><td>22.3071</td><td>22.1457</td><td>NaN</td><td>20.7352</td><td>21.3769</td><td>21.5475</td><td>21.9611</td><td>23.7328</td><td>6</td><td>6</td><td>6</td><td>42.5</td><td>42.5</td><td>42.5</td><td>22.54</td><td>0</td><td>20.773</td><td>95396000</td><td>70</td><td></td><td>gi|121296508|gb|ABM53755.1|;gi|121296498|gb|ABM53750.1|;gi|1048067242|ref|XP_017486155.1|;NODE_594_length_30961_cov_727.715686_True_30400</td><td>gi|121296</td><td>1559</td><td>gi|121296508|gb|ABM53755.1| mite allergen Tyr p 7 [Tyrophagus putrescentiae];gi|121296498|gb|ABM53750.1| mite allergen Tyr p 7 [Tyrophagus putrescentiae];gi|1048067242|ref|XP_017486155.1| PREDICTED: mite allergen Lep d 7-like [Rhagoletis zephyria];NODE_594</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 8:AGG10560.1 MISLEADING - not detected, only in the raw dataset 3X6 and 3X3</td><td>gi|452215228|gb|AGG10560.1| Tyr p 8 allergen [Tyrophagus putrescentiae];gi|1679377507|sp|M1RIR6.1|GSTM_TYRPU RecName: Full=Glutathione S-transferase;AltName: Full=GST class-mu;AltName: Allergen=Tyr p 8</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td></td><td>gi|452215228|gb|AGG10560.1| Tyr p 8 allergen [Tyrophagus putrescentiae];gi|1679377507|sp|M1RIR6.1|GSTM_TYRPU RecName: Full=Glutathione S-transferase;AltName: Full=GST class-mu;AltName: Allergen=Tyr p 8</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td>Tyr p 10: AAT40866.1</td><td>gi|48249227|gb|AAT40866.1|;NODE_1891_length_12805_cov_683.053255_False_8676</td><td colspan="5"></td></tr>
<tr><td>28.8993</td><td>28.9193</td><td>29.1606</td><td>29.2186</td><td>28.7058</td><td>29.1168</td><td>29.0539</td><td>29.6203</td><td>29.4852</td><td>31</td><td>31</td><td>0</td><td>65.1</td><td>65.1</td><td>0</td><td>32.954</td><td>0</td><td>323.31</td><td>2.72E+10</td><td>1009</td><td></td><td>gi|48249227|gb|AAT40866.1|</td><td>gi|482492</td><td>1728</td><td>gi|48249227|gb|AAT40866.1| tropomyosin, partial [Tyrophagus putrescentiae]</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 13: AAU11502.1</td><td>gi|51860756|gb|AAU11502.1|;gi|1048052294|ref|XP_017460914.1|;gi|156938917|gb|ABU97480.1|;NODE_965_length_22506_cov_711.638323_False_16202</td><td colspan="5"></td></tr>
<tr><td>25.9317</td><td>25.3463</td><td>25.5325</td><td>25.2698</td><td>25.3834</td><td>25.9497</td><td>25.6577</td><td>25.8563</td><td>26.1056</td><td>13</td><td>8</td><td>8</td><td>74.8</td><td>62.6</td><td>62.6</td><td>14.573</td><td>0</td><td>64.017</td><td>9.85E+08</td><td>110</td><td></td><td>gi|51860756|gb|AAU11502.1|;gi|1048052294|ref|XP_017460914.1|;gi|156938917|gb|ABU97480.1|;NODE_965_length_22506_cov_711.638323_False_16202</td><td>gi|518607</td><td>1075</td><td>gi|51860756|gb|AAU11502.1| fatty acid-biding protein [Tyrophagus putrescentiae];gi|1048052294|ref|XP_017460914.1| PREDICTED: fatty acid-binding protein-like [Rhagoletis zephyria];gi|156938917|gb|ABU97480.1| allergen Tyr p 13 [Tyrophagus putrescentiae];NODE</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 20</td><td>gi|1048056749|ref|XP_017461640.1|;NODE_808_length_25670_cov_703.024790_False_24626;NODE_808_length_25670_cov_703.024790_False_25355;gi|1048044186|ref|XP_017493521.1|;NODE_808_length_25670_cov_703.024790_False_24948</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td>GenPept: QOI58528.1</td><td>>gi|1914565355|gb|QOI58528.1| arginine kinase [Tyrophagus putrescentiae]
MVDQATLDKLEAGFKKLQSSGDACHSLLKKYLTEDVFNKLKDKKTGMGATLLDVIQSGVENLDSGVGLYA
PDAEAYTLFADLFNPVIEGYHGGFKSTDKHPPSDFGDINQLVNVDPNNEFVISTRVRCGRSLQGYPFNPC
LTEAQYKEMEEKVKAQLESFEGELKGTYYPLTGMDKATQQQLIDDHFLFKEGDRFLQAANACRFWPTGRG
IFHNASKTFLMWVNEEDHLRIISMQKGGDLKEVFGRLVKAVQHIEKKIPFSRDDRLGFLTFCPTNLGTTI
RASVHIKLPKLAADRKKLEEVAAKYNLQVRGTAGEHTESVGGVYDISNKRRMGLTEYQAVKEMQDGILEL
IKIEKSL</td><td colspan="5"></td></tr>
<tr><td>26.5895</td><td>26.604</td><td>26.5643</td><td>27.1855</td><td>26.7223</td><td>27.1608</td><td>27.2026</td><td>27.5961</td><td>27.9185</td><td>34</td><td>34</td><td>23</td><td>78.7</td><td>78.7</td><td>55.3</td><td>40.367</td><td>0</td><td>323.31</td><td>6E+09</td><td>585</td><td></td><td>gi|1048056749|ref|XP_017461640.1|;NODE_808_length_25670_cov_703.024790_False_24626;gi|1048044186|ref|XP_017493521.1|;NODE_808_length_25670_cov_703.024790_False_25355;NODE_808_length_25670_cov_703.024790_False_24948</td><td>gi|104805</td><td>1222</td><td>gi|1048056749|ref|XP_017461640.1| PREDICTED: arginine kinase-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 28: AOD75395.1</td><td>gi|1055365842|gb|AOD75395.1|</td><td colspan="5"></td></tr>
<tr><td>23.6227</td><td>23.5049</td><td>23.5709</td><td>23.779</td><td>23.5142</td><td>23.6511</td><td>24.3719</td><td>24.4683</td><td>24.7205</td><td>15</td><td>5</td><td>0</td><td>22.9</td><td>7.1</td><td>0</td><td>72.31</td><td>0</td><td>42.461</td><td>3.31E+08</td><td>90</td><td></td><td>gi|1055365842|gb|AOD75395.1|</td><td>gi|105536</td><td>1716</td><td>gi|1055365842|gb|AOD75395.1| heat shock-like protein [Tyrophagus putrescentiae]</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 34-39: ACL36923.1</td><td>gi|219815476|gb|ACL36923.1|;gi|1679377553|sp|D2DGW3.1|TNNC_TYRPU;NODE_312_length_45145_cov_683.923797_True_27198;NODE_312_length_45145_cov_683.923797_True_27389</td><td colspan="5"></td></tr>
<tr><td>27.0252</td><td>27.1629</td><td>27.3599</td><td>27.4966</td><td>27.4192</td><td>27.2161</td><td>27.8155</td><td>27.9269</td><td>27.5285</td><td>13</td><td>13</td><td>13</td><td>47.7</td><td>47.7</td><td>47.7</td><td>17.692</td><td>0</td><td>210.46</td><td>3.76E+09</td><td>488</td><td></td><td>gi|219815476|gb|ACL36923.1|;gi|1679377553|sp|D2DGW3.1|TNNC_TYRPU;NODE_312_length_45145_cov_683.923797_True_27198;NODE_312_length_45145_cov_683.923797_True_27389</td><td>gi|219815</td><td>1724</td><td>gi|219815476|gb|ACL36923.1| troponin C [Tyrophagus putrescentiae];gi|1679377553|sp|D2DGW3.1|TNNC_TYRPU RecName: Full=Troponin C;AltName: Full=Allergen Tyr p 24;AltName: Allergen=Tyr p 24.0101;NODE_312_length_45145_cov_683.923797_True_27198 troponin C</td><td></td><td></td></tr>
<tr><td colspan="20"></td><td>Tyr p 35-new group (?! Tyr p 35 ~ Der f Alt a 10): AOD75396.1 MISLEADING - not detected, only in the raw dataset 3X6, but not 3X3</td><td>gi|1055365860|gb|AOD75396.1| aldehyde dehydrogenase-like protein [Tyrophagus putrescentiae]</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td></td><td>Not detected</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td>Tyr p 36: AOD75399.1</td><td>NODE_503_length_34863_cov_743.299787_False_19189;gi|1055365943|gb|AOD75399.1|</td><td colspan="5"></td></tr>
<tr><td colspan="20"></td><td></td><td>Not detected</td><td colspan="5"></td></tr>
<tr><td>21.4709</td><td>21.676</td><td>21.8355</td><td>21.8534</td><td>21.8519</td><td>21.9841</td><td>22.325</td><td>22.2814</td><td>23.4107</td><td>17</td><td>2</td><td>1</td><td>33.4</td><td>8.6</td><td>6.3</td><td>72.523</td><td>0</td><td>32.367</td><td>73307000</td><td>41</td><td></td><td>gi|1023044021|gb|ANA96231.1|;NODE_1743_length_13677_cov_726.259213_False_13674</td><td>gi|102304</td><td>45</td><td>gi|1023044021|gb|ANA96231.1| heat shock protein [Tyrophagus putrescentiae]</td><td></td><td></td></tr>
<tr><td>22.9104</td><td>22.9829</td><td>23.162</td><td>23.0652</td><td>22.6067</td><td>22.6328</td><td>23.4892</td><td>23.8804</td><td>23.9126</td><td>24</td><td>24</td><td>11</td><td>43.6</td><td>43.6</td><td>23.9</td><td>72.754</td><td>0</td><td>149.12</td><td>4.42E+08</td><td>167</td><td></td><td>gi|1023044023|gb|ANA96232.1|;NODE_17362_length_932_cov_1327.148233_False_931;gi|1048068998|ref|XP_017486664.1|;NODE_827_length_25396_cov_716.219171_False_25393;NODE_8561_length_2196_cov_809.535264_False_407;NODE_827_length_25396_cov_716.219171_False_24866</td><td>gi|102304</td><td>46</td><td>gi|1023044023|gb|ANA96232.1| heat shock protein [Tyrophagus putrescentiae]</td><td></td><td></td></tr>
<tr><td>24.7257</td><td>24.7288</td><td>25.2873</td><td>24.5634</td><td>24.8494</td><td>25.1905</td><td>25.0271</td><td>25.8517</td><td>26.5334</td><td>7</td><td>7</td><td>5</td><td>37.9</td><td>37.9</td><td>30.6</td><td>13.32</td><td>0</td><td>131.46</td><td>1.06E+09</td><td>121</td><td></td><td>gi|1048046021|ref|XP_017494516.1|;gi|1048057783|ref|XP_017462204.1|;NODE_1835_length_13132_cov_679.792995_True_1790;NODE_6017_length_3616_cov_670.828981_False_2792;NODE_387_length_39374_cov_704.810957_True_437;gi|1048019894|ref|XP_017488107.1|;gi|1048057265|ref|XP_017461918.1|;NODE_12154_length_1371_cov_573.113982_False_1074;gi|1048029566|ref|XP_017488644.1|;gi|1048031409|ref|XP_017489640.1|;gi|1048003620|ref|XP_017481150.1|;NODE_18224_length_889_cov_697.359712_False_887;NODE_34149_length_500_cov_587.260674_True_154;NODE_1970_length_12402_cov_725.800680_False_848;NODE_4291_length_5462_cov_1425.463103_True_570;gi|1048043604|ref|XP_017493206.1|;NODE_4291_length_5462_cov_1425.463103_True_134;NODE_25733_length_641_cov_739.165529_False_640;gi|1048054319|ref|XP_017481239.1|;NODE_2762_length_9065_cov_1244.131299_True_6664;NODE_6214_length_3453_cov_728.520895_True_438</td><td>gi|104804</td><td>58</td><td>gi|1048046021|ref|XP_017494516.1| PREDICTED: histone H2A-like [Rhagoletis zephyria];gi|1048057783|ref|XP_017462204.1| PREDICTED: histone H2A-like [Rhagoletis zephyria];NODE_1835_length_13132_cov_679.792995_True_1790 histone H2A;NODE_6017_length_3616_cov_67</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>20.9272</td><td>NaN</td><td>NaN</td><td>21.4665</td><td>NaN</td><td>13</td><td>1</td><td>0</td><td>35.3</td><td>3.3</td><td>0</td><td>49.908</td><td>0</td><td>11.852</td><td>19063000</td><td>11</td><td></td><td>gi|1048004366|ref|XP_017484678.1|;NODE_398_length_38920_cov_859.184536_False_13070;NODE_398_length_38920_cov_859.184536_False_11888;NODE_29387_length_569_cov_754.180934_False_566</td><td>gi|104800</td><td>60</td><td>gi|1048004366|ref|XP_017484678.1| PREDICTED: tubulin alpha-1 chain [Rhagoletis zephyria]</td><td></td><td></td></tr>
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<tr><td>NaN</td><td>20.0517</td><td>19.8935</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>20.9224</td><td>NaN</td><td>2</td><td>2</td><td>2</td><td>31.5</td><td>31.5</td><td>31.5</td><td>8.3266</td><td>0</td><td>5.3748</td><td>10244000</td><td>10</td><td></td><td>NODE_629_length_30016_cov_744.042121_False_17807;gi|1048009285|ref|XP_017465425.1|</td><td>NODE_62!</td><td>69</td><td>NODE_629_length_30016_cov_744.042121_False_17807 Vacuolar protein sorting-associated protein 29;gi|1048009285|ref|XP_017465425.1| PREDICTED: vacuolar protein sorting-associated protein 29-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>22.6807</td><td>22.8335</td><td>22.5904</td><td>22.4343</td><td>21.8059</td><td>22.3575</td><td>22.9715</td><td>23.5047</td><td>24.4187</td><td>12</td><td>12</td><td>12</td><td>40</td><td>40</td><td>40</td><td>34.418</td><td>0</td><td>141.66</td><td>3.15E+08</td><td>122</td><td></td><td>gi|1048009287|ref|XP_017465427.1|;NODE_629_length_30016_cov_744.042121_True_16453;NODE_629_length_30016_cov_744.042121_True_16034;NODE_629_length_30016_cov_744.042121_True_15704</td><td>gi|104800</td><td>70</td><td>gi|1048009287|ref|XP_017465427.1| PREDICTED: succinyl-CoA ligase subunit alpha, mitochondrial-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>20.6192</td><td>20.0366</td><td>20.7265</td><td>19.8114</td><td>19.9141</td><td>19.7837</td><td>NaN</td><td>20.5449</td><td>21.2845</td><td>6</td><td>6</td><td>6</td><td>17.8</td><td>17.8</td><td>17.8</td><td>50.421</td><td>0</td><td>12.436</td><td>30875000</td><td>34</td><td></td><td>gi|1048009289|ref|XP_017465428.1|;NODE_1242_length_18418_cov_743.663835_False_2151</td><td>gi|104800</td><td>71</td><td>gi|1048009289|ref|XP_017465428.1| PREDICTED: programmed cell death protein 4-like [Rhagoletis zephyria];NODE_1242_length_18418_cov_743.663835_False_2151 programmed cell death protein 4</td><td></td><td></td></tr>
<tr><td>20.6158</td><td>20.5724</td><td>20.7846</td><td>21.2705</td><td>21.2287</td><td>21.2943</td><td>21.2245</td><td>21.928</td><td>22.2225</td><td>18</td><td>18</td><td>18</td><td>59</td><td>59</td><td>59</td><td>47.139</td><td>0</td><td>92.853</td><td>1.29E+08</td><td>103</td><td></td><td>gi|1048009291|ref|XP_017465429.1|;NODE_1242_length_18418_cov_743.663835_False_5764;gi|1048068219|ref|XP_017486244.1|</td><td>gi|104800</td><td>72</td><td>gi|1048009291|ref|XP_017465429.1| PREDICTED: 26S protease regulatory subunit 6B-like [Rhagoletis zephyria];NODE_1242_length_18418_cov_743.663835_False_5764 26S proteasome regulatory subunit 6B</td><td></td><td></td></tr>
<tr><td>20.8943</td><td>20.9342</td><td>21.2087</td><td>21.6356</td><td>21.1499</td><td>21.3438</td><td>21.7538</td><td>22.1537</td><td>22.7665</td><td>61</td><td>61</td><td>37</td><td>25.8</td><td>25.8</td><td>16.2</td><td>421.64</td><td>0</td><td>323.31</td><td>3.08E+08</td><td>296</td><td></td><td>gi|1048009299|ref|XP_017465434.1|;NODE_474_length_36110_cov_739.120399_False_25484;NODE_474_length_36110_cov_739.120399_False_15315;NODE_30563_length_550_cov_393.234343_False_547;NODE_30566_length_550_cov_358.822222_False_547;NODE_474_length_36110_cov_739.120399_False_26029;NODE_474_length_36110_cov_739.120399_False_17051;NODE_474_length_36110_cov_739.120399_False_17359;NODE_474_length_36110_cov_739.120399_False_29260;NODE_474_length_36110_cov_739.120399_False_27538;NODE_474_length_36110_cov_739.120399_False_18405;NODE_474_length_36110_cov_739.120399_False_26675;NODE_474_length_36110_cov_739.120399_False_28831;NODE_474_length_36110_cov_739.120399_False_16084;NODE_474_length_36110_cov_739.120399_False_19103</td><td>gi|104800</td><td>74</td><td>gi|1048009299|ref|XP_017465434.1| PREDICTED: muscle M-line assembly protein unc-89-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>24.1128</td><td>24.2197</td><td>24.3156</td><td>24.0829</td><td>23.5261</td><td>23.8595</td><td>24.4828</td><td>25.2071</td><td>25.6665</td><td>42</td><td>42</td><td>42</td><td>50.1</td><td>50.1</td><td>50.1</td><td>94.606</td><td>0</td><td>300.6</td><td>1.88E+09</td><td>481</td><td></td><td>gi|1048009305|ref|XP_017465437.1|;NODE_474_length_36110_cov_739.120399_False_3109;NODE_474_length_36110_cov_739.120399_False_3731;NODE_474_length_36110_cov_739.120399_False_1878;NODE_474_length_36110_cov_739.120399_False_1458;NODE_474_length_36110_cov_739.120399_False_3975;gi|1048041019|ref|XP_017477399.1|</td><td>gi|104800</td><td>76</td><td>gi|1048009305|ref|XP_017465437.1| PREDICTED: probable aconitate hydratase, mitochondrial [Rhagoletis zephyria];NODE_474_length_36110_cov_739.120399_False_3109 probable aconitate hydratase, mitochondrial</td><td></td><td></td></tr>
<tr><td>20.6209</td><td>20.7349</td><td>20.6035</td><td>20.1108</td><td>NaN</td><td>19.8797</td><td>NaN</td><td>21.524</td><td>21.371</td><td>3</td><td>3</td><td>3</td><td>29.6</td><td>29.6</td><td>29.6</td><td>22.314</td><td>0</td><td>25.506</td><td>24554000</td><td>20</td><td></td><td>gi|1048009317|ref|XP_017465444.1|;NODE_168_length_56594_cov_755.832912_True_18045</td><td>gi|104800</td><td>78</td><td>gi|1048009317|ref|XP_017465444.1| PREDICTED: protein SCO1 homolog, mitochondrial-like [Rhagoletis zephyria];NODE_168_length_56594_cov_755.832912_True_18045 protein SCO1 homolog, mitochondrial-like</td><td></td><td></td></tr>
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<tr><td>NaN</td><td>NaN</td><td>19.4376</td><td>NaN</td><td>19.5244</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>3</td><td>3</td><td>3</td><td>12.5</td><td>12.5</td><td>12.5</td><td>50.488</td><td>0</td><td>7.0146</td><td>3924100</td><td>8</td><td></td><td>gi|1048009347|ref|XP_017465462.1|;NODE_52_length_90661_cov_730.284507_True_38828</td><td>gi|104800</td><td>81</td><td>gi|1048009347|ref|XP_017465462.1| PREDICTED: carboxypeptidase E-like [Rhagoletis zephyria];NODE_52_length_90661_cov_730.284507_True_38828 carboxypeptidase E-like</td><td></td><td></td></tr>
<tr><td>22.4385</td><td>22.5511</td><td>22.6819</td><td>22.2299</td><td>22.123</td><td>22.1155</td><td>21.8858</td><td>22.7459</td><td>22.8587</td><td>8</td><td>8</td><td>8</td><td>44.5</td><td>44.5</td><td>44.5</td><td>23.168</td><td>0</td><td>32.619</td><td>1.26E+08</td><td>51</td><td></td><td>gi|1048009357|ref|XP_017465468.1|;NODE_2560_length_9786_cov_729.145823_True_9499;NODE_2560_length_9786_cov_729.145823_True_9129</td><td>gi|104800</td><td>83</td><td>gi|1048009357|ref|XP_017465468.1| PREDICTED: FK506-binding protein 2-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>19.9836</td><td>19.094</td><td>NaN</td><td>20.1102</td><td>NaN</td><td>NaN</td><td>NaN</td><td>4</td><td>4</td><td>4</td><td>31.7</td><td>31.7</td><td>31.7</td><td>21.079</td><td>0</td><td>12.537</td><td>13712000</td><td>15</td><td></td><td>gi|1048009369|ref|XP_017465475.1|;NODE_983_length_22232_cov_742.238445_False_18437</td><td>gi|104800</td><td>85</td><td>gi|1048009369|ref|XP_017465475.1| PREDICTED: ADP-ribosylation factor-like protein 8B [Rhagoletis zephyria];NODE_983_length_22232_cov_742.238445_False_18437 ADP-ribosylation factor-like protein 8A</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>NaN</td><td>18.0286</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>19.4044</td><td>3</td><td>3</td><td>3</td><td>9.5</td><td>9.5</td><td>9.5</td><td>46.718</td><td>0</td><td>10.317</td><td>4027400</td><td>11</td><td></td><td>gi|1048009371|ref|XP_017465476.1|;NODE_2765_length_9058_cov_737.505165_True_7116</td><td>gi|104800</td><td>86</td><td>gi|1048009371|ref|XP_017465476.1| PREDICTED: lissencephaly-1 homolog [Rhagoletis zephyria];NODE_2765_length_9058_cov_737.505165_True_7116 lissencephaly-1 homolog</td><td></td><td></td></tr>
<tr><td>26.7669</td><td>26.7354</td><td>26.657</td><td>26.3274</td><td>27.3869</td><td>26.8688</td><td>25.7593</td><td>26.9999</td><td>27.7507</td><td>6</td><td>6</td><td>6</td><td>35.2</td><td>35.2</td><td>35.2</td><td>14.729</td><td>0</td><td>125.01</td><td>2.02E+09</td><td>120</td><td></td><td>gi|1048043433|ref|XP_017493110.1|;gi|1048040747|ref|XP_017477261.1|;gi|1048046176|ref|XP_017494602.1|;gi|1048009576|ref|XP_017465584.1|;NODE_59_length_86816_cov_723.476758_True_59991;NODE_1134_length_19738_cov_717.615658_True_16142;NODE_59_length_86816_cov_723.476758_True_59183;gi|1048067685|ref|XP_017463961.1|;NODE_59_length_86816_cov_723.476758_True_58938;NODE_111_length_67919_cov_695.680921_True_57027;NODE_59_length_86816_cov_723.476758_True_59701;gi|1048010549|ref|XP_017466105.1|</td><td>gi|104804</td><td>87</td><td>gi|1048043433|ref|XP_017493110.1| PREDICTED: ubiquitin-60S ribosomal protein L40 [Rhagoletis zephyria];gi|1048040747|ref|XP_017477261.1| PREDICTED: ubiquitin-60S ribosomal protein L40-like [Rhagoletis zephyria];gi|1048046176|ref|XP_017494602.1| PREDICTED:</td><td></td><td></td></tr>
<tr><td>23.3729</td><td>23.2535</td><td>23.3934</td><td>23.3141</td><td>23.1139</td><td>23.3592</td><td>23.6432</td><td>23.9992</td><td>24.1233</td><td>11</td><td>7</td><td>7</td><td>58</td><td>41.1</td><td>41.1</td><td>24.131</td><td>0</td><td>47.992</td><td>3.12E+08</td><td>86</td><td></td><td>gi|1048019501|ref|XP_017487889.1|;NODE_1063_length_20806_cov_709.760445_False_20803;NODE_1063_length_20806_cov_709.760445_False_20221</td><td>gi|104801</td><td>105</td><td>gi|1048019501|ref|XP_017487889.1| PREDICTED: heat shock 70 kDa protein C-like, partial [Rhagoletis zephyria];NODE_1063_length_20806_cov_709.760445_False_20803 Hsp70 family protein</td><td></td><td></td></tr>
<tr><td>20.6912</td><td>20.5888</td><td>20.9452</td><td>20.5777</td><td>NaN</td><td>20.3924</td><td>21.2676</td><td>21.6054</td><td>22.1519</td><td>10</td><td>10</td><td>10</td><td>41.5</td><td>41.5</td><td>41.5</td><td>32.275</td><td>0</td><td>63.483</td><td>50182000</td><td>44</td><td></td><td>gi|1048019607|ref|XP_017487946.1|;NODE_9_length_186394_cov_717.866013_False_105413;NODE_9_length_186394_cov_717.866013_False_105583;gi|1048021995|ref|XP_017471532.1|</td><td>gi|104801</td><td>108</td><td>gi|1048019607|ref|XP_017487946.1| PREDICTED: succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial-like [Rhagoletis zephyria];NODE_9_length_186394_cov_717.866013_False_105413 Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitoc</td><td></td><td></td></tr>
<tr><td>20.8165</td><td>20.9308</td><td>21.0101</td><td>20.8203</td><td>NaN</td><td>20.9866</td><td>20.5002</td><td>20.9742</td><td>21.567</td><td>3</td><td>3</td><td>3</td><td>18.8</td><td>18.8</td><td>18.8</td><td>34.054</td><td>0</td><td>21.089</td><td>36578000</td><td>26</td><td></td><td>gi|1048019611|ref|XP_017487949.1|;NODE_888_length_24016_cov_715.014691_True_2591</td><td>gi|104801</td><td>109</td><td>gi|1048019611|ref|XP_017487949.1| PREDICTED: glyoxalase domain-containing protein 4-like [Rhagoletis zephyria];NODE_888_length_24016_cov_715.014691_True_2591 glyoxalase I</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>NaN</td><td>19.2844</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>20.1411</td><td>3</td><td>3</td><td>3</td><td>9.3</td><td>9.3</td><td>9.3</td><td>59.846</td><td>0</td><td>6.639</td><td>6255300</td><td>10</td><td></td><td>gi|1048019617|ref|XP_017487952.1|;NODE_70_length_82317_cov_789.187073_False_43024;NODE_70_length_82317_cov_789.187073_False_41664</td><td>gi|104801</td><td>111</td><td>gi|1048019617|ref|XP_017487952.1| PREDICTED: gamma-glutamyltranspeptidase 1-like, partial [Rhagoletis zephyria];NODE_70_length_82317_cov_789.187073_False_43024 gamma-glutamyltranspeptidase 1-like isoform X2</td><td></td><td></td></tr>
<tr><td>22.9979</td><td>22.4685</td><td>22.8598</td><td>22.3853</td><td>22.1983</td><td>22.3992</td><td>22.8877</td><td>23.2473</td><td>23.9376</td><td>6</td><td>5</td><td>4</td><td>36</td><td>30.4</td><td>25.2</td><td>23.995</td><td>0</td><td>14.482</td><td>1.17E+08</td><td>40</td><td></td><td>gi|1048019739|ref|XP_017488019.1|;NODE_435_length_37646_cov_706.286372_False_8865</td><td>gi|104801</td><td>113</td><td>gi|1048019739|ref|XP_017488019.1| PREDICTED: endochitinase At2g43620-like [Rhagoletis zephyria];NODE_435_length_37646_cov_706.286372_False_8865 chitinase 4-like</td><td></td><td></td></tr>
<tr><td>21.0101</td><td>21.1242</td><td>21.1574</td><td>20.9145</td><td>20.7708</td><td>20.9449</td><td>21.3125</td><td>21.5527</td><td>21.9191</td><td>18</td><td>18</td><td>17</td><td>23.1</td><td>23.1</td><td>21.9</td><td>127.84</td><td>0</td><td>153.85</td><td>99313000</td><td>114</td><td></td><td>gi|1048019757|ref|XP_017488029.1|;NODE_721_length_27587_cov_716.399353_False_21255;NODE_721_length_27587_cov_716.399353_False_18804;NODE_721_length_27587_cov_716.399353_False_20096;NODE_721_length_27587_cov_716.399353_False_21563;NODE_721_length_27587_cov_716.399353_False_19185</td><td>gi|104801</td><td>116</td><td>gi|1048019757|ref|XP_017488029.1| PREDICTED: contactin-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>19.7223</td><td>19.9715</td><td>20.1493</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>20.5768</td><td>7</td><td>6</td><td>6</td><td>16.1</td><td>13.8</td><td>13.8</td><td>55.084</td><td>0</td><td>16.616</td><td>14259000</td><td>16</td><td></td><td>gi|1048019799|ref|XP_017488052.1|;NODE_758_length_26962_cov_675.952800_True_7054;NODE_2888_length_8716_cov_721.382173_False_4958;NODE_2888_length_8716_cov_721.382173_False_5366;NODE_758_length_26962_cov_675.952800_True_8352;NODE_758_length_26962_cov_675.952800_False_6585;NODE_9_length_186394_cov_717.866013_True_134495;gi|1048045425|ref|XP_017494191.1|</td><td>gi|104801</td><td>118</td><td>gi|1048019799|ref|XP_017488052.1| PREDICTED: uncharacterized protein LOC108376358 [Rhagoletis zephyria];NODE_758_length_26962_cov_675.952800_True_7054 Septin domain containing protein</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>23.4886</td><td>23.5236</td><td>7</td><td>2</td><td>2</td><td>30.7</td><td>8.9</td><td>8.9</td><td>41.631</td><td>0</td><td>8.7143</td><td>25734000</td><td>6</td><td></td><td>gi|1048019801|ref|XP_017488054.1|;NODE_4145_length_5684_cov_491.632439_False_5011</td><td>gi|104801</td><td>119</td><td>gi|1048019801|ref|XP_017488054.1| PREDICTED: uncharacterized protein LOC108376359 [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>21.9806</td><td>21.8465</td><td>21.9586</td><td>22.0683</td><td>22.1568</td><td>22.1833</td><td>22.0249</td><td>22.4678</td><td>22.6577</td><td>49</td><td>49</td><td>27</td><td>40.3</td><td>40.3</td><td>22.4</td><td>188.32</td><td>0</td><td>323.31</td><td>4.13E+08</td><td>277</td><td></td><td>gi|1048019831|ref|XP_017488071.1|;NODE_115_length_66846_cov_694.036517_True_2588;NODE_115_length_66846_cov_694.036517_True_817;NODE_115_length_66846_cov_694.036517_True_2025;NODE_115_length_66846_cov_694.036517_True_1367</td><td>gi|104801</td><td>120</td><td>gi|1048019831|ref|XP_017488071.1| PREDICTED: spectrin alpha chain-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>21.9356</td><td>21.9462</td><td>21.9272</td><td>22.106</td><td>22.3739</td><td>22.4422</td><td>21.8295</td><td>22.4702</td><td>22.8897</td><td>37</td><td>18</td><td>18</td><td>55.2</td><td>25.9</td><td>25.9</td><td>119.31</td><td>0</td><td>132.86</td><td>1.7E+08</td><td>116</td><td></td><td>gi|1048019833|ref|XP_017488072.1|;NODE_115_length_66846_cov_694.036517_True_8543;NODE_115_length_66846_cov_694.036517_True_7912;NODE_115_length_66846_cov_694.036517_True_9249</td><td>gi|104801</td><td>121</td><td>gi|1048019833|ref|XP_017488072.1| PREDICTED: spectrin alpha chain-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
<tr><td>NaN</td><td>NaN</td><td>NaN</td><td>21.0403</td><td>NaN</td><td>NaN</td><td>21.67</td><td>NaN</td><td>21.4268</td><td>2</td><td>2</td><td>2</td><td>8.2</td><td>8.2</td><td>8.2</td><td>39.979</td><td>0</td><td>6.3211</td><td>27991000</td><td>12</td><td></td><td>gi|1048019846|ref|XP_017488079.1|;NODE_502_length_34908_cov_702.237225_False_16871;NODE_502_length_34908_cov_702.237225_False_17787</td><td>gi|104801</td><td>122</td><td>gi|1048019846|ref|XP_017488079.1| PREDICTED: toll-interacting protein-like [Rhagoletis zephyria];NODE_502_length_34908_cov_702.237225_False_16871 toll-interacting protein isoform X1;NODE_502_length_34908_cov_702.237225_False_17787 toll-interacting protein-</td><td></td><td></td></tr>
<tr><td>20.0709</td><td>19.7843</td><td>20.6255</td><td>19.2162</td><td>NaN</td><td>19.6673</td><td>20.4149</td><td>19.9277</td><td>21.4615</td><td>11</td><td>11</td><td>11</td><td>21.9</td><td>21.9</td><td>21.9</td><td>88.99</td><td>0</td><td>36.32</td><td>26927000</td><td>34</td><td></td><td>gi|1048019924|ref|XP_017488123.1|;NODE_2255_length_11026_cov_677.404703_True_4307;NODE_2255_length_11026_cov_677.404703_True_4011</td><td>gi|104801</td><td>124</td><td>gi|1048019924|ref|XP_017488123.1| PREDICTED: protein transport protein Sec23A-like [Rhagoletis zephyria];NODE_2255_length_11026_cov_677.404703_True_4307 protein transport protein Sec23A isoform X1</td><td></td><td></td></tr>
<tr><td>19.327</td><td>18.9794</td><td>NaN</td><td>NaN</td><td>NaN</td><td>NaN</td><td>19.7769</td><td>19.8631</td><td>NaN</td><td>4</td><td>4</td><td>4</td><td>5.1</td><td>5.1</td><td>5.1</td><td>133.79</td><td>0</td><td>10.014</td><td>8902800</td><td>14</td><td></td><td>gi|1048019926|ref|XP_017488124.1|;NODE_2255_length_11026_cov_677.404703_True_302;gi|1048006906|ref|XP_017462107.1|</td><td>gi|104801</td><td>125</td><td>gi|1048019926|ref|XP_017488124.1| PREDICTED: DNA-directed RNA polymerase II subunit RPB2-like [Rhagoletis zephyria];NODE_2255_length_11026_cov_677.404703_True_302 DNA-directed RNA polymerase II subunit RPB2</td><td></td><td></td></tr>
<tr><td>22.2258</td><td>22.369</td><td>22.6218</td><td>23.1172</td><td>22.0627</td><td>22.981</td><td>23.6617</td><td>24.2509</td><td>24.6067</td><td>15</td><td>15</td><td>15</td><td>44.6</td><td>44.6</td><td>44.6</td><td>48.487</td><td>0</td><td>115.93</td><td>4.43E+08</td><td>120</td><td></td><td>gi|1048019981|ref|XP_017488154.1|;NODE_3823_length_6229_cov_692.549887_False_4379;NODE_3823_length_6229_cov_692.549887_False_3591;NODE_3823_length_6229_cov_692.549887_False_3610;NODE_1215_length_18722_cov_714.702630_True_7721;gi|1048035070|ref|XP_017491624.1|</td><td>gi|104801</td><td>128</td><td>gi|1048019981|ref|XP_017488154.1| PREDICTED: inosine-5-monophosphate dehydrogenase 2-like [Rhagoletis zephyria]</td><td></td><td></td></tr>
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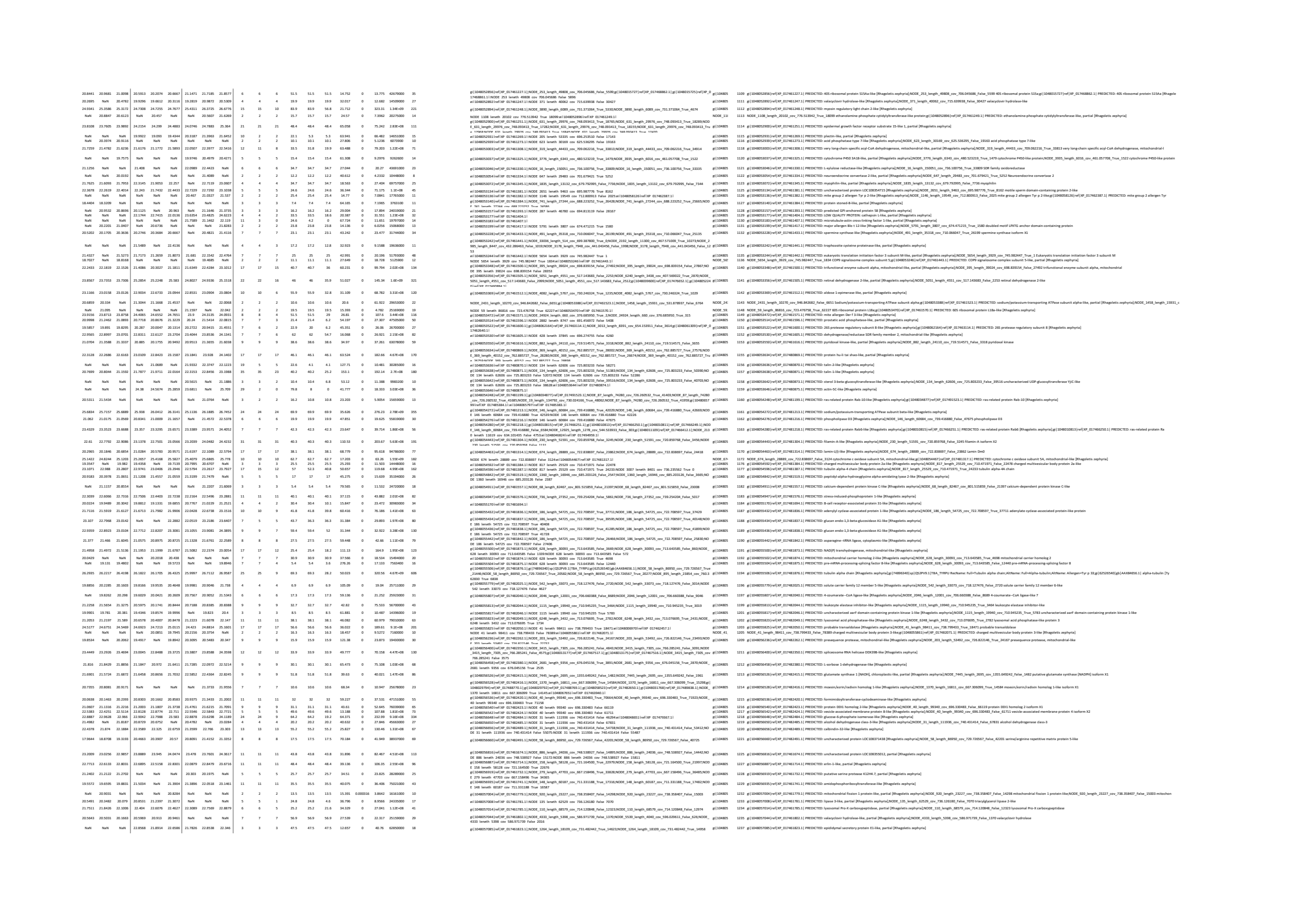


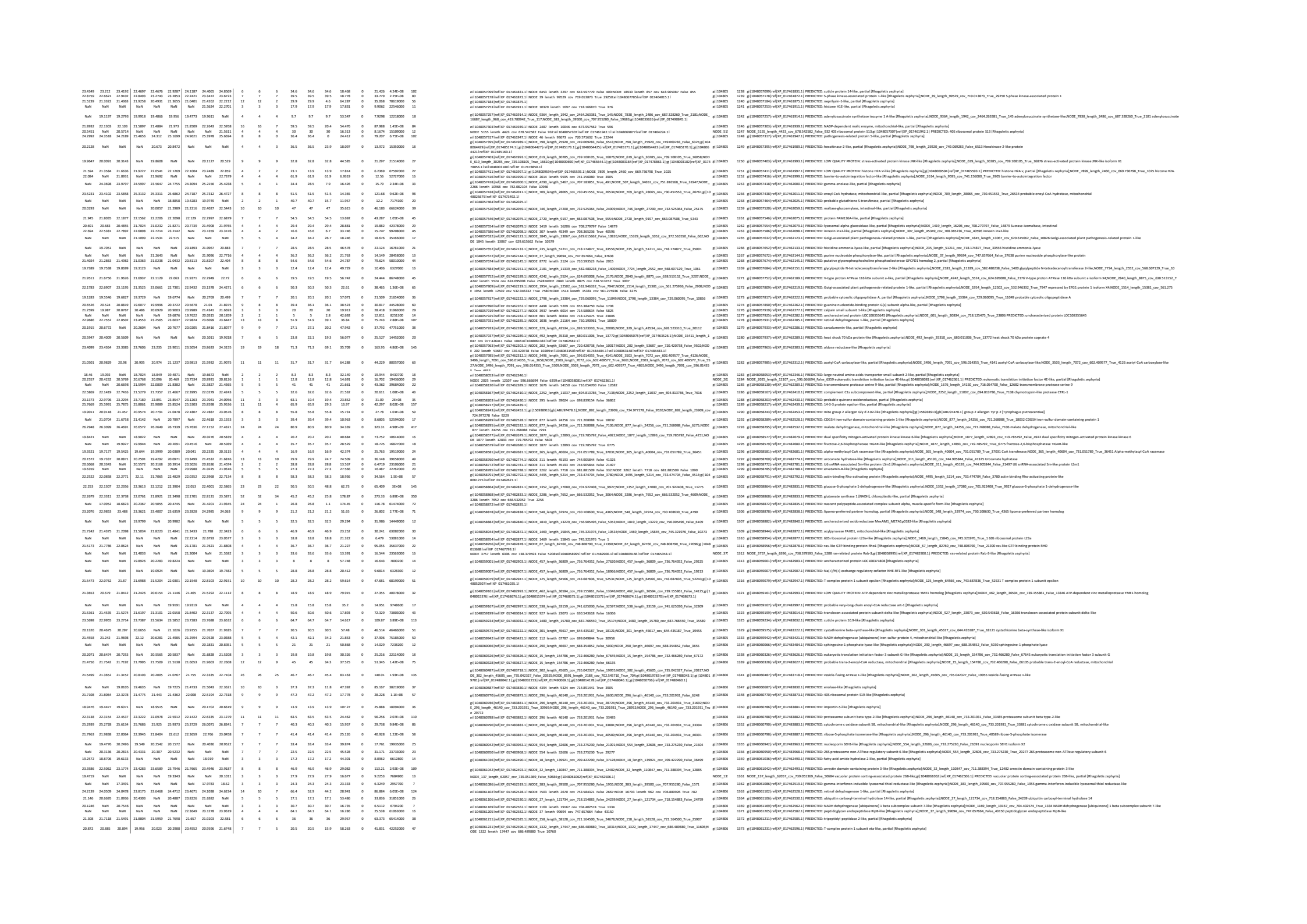


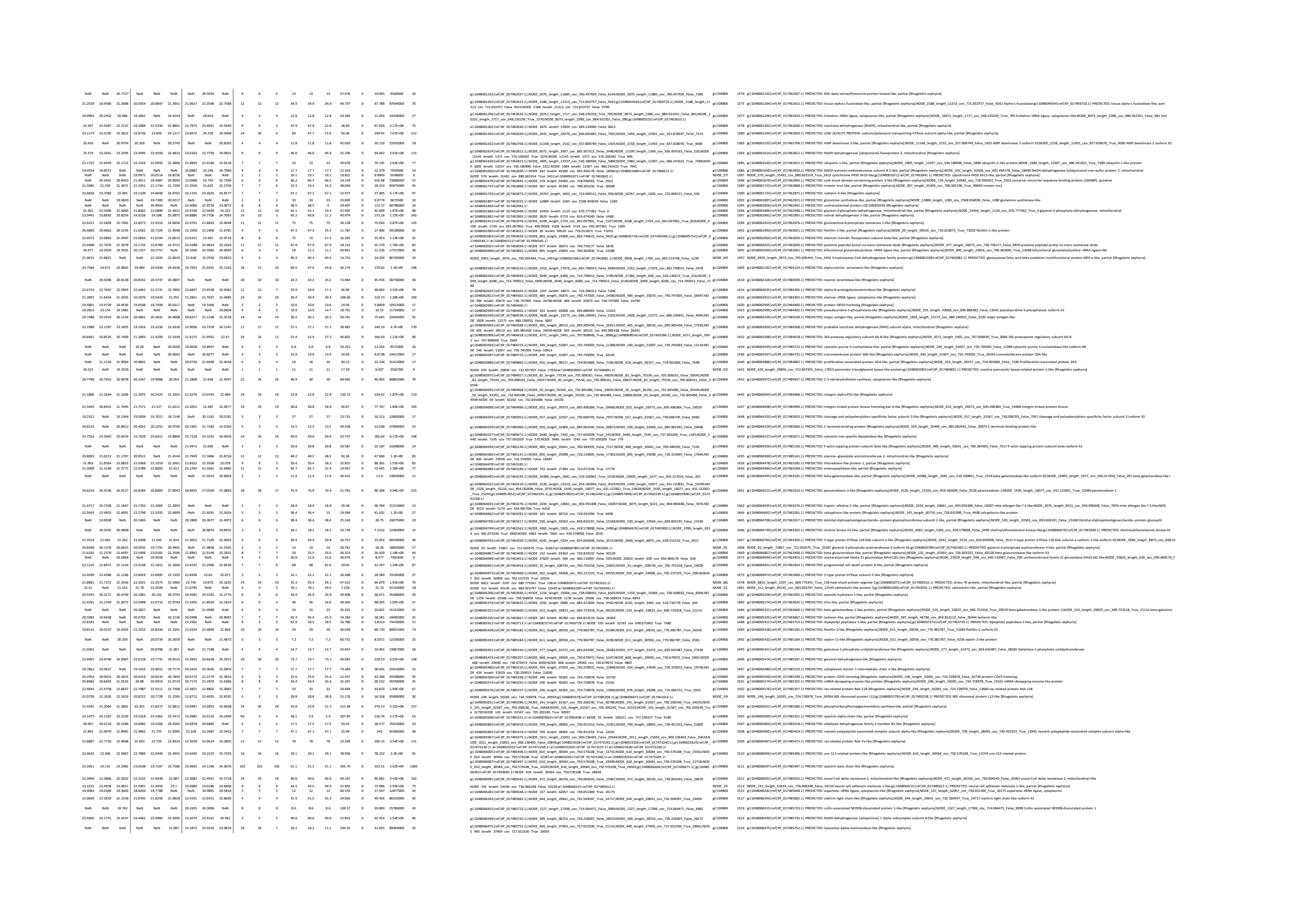




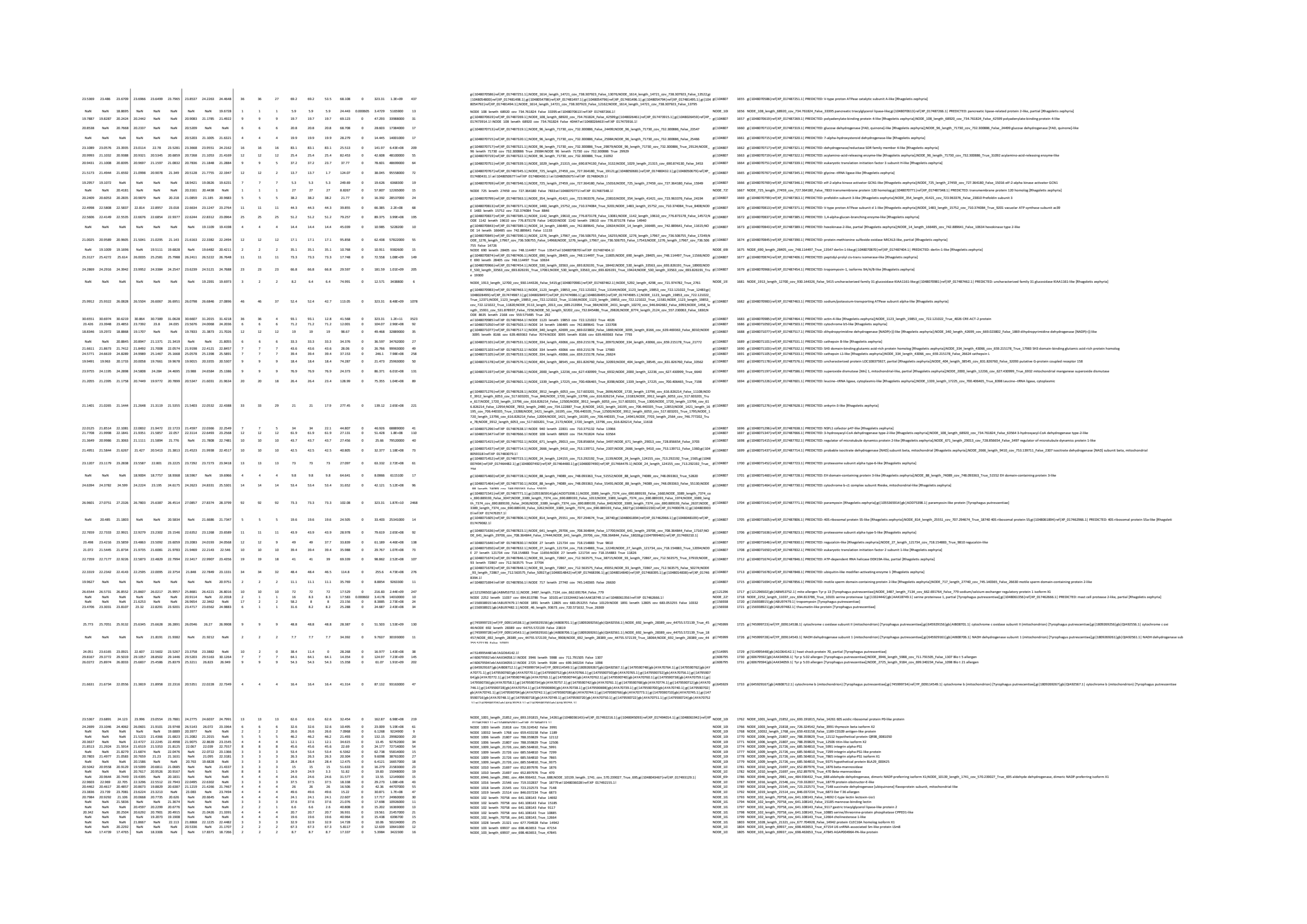






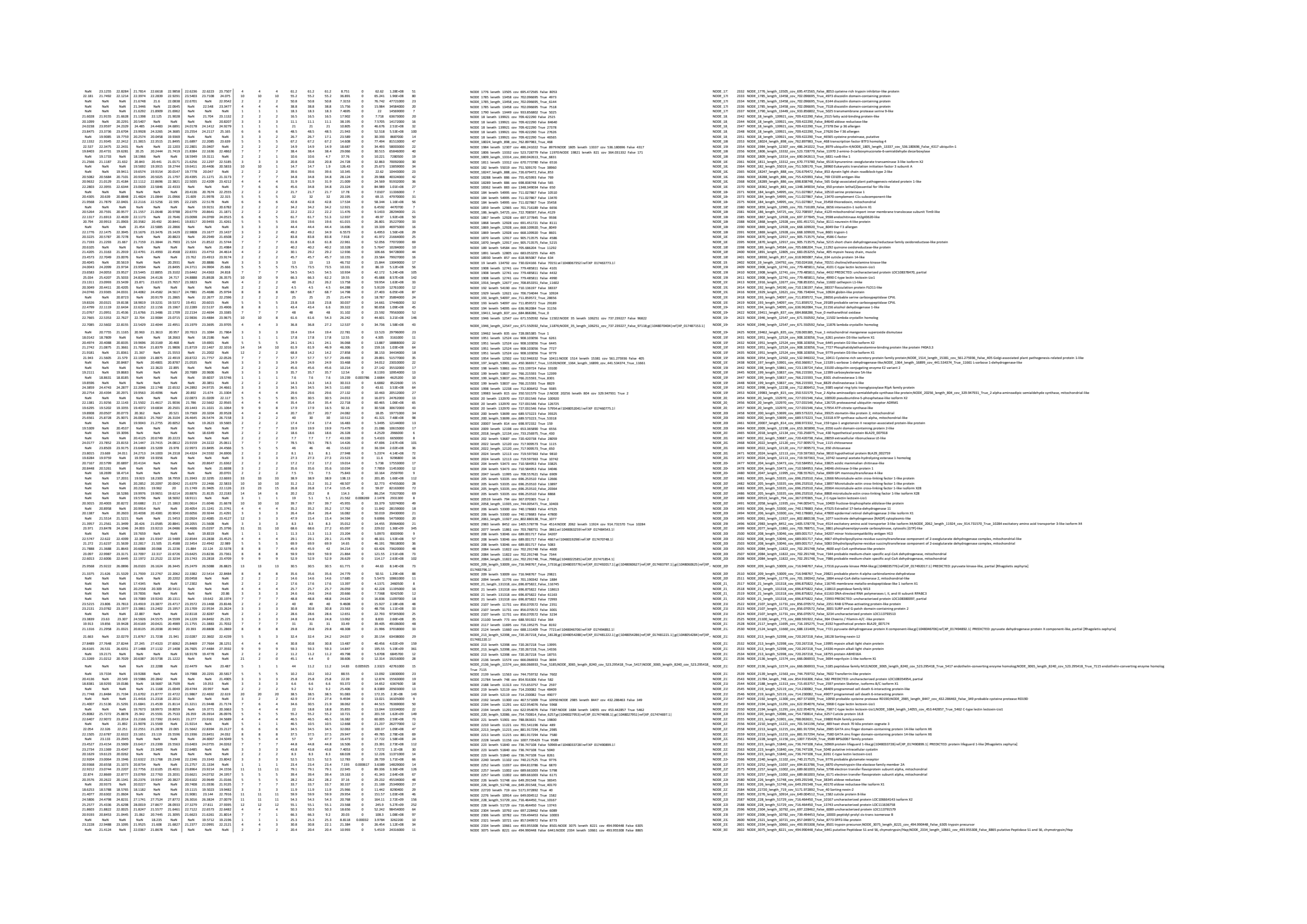


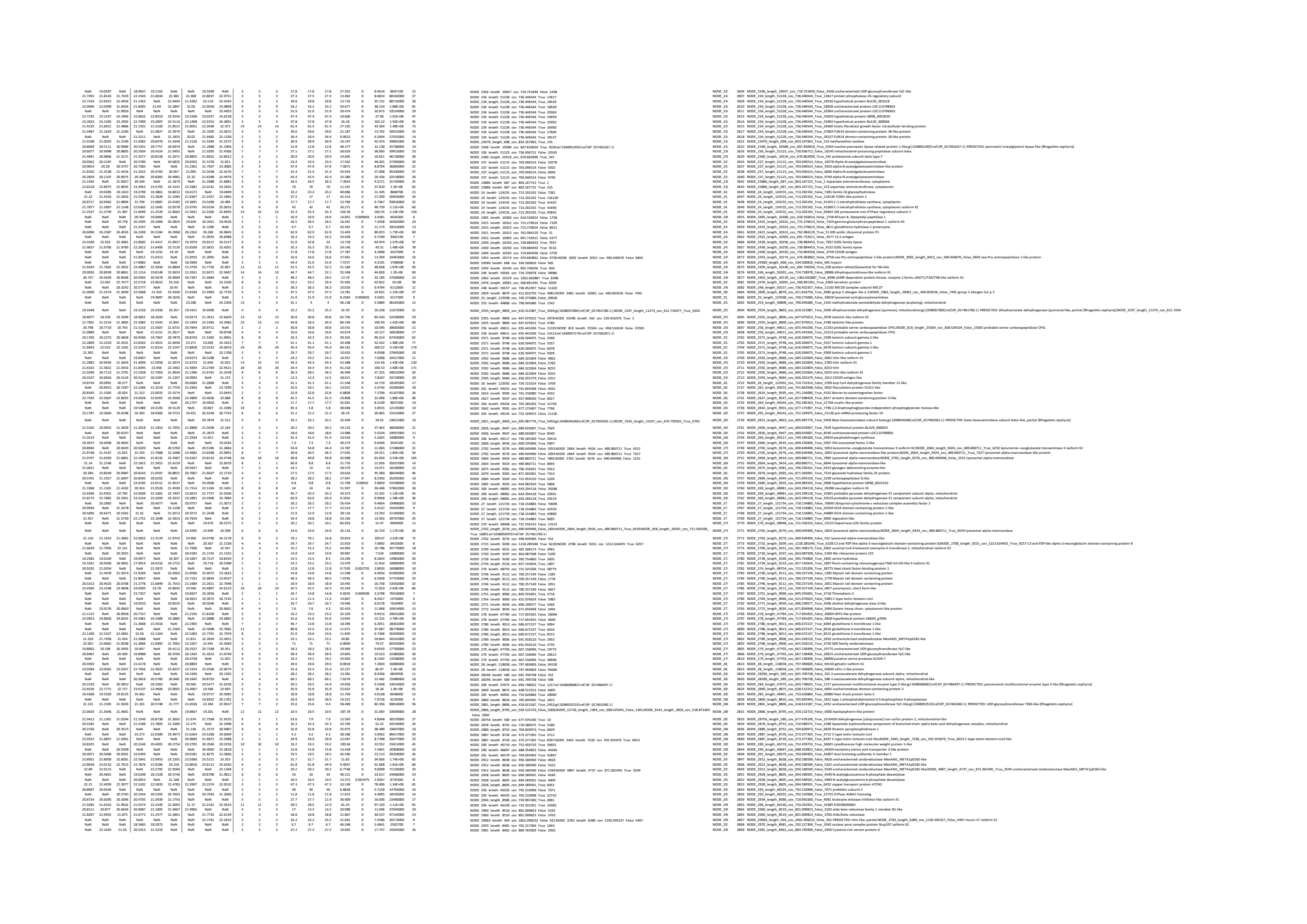
22.2082	22.2515	22.3259	21.9958	22.0585	22.4433	21.8307	22.6539	23.285	25	25	24	38.7	38.7	37.1	98.864	0	182.38	3.24E+08	200	gi|1048066542|ref|XP_017485789.1|;NODE_1542_length_15201_cov_732.203420_True_8423;NODE_1542_length_15201_cov_732.203420_True_6347;NODE_1542_length_15201_cov_732.203420_True_9427;NODE_1542_length_15201_cov_732.203420_True_7443;NODE_1542_length_15201_cov_732.203420_Tr [...ue_6858]	gi|104806	1525	gi|1048066542|ref|XP_017485789.1| PREDICTED: puromycin-sensitive aminopeptidase-like [Rhagoletis zephyria]
23.0301	22.9416	23.1395	22.9364	22.8617	23.268	22.7465	23.4035	23.8361	33	33	28	51.9	51.9	44.8	91.37	0	189.71	5.71E+08	263	gi|1048066544|ref|XP_017485790.1|;NODE_1542_length_15201_cov_732.203420_False_5597;NODE_1542_length_15201_cov_732.203420_False_2996;NODE_1542_length_15201_cov_732.203420_False_4816;NODE_1542_length_15201_cov_732.203420_False_5760;NODE_1542_length_15201_cov_732.203420_ [...False_4459]	gi|104806	1526	gi|1048066544|ref|XP_017485790.1| PREDICTED: puromycin-sensitive aminopeptidase-like protein [Rhagoletis zephyria]
21.2792	21.2687	21.2202	21.7548	21.6097	21.6554	21.584	21.8727	22.1336	7	7	7	50.8	50.8	50.8	21.979	0	21.658	64342000	52	gi|1048066546|ref|XP_017485791.1|;NODE_1542_length_15201_cov_732.203420_False_10489;NODE_1542_length_15201_cov_732.203420_False_10805;NODE_1542_length_15201_cov_732.203420_False_10987;gi|1048005810|ref|XP_017491462.1|	gi|104806	1527	gi|1048066546|ref|XP_017485791.1| PREDICTED: GTP-binding protein SAR1-like [Rhagoletis zephyria]
19.0668	18.6891	19.2705	19.4657	18.7631	19.6824	20.0994	21.9343	22.4668	9	9	9	27.7	27.7	27.7	51.389	0	27.883	48987000	47	gi|1048066623|ref|XP_017485831.1|;NODE_389_length_39244_cov_743.346449_True_8029;NODE_389_length_39244_cov_743.346449_True_7152;NODE_389_length_39244_cov_743.346449_True_8690;NODE_389_length_39244_cov_743.346449_True_9209;gi|1048018640|ref|XP_017470396.1|	gi|104806	1529	gi|1048066623|ref|XP_017485831.1| PREDICTED: protein henna-like [Rhagoletis zephyria]
20.6215	20.7434	20.8467	20.4941	20.6523	21.274	21.8555	22.7638	22.9364	17	17	11	38.9	38.9	27.7	81.878	0	103.4	1.24E+08	84	gi|1048066625|ref|XP_017485832.1|;NODE_389_length_39244_cov_743.346449_False_19029;gi|1048066295|ref|XP_017485656.1|	gi|104806	1530	gi|1048066625|ref|XP_017485832.1| PREDICTED: LOW QUALITY PROTEIN: trifunctional purine biosynthetic protein adenosine-3-like [Rhagoletis zephyria]
23.6319	23.4554	23.7831	25.1839	24.8549	24.858	25.2329	25.5909	24.7602	8	8	8	59.7	59.7	59.7	23.214	0	65.132	4.25E+08	74	gi|1048066649|ref|XP_017485845.1|;NODE_1173_length_19149_cov_733.018854_True_1211;NODE_1173_length_19149_cov_733.018854_True_1799	gi|104806	1531	gi|1048066649|ref|XP_017485845.1| PREDICTED: probable peroxisomal membrane protein PEX13 [Rhagoletis zephyria];NODE_1173_length_19149_cov_733.018854_True_1211 DFP2-like protein
22.2254	22.3069	22.3437	22.4344	22.0239	22.5669	22.1428	22.7899	23.3159	19	19	14	44.9	44.9	31.4	53.875	0	149.56	3.06E+08	141	gi|1048066667|ref|XP_017485854.1|;NODE_29284_length_571_cov_708.740310_True_176;NODE_3393_length_7368_cov_693.972788_True_6736;gi|1048066230|ref|XP_017485619.1|	gi|104806	1533	gi|1048066667|ref|XP_017485854.1| PREDICTED: NADH-ubiquinone oxidoreductase 49 kDa subunit-like [Rhagoletis zephyria]
NaN	NaN	19.2331	NaN	NaN	21.0623	NaN	NaN	22.0185	2	2	2	17.2	17.2	17.2	23.438	0	5.7866	11977000	11	NODE_3393_length_7368_cov_693.972788_True_5804;gi|1048066669|ref|XP_017485856.1|	NODE_33	1534	NODE_3393_length_7368_cov_693.972788_True_5804 L-serine dehydratase/L-threonine deaminase-like;gi|1048066669|ref|XP_017485856.1| PREDICTED: L-serine dehydratase/L-threonine deaminase-like [Rhagoletis zephyria]
NaN	NaN	NaN	19.1775	19.4844	19.9029	19.4884	20.522	20.2844	4	4	4	14.1	14.1	14.1	48.689	0	14.02	13811000	21	gi|1048066681|ref|XP_017485863.1|;NODE_206_length_53300_cov_740.178683_True_32972;NODE_206_length_53300_cov_740.178683_True_33344;NODE_206_length_53300_cov_740.178683_True_31851	gi|104806	1536	gi|1048066681|ref|XP_017485863.1| PREDICTED: flotillin-2-like [Rhagoletis zephyria]
22.437	23.1906	22.718	22.0683	22.2375	23.4467	23.1814	23.9151	24.2597	4	2	0	13.2	6.5	0	47.024	0	98.849	1.49E+08	73	gi|1048066699|ref|XP_017485873.1|	gi|104806	1538	gi|1048066699|ref|XP_017485873.1| PREDICTED: enolase [Rhagoletis zephyria]
20.7945	20.6564	20.8691	20.5398	20.6266	20.7018	21.251	21.5237	21.8922	17	17	17	38.8	38.8	38.8	74.951	0	101.61	1.1E+08	107	gi|1048066718|ref|XP_017485883.1|;NODE_915_length_23347_cov_724.681350_True_11311;NODE_915_length_23347_cov_724.681350_True_10340;NODE_915_length_23347_cov_724.681350_True_11110;NODE_915_length_23347_cov_724.681350_True_9897;NODE_915_length_23347_cov_724.681350_True_12239;NODE_915_length_23347_cov_724.681350_True_10887	gi|104806	1540	gi|1048066718|ref|XP_017485883.1| PREDICTED: NADPH--cytochrome P450 reductase-like [Rhagoletis zephyria]
NaN	NaN	NaN	20.7729	20.7423	NaN	NaN	NaN	NaN	5	5	3	16.2	16.2	8.7	72.552	0	31.207	9467100	18	gi|1048066738|ref|XP_017485893.1|;NODE_1169_length_19167_cov_704.402574_False_16727	gi|104806	1542	gi|1048066738|ref|XP_017485893.1| PREDICTED: uncharacterized protein DDB_G0283697-like [Rhagoletis zephyria]
20.8685	20.56	NaN	20.7113	20.9338	21.0817	NaN	21.3375	21.9019	7	7	7	32.4	32.4	32.4	49.651	0	26.985	38422000	26	gi|1048066744|ref|XP_017485896.1|;NODE_7079_length_2883_cov_719.977369_True_1149;gi|1048023623|ref|XP_017472399.1|;NODE_7079_length_2883_cov_719.977369_True_957	gi|104806	1543	gi|1048066744|ref|XP_017485896.1| PREDICTED: histone-binding protein RBBP4-like [Rhagoletis zephyria];NODE_7079_length_2883_cov_719.977369_True_1149 probable histone-binding protein Caf1
NaN	NaN	NaN	19.9112	19.0817	19.979	NaN	NaN	20.4452	4	4	4	15	15	15	52.838	0	8.537	10663000	17	gi|1048066769|ref|XP_017485909.1|;NODE_113_length_67169_cov_701.942397_False_61692;NODE_113_length_67169_cov_701.942397_False_60697	gi|104806	1544	gi|1048066769|ref|XP_017485909.1| PREDICTED: pantetheinase-like [Rhagoletis zephyria];NODE_113_length_67169_cov_701.942397_False_61692 pantetheinase-like
19.3944	19.5197	20.0427	20.4018	20.3526	20.1702	19.9825	20.6509	20.4955	5	5	5	15.1	15.1	15.1	57.163	0	16.703	24950000	31	gi|1048066857|ref|XP_017485952.1|;NODE_1044_length_21032_cov_700.449302_False_15768	gi|104806	1545	gi|1048066857|ref|XP_017485952.1| PREDICTED: T-complex protein 1 subunit delta-like [Rhagoletis zephyria];NODE_1044_length_21032_cov_700.449302_False_15768 T-complex protein 1 subunit delta-like
NaN	NaN	NaN	NaN	NaN	20.2227	NaN	20.5991	21.021	3	3	3	23.3	23.3	23.3	19.838	0	6.8026	17520000	15	gi|1048066863|ref|XP_017485956.1|;NODE_1044_length_21032_cov_700.449302_True_20037;gi|1048023190|ref|XP_017472169.1|	gi|104806	1546	gi|1048066863|ref|XP_017485956.1| PREDICTED: myosin regulatory light chain sqh-like [Rhagoletis zephyria];NODE_1044_length_21032_cov_700.449302_True_20037 myosin regulatory light chain sqh
20.9311	20.859	NaN	20.7118	NaN	21.2261	NaN	20.9535	21.2303	2	2	2	15.2	15.2	15.2	23.39	0	12.132	30855000	17	gi|1048066881|ref|XP_017485964.1|;NODE_392_length_39047_cov_696.121538_False_1421;NODE_392_length_39047_cov_696.121538_False_2057	gi|104806	1547	gi|1048066881|ref|XP_017485964.1| PREDICTED: selenoprotein T-like [Rhagoletis zephyria];NODE_392_length_39047_cov_696.121538_False_1421 selenoprotein T2-like;NODE_392_length_39047_cov_696.121538_False_2057 thioredoxin reductase-like selenoprotein T
20.5294	20.5667	21.012	21.1591	21.0307	21.1011	21.5145	22.276	23.0586	71	71	71	20	20	20	646.63	0	323.31	3.26E+08	295	gi|1048066998|ref|XP_017486023.1|;NODE_2555_length_9800_cov_647.075013_True_0;NODE_1744_length_13666_cov_645.230622_False_5298;NODE_1873_length_12910_cov_649.430338_True_7611;NODE_1744_length_13666_cov_645.230622_False_2576;NODE_1873_length_12910_cov_649.430338_True_10333;NODE_1744_length_13666_cov_645.230622_False_13664;NODE_1873_length_12910_cov_649.430338_True_5057;NODE_1744_length_13666_cov_645.230622_False_7852;NODE_1873_length_12910_cov_649.430338_True_2;NODE_1873_length_12910_cov_649.430338_True_11758;NODE_1744_length_13666_cov_645.230622_False_1151;NODE_6764_length_3100_cov_688.726437_False_1436;NODE_1744_length_13666_cov_645.230622_False_9323;NODE_1873_length_12910_cov_649.430338_True_3586;NODE_6764_length_3100_cov_688.726437_False_1800;NODE_21064_length_774_cov_666.785814_False_770;NODE_1744_length_13666_cov_645.230622_False_9621;NODE_1744_length_13666_cov_645.230622_False_522;NODE_1873_length_12910_cov_649.430338_True_12387;NODE_1873_length_12910_cov_649.430338_True_3275	gi|104806	1548	gi|1048066998|ref|XP_017486023.1| PREDICTED: twitchin-like, partial [Rhagoletis zephyria]
20.913	20.9018	20.9704	21.1939	21.4578	21.3489	20.4844	21.5935	22.5871	7	7	6	22.8	22.8	18.4	53.462	0	76.314	56842000	54	gi|1048067023|ref|XP_017486037.1|;NODE_14148_length_1151_cov_1065.334854_False_475;NODE_4762_length_4906_cov_715.223459_True_4347	gi|104806	1549	gi|1048067023|ref|XP_017486037.1| PREDICTED: 26S proteasome non-ATPase regulatory subunit 12-like [Rhagoletis zephyria]
28.4688	28.3819	28.3772	28.6043	28.4588	28.7644	28.8329	29.0628	29.2602	31	18	1	87.8	63	7.4	41.805	0	323.31	1.47E+10	765	gi|1048067065|ref|XP_017486058.1|;gi|1048067063|ref|XP_017486057.1|;gi|1048067061|ref|XP_017486056.1|;gi|1048067059|ref|XP_017486055.1|;gi|1048067057|ref|XP_017486054.1|;gi|1048067055|ref|XP_017486053.1|;NODE_8298_length_2293_cov_763.758266_True_2	gi|104806	1551	gi|1048067065|ref|XP_017486058.1| PREDICTED: actin, cytoplasmic A3a [Rhagoletis zephyria];gi|1048067063|ref|XP_017486057.1| PREDICTED: actin, cytoplasmic A3a [Rhagoletis zephyria];gi|1048067061|ref|XP_017486056.1| PREDICTED: actin, cytoplasmic A3a [Rhagole
22.9713	22.9864	23.054	23.2202	22.4806	23.1492	22.8125	23.257	23.8019	9	9	9	43.2	43.2	43.2	30.437	0	113.49	3.49E+08	142	gi|1048067146|ref|XP_017486100.1|;NODE_2411_length_10339_cov_705.199922_False_7102;NODE_2411_length_10339_cov_705.199922_False_9757;NODE_2411_length_10339_cov_705.199922_False_7438;NODE_2826_length_8910_cov_722.296330_True_7011	gi|104806	1554	gi|1048067146|ref|XP_017486100.1| PREDICTED: fructose-1,6-bisphosphatase 1-like, partial [Rhagoletis zephyria]
23.6657	23.7553	23.6438	24.6585	23.6102	24.5077	24.346	24.8862	24.732	11	11	6	63.1	63.1	40.6	28.267	0	48.015	5.18E+08	120	gi|1048067164|ref|XP_017486111.1|;gi|1048067166|ref|XP_017486112.1|;NODE_509_length_34614_cov_716.111462_False_22347;NODE_509_length_34614_cov_716.111462_False_23206	gi|104806	1555	gi|1048067164|ref|XP_017486111.1| PREDICTED: trypsin alpha-3-like [Rhagoletis zephyria];gi|1048067166|ref|XP_017486112.1| PREDICTED: trypsin alpha-3-like, partial [Rhagoletis zephyria]
20.3332	20.0433	20.3608	20.3186	19.9198	20.4551	20.8292	21.537	20.7639	9	9	9	41.5	41.5	41.5	41.119	0	48.174	42860000	37	gi|1048067217|ref|XP_017486142.1|;NODE_159_length_58072_cov_727.098299_False_14209	gi|104806	1556	gi|1048067217|ref|XP_017486142.1| PREDICTED: uroporphyrinogen decarboxylase-like [Rhagoletis zephyria];NODE_159_length_58072_cov_727.098299_False_14209 uroporphyrinogen decarboxylase
21.0469	20.8816	21.0276	20.9826	20.785	21.1986	20.7381	21.4573	22.1056	4	4	4	23.8	23.8	23.8	20.204	0	33.457	32946000	23	gi|1048067221|ref|XP_017486144.1|;NODE_4157_length_5666_cov_717.418286_False_1801;NODE_4157_length_5666_cov_717.418286_False_1650;gi|1048026694|ref|XP_017474038.1|;gi|1048026692|ref|XP_017474037.1|	gi|104806	1557	gi|1048067221|ref|XP_017486144.1| PREDICTED: signal peptidase complex catalytic subunit SEC11A-like [Rhagoletis zephyria];NODE_4157_length_5666_cov_717.418286_False_1801 signal peptidase complex catalytic subunit SEC11A
23.8983	23.8798	23.9638	23.9907	24.0158	24.2682	23.9184	24.3021	24.628	24	24	7	71.9	71.9	20.4	55.954	0	133.68	1.21E+09	313	gi|1048067238|ref|XP_017486153.1|;NODE_2642_length_9501_cov_677.173407_True_7041	gi|104806	1558	gi|1048067238|ref|XP_017486153.1| PREDICTED: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like [Rhagoletis zephyria]
19.8689	19.1819	19.8232	19.4306	19.3599	19.8265	19.6466	19.6432	20.12	5	5	3	22.8	22.8	10.6	40.544	0	16.387	13054000	26	gi|1048067270|ref|XP_017463727.1|;NODE_9619_length_1869_cov_637.710584_False_754	gi|104806	1561	gi|1048067270|ref|XP_017463727.1| PREDICTED: secernin-2-like, partial [Rhagoletis zephyria];NODE_9619_length_1869_cov_637.710584_False_754 secernin-2-like isoform X3
20.0682	20.1388	19.904	21.1287	21.276	21.3379	20.7247	21.0899	NaN	3	3	3	21.7	21.7	21.7	18.14	0	7.5103	23728000	17	gi|1048067507|ref|XP_017463858.1|;NODE_965_length_22506_cov_711.638323_True_22336;NODE_965_length_22506_cov_711.638323_True_21964	gi|104806	1563	gi|1048067507|ref|XP_017463858.1| PREDICTED: serpin B10-like, partial [Rhagoletis zephyria]
20.5995	20.7344	20.6807	NaN	20.2685	20.3786	20.6911	20.8272	20.9991	4	4	4	19.5	19.5	19.5	34.939	0	20.354	23517000	25	gi|1048067547|ref|XP_017463881.1|;NODE_690_length_28405_cov_748.114497_True_24498;NODE_690_length_28405_cov_748.114497_True_25668	gi|104806	1564	gi|1048067547|ref|XP_017463881.1| PREDICTED: isoaspartyl peptidase/L-asparaginase-like, partial [Rhagoletis zephyria];NODE_690_length_28405_cov_748.114497_True_24498 isoaspartyl peptidase/L-asparaginase-like
21.316	21.6345	21.5759	21.665	21.5669	21.9952	21.972	22.058	22.668	10	10	4	47.3	47.3	21.1	32.926	0	59.491	1.17E+08	75	gi|1048067611|ref|XP_017463917.1|;NODE_11695_length_1438_cov_481.934924_True_874;NODE_11734_length_1432_cov_494.122731_False_585;gi|1048014478|ref|XP_017468206.1|;gi|1048014476|ref|XP_017468205.1|	gi|104806	1566	gi|1048067611|ref|XP_017463917.1| PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial-like, partial [Rhagoletis zephyria]
22.2158	NaN	21.5783	21.6091	22.0404	21.8393	21.6488	21.8551	22.0246	8	8	3	35	35	15.9	34.939	0	36.619	79899000	40	gi|1048067742|ref|XP_017463991.1|	gi|104806	1567	gi|1048067742|ref|XP_017463991.1| PREDICTED: deoxyribose-phosphate aldolase-like [Rhagoletis zephyria]
20.3825	NaN	20.7621	NaN	19.614	20.4283	NaN	20.9207	21.666	5	5	5	32.6	32.6	32.6	25.648	0	19.293	22504000	27	gi|1048067780|ref|XP_017464013.1|;NODE_1655_length_14391_cov_793.435268_True_13688;NODE_1655_length_14391_cov_793.435268_True_13289	gi|104806	1568	gi|1048067780|ref|XP_017464013.1| PREDICTED: neutral alpha-glucosidase AB-like [Rhagoletis zephyria];NODE_1655_length_14391_cov_793.435268_True_13688 neutral alpha-glucosidase AB
21.3803	21.2499	21.3276	21.7899	21.4344	22.5066	20.9579	NaN	21.8789	7	2	2	82.8	34.4	34.4	13.564	0	19.27	53967000	28	gi|1048067933|ref|XP_017464100.1|	gi|104806	1573	gi|1048067933|ref|XP_017464100.1| PREDICTED: aldehyde dehydrogenase, cytosolic 2-like, partial [Rhagoletis zephyria]
21.3217	21.1955	20.8076	21.2216	21.0876	21.8592	20.2099	21.7587	22.1533	2	1	1	15.8	9.9	9.9	19.448	0	179.18	47373000	24	gi|1048067960|ref|XP_017464117.1|;NODE_307_length_45349_cov_708.365236_True_31488	gi|104806	1574	gi|1048067960|ref|XP_017464117.1| PREDICTED: innexin inx2-like, partial [Rhagoletis zephyria];NODE_307_length_45349_cov_708.365236_True_31488 Innexin inx2
23.4493	23.6196	23.6008	23.3063	23.4892	23.7231	22.4032	23.526	24.2165	13	13	1	68.3	68.3	3.4	30.807	0	66.806	4.72E+08	149	gi|1048068055|ref|XP_017464170.1|	gi|104806	1575	gi|1048068055|ref|XP_017464170.1| PREDICTED: sorbitol dehydrogenase-like [Rhagoletis zephyria]
20.3003	19.8005	20.1934	20.756	NaN	20.444	20.7244	20.8652	20.3585	3	3	3	13.9	13.9	13.9	35.846	0	27.96	18677000	21	gi|1048068107|ref|XP_017486182.1|;NODE_2423_length_10300_cov_730.958224_False_2844	gi|104806	1576	gi|1048068107|ref|XP_017486182.1| PREDICTED: ubiquitin-like-conjugating enzyme ATG3 [Rhagoletis zephyria];NODE_2423_length_10300_cov_730.958224_False_2844 ubiquitin-like-conjugating enzyme ATG3
21.7802	21.5635	21.8828	21.8442	21.9832	22.2384	21.1388	21.8651	22.7088	11	11	11	43.7	43.7	43.7	34.942	0	47.411	1.06E+08	62	gi|1048068111|ref|XP_017486185.1|;NODE_4257_length_5503_cov_763.142438_True_709;NODE_4257_length_5503_cov_763.142438_True_149	gi|104806	1577	gi|1048068111|ref|XP_017486185.1| PREDICTED: ester hydrolase C11orf54 homolog [Rhagoletis zephyria];NODE_4257_length_5503_cov_763.142438_True_709 ester hydrolase C11orf54 homolog
21.9017	21.6383	21.7307	22.1463	22.1379	22.4438	20.8196	21.7077	22.332	8	8	8	51.6	51.6	51.6	24.265	0	70.036	1.35E+08	78	gi|1048068113|ref|XP_017486186.1|;NODE_8621_length_2172_cov_743.175720_True_407	gi|104806	1578	gi|1048068113|ref|XP_017486186.1| PREDICTED: methylthioribulose-1-phosphate dehydratase-like [Rhagoletis zephyria];NODE_8621_length_2172_cov_743.175720_True_407 methylthioribulose-1-phosphate dehydratase
23.0588	22.6157	22.8736	22.8429	22.9607	22.9643	23.0717	23.3038	23.5776	11	11	11	56.2	56.2	56.2	38.605	0	177.25	4.08E+08	134	gi|1048068267|ref|XP_017486270.1|;NODE_175_length_55635_cov_670.799532_False_11280;NODE_175_length_55635_cov_670.799532_False_10721;NODE_175_length_55635_cov_670.799532_False_11564	gi|104806	1582	gi|1048068267|ref|XP_017486270.1| PREDICTED: eukaryotic translation initiation factor 3 subunit I-like [Rhagoletis zephyria]
20.4366	20.3746	20.0454	20.4934	19.2643	20.8157	20.0059	20.1353	20.4044	10	10	6	8.3	8.3	4.5	241.74	0	39.513	27222000	50	gi|1048068303|ref|XP_017486290.1|;NODE_1757_length_13610_cov_667.159720_True_3593;NODE_1757_length_13610_cov_667.159720_True_3011;NODE_18448_length_879_cov_451.311893_True_2;NODE_18108_length_894_cov_407.008343_True_2	gi|104806	1583	gi|1048068303|ref|XP_017486290.1| PREDICTED: CAD protein-like [Rhagoletis zephyria]
22.9955	22.826	23.1501	23.5525	23.0273	23.6134	24.4196	24.7683	25.1286	11	11	11	48.5	48.5	48.5	41.277	0	97.094	5.22E+08	128	gi|1048068369|ref|XP_017486328.1|;NODE_909_length_23512_cov_713.183698_True_15073;NODE_909_length_23512_cov_713.183698_True_13475;NODE_909_length_23512_cov_713.183698_True_15550;NODE_909_length_23512_cov_713.183698_True_14435	gi|104806	1584	gi|1048068369|ref|XP_017486328.1| PREDICTED: phosphoserine aminotransferase-like [Rhagoletis zephyria]
NaN	NaN	16.4699	16.6481	16.6726	20.6863	22.0848	22.4189	23.0134	40	40	3	26.5	26.5	1.5	278.8	0	231.53	1.86E+08	132	gi|1048068440|ref|XP_017486368.1|;NODE_374_length_39911_cov_715.537008_False_30368	gi|104806	1586	gi|1048068440|ref|XP_017486368.1| PREDICTED: fatty acid synthase-like [Rhagoletis zephyria]
19.6259	NaN	20.1797	20.5157	20.3033	NaN	21.0843	NaN	21.0022	5	5	5	30.5	30.5	30.5	30.196	0	15.77	22863000	16	gi|1048068467|ref|XP_017486382.1|;NODE_159_length_58072_cov_727.098299_True_42873;NODE_159_length_58072_cov_727.098299_True_43214;NODE_159_length_58072_cov_727.098299_True_42344	gi|104806	1587	gi|1048068467|ref|XP_017486382.1| PREDICTED: palmitoyl-protein thioesterase 1-like [Rhagoletis zephyria]
23.4276	23.173	23.5958	23.7338	23.8596	23.8712	23.3868	23.6262	24.1307	9	9	9	50.5	50.5	50.5	34.006	0	85.511	3.79E+08	122	gi|1048068537|ref|XP_017486420.1|;NODE_488_length_35676_cov_738.615873_False_33561;NODE_488_length_35676_cov_738.615873_False_33719;NODE_488_length_35676_cov_738.615873_False_33049;NODE_488_length_35676_cov_738.615873_False_33939;NODE_488_length_35676_cov_738.615873_False_33338	gi|104806	1591	gi|1048068537|ref|XP_017486420.1| PREDICTED: glycogenin-1-like [Rhagoletis zephyria]
20.6922	20.9071	20.851	20.4391	NaN	NaN	NaN	21.6998	22.1569	4	4	4	18.1	18.1	18.1	30.23	0	19.784	30189000	20	gi|1048068545|ref|XP_017486426.1|;NODE_442_length_37388_cov_750.421557_False_10896	gi|104806	1592	gi|1048068545|ref|XP_017486426.1| PREDICTED: 60S ribosomal protein L7a-like [Rhagoletis zephyria];NODE_442_length_37388_cov_750.421557_False_10896 ribosomal protein L7a
21.2255	21.1533	21.3618	21.5904	21.0332	21.3872	21.7302	22.1524	22.3407	16	16	16	47.9	47.9	47.9	48.423	0	81.684	97053000	85	gi|1048068703|ref|XP_017486507.1|;NODE_2908_length_8648_cov_604.671360_False_8233;NODE_6914_length_3001_cov_530.121860_True_107;NODE_2908_length_8648_cov_604.671360_False_7024;NODE_2908_length_8648_cov_604.671360_False_8647	gi|104806	1595	gi|1048068703|ref|XP_017486507.1| PREDICTED: elongation factor Tu-like [Rhagoletis zephyria];NODE_2908_length_8648_cov_604.671360_False_8233 elongation factor Tu, mitochondrial
NaN	20.2545	21.0243	20.2264	21.0032	21.0408	20.3532	21.1899	21.4307	6	6	3	41.7	41.7	23.6	28.117	0	16.937	26625000	28	gi|1048068705|ref|XP_017486508.1|;NODE_6669_length_3163_cov_491.038288_True_1417;NODE_6680_length_3153_cov_510.043577_True_1386;NODE_6680_length_3153_cov_510.043577_True_1693;NODE_6669_length_3163_cov_491.038288_True_1706	gi|104806	1596	gi|1048068705|ref|XP_017486508.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial-like [Rhagoletis zephyria]
20.8219	NaN	20.8896	NaN	NaN	NaN	NaN	NaN	NaN	2	2	2	10	10	10	26.807	0.000315	3.8135	13426000	13	gi|1048068764|ref|XP_017486540.1|;NODE_3545_length_6954_cov_644.510654_False_6917	gi|104806	1597	gi|1048068764|ref|XP_017486540.1| PREDICTED: superoxide dismutase [Cu-Zn]-like, partial [Rhagoletis zephyria];NODE_3545_length_6954_cov_644.510654_False_6917 Superoxide dismutase [Cu-Zn]
NaN	NaN	19.5124	NaN	NaN	20.0292	NaN	NaN	NaN	3	3	3	7.7	7.7	7.7	47.933	0	4.611	3815600	11	gi|1048068835|ref|XP_017486576.1|;NODE_557_length_32567_cov_730.006705_True_17147;NODE_557_length_32567_cov_730.006705_True_17352	gi|104806	1599	gi|1048068835|ref|XP_017486576.1| PREDICTED: heat shock factor protein-like [Rhagoletis zephyria]
22.5149	22.5942	22.6045	22.6687	22.5835	22.8368	22.1362	22.7795	23.1773	20	20	20	52.6	52.6	52.6	55.934	0	146.24	4.7E+08	195	gi|1048068837|ref|XP_017486577.1|;NODE_557_length_32567_cov_730.006705_False_30618;NODE_557_length_32567_cov_730.006705_False_29604;NODE_557_length_32567_cov_730.006705_False_30902	gi|104806	1600	gi|1048068837|ref|XP_017486577.1| PREDICTED: xaa-Pro dipeptidase-like [Rhagoletis zephyria];NODE_557_length_32567_cov_730.006705_False_30618 xaa-Pro dipeptidase
23.2988	23.3573	23.447	23.4854	23.3237	23.2832	23.3003	23.7495	24.2598	39	39	34	65.2	65.2	56.1	89.066	0	323.31	8.14E+08	290	gi|1048068952|ref|XP_017486639.1|;NODE_391_length_39090_cov_734.817548_True_3569;NODE_391_length_39090_cov_734.817548_True_5341;NODE_391_length_39090_cov_734.817548_True_5877	gi|104806	1601	gi|1048068952|ref|XP_017486639.1| PREDICTED: transitional endoplasmic reticulum ATPase-like [Rhagoletis zephyria];NODE_391_length_39090_cov_734.817548_True_3569 Transitional endoplasmic reticulum ATPase TER94
23.5909	23.468	23.7026	23.7388	23.1885	23.6356	23.7916	24.4633	24.9334	11	11	11	59.7	59.7	59.7	20.867	0	115.31	7.84E+08	178	gi|1048068994|ref|XP_017486661.1|;NODE_336_length_42956_cov_721.378966_True_26720;NODE_336_length_42956_cov_721.378966_True_27125	gi|104806	1602	gi|1048068994|ref|XP_017486661.1| PREDICTED: ATP synthase subunit d, mitochondrial-like [Rhagoletis zephyria];NODE_336_length_42956_cov_721.378966_True_26720 ATP synthase subunit d, mitochondrial-like
NaN	NaN	21.1346	21.3082	NaN	NaN	NaN	22.4642	22.5919	5	5	5	19.1	19.1	19.1	44.098	0	15.129	26555000	16	gi|1048069010|ref|XP_017486670.1|;NODE_565_length_32137_cov_736.652671_True_11478;NODE_565_length_32137_cov_736.652671_True_12411	gi|104806	1605	gi|1048069010|ref|XP_017486670.1| PREDICTED: carboxypeptidase B-like [Rhagoletis zephyria];NODE_565_length_32137_cov_736.652671_True_11478 carboxypeptidase B-like
23.2724	23.2234	23.277	25.1456	24.9842	25.2689	23.5009	24.1786	24.834	43	43	35	61.1	61.1	50.7	95.906	0	323.31	2.44E+09	549	gi|1048069056|ref|XP_017486696.1|;NODE_309_length_45340_cov_718.561798_False_13631;NODE_309_length_45340_cov_718.561798_False_10854;NODE_309_length_45340_cov_718.561798_False_12138;NODE_309_length_45340_cov_718.561798_False_12919;NODE_309_length_45340_cov_718.561798_False_11901;NODE_309_length_45340_cov_718.561798_False_11689	gi|104806	1606	gi|1048069056|ref|XP_017486696.1| PREDICTED: sucrase-isomaltase, intestinal-like [Rhagoletis zephyria]
21.5759	21.7965	21.7596	21.7115	21.0717	22.1713	22.2609	22.1441	22.5519	24	24	24	38.4	38.4	38.4	97.324	0	61.166	94454000	80	gi|1048069087|ref|XP_017486714.1|;NODE_793_length_25978_cov_712.349497_False_6077;NODE_793_length_25978_cov_712.349497_False_4311;NODE_793_length_25978_cov_712.349497_False_4831;NODE_793_length_25978_cov_712.349497_False_6593;NODE_793_length_25978_cov_712.349497_False_5033;NODE_793_length_25978_cov_712.349497_False_6735	gi|104806	1609	gi|1048069087|ref|XP_017486714.1| PREDICTED: ubiquitin carboxyl-terminal hydrolase 5-like [Rhagoletis zephyria]
19.8025	20.1067	20.1325	20.5388	19.9255	20.7713	21.1017	21.4271	21.6723	8	8	8	32.9	32.9	32.9	33.661	0	18.744	29762000	37	gi|1048069192|ref|XP_017486770.1|;NODE_4132_length_5699_cov_722.413182_False_1258;NODE_4132_length_5699_cov_722.413182_False_903	gi|104806	1612	gi|1048069192|ref|XP_017486770.1| PREDICTED: hydroxymethylglutaryl-CoA lyase, mitochondrial-like, partial [Rhagoletis zephyria];NODE_4132_length_5699_cov_722.413182_False_1258 Hydroxymethylglutaryl-CoA lyase, mitochondrial
20.5099	21.3294	21.0881	20.8715	20.9421	21.0737	NaN	20.7874	21.0587	5	5	5	20.3	20.3	20.3	35.105	0	12.611	50216000	38	gi|1048069241|ref|XP_017486795.1|;NODE_4451_length_5256_cov_674.763507_True_4062;NODE_9771_length_1830_cov_663.619155_True_157	gi|104806	1613	gi|1048069241|ref|XP_017486795.1| PREDICTED: histidine-rich glycoprotein-like [Rhagoletis zephyria];NODE_4451_length_5256_cov_674.763507_True_4062 adhesion G- coupled receptor G7-like protein
19.3835	19.4611	19.5025	19.1486	18.6097	19.4232	19.4775	19.8965	19.9275	8	7	7	12.8	11.8	11.8	110	0	23.746	19154000	39	gi|1048069253|ref|XP_017486801.1|;NODE_16_length_150051_cov_736.100756_False_75825;NODE_16_length_150051_cov_736.100756_False_76870;NODE_16_length_150051_cov_736.100756_False_77802;NODE_16_length_150051_cov_736.100756_False_78048;NODE_16_length_150051_cov_736.100756_False_77626;gi|1048042477|ref|XP_017478175.1|	gi|104806	1614	gi|1048069253|ref|XP_017486801.1| PREDICTED: 116 kDa U5 small nuclear ribonucleoprotein component-like [Rhagoletis zephyria]
NaN	NaN	22.9978	22.7039	NaN	22.488	23.4885	23.7099	NaN	8	1	0	17.2	3.7	0	71.364	0	20.433	65054000	21	gi|1048069293|ref|XP_017486823.1|;gi|1048069891|ref|XP_017464233.1|	gi|104806	1615	gi|1048069293|ref|XP_017486823.1| PREDICTED: heat shock 70 kDa protein cognate 4 [Rhagoletis zephyria]
22.294	22.3032	22.2385	22.8588	22.6252	22.9296	22.8294	23.1081	23.3753	18	18	17	50.5	50.5	48.6	45.822	0	114.24	3.56E+08	147	gi|1048069315|ref|XP_017486833.1|;NODE_5495_length_4080_cov_735.795031_True_2743;NODE_5495_length_4080_cov_735.795031_True_3112;NODE_5495_length_4080_cov_735.795031_True_3363;NODE_5495_length_4080_cov_735.795031_True_2487;NODE_5495_length_4080_cov_735.795031_True_2194	gi|104806	1617	gi|1048069315|ref|XP_017486833.1| PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like [Rhagoletis zephyria]
22.2282	22.177	22.1315	22.2219	22.0959	22.664	23.0558	23.1829	23.2097	8	8	8	57	57	57	23.496	0	37.764	1.63E+08	54	gi|1048069385|ref|XP_017486868.1|;NODE_15_length_154786_cov_732.466280_True_101983	gi|104806	1618	gi|1048069385|ref|XP_017486868.1| PREDICTED: 5-formyltetrahydrofolate cyclo-ligase-like [Rhagoletis zephyria];NODE_15_length_154786_cov_732.466280_True_101983 5-formyltetrahydrofolate cyclo-ligase
20.8606	20.629	20.6176	21.0715	NaN	20.9916	21.4363	21.4629	22.2135	8	8	8	27.1	27.1	27.1	50.704	0	34.503	56191000	35	gi|1048069393|ref|XP_017486874.1|;NODE_15_length_154786_cov_732.466280_True_88876;gi|1048050281|ref|XP_017480225.1|	gi|104806	1619	gi|1048069393|ref|XP_017486874.1| PREDICTED: eukaryotic translation initiation factor 2 subunit 3-like [Rhagoletis zephyria];NODE_15_length_154786_cov_732.466280_True_88876 eukaryotic translation initiation factor 2 subunit 3-like
19.736	19.3721	19.9751	19.8054	NaN	19.9296	NaN	19.814	20.5209	6	6	6	51.4	51.4	51.4	21.109	0	16.891	22102000	23	gi|1048069395|ref|XP_017486875.1|;NODE_15_length_154786_cov_732.466280_False_88354	gi|104806	1620	gi|1048069395|ref|XP_017486875.1| PREDICTED: uncharacterized protein LOC108375287 [Rhagoletis zephyria];NODE_15_length_154786_cov_732.466280_False_88354 PREDICTED: uncharacterized protein LOC108375287
21.3148	21.2692	21.3312	21.2689	21.4988	21.87	21.4278	21.7174	22.3236	13	13	2	32.8	32.8	5.5	65.353	0	92.968	1.58E+08	126	gi|1048069401|ref|XP_017486878.1|;NODE_3606_length_6784_cov_521.923168_True_3318;NODE_2931_length_8592_cov_552.820194_False_5254;gi|1048027339|ref|XP_017474372.1|;gi|1048027337|ref|XP_017474371.1|	gi|104806	1623	gi|1048069401|ref|XP_017486878.1| PREDICTED: UDP-glucose 4-epimerase-like [Rhagoletis zephyria]
20.0315	NaN	20.3563	20.2978	20.5367	20.6656	20.5616	20.6997	21.6882	10	10	10	13.2	13.2	13.2	110.4	0	56.084	40779000	47	gi|1048069421|ref|XP_017486889.1|;NODE_60_length_86167_cov_723.652151_False_41093;NODE_60_length_86167_cov_723.652151_False_39999	gi|104806	1624	gi|1048069421|ref|XP_017486889.1| PREDICTED: sodium/calcium exchanger 3-like [Rhagoletis zephyria];NODE_60_length_86167_cov_723.652151_False_41093 sodium/calcium exchanger 3-like
21.7723	21.9236	22.0138	21.4132	21.2657	21.8897	21.7213	22.2838	22.7274	17	17	17	42.2	42.2	42.2	71.815	0	169.83	1.84E+08	137	gi|1048069443|ref|XP_017486901.1|;NODE_2618_length_9582_cov_744.834156_False_3923;NODE_2618_length_9582_cov_744.834156_False_4667;NODE_2618_length_9582_cov_744.834156_False_2599;NODE_2618_length_9582_cov_744.834156_False_3187;NODE_2618_length_9582_cov_744.834156_False_2803	gi|104806	1626	gi|1048069443|ref|XP_017486901.1| PREDICTED: plastin-2-like [Rhagoletis zephyria]
19.1753	19.059	19.3654	20.1398	19.5118	20.0135	21.0212	21.6629	21.2357	17	17	17	27.1	27.1	27.1	106.2	0	96.755	61845000	76	gi|1048069492|ref|XP_017486928.1|;NODE_464_length_36455_cov_743.745495_True_24765;NODE_464_length_36455_cov_743.745495_True_25874;NODE_464_length_36455_cov_743.745495_True_23913;NODE_464_length_36455_cov_743.745495_True_27363;NODE_464_length_36455_cov_743.745495_True_27071;NODE_464_length_36455_cov_743.745495_True_24283	gi|104806	1627	gi|1048069492|ref|XP_017486928.1| PREDICTED: vinculin-like [Rhagoletis zephyria]
23.5914	23.8716	23.7276	24.0056	22.7732	24.2163	24.0221	24.4145	24.9273	24	24	24	83	83	83	41.973	0	323.31	1.24E+09	304	gi|1048069494|ref|XP_017486930.1|;NODE_464_length_36455_cov_743.745495_False_28830;NODE_464_length_36455_cov_743.745495_False_28368;NODE_464_length_36455_cov_743.745495_False_29529;NODE_464_length_36455_cov_743.745495_False_29032	gi|104806	1628	gi|1048069494|ref|XP_017486930.1| PREDICTED: 3-ketoacyl-CoA thiolase, mitochondrial-like [Rhagoletis zephyria]
20.0624	NaN	NaN	20.7748	NaN	20.8793	NaN	21.2428	22.1085	5	5	4	24.9	24.9	20.7	32.471	0	14.136	25303000	25	gi|1048069498|ref|XP_017486932.1|;NODE_464_length_36455_cov_743.745495_True_35895;NODE_1118_length_19892_cov_710.504965_False_14479;NODE_464_length_36455_cov_743.745495_True_35428	gi|104806	1629	gi|1048069498|ref|XP_017486932.1| PREDICTED: pyrroline-5-carboxylate reductase 3-like [Rhagoletis zephyria];NODE_464_length_36455_cov_743.745495_True_35895 pyrroline-5-carboxylate reductase 3-like;NODE_1118_length_19892_cov_710.504965_False_14479 pyrroline
22.8915	22.9192	22.9816	23.0261	23.0834	23.0539	22.877	23.2294	23.619	15	15	15	58.2	58.2	58.2	33.969	0	111.71	3.69E+08	203	NODE_654_length_29324_cov_725.602822_True_4078;gi|1048069506|ref|XP_017486937.1|;gi|1048028993|ref|XP_017475242.1|	NODE_65	1630	NODE_654_length_29324_cov_725.602822_True_4078 Proteasome subunit alpha type-1;gi|1048069506|ref|XP_017486937.1| PREDICTED: proteasome subunit alpha type-1-like [Rhagoletis zephyria]
NaN	20.0236	20.1684	19.7102	NaN	NaN	NaN	NaN	NaN	4	4	4	17.5	17.5	17.5	30.601	0	12.951	12720000	15	gi|1048069516|ref|XP_017486944.1|;NODE_219_length_52119_cov_714.230082_False_15139	gi|104806	1631	gi|1048069516|ref|XP_017486944.1| PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member B-like, partial [Rhagoletis zephyria]
23.8286	23.2137	23.6393	NaN	23.7792	23.2027	NaN	23.3886	23.7772	3	3	3	16.3	16.3	16.3	20.786	0	11.174	1.13E+08	46	gi|1048069560|ref|XP_017486969.1|;NODE_2186_length_11317_cov_676.711863_False_9993	gi|104806	1632	gi|1048069560|ref|XP_017486969.1| PREDICTED: acyl carrier protein, mitochondrial-like [Rhagoletis zephyria];NODE_2186_length_11317_cov_676.711863_False_9993 acyl carrier protein, mitochondrial isoform X1
NaN	NaN	NaN	NaN	NaN	20.0364	19.2383	20.3853	NaN	2	2	2	28	28	28	18.757	0	10.443	5824200	8	gi|1048069695|ref|XP_017487040.1|;NODE_162_length_57653_cov_710.035105_False_22418	gi|104806	1634	gi|1048069695|ref|XP_017487040.1| PREDICTED: ubiquitin-conjugating enzyme E2 A [Rhagoletis zephyria];NODE_162_length_57653_cov_710.035105_False_22418 ubiquitin-conjugating enzyme E2 A
22.1923	22.0931	22.0496	22.211	22.17	22.5109	22.7432	22.5147	22.967	6	6	3	56.4	56.4	28.2	17.984	0	24.601	79376000	46	gi|1048069729|ref|XP_017487060.1|;NODE_2024_length_12113_cov_719.597363_False_3562	gi|104806	1636	gi|1048069729|ref|XP_017487060.1| PREDICTED: UMP-CMP kinase-like, partial [Rhagoletis zephyria]
20.7851	20.619	21.4723	NaN	NaN	20.5753	NaN	20.9694	NaN	5	4	3	27.2	21.6	16.4	29.864	0	53.799	19335000	24	gi|1048069758|ref|XP_017487077.1|;NODE_895_length_23854_cov_760.362830_True_7148	gi|104806	1637	gi|1048069758|ref|XP_017487077.1| PREDICTED: tubulin alpha chain-like [Rhagoletis zephyria];NODE_895_length_23854_cov_760.362830_True_7148 Tubulin alpha-1A chain
23.0054	23.0471	23.0555	23.0013	22.8452	22.8651	21.8326	22.946	23.6922	5	5	1	56.4	56.4	8.5	10.513	0	103.31	2E+08	119	gi|1048069848|ref|XP_017464209.1|	gi|104806	1638	gi|1048069848|ref|XP_017464209.1| PREDICTED: adenosine kinase-like, partial [Rhagoletis zephyria]
22.0465	22.1087	22.4918	22.4375	21.794	22.358	21.5443	22.7363	23.4274	9	9	4	62.7	62.7	27.4	23.515	0	86.256	1.47E+08	87	gi|1048069921|ref|XP_017464250.1|;NODE_7215_length_2811_cov_776.097242_False_1385;NODE_6894_length_3015_cov_746.279054_True_1630;NODE_12304_length_1352_cov_999.215883_False_779	gi|104806	1640	gi|1048069921|ref|XP_017464250.1| PREDICTED: probable chitinase 2, partial [Rhagoletis zephyria]
20.2382	19.6317	20.4812	20.5508	NaN	NaN	20.6641	22.0069	22.0813	6	2	2	39.2	15.3	15.3	23.705	0	26.42	30301000	22	gi|1048069938|ref|XP_017464259.1|;NODE_2571_length_9748_cov_626.504075_True_3799	gi|104806	1641	gi|1048069938|ref|XP_017464259.1| PREDICTED: laminin-like protein lam-2, partial [Rhagoletis zephyria]
NaN	20.2463	19.9429	19.5764	19.4875	NaN	19.9651	20.5853	21.2125	2	2	1	14.7	14.7	8.8	15.842	0	5.3288	17934000	17	gi|1048070034|ref|XP_017464316.1|;NODE_1708_length_13844_cov_702.977518_False_8198	gi|104807	1644	gi|1048070034|ref|XP_017464316.1| PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit 3-like, partial [Rhagoletis zephyria];NODE_1708_length_13844_cov_702.977518_False_8198 phosphatase 2B at 14D-like protein
21.912	21.7796	22.1357	22.1068	22.2493	22.4404	21.1346	22.8109	22.7387	6	6	6	61.5	61.5	61.5	13.616	0	29.002	88138000	49	gi|1048070334|ref|XP_017487117.1|;NODE_848_length_24957_cov_661.678379_True_19078	gi|104807	1646	gi|1048070334|ref|XP_017487117.1| PREDICTED: V-type proton ATPase subunit F-like [Rhagoletis zephyria];NODE_848_length_24957_cov_661.678379_True_19078 V-type proton ATPase subunit F
21.5813	21.6611	21.87	21.1885	21.7032	22.4528	21.1889	21.876	22.0622	10	10	10	60	60	60	31.393	0	29.531	91297000	47	gi|1048070474|ref|XP_017487189.1|;NODE_149_length_59631_cov_731.653166_False_30880;NODE_149_length_59631_cov_731.653166_False_30320;NODE_149_length_59631_cov_731.653166_False_30036	gi|104807	1647	gi|1048070474|ref|XP_017487189.1| PREDICTED: putative hydroxypyruvate isomerase [Rhagoletis zephyria];NODE_149_length_59631_cov_731.653166_False_30880 hydroxypyruvate isomerase-like protein
NaN	NaN	NaN	18.6379	NaN	18.9771	19.4847	19.7295	20.2649	11	11	11	7.1	7.1	7.1	303.06	0	39.003	16435000	31	gi|1048070484|ref|XP_017487195.1|;NODE_441_length_37407_cov_693.046129_True_21250;NODE_441_length_37407_cov_693.046129_True_32500	gi|104807	1648	gi|1048070484|ref|XP_017487195.1| PREDICTED: dmX-like protein 2 [Rhagoletis zephyria];NODE_441_length_37407_cov_693.046129_True_21250 dmX-like protein 2
21.1064	21.3215	21.074	21.4651	NaN	21.2277	21.5708	22.034	22.7154	9	9	9	32.6	32.6	32.6	44.004	0	37.43	72358000	51	gi|1048070510|ref|XP_017487209.1|;NODE_97_length_71692_cov_706.114005_False_41118	gi|104807	1650	gi|1048070510|ref|XP_017487209.1| PREDICTED: adenylyltransferase and sulfurtransferase MOCS3-like [Rhagoletis zephyria];NODE_97_length_71692_cov_706.114005_False_41118 adenylyltransferase and sulfurtransferase MOCS3
23.5552	23.7447	23.5918	24.4606	24.2194	24.643	24.6735	25.1106	25.5621	14	14	12	65.8	65.8	59.6	35.295	0	130.29	8.52E+08	236	gi|1048070516|ref|XP_017487213.1|;NODE_97_length_71692_cov_706.114005_False_32414;NODE_97_length_71692_cov_706.114005_False_31646	gi|104807	1652	gi|1048070516|ref|XP_017487213.1| PREDICTED: delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial-like [Rhagoletis zephyria];NODE_97_length_71692_cov_706.114005_False_32414 delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
21.902	21.6845	21.7313	21.8195	21.3764	21.7611	21.3054	21.7569	21.5352	6	5	5	35.8	32.5	32.5	27.166	0	16.605	60352000	37	gi|1048070580|ref|XP_017487247.1|;NODE_327_length_43692_cov_738.782478_True_41028;gi|1048037451|ref|XP_017475498.1|	gi|104807	1654	gi|1048070580|ref|XP_017487247.1| PREDICTED: peroxiredoxin-4-like [Rhagoletis zephyria];NODE_327_length_43692_cov_738.782478_True_41028 peroxiredoxin-4-like protein



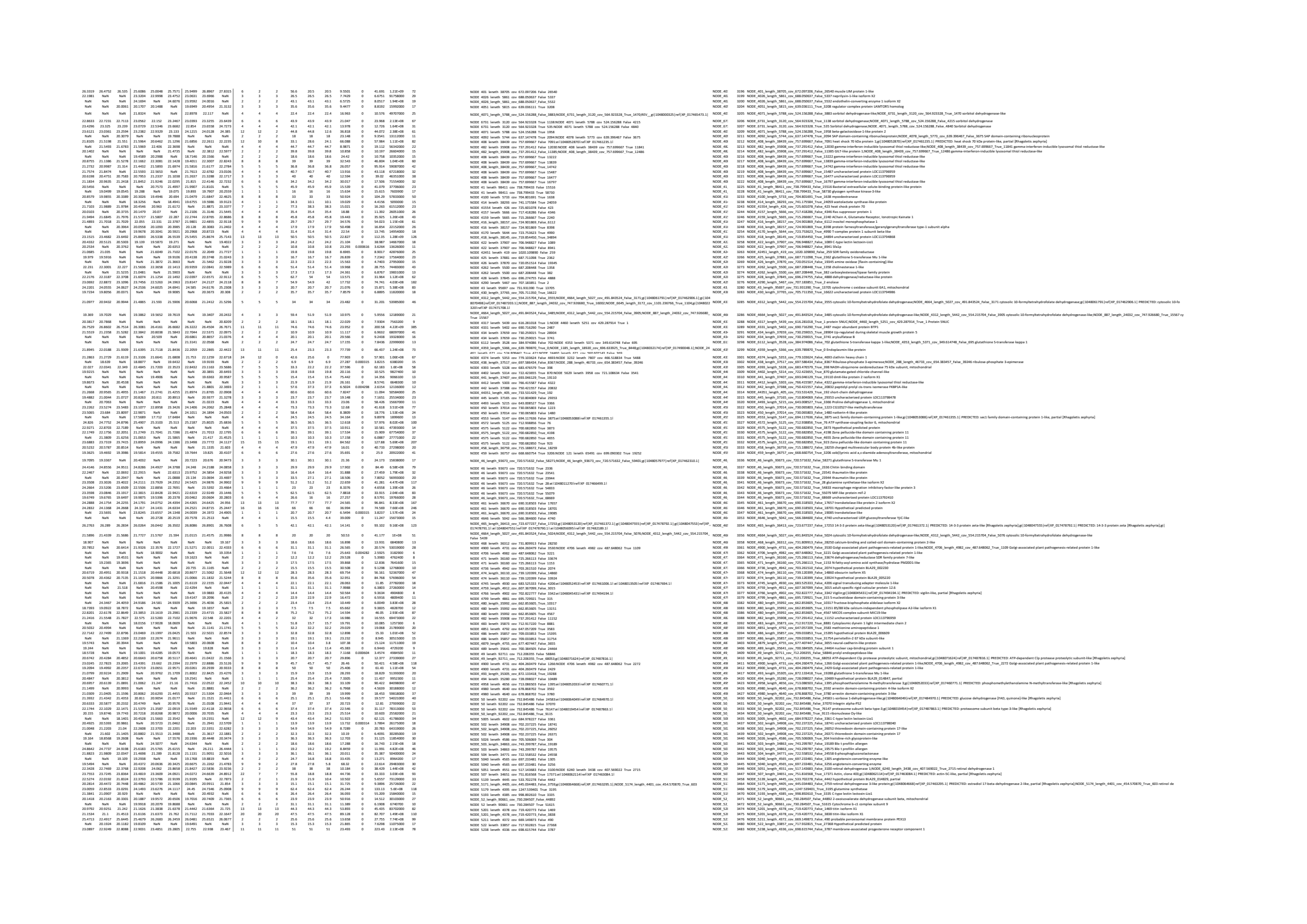








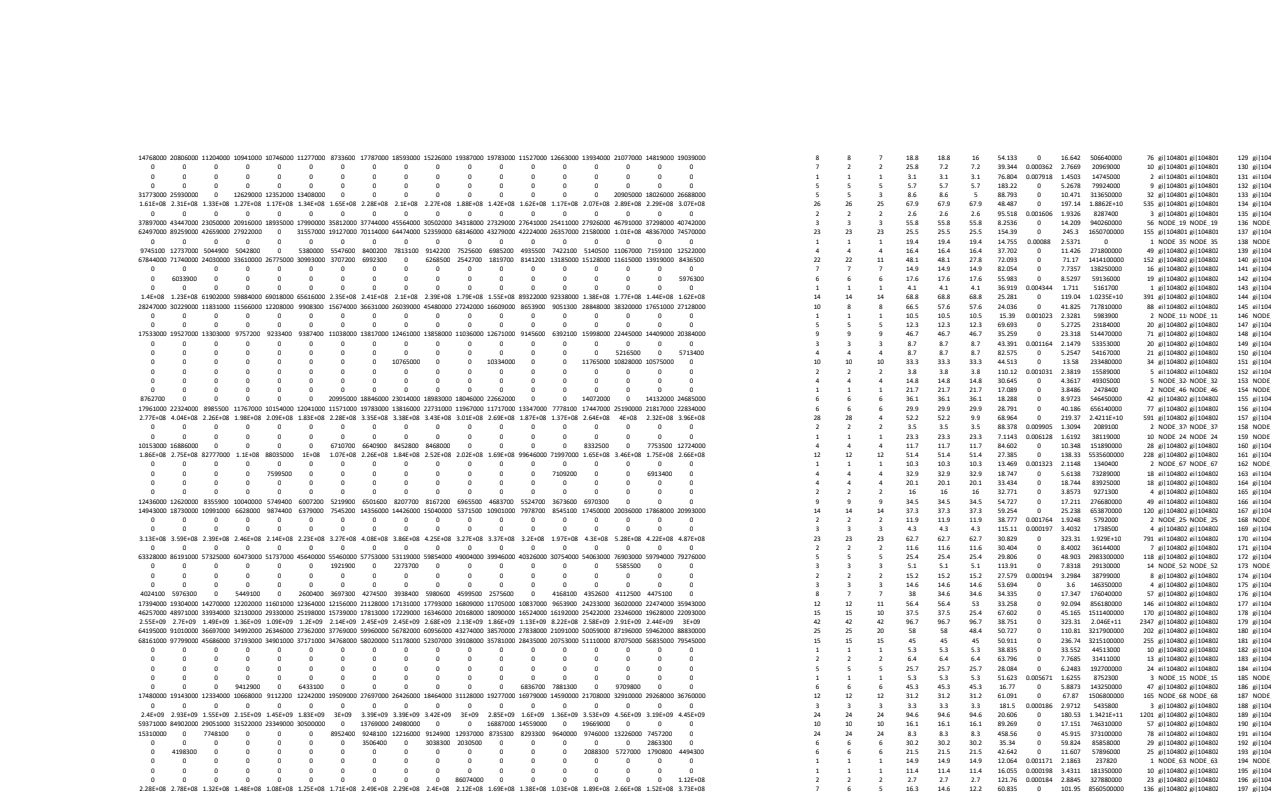


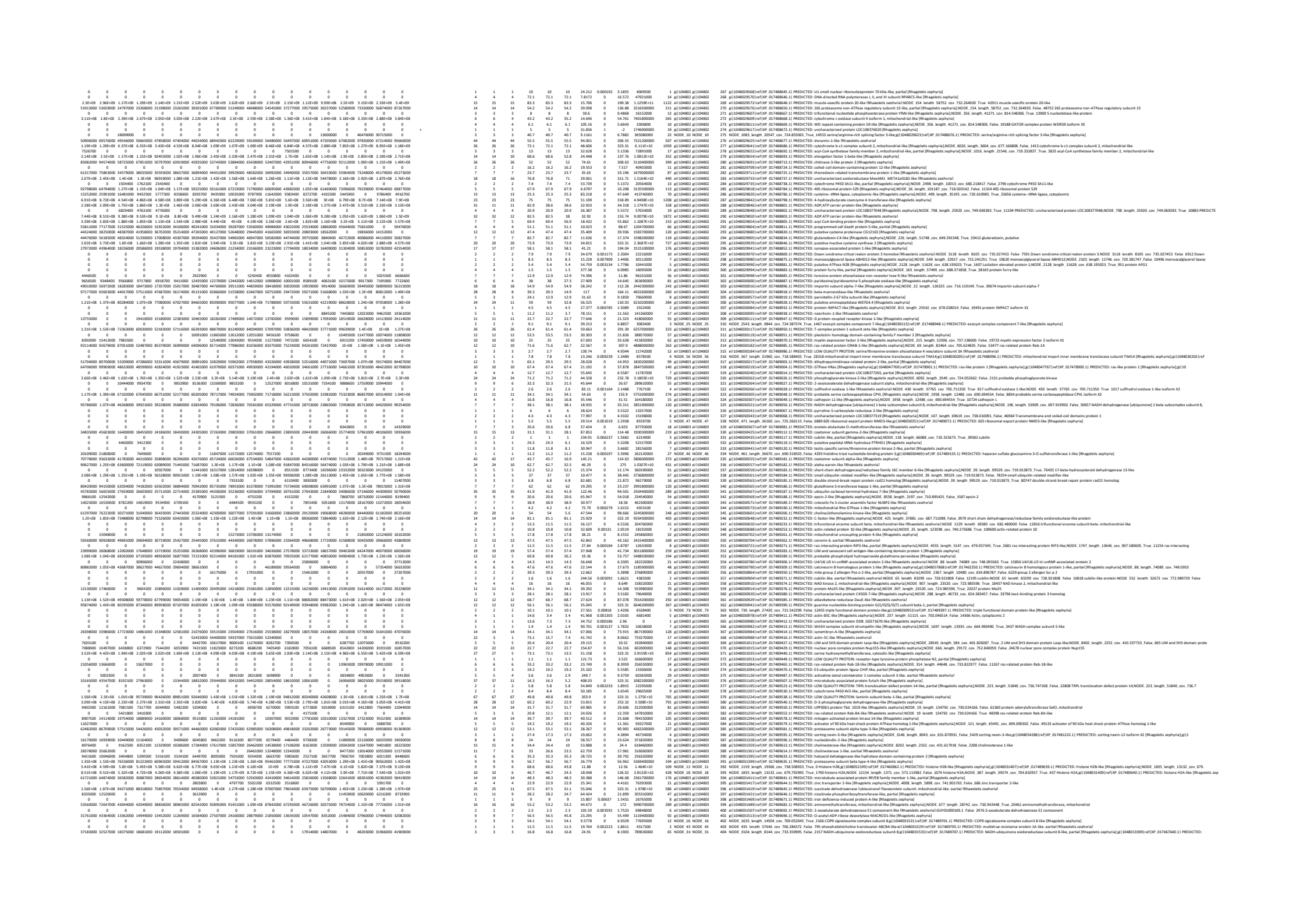


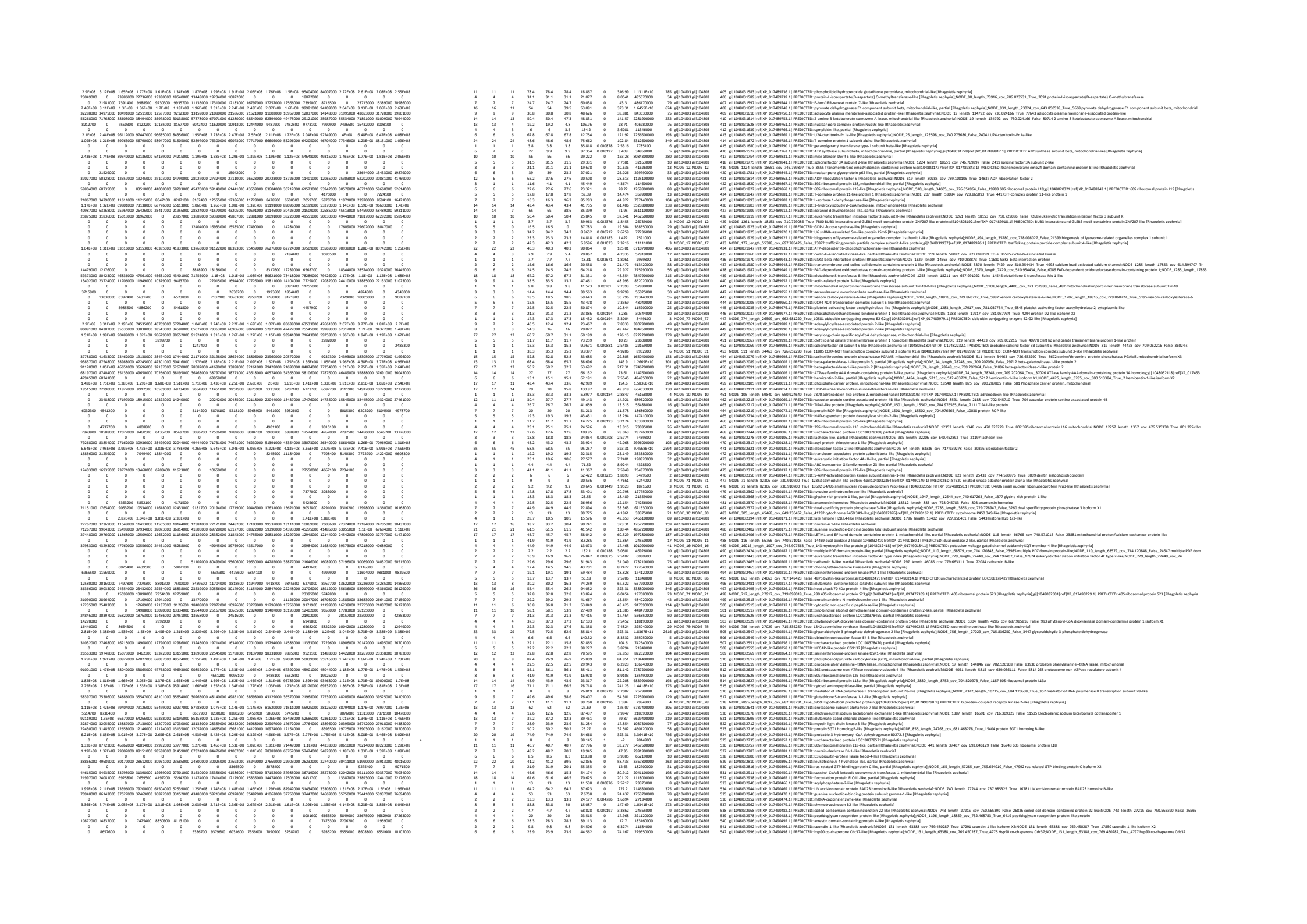


22.1467	21.7875	22.243	23.4108	23.1964	22.8646	23.9596	23.3361	23.8282	7	6	6	55.4	46.8	46.8	15.393	0	33.187	1.71E+08	48	NODE 731 length 27401 cov 690.298801 False 4407	NODE_73	3788	NODE_731_length_27401_cov_690.298801_False_4407 myosin heavy chain, muscle-like
NaN	23.2943	22.9751	22.8647	22.8005	22.8999	23.1454	23.0602	23.5806	3	3	3	24	24	24	16.372	0	8.994	1.14E+08	20	NODE 737 length 27299 cov 674.945970 False 8983	NODE_73	3793	NODE_737_length_27299_cov_674.945970_False_8983 glucose-6-phosphate 1-dehydrogenase-like
NaN	19.5826	19.6424	NaN	NaN	NaN	NaN	20.3658	20.82	3	3	3	18.3	18.3	18.3	21.054	0	9.2739	10700000	16	NODE 739 length 27272 cov 671.282801 False 2642:gi|1048064843|ref|XP 017463394.1|	NODE_73	3796	NODE_739_length_27272_cov_671.282801_False_2642 AP-2 complex subunit mu;gi|1048064843|ref|XP_017463394.1| PREDICTED: AP-2 complex subunit mu-like, partial [Rhagoletis zephyria]
NaN	NaN	NaN	NaN	NaN	NaN	20.5624	21.2969	NaN	3	3	3	20.8	20.8	20.8	18.373	0	6.5793	13846000	16	NODE 739 length 27272 cov 671.282801 False 5401	NODE_73	3797	NODE_739_length_27272_cov_671.282801_False_5401 sodium/potassium-transporting ATPase subunit beta-like
21.8648	20.6894	21.1206	23.5898	23.1072	23.5837	24.6067	24.8789	25.4565	11	10	3	48.9	46.1	16.2	40.768	0	42.289	4.43E+08	80	NODE 74 length 78248 cov 709.202064 False 29074	NODE_74_	3798	NODE_74_length_78248_cov_709.202064_False_29074 beta-galactosidase-1-like protein 2
NaN	NaN	NaN	20.606	22.1768	22.3196	NaN	NaN	NaN	2	2	2	70.9	70.9	70.9	6.0507	0	8.9342	20809000	9	NODE 7429 length 2707 cov 526.438914 True 691	NODE_74	3805	NODE_7429_length_2707_cov_526.438914_True_691 complement C1r-A subcomponent-like
22.7462	22.6011	22.7745	22.2902	21.9209	22.6965	22.615	23.2829	23.8323	11	11	10	66.7	66.7	61.6	30.303	0	75.438	1.9E+08	85	NODE 7445 length 2695 cov 1355.649242 False 2692	NODE_74	3806	NODE_7445_length_2695_cov_1355.649242_False_2692 putative glutamate synthase [NADPH] isoform X3
NaN	NaN	NaN	21.2728	21.3545	21.6267	21.2189	22.3059	22.6009	7	7	7	47.7	47.7	47.7	23.741	0	33.901	73245000	36	NODE 746 length 27200 cov 732.525364 False 22888	NODE_74	3810	NODE_746_length_27200_cov_732.525364_False_22888 sucrase-isomaltase, intestinal-like
NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.6836	21.8599	2	2	2	28.6	28.6	28.6	17.727	0	13.247	17610000	9	NODE 746 length 27200 cov 732.525364 False 23383	NODE_74	3811	NODE_746_length_27200_cov_732.525364_False_23383 sucrase-isomaltase, intestinal-like
NaN	NaN	NaN	NaN	NaN	20.6293	NaN	21.4416	22.5522	4	4	4	28	28	28	17.734	0	16.583	28877000	14	NODE 746 length 27200 cov 732.525364 False 25693	NODE_74	3813	NODE_746_length_27200_cov_732.525364_False_25693 maltase-glucoamylase, intestinal
20.4983	20.5712	20.7527	NaN	NaN	NaN	NaN	NaN	NaN	4	4	4	13.6	13.6	13.6	37.008	0	66.888	9835100	10	NODE 746 length 27200 cov 732.525364 True 20154:gi|1048065196|ref|XP 017463589.1|	NODE_74	3814	NODE_746_length_27200_cov_732.525364_True_20154 venom acid phosphatase Acph-1-like
21.0513	20.976	21.8366	19.8728	NaN	NaN	NaN	NaN	NaN	3	3	3	24.2	24.2	24.2	25.691	0	17.475	20571000	13	NODE 746 length 27200 cov 732.525364 True 21166	NODE_74	3815	NODE_746_length_27200_cov_732.525364_True_21166 prostatic acid phosphatase-like
18.4794	19.1396	19.2485	NaN	NaN	NaN	NaN	NaN	NaN	1	1	1	18.4	18.4	18.4	10.968	0.000604	3.4495	3167100	8	NODE 746 length 27200 cov 732.525364 True 21891	NODE_74	3816	NODE_746_length_27200_cov_732.525364_True_21891 prostatic acid phosphatase-like
22.4858	22.9367	23.0492	22.2591	22.4569	23.0723	20.8964	22.6837	23.8748	5	5	5	37.8	37.8	37.8	19.879	0	17.559	1.23E+08	33	NODE 75 length 78014 cov 690.976436 False 71446	NODE_75_	3818	NODE_75_length_78014_cov_690.976436_False_71446 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13
NaN	NaN	NaN	NaN	NaN	NaN	21.2844	22.0868	NaN	4	4	4	23.1	23.1	23.1	23.681	0	7.6152	16057000	9	NODE 75 length 78014 cov 690.976436 True 16116	NODE_75_	3819	NODE_75_length_78014_cov_690.976436_True_16116 phosphoribosyl pyrophosphate synthase-associated protein 2
NaN	20.3056	20.5797	20.341	20.9379	21.2703	21.6131	21.965	21.615	5	5	5	40.2	40.2	40.2	24.789	0	16.996	35577000	23	NODE 75 length 78014 cov 690.976436 True 16673	NODE_75_	3820	NODE_75_length_78014_cov_690.976436_True_16673 phosphoribosyl pyrophosphate synthase-associated protein 2 isoform X2
NaN	NaN	NaN	19.8585	20.1789	19.6836	19.9809	20.5897	21.384	7	7	7	23.7	23.7	23.7	52.393	0	34.484	23078000	27	NODE 75 length 78014 cov 690.976436 True 67199	NODE_75_	3822	NODE_75_length_78014_cov_690.976436_True_67199 Protein CBG13257
24.1024	24.0972	24.0127	23.9083	23.9209	24.5777	23.9771	24.2618	24.8257	14	12	3	57.6	55.1	24.8	34.08	0	48.901	7.54E+08	166	NODE 7503 length 2670 cov 753.584321 False 2156	NODE_75	3823	NODE_7503_length_2670_cov_753.584321_False_2156 retinal dehydrogenase 1 isoform X2
22.5364	22.51	22.5835	22.2303	22.2367	22.8251	22.9457	23.0404	23.847	4	4	4	41.9	41.9	41.9	10.147	0	13.102	1.06E+08	34	NODE 751 length 27076 cov 717.293883 True 3080	NODE_75	3824	NODE_751_length_27076_cov_717.293883_True_3080 protein obstructor-E
21.6382	21.8444	21.8105	21.3856	21.7286	21.8243	22.3322	22.6958	22.9724	4	4	4	64.5	64.5	64.5	7.1831	0	10.005	1.19E+08	48	NODE 751 length 27076 cov 717.293883 True 3654	NODE_75	3826	NODE_751_length_27076_cov_717.293883_True_3654 protein obstructor-E
19.9127	20.1368	20.0988	NaN	NaN	19.8651	NaN	NaN	20.4178	3	3	3	8.3	8.3	8.3	65.356	0	12.656	10916000	16	NODE 7534 length 2657 cov 718.792083 True 958:gi|1048067576|ref|XP 017463898.1|	NODE_75	3828	NODE_7534_length_2657_cov_718.792083_True_958 exportin-2-like;gi|1048067576|ref|XP_017463898.1| PREDICTED: exportin-2-like, partial [Rhagoletis zephyria]
NaN	NaN	NaN	NaN	NaN	NaN	21.9989	22.2518	22.764	8	8	3	28.3	28.3	7.5	44.008	0	27.628	42895000	29	NODE 758 length 26962 cov 675.952800 True 2887	NODE_75	3830	NODE_758_length_26962_cov_675.952800_True_2887 p-loop containing nucleoside triphosphate hydrolase
25.3425	25.1522	25.2491	26.4711	26.0525	26.1218	24.9041	25.1921	25.4407	12	12	7	61.8	61.8	36.7	22.924	0	100.19	1.94E+09	235	NODE 76 length 77980 cov 709.829426 False 25058:gi|1048033876|ref|XP 017490976.1|	NODE_76_	3836	NODE_76_length_77980_cov_709.829426_False_25058 protein lethal(2)essential for life-like;gi|1048033876|ref|XP_017490976.1| PREDICTED: alpha-crystallin A chain-like [Rhagoletis zephyria]
22.1058	22.4009	22.6636	21.6335	21.9113	22.1835	22.1669	22.6257	23.297	6	6	6	30.6	30.6	30.6	26.294	0	29.204	79136000	28	NODE 76 length 77980 cov 709.829426 False 54887:gi|1048052876|ref|XP 017461238.1|	NODE_76_	3837	NODE_76_length_77980_cov_709.829426_False_54887 40S ribosomal protein S3a;gi|1048052876|ref|XP_017461238.1| PREDICTED: 40S ribosomal protein S3a-like, partial [Rhagoletis zephyria]
22.5038	22.7604	22.1947	22.7303	22.5699	23.1026	23.2244	23.5732	24.1102	9	9	9	46.4	46.4	46.4	26.917	0	34.12	3.09E+08	106	NODE 760 length 26909 cov 677.370857 True 3946	NODE_76	3840	NODE_760_length_26909_cov_677.370857_True_3946 Platelet-activating factor acetylhydrolase IB subunit gamma
21.4734	21.2382	21.2494	21.2241	20.7953	21.7268	21.8242	22.4311	23.2945	6	6	6	67.5	67.5	67.5	14.269	0	84.389	1.27E+08	80	NODE 760 length 26909 cov 677.370857 True 4632	NODE_76	3841	NODE_760_length_26909_cov_677.370857_True_4632 GDSL family lipase
21.9076	21.8974	21.8952	22.6183	22.6429	22.9085	21.6286	23.2015	23.8271	2	2	2	43.3	43.3	43.3	7.1382	0	11.644	1.37E+08	39	NODE 765 length 26795 cov 715.856021 True 15292	NODE_76	3844	NODE_765_length_26795_cov_715.856021_True_15292 glucosylceramidase-like protein
20.7381	20.6277	20.5901	21.6372	21.1077	21.2163	20.9391	21.8732	22.2711	2	2	2	31.7	31.7	31.7	9.4945	0	5.861	53257000	32	NODE 765 length 26795 cov 715.856021 True 15575	NODE_76	3845	NODE_765_length_26795_cov_715.856021_True_15575 glucosylceramidase-like
21.9645	NaN	NaN	22.7053	22.3787	22.7666	22.1862	22.9715	23.4967	6	6	6	53.1	53.1	53.1	14.74	0	12.308	98303000	29	NODE 765 length 26795 cov 715.856021 True 16000	NODE_76	3846	NODE_765_length_26795_cov_715.856021_True_16000 glucosylceramidase-like
20.9313	21.4361	21.0802	22.7119	22.7259	22.5149	20.9477	22.213	22.9791	10	10	10	46.9	46.9	46.9	31.97	0	62.907	1.24E+08	56	NODE 769 length 26648 cov 711.626970 True 12907:gi|1048064571|ref|XP 017463239.1|:gi|1048066809|ref|XP 017485929.1|	NODE_76	3849	NODE_769_length_26648_cov_711.626970_True_12907 cathepsin B;gi|1048064571|ref|XP_017463239.1| PREDICTED: cathepsin B-like, partial [Rhagoletis zephyria]
NaN	NaN	NaN	20.1963	NaN	20.4727	NaN	20.9588	21.2988	4	4	4	13	13	13	43.289	0	9.534	15719000	15	NODE 769 length 26648 cov 711.626970 True 1692	NODE_76	3850	NODE_769_length_26648_cov_711.626970_True_1692 serpin family protein
NaN	NaN	NaN	21.3848	21.1651	21.3819	NaN	NaN	NaN	8	8	8	28.4	28.4	28.4	47.502	0	42.175	29393000	22	NODE 769 length 26648 cov 711.626970 True 4786	NODE_76	3851	NODE_769_length_26648_cov_711.626970_True_4786 serpin family protein
25.3056	25.5512	25.2951	25.354	25.8331	25.7243	23.8694	25.6701	26.2718	7	7	6	45.7	45.7	39.1	17.101	0	139.59	1.08E+09	279	NODE 770 length 26597 cov 711.175910 False 3437:NODE 465 length 36413 cov 723.677237 False 11173	NODE_77	3853	NODE_770_length_26597_cov_711.175910_False_3437 14-3-3 protein epsilon
NaN	NaN	NaN	19.1477	20.1446	NaN	20.5771	21.1372	21.8421	4	4	4	44.2	44.2	44.2	13.83	0	15.325	22693000	26	NODE 770 length 26597 cov 711.175910 False 9344	NODE_77	3855	NODE_770_length_26597_cov_711.175910_False_9344 Phosphoserine phosphatase
24.0385	24.1695	24.1565	22.9217	24.4886	24.2123	20.9269	23.4359	24.7882	6	6	4	37.4	37.4	35	35.948	0	46.841	3.28E+08	49	NODE 775 length 26434 cov 710.296562 False 10267	NODE_77	3861	NODE_775_length_26434_cov_710.296562_False_10267 PREDICTED: calphotin-like, partial
22.1382	21.9754	21.487	NaN	NaN	NaN	21.1589	22.0886	22.0712	3	3	3	28.7	28.7	28.7	27.364	0	21.088	36156000	18	NODE 7767 length 2529 cov 723.088116 True 2	NODE_77	3863	NODE_7767_length_2529_cov_723.088116_True_2 C-type lectin lectoxin-Lio1
NaN	NaN	NaN	18.3843	NaN	NaN	18.4634	NaN	19.4004	2	2	2	23.6	23.6	23.6	11.836	0.000319	3.9528	3356000	10	NODE 7776 length 2524 cov 622.100041 False 1087:NODE 7836 length 2487 cov 645.348684 False 1075	NODE_77	3864	NODE_7776_length_2524_cov_622.100041_False_1087 long-chain-fatty-acid--CoA ligase 4-like;NODE_7836_length_2487_cov_645.348684_False_1075 long-chain-fatty-acid--CoA ligase 4-like
NaN	NaN	20.1033	20.353	20.3587	20.5135	NaN	NaN	NaN	1	1	1	30.8	30.8	30.8	12.331	0	19.977	10815000	15	NODE 779 length 26342 cov 635.046677 False 5734	NODE_77	3868	NODE_779_length_26342_cov_635.046677_False_5734 NDRG3-like protein
24.2137	24.229	24.4061	NaN	24.0002	NaN	23.8753	NaN	NaN	4	4	4	49.2	49.2	49.2	13.563	0	48.42	1.39E+08	30	NODE 78 length 76615 cov 746.913009 False 71374	NODE_78_	3870	NODE_78_length_76615_cov_746.913009_False_71374 cuticle protein, putative
21.9924	22.2481	22.411	20.8953	20.5446	NaN	21.6027	21.6341	21.4646	9	9	9	38.2	38.2	38.2	32.866	0	107.65	87317000	56	NODE 789 length 26146 cov 876.478173 False 20427	NODE_78	3878	NODE_789_length_26146_cov_876.478173_False_20427 hypothetical protein QR98_0103690
NaN	NaN	20.6049	NaN	21.0559	NaN	20.0863	21.2403	NaN	4	4	4	16.5	16.5	16.5	26.578	0	8.4729	18681000	24	NODE 789 length 26146 cov 876.478173 False 25813	NODE_78	3879	NODE_789_length_26146_cov_876.478173_False_25813 chromobox protein homolog 6 isoform X2
NaN	NaN	NaN	NaN	NaN	NaN	20.3117	NaN	20.8115	10	3	3	21.2	7.4	7.4	78.291	0	8.4561	7865100	10	NODE 79 length 76496 cov 660.700619 False 26345	NODE_79_	3881	NODE_79_length_76496_cov_660.700619_False_26345 uncharacterized family 31 glucosidase KIAA1161-like
21.9272	22.1339	22.1211	21.6064	21.8676	21.9344	22.0346	22.3363	22.6315	21	21	21	39.7	39.7	39.7	85.07	0	94.83	2.33E+08	128	NODE 79 length 76496 cov 660.700619 False 41202	NODE_79_	3882	NODE_79_length_76496_cov_660.700619_False_41202 uncharacterized family 31 glucosidase KIAA1161-like
NaN	20.8916	21.3114	NaN	NaN	NaN	NaN	NaN	NaN	2	2	2	11.6	11.6	11.6	22.273	0.002759	2.8054	13168000	7	NODE 7945 length 2441 cov 705.491199 False 1514	NODE_79	3884	NODE_7945_length_2441_cov_705.491199_False_1514 neural cell adhesion molecule 1-like
NaN	NaN	NaN	NaN	NaN	NaN	18.898	19.3493	19.6611	3	3	3	3.2	3.2	3.2	171.88	0	9.1656	3028600	10	NODE 795 length 25951 cov 734.886392 False 23197:gi|1048069216|ref|XP 017486783.1|	NODE_79	3885	NODE_795_length_25951_cov_734.886392_False_23197 RING finger protein nhl-1-like
20.6591	21.024	21.023	21.302	20.9205	21.3778	21.0287	21.5717	21.3955	2	2	2	52.2	52.2	52.2	7.5317	0	39.389	41810000	25	NODE 7963 length 2433 cov 491.613120 True 1418:NODE 8059 length 2392 cov 484.810441 True 1383	NODE_79	3886	NODE_7963_length_2433_cov_491.613120_True_1418 galactose mutarotase;NODE_8059_length_2392_cov_484.810441_True_1383 galactose mutarotase
21.5454	21.8584	NaN	22.3745	22.7963	22.3597	21.634	21.6744	22.6861	3	3	3	30.9	30.9	30.9	6.283	0	30.686	58511000	20	NODE 80 length 76295 cov 746.454538 False 36443	NODE_80_	3888	NODE_80_length_76295_cov_746.454538_False_36443 cuticular protein, putative
21.7383	21.555	21.841	21.9572	22.0372	22.0035	21.7838	22.5703	22.8967	3	3	2	9.7	9.7	4.1	29.735	0	59.159	79017000	35	NODE 80 length 76295 cov 746.454538 False 4430	NODE_80_	3889	NODE_80_length_76295_cov_746.454538_False_4430 ribosomal protein S6
NaN	21.5288	21.3419	21.9934	21.7188	22.181	22.5958	22.7981	22.6027	5	5	5	21.1	21.1	21.1	38.331	0	23.254	70808000	38	NODE 80 length 76295 cov 746.454538 True 11890	NODE_80_	3892	NODE_80_length_76295_cov_746.454538_True_11890 succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial-like
22.9064	22.9686	22.8613	22.7842	22.8431	23.383	22.7692	23.3961	24.1848	6	6	6	52.2	52.2	52.2	22.449	0	100.97	3.47E+08	100	NODE 80 length 76295 cov 746.454538 True 12813:gi|1048052323|ref|XP 017460931.1|	NODE_80_	3893	NODE_80_length_76295_cov_746.454538_True_12813 ADP-forming succinate--CoA ligase subunit beta;gi|1048052323|ref|XP_017460931.1| PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta-like [Rhagoletis zephyria]
19.465	18.991	NaN	NaN	NaN	NaN	NaN	NaN	NaN	3	3	3	11.4	11.4	11.4	52.852	0	8.7932	3560900	9	NODE 80 length 76295 cov 746.454538 True 30188	NODE_80_	3894	NODE_80_length_76295_cov_746.454538_True_30188 complement C3-like
NaN	19.2023	NaN	NaN	NaN	NaN	NaN	NaN	20.3843	3	3	3	7	7	7	76.925	0	5.4928	6150400	8	NODE 80 length 76295 cov 746.454538 True 31735:NODE 2373 length 10453 cov 695.578188 False 2981	NODE_80_	3895	NODE_80_length_76295_cov_746.454538_True_31735 Complement C3
21.865	22.0642	22.5492	22.6718	22.7268	22.7878	22.9312	22.1491	23.263	2	2	2	27.6	27.6	27.6	18.865	0	12.972	1.05E+08	29	NODE 80 length 76295 cov 746.454538 True 43583	NODE_80_	3896	NODE_80_length_76295_cov_746.454538_True_43583 DFP2-like protein 25
23.6678	23.7039	23.9667	23.7972	23.7722	23.784	23.4609	23.9353	23.8738	4	4	4	45.3	45.3	45.3	13.042	0	42.466	2.03E+08	53	NODE 80 length 76295 cov 746.454538 True 49906	NODE_80_	3897	NODE_80_length_76295_cov_746.454538_True_49906 cuticular protein, putative
NaN	19.9185	20.354	NaN	NaN	NaN	NaN	NaN	NaN	3	3	3	21.8	21.8	21.8	25.023	0	10.515	8538800	11	NODE 80 length 76295 cov 746.454538 True 66539	NODE_80_	3898	NODE_80_length_76295_cov_746.454538_True_66539 putative ferric-chelate reductase 1 homolog
25.9361	25.447	25.6062	25.8288	25.6636	25.9158	26.5478	26.5638	26.2306	15	7	3	67.1	41.1	24	16.261	0	26.79	1.08E+09	111	NODE 808 length 25670 cov 703.024790 False 18112:NODE 207 length 53084 cov 723.865093 False 46108	NODE_80	3905	NODE_808_length_25670_cov_703.024790_False_18112 arginine kinase
26.5314	26.1988	26.4117	27.3968	26.9574	27.3622	26.8391	27.5253	27.8173	7	5	5	53.8	41.5	41.5	12.522	0	46.272	2.03E+09	69	NODE 808 length 25670 cov 703.024790 False 18433	NODE_80	3906	NODE_808_length_25670_cov_703.024790_False_18433 arginine kinase
NaN	NaN	NaN	21.0815	NaN	21.2671	21.0523	21.6549	22.3756	3	3	3	17.2	17.2	17.2	29.709	0	9.0606	35987000	16	NODE 8088 length 2383 cov 602.454897 True 153:NODE 8084 length 2384 cov 603.037355 False 2364	NODE_80	3909	NODE_8088_length_2383_cov_602.454897_True_153 sodium-driven chloride bicarbonate exchanger isoform X4;NODE_8084_length_2384_cov_603.037355_False_2364 sodium-driven chloride bicarbonate exchanger isoform X4
21.3231	21.2665	21.91	20.1377	NaN	20.1914	22.4807	23.0307	23.4799	3	3	3	14.2	14.2	14.2	30.697	0	58.127	52964000	38	NODE 812 length 25571 cov 748.469901 False 1801	NODE_81	3914	NODE_812_length_25571_cov_748.469901_False_1801 hypothetical protein BLA29_012342
20.6725	20.5678	20.7212	20.8415	20.6906	20.8006	20.7638	20.994	21.3472	7	7	7	26.8	26.8	26.8	44.683	0	20.684	30686000	33	NODE 819 length 25504 cov 658.534324 False 16969:gi|1048067691|ref|XP 017463965.1|	NODE_81	3921	NODE_819_length_25504_cov_658.534324_False_16969 inactive pancreatic lipase-related protein 1-like;gi|1048067691|ref|XP_017463965.1| PREDICTED: inactive pancreatic lipase-related protein 1-like [Rhagoletis zephyria]
23.3691	23.2508	22.9051	22.4033	21.5451	23.2585	24.1084	24.1009	24.6471	3	2	2	40	33.3	33.3	17.693	0	82.332	2.06E+08	52	NODE 82 length 75534 cov 705.008161 False 47003	NODE_82_	3922	NODE_82_length_75534_cov_705.008161_False_47003 Cuticle protein 14 isoform a
23.2107	23.6065	23.7259	22.8502	NaN	23.4429	23.7847	24.0628	24.5563	1	1	1	32.9	32.9	32.9	7.2771	0	36.426	1.28E+08	23	NODE 82 length 75534 cov 705.008161 False 47260	NODE_82_	3923	NODE_82_length_75534_cov_705.008161_False_47260 adult-specific rigid cuticular protein 15.7-like
24.1483	23.8135	24.0363	23.9916	23.6194	24.0701	22.7229	23.9187	23.6899	3	3	3	39.2	39.2	39.2	11.005	0	21.859	2.3E+08	46	NODE 82 length 75534 cov 705.008161 True 59581	NODE_82_	3925	NODE_82_length_75534_cov_705.008161_True_59581 glutathione S-transferase Mu 1-like
NaN	NaN	NaN	NaN	21.7645	22.0401	NaN	NaN	NaN	2	2	2	18.2	18.2	18.2	9.8612	0.000317	3.8886	28139000	10	NODE 82 length 75534 cov 705.008161 True 59879	NODE_82_	3926	NODE_82_length_75534_cov_705.008161_True_59879 glutathione S-transferase Mu 5
19.9905	NaN	20.3077	19.8463	NaN	NaN	20.8251	20.8732	NaN	2	2	2	38.7	38.7	38.7	11.98	0	6.5345	10834000	13	NODE 8222 length 2325 cov 717.951101 False 1162	NODE_82	3928	NODE_8222_length_2325_cov_717.951101_False_1162 peptidase S10, serine carboxypeptidase
21.0685	21.309	21.0563	21.9934	22.2075	22.6254	22.2237	22.6458	22.0812	3	3	3	32.3	32.3	32.3	20.075	0	22.6	90211000	42	NODE 8237 length 2319 cov 702.685954 False 1657	NODE_82	3930	NODE_8237_length_2319_cov_702.685954_False_1657 DFP2-like protein
NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.485	22.0828	3	3	3	29.4	29.4	29.4	18.176	0	11.482	17171000	8	NODE 824 length 25427 cov 742.683115 True 22930	NODE_82	3932	NODE_824_length_25427_cov_742.683115_True_22930 cholinesterase 1-like
21.4073	21.6449	21.6167	21.558	21.4996	21.9844	21.4815	21.6235	NaN	4	4	4	13.5	13.5	13.5	50.845	0	60.903	40041000	25	NODE 8253 length 2315 cov 723.318584 False 2314	NODE_82	3933	NODE_8253_length_2315_cov_723.318584_False_2314 CD109 antigen-like
NaN	20.5009	20.7503	21.8415	20.7896	21.5094	21.1642	21.662	21.9382	4	4	4	39	39	39	19.055	0	18.958	28437000	32	NODE 8253 length 2315 cov 723.318584 False 532	NODE_82	3934	NODE_8253_length_2315_cov_723.318584_False_532 CD109 antigen-like
NaN	21.6994	21.6297	21.983	21.245	22.1326	NaN	NaN	NaN	2	2	2	13.6	13.6	13.6	20.873	0	21.588	31817000	13	NODE 8421 length 2245 cov 524.184018 True 888:NODE 8281 length 2306 cov 518.107508 True 918	NODE_84	3936	NODE_8421_length_2245_cov_524.184018_True_888 CD109 antigen-like protein;NODE_8281_length_2306_cov_518.107508_True_918 CD109 antigen-like protein
NaN	17.7601	NaN	18.431	NaN	NaN	NaN	19.3674	19.4924	1	1	1	14.4	14.4	14.4	12.377	0	4.3008	3939700	10	NODE 832 length 25313 cov 715.847929 False 21520	NODE_83	3938	NODE_832_length_25313_cov_715.847929_False_21520 vesicular glutamate transporter 1-like
NaN	NaN	NaN	NaN	NaN	NaN	20.5558	NaN	21.4751	1	1	1	8.3	8.3	8.3	17.99	0	5.5886	8037000	5	NODE 8388 length 2256 cov 723.361654 True 710	NODE_83	3941	NODE_8388_length_2256_cov_723.361654_True_710 putative glycine receptor subunit alpha-3-like
24.6197	24.8913	24.7267	24.4588	23.5152	24.3731	24.2508	24.6322	25.7377	2	2	2	49.2	49.2	49.2	7.2182	0	91.479	3.79E+08	46	NODE 84 length 75055 cov 730.418667 True 47353	NODE_84_	3943	NODE_84_length_75055_cov_730.418667_True_47353 adenosine kinase
24.2589	24.3891	24.6524	24.7679	24.7343	24.6145	25.094	25.243	25.3643	2	2	2	25.8	25.8	25.8	9.886	0	8.5858	4.55E+08	38	NODE 843 length 25132 cov 716.241656 False 2607	NODE_84	3946	NODE_843_length_25132_cov_716.241656_False_2607 smoothelin-like protein
22.9666	23.0154	23.3299	23.8046	23.3633	23.5115	23.68	24.0441	24.3828	4	4	4	50.7	50.7	50.7	7.1079	0	12.46	2.9E+08	49	NODE 843 length 25132 cov 716.241656 False 3005	NODE_84	3947	NODE_843_length_25132_cov_716.241656_False_3005 Smoothelin-like protein 1
NaN	NaN	NaN	21.3911	NaN	NaN	21.7053	NaN	NaN	3	3	3	10.6	10.6	10.6	23.749	0	5.2679	23732000	11	NODE 843 length 25132 cov 716.241656 False 3406	NODE_84	3948	NODE_843_length_25132_cov_716.241656_False_3406 smoothelin-like protein
19.432	NaN	NaN	19.5641	19.4695	19.7341	NaN	19.8092	20.522	1	1	1	28.6	28.6	28.6	6.6758	0.00061	3.5291	8986100	19	NODE 843 length 25132 cov 716.241656 False 369	NODE_84	3949	NODE_843_length_25132_cov_716.241656_False_369 smoothelin-like protein
NaN	20.8715	NaN	20.9971	20.7871	20.8976	21.3911	21.3028	21.6386	3	3	3	17.5	17.5	17.5	30.02	0	16.351	27362000	21	NODE 848 length 24957 cov 661.678379 True 2926	NODE_84	3952	NODE_848_length_24957_cov_661.678379_True_2926 synaptophysin-like protein
19.789	19.8403	19.7277	NaN	NaN	NaN	NaN	NaN	20.3404	2	2	2	12.1	12.1	12.1	23.836	0	5.1283	10703000	17	NODE_8977_length_2051_cov_393.142285_True_1276;NODE_8571_length_2194_cov_375.468911_True_1383;NODE_8377_length_2260_cov_1112.263039_ True 65	NODE_89	3954	NODE_8977_length_2051_cov_393.142285_True_1276 transmembrane protein 79-like;NODE_8571_length_2194_cov_375.468911_True_1383 transmembrane protein 79-like;NODE_8377_length_2260_cov_1112.263039_True_65 transmembrane protein 79-like
21.1541	21.1654	21.3441	21.1661	20.7939	21.2747	NaN	21.4016	21.5644	2	2	2	17.8	17.8	17.8	11.321	0	11.248	36182000	26	NODE 86 length 74613 cov 706.678425 True 36373	NODE_86_	3956	NODE_86_length_74613_cov_706.678425_True_36373 transmembrane emp24 domain-containing protein bai-like
NaN	20.4015	20.8084	20.8091	NaN	21.1014	NaN	NaN	21.509	1	1	1	8.4	8.4	8.4	14.814	0.000592	3.2954	20508000	14	NODE 86 length 74613 cov 706.678425 True 46587	NODE_86_	3958	NODE_86_length_74613_cov_706.678425_True_46587 probable cathepsin C
NaN	NaN	NaN	19.6758	NaN	NaN	NaN	NaN	20.6168	3	2	2	24.3	18.1	18.1	22.852	0	8.3883	6601400	10	NODE 861 length 24746 cov 633.272569 True 12893	NODE_86	3961	NODE_861_length_24746_cov_633.272569_True_12893 cathepsin L1-like
NaN	NaN	NaN	20.2807	20.1724	21.2177	NaN	NaN	NaN	5	4	4	29.2	26.3	26.3	27.216	0	10.828	10839000	7	NODE 8615 length 2178 cov 676.451719 False 2177	NODE_86	3962	NODE_8615_length_2178_cov_676.451719_False_2177 C-type lectin lectoxin-Lio1
19.5033	19.6155	NaN	NaN	21.054	19.988	20.7881	21.7028	22.3824	14	14	14	29.5	29.5	29.5	72.555	0	35.33	49917000	42	NODE 862 length 24674 cov 702.974654 False 24248	NODE_86	3963	NODE_862_length_24674_cov_702.974654_False_24248 beta-glucuronidase-like isoform X3
NaN	NaN	NaN	19.8014	19.9175	20.0603	20.7016	21.1275	NaN	4	4	4	11.5	11.5	11.5	47.929	0	11.329	16994000	19	NODE 862 length 24674 cov 702.974654 False 5876	NODE_86	3964	NODE_862_length_24674_cov_702.974654_False_5876 tetratricopeptide repeat protein 38-like
23.4906	23.5671	23.5359	23.4241	23.2641	23.8461	22.6366	23.5154	24.189	6	6	6	30.4	30.4	30.4	36.406	0	30.635	2.39E+08	101	NODE 864 length 24558 cov 756.378811 True 12927	NODE_86	3965	NODE_864_length_24558_cov_756.378811_True_12927 Carbonic anhydrase 7-like protein
NaN	NaN	NaN	20.4004	20.7303	21.8541	NaN	NaN	NaN	6	6	6	30.1	30.1	30.1	33.467	0	10.959	15253000	11	NODE 8652 length 2164 cov 482.280228 True 2:NODE 8580 length 2191 cov 488.660581 True 177	NODE_86	3966	NODE_8652_length_2164_cov_482.280228_True_2 Group 1 mite allergen-like protein (Cysteine protease);NODE_8580_length_2191_cov_488.660581_True_177 cathepsin L1-like
19.9059	19.9844	20.1177	19.8273	19.5884	NaN	20.2044	20.4584	NaN	5	5	5	28.9	28.9	28.9	26.066	0	15.204	17682000	21	NODE 87 length 74280 cov 726.260532 True 28370	NODE_87_	3972	NODE_87_length_74280_cov_726.260532_True_28370 Thymidylate kinase
NaN	NaN	21.5167	21.4249	NaN	NaN	NaN	NaN	NaN	2	2	2	9.6	9.6	9.6	26.417	0	8.7928	19131000	8	NODE 874 length 24332 cov 691.935659 True 19120	NODE_87	3980	NODE_874_length_24332_cov_691.935659_True_19120 N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase-like
21.5354	NaN	NaN	23.9954	23.8124	23.9973	23.2711	23.0947	23.9255	8	8	8	43.3	43.3	43.3	25.48	0	21.448	2.74E+08	64	NODE 876 length 24266 cov 715.666722 False 6630	NODE_87	3981	NODE_876_length_24266_cov_715.666722_False_6630 maltase-glucoamylase, intestinal-like
NaN	NaN	NaN	18.2182	19.1019	18.7653	NaN	NaN	NaN	1	1	1	7.8	7.8	7.8	18.793	0	4.2651	2488700	10	NODE 876 length 24266 cov 715.666722 False 6737	NODE_87	3982	NODE_876_length_24266_cov_715.666722_False_6737 maltase-glucoamylase, intestinal-like
22.788	22.5329	22.5331	23.623	23.9363	24.6945	22.3417	23.4333	24.4668	5	5	3	43.2	43.2	35.5	17.649	0	114.37	2.46E+08	55	NODE 876 length 24266 cov 715.666722 False 7251	NODE_87	3983	NODE_876_length_24266_cov_715.666722_False_7251 Sucrase-isomaltase, intestinal
21.0782	20.3986	20.7778	23.7586	23.4625	23.8888	21.7222	22.0916	23.3355	5	5	5	25	25	25	16.744	0	24.327	1.7E+08	41	NODE 876 length 24266 cov 715.666722 False 7990	NODE_87	3984	NODE_876_length_24266_cov_715.666722_False_7990 sucrase-isomaltase, intestinal-like
20.8598	20.4144	20.3504	24.8835	24.426	25.0311	23.131	23.2166	23.717	8	8	8	42.5	42.5	42.5	30.549	0	38.902	4.8E+08	95	NODE 876 length 24266 cov 715.666722 False 9163	NODE_87	3986	NODE_876_length_24266_cov_715.666722_False_9163 sucrase-isomaltase, intestinal isoform X2
NaN	NaN	NaN	20.1444	19.9991	20.2145	NaN	NaN	NaN	1	1	1	8.3	8.3	8.3	16.063	0.001445	3.0926	8415500	12	NODE 876 length 24266 cov 715.666722 True 13345	NODE_87	3987	NODE_876_length_24266_cov_715.666722_True_13345 ras guanine nucleotide exchange factor E-like
NaN	NaN	20.552	NaN	NaN	20.079	NaN	NaN	21.5754	3	3	3	10.1	10.1	10.1	65.608	0	18.828	17224000	16	NODE 877 length 24256 cov 721.268088 False 20455	NODE_87	3988	NODE_877_length_24256_cov_721.268088_False_20455 importin subunit alpha-3
NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.3437	22.3144	3	3	3	31.5	31.5	31.5	15.877	0	7.6976	21887000	13	NODE 8772 length 2124 cov 710.593523 False 1180	NODE_87	3989	NODE_8772_length_2124_cov_710.593523_False_1180 glycerophosphocholine phosphodiesterase GPCPD1-like isoform X1
19.6958	NaN	NaN	NaN	NaN	NaN	NaN	21.7809	21.9978	3	3	3	19.2	19.2	19.2	32.581	0	50.016	17011000	16	NODE 8798 length 2114 cov 743.692569 True 0	NODE_87	3992	NODE_8798_length_2114_cov_743.692569_True_0 Twitchin
20.4908	20.5249	20.7829	20.9587	20.3905	20.6853	NaN	NaN	22.0856	3	3	3	16.1	16.1	16.1	20.269	0	7.4086	29005000	20	NODE 8798 length 2114 cov 743.692569 True 1193	NODE_87	3993	NODE_8798_length_2114_cov_743.692569_True_1193 Hypothetical predicted protein
20.3705	20.0821	20.3637	20.642	19.9566	20.8885	NaN	21.1267	21.707	4	4	3	21.2	21.2	13.7	23.906	0	13.901	26353000	27	NODE 8913 length 2076 cov 648.927759 False 1411:NODE 8799 length 2114 cov 638.049053 False 1405	NODE_89	3997	NODE_8913_length_2076_cov_648.927759_False_1411 glutathione S-transferase;NODE_8799_length_2114_cov_638.049053_False_1405 glutathione S-transferase
22.8062	22.6618	22.9885	22.6982	22.736	22.9269	23.0095	23.4133	24.0624	6	4	4	31.3	24	24	26.01	0	32.944	99663000	50	NODE 8822 length 2107 cov 689.775341 True 1408	NODE_88	4000	NODE_8822_length_2107_cov_689.775341_True_1408 heat shock protein cognate 5
NaN	NaN	NaN	NaN	NaN	NaN	21.2271	NaN	22.1111	1	1	1	8	8	8	25.392	0	4.5294	19777000	11	NODE 8826 length 2106 cov 724.047294 True 126	NODE_88	4001	NODE_8826_length_2106_cov_724.047294_True_126 staphylococcal nuclease domain-containing protein 1-like
NaN	21.7866	NaN	NaN	NaN	NaN	21.2559	22.3867	23	3	3	3	44.3	44.3	44.3	12	0	7.5375	41071000	17	NODE 8826 length 2106 cov 724.047294 True 1780	NODE_88	4002	NODE_8826_length_2106_cov_724.047294_True_1780 staphylococcal nuclease domain-containing protein 1-like
21.1188	21.0998	21.3528	20.6775	NaN	20.8405	20.9888	21.7463	22.5259	8	8	8	32.6	32.6	32.6	34.624	0	68.742	74371000	48	NODE 8826 length 2106 cov 724.047294 True 791	NODE_88	4003	NODE_8826_length_2106_cov_724.047294_True_791 staphylococcal nuclease domain-containing protein 1-like
NaN	23.2271	23.0438	23.1808	23.6146	23.9099	23.0712	23.836	24.548	4	4	4	38.4	38.4	38.4	21.71	0	44.761	1.65E+08	52	NODE 886 length 24036 cov 748.538927 False 14220	NODE_88	4006	NODE_886_length_24036_cov_748.538927_False_14220 peritrophic membrane chitin binding protein, putative
24.91	24.5601	24.9511	24.7962	24.828	24.9569	24.9237	25.2403	25.4812	14	14	14	51.2	51.2	51.2	28.096	0	110.76	1.52E+09	220	NODE 89 length 74004 cov 737.655289 True 44618:gi|1048044854|ref|XP 017493883.1|	NODE_89_	4007	NODE_89_length_74004_cov_737.655289_True_44618 nucleoside diphosphate kinase
19.2063	NaN	19.5145	19.4568	20.089	20.4839	NaN	NaN	NaN	2	2	2	16.2	16.2	16.2	14.932	0	4.9066	10373000	13	NODE 89 length 74004 cov 737.655289 True 7598	NODE_89_	4009	NODE_89_length_74004_cov_737.655289_True_7598 serine hydrolase
21.3622	21.0197	21.8737	23.8997	23.8243	24.5901	21.4899	22.1131	22.2916	6	6	6	60	60	60	12.042	0	16.06	1.62E+08	39	NODE 891 length 23916 cov 827.073258 False 4237	NODE_89	4012	NODE_891_length_23916_cov_827.073258_False_4237 cysteine proteinase COT44-like
21.5756	21.3767	21.5156	22.1332	22.6275	23.012	20.0575	21.434	20.9975	2	2	2	9.4	9.4	9.4	28.852	0	96.942	69235000	38	NODE 891 length 23916 cov 827.073258 False 5540	NODE_89	4013	NODE_891_length_23916_cov_827.073258_False_5540 cathepsin L-like
21.9953	NaN	22.0353	21.5771	NaN	21.2764	22.8373	22.6966	NaN	4	2	2	60.7	21.4	21.4	6.1512	0	6.7039	61769000	18	NODE 893 length 23908 cov 692.746615 False 9287	NODE_89	4014	NODE_893_length_23908_cov_692.746615_False_9287 electron transfer flavoprotein subunit beta/FixA family protein
22.0956	22.1371	22.184	21.3597	20.9769	21.289	22.1539	22.7317	23.3985	4	4	4	48	48	48	11.073	0	21.236	1.33E+08	44	NODE 893 length 23908 cov 692.746615 False 9971	NODE_89	4015	NODE_893_length_23908_cov_692.746615_False_9971 Electron transfer flavoprotein subunit beta
20.2963	20.6245	20.272	20.9528	21.1314	21.0909	19.5567	NaN	NaN	2	2	2	39	39	39	9.4367	0	7.3218	15582000	20	NODE 893 length 23908 cov 692.746615 True 15587	NODE_89	4017	NODE_893_length_23908_cov_692.746615_True_15587 lysosomal protective protein-like
23.7068	NaN	23.6568	22.6076	22.8109	23.337	21.9741	22.912	23.5606	3	3	3	68.6	68.6	68.6	7.9689	0	36.511	1.38E+08	35	NODE 894 length 23889 cov 665.252622 True 1253	NODE_89	4019	NODE_894_length_23889_cov_665.252622_True_1253 alpha-crystallin A chain-like
24.6619	24.8367	24.6732	24.0962	24.5688	24.7957	23.8226	24.2818	24.9805	5	5	5	41.6	41.6	41.6	21.194	0	72.027	8.08E+08	148	NODE 894 length 23889 cov 665.252622 True 1508	NODE_89	4020	NODE_894_length_23889_cov_665.252622_True_1508 alpha-crystallin A chain-like
22.1121	21.8928	22.0928	22.3772	22.3506	22.8635	22.0865	22.1405	22.6805	9	9	9	44.9	44.9	44.9	29.293	0	110.24	1.58E+08	67	NODE 895 length 23854 cov 760.362830 False 23478:gi|1048037059|ref|XP 017492720.1|	NODE_89	4021	NODE_895_length_23854_cov_760.362830_False_23478 pathogenesis-related protein 5-like;gi|1048037059|ref|XP_017492720.1| PREDICTED: pathogenesis-related protein 5-like, partial [Rhagoletis zephyria]
19.872	20.322	NaN	19.5279	NaN	NaN	NaN	20.4387	22.1162	12	12	2	25	25	4	99.201	0	34.447	28246000	32	NODE 895 length 23854 cov 760.362830 True 14560	NODE_89	4022	NODE_895_length_23854_cov_760.362830_True_14560 bifunctional glutamate/proline--tRNA ligase isoform X6
19.0096	NaN	NaN	NaN	NaN	NaN	NaN	19.5255	NaN	1	1	1	14.6	14.6	14.6	10.401	0.001973	2.9524	2856600	7	NODE 895 length 23854 cov 760.362830 True 7664	NODE_89	4024	NODE_895_length_23854_cov_760.362830_True_7664 alpha tubulin
NaN	NaN	20.2307	NaN	NaN	20.76	NaN	20.6829	21.5097	2	2	2	22.6	22.6	22.6	17.98	0	10.324	17231000	17	NODE 9 length 186394 cov 717.866013 False 103562:gi|1048011843|ref|XP 017466809.1|:gi|1048011841|ref|XP 017466808.1|	NODE_9_l	4028	NODE_9_length_186394_cov_717.866013_False_103562 protein mago nashi homolog;gi|1048011843|ref|XP_017466809.1| PREDICTED: protein mago nashi [Rhagoletis zephyria];gi|1048011841|ref|XP_017466808.1| PREDICTED: protein mago nashi [Rhagoletis zephyria]
NaN	NaN	NaN	NaN	NaN	NaN	19.8083	20.271	20.0303	7	1	1	42.9	8.2	8.2	20.594	0	5.1671	5030300	9	NODE 9 length 186394 cov 717.866013 True 148615	NODE_9_l	4030	NODE_9_length_186394_cov_717.866013_True_148615 uncharacterized UDP-glucosyltransferase YjiC-like
22.6114	22.5488	22.7627	23.3738	23.0994	23.661	22.6764	23.1621	23.4811	2	2	2	21.9	21.9	21.9	12.722	0	7.9648	90654000	27	NODE 90 length 73916 cov 706.023531 True 57988	NODE_90_	4032	NODE_90_length_73916_cov_706.023531_True_57988 S-formylglutathione hydrolase
NaN	NaN	NaN	22.2016	22.3423	22.5144	NaN	21.8202	NaN	3	3	3	25.7	25.7	25.7	16.38	0	8.9749	36125000	15	NODE 90 length 73916 cov 706.023531 True 58337	NODE_90_	4033	NODE_90_length_73916_cov_706.023531_True_58337 S-formylglutathione hydrolase-like
20.2544	20.273	NaN	NaN	NaN	NaN	NaN	NaN	21.6664	3	3	3	37.5	37.5	37.5	9.3347	0	6.1646	12675000	8	NODE 90 length 73916 cov 706.023531 True 58741	NODE_90_	4034	NODE_90_length_73916_cov_706.023531_True_58741 S-formylglutathione hydrolase
NaN	NaN	NaN	21.862	21.8465	22.0465	NaN	NaN	NaN	2	2	2	19.1	19.1	19.1	17.051	0	7.3521	27432000	11	NODE 9070 length 2026 cov 710.212582 False 457	NODE_90	4035	NODE_9070_length_2026_cov_710.212582_False_457 cytosolic 10-formyltetrahydrofolate dehydrogenase-like
20.8456	20.7836	20.9759	NaN	NaN	NaN	NaN	20.6041	20.5829	7	7	7	12.7	12.7	12.7	76.095	0	16.874	18453000	23	NODE 910 length 23461 cov 639.886525 True 11973	NODE_91	4037	NODE_910_length_23461_cov_639.886525_True_11973 myogenesis-regulating glycosidase-like
25.2409	24.6285	25.029	25.6672	24.4046	25.0665	26.9053	26.2181	24.3072	3	3	3	13.5	13.5	13.5	17.958	0	19.475	7.34E+08	86	NODE 911 length 23459 cov 729.644462 True 4816	NODE_91	4039	NODE_911_length_23459_cov_729.644462_True_4816 cuticle protein 10.9-like
29.9863	29.9856	30.1009	29.9586	29.7323	29.8446	28.8545	29.6592	29.8959	3	3	3	21.6	21.6	21.6	15.195	0	121.29	1.09E+10	1422	NODE 911 length 23459 cov 729.644462 True 673	NODE_91	4040	NODE_911_length_23459_cov_729.644462_True_673 cuticle protein 10.9-like
19.4278	19.3196	18.9801	NaN	NaN	NaN	18.4462	19.0839	20.3074	12	2	2	38	10.9	10.9	34.758	0	26.26	8368400	19	NODE 9123 length 2006 cov 795.240902 False 1081:gi|1048050762|ref|XP 017480476.1|	NODE_91	4042	NODE_9123_length_2006_cov_795.240902_False_1081 retinal dehydrogenase 1
21.8105	21.8294	NaN	NaN	NaN	NaN	NaN	22.6822	NaN	3	3	3	54.2	54.2	54.2	9.5194	0	19.073	45573000	15	NODE 9136 length 2004 cov 431.904053 False 1463:NODE 9127 length 2006 cov 430.452588 True 542	NODE_91	4044	NODE_9136_length_2004_cov_431.904053_False_1463 cuticle protein 6-like;NODE_9127_length_2006_cov_430.452588_True_542 cuticle protein 16.8
21.1918	20.6402	21.1167	21.8312	21.632	21.7265	22.2885	22.3506	22.656	6	6	6	30.9	30.9	30.9	38.2	0	61.464	67601000	70	NODE 9136 length 2004 cov 431.904053 False 1168:NODE 9127 length 2006 cov 430.452588 True 792	NODE_91	4045	NODE_9136_length_2004_cov_431.904053_False_1168 hypothetical protein QR98_0003620;NODE_9127_length_2006_cov_430.452588_True_792 uncharacterized protein LOC113795033
21.2308	21.13	21.3627	21.499	21.5912	21.6543	21.634	22.0838	22.3785	6	6	6	39.8	39.8	39.8	19.7	0	20.078	87560000	71	NODE 920 length 23227 cov 738.358407 True 15319	NODE_92	4049	NODE_920_length_23227_cov_738.358407_True_15319 GTP:AMP phosphotransferase AK3, mitochondrial-like
21.6642	21.6189	21.6167	21.6236	21.3905	21.7488	21.4752	22.0763	22.4607	6	6	6	31.3	31.3	31.3	31.634	0	75.754	93853000	51	NODE 9257 length 1970 cov 607.319582 False 1183:NODE 9375 length 1939 cov 607.606157 True 765	NODE_92	4050	NODE_9257_length_1970_cov_607.319582_False_1183 staphylococcal nuclease domain-containing protein 1-like protein;NODE_9375_length_1939_cov_607.606157_True_765 staphylococcal nuclease domain-containing protein 1-like protein
20.6614	21.1452	21.2564	20.6219	NaN	NaN	20.8656	21.3001	21.5702	7	7	1	39	39	6.8	22.683	0	29.253	36340000	26	NODE 9257 length 1970 cov 607.319582 False 1801	NODE_92	4051	NODE_9257_length_1970_cov_607.319582_False_1801 staphylococcal nuclease domain-containing protein 1-like
NaN	NaN	NaN	21.2341	NaN	NaN	NaN	21.5912	NaN	3	3	3	22.7	22.7	22.7	23.079	0	7.3078	21644000	9	NODE 926 length 23085 cov 704.720408 True 4747	NODE_92	4052	NODE_926_length_23085_cov_704.720408_True_4747 beta-galactosidase-1-like protein 2
NaN	NaN	19.7924	21.0683	20.4409	20.1708	NaN	20.4613	NaN	4	4	4	19.1	19.1	19.1	34.67	0	10.3	18788000	18	NODE 926 length 23085 cov 704.720408 True 5344	NODE_92	4053	NODE_926_length_23085_cov_704.720408_True_5344 beta-galactosidase-1-like protein 2
22.753	22.8142	23.0708	22.5916	22.4919	23.0475	22.4611	23.2057	23.7275	7	5	5	28.8	19.6	19.6	29.555	0	25.245	1.29E+08	43	NODE 931 length 23024 cov 643.850538 False 2688:gi|1048051663|ref|XP 017460563.1|	NODE_93	4057	NODE_931_length_23024_cov_643.850538_False_2688 phosphate carrier protein, mitochondrial-like;gi|1048051663|ref|XP_017460563.1| PREDICTED: phosphate carrier protein, mitochondrial-like, partial [Rhagoletis zephyria]
22.0058	22.1448	22.043	21.8688	22.3045	22.4533	21.7619	22.489	23.3015	5	5	5	56.3	56.3	56.3	18.469	0	39.875	72154000	28	NODE 939 length 22888 cov 643.735646 False 14297	NODE_93	4060	NODE_939_length_22888_cov_643.735646_False_14297 mesh-like CUB and sushi domain-containing protein
20.0942	NaN	NaN	NaN	20.1357	NaN	NaN	NaN	NaN	2	2	2	12.2	12.2	12.2	16.962	0.00032	3.971	11731000	12	NODE 939 length 22888 cov 643.735646 False 14784	NODE_93	4061	NODE_939_length_22888_cov_643.735646_False_14784 protein mesh-like
22.0327	22.051	22.0694	21.8684	21.7102	22.0118	NaN	22.5326	23.0152	2	2	2	20.6	20.6	20.6	22.078	0	12.155	71184000	31	NODE 939 length 22888 cov 643.735646 False 15157	NODE_93	4062	NODE_939_length_22888_cov_643.735646_False_15157 protein mesh-like
21.8467	21.7289	21.872	21.5708	21.6272	21.9557	21.2393	22.1267	22.5457	10	10	10	54	54	54	31.42	0	47.152	1.48E+08	81	NODE 939 length 22888 cov 643.735646 False 16037	NODE_93	4063	NODE_939_length_22888_cov_643.735646_False_16037 protein mesh-like
22.2807	21.917	22.1965	22.0592	22.1356	22.4978	22.511	22.5547	23.125	12	12	12	38.1	38.1	38.1	42.452	0	36.563	1.27E+08	76	NODE_939_length_22888_cov_643.735646_False_17104;NODE_586_length_31161_cov_751.506848_False_20296;gi|1048030423|ref|XP_017489111.1|	NODE_93	4064	NODE_939_length_22888_cov_643.735646_False_17104 mesh-like CUB and sushi domain-containing protein
21.4401	21.4776	21.6616	21.0481	21.0678	21.5563	21.2121	21.7536	22.344	4	4	4	56.2	56.2	56.2	11.46	0	30.131	71982000	55	NODE 939 length 22888 cov 643.735646 False 17373	NODE_93	4065	NODE_939_length_22888_cov_643.735646_False_17373 mesh-like CUB and sushi domain-containing protein
NaN	19.6002	20.2022	20.4751	20.2364	20.4489	19.8011	20.5743	NaN	3	3	3	23.5	23.5	23.5	23.046	0	9.4673	17967000	17	NODE 94 length 72866 cov 706.657497 True 39051	NODE_94_	4066	NODE_94_length_72866_cov_706.657497_True_39051 serine protease 7
NaN	NaN	NaN	21.3886	NaN	21.5754	NaN	NaN	NaN	5	3	3	35.7	20.4	20.4	34.517	0	18.565	15510000	13	NODE 940 length 22831 cov 710.375132 False 14919	NODE_94	4067	NODE_940_length_22831_cov_710.375132_False_14919 NSFL1 cofactor p47
23.1394	23.5796	23.2726	23.818	23.1891	24.2397	24.5485	24.2923	24.3929	9	7	7	77	55.6	55.6	14.878	0	48.584	4.59E+08	128	NODE 946 length 22745 cov 682.171662 True 1272	NODE_94	4071	NODE_946_length_22745_cov_682.171662_True_1272 ATP synthase subunit alpha, mitochondrial
20.2358	NaN	NaN	NaN	NaN	20.0555	NaN	NaN	NaN	5	5	5	23.2	23.2	23.2	26.613	0	9.5786	10029000	19	NODE 946 length 22745 cov 682.171662 True 14607:gi|1048046356|ref|XP 017494703.1|	NODE_94	4072	NODE_946_length_22745_cov_682.171662_True_14607 26S proteasome non-ATPase regulatory subunit 10-like;gi|1048046356|ref|XP_017494703.1| PREDICTED: 26S proteasome non-ATPase regulatory subunit 10-like [Rhagoletis zephyria]
26.028	26.0559	25.9892	26.1993	25.4326	26.4066	26.3759	26.9914	26.8741	8	6	6	30.4	23.3	23.3	25.762	0	49.655	1.23E+09	97	NODE 946 length 22745 cov 682.171662 True 26	NODE_94	4073	NODE_946_length_22745_cov_682.171662_True_26 ATP synthase subunit alpha, mitochondrial-like

21.0928	21.0363	20.7033	NaN	NaN	NaN	NaN	NaN	NaN	3	3	3	26.6	26.6	26.6	12.714	0	7.5863	13311000	9	NODE_949_length_22698_cov_723.510180_False_328	NODE_949_length_22698_cov_723.510180_False_328 transmembrane protein 53-like protein
NaN	NaN	20.2545	NaN	NaN	NaN	NaN	NaN	21.4477	4	4	4	41.6	41.6	41.6	16.517	0	11.36	11014000	11	NODE_949_length_22698_cov_723.510180_False_801	NODE_949_length_22698_cov_723.510180_False_801 transmembrane protein 53-like protein
18.8914	18.8031	18.7059	18.837	NaN	18.8387	NaN	19.8045	20.0953	2	2	2	13.7	13.7	13.7	30.547	0	51.293	7436000	18	NODE_95_length_72031_cov_728.552462_False_2550	NODE_95_length_72031_cov_728.552462_False_2550 insulin-like growth factor 2 mRNA-binding protein 1 isoform X3
21.6953	21.6565	21.9433	20.4067	19.936	21.2963	21.578	22.6624	23.1589	17	17	17	46.9	46.9	46.9	54.41	0	118.79	1.12E+08	69	NODE_95_length_72031_cov_728.552462_False_61381	NODE_95_length_72031_cov_728.552462_False_61381 dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
19.7391	20.1273	19.9746	20.7101	19.8473	20.8283	19.8611	20.3835	20.679	5	5	5	27.4	27.4	27.4	33.687	0	16.203	37956000	48	NODE_957_length_22591_cov_682.473775_True_10625	NODE_957_length_22591_cov_682.473775_True_10625 lysosomal alpha-mannosidase
19.4907	19.5618	19.6195	20.3896	19.1619	20.0299	19.0511	20.3729	20.3946	5	5	5	28.1	28.1	28.1	25.847	0	12.895	20539000	32	NODE_957_length_22591_cov_682.473775_True_11481	NODE_957_length_22591_cov_682.473775_True_11481 lysosomal alpha-mannosidase-like
22.5661	21.9237	22.1043	NaN	NaN	NaN	21.3824	22.125	22.6189	5	3	3	36.1	24.2	24.2	21.933	0	18.74	52364000	33	NODE_957_length_22591_cov_682.473775_True_12841;gi|104809103|ref|XP_017488942.1|;NODE_6817_length_3063_cov_666.145279_True_2261	NODE_957_length_22591_cov_682.473775_True_12841 chitinase 4-like
21.7704	NaN	NaN	NaN	NaN	NaN	22.6727	23.304	NaN	1	1	1	8.5	8.5	8.5	23.249	0.000597	3.3629	61215000	14	NODE_957_length_22591_cov_682.473775_True_9074	NODE_957_length_22591_cov_682.473775_True_9074 lysosomal alpha-mannosidase-like
NaN	NaN	NaN	NaN	NaN	NaN	19.0955	20.404	NaN	3	3	3	13.4	13.4	13.4	46.516	0	13.47	4438100	6	NODE_96_length_71730_cov_712.300886_True_59252	NODE_96_length_71730_cov_712.300886_True_59252 la-related protein 1B isoform X1
22.626	22.1515	22.159	22.531	22.0751	22.5832	22.4063	22.9979	23.6992	7	7	6	61.7	61.7	55.8	16.692	0	35.671	1.53E+08	58	NODE_9664_length_1859_cov_703.489468_False_1201	NODE_9664_length_1859_cov_703.489468_False_1201 glutamate dehydrogenase, mitochondrial
NaN	NaN	NaN	21.8029	NaN	NaN	21.4462	22.6116	NaN	4	4	4	22.2	22.2	22.2	20.917	0	9.6183	46173000	15	NODE_9664_length_1859_cov_703.489468_False_1759	NODE_9664_length_1859_cov_703.489468_False_1759 glutamate dehydrogenase, mitochondrial-like
NaN	NaN	22.4388	21.7803	NaN	22.674	21.6511	22.2797	23.7896	2	2	2	22	22	22	18.232	0	11.84	67697000	28	NODE_9664_length_1859_cov_703.489468_False_800	NODE_9664_length_1859_cov_703.489468_False_800 glutamate dehydrogenase, mitochondrial
NaN	NaN	NaN	NaN	NaN	NaN	21.0714	21.4423	21.9584	4	4	4	22.1	22.1	22.1	30.309	0	66.626	17574000	16	NODE_973_length_22370_cov_727.407797_True_12544	NODE_973_length_22370_cov_727.407797_True_12544 immunogenic protein
22.7783	22.6622	22.9518	22.9723	22.9141	22.7912	22.9393	23.1561	23.4527	10	10	3	46.3	46.3	12.4	37.699	0	70.939	2.42E+08	97	NODE_9786_length_1827_cov_419.374718_False_1824	NODE_9786_length_1827_cov_419.374718_False_1824 gastric triacylglycerol lipase-like
21.1469	NaN	21.241	NaN	NaN	NaN	NaN	21.6882	21.9132	2	2	2	25.2	25.2	25.2	11.935	0	14.953	34864000	18	NODE_983_length_22232_cov_742.238445_False_1912	NODE_983_length_22232_cov_742.238445_False_1912 U6 snRNA-associated Sm-like protein LSm3
19.6278	19.7724	19.6336	NaN	NaN	NaN	NaN	NaN	NaN	4	4	4	32.7	32.7	32.7	17.393	0	25.486	5849500	15	NODE_985_length_22206_cov_640.452892_True_20763	NODE_985_length_22206_cov_640.452892_True_20763 lachesin-like
NaN	NaN	NaN	20.5185	21.4408	21.7193	NaN	NaN	NaN	10	8	8	41.7	33.9	33.9	43.173	0	77.609	37723000	28	NODE_9865_length_1808_cov_595.561894_True_494;NODE_4366_length_5361_cov_517.613645_False_3086	NODE_9865_length_1808_cov_595.561894_True_494 C-type lectin lectoxin-Lio1
22.2506	22.2638	22.3779	22.0892	22.2625	22.2451	22.4075	22.6818	23.2694	6	6	6	29.1	29.1	29.1	28.641	0	20.46	1.45E+08	60	NODE_99_length_71160_cov_740.022825_True_4757	NODE_99_length_71160_cov_740.022825_True_4757 hypothetical protein QR98_0039000
22.0559	22.1458	22.4119	21.9802	22.308	22.3055	22.5988	22.6216	22.8061	7	7	7	29.8	29.8	29.8	28.687	0	28.873	1.26E+08	63	NODE_99_length_71160_cov_740.022825_True_85417	NODE_99_length_71160_cov_740.022825_True_85417 tetratricopeptide repeat protein
19.7232	NaN	19.5361	19.2443	19.2077	NaN	18.9968	19.7981	20.8739	2	2	2	20.6	20.6	20.6	20.062	0	13.168	11011000	18	NODE_992_length_22012_cov_665.666576_True_17286	NODE_992_length_22012_cov_665.666576_True_17286 GA25141
21.6612	21.4557	21.6511	22.2475	22.2427	22.1564	22.5452	22.5207	22.4561	9	2	2	51.8	10.7	10.7	31.416	0	53.593	76451000	23	NODE_9922_length_1795_cov_460.276437_False_1712	NODE_9922_length_1795_cov_460.276437_False_1712 gastric triacylglycerol lipase-like
19.0561	NaN	NaN	18.2792	18.7757	19.0686	18.8577	19.3268	19.886	3	3	3	28.9	28.9	28.9	23.998	0	26.371	8738900	23	NODE_9958_length_1784_cov_692.514748_False_753	NODE_9958_length_1784_cov_692.514748_False_753 probable 3-hydroxyacyl-CoA dehydrogenase B0272.3









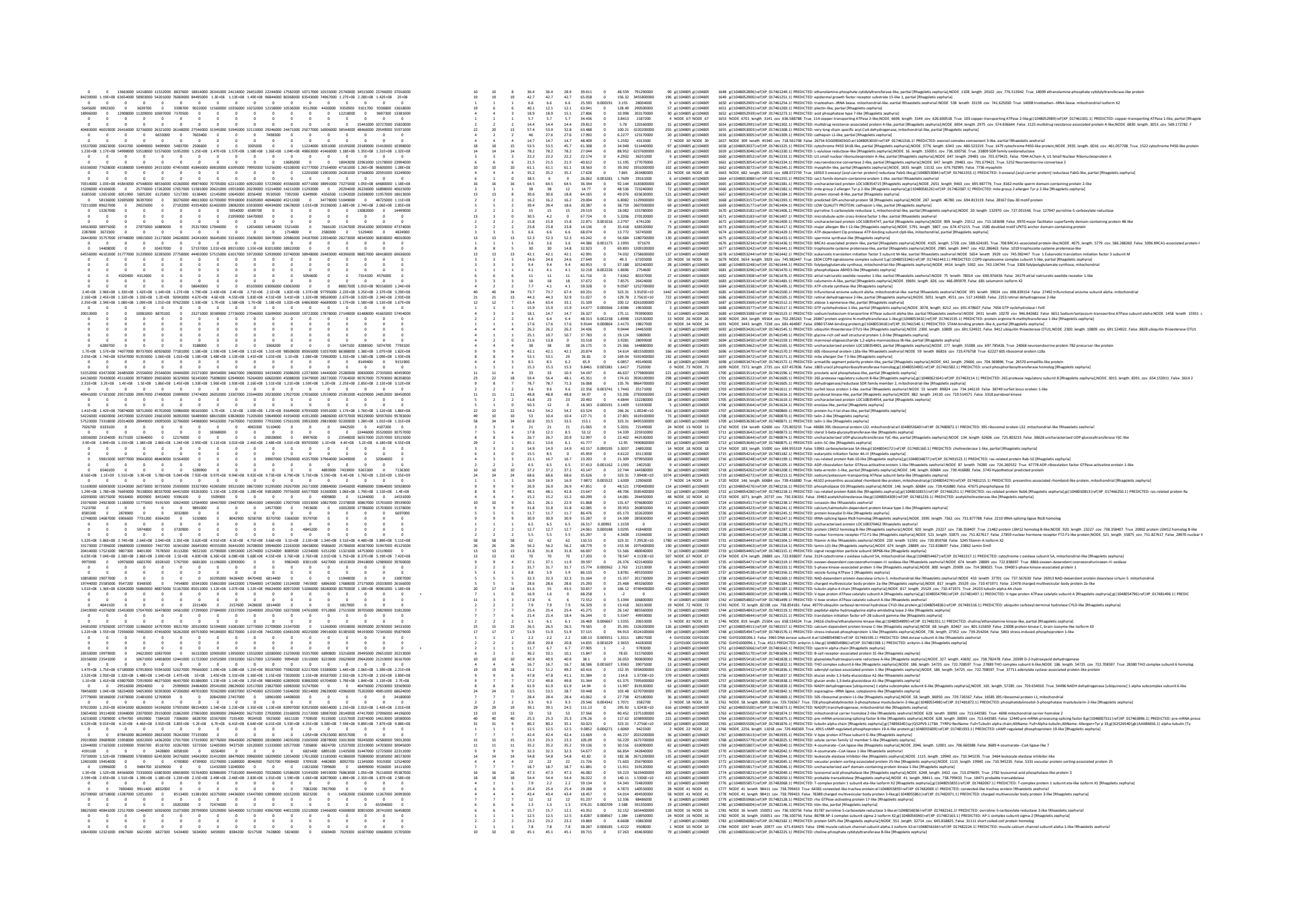




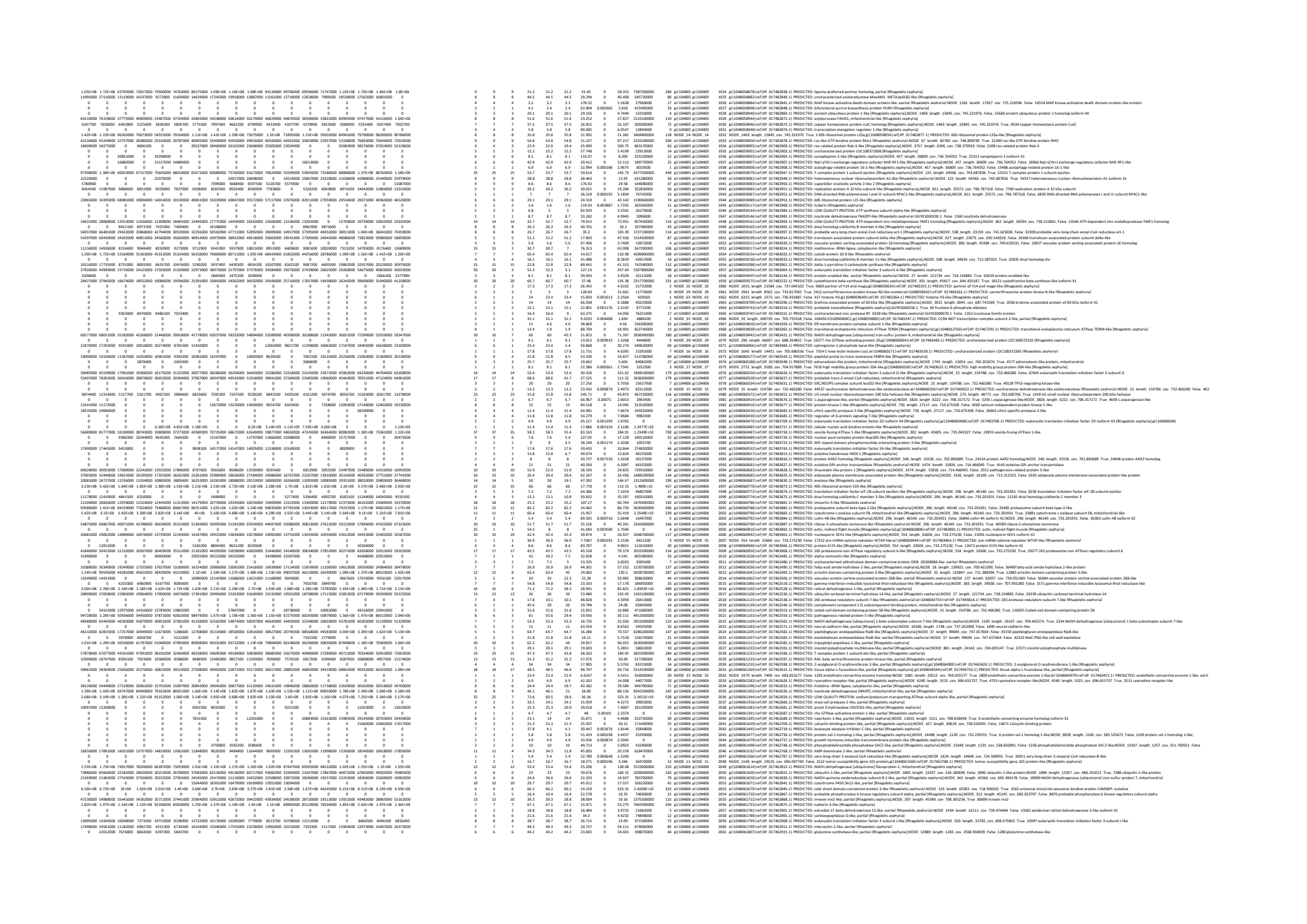


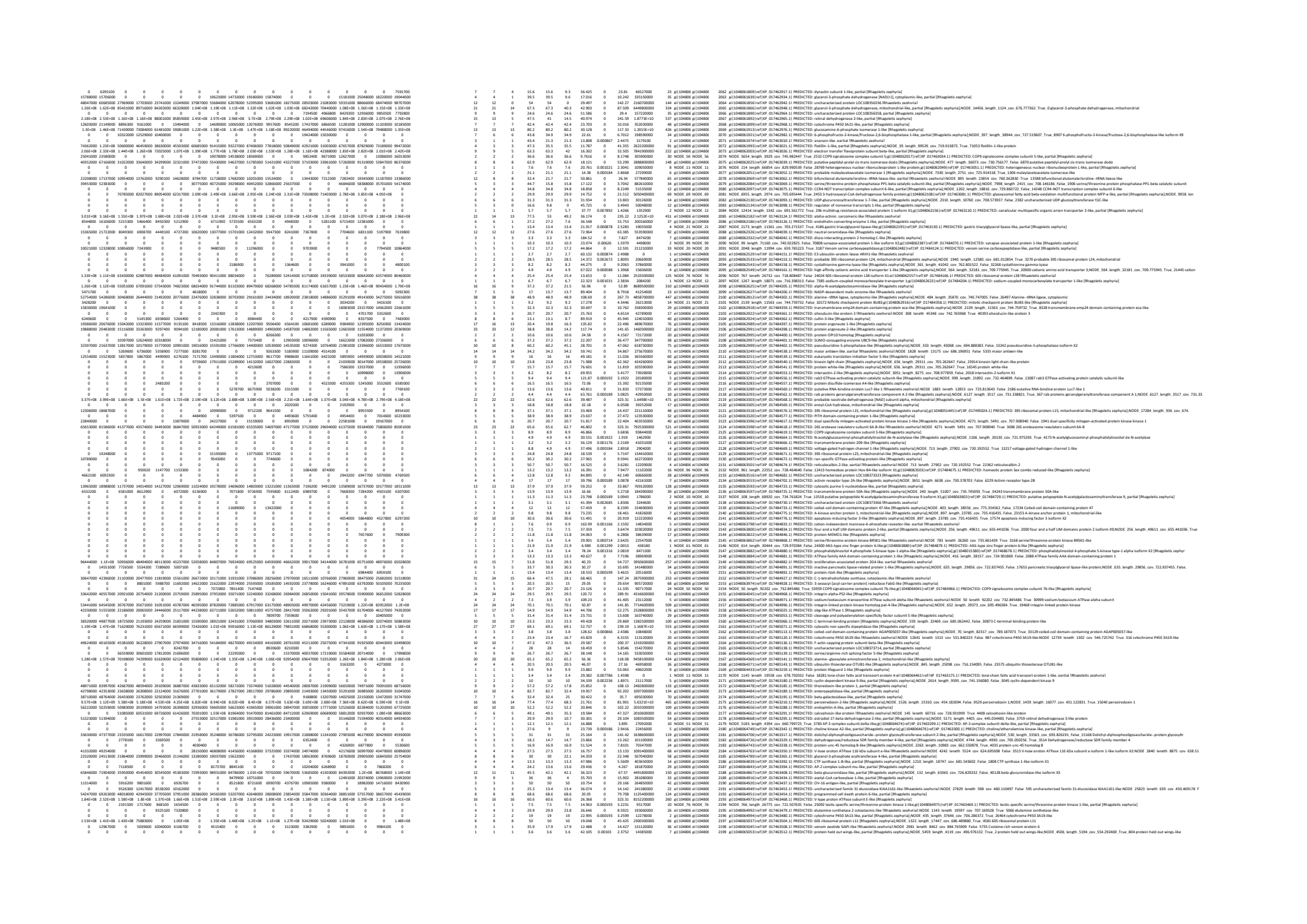






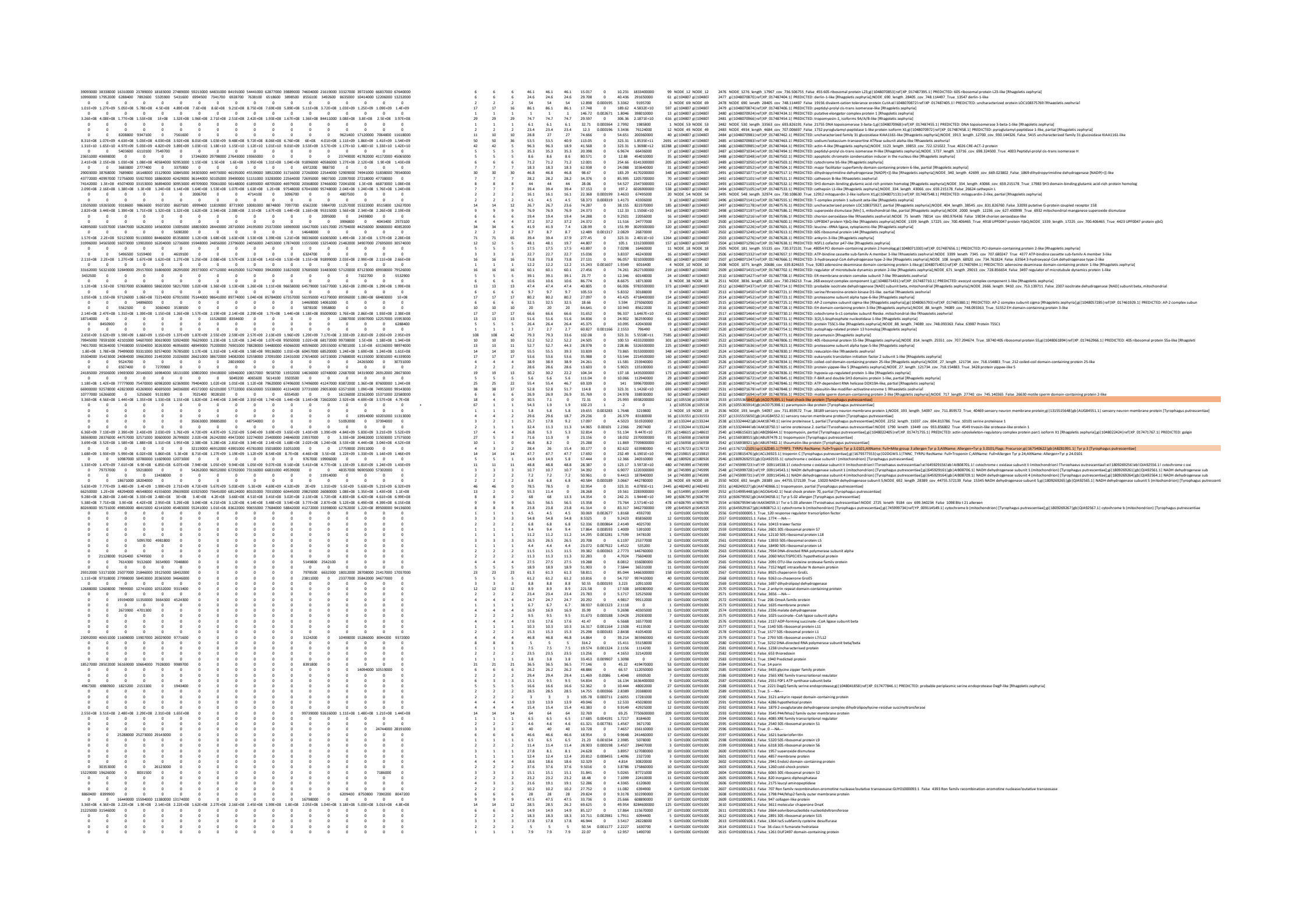


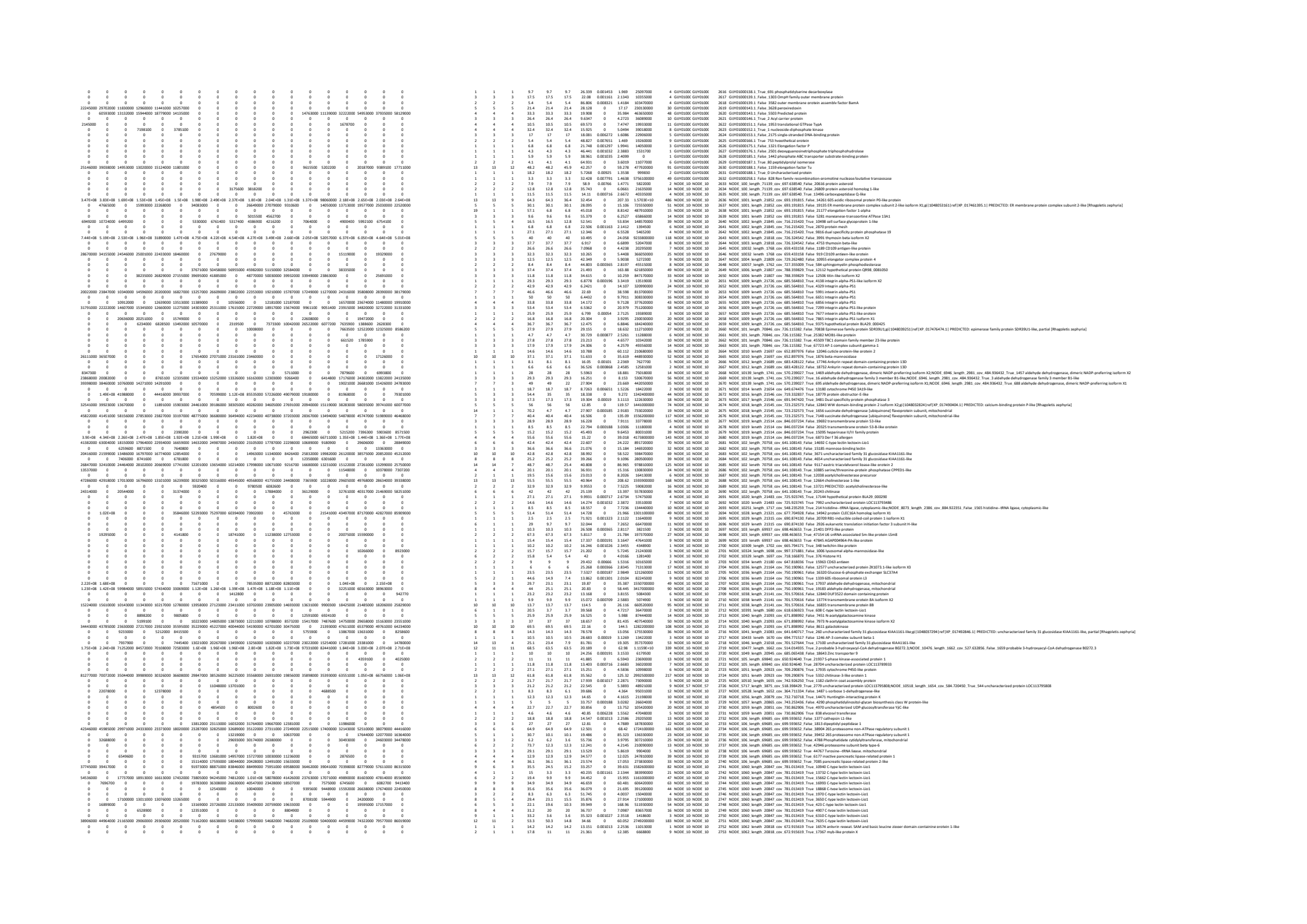


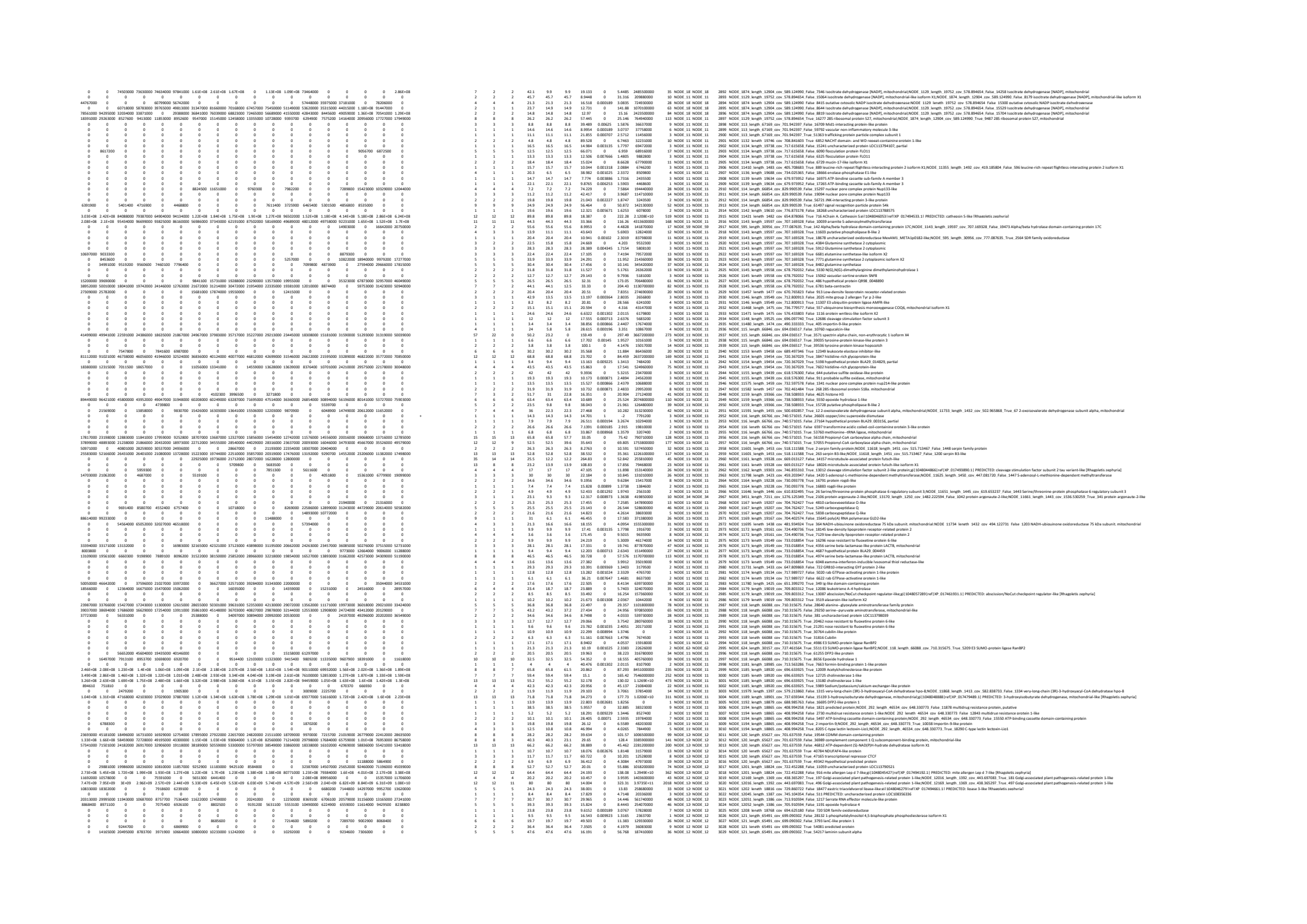




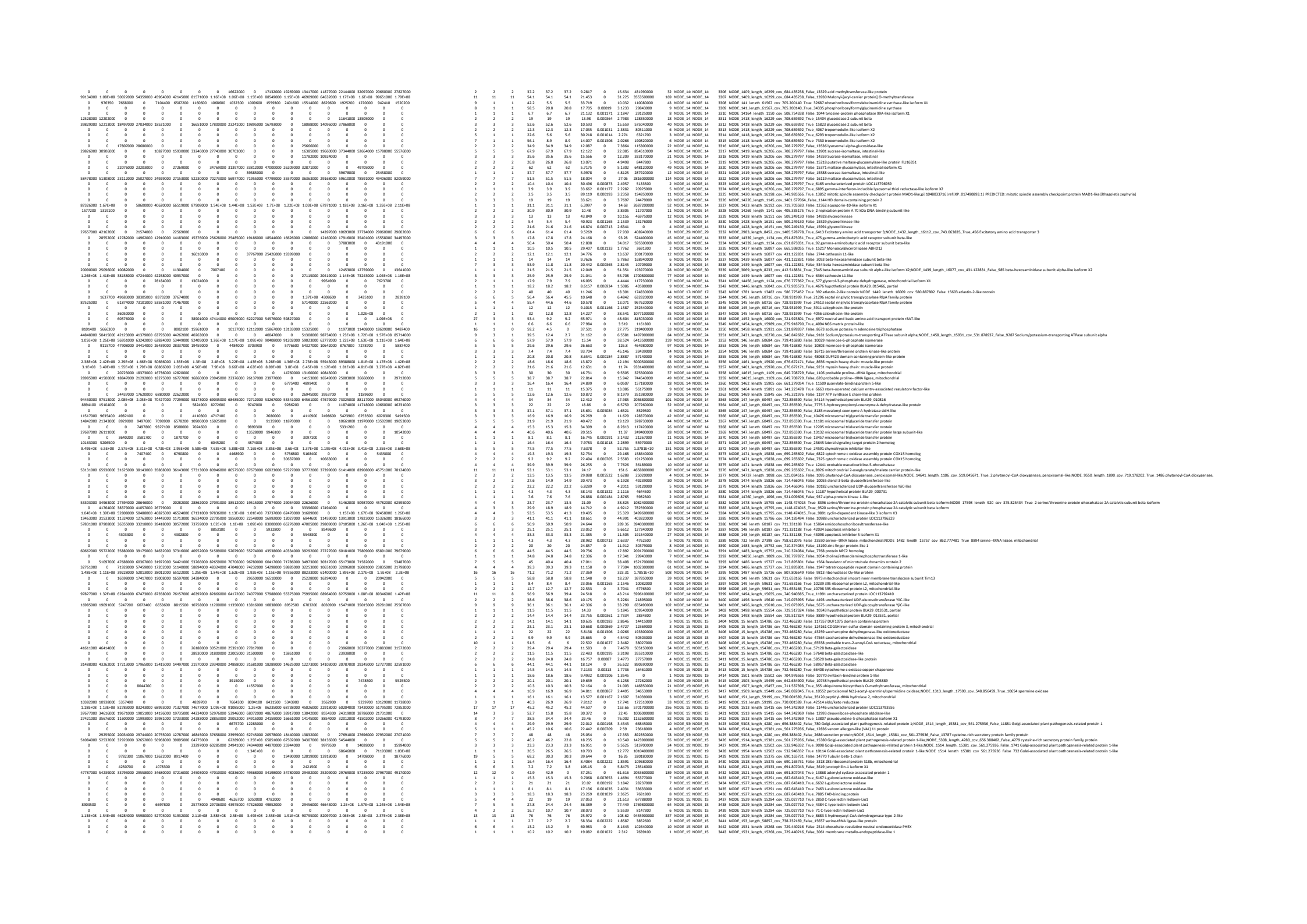


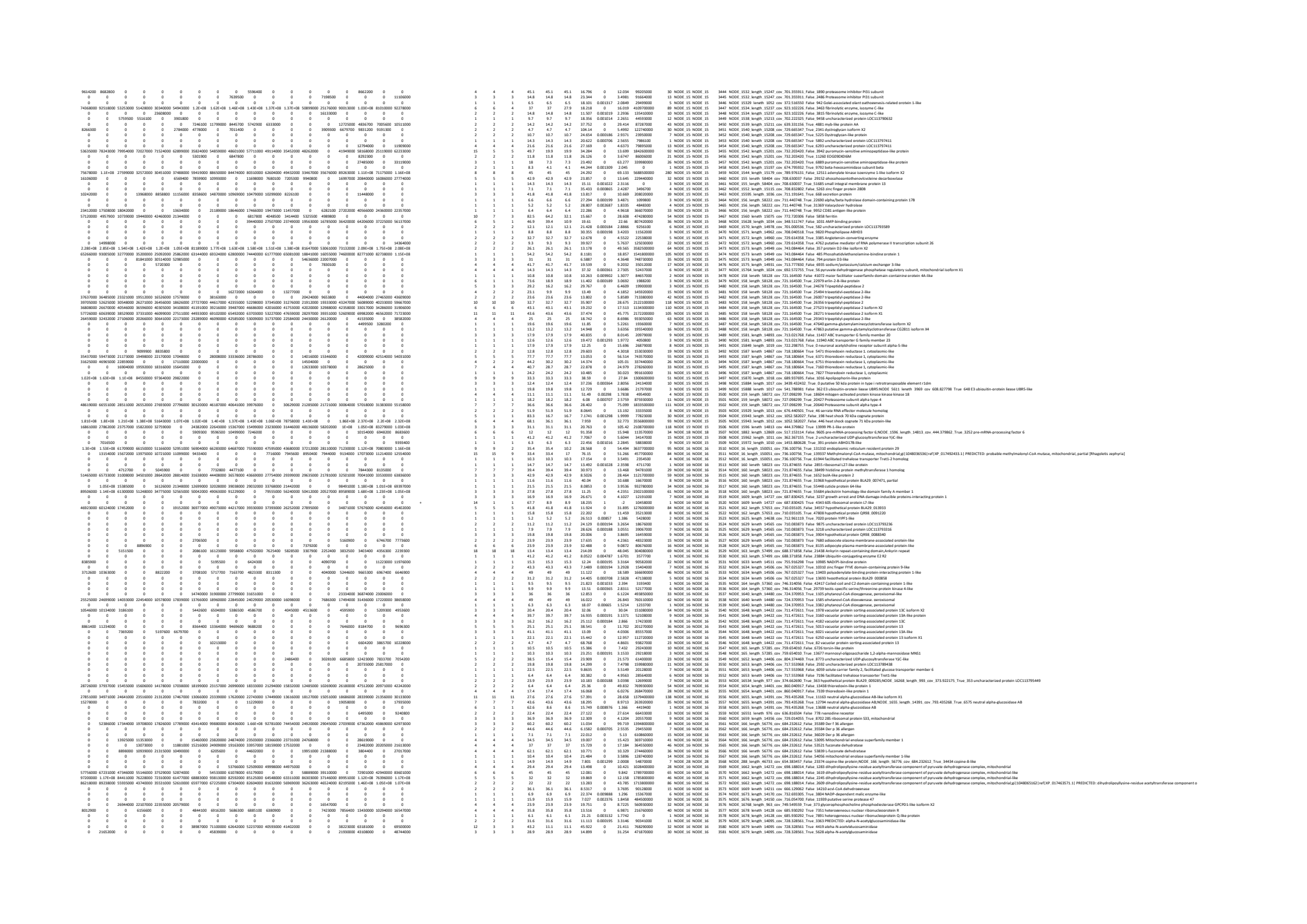








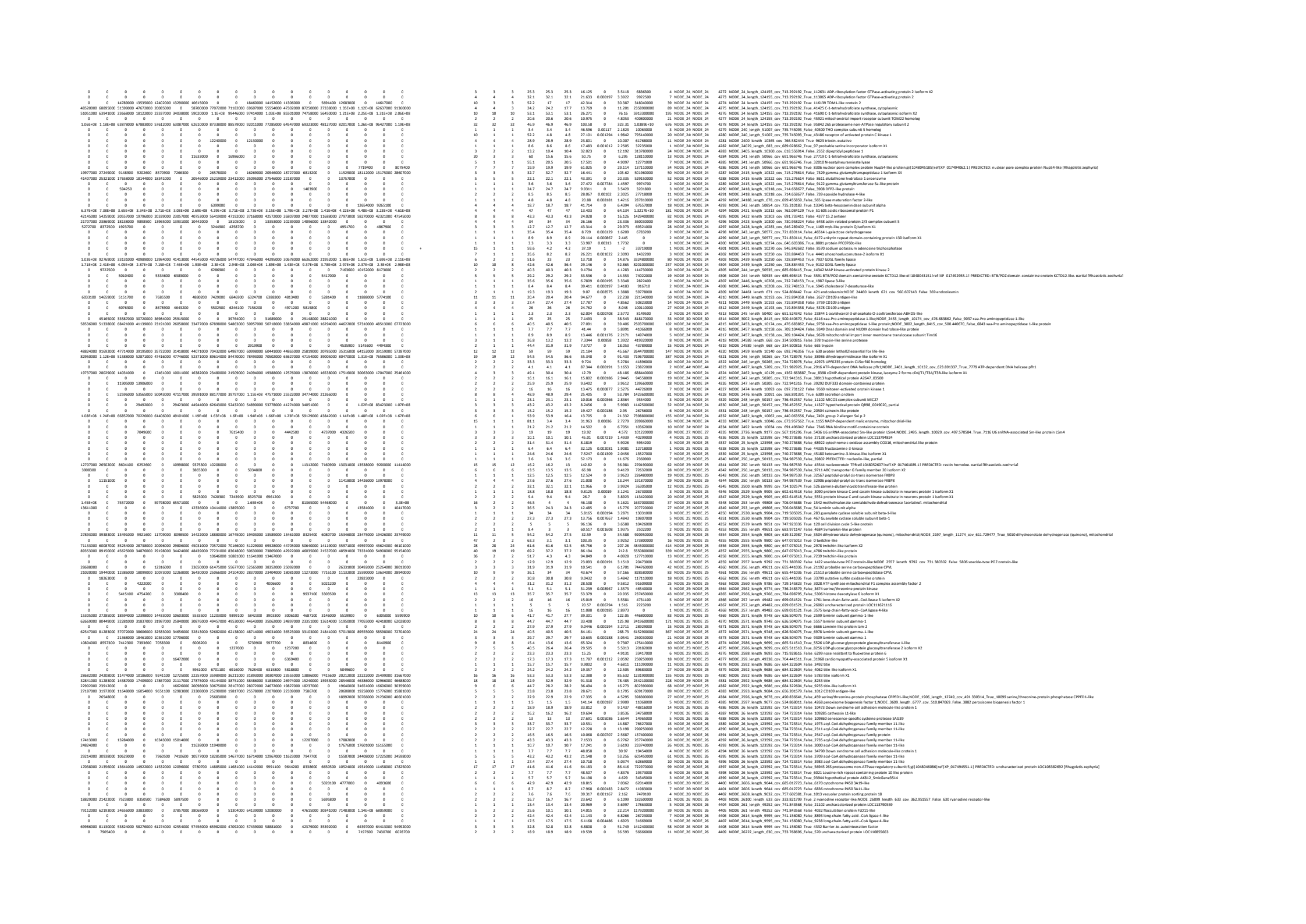


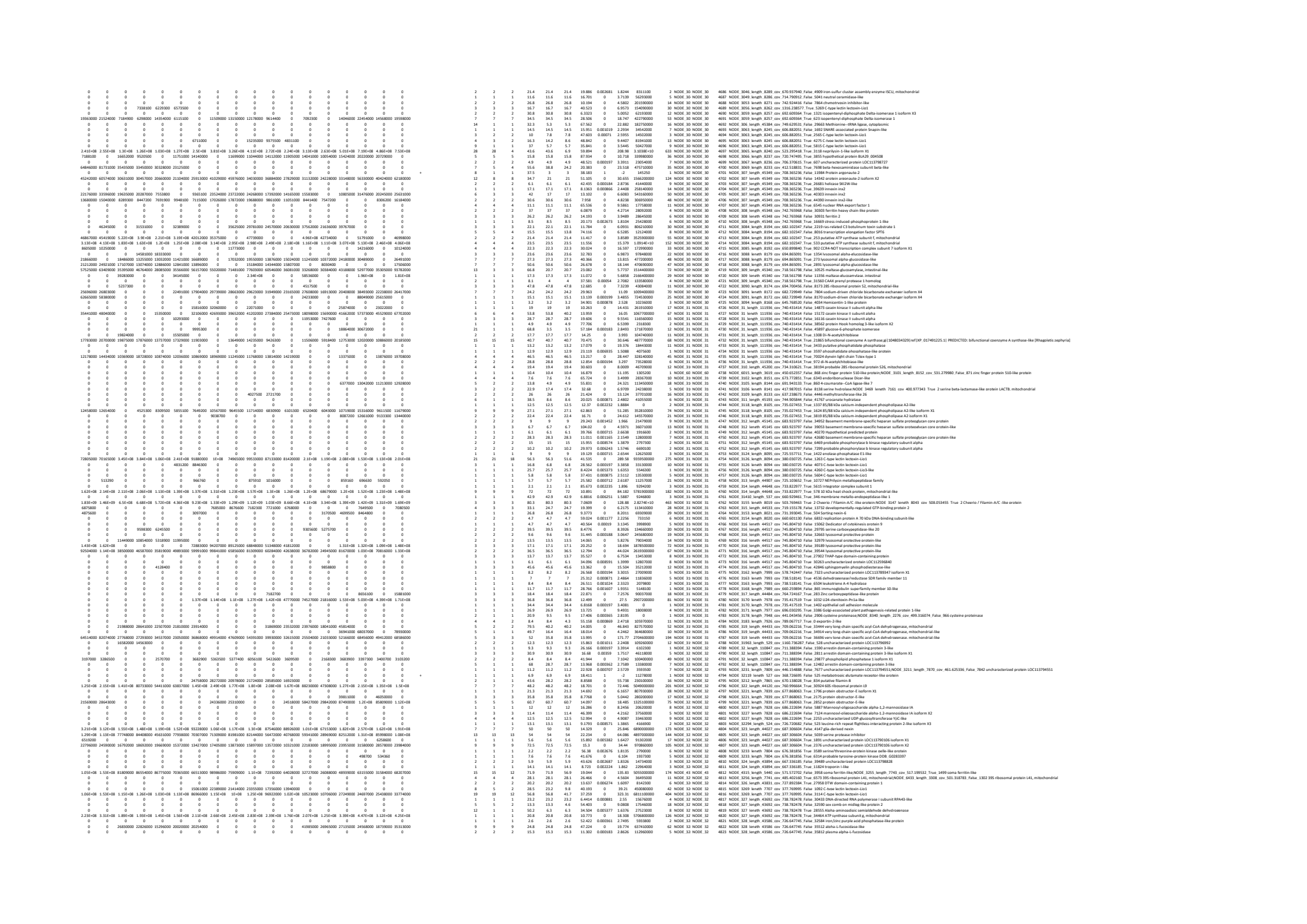


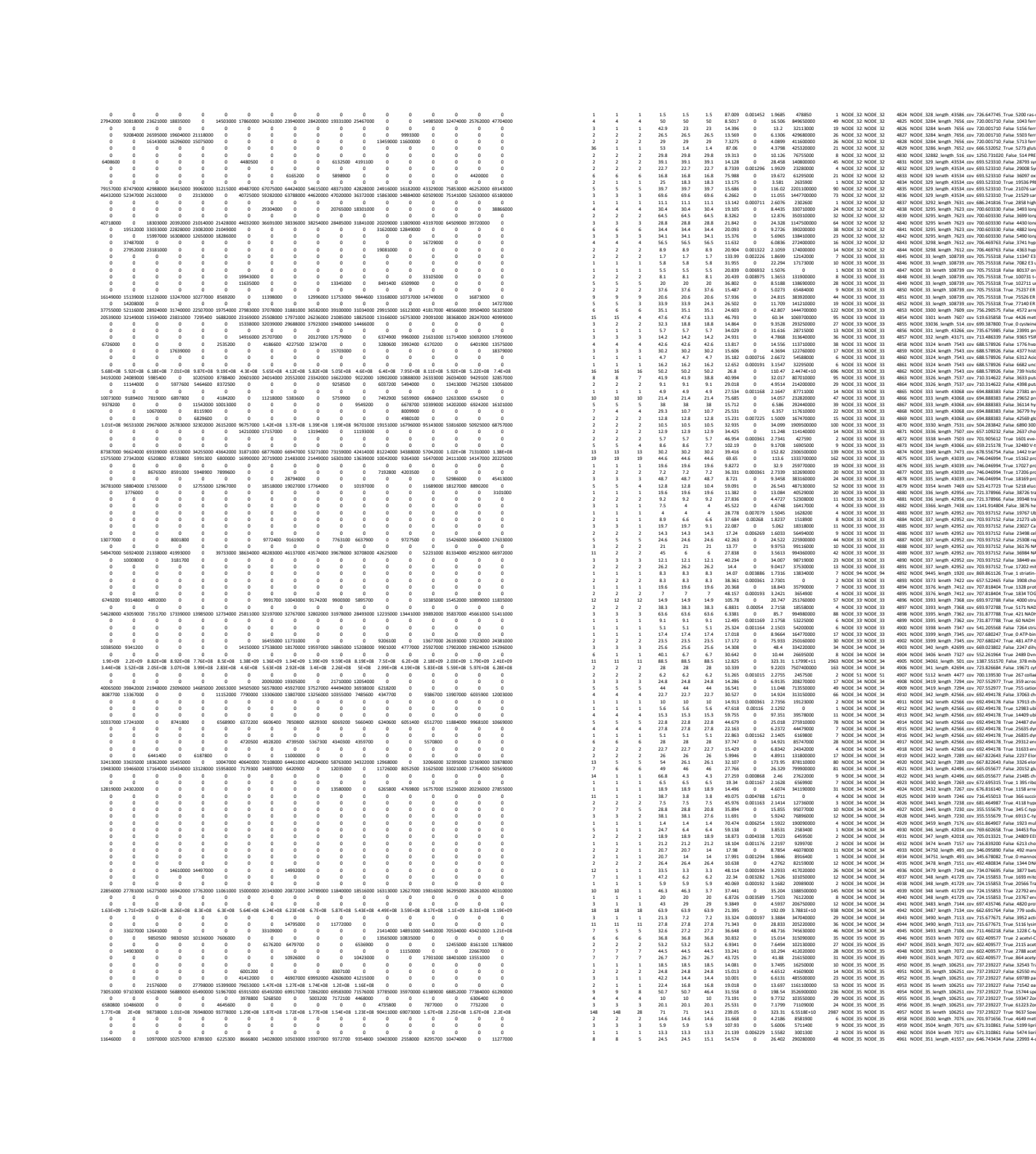
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2.49E+08	2.89E+08	2.29E+08	3.33E+08	2.08E+08	3.04E+08	2.22E+08	2.42E+08	2.81E+08	2.92E+08	2.32E+08	2.39E+08	1.31E+08	79867000	2.74E+08	4.23E+08	2.81E+08	2.64E+08	5	5	5	68.6	68.6	68.6	8.2403	0	44.383	7071100000	145	NODE_16_NODE_16	3583	NODE_1679_length_14095_cov_728.328561_True_6900 uncharacterized protein LOC113788571
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	32.9	32.9	32.9	19.611	0	6.6677	54028000	6	NODE_16_NODE_16	3584	NODE_168_length_56594_cov_755.832912_False_19578 DNA-directed RNA polymerases I, II, and III subunit RPABC1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	39.6	39.6	39.6	11.747	0	3.9278	24396000	9	NODE_16_NODE_16	3585	NODE_168_length_56594_cov_755.832912_False_19768 DNA-directed RNA polymerases I, II, and III subunit RPABC1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	2	12.1	9	9	36.452	0	5.4276	47069000	8	NODE_16_NODE_16	3586	NODE_1684_length_14055_cov_453.442857_True_1564 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	2	2	32.6	13.2	13.2	36.614	0	6.1254	24220000	7	NODE_16_NODE_16	3587	NODE_1684_length_14055_cov_453.442857_True_5462 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	2	21.3	8.5	8.5	23.751	0.006645	1.5171	27188000	2	NODE_16_NODE_16	3588	NODE_1684_length_14055_cov_453.442857_True_631 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	58527000	68735000	72924000	0	0	0	0	0	0	0	0	7	2	2	24.8	8.5	8.5	39.143	0.000191	3.1585	382920000	15	NODE_16_NODE_16	3589	NODE_1684_length_14055_cov_453.442857_True_6869 C-type lectin lectoxin-Lio1
0	0	20275000	0	14472000	15769000	29180000	57714000	43381000	88949000	44082000	31909000	0	0	0	0	0	0	4	3	2	35.3	26.6	20.1	15.029	0	103.41	850230000	42	NODE_16_NODE_16	3590	NODE_16840_length_959_cov_321.561947_True_68 cystatin-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	7.4	7.4	7.4	34.858	0.000199	3.4531	6164800	4	NODE_16_NODE_16	3591	NODE_1686_length_14042_cov_655.930793_True_3651 GATA zinc finger domain-containing protein 14-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	5.7	5.7	5.7	17.608	0.008177	1.42	13446000	5	NODE_16_NODE_16	3592	NODE_169_length_56449_cov_741.151115_True_25616 carboxypeptidase-like protein 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	5	5	86.7	86.7	86.7	9.2935	0	9.5422	49975000	8	NODE_16_NODE_16	3593	NODE_169_length_56449_cov_741.151115_True_26802 N-fatty-acyl-amino acid synthase/hydrolase PM20D1
0	17580000	0	0	0	0	0	0	0	0	0	0	0	0	0	17307000	0	15205000	1	1	1	10.2	10.2	10.2	17.127	0.000867	2.4504	123870000	17	NODE_16_NODE_16	3594	NODE_169_length_56449_cov_741.151115_True_27120 N-fatty-acyl-amino acid synthase/hydrolase PM20D1-like
0	0	0	0	0	0	0	3897200	3934200	4566100	2821400	2227400	0	0	3184500	6090900	0	0	5	5	5	9.8	9.8	9.8	94.384	0	6.5057	67794000	28	NODE_16_NODE_16	3595	NODE_169_length_56449_cov_741.151115_True_38687 mannosyl-oligosaccharide glucosidase-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	31	31	31	8.0548	0	4.9542	0	1	NODE_16_NODE_16	3596	NODE_16947_length_953_cov_785.397550_True_346 DFP2-like protein
2.07E+08	2.36E+08	1.27E+08	1.21E+08	1.01E+08	1.05E+08	1.52E+08	1.77E+08	1.8E+08	2.07E+08	1.68E+08	1.34E+08	72227000	66580000	1.47E+08	2.46E+08	1.38E+08	1.95E+08	14	14	14	57.4	57.4	57.4	29.302	0	125.19	1.2938E+10	410	NODE_16_NODE_16	3597	NODE_16948_length_953_cov_754.871938_True_0 glutamate receptor kainate-like protein
10766000	0	0	8659600	0	6490300	0	9888700	7377900	10330000	7076400	5764800	0	0	5557000	10774000	0	0	5	5	3	13.8	13.8	10	58.896	0	23.39	183820000	38	NODE_16_NODE_16	3598	NODE_1697_length_13935_cov_664.990490_False_10355 inositol hexakisphosphate kinase 3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	5.4	5.4	5.4	24.665	0.00102	2.3007	47226000	10	NODE_16_NODE_16	3599	NODE_1697_length_13935_cov_664.990490_False_8696 inositol hexakisphosphate kinase 3
1.34E+08	1.39E+08	74068000	59225000	68388000	17360000	10003000	5914200	6893700	7770100	5513900	0	2705700	2688700	2859200	3122300	6997900	988580	68	68	68	54	54	54	197.76	0	323.31	7109800000	593	NODE_17_NODE_17	3600	NODE_17_length_144846_cov_702.126168_False_128883 vitellogenin-like protein
93160000	82037000	31667000	22546000	35362000	11578000	21048000	20702000	0	16927000	0	0	0	7169200	0	0	0	0	13	13	13	41.5	41.5	41.5	45.151	0	165.61	1234000000	86	NODE_17_NODE_17	3601	NODE_17_length_144846_cov_702.126168_False_130141 vitellogenin-like protein
11717000	13790000	0	0	0	0	0	0	0	5505300	0	0	0	0	0	9713700	6094800	0	4	4	4	15.9	15.9	15.9	39.571	0	9.3819	98008000	31	NODE_17_NODE_17	3602	NODE_17_length_144846_cov_702.126168_False_84756 phenylalanine-tRNA ligase [
55447000	65646000	44332000	31357000	39771000	0	0	0	0	0	0	0	0	0	0	0	0	0	12	12	12	44	44	44	36.285	0	82.877	702880000	52	NODE_17_NODE_17	3603	NODE_17_length_144846_cov_702.126168_True_12889 uncharacterized protein LOC113799427
1.03E+08	86575000	81741000	65973000	82088000	28163000	0	0	0	0	869590	0	0	278520	0	0	0	760510	35	35	35	54.8	54.8	54.8	97.692	0	220.76	4397900000	239	NODE_17_NODE_17	3604	NODE_17_length_144846_cov_702.126168_True_13913 uncharacterized protein LOC113799427
2.27E+08	2.61E+08	1.38E+08	87602000	1.22E+08	23393000	3209000	2926900	1445300	1646300	3192000	0	0	436540	1837700	0	1335900	6061200	33	33	33	50.5	50.5	50.5	94.047	0	285.33	6385300000	314	NODE_17_NODE_17	3605	NODE_17_length_144846_cov_702.126168_True_16715 uncharacterized protein LOC113799427
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	6.7	6.7	6.7	41.359	0	9.5664	27273000	11	NODE_17_NODE_17	3606	NODE_17_length_144846_cov_702.126168_True_26792 phosphatidylinositol 3-kinase 1-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	10284000	14980000	9079900	10435000	5	5	5	18.9	18.9	18.9	43.169	0	9.9877	153600000	34	NODE_17_NODE_17	3607	NODE_17_length_144846_cov_702.126168_True_30222 Rho GTPase-activating protein 100F
0	0	0	0	0	0	0	7681600	0	0	5172300	3723500	0	0	0	17756000	0	13287000	5	5	5	22.7	22.7	22.7	31.81	0	8.9031	93132000	19	NODE_17_NODE_17	3608	NODE_17_length_144846_cov_702.126168_True_31373 rho GTPase-activating protein-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	6.5	6.5	6.5	40.891	0.002239	1.9026	24752000	6	NODE_17_NODE_17	3609	NODE_17_length_144846_cov_702.126168_True_32589 Rho GTPase-activating protein 100F
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1.9	1.9	1.9	76.636	0.003587	1.7473	3058700	3	NODE_17_NODE_17	3610	NODE_17_length_144846_cov_702.126168_True_42956 probable global transcription activator SNF2L2
0	0	0	3503700	0	0	5376700	0	0	0	0	6098200	0	0	7134800	8113700	5085800	0	2	2	2	17.7	17.7	17.7	21.29	0	7.8007	89965000	25	NODE_17_NODE_17	3611	NODE_17_length_144846_cov_702.126168_True_87417 ethylmalonyl-CoA decarboxylase-like
78106000	94489000	35681000	32862000	43085000	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	41.2	41.2	41.2	26.552	0	53.881	551890000	37	NODE_17_NODE_17	3612	NODE_17_length_144846_cov_702.126168_True_8755 beta-1,3-glucan-binding protein precursor
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	30	30	30	26.982	0	9.5476	24515000	8	NODE_17_NODE_17	3613	NODE_17_length_144846_cov_702.126168_True_88049 ethylmalonyl-CoA decarboxylase-like
2.81E+08	3.05E+08	1.8E+08	1.18E+08	1.63E+08	43527000	1419600	2847300	1371400	1305800	3656100	0	1477700	1355000	1617800	853670	1828700	2434800	47	47	47	52.2	52.2	52.2	130.86	0	323.31	1.0035E+10	481	NODE_17_NODE_17	3614	NODE_17_length_144846_cov_702.126168_True_9404 apolipophorins-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	7.4	7.4	7.4	37.235	0	5.6025	7020900	6	NODE_17_NODE_17	3615	NODE_170_length_56447_cov_647.576748_False_16377 protein PFF0380w-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	3.4	3.4	3.4	52.29	0.000189	3.0859	17174000	3	NODE_17_NODE_17	3616	NODE_170_length_56447_cov_647.576748_False_17777 protein PFF0380w-like
0	0	0	39844000	0	31704000	0	0	0	0	0	0	0	8931600	0	0	0	0	12	2	2	46.9	8.3	8.3	26.685	0.00071	2.5961	229600000	20	NODE_17_NODE_17	3617	NODE_170_length_56447_cov_647.576748_False_9933 putative glucosylceramidase 3
41395000	16627000	17782000	18458000	16340000	12226000	0	0	0	0	0	10936000	10486000	8377700	0	0	0	41160000	5	5	5	41.9	41.9	41.9	27.561	0	16.173	539990000	47	NODE_17_NODE_17	3618	NODE_1704_length_13861_cov_740.135955_True_10911 Phenazine biosynthesis-like domain-containing protein
25152000	0	0	0	0	0	0	0	0	0	0	0	34880000	20807000	35204000	1.69E+08	52082000	1.35E+08	3	3	3	30.8	30.8	30.8	23.385	0	99.19	837380000	38	NODE_33_NODE_33	3619	NODE_3348_length_7491_cov_445.766407_False_5397 hypothetical protein BV898_14315;NODE_1705_length_13859_cov_431.937627_False_10092 hypothetical protein BV898_14315
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	3.9	3.9	3.9	44.506	0.007649	1.4686	563580000	6	NODE_17_NODE_17	3620	NODE_1706_length_13851_cov_697.366990_False_2659 alpha 1:2 mannosidase precursor-like protein
0	0	0	0	0	0	0	20569000	0	0	0	0	0	0	0	18513000	0	0	4	4	4	30.4	30.4	30.4	29.471	0	16.728	84649000	15	NODE_17_NODE_17	3621	NODE_1706_length_13851_cov_697.366990_False_5372 putative cysteine proteinase;gi	1048030256	ref	XP_017489023.1	PREDICTED: cysteine proteinase 15A-like, partial [Rhagoletis zephyria]
0	0	0	0	12548000	0	15418000	30283000	16216000	43928000	20721000	17477000	9792200	7978100	14837000	15548000	14261000	19840000	10	10	10	49.1	49.1	49.1	30.397	0	22.755	629280000	66	NODE_17_NODE_17	3622	NODE_1706_length_13851_cov_697.366990_False_9428 cathepsin L1-like
0	0	5646700	4529600	0	4857500	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	7.9	7.9	7.9	13.831	0.001161	2.1309	30133000	14	NODE_17_NODE_17	3623	NODE_171_length_55957_cov_721.538550_True_47698 hypothetical protein QR98_0091080
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	34.8	22.7	22.7	7.5206	0	78.688	127220000	14	NODE_17_NODE_17	3624	NODE_171_length_55957_cov_721.538550_True_54664 calpain-9 isoform X1
0	0	0	0	0	11821000	0	0	0	0	0	0	22091000	0	0	0	0	0	3	3	3	21.4	21.4	21.4	16.361	0	4.5088	177700000	9	NODE_17_NODE_17	3625	NODE_1712_length_13825_cov_711.553377_False_5040 cytochrome b reductase 1-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	7.9	7.9	7.9	25.957	0	10.405	103410000	16	NODE_17_NODE_17	3626	NODE_1712_length_13825_cov_711.553377_False_6028 cytochrome b561-like isoform X1
0	0	0	29362000	29375000	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	21.6	21.6	21.6	40.633	0	16.535	324860000	22	NODE_17_NODE_17	3627	NODE_1714_length_13820_cov_542.759535_True_4159 glucose dehydrogenase [FAD, quinone]-like isoform X4;NODE_4687_length_4998_cov_502.644548_True_4193 glucose dehydrogenase [FAD, quinone]-like isoform X4
0	0	21587000	17546000	11568000	15086000	0	0	0	0	0	0	0	0	0	18461000	12990000	0	3	3	3	31.1	31.1	31.1	24.736	0	11.415	329180000	35	NODE_17_NODE_17	3628	NODE_1714_length_13820_cov_542.759535_True_5166 glucose dehydrogenase [FAD, quinone]-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	27.9	27.9	27.9	10.246	0	38.6	134610000	19	NODE_17_NODE_17	3629	NODE_17654_length_917_cov_506.967517_True_306 CD151 antigen-like;NODE_17145_length_943_cov_494.540541_False_631 CD151 antigen-like
28792000	55978000	33402000	32672000	30820000	26711000	40867000	44751000	54984000	78250000	54764000	51340000	16067000	0	24500000	28485000	39832000	41624000	8	8	8	43.7	43.7	43.7	26.076	0	44.55	1512700000	101	NODE_17_NODE_17	3630	NODE_1718_length_13805_cov_694.795200_True_0 serpin family protein;gi	1048068019	ref	XP_017464150.1	PREDICTED: plasminogen activator inhibitor 2-like [Rhagoletis zephyria]
0	0	0	0	0	0	8511100	0	0	14246000	0	6470100	0	0	0	0	0	0	8	8	8	35.3	35.3	35.3	46.914	0	64.171	136770000	26	NODE_17_NODE_17	3631	NODE_1718_length_13805_cov_694.795200_True_10475 calsequestrin-2-like protein
26513000	20915000	11736000	6771400	7740200	8223700	9508100	13152000	11106000	14383000	10190000	7527800	4732900	0	6122400	7888000	7062500	11071000	3	3	3	23.4	23.4	23.4	25.878	0	19.025	477180000	81	NODE_17_NODE_17	3632	NODE_1718_length_13805_cov_694.795200_True_9756 calsequestrin-2-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	2.9	2.9	2.9	39.534	0.001308	2.0363	17037000	3	NODE_17_NODE_17	3633	NODE_172_length_55894_cov_701.987679_False_55892 disabled homolog 2 isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	22.8	22.8	22.8	28.778	0	4.5566	24280000	11	NODE_17_NODE_17	3634	NODE_172_length_55894_cov_701.987679_False_7910 Selenoprotein P - N terminal domain containing protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	35	35	35	8.8072	0	5.8539	73480000	17	NODE_17_NODE_17	3635	NODE_1720_length_13796_cov_616.826214_False_7718 PREDICTED: ankyrin-3-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.1	4.1	4.1	49.034	0.00087	2.4792	17142000	5	NODE_17_NODE_17	3636	NODE_1721_length_13784_cov_655.508559_False_4930 afadin isoform X9
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	5.6	5.6	5.6	24.166	0.003741	1.7445	28746000	2	NODE_17_NODE_17	3637	NODE_1722_length_13783_cov_650.911349_False_13104 Heme peroxidase-like protein
43200000	55358000	0	17959000	17532000	13030000	0	0	0	0	0	0	11715000	12546000	40943000	22095000	30666000	43256000	6	2	2	67.4	32.6	32.6	14.286	0	22.271	616820000	35	NODE_17_NODE_17	3638	NODE_1723_length_13780_cov_717.779089_False_7272 uncharacterized oxidoreductase MexAM1_META1p0182-like
0	0	15984000	18391000	0	11692000	0	0	0	0	0	0	0	0	0	0	0	0	8	2	2	58.2	26.6	26.6	16.828	0	8.3397	347320000	23	NODE_17_NODE_17	3639	NODE_1723_length_13780_cov_717.779089_False_7763 uncharacterized oxidoreductase MexAM1_META1p0182-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	13.7	13.7	13.7	11.165	0.003282	1.7636	6658700	2	NODE_17_NODE_17	3640	NODE_1723_length_13780_cov_717.779089_False_8315 SDR family oxidoreductase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.9	4.9	4.9	28.88	0.003283	1.7654	61493000	6	NODE_17_NODE_17	3641	NODE_1727_length_13753_cov_716.367572_True_1011 perivitellin-2 67 kDa subunit-like
49830000	29653000	42964000	54938000	46394000	44122000	77722000	81765000	68002000	78583000	67461000	72276000	69940000	24364000	70882000	53843000	71088000	40111000	4	4	4	45.1	45.1	45.1	11.408	0	5.767	1597700000	57	NODE_17_NODE_17	3642	NODE_173_length_55685_cov_732.659680_False_49229 cytochrome b-c1 complex subunit 6, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	7.1	7.1	7.1	98.49	0	6.8324	3235800	14	NODE_17_NODE_17	3643	NODE_173_length_55685_cov_732.659680_True_41621 autophagy-related protein 9A isoform X1
0	11565000	0	0	8486300	0	0	0	0	0	0	0	0	0	0	11309000	0	10820000	4	4	4	14.9	14.9	14.9	60.462	0	13.53	108190000	20	NODE_17_NODE_17	3644	NODE_173_length_55685_cov_732.659680_True_46865 glycerol kinase 3-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	31.9	31.9	31.9	15.465	0	3.6115	24574000	6	NODE_17_NODE_17	3645	NODE_1735_length_13717_cov_467.385815_False_12681 GNAT family acetyltransferase-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	8.8	8.8	8.8	13.2	0.00936	1.3359	96694000	12	NODE_17_NODE_17	3646	NODE_17363_length_932_cov_538.628278_False_745 serine/arginine repetitive matrix protein 2-like isoform X6
17224000	14867000	7909200	0	0	0	19255000	22885000	21420000	13640000	25446000	14622000	10995000	0	13914000	15294000	13787000	15448000	7	7	7	36.7	36.7	36.7	36.9	0	69.249	621380000	76	NODE_17_NODE_17	3647	NODE_1737_length_13716_cov_698.324500_False_1283 serine-rich 25 kDa antigen protein-like
0	0	0	0	0	0	0	4265600	2948800	0	4186500	0	0	0	0	0	0	0	12	2	2	26.6	5	5	68.356	0	3.891	27164000	14	NODE_17_NODE_17	3648	NODE_1744_length_13666_cov_645.230622_False_13664 twitchin
0	20490000	0	0	6453800	5411000	0	0	0	0	0	9515600	0	0	0	18349000	12074000	0	5	5	5	15.8	15.8	15.8	47.956	0	9.2121	153390000	32	NODE_17_NODE_17	3649	NODE_1745_length_13654_cov_765.202074_False_10262 DNA damage-binding protein 1
8236300	0	0	0	0	0	0	0	0	0	0	0	0	0	17098000	22819000	16449000	22393000	3	3	3	20.8	20.8	20.8	18.666	0	25.093	204230000	32	NODE_17_NODE_17	3650	NODE_1745_length_13654_cov_765.202074_False_2035 glycosyl hydrolase
0	0	7732600	9488900	5807500	8186300	0	0	0	0	0	0	19638000	20436000	0	11175000	0	0	2	2	2	47.7	47.7	47.7	7.2014	0	6.4957	168300000	22	NODE_17_NODE_17	3651	NODE_1745_length_13654_cov_765.202074_False_2294 cellulose binding domain-containing protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	16536000	28032000	0	28085000	3	3	3	37.7	37.7	37.7	12.533	0	24.815	120930000	17	NODE_17_NODE_17	3652	NODE_1745_length_13654_cov_765.202074_False_3054 glycosyl hydrolase
0	0	5989800	6245300	6746400	0	0	0	0	0	0	0	0	6313800	0	0	0	0	2	2	2	34	34	34	11.289	0	4.9169	166630000	20	NODE_17_NODE_17	3653	NODE_1745_length_13654_cov_765.202074_False_6811 DNA damage-binding protein 1-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	15	15	15	12.788	0.004486	1.6928	9150900	3	NODE_17_NODE_17	3654	NODE_1745_length_13654_cov_765.202074_False_7028 DNA damage-binding protein 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	16.8	16.8	16.8	21.034	0	3.8294	24730000	10	NODE_17_NODE_17	3655	NODE_1745_length_13654_cov_765.202074_False_7624 DNA damage-binding protein 1-like
6834200	0	0	0	0	0	3984500	6689700	5295000	6016800	5113400	3475100	0	0	4041600	11403000	0	0	6	6	6	27.1	27.1	27.1	29.946	0	11.293	146290000	38	NODE_17_NODE_17	3656	NODE_1745_length_13654_cov_765.202074_False_8387 DNA damage-binding protein 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	37.6	37.6	37.6	15.871	0	3.8665	13511000	5	NODE_17_NODE_17	3657	NODE_1748_length_13642_cov_703.859351_True_9461 PHD finger-like domain-containing protein 5A;gi	1048028268	ref	XP_017474862.1	PREDICTED: uncharacterized protein CG9548 [Rhagoletis zephyria]
1.17E+08	83454000	33283000	36044000	26745000	43565000	1E+08	1.24E+08	1.16E+08	1.16E+08	78228000	56734000	1.42E+08	90604000	3.44E+08	3.73E+08	2.3E+08	4E+08	10	10	10	77.2	77.2	77.2	17.286	0	95.438	9940200000	236	NODE_17_NODE_17	3658	NODE_17487_length_926_cov_693.936854_False_624 DM9 domain-containing protein isoform 2
1.68E+08	1.52E+08	51195000	52208000	38994000	63175000	1.25E+08	2.04E+08	1.7E+08	2.03E+08	1.39E+08	95567000	1.7E+08	1.03E+08	4.19E+08	5.71E+08	3.98E+08	6.22E+08	5	5	5	52.3	52.3	52.3	12.515	0	81.933	7021700000	121	NODE_17_NODE_17	3659	NODE_17487_length_926_cov_693.936854_False_925 lysosomal alpha-mannosidase-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	21.9	21.9	21.9	34.062	0	5.0886	27168000	5	NODE_17_NODE_17	3660	NODE_175_length_55635_cov_670.799532_False_1155 28S ribosomal protein S7, mitochondrial-like
0	0	0	0	0	0	0	0	0	6031600	0	0	0	0	0	0	0	8560600	5	5	5	19.2	19.2	19.2	41.903	0	9.1729	118650000	27	NODE_17_NODE_17	3661	NODE_175_length_55635_cov_670.799532_False_22632 nucleoporin Nup43
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	2.6	2.6	2.6	70.467	0.008457	1.4134	0	2	NODE_17_NODE_17	3662	NODE_175_length_55635_cov_670.799532_True_12301 putative RNA-binding protein 15
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	10.8	10.8	10.8	44.03	0.000195	3.3282	41363000	10	NODE_17_NODE_17	3663	NODE_175_length_55635_cov_670.799532_True_23061 mitochondrial inner membrane protein OXA1L;gi	1048068271	ref	XP_017486273.1	PREDICTED: mitochondrial inner membrane protein OXA1L-like, partial [Rhagoletis zephyria]
14593000	22048000	7496700	7870700	10254000	7520000	6179400	10525000	8824000	8930300	7402700	5322000	4598100	5568400	8417600	14036000	8955800	13482000	10	10	10	31.9	31.9	31.9	49.98	0	92.602	486540000	107	NODE_17_NODE_17	3664	NODE_1753_length_13619_cov_663.617738_True_7949 protein slit-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	137.17	0.001316	2.0792	3355000	2	NODE_17_NODE_17	3665	NODE_1754_length_13615_cov_692.123599_False_11074 integrator complex subunit 7-like
24475000	19968000	16032000	15973000	13016000	13015000	31405000	31171000	30776000	27299000	26971000	15302000	20619000	14766000	34206000	55268000	39797000	49895000	12	12	12	63.4	63.4	63.4	29.957	0	45.105	1778800000	121	NODE_17_NODE_17	3666	NODE_1756_length_13613_cov_703.874539_False_1493 aldo-keto reductase family 1 member B10-like
0	0	0	8820000	9157400	17692000	0	0	0	0	0	0	27388000	7741700	6485700	0	0	0	4	4	4	40.4	40.4	40.4	11.117	0	8.005	470380000	24	NODE_17_NODE_17	3667	NODE_1756_length_13613_cov_703.874539_False_1833 aldo/keto reductase
0	56779000	34210000	0	29522000	32467000	0	0	0	0	0	0	0	0	0	35556000	24267000	0	2	2	2	12.3	12.3	12.3	23.344	0	4.2847	513170000	29	NODE_17_NODE_17	3668	NODE_1756_length_13613_cov_703.874539_True_10139 pancreatic lipase-related protein 2-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	1	1	17.8	2	2	81.72	0.000189	3.0843	86616000	12	NODE_17_NODE_17	3669	NODE_1757_length_13610_cov_667.159720_True_1 CAD protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	2	2	32	9.2	9.2	55.881	0.008977	1.3671	20469000	7	NODE_17_NODE_17	3670	NODE_1757_length_13610_cov_667.159720_True_3593 CAD protein isoform X2
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	2	16.3	7.4	7.4	46.768	0.001032	2.3917	56936000	7	NODE_17_NODE_17	3671	NODE_1757_length_13610_cov_667.159720_True_5228 CAD protein
7E+08	1.04E+09	4.5E+08	4.8E+08	1.76E+08	4.1E+08	5.21E+08	8.83E+08	8.51E+08	9.07E+08	6.71E+08	5.51E+08	1.94E+08	1.15E+08	4.51E+08	5.37E+08	3.8E+08	5.95E+08	13	13	13	87.8	87.8	87.8	13.606	0	248.64	3.7781E+10	396	NODE_17_NODE_17	3672	NODE_176_length_55603_cov_729.977191_False_39668 myosin regulatory light polypeptide 9-like
81862000	1.07E+08	59729000	51053000	58069000	57252000	79264000	86368000	1.18E+08	1.2E+08	97599000	97582000	30059000	29737000	45665000	1.13E+08	64147000	61397000	1	1	1	30.5	30.5	30.5	6.9099	0	42.921	2205900000	116	NODE_17_NODE_17	3673	NODE_176_length_55603_cov_729.977191_False_42181 regulatory myosin light chain
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	6.2	6.2	6.2	48.39	0.00019	3.0953	45186000	10	NODE_17_NODE_17	3674	NODE_176_length_55603_cov_729.977191_True_28106 ras guanine nucleotide exchange factor R-like isoform X3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	30.9	30.9	30.9	5.8467	0.001451	1.9639	49791000	4	NODE_17_NODE_17	3675	NODE_176_length_55603_cov_729.977191_True_34628 sorbin and SH3 domain-containing protein 2-like isoform X28
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	14.4	14.4	14.4	33.788	0	7.6647	58994000	14	NODE_17_NODE_17	3676	NODE_176_length_55603_cov_729.977191_True_35023 ras guanine nucleotide exchange factor R-like isoform X3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	11.6	11.6	11.6	10.039	0.007896	1.4285	22459000	8	NODE_17_NODE_17	3677	NODE_176_length_55603_cov_729.977191_True_36470 Hypothetical predicted protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	18.5	18.5	18.5	7.7539	0.000869	2.4672	21696000	4	NODE_17_NODE_17	3678	NODE_176_length_55603_cov_729.977191_True_36723 sorbin and SH3 domain-containing protein 1 isoform X4
0	0	20549000	17305000	16062000	11982000	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	17.4	17.4	17.4	16.175	0	4.8719	226450000	19	NODE_17_NODE_17	3679	NODE_1760_length_13597_cov_684.576134_True_8636 RUN domain-containing protein 1-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	16.2	16.2	16.2	10.623	0	4.3725	134010000	7	NODE_17_NODE_17	3680	NODE_1760_length_13597_cov_684.576134_True_9074 RUN domain-containing protein 1-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	3.3	3.3	3.3	40.925	0.003132	1.7742	988430	1	NODE_17_NODE_17	3681	NODE_1762_length_13579_cov_779.801316_False_11311 choice-of-anchor A family protein
43639000	50148000	46767000	36630000	21410000	33389000	36331000	45900000	60238000	65954000	54235000	49727000	20822000	4924900	29114000	29828000	35421000	25472000	5	5	5	64.8	64.8	64.8	9.6192	0	33.431	1900800000	202	NODE_17_NODE_17	3682	NODE_1762_length_13579_cov_779.801316_False_12399 cuticular protein-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	2	2	45.7	8.6	8.6	23.718	0.000192	3.1932	17095000	5	NODE_17_NODE_17	3683	NODE_17621_length_919_cov_498.515046_True_2 Secernin-2-like protein;NODE_17925_length_903_cov_514.995283_False_809 Secernin-2-like protein
1.34E+08	1.1E+08	38125000	43875000	55338000	55685000	1.21E+08	1.98E+08	1.14E+08	1.75E+08	1.26E+08	1.38E+08	47080000	39513000	87430000	88896000	67501000	1.24E+08	4	2	2	35.1	14.5	14.5	23.499	0	193.15	2972100000	90	NODE_17_NODE_17	3684	NODE_1763_length_13579_cov_643.766933_False_10728 mite allergen Der f 3-like
21220000	40155000	16030000	15327000	11249000	12581000	20988000	29175000	24698000	30138000	22487000	17644000	12727000	9699200	19763000	23639000	18072000	20891000	7	7	7	20	20	20	42.156	0	10.962	860140000	92	NODE_17_NODE_17	3685	NODE_177_length_55388_cov_697.785426_False_55170 N-acetylserotonin O-methyltransferase-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	6.6	6.6	6.6	49.789	0.001922	1.9189	6070200	5	NODE_17_NODE_17	3686	NODE_177_length_55388_cov_697.785426_True_29400 TBC1 domain family member 22B
0	0	0	0	0	0	0	25137000	18561000	30075000	16261000	10575000	0	0	0	0	0	0	2	2	2	17.5	17.5	17.5	16.304	0.000193	3.2604	187290000	25	NODE_17_NODE_17	3687	NODE_1775_length_13514_cov_703.145479_True_2643 complement C1s subcomponent
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	7.5	7.5	7.5	17.816	0.001021	2.3047	68006000	3	NODE_17_NODE_17	3688	NODE_1775_length_13514_cov_703.145479_True_4333 complement C1s subcomponent
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	14.1	14.1	14.1	17.515	0.001016	2.2803	177900000	12	NODE_17_NODE_17	3689	NODE_1775_length_13514_cov_703.145479_True_434 transmembrane protease serine 9-like
0	0	0	0	0	0	0	24348000	0	0	0	6836400	0	0	0	0	0	0	2	2	2	11.8	11.8	11.8	25.798	0.001018	2.2908	89103000	7	NODE_17_NODE_17	3690	NODE_1775_length_13514_cov_703.145479_True_6272 complement C1s subcomponent
0	0	0	0	0	0	24913000	45809000	26916000	43337000	23785000	19349000	23364000	21815000	37949000	41568000	34302000	48873000	4	4	3	25	25	25	18.027	0	11.756	916260000	67	NODE_17_NODE_17	3691	NODE_1775_length_13514_cov_703.145479_True_822 chymotrypsin-like protease CTRL-1
1.52E+08	1.39E+08	59114000	68244000	63200000	66302000	55414000	1.03E+08	85333000	89734000	65752000	66206000	45779000	41042000	64744000	1.12E+08	89939000	1.13E+08	4	4	4	61.2	61.2	61.2	8.751	0	32.3	2697600000	111	NODE_17_NODE_17	3692	NODE_1776_length_13505_cov_695.472565_False_8053 cysteine rich trypsin inhibitor-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	2.3	2.3	2.3	52.705	0.000706	2.5658	280820	2	NODE_17_NODE_17	3693	NODE_1778_length_13489_cov_704.014813_True_9524 probable serine/threonine-protein kinase DDB_G0282963
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	33.7	33.7	33.7	22.533	0	10.226	63665000	15	NODE_17_NODE_17	3694	NODE_1783_length_13470_cov_721.192322_False_6621 ectonucleotide pyrophosphatase/phosphodiesterase family member 6-like
34685000	0	18858000	21761000	20144000	16732000	0	27632000	0	20702000	33418000	13331000	11487000	12614000	18714000	30275000	0	0	5	5	5	34.5	34.5	34.5	25.748	0	16.379	639460000	51	NODE_17_NODE_17	3695	NODE_1783_length_13470_cov_721.192322_False_9148 ectonucleotide pyrophosphatase/phosphodiesterase family member 6-like
0	0	6545200	6433500	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	42.1	42.1	42.1	16.678	0	6.3797	43541000	13	NODE_17_NODE_17	3696	NODE_1785_length_13458_cov_702.096695_False_3132 serine--pyruvate aminotransferase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	3	19.5	14.5	14.5	33.545	0	3.9649	53206000	13	NODE_17_NODE_17	3697	NODE_1785_length_13458_cov_702.096695_False_4047 serine--pyruvate aminotransferase
1.48E+08	1.53E+08	47836000	64588000	50124000	52761000	1.27E+08	1.86E+08	1.49E+08	1.75E+08	1.54E+08	1.16E+08	1.3E+08	1.18E+08	2.33E+08	4.04E+08	3.6E+08	4.64E+08	9	9	9	55.2	55.2	55.2	36.891	0	68.942	5818100000	187	NODE_17_NODE_17	3698	NODE_1785_length_13458_cov_702.096695_True_4973 discoidin domain-containing protein
61562000	65263000	15504000	17585000	16364000	17099000	57996000	77172000	58810000	59596000	50740000	38998000	48272000	36097000	1.74E+08	1.73E+08	1.23E+08	2.2E+08	2	2	2	50.8	50.8	50.8	7.3153	0	91.317	1806800000	54	NODE_17_NODE_17	3699	NODE_1785_length_13458_cov_702.096695_True_6144 discoidin domain-containing protein
0	0	0	0	0	0	0	27179000	0	0	0	0	0	0	0	35623000	1.05E+08	0	1	1	1	38.7	38.7	38.7	6.8835	0	14.207	338490000	29	NODE_17_NODE_17	3700	NODE_1785_length_13458_cov_702.096695_True_7271 discoidin domain-containing protein
0	0	0	0	0	0	17512000	36515000	23235000	0	0	28936000	36091000	36444000	54131000	79872000	46606000	1.19E+08	2	2	2	30.9	30.9	30.9	15.756	0	47.327	767160000	43	NODE_17_NODE_17	3701	NODE_1785_length_13458_cov_702.096695_True_7518 discoidin domain-containing protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	28.2	18.3	18.3	7.4695	0.00019	3.109	92549000	2	NODE_17_NODE_17	3702	NODE_1790_length_13449_cov_933.856802_True_5025 transmembrane protease serine 9-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	10.3	10.3	10.3	16.992	0	4.8568	3612300	4	NODE_17_NODE_17	3703	NODE_1790_length_13449_cov_933.856802_True_6157 Der f 3 allergen
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	10.1	10.1	10.1	16.98	0.001318	2.0881	3105200	2	NODE_17_NODE_17	3704	NODE_1792_length_13440_cov_472.971162_True_3955 hypothetical protein DRP01_10620, partial;NODE_2247_length_11070_cov_440.820245_True_3134 hypothetical protein DRP01_10620, partial
0	0	0	0	3810600	0	0	0	0	0	0	0	0	2767200	0	0	0	0	3	3	3	5	5	5	62.584	0.001034	2.4001	29205000	8	NODE_17_NODE_17	3705	NODE_1797_length_13397_cov_791.291411_True_11538 Putative phosphoenolpyruvate synthase
0	0	6019600	6021400	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	5.8	5.8	5.8	74.593	0	12.126	81041000	22	NODE_17_NODE_17	3706	NODE_1797_length_13397_cov_791.291411_True_9000 Cleft lip and palate transmembrane protein 1-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	13.6	13.6	13.6	10.207	0.009898	1.3038	54836000	7	NODE_17_NODE_17	3707	NODE_1798_length_13384_cov_729.060095_True_12546 oligopeptidase A
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	20.4	20.4	20.4	17.58	0.001171	2.1875	3227100	2	NODE_17_NODE_17	3708	NODE_1798_length_13384_cov_729.060095_True_12813 probable cytosolic oligopeptidase A
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.6	4.6	4.6	40.415	0	3.6961	458730	1	NODE_18_NODE_18	3709	NODE_18_length_139921_cov_709.422290_False_137117 ubiquitin carboxyl-terminal hydrolase 36-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32456000	47691000	41475000	2	2	2	32	32	32	8.6366	0	3.7216	288920000	19	NODE_18_NODE_18	3710	NODE_18_length_139921_cov_709.422290_False_1718 cellular retinoic acid binding protein
17233000	25533000	0	0	0	18887000	9479300	23296000	20018000	20625000	18405000	14358000	29119000	22151000	17869000	67586000	53100000	75887000	4	4	4	18.4	18.4	18.4	17.902	0	9.2148	924270000	54	NODE_18_NODE_18	3711	NODE_18_length_139921_cov_709.422290_False_2515 fatty acid-binding protein-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	16.8	16.8	16.8	14.868	0.001297	1.9966	2483600	3	NODE_18_NODE_18	3712	NODE_18_length_139921_cov_709.422290_False_28773 activating signal cointegrator 1 complex subunit 1-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	10.3	10.3	10.3	34.237	0.000187	2.9853	16538000	2	NODE_18_NODE_18	3713	NODE_18_length_139921_cov_709.422290_False_34589 uncharacterized oxidoreductase ZK1290.5-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	11.6	11.6	11.6	16.141	0.000187	2.9849	255860000	19	NODE_18_NODE_18	3714	NODE_18_length_139921_cov_709.422290_False_37551 fatty-acid amide hydrolase 2-like
0	0	0	0	0	4644000	0	0	0	0	0	0	8217300	4894300	0	18683000	18581000	24355000	3	3	3	30.6	30.6	30.6	14.404	0	41.946	206920000	28	NODE_18_NODE_18	3715	NODE_18_length_139921_cov_709.422290_False_6753 fatty acid-binding protein-like
16314000	0	0	16326000	15021000	16721000	12868000	14202000	17111000	14966000	14976000	19847000	10900000	18802000	13976000	19906000	13576000	23074000	10	10	10	34.2	34.2	34.2	38.195	0	32.013	571360000	59	NODE_18_NODE_18	3716	NODE_18_length_139921_cov_709.422290_False_84640 aldose reductase-like
0	0	0	0	0	0	3839500	7812100	5690700	0	4841700	5895300	0	0	0	0	6071200	0	3	3	3	17.9	17.9	17.9	23.16	0	8.9056	98620000	30	NODE_18_NODE_18	3717	NODE_18_length_139921_cov_709.422290_False_88323 cAMP-specific 3
6904100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11231000	7538500	10143000	4	4	4	27.4	27.4	27.4	28.117	0	15.115	106380000	21	NODE_18_NODE_18	3718	NODE_18_length_139921_cov_709.422290_False_89049 cAMP-specific 3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	14.7	14.7	14.7	40.414	0	15.249	16003000	14	NODE_18_NODE_18	3719	NODE_18_length_139921_cov_709.422290_False_90473 cAMP-specific 3,5-cyclic phosphodiesterase-like

2.81E+08	3.56E+08	20271000	99840000	67607000	78221000	1.47E+08	2.7E+08	2.04E+08	2.01E+08	1.74E+08	2.04E+08	87012000	0	1.89E+08	4.04E+08	2.05E+08	3.07E+08	1	1	1	21	21	21	10.805	0	136.29	4780100000	68	NODE 18	NODE 18	3720	NODE 18 length 139921 cov 709.422290 True 27378 Der p 36 allergen
2.6E+08	1.39E+08	88016000	1.06E+08	85253000	1.04E+08	2.07E+08	3.69E+08	2.72E+08	3.27E+08	2.58E+08	1.7E+08	1.55E+08	1.21E+08	2.25E+08	3.88E+08	2.73E+08	4.51E+08	6	6	6	48.5	48.5	48.5	21.943	0	92.749	9899200000	175	NODE 18	NODE 18	3721	NODE 18 length 139921 cov 709.422290 True 27626 Der f 36 allergen
0	0	8316700	0	0	0	0	0	0	0	0	0	7502900	0	0	0	0	0	4	4	4	38.6	38.6	38.6	14.76	0	12.611	242810000	26	NODE 18	NODE 18	3722	NODE 18 length 139921 cov 709.422290 True 33114 guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase MESH1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	18.5	18.5	18.5	16.918	0	3.6953	81810000	13	NODE 18	NODE 18	3723	NODE 18 length 139921 cov 709.422290 True 46083 cathepsin O isoform X2
0	0	0	4736700	0	0	6552000	8184200	8350600	0	0	3368900	0	0	0	0	0	0	4	4	2	31.4	31.4	17.1	23.589	0	37.002	93254000	22	NODE 18	NODE 18	3724	NODE 18 length 139921 cov 709.422290 True 46565 cysteine proteinase, putative
14705000	19027000	13736000	15321000	9799000	14012000	10878000	22230000	17044000	20326000	16660000	14714000	20323000	14189000	26537000	51483000	30582000	36732000	2	2	2	30.2	30.2	30.2	6.92	0	15.528	583450000	66	NODE 18	NODE 18	3725	NODE 180 length 55321 cov 736.849980 False 37420 mitochondrial import receptor subunit TOM40 homolog 1-like
0	0	6586100	6327700	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	33.3	33.3	33.3	13.462	0	8.7147	83956000	18	NODE 18	NODE 18	3726	NODE 180 length 55321 cov 736.849980 False 43259 UPF0160 protein MYG1, mitochondrial isoform X2
0	11176000	0	0	0	0	6921700	8081900	9452000	8573100	8276200	6472000	0	0	8023900	15239000	9157600	14625000	8	8	8	18.6	18.6	18.6	62.827	0	44.628	271040000	63	NODE 18	NODE 18	3727	NODE 180 length 55321 cov 736.849980 True 28261 inner nuclear membrane protein Man1;gi|1048047539|ref|XP 017478783.1| PREDICTED: inner nuclear membrane protein Man1-like [Rhagoletis zephyria]
2.07E+08	2.33E+08	1.09E+08	74558000	58073000	49474000	86320000	1.32E+08	1.32E+08	89226000	1.32E+08	74156000	83864000	26812000	53225000	1.05E+08	1.02E+08	1.07E+08	6	6	6	67.2	67.2	67.2	14.608	0	135.62	3229800000	117	NODE 18	NODE 18	3728	NODE 18024 length 898 cov 762.897983 True 468 transcription factor BTF3 homolog 4
29513000	35066000	25053000	22681000	18077000	16577000	0	19279000	0	19182000	23330000	20235000	0	11871000	24036000	32053000	0	34367000	2	2	2	14.9	14.9	14.9	18.687	0	26.451	604520000	48	NODE 19	NODE 19	3729	NODE 1984 length 12307 cov 486.241022 True 8979 ubiquilin-4;NODE 1805 length 13337 cov 536.180696 False 4317 ubiquilin-1
0	0	0	20801000	0	15033000	13646000	21829000	15444000	18408000	19420000	13086000	0	0	17698000	26134000	33661000	29533000	2	2	2	17.9	17.9	17.9	16.912	0	22.273	499420000	41	NODE 19	NODE 19	3730	NODE 1984 length 12307 cov 486.241022 True 6942 ubiquilin-1-like protein;NODE 1805 length 13337 cov 536.180696 False 6336 ubiquilin-1-like protein
27331000	35783000	0	18018000	9536200	14985000	35027000	47525000	40870000	56443000	51264000	24357000	24842000	13228000	49818000	68414000	42655000	74755000	10	10	10	62.8	62.8	62.8	29.066	0	35.693	1918500000	114	NODE 18	NODE 18	3731	NODE 1806 length 13332 cov 523.728779 False 11970 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	18.8	18.8	18.8	31.195	0.000198	3.438	10747000	4	NODE 18	NODE 18	3732	NODE 1808 length 13319 cov 934.430262 True 6633 neprilysin-1-like;NODE 2330 length 10681 cov 489.464239 False 6699 peptidase family M13
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	18.4	18.4	18.4	11.296	0	3.7482	11977000	4	NODE 23	NODE 23	3733	NODE 2330 length 10681 cov 489.464239 False 5147 membrane metallo-endopeptidase-like 1;NODE_1808_length_13319_cov_934.430262_True_8175 membrane metallo-endopeptidase-like 1
16147000	0	9649000	9638800	8400700	9876000	0	10619000	12622000	0	0	0	0	7068900	19270000	0	0	21123000	9	1	1	45.2	4.7	4.7	37.76	0	3.7256	255990000	30	NODE 18	NODE 18	3734	NODE 1809 length 13314 cov 690.042613 True 6831 ruvB-like 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	10.2	10.2	10.2	14.32	0.000186	2.9444	17724000	7	NODE 18	NODE 18	3735	NODE 1809 length 13314 cov 690.042613 True 9114 17-beta-hydroxysteroid dehydrogenase 13-like isoform X1
0	0	14612000	14660000	16090000	0	0	0	0	0	0	0	11227000	11774000	0	0	0	0	3	3	3	20.5	20.5	20.5	22.949	0	4.4875	140170000	26	NODE 18	NODE 18	3736	NODE 1811 length 13312 cov 670.773780 False 5179 kynurenine--oxoglutarate transaminase 3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	24	24	24	5.9147	0.000198	3.419	282660000	15	NODE 18	NODE 18	3737	NODE 1811 length 13312 cov 670.773780 False 5348 Kynurenine--oxoglutarate transaminase 3
89818000	1.02E+08	38299000	36647000	31395000	30713000	32139000	45669000	43504000	49184000	29386000	25007000	24018000	25597000	49058000	1.06E+08	47341000	81301000	5	5	5	31	31	31	24.728	0	144.88	2071500000	80	NODE 18	NODE 18	3738	NODE 1811 length 13312 cov 670.773780 False 6516 kynurenine--oxoglutarate transaminase 3-like isoform X2
1.22E+08	1.24E+08	61684000	48328000	70803000	0	0	0	0	0	0	0	0	0	0	0	0	0	44	3	3	35.2	3.1	3.1	160.87	0	6.9112	494310000	28	NODE 18	NODE 18	3739	NODE 1816 length 13241 cov 477.333308 False 13239 Apolipophorin-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	5217900	0	0	8457800	0	5	4	3	16.5	12.9	9.7	53.956	0	6.9226	96280000	18	NODE 18	NODE 18	3740	NODE 1816 length 13241 cov 477.333308 True 5200 glycosyl transferase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	3.9	3.9	3.9	111.85	0	4.9047	3780500	7	NODE 18	NODE 18	3741	NODE 182 length 55019 cov 751.509170 True 32652 RING finger and SPRY domain-containing protein 1-like
2367800	0	0	0	0	0	3065800	0	0	0	0	1847700	0	0	0	0	2008700	0	48	1	1	51.3	1.9	1.9	126.43	0	66.57	30023000	22	NODE 18	NODE 18	3742	NODE 182 length 55019 cov 751.509170 True 38960 Eukaryotic translation initiation factor 3 subunit A
8802200	12579000	0	0	0	0	5660400	7569000	6521600	7741800	5847000	5552000	0	0	12170000	14557000	12463000	0	2	2	2	39.6	39.6	39.6	10.345	0	43.885	171590000	46	NODE 18	NODE 18	3743	NODE 18247 length 888 cov 726.679472 False 853 dynein light chain roadblock-type 2-like
0	0	11280000	3510400	3453300	6660200	11135000	26062000	6713500	40070000	11180000	12210000	19445000	4654400	2524500	8628100	2245600	9030700	7	7	7	31.3	31.3	31.3	31.686	0	26.798	572660000	65	NODE 18	NODE 18	3744	NODE 1825 length 13199 cov 715.748707 False 898 C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	7.7	7.7	7.7	49.349	0	6.3778	29688000	8	NODE 18	NODE 18	3745	NODE 1827 length 13179 cov 670.779717 False 2868 RIMS-binding protein 2-like isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	24.4	24.4	24.4	9.7438	0.001297	1.9942	5891800	3	NODE 18	NODE 18	3746	NODE 1827 length 13179 cov 670.779717 False 4036 RIMS-binding protein 2-like isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	40.5	40.5	40.5	9.6897	0.000193	3.259	10623000	5	NODE 18	NODE 18	3747	NODE_1827_length_13179_cov_670.779717_False_4306 RIMS-binding protein 2-like isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	27.9	27.9	27.9	21.404	0	4.0599	43838000	12	NODE 18	NODE 18	3748	NODE 1827 length 13179 cov 670.779717 False 4947 RIMS-binding protein 2-like isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	5.2	5.2	5.2	62.99	0.000193	3.2512	26636000	6	NODE 18	NODE 18	3749	NODE_1827_length_13179_cov_670.779717_False_8252 RIMS-binding protein 2-like protein
22387000	27055000	17914000	17578000	16885000	18703000	21801000	26206000	24610000	29219000	21648000	21276000	15156000	11073000	18848000	22404000	15473000	19211000	8	8	8	38.7	38.7	38.7	28.124	0	41.479	911910000	81	NODE 18	NODE 18	3750	NODE 18288 length 886 cov 755.425993 False 769 CD109 antigen-like
1.46E+08	1.08E+08	0	0	0	0	0	84331000	0	87297000	64826000	0	0	0	0	86850000	0	1.02E+08	1	1	1	40.7	40.7	40.7	5.8546	0	5.6779	1209100000	49	NODE 18	NODE 18	3751	NODE 18288 length 886 cov 755.425993 False 885 CD109 antigen-like protein
0	43196000	32694000	19682000	25614000	21406000	31765000	86295000	33353000	1.08E+08	50415000	56362000	37726000	37097000	65481000	50365000	63483000	64156000	5	5	5	38.3	38.3	38.3	21.009	0	25.894	1366500000	82	NODE 18	NODE 18	3752	NODE 18289 length 886 cov 698.838748 False 565 Golgi-associated plant pathogenesis-related protein 1-like
18787000	24915000	10962000	9961700	14469000	7136500	0	0	0	0	0	11692000	5549100	5538000	7614500	0	0	20247000	5	5	5	21.5	21.5	21.5	39.24	0	12.587	284060000	45	NODE 18	NODE 18	3753	NODE 183 length 55000 cov 684.955319 True 50798 cytochrome P450 3A11-like
0	889690	0	0	0	0	0	864960	0	0	0	0	0	0	0	2322800	0	2544700	3	3	3	24.6	24.6	24.6	12.643	0	22.151	20611000	16	NODE 18	NODE 18	3754	NODE 1830 length 13153 cov 704.077493 False 6818 hypothetical protein BLA29 005011
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	17.4	17.4	17.4	29.495	0	6.0548	32305000	9	NODE 18	NODE 18	3755	NODE 1830 length 13153 cov 704.077493 False 7647 hypothetical protein BLA29 005011
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	19.7	19.7	19.7	29.455	0	5.412	66633000	15	NODE 18	NODE 18	3756	NODE_1830_length_13153_cov_704.077493_False_8257 uncharacterized protein LOC113791953
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	50.6	50.6	50.6	9.2392	0.000188	3.0621	17611000	5	NODE 18	NODE 18	3757	NODE 18342 length 884 cov 726.051870 False 730 DFP2-like protein
1.62E+08	1.75E+08	81798000	90769000	69819000	49380000	45675000	45213000	43984000	63563000	35354000	18707000	8196600	6660400	15346000	25571000	15330000	19769000	10	9	9	54.4	43.6	43.6	23.324	0	89.632	3174200000	126	NODE 18	NODE 18	3758	NODE 18362 length 883 cov 1348.349034 False 650 protein lethal(2)essential for life-like
0	0	0	0	0	0	0	0	0	0	0	0	17407000	16298000	40448000	22562000	0	57250000	4	4	4	35.7	35.7	35.7	17.78	0	18.966	282080000	25	NODE 18	NODE 18	3759	NODE 184 length 54995 cov 711.027867 False 10510 serine proteinase 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	19.6	19.6	19.6	6.0827	0.001453	1.9722	214670000	11	NODE 18	NODE 18	3760	NODE 184 length 54995 cov 711.027867 False 12924 serine protease
46668000	53351000	24038000	22867000	16165000	21143000	34345000	46925000	21804000	51516000	30380000	24067000	16467000	18547000	35183000	38016000	0	41958000	6	6	6	35.9	35.9	35.9	20.195	0	202.97	1226900000	85	NODE 18	NODE 18	3761	NODE 184 length 54995 cov 711.027867 False 13470 complement C1s subcomponent-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	23.5	23.5	23.5	7.439	0.000879	2.5356	35424000	7	NODE 18	NODE 18	3762	NODE 184 length 54995 cov 711.027867 False 14417 transmembrane protease serine 9-like
0	0	0	0	0	0	32734000	45185000	25185000	53344000	27580000	18630000	0	0	13540000	0	0	0	3	3	3	20	20	20	20.459	0	6.4766	473960000	24	NODE 18	NODE 18	3763	NODE_184_length_54995_cov_711.027867_False_14995 serine protease-like protein 3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	14.5	14.5	14.5	17.519	0.00434	1.7061	4705700	2	NODE 18	NODE 18	3764	NODE 184 length 54995 cov 711.027867 False 16288 trypsin precursor
63532000	84514000	40057000	43471000	37410000	35183000	63259000	69499000	70991000	79577000	53435000	52715000	30080000	26695000	71558000	81167000	83805000	68310000	9	9	8	58.5	58.5	49.1	17.534	0	44.125	1774600000	143	NODE 18	NODE 18	3765	NODE 184 length 54995 cov 711.027867 True 35458 thioredoxin, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	9.5	9.5	9.5	41.595	0.001175	2.2114	5614900	1	NODE 18	NODE 18	3766	NODE 1842 length 13099 cov 778.891981 True 10633 beta-galactosidase-1-like protein 2
0	0	3795400	4938000	0	5007500	0	0	0	0	0	0	0	0	0	0	0	0	4	3	3	13.6	10	10	38.686	0	3.6802	33865000	11	NODE 18	NODE 18	3767	NODE 1842 length 13099 cov 778.891981 True 11740 beta-galactosidase-1-like protein 2
0	0	0	0	19640000	0	83195000	1.52E+08	1.4E+08	1.23E+08	1.08E+08	51346000	0	0	87024000	0	1.07E+08	2.34E+08	3	1	1	48.3	25.3	25.3	9.6992	0	83.632	1603200000	38	NODE 18	NODE 18	3768	NODE 1843 length 13096 cov 731.197378 True 8617 enoyl-CoA hydratase domain-containing protein 3, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	11.5	11.5	11.5	12.485	0.003734	1.7378	29350000	6	NODE 18	NODE 18	3769	NODE 18442 length 879 cov 677.490291 False 404 probable proline--tRNA ligase, mitochondrial
17104000	18253000	0	0	0	0	8289600	0	0	0	0	0	0	0	8168900	0	0	0	2	2	2	23	23	23	12.042	0	5.018	149850000	22	NODE 18	NODE 18	3770	NODE_18442_length_879_cov_677.490291_False_687 probable proline--tRNA ligase, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	16.2	16.2	16.2	9.0814	0.001319	2.0893	1066900	1	NODE 18	NODE 18	3771	NODE 18444 length 879 cov 490.010922 False 595 nicotinamide riboside kinase 2-like;NODE 7786 length 2516 cov 664.726534 False 598 Nicotinamide riboside kinase 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	17.6	17.6	17.6	17.049	0	4.6567	8980900	8	NODE 18	NODE 18	3772	NODE 1846 length 13066 cov 725.461464 True 3125 globin D, coelomic
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	24.4	24.4	24.4	8.9202	0.003285	1.7689	39029000	6	NODE 18	NODE 18	3773	NODE 1847 length 13057 cov 712.461544 True 11276 triokinase/FMN cyclase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	23.4	23.4	23.4	21.834	0	9.8091	23672000	9	NODE 18	NODE 18	3774	NODE 1847 length 13057 cov 712.461544 True 11559 triokinase/FMN cyclase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	29.4	29.4	29.4	22.839	0	9.2269	288080000	17	NODE 18	NODE 18	3775	NODE 1847 length 13057 cov 712.461544 True 12238 dihydroxyacetone kinase
0	0	0	0	0	14133000	0	0	0	0	0	12853000	0	0	0	0	0	0	3	3	3	38.8	38.8	38.8	11.448	0	4.7299	324360000	24	NODE 18	NODE 18	3776	NODE 1852 length 13033 cov 712.880105 False 677 microtubule-associated proteins 1A/1B light chain 3A
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	1	35.5	6.5	6.5	17.612	0.006234	1.5605	10033000	4	NODE 18	NODE 18	3777	NODE 1854 length 13017 cov 722.139948 True 10936 adenylate kinase 2, mitochondrial isoform X1
1.31E+08	1.5E+08	69165000	78929000	65821000	68549000	1.27E+08	1.29E+08	1.45E+08	1.64E+08	1.11E+08	1.1E+08	87479000	46307000	1.29E+08	1.74E+08	1.15E+08	1.91E+08	6	6	2	92.5	92.5	34.3	7.1422	0	53.263	5269100000	181	NODE 18	NODE 18	3778	NODE 18567 length 874 cov 507.141636 True 2 SDR family oxidoreductase
0	0	8339600	6282000	5907200	6141900	0	0	0	0	0	0	9727600	0	0	0	0	0	7	7	1	17.3	17.3	4.6	55.678	0	11.329	125320000	30	NODE 18	NODE 18	3779	NODE_1859_length_12965_cov_701.716189_False_5910 intersectin-1 isoform X1
5986800	10027000	4034000	0	7368500	4845700	4839500	9221500	5308800	0	6881700	5164400	0	10260000	3673600	12241000	6647900	9732600	3	3	3	47.5	47.5	47.5	12.921	0	11.231	198030000	43	NODE 18	NODE 18	3780	NODE 1859 length 12965 cov 701.716189 False 6656 intersectin-1 isoform X1
0	0	20045000	0	0	0	0	0	0	0	0	0	12955000	0	0	0	0	0	4	4	4	46.5	46.5	46.5	11.476	0	10.2	69931000	13	NODE 18	NODE 18	3781	NODE 186 length 54725 cov 722.708597 False 4129 mitochondrial import inner membrane translocase subunit Tim9-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	20	20	20	12.059	0	6.2302	21636000	5	NODE 18	NODE 18	3782	NODE 186 length 54725 cov 722.708597 True 10315 probable D-lactate dehydrogenase, mitochondrial
0	5427700	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8344800	0	5	5	5	26.2	26.2	26.2	30.383	0	23.845	107390000	19	NODE 18	NODE 18	3783	NODE 186 length 54725 cov 722.708597 True 12425 probable D-lactate dehydrogenase, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	18	18	18	10.737	0.000714	2.6515	7585700	6	NODE 18	NODE 18	3784	NODE 186 length 54725 cov 722.708597 True 9672 probable D-lactate dehydrogenase, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	16	16	16	17.987	0.00538	1.6391	0	1	NODE 18	NODE 18	3785	NODE 186 length 54725 cov 722.708597 True 9959 probable D-lactate dehydrogenase, mitochondrial
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	20.6	20.6	20.6	16.465	0.007914	1.4459	3434700	2	NODE 18	NODE 18	3786	NODE_18626_length_871_cov_722.453431_True_114 hemicentin-2 isoform X1
0	0	1532600	1133500	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	28.3	28.3	28.3	6.3145	0	3.4978	6293400	6	NODE 18	NODE 18	3787	NODE 18652 length 870 cov 484.710429 False 867 cold and drought-regulated protein CORA-like
0	0	1.11E+08	0	30807000	67841000	0	0	0	0	0	0	1.05E+08	79556000	1.01E+08	1.42E+08	1.17E+08	1.45E+08	9	8	8	71.3	71.3	71.3	12.937	0	80.061	2387800000	74	NODE 18	NODE 18	3788	NODE 1867 length 12928 cov 697.377845 True 9598 endochitinase At2g43620-like
0	0	30428000	21794000	10668000	20374000	0	0	0	0	0	0	87311000	29318000	0	0	0	0	4	4	4	52.7	52.7	52.7	8.7318	0	6.9214	1486000000	39	NODE 18	NODE 18	3789	NODE 1867 length 12928 cov 697.377845 True 9985 chitinase 4-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	21.1	21.1	21.1	17.733	0	5.0591	87350000	17	NODE 18	NODE 18	3790	NODE 1868 length 12928 cov 691.451721 False 5889 neurexin-4-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	12.8	12.8	12.8	20.442	0.008598	1.4021	27075000	5	NODE 18	NODE 18	3791	NODE 1868 length 12928 cov 691.451721 False 6466 neurexin-4-like isoform X2;gi|1048037445|ref|XP 017475495.1| PREDICTED: neurexin-4 isoform X3 [Rhagoletis zephyria];gi|1048037443|ref|XP 017475493.1| PREDICTED: neurexin-4 isoform X2 [Rhagoletis zephyria];gi
9089800	14702000	9693200	8864600	7573700	6891200	4864300	7501200	8311600	5942100	7511500	4575300	5349900	4773900	9267400	8453100	0	7771000	10	10	10	31.3	31.3	31.3	61.015	0	28.898	407380000	83	NODE 18	NODE 18	3792	NODE 1868 length 12928 cov 691.451721 False 8111 neurexin-4-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	14.6	14.6	14.6	10.941	0.000715	2.6627	83147000	12	NODE 18	NODE 18	3793	NODE_1868_length_12928_cov_691.451721_False_9544 neurexin-4 isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	9.3	9.3	9.3	23.483	0	4.7076	140960000	13	NODE 18	NODE 18	3794	NODE 1868 length 12928 cov 691.451721 True 11855 uncharacterized protein LOC113793005
0	0	0	0	0	0	37210000	50872000	39062000	49177000	36661000	35898000	0	0	0	0	0	0	5	5	5	56.9	56.9	56.9	16.696	0	17.979	577440000	51	NODE 18	NODE 18	3795	NODE 1869 length 12928 cov 668.109920 True 8049 Der f 3 allergen
1.19E+08	1.12E+08	45097000	46716000	49106000	54379000	82074000	1.13E+08	88258000	1.08E+08	68016000	78613000	56560000	57686000	92899000	1.27E+08	65910000	1.14E+08	3	3	2	49.2	49.2	34.9	6.5573	0	5.0235	3727100000	81	NODE 18	NODE 18	3796	NODE 1869 length 12928 cov 668.109920 True 8601 trypsin-1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	7.6	7.6	7.6	18.216	0.008859	1.3822	3543500	1	NODE 18	NODE 18	3797	NODE 187 length 54715 cov 652.073582 False 26057 Nicastrin-like Protein
1296000	0	70499000	66412000	10692000	56479000	3474300	10049000	3380300	10238000	0	9293600	2.16E+08	16057000	4954400	5932200	4923800	5868600	9	4	4	51.5	20.9	20.9	18.454	0	19.063	643610000	58	NODE 18	NODE 18	3798	NODE 187 length 54715 cov 652.073582 True 47806 glutathione S-transferase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	28.3	28.3	28.3	10.491	0	17.353	61359000	13	NODE 18	NODE 18	3799	NODE 187 length 54715 cov 652.073582 True 49055 COX assembly mitochondrial protein homolog
23795000	23764000	0	0	0	0	7307800	18718000	0	21154000	0	14362000	0	0	6201200	29695000	20642000	25850000	2	2	2	83.8	83.8	83.8	7.918	0	71.571	362510000	51	NODE 18	NODE 18	3800	NODE 1870 length 12917 cov 905.713575 False 4586 C-factor
64655000	53599000	29180000	31738000	21653000	20279000	34069000	40703000	38798000	50291000	35668000	32321000	20275000	7860600	33572000	43154000	32932000	38951000	8	8	8	61.8	61.8	61.8	22.961	0	215.14	1672700000	157	NODE 18	NODE 18	3801	NODE 1870 length 12917 cov 905.713575 False 5215 short chain dehydrogenase/reductase family oxidoreductase-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	23.8	23.8	23.8	7.1531	0.000187	2.9979	9040300	2	NODE 18	NODE 18	3802	NODE_1871_length_12915_cov_956.452488_True_3808 uncharacterized isomerase BH0283-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	17.3	17.3	17.3	31.406	0	5.7805	14940000	10	NODE 18	NODE 18	3803	NODE 1871 length 12915 cov 956.452488 True 4053 phenazine biosynthesis-like domain-containing protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	21.4	21.4	21.4	17.745	0	4.5347	43576000	7	NODE 18	NODE 18	3804	NODE 1872 length 12915 cov 719.707076 True 2591 Putative phosphoenolpyruvate synthase
0	0	7240400	4778100	2880600	4515700	0	0	0	0	0	0	0	4578700	0	0	0	0	9	9	9	13.7	13.7	13.7	116.8	0	27.276	129600000	34	NODE 18	NODE 18	3805	NODE 1872 length 12915 cov 719.707076 False 5720 putative phosphoenolpyruvate synthase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	40	1	1	61.2	1.2	1.2	99.296	0.001452	1.9649	2174400	4	NODE 18	NODE 18	3806	NODE 1873 length 12910 cov 649.430338 True 7611 twitchin
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	4	12.9	12.9	12.9	55.797	0	5.746	22831000	9	NODE 18	NODE 18	3807	NODE 1877 length 12893 cov 719.785792 True 1482 glutamate-rich WD repeat-containing protein 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	22.7	22.7	22.7	16.812	0.000707	2.5694	7026500	2	NODE 18	NODE 18	3808	NODE 188 length 54608 cov 694.950397 True 11269 zwei Ig domain protein zig-4-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	18.1	18.1	18.1	34.532	0	7.8246	76224000	9	NODE 18	NODE 18	3809	NODE_1881_length_12881_cov_830.112194_True_2 protein diaphanous isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	35.3	35.3	35.3	7.387	0.000872	2.4915	0	1	NODE 18	NODE 18	3810	NODE 1881 length 12881 cov 830.112194 True 3373 protein diaphanous-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.1	4.1	4.1	34.929	0	12.568	16634000	6	NODE 18	NODE 18	3811	NODE 1881 length 12881 cov 830.112194 True 996 protein diaphanous homolog 2 isoform X4
18323000	9323400	23348000	15565000	6934700	0	27233000	5499600	16902000	9544600	17566000	20233000	0	0	12971000	13929000	36221000	8658400	6	6	6	38.4	38.4	38.4	28.594	0	78.592	305410000	44	NODE 18	NODE 18	3812	NODE 1883 length 12853 cov 723.813643 False 8331 perilipin-like protein
0	0	15378000	14650000	6984700	9834100	0	0	0	0	0	0	5397900	1816400	0	0	0	0	4	4	4	56.8	56.8	56.8	9.4357	0	9.1352	126570000	25	NODE 18	NODE 18	3813	NODE 1883 length 12853 cov 723.813643 False 8622 lipid storage droplets surface-binding protein 2
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	56	56	56	11.281	0	9.7192	35977000	5	NODE 18	NODE 18	3814	NODE 1885 length 12834 cov 726.796932 True 4565 DFP2-like protein
0	0	0	15881000	0	0	0	0	0	0	0	0	12861000	13847000	0	0	0	0	3	3	3	50	50	50	10.328	0	9.5651	464690000	27	NODE 18	NODE 18	3815	NODE 189 length 54584 cov 705.686204 True 11292 quinone oxidoreductase-like protein
0	9684700	5081800	0	0	0	7703900	9035400	8215200	10631000	11647000	11226000	0	0	9806500	0	10143000	13133000	3	3	3	17.4	17.4	17.4	34.234	0	10.849	193920000	34	NODE 18	NODE 18	3816	NODE_189_length_54584_cov_705.686204_True_11579 prostaglandin reductase 3
0	8973000	0	0	0	0	8434100	11067000	12466000	12205000	0	0	0	0	0	0	0	9956700	3	3	3	15	15	15	24.281	0	4.0896	167350000	27	NODE 18	NODE 18	3817	NODE 189 length 54584 cov 705.686204 True 20234 probable lysosomal cobalamin transporter
5.13E+08	4.6E+08	1.1E+08	66771000	50604000	65766000	2.76E+08	3.98E+08	5.02E+08	2.33E+08	4.1E+08	1.95E+08	91296000	43169000	1.76E+08	3.3E+08	2.03E+08	2.49E+08	5	3	3	30.1	30.1	30.1	12.936	0	148.06	6538700000	171	NODE 18	NODE 18	3818	NODE 1891 length 12805 cov 683.053255 False 405 myosin heavy chain, muscle
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	13.3	13.3	13.3	10.155	0.000188	3.0447	61154000	6	NODE 18	NODE 18	3819	NODE 18930 length 857 cov 618.965087 False 634 cuticle protein 14-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	19	19	19	9.3417	0.00374	1.7441	5536700	2	NODE 19	NODE 19	3820	NODE 19 length 134792 cov 730.024166 False 25128 sister chromatid cohesion protein PDS5 homolog B
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	13.7	13.7	13.7	16.918	0.001011	2.24	8680100	2	NODE 19	NODE 19	3821	NODE 19 length 134792 cov 730.024166 False 38388 ATP synthase subunit C lysine N-methyltransferase
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	15.3	15.3	15.3	8.3927	0.001301	2.0088	87066000	9	NODE 19	NODE 19	3822	NODE 19 length 134792 cov 730.024166 False 50335 Krueppel homolog 2
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	14.4	14.4	14.4	16.744	0.000185	2.9264	59030000	3	NODE 19	NODE 19	3823	NODE 19 length 134792 cov 730.024166 False 51016 transmembrane protein 33-like isoform X1
13140000	21518000	6575000	7232900	16428000	0	0	7346800	7585900	7758300	0	8603800	0	7393300	10740000	15121000	9607100	16349000	7	7	7	25.7	25.7	25.7	46.732	0	33.57	303080000	44	NODE 19	NODE 19	3824	NODE 19 length 134792 cov 730.024166 False 70151 choline/ethanolamine kinase-like;gi|1048067352|ref|XP 017463773.1| PREDICTED: choline kinase alpha-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	17.9	17.9	17.9	20.707	0	4.8533	60074000	10	NODE 19	NODE 19	3825	NODE_19_length_134792_cov_730.024166_True_107686 nardilysin-like protein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	9.8	9.8	9.8	12.584	0.006225	1.5547	49383000	8	NODE 19	NODE 19	3826	NODE 19 length 134792 cov 730.024166 True 108206 nardilysin-like
31005000	37139000	14584000	10046000	11452000	9505600	11391000	21357000	17873000	20849000	14806000	16413000	8932600	6476700	18878000	34849000	26192000	31207000	21	21	11	36.2	36.2	22.1	91.689	0	89.713	1353900000	201	NODE 19	NODE 19	3827	NODE 19 length 134792 cov 730.024166 True 108549 nardilysin-like
38541000	47323000	16284000	17690000	19662000	17710000	20268000	27359000	26175000	31245000	20676000	13540000	11441000	0	0	0	0	29782000	2	2	2	32.9	32.9	32.9	9.1072	0	7.7066	522000000	37	NODE 19	NODE 19	3828	NODE 19 length 134792 cov 730.024166 True 72168 adipocyte plasma membrane-associated protein-like protein
32091000	33804000	19571000	22219000	16877000	18446000	10970000	21067000	20286000	25105000	17967000	19501000	12716000	12445000	0	24009000	21422000	25034000	13	13	13	46.1	46.1	46.1	47.475	0	144.83	858900000	95	NODE 19	NODE 19	3829	NODE 19 length 134792 cov 730.024166 True 72565 adipocyte plasma membrane-associated protein-like protein
17759000	23752000	29290000	23291000	17593000	19638000	24623000	27636000	32728000	20555000	22102000	16620000	44514000	13172000	28632000	0	17776000	32551000	11	11	11	46.9	46.9	46.9	20.65	0	32.092	791390000	82	NODE 19	NODE 19	3830	NODE 1900 length 12763 cov 730.251810 False 7384 60S ribosomal protein L6
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	14	14	14	14.204	0.006649	1.5208	179850000	12	NODE 19	NODE 19	3831	NODE 1900 length 12763 cov 730.251810 False 7748 60S ribosomal protein L6-like
28937000	27493000	17335000	13955000	11946000	10146000	14746000	25224000	24484000	19423000	19389000	16818000	19166000	15068000	16480000	34011000	21283000	34658000	23	23	23	40.1	40.1	40.1	74.475	0	163.16	1282300000	167	NODE 19	NODE 19	3832	NODE_1900_length_12763_cov_730.251810_True_3530 eukaryotic translation initiation factor 3 subunit C
0	0	0	0	0	0	0	0	0	0	0	0	23164000	10278000	0	0	0	0	3	3	3	12.2	12.2	12.2	21.206	0	14.084	144040000	19	NODE 19	NODE 19	3833	NODE 1900 length 12763 cov 730.251810 True 5437 eukaryotic translation initiation factor 3 subunit C-like
0	0	48958000	0	0	0	0	0	0	0	0	0	20945000	19117000	0	0	0	0	4	4	4	26.2	26.2	26.2	20.976	0	7.9535	302130000	34	NODE 19	NODE 19	3834	NODE 1900 length 12763 cov 730.251810 True 5951 eukaryotic translation initiation factor 3 subunit C isoform X1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	20.7	20.7	20.7	6.8427	0	4.2035	3089700	2	NODE 65	NODE 65	3835	NODE 65150 length 303 cov 319.923387 False 175 related to endothelial zinc finger protein induced by tumor necrosis factor alpha;NODE 19010 length 854 cov 513.105131 False 767 gastrula zinc finger protein XlCGF7.1-like isoform X3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	4.3	4.3	4.3	120.64	0.001026	2.3434	4371500	2	NODE 19	NODE 19	3836	NODE 1902 length 12758 cov 709.795481 False 12296 protein still life, isoform SIF type 1 isoform X2;gi|1048043363|ref|XP 017493072.1| PREDICTED: G-box-binding factor [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.4	4.4	4.4	40.828	0	3.7835	2988100	3	NODE 19	NODE 19	3837	NODE 1902 length 12758 cov 709.795481 False 7912 Protein still life, isoforms C/SIF type 2
0	0	17434000	19597000	15352000	18111000	0	0	0	0	0	0	15998000	0	0	0	29589000	0	3	2	2	41.5	24.6	24.6	16.517	0	43.887	491880000	36	NODE 19	NODE 19	3838	NODE 1903 length 12754 cov 714.913851 True 3442 lysosomal acid phosphatase-like protein 3
2082700	1652100	0	0	0	0	0	2166800	0	0	1952200	0	0	0	0	0	0	0	3	3	3	3.6	3.6	3.6	165.99	0	7.1103	39946000	22	NODE 19	NODE 19	3839	NODE_1905_length_12749_cov_702.697574_True_2 titin-like isoform X1
0	0	0	0	0	0	0	0	5091000	0	4755100	0	0	0	0	0	0	0	5	5	5	4.4	4.4	4.4	186.18	0	10.544	62013000	20	NODE 19	NODE 19	3840	NODE 1905 length 12749 cov 702.697574 True 4794 titin-like isoform X2
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	8.9	8.9	8.9	12.684	0.00991	1.3129	0	4	NODE 19	NODE 19	3841	NODE 1906 length 12749 cov 491.330314 True 11117 serine/threonine-protein phosphatase CPPED1-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	6115500	11240000	0	0	2	2	2	3.4	3.4	3.4	75.029	0	3.6452	56110000	10	NODE 19	NODE 19	3842	NODE 1906 length 12749 cov 491.330314 True 6471 copine-8-like isoform X2;NODE 2596 length 9678 cov 490.836641 False 4502 copine-8-like isoform X3
4.66E+08	8.59E+08	3.29E+08	3.27E+08	2.71E+08	2.09E+08	3.01E+08	4.64E+08	4.41E+08	4.15E+08	3.7E+08	2.16E+08	2E+08	1.6E+08	5.75E+08	6.38E+08	3.71E+08	8.56E+08	5	5	5	84.7	84.7	84.7	10.331	0	126.26	2.0041E+10	194	NODE 19	NODE 19	3843	NODE 1908 length 12741 cov 779.485811 False 4101 C-type lectin lectoxin-Lio1
2.58E+08	3.2E+08	3.65E+08	3.04E+08	2.37E+08	2.66E+08	1.8E+08	2.92E+08	1.89E+08	2.68E+08	2.12E+08	1.72E+08	2.43E+08	1.41E+08	1.88E+08	2.81E+08	1.82E+08	3.1E+08	10	10	10	78.8	78.8	78.8	10.934	0	86.88	1.0382E+10	208	NODE 19	NODE 19	3844	NODE 1908 length 12741 cov 779.485811 False 4432 PREDICTED: uncharacterized protein LOC108378470, partial
5.79E+08	1.28E+09	3.99E+08	4.7E+08	4.03E+08	3.36E+08	3.79E+08	5.13E+08	4.51E+08	4.78E+08	4.16E+08	3.14E+08	3.13E+08	2.52E+08	7.03E+08	9.98E+08	6.42E+08	1.18E+09	12	12	10	67.4	67.4	63.4	19.55	0	174.06	2.6684E+10	370	NODE 19	NODE 19	3845	NODE 1908 length 12741 cov 779.485811 False 4990 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	9.3	9.3	9.3	29.276	0.000196	3.3601	89312000	10	NODE 19	NODE 19	3846	NODE_191_length_54244_cov_736.966248_False_4549 diacylglycerol O-acyltransferase 1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	12.9	12.9	12.9	32.17	0	5.0485	106660000	11	NODE 19	NODE 19	3847	NODE 191 length 54244 cov 736.966248 False 8218 diacylglycerol O-acyltransferase 1
26817000	28788000	11371000	27808000	28641000	27955000	0	0	0	0	0	0	16965000	20467000	42905000	47574000	34319000	52897000	2	2	2	41.7	41.7	41.7	11.21	0	43.312	765710000	70	NODE 19	NODE 19	3848	NODE_191_length_54244_cov_736.966248_True_12443 vesicle-associated membrane protein-associated protein B/C
207720	290010	9286700	6072300	0	3210100	0	0	0	0	0	0	3720200	0	248650	0	0	0	1	1	1	26.6	26.6	26.6	7.2069	0	3.6656	45454000	27	NODE 19	NODE 19	3849	NODE 1916 length 12677 cov 708.853351 False 10952 cathepsin L1-like
2.56E+08	2.58E+08	1.36E+08	1.16E+08	84477000	83597000	1.38E+08	1.65E+08	1.78E+08	1.9E+08	1.37E+08	1.25E+08	43069000	33340000	1.19E+08	1.39E+08	1.04E+08	1.3E+08	4	2	2	40	26.2	26.2	13.758	0	107.52	5962900000	91	NODE 19	NODE 19	3850	NODE 1916 length 12677 cov 708.853351 False 11602 cathepsin L1-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	13.3	13.3	13.3	10.73	0.009232	1.347	0	1	NODE 19	NODE 19	3851	NODE 1916 length 12677 cov 708.853351 True 3034 dentin sialophosphoprotein
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	3.7	3.7	3.7	34.339	0.001315	2.0729	5116100	1	NODE 19	NODE 19	3852	NODE 1916 length 12677 cov 708.853351 True 3576 neurofilament medium polypeptide-like
0	0	7763800	8417600	0	0	0	0	0	11255000	0	0	0	0	0	0	0	0	2	2	2	4.5	4.5	4.5	64.288	0	4.0934	96837000	15	NODE 19	NODE 19	3853	NODE 192 length 54190 cov 710.136197 False 38337 flocculation protein FLO11-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	17.9	17.9	17.9	12.413	0.001012	2.2516	16480000	4	NODE 19	NODE 19	3854	NODE 192 length 54190 cov 710.136197 True 6063 ABC transporter G family member 23-like
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4.7	4.7	4.7	33.91	0.007658	1.4747	5943400	2	NODE 19	NODE 19	3855	NODE_1924_length_12650_cov_713.341088_True_1850 guanylate cyclase soluble subunit alpha-1-like
1.94E+08	2.24E+08	1.08E+08	1.17E+08	1.29E+08	1.25E+08	2.14E+08	2.79E+08	2.54E+08	2.71E+08	2.54E+08	2.34E+08	1.95E+08	1.98E+08	3.21E+08	4.9E+08	3.73E+08	3.89E+08	9	9	9	67.2	67.2	67.2	14.798	0	48.617	1.1123E+10	327	NODE 19	NODE 19	3856	NODE 1929 length 12621 cov 706.734044 True 10924 globin-like protein
25158000	41318000	22152000	22197000	15482000	21373000	0	0	0	25946000	20718000	27959000	16003000	16513000	29314000	55246000	38663000	49514000	4	4	4	31.8	31.8	31.8	21.658	0	15.331	828230000	56	NODE 19	NODE 19	3857	NODE 193 length 54097 cov 711.859572 False 7842 thioredoxin reductase 3 isoform X1



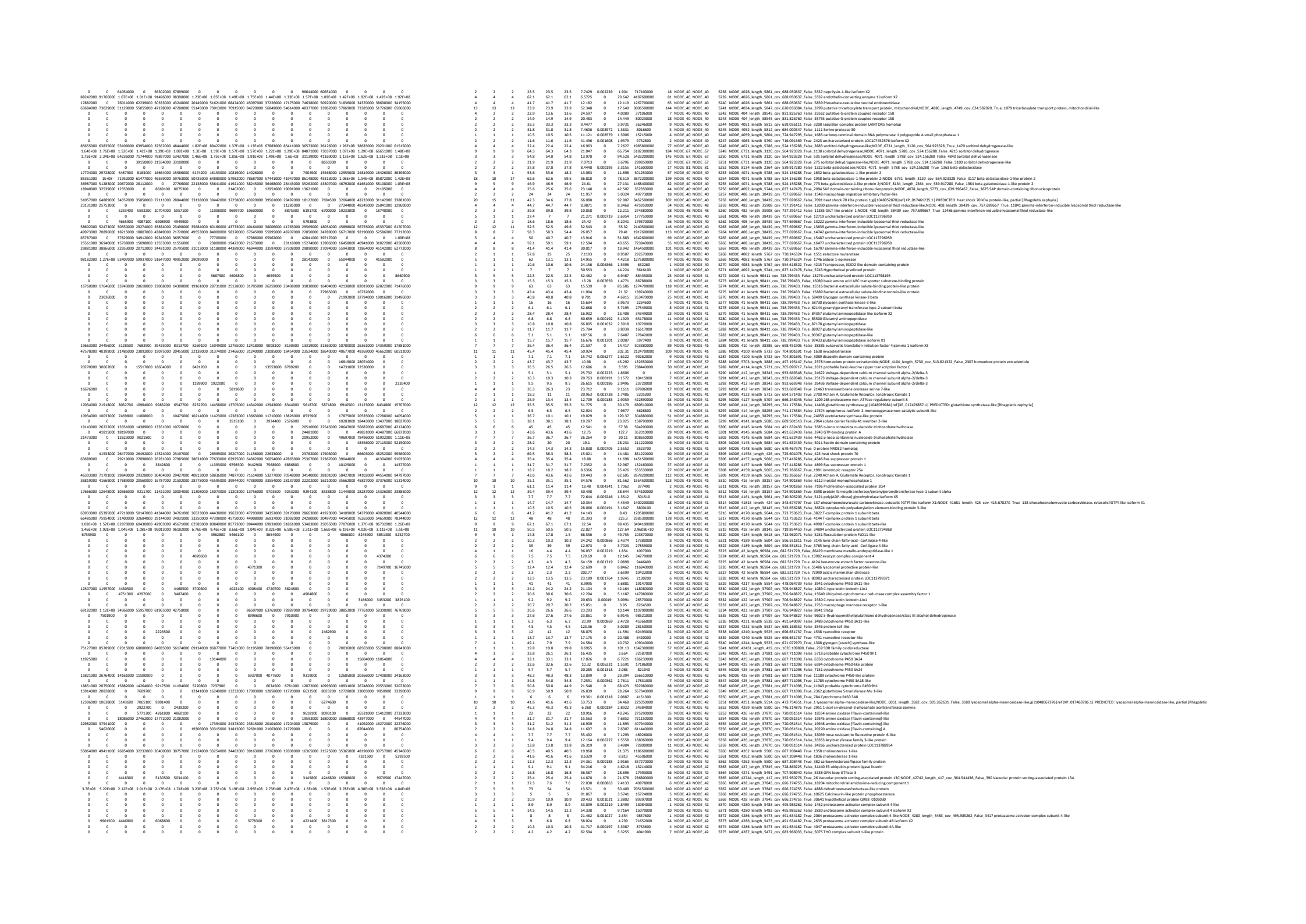


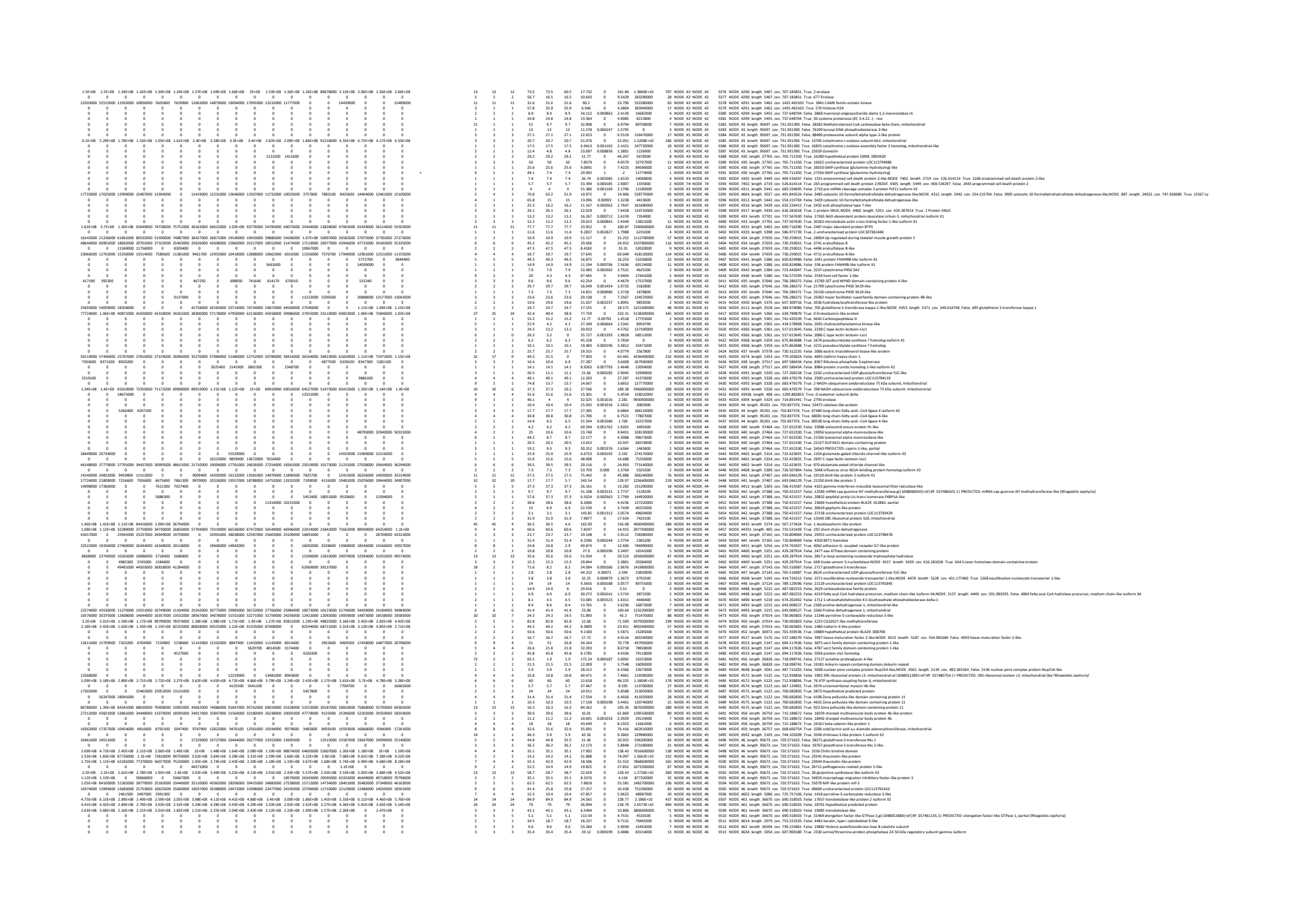


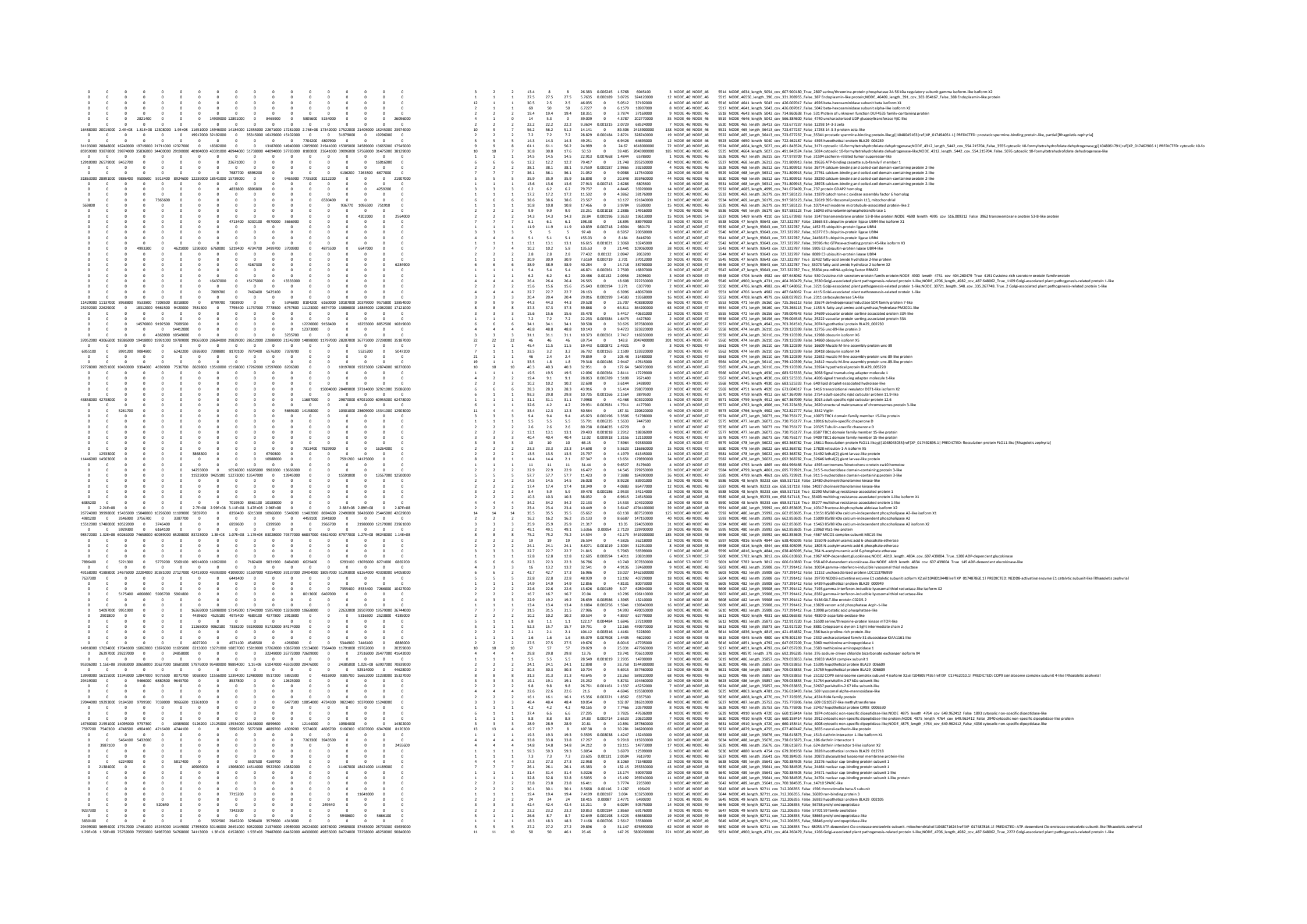


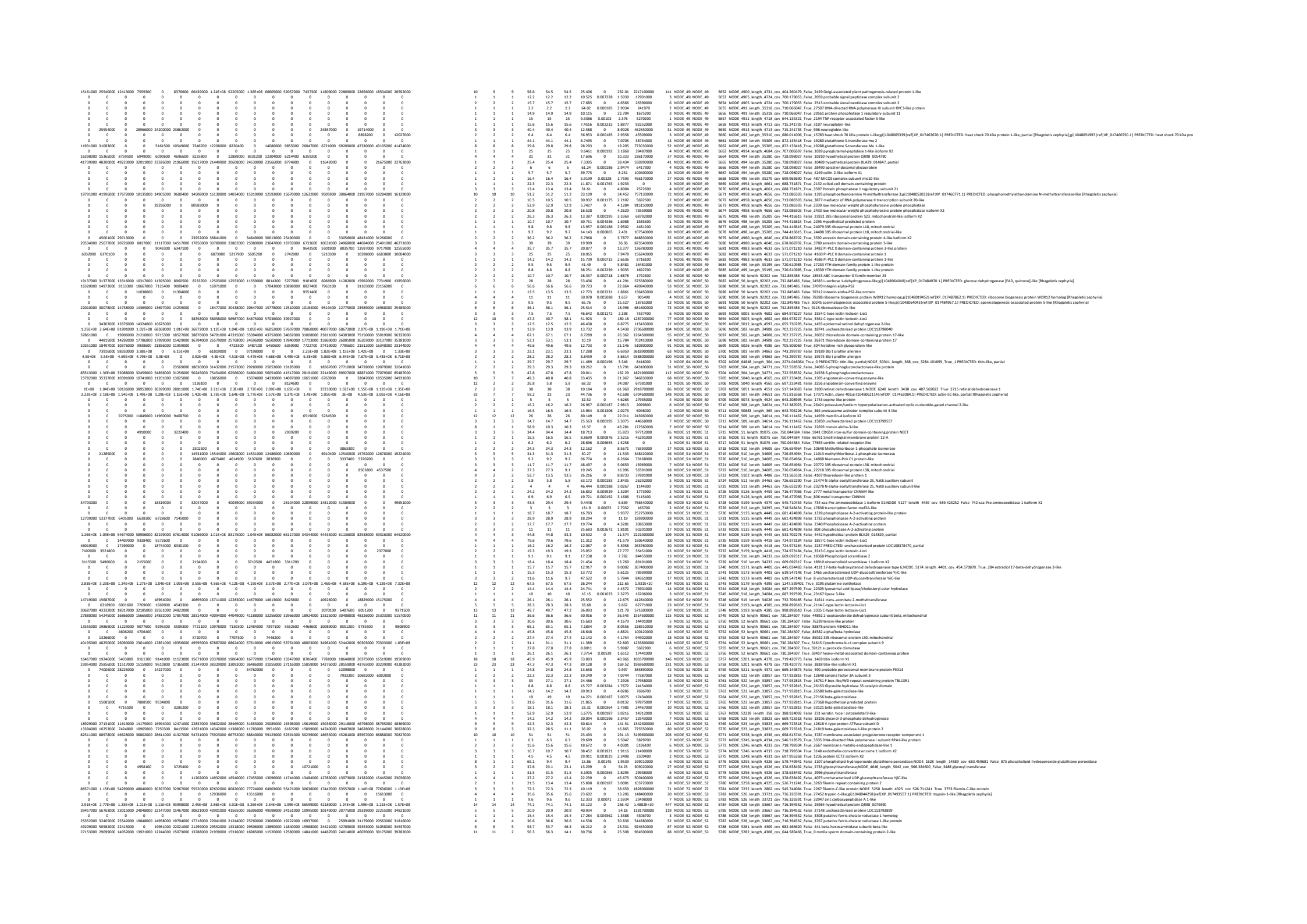


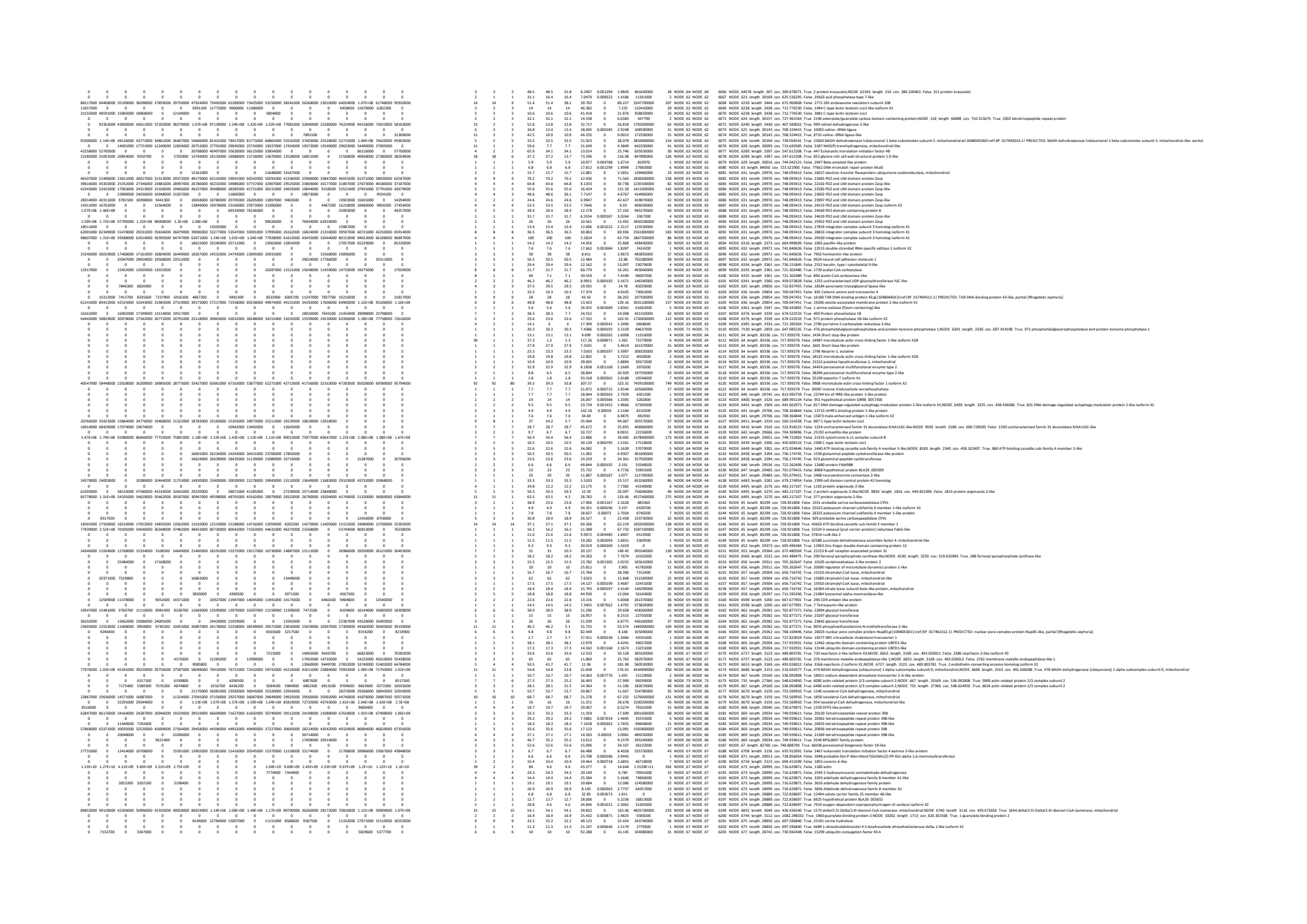


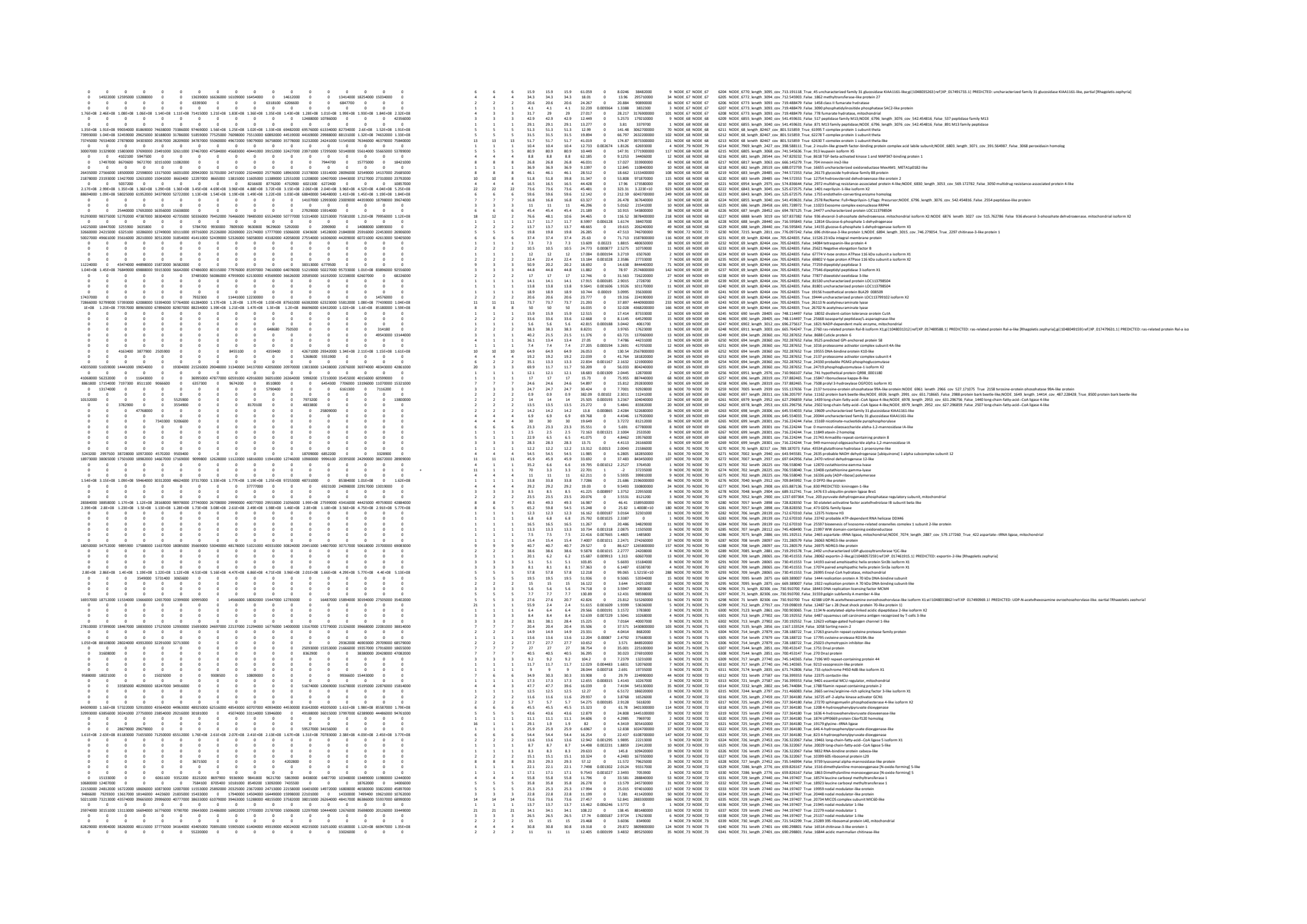


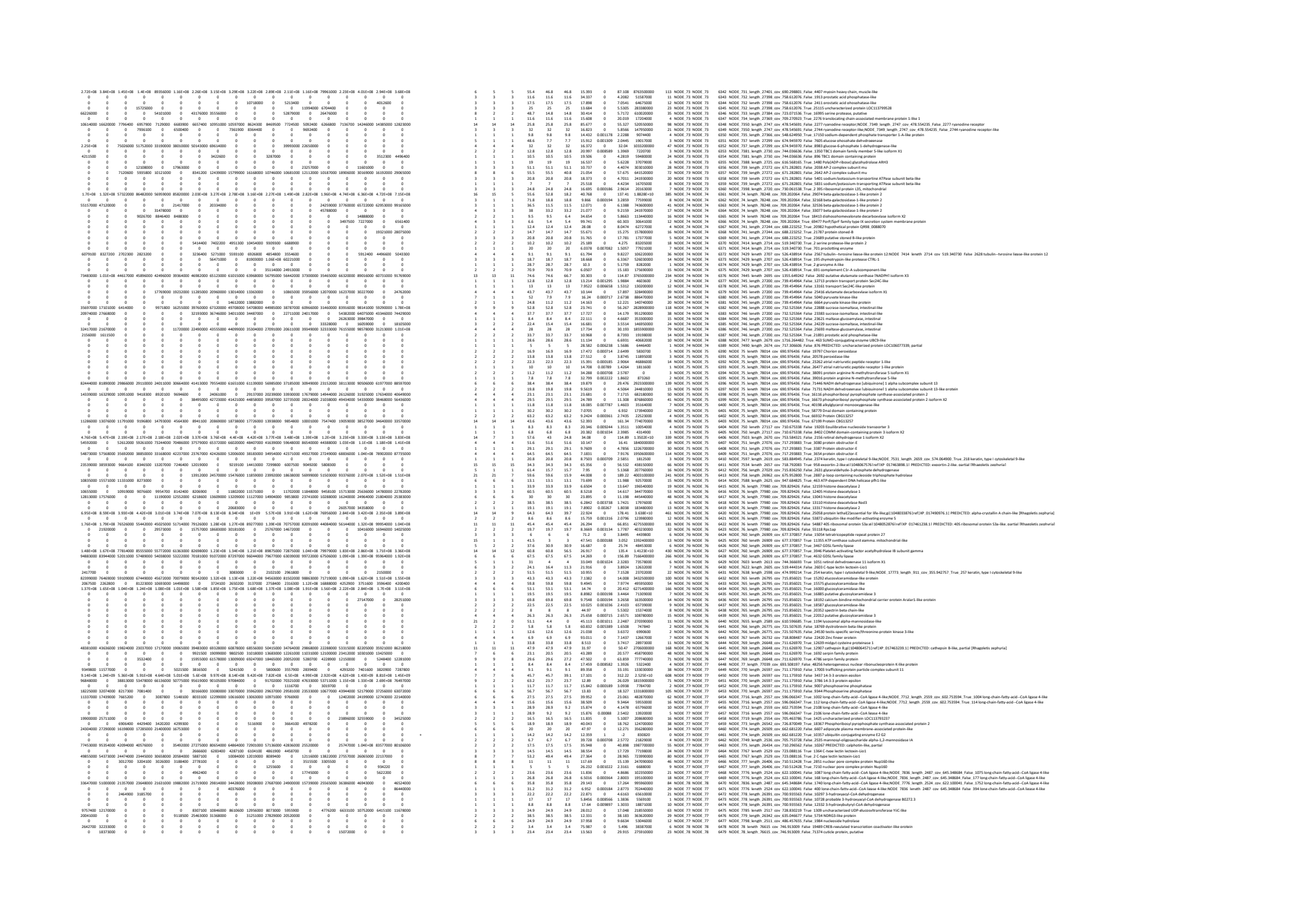


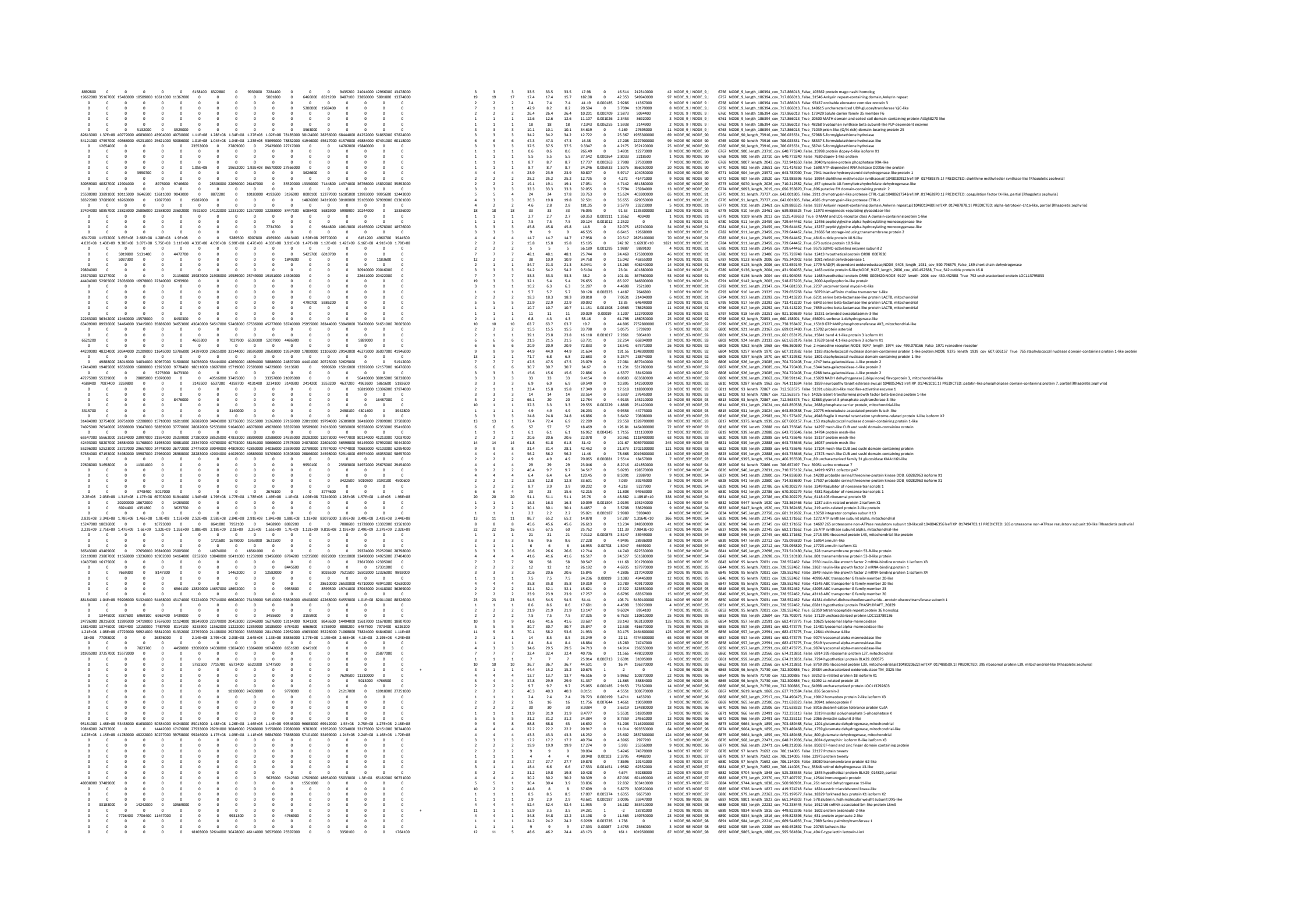


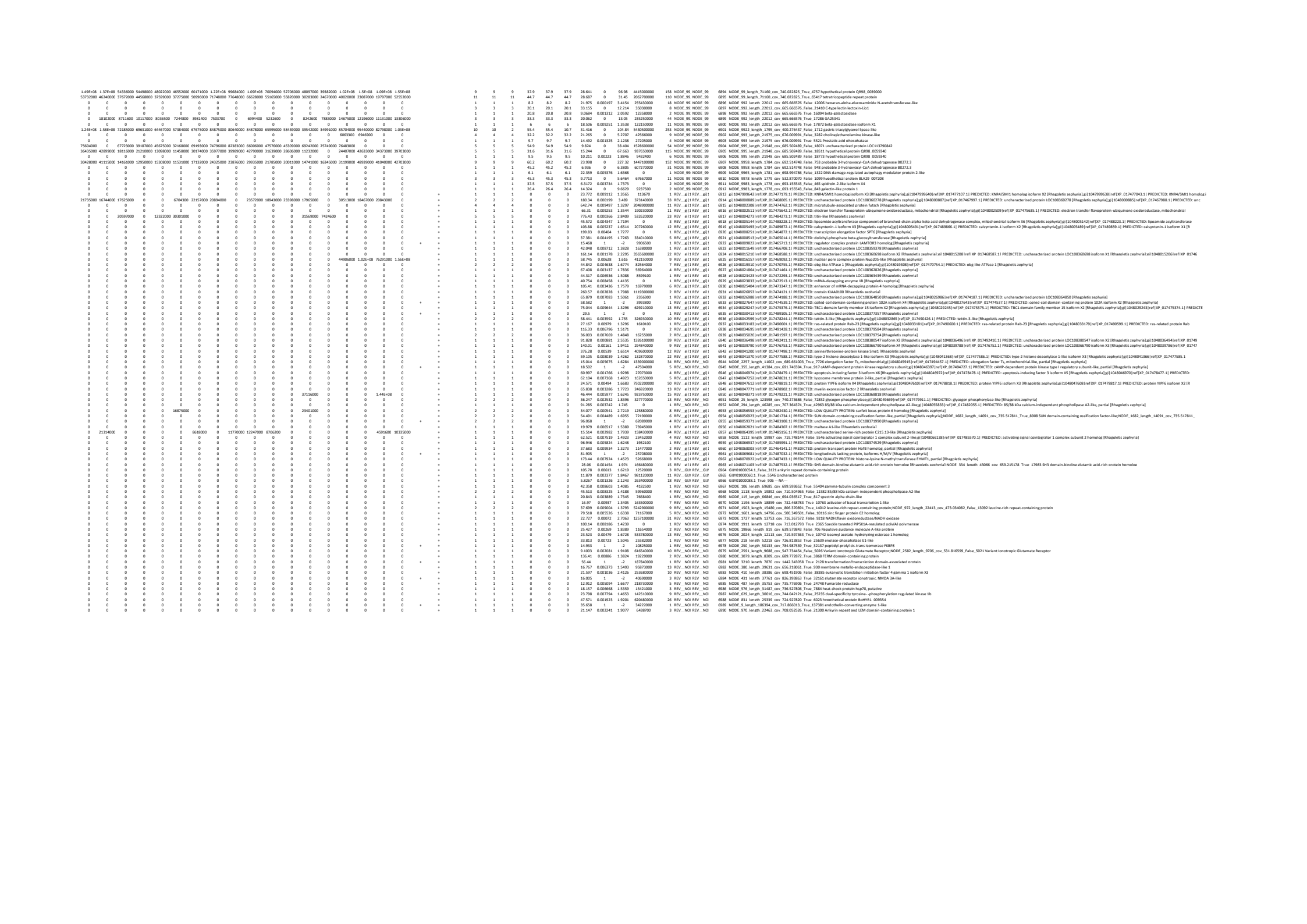




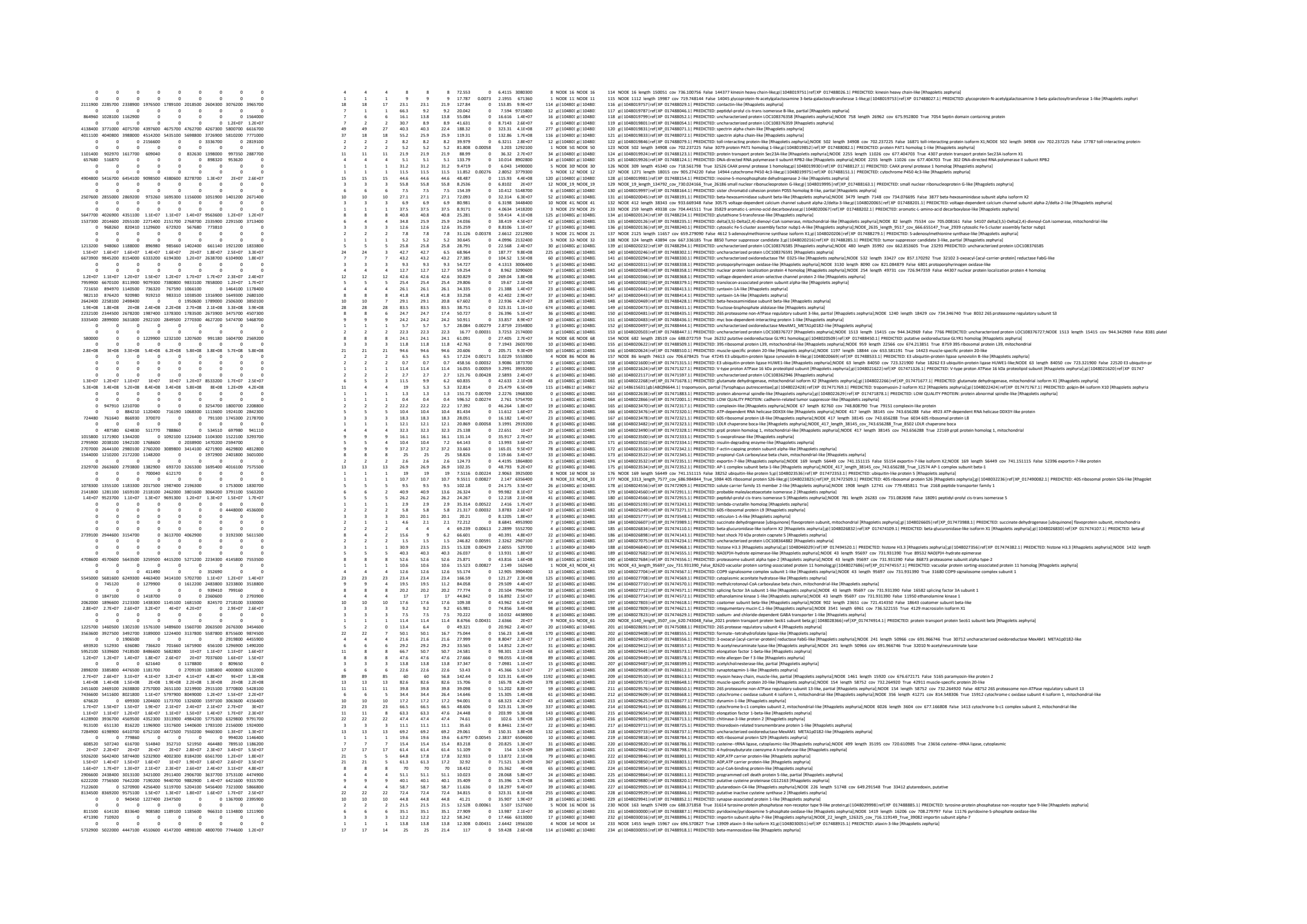


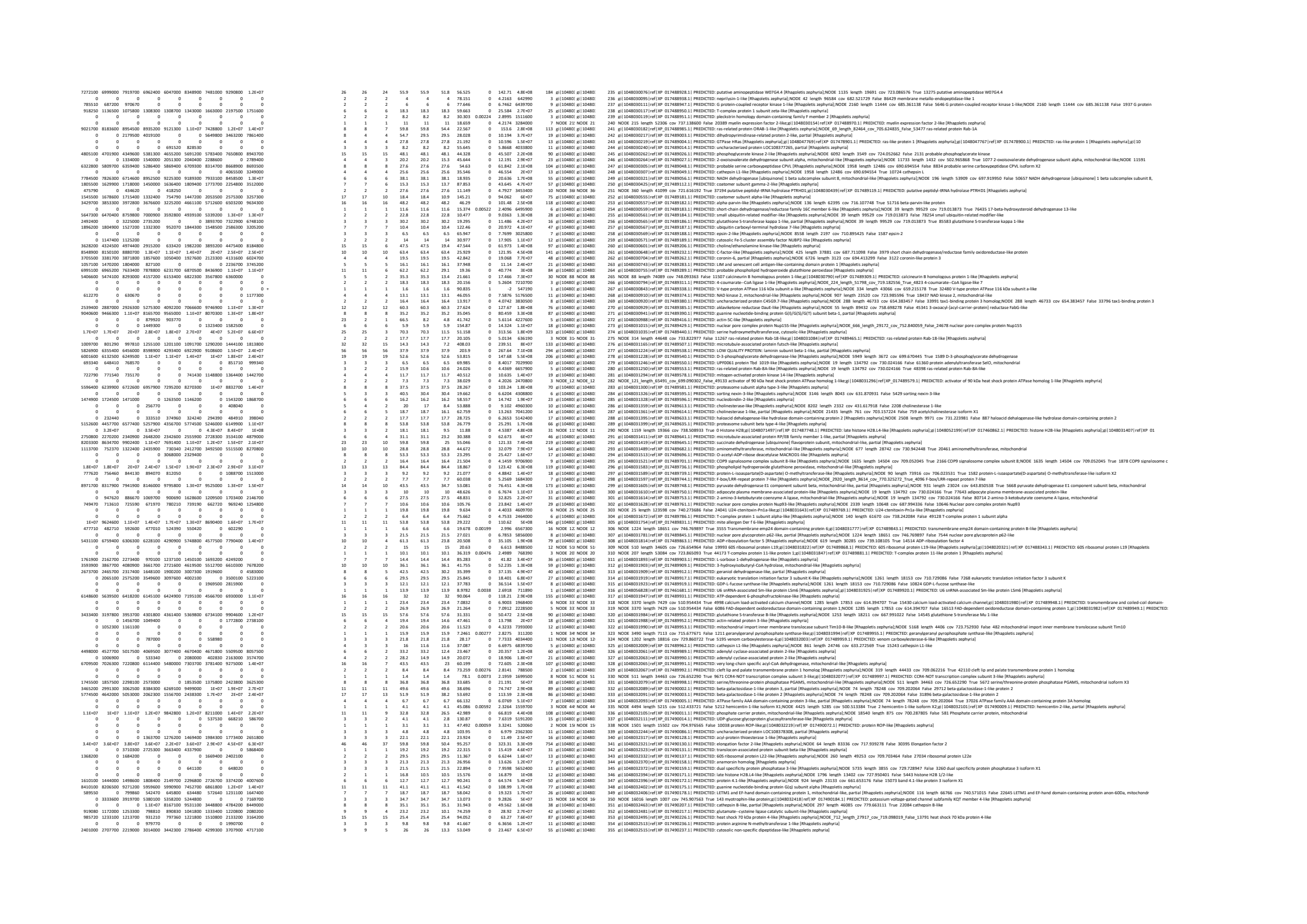




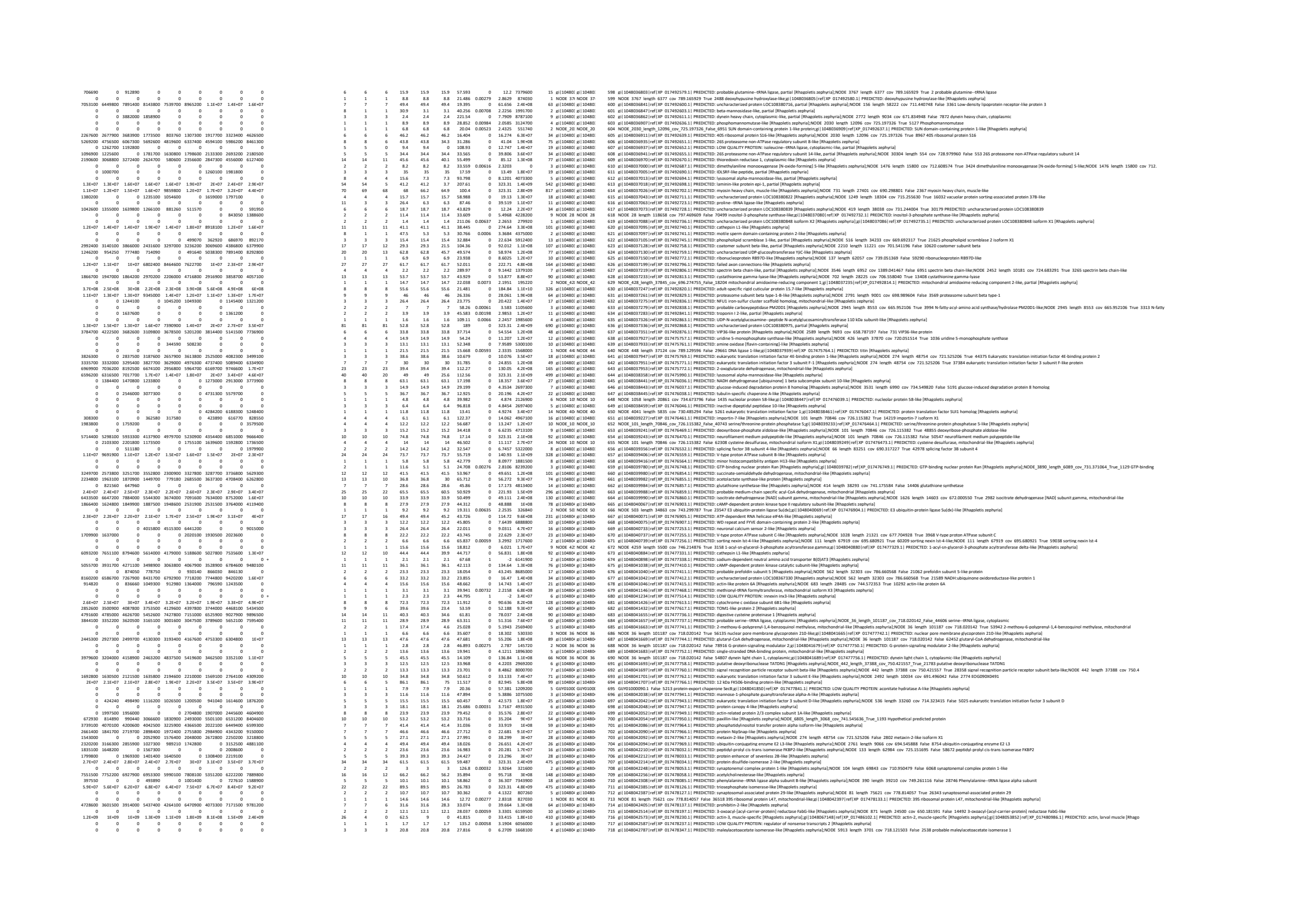


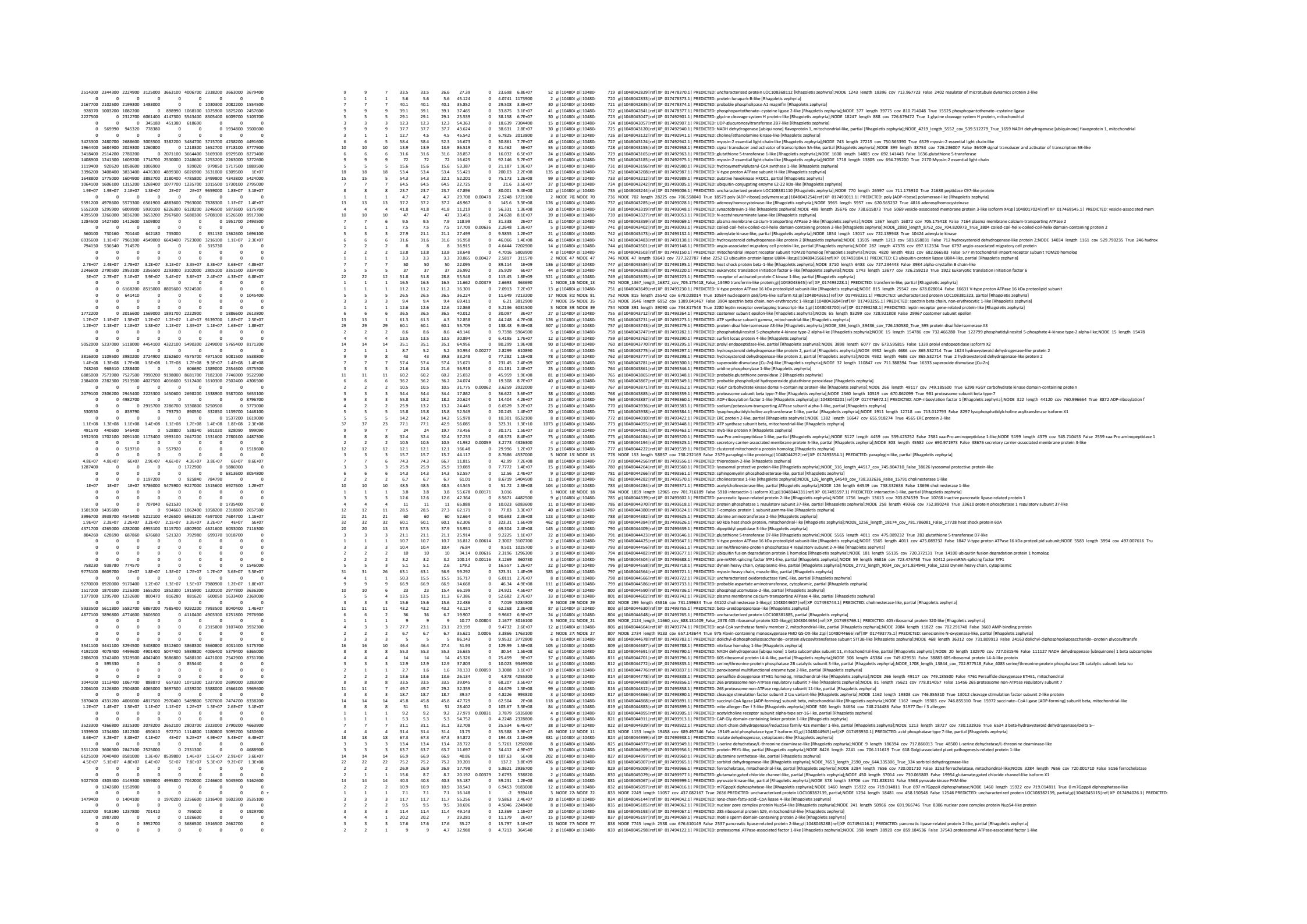
LFQ intensity Dog1	LFQ intensity Dog2	LFQ intensity Dog3	LFQ intensity Kop1	LFQ intensity Kop2	LFQ intensity Kop3	LFQ intensity Phi1	LFQ intensity Phi2	LFQ intensity Phi3	C: Only identified by site	C: Reverse	C: Potential contaminant	N: Peptides	N: Razor + unique peptides	N: Unique peptides	N: Sequence coverage [%]	N: Unique + razor sequence coverage [%]	N: Unique sequence coverage [%]	N: Mol. weight [kDa]	N: Q-value	N: Score	N: Intensity	N: MS/MS count	T: Protein IDs	T: Majority protein IDs	T: id	T: Fasta headers
0	0	0	0	0	0	0	0	0				1	1	1	4.1	4.1	4.1	25.012	0.00522	2.4111	9E+07	15	gi|45221	gi|45221	1723	gi|452215228|gb|AGG10560.1| Tyr p 8 allergen [Tyrophagus putrescentiae];gi|1679377507|sp|M1RIR6.1|GSTM TYRPU RecName: Full=Glutathione S-transferase;AltName: Full=GST class-mu;AltName: Allergen=Tyr p 8
0	0	0	0	0	0	0	0	0	+		+	10	1	1	12.9	1.8	1.8	63.165	1	-2	1176100	1	CON EN	CON EN	0	
6.2E+09	9.5E+09	7.5E+09	1.2E+09	4.8E+09	5.8E+09	9.2E+08	2.3E+09	1.9E+10			+	5	5	5	31.6	31.6	31.6	24.409	0	56.785	5.9E+10	851	CON P0	CON P0	1	
1.2E+07	2.6E+07	2.5E+07	2.1E+07	2.6E+07	9.3E+07	9319100	3.4E+07	9236300			+	37	22	8	71.4	49.2	27.1	51.621	0	323.31	1.6E+09	411	CON P0	CON P0	2	
0	0	0	0	0	0	0	0	0			+	11	2	2	19.6	8.8	8.8	57.769	0	4.1902	2597100	7	CON P0	CON P0	3	
0	3396500	0	7384900	7087100	5.2E+07	0	6671100	0			+	39	3	3	54.6	6.2	6.2	60.044	0	7.8252	1.3E+08	18	CON P0	CON P0	4	
0	0	2418900	2032700	0	0	0	0	0			+	1	1	1	9.5	9.5	9.5	22.975	0.00032	3.9054	6825400	7	CON P0	CON P0	5	
0	0	2328400	3002700	0	2027700	0	2691500	0			+	1	1	1	9.1	9.1	9.1	23.583	0.00032	3.8802	1.7E+07	15	CON P0	CON P0	6	
0	0	562280	496610	362810	0	0	0	0			+	1	1	1	10.7	10.7	10.7	18.974	0	5.1621	2577300	5	CON P0	CON P0	7	
0	1651200	1253900	865910	0	0	0	2283600	0			+	3	3	3	27.8	27.8	27.8	18.281	0	8.8832	1E+07	12	CON P0	CON P0	8	
0	908100	3871400	1141900	0	0	0	1933500	1146400			+	13	11	11	27.4	25	25	69.366	0	28.276	3.1E+07	31	CON P0	CON P0	9	
3041700	2284000	1526600	1.5E+07	6597100	2086600	1826900	1142300	0			+	25	25	23	50.4	50.4	47.9	69.293	0	91.029	1.4E+08	111	CON P0	CON P0	10	
1E+07	2E+07	1.6E+07	2.7E+07	3.3E+07	2.2E+08	7252600	2.9E+07	8137500			+	40	28	1	54.6	43.1	3	59.998	0	232.27	2.3E+09	303	CON P04	CON P04	11	
3.9E+08	6.5E+08	7.8E+08	6.7E+08	7.1E+08	8.9E+08	1.9E+08	7.9E+08	3.9E+08			+	41	37	31	58.5	57.9	50.6	66.017	0	323.31	3E+10	1857	CON P04	CON P04	12	
0	0	0	0	0	0	0	0	0			+	12	2	2	24.8	6.5	6.5	44.091	0.00171	3.0103	2330000	4	CON P08	CON P08	13	
7106500	2E+07	1.9E+07	2.9E+07	3.5E+07	3E+08	7045100	3.1E+07	6730400			+	37	33	16	73.4	68.1	41.2	51.267	0	323.31	2.8E+09	414	CON P08	CON P08	14	
0	0	0	0	0	0	0	0	0			+	1	1	1	3	3	3	59.733	0	4.9323	1082900	1	CON P09	CON P09	15	
2.3E+08	4.3E+08	4E+08	3.8E+08	5.6E+08	4.2E+08	1.2E+08	5.6E+08	1.4E+08			+	41	41	30	59.7	59.7	50.3	59.51	0	323.31	3.1E+10	2063	CON P1	CON P1	16	
1217400	0	0	8088300	0	0	0	910060	3405100			+	16	11	2	41.7	34.1	7.6	49.586	0	42.762	5E+07	28	CON P1	CON P1	17	
1.2E+07	2.3E+07	3E+07	2.3E+07	2.7E+07	3.9E+07	6098900	2.7E+07	1.3E+07			+	37	19	7	52.4	36.9	12.7	62.378	0	113.17	1.1E+09	306	CON P1	CON P1	18	
4E+07	0	0	4.4E+07	0	0	0	0	7.7E+07			+	11	9	7	28.1	25.4	21.5	63.91	0	44.163	1.8E+08	22	CON P1	CON P1	19	
2.1E+08	2.9E+08	3.9E+08	3.2E+08	2.8E+08	3.7E+08	8.6E+07	3.4E+08	2.7E+08			+	41	40	40	67.4	67.4	67.4	62.129	0	323.31	1.6E+10	1641	CON P3	CON P3	20	
0	0	0	0	0	0	0	0	0			+	61	1	1	87.8	5.6	5.6	65.865	0	12.793	3.9E+07	7	CON P3	CON P3	21	
3.7E+08	6.7E+08	7.4E+08	6E+08	8.2E+08	4E+08	1.9E+08	7.7E+08	2.7E+08			+	61	61	1	87.6	87.6	4.7	65.432	0	323.31	1.7E+10	1421	CON P3	CON P3	22	
0	0	0	0	1.2E+07	8.4E+07	0	5398400	0			+	39	2	1	54.4	5.7	2.7	60.024	0	30.467	1.6E+08	21	CON P4	CON P4	23	
0	0	0	0	0	0	0	0	0			+	4	4	4	41	41	41	11.703	0	10.584	1.6E+07	13	CON P6	CON P6	24	
553020	1975900	1138600	1974200	6555500	5.7E+07	1213000	5066500	0			+	27	15	5	65.7	45.6	22	48.105	0	181.01	3E+08	98	CON Q0	CON Q0	25	
0	0	0	0	0	0	0	0	0			+	3	2	2	11.4	9.7	9.7	46.213	0	8.3535	2462800	2	CON Q1	CON Q1	26	;;
0	0	0	0	0	0	0	0	0			+	7	2	0	9.6	4.1	0	58.923	0	27.959	1.1E+08	38	CON Q3	CON Q3	27	;
0	0	0	0	0	0	0	0	0			+	1	1	1	4.5	4.5	4.5	22.06	0.00279	2.8719	7845200	8	CON Q3	CON Q3	28	
0	0	0	0	0	0	0	0	0			+	1	1	1	3.5	3.5	3.5	33.012	0.0073	2.1924	981650	2	CON Q3	CON Q3	29	
0	0	0	0	0	0	0	0	0			+	12	1	1	23.7	3.6	3.6	51.606	0	7.5912	2189700	2	CON Q9	CON Q9	30	;
0	0	0	0	0	0	0	0	0	+		+	2	1	1	5.4	2.7	2.7	62.87	1	-2	2905100	0	CON Q3	CON Q3	31	
1787500	1490000	2612400	0	3882800	2504300	1074000	4149600	1318800			+	6	6	6	4.8	4.8	4.8	248.07	0	21.828	2.9E+07	31	CON Q5	CON Q5	32	
0	0	0	0	0	0	0	0	0			+	25	1	1	36.8	1.7	1.7	62.936	0.00429	2.607	3606800	2	CON Q5	CON Q5	33	
0	0	0	0	0	0	0	0	0			+	20	1	1	31.9	4	4	50.133	0.0006	3.3563	4.1E+07	2	CON Q6	CON Q6	34	
0	0	0	0	0	0	0	0	0			+	12	8	8	27.3	23.8	23.8	64.895	0	17.737	1.3E+07	10	CON Q9	CON Q9	35	;
0	0	1117100	0	1026300	733730	0	0	0			+	4	4	4	10.2	10.2	10.2	50.525	0	7.7616	6185100	10	CON Q6	CON Q6	36	;
994960	1543700	1715900	1612900	1968100	2067500	0	2575100	0			+	10	7	7	27.4	22.5	22.5	56.964	0	35.855	3.5E+07	39	CON Q8	CON Q8	37	;
0	1757600	1716900	1839600	2815500	0	0	2753200	0			+	14	10	8	30.6	25.8	21.8	61.802	0	46.209	2.7E+07	26	CON Q7	CON Q7	38	
1638800	2032500	3880600	2596700	2325700	3510600	781610	2962100	2512200			+	6	6	6	6.7	6.7	6.7	282.39	0	136.43	5.5E+07	76	CON Q8	CON Q8	39	
0	0	0	0	0	0	0	0	0	+		+	20	1	1	27.9	2.4	2.4	61.766	1	-2	647100	1	CON Q9	CON Q9	40	
0	0	0	0	0	0	0	0	0			+	1	1	1	3.1	3.1	3.1	48.131	0.00617	2.3247	647200	2	CON Q9	CON Q9	41	
0	0	0	0	0	0	0	0	0	+		+	22	1	1	44.1	3	3	48.161	1	-2	0	1	CON Q9	CON Q9	42	
0	0	0	0	0	0	0	0	0			+	5	1	0	8.2	2.3	0	57.382	0.00171	3.013	1402900	2	CON Q9	CON Q9	43	
1909500	0	1540100	3546400	3398600	2414300	0	0	0			+	5	5	5	43.1	43.1	43.1	16.622	0	26.647	2.4E+07	27	CON Str	CON Str	44	
2906500	3350700	3742400	3789100	3785200	4148300	5254100	5097600	1.1E+07				17	2	1	33.4	8.6	6.3	72.523	0	32.367	7.3E+07	41	gi|10230	gi|10230	45	gi|1023044021|gb|ANA96231.1| heat shock protein [Tyrophagus putrescentiae]
7883200	8289700	9385600	8776600	6387000	6503400	1.2E+07	1.5E+07	1.6E+07				24	24	11	43.6	43.6	23.9	72.754	0	149.12	4.4E+08	167	gi|10230	gi|10230	46	gi|1023044023|gb|ANA96232.1| heat shock protein [Tyrophagus putrescentiae]
3.8E+07	4.1E+07	4.5E+07	4.4E+07	1.9E+07	4.3E+07	5E+07	6E+07	6.9E+07				11	11	5	18.7	18.7	7.2	59.463	0	133.38	1.8E+09	167	gi|10479	gi|10479	47	gi|1047999330|ref|XP 017487347.1| PREDICTED: ATP synthase subunit alpha, mitochondrial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	2.7	2.7	2.7	45.9	0.00709	2.2301	1152600	1	gi|10479	gi|10479	48	gi|1047999538|ref|XP 017472647.1| PREDICTED: stromal membrane-associated protein 1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	2.3	2.3	2.3	44.401	0.00547	2.399	7.5E+08	33	gi|10480	gi|10480	49	gi|1048000231|ref|XP 017465036.1| PREDICTED: oxygen-dependent coproporphyrinogen-III oxidase [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				3	1	0	3.8	1.4	0	138.6	0	24.418	2.7E+07	9	gi|10480	gi|10480	50	gi|1048002029|ref|XP 017473440.1| PREDICTED: plasma membrane calcium-transporting ATPase 2 isoform X1 [Rhagoletis zephyria];gi|1048002045|ref|XP 017473499.1| PREDICTED: plasma membrane calcium-transporting ATPase 2 isoform X6 [Rhagoletis zephyria];gi|10480
0	0	0	0	0	0	0	0	0				10	2	2	14.8	3.8	3.8	94.611	0.00062	3.654	2.5E+08	17	gi|10480	gi|10480	51	gi|1048002070|ref|XP 017473640.1| PREDICTED: elongation factor 2 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	19.3	19.3	19.3	10.345	0	4.6162	1689600	2	NODE 12	NODE 12	52	NODE 124 length 64648 cov 707.713235 True 49956 ras-related C3 botulinum toxin substrate 3 isoform X1;gi|1048046779|ref|XP 017494934.1| PREDICTED: ras-related C3 botulinum toxin substrate 1-like [Rhagoletis zephyria];gi|1048029520|ref|XP 017488619.1| PREDI
0	0	0	0	0	0	0	0	0				1	1	1	19.1	19.1	19.1	7.6422	0.00301	2.7419	1E+07	5	gi|10480	gi|10480	53	gi|1048062099|ref|XP 017463076.1| PREDICTED: protein transport protein Sec61 gamma-2 subunit [Rhagoletis zephyria];gi|1048002348|ref|XP 017474952.1| PREDICTED: protein transport protein Sec61 gamma-2 subunit [Rhagoletis zephyria];gi|1048002346|ref|XP 01747
0	0	0	0	0	0	0	0	0				2	1	1	13.3	10	10	37.726	0	13.895	2.2E+07	8	gi|10480	gi|10480	54	gi|1048002357|ref|XP 017474988.1| PREDICTED: serine/threonine-protein phosphatase beta isoform [Rhagoletis zephyria];gi|1048002355|ref|XP 017474981.1| PREDICTED: serine/threonine-protein phosphatase beta isoform [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+			1	1	1	1.8	1.8	1.8	72.351	1	-2	4275900	3	gi|10480	gi|10480	55	gi|1048002651|ref|XP 017476289.1| PREDICTED: coiled-coil domain-containing protein 65 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				2	2	2	2.2	2.2	2.2	194.13	0.00871	2.1143	3133400	2	gi|10480	gi|10480	56	gi|1048002872|ref|XP 017477314.1| PREDICTED: PERQ amino acid-rich with GYF domain-containing protein CG11148 isoform X2 [Rhagoletis zephyria];gi|1048002870|ref|XP 017477307.1| PREDICTED: PERQ amino acid-rich with GYF domain-containing protein CG11148 isofo
0	0	0	0	0	0	0	0	0				4	4	4	0.5	0.5	0.5	1455.1	0	5.181	6.7E+07	4	gi|10480	gi|10480	57	gi|1048002955|ref|XP 017477784.1| PREDICTED: nesprin-1 isoform X2 [Rhagoletis zephyria];gi|1048002953|ref|XP 017477776.1| PREDICTED: nesprin-1 isoform X1 [Rhagoletis zephyria];gi|1048002959|ref|XP 017477803.1| PREDICTED: nesprin-1 isoform X4 [Rhagoletis ze
2.8E+07	2.8E+07	4.1E+07	2.5E+07	3E+07	3.8E+07	3.4E+07	6.1E+07	9.7E+07				7	7	5	37.9	37.9	30.6	13.32	0	131.46	1.1E+09	121	gi|10480	gi|10480	58	gi|1048046021|ref|XP 017494516.1| PREDICTED: histone H2A-like [Rhagoletis zephyria];gi|1048057783|ref|XP 017462204.1| PREDICTED: histone H2A-like [Rhagoletis zephyria];NODE 1835 length 13132 cov 679.792995 True 1790 histone H2A;NODE 6017 length 3616 cov 67
0	0	0	0	0	0	0	0	0				7	1	1	17.8	4.2	4.2	35.557	0	26.473	1.4E+07	7	gi|10480	gi|10480	59	gi|1048003646|ref|XP 017481271.1| PREDICTED: glyceraldehyde-3-phosphate dehydrogenase [Rhagoletis zephyria]
0	0	0	0	1994000	0	0	2897800	0				13	1	0	35.3	3.3	0	49.908	0	11.852	1.9E+07	11	gi|10480	gi|10480	60	gi|1048004366|ref|XP 017484678.1| PREDICTED: tubulin alpha-1 chain [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+			1	1	1	2.3	2.3	2.3	127.55	1	-2	2214400	1	gi|10480	gi|10480	61	gi|1048004756|ref|XP 017486578.1| PREDICTED: uncharacterized protein LOC108375015 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	2.1	2.1	2.1	68.049	0.00274	2.7512	745350	5	gi|10480	gi|10480	62	gi|1048004810|ref|XP 017486821.1| PREDICTED: transketolase-like protein 2 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				4	1	1	6.6	3	3	97.498	0.00938	2.0748	0	1	gi|10480	gi|10480	63	gi|1048005537|ref|XP 017490153.1| PREDICTED: glycogen phosphorylase isoform X1 [Rhagoletis zephyria];gi|1048005539|ref|XP 017490160.1| PREDICTED: glycogen phosphorylase isoform X2 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				10	2	2	6.6	1.7	1.7	224.29	0.00849	2.1256	4511400	1	gi|10480	gi|10480	64	gi|1048006791|ref|XP 017461556.1| PREDICTED: myosin heavy chain, muscle isoform X11 [Rhagoletis zephyria];gi|1048006789|ref|XP 017461550.1| PREDICTED: myosin heavy chain, muscle isoform X10 [Rhagoletis zephyria];gi|1048006785|ref|XP 017461536.1| PREDICTED:
0	0	0	0	0	0	0	0	0				3	1	1	10.9	4.6	4.6	34.554	0	4.9371	1.1E+07	6	gi|10480	gi|10480	65	gi|1048069062|ref|XP 017486699.1| PREDICTED: serine/threonine-protein phosphatase alpha-2 isoform [Rhagoletis zephyria];gi|1048007133|ref|XP 017463176.1| PREDICTED: serine/threonine-protein phosphatase alpha-1 isoform [Rhagoletis zephyria];NODE 6916 length
0	0	0	0	0	0	0	0	0				1	1	1	3.8	3.8	3.8	44.534	0.00525	2.4485	4198100	3	gi|10480	gi|10480	66	gi|1048008695|ref|XP 017465112.1| PREDICTED: tenascin isoform X2 [Rhagoletis zephyria];gi|1048008693|ref|XP 017465111.1| PREDICTED: tenascin isoform X1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				2	1	1	6.6	3.5	3.5	44.742	0.00059	3.3353	248410	1	gi|10480	gi|10480	67	gi|1048009190|ref|XP 017465372.1| PREDICTED: 26S protease regulatory subunit 10B [Rhagoletis zephyria];NODE 6230 length 3444 cov 675.969608 False 2914 26S proteasome regulatory subunit 10B-like
0	0	0	0	0	0	0	1013900	1297100				7	7	7	8.8	8.8	8.8	138.14	0	17.632	9764500	15	gi|10480	gi|10480	68	gi|1048009281|ref|XP 017465423.1| PREDICTED: neuroglian-like [Rhagoletis zephyria];NODE 983 length 22232 cov 742.238445 False 6443 neuronal cell adhesion molecule-like protein
0	1086800	973930	0	0	0	0	1987300	0				2	2	2	31.5	31.5	31.5	8.3266	0	5.3748	1E+07	10	NODE 62	NODE 62	69	NODE 629 length 30016 cov 744.042121 False 17807 Vacuolar protein sorting-associated protein 29;gi|1048009285|ref|XP 017465425.1| PREDICTED: vacuolar protein sorting-associated protein 29-like [Rhagoletis zephyria]
6723100	7474400	6315000	5667400	3666200	5373700	8224700	1.2E+07	2.2E+07				12	12	12	40	40	40	34.418	0	141.66	3.2E+08	122	gi|10480	gi|10480	70	gi|1048009287|ref|XP 017465427.1| PREDICTED: succinyl-CoA ligase subunit alpha, mitochondrial-like [Rhagoletis zephyria]
1610600	1075500	1735000	920060	987990	902590	0	1529800	2554300				6	6	6	17.8	17.8	17.8	50.421	0	12.436	3.1E+07	34	gi|10480	gi|10480	71	gi|1048009289|ref|XP 017465428.1| PREDICTED: programmed cell death protein 4-like [Rhagoletis zephyria];NODE 1242 length 18418 cov 743.663835 False 2151 programmed cell death protein 4
1606900	1559200	1806300	2529600	2457400	2571800	2450300	3990200	4893600				18	18	18	59	59	59	47.139	0	92.853	1.3E+08	103	gi|10480	gi|10480	72	gi|1048009291|ref|XP 017465429.1| PREDICTED: 26S protease regulatory subunit 6B-like [Rhagoletis zephyria];NODE 1242 length 18418 cov 743.663835 False 5764 26S proteasome regulatory subunit 6B
0	0	0	0	0	0	0	0	0				3	3	3	6.2	6.2	6.2	71.552	0	4.51	1894200	3	gi|10480	gi|10480	73	gi|1048009297|ref|XP 017465433.1| PREDICTED: protein PTCD3 homolog, mitochondrial-like [Rhagoletis zephyria]
1949000	2003600	2423500	3258100	2326800	2661500	3536200	4665800	7134900				61	61	37	25.8	25.8	16.2	421.64	0	323.31	3.1E+08	296	gi|10480	gi|10480	74	gi|1048009299|ref|XP 017465434.1| PREDICTED: muscle M-line assembly protein unc-89-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	8.8	8.8	8.8	15.884	0	4.1976	2559700	3	NODE 47	NODE 47	75	NODE 474 length 36110 cov 739.120399 False 10529 protein quiver-like;gi|1048009303|ref|XP 017465436.1| PREDICTED: uncharacterized protein LOC108358545 [Rhagoletis zephyria]
1.8E+07	2E+07	2.1E+07	1.8E+07	1.2E+07	1.5E+07	2.3E+07	3.9E+07	5.3E+07				42	42	42	50.1	50.1	50.1	94.606	0	300.6	1.9E+09	481	gi|10480	gi|10480	76	gi|1048009305|ref|XP 017465437.1| PREDICTED: probable aconitate hydratase, mitochondrial [Rhagoletis zephyria];NODE 474 length 36110 cov 739.120399 False 3109 probable aconitate hydratase, mitochondrial
0	0	0	0	0	0	0	0	0				1	1	1	15.2	15.2	15.2	14.041	0.00061	3.5555	0	1	NODE 16	NODE 16	77	NODE 168 length 56594 cov 755.832912 False 16866 notchless protein homolog 1 isoform X2;gi|1048009315|ref|XP 017465443.1| PREDICTED: notchless protein homolog 1 [Rhagoletis zephyria]
1612500	1745100	1593200	1132300	0	964690	0	3015500	2712200				3	3	3	29.6	29.6	29.6	22.314	0	25.506	2.5E+07	20	gi|10480	gi|10480	78	gi|1048009317|ref|XP 017465444.1| PREDICTED: protein SCO1 homolog, mitochondrial-like [Rhagoletis zephyria];NODE 168 length 56594 cov 755.832912 True 18045 protein SCO1 homolog, mitochondrial-like
4237500	4523300	4514300	4701600	4862200	5821800	4215000	5922600	7859900				7	7	7	47.7	47.7	47.7	23.503	0	62.577	1.7E+08	76	gi|10480	gi|10480	79	gi|1048009333|ref|XP 017465453.1| PREDICTED: ras-related protein Rab-5B-like [Rhagoletis zephyria];gi|1048012503|ref|XP 017467161.1| PREDICTED: ras-related protein Rab-5B [Rhagoletis zephyria];gi|1048012501|ref|XP 017467160.1| PREDICTED: ras-related protei
0	0	0	0	0	0	0	0	0				4	4	4	9.4	9.4	9.4	68.407	0	5.155	5481100	7	gi|10480	gi|10480	80	gi|1048009337|ref|XP 017465457.1| PREDICTED: MAGUK p55 subfamily member 6-like [Rhagoletis zephyria];NODE 52 length 90661 cov 730.284507 False 63349 MAGUK p55 subfamily member 6-like isoform X2
0	0	710070	0	754090	0	0	0	0				3	3	3	12.5	12.5	12.5	50.488	0	7.0146	3924100	8	gi|10480	gi|10480	81	gi|1048009347|ref|XP 017465462.1| PREDICTED: carboxypeptidase E-like [Rhagoletis zephyria];NODE 52 length 90661 cov 730.284507 True 38828 carboxypeptidase E-like
0	0	0	0	0	0	0	0	0				4	4	4	2.5	2.5	2.5	249.24	0	9.3513	6737400	12	gi|10480	gi|10480	82	gi|1048009353|ref|XP 017465466.1| PREDICTED: dnaJ homolog subfamily C member 13-like [Rhagoletis zephyria];NODE 3236 length 7798 cov 738.497482 True 1972 dnaJ homolog subfamily C member 13-like isoform X1
5684100	6145300	6728600	4919000	4567700	4544000	3875000	7034100	7605700				8	8	8	44.5	44.5	44.5	23.168	0	32.619	1.3E+08	51	gi|10480	gi|10480	83	gi|1048009357|ref|XP 017465468.1| PREDICTED: FK506-binding protein 2-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				2	2	2	13.5	13.5	13.5	25.876	0	5.6319	2E+07	6	gi|10480	gi|10480	84	gi|1048009359|ref|XP 017465469.1| PREDICTED: uridine diphosphate glucose pyrophosphatase-like [Rhagoletis zephyria];NODE 2560 length 9786 cov 729.145823 False 7283 uridine diphosphate glucose pyrophosphatase-like
0	0	1036700	559600	0	1131800	0	0	0				4	4	4	31.7	31.7	31.7	21.079	0	12.537	1.4E+07	15	gi|10480	gi|10480	85	gi|1048009369|ref|XP 017465475.1| PREDICTED: ADP-ribosylation factor-like protein 8B [Rhagoletis zephyria];NODE 983 length 22232 cov 742.238445 False 18437 ADP-ribosylation factor-like protein 8A
0	0	0	267400	0	0	0	0	693900				3	3	3	9.5	9.5	9.5	46.718	0	10.317	4027400	11	gi|10480	gi|10480	86	gi|1048009371|ref|XP 017465476.1| PREDICTED: lissencephaly-1 homolog [Rhagoletis zephyria];NODE 2765 length 9058 cov 737.505165 True 7116 lissencephaly-1 homolog
1.1E+08	1.1E+08	1.1E+08	8.4E+07	1.8E+08	1.2E+08	5.7E+07	1.3E+08	2.3E+08				6	6	6	35.2	35.2	35.2	14.729	0	125.01	2E+09	120	gi|10480	gi|10480	87	gi|1048043433|ref|XP 017493110.1| PREDICTED: ubiquitin-60S ribosomal protein L40 [Rhagoletis zephyria];gi|1048040747|ref|XP 017477261.1| PREDICTED: ubiquitin-60S ribosomal protein L40-like [Rhagoletis zephyria];gi|1048046176|ref|XP 017494602.1| PREDICTED:
0	0	0	0	0	0	0	0	0				12	2	2	33	9	9	49.869	0.00031	3.7222	9460100	6	gi|10480	gi|10480	88	gi|1048009784|ref|XP 017465693.1| PREDICTED: tubulin beta-2 chain [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+			1	1	1	14.1	14.1	14.1	10.515	1	-2	6.3E+07	12	gi|10480	gi|10480	89	gi|1048009861|ref|XP 017465732.1| PREDICTED: mitochondrial import inner membrane translocase subunit Tim10 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				13	2	0	30.2	7.4	0	50.147	0	6.2144	5300600	3	gi|10481	gi|10481	90	gi|1048011327|ref|XP 017466531.1| PREDICTED: tubulin beta-1 chain [Rhagoletis zephyria];gi|1048042894|ref|XP 017478405.1| PREDICTED: tubulin beta-3 chain [Rhagoletis zephyria];gi|1048042892|ref|XP 017478404.1| PREDICTED: tubulin beta-3 chain [Rhagoletis ze
0	0	0	0	0	0	0	0	0				1	1	1	6.9	6.9	6.9	24.628	0.00826	2.1391	1.2E+07	2	gi|10481	gi|10481	91	gi|1048013078|ref|XP 017467465.1| PREDICTED: alpha-tubulin N-acetyltransferase 1-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				10	1	1	12.3	1.1	1.1	103.83	0.00731	2.1962	8.1E+07	8	gi|10481	gi|10481	92	gi|1048013449|ref|XP 017467664.1| PREDICTED: alpha-actinin, sarcomeric isoform X3 [Rhagoletis zephyria];gi|1048013447|ref|XP 017467663.1| PREDICTED: alpha-actinin, sarcomeric isoform X2 [Rhagoletis zephyria];gi|1048013445|ref|XP 017467662.1| PREDICTED: alp
0	0	0	0	0	0	0	0	0				5	1	1	10.2	3.4	3.4	50.04	0	7.1268	9177400	4	gi|10481	gi|10481	93	gi|1048013784|ref|XP 017467841.1| PREDICTED: rab GDP dissociation inhibitor alpha-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				15	1	1	41.8	3.8	3.8	54.127	0.00058	3.1631	1904100	3	gi|10481	gi|10481	94	gi|1048014277|ref|XP 017468100.1| PREDICTED: ATP synthase subunit beta, mitochondrial [Rhagoletis zephyria];gi|1048023154|ref|XP 017472150.1| PREDICTED: ATP synthase subunit beta, mitochondrial-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				2	2	2	1.7	1.7	1.7	124.71	0.00224	2.9085	7182500	4	gi|10481	gi|10481	95	gi|1048015042|ref|XP 017468499.1| PREDICTED: protein diaphanous [Rhagoletis zephyria];gi|1048015040|ref|XP 017468498.1| PREDICTED: protein diaphanous [Rhagoletis zephyria];gi|1048015038|ref|XP 017468497.1| PREDICTED: protein diaphanous [Rhagoletis zephyria
0	0	0	0	0	0	0	0	0	+			1	1	1	6.1	6.1	6.1	28.671	1	-2	3.3E+07	5	gi|10481	gi|10481	96	gi|1048015191|ref|XP 017468578.1| PREDICTED: uncharacterized protein LOC108360695 isoform X1 [Rhagoletis zephyria];gi|1048015189|ref|XP 017468577.1| PREDICTED: uncharacterized protein LOC108360695 isoform X1 [Rhagoletis zephyria];gi|1048015187|ref|XP 01746
0	0	0	0	0	0	0	0	0				4	1	1	11.9	2.4	2.4	67.975	0	8.8105	1.2E+07	5	gi|10481	gi|10481	97	gi|1048016646|ref|XP 017469351.1| PREDICTED: V-type proton ATPase catalytic subunit A [Rhagoletis zephyria];gi|1048016644|ref|XP 017469350.1| PREDICTED: V-type proton ATPase catalytic subunit A [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+			1	1	1	0.3	0.3	0.3	487.98	1	-2	1.4E+07	2	gi|10481	gi|10481	98	gi|1048016756|ref|XP 017469411.1| PREDICTED: dynein beta chain, ciliary, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+			1	1	1	3.3	3.3	3.3	82.15	1	-2	4936600	3	gi|10481	gi|10481	99	gi|1048016801|ref|XP 017469434.1| PREDICTED: kelch-like protein 10 isoform X1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	0.3	0.3	0.3	295.71	0.00615	2.3075	3006600	9	gi|10481	gi|10481	100	gi|1048016925|ref|XP 017469500.1| PREDICTED: eIF-2-alpha kinase activator GCN1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	1.5	1.5	1.5	121.81	0.00225	2.9209	713310	1	gi|10481	gi|10481	101	gi|1048017620|ref|XP 017469866.1| PREDICTED: TATA element modulatory factor isoform X2 [Rhagoletis zephyria];gi|1048017618|ref|XP 017469865.1| PREDICTED: TATA element modulatory factor isoform X1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0				1	1	1	24.6	24.6	24.6	6.5665	0	11.755	4518300	11	NODE 25	NODE 25	102	NODE 2590 length 9688 cov 720.833904 False 7723 GTP-binding protein;gi|1048064150|ref|XP 017485025.1| PREDICTED: obg-like ATPase 1 [Rhagoletis zephyria];gi|1048019310|ref|XP 017470755.1| PREDICTED: obg-like ATPase 1 [Rhagoletis zephyria];gi|1048019308|ref|
0	0	0	0	0	0	0	0	0				2	2	2	9	9	9	37.624	0.0006	3.3782	1926200	2	gi|10481	gi|10481	103	gi|1048019452|ref|XP 017487862.1| PREDICTED: ribosome biogenesis protein WDR12 homolog [Rhagoletis zephyria];NODE 50 length 92202 cov 732.845486 False 78288 ribosome biogenesis protein WDR12 homolog
0	0	0	0	0	0	0	0	0				2	2	2	17	17	17	15.838	0	4.0811	2042600	4	gi|10481	gi|10481	104	gi|1048019462|ref|XP 017487868.1| PREDICTED: 60S ribosomal protein L27-like [Rhagoletis zephyria];NODE 50 length 92202 cov 732.845486 True 72703 60S ribosomal protein L27
1.1E+07	9999900	1.1E+07	1E+07	9077900	1.1E+07	1.3E+07	1.7E+07	1.8E+07				11	7	7	58	41.1	41.1	24.131	0	47.992	3.1E+08	86	gi|10481	gi|10481	105	gi|1048019501|ref|XP 017487889.1| PREDICTED: heat shock 70 kDa protein C-like, partial [Rhagoletis zephyria];NODE 1063 length 20806 cov 709.760445 False 20803 Hsp70 family protein
0	0	0	0	0	0	0	0	0				1	1	1	19.6	19.6	19.6	11.474	0.00061	3.5166	205930	2	NODE 38	NODE 38	106	NODE 3857 length 6154 cov 437.127890 False 4481 basic proline-rich protein-like;NODE 2870 length 8778 cov 460.930987 True 7899 basic proline-rich protein-like;gi|1048019523|ref|XP 017487900.1| PREDICTED: basic proline-rich protein-like [Rhagoletis zephyria
0	0	0	0	0	0	0	0	0				3	3	3	3.8	3.8	3.8	165.59	0	6.8711	2907000	7	gi|10481	gi|10481	107	gi|1048019564|ref|XP 017487922.1| PREDICTED: mitogen-activated protein kinase kinase kinase 15-like [Rhagoletis zephyria];NODE 15 length 154786 cov 732.466280 False 138998 mitogen-activated protein kinase kinase kinase 15 isoform X4
1693100	1577100	2019000	1565000	0	1376300	2524600	3190500	4659900				10	10	10	41.5	41.5	41.5	32.275	0	63.483	5E+07	44	gi|10481	gi|10481	108	gi|1048019607|ref|XP 017487946.1| PREDICTED: succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial-like [Rhagoletis zephyria];NODE 9 length 186394 cov 717.866013 False 105413 Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitoc
1846700	1999000	2111900	1851500	0	2077700	1483100	2060000	3106900				3	3	3	18.8	18.8	18.8	34.054	0	21.089	3.7E+07	26	gi|10481	gi|10481	109	gi|1048019611|ref|XP 017487949.1| PREDICTED: glyoxalase domain-containing protein 4-like [Rhagoletis zephyria];NODE 888 length 24016 cov 715.014691 True 2591 glyoxalase I
0	0	0	0	0	0	0	0	0				2	2	2	14	14	14	35.238	0	6.9271	1981200	7	NODE 88	NODE 88	110	NODE 888 length 24016 cov 715.014691 False 4951 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial;gi|1048019613|ref|XP 017487950.1| PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial-like [Rhagoletis zephyria]
0	0	0	638520	0	0	0	0	1156300				3	3	3	9.3	9.3	9.3	59.846	0	6.639	6255300	10	gi|10481	gi|10481	111	gi|1048019617|ref|XP 017487952.1| PREDICTED: gamma-glutamyltranspeptidase 1-like, partial [Rhagoletis zephyria];NODE 70 length 82317 cov 789.187073 False 43024 gamma-glutamyltranspeptidase 1-like isoform X2
0	0	0	0	0	0	0	0	0				1	1	1	12.1	12.1	12.1	16.036	0.00275	2.7934	1316400	1	NODE 44	NODE 44	112	NODE 4409 length 5305 cov 646.652952 True 2650 DDRGK domain-containing protein 1;gi|1048019696|ref|XP 017487994.1| PREDICTED: DDRGK domain-containing protein 1-like [Rhagoletis zephyria]
8376400	5803700	7611800	5478500	4812200	5531400	7760600	9956800	1.6E+07				6	5	4	36	30.4	25.2	23.995	0	14.482	1.2E+08	40	gi|10481	gi|10481	113	gi|1048019739|ref|XP 017488019.1| PREDICTED: endochitinase At2g43620-like [Rhagoletis zephyria];NODE 435 length 37646 cov 706.286372 False 8865 chitinase 4-like

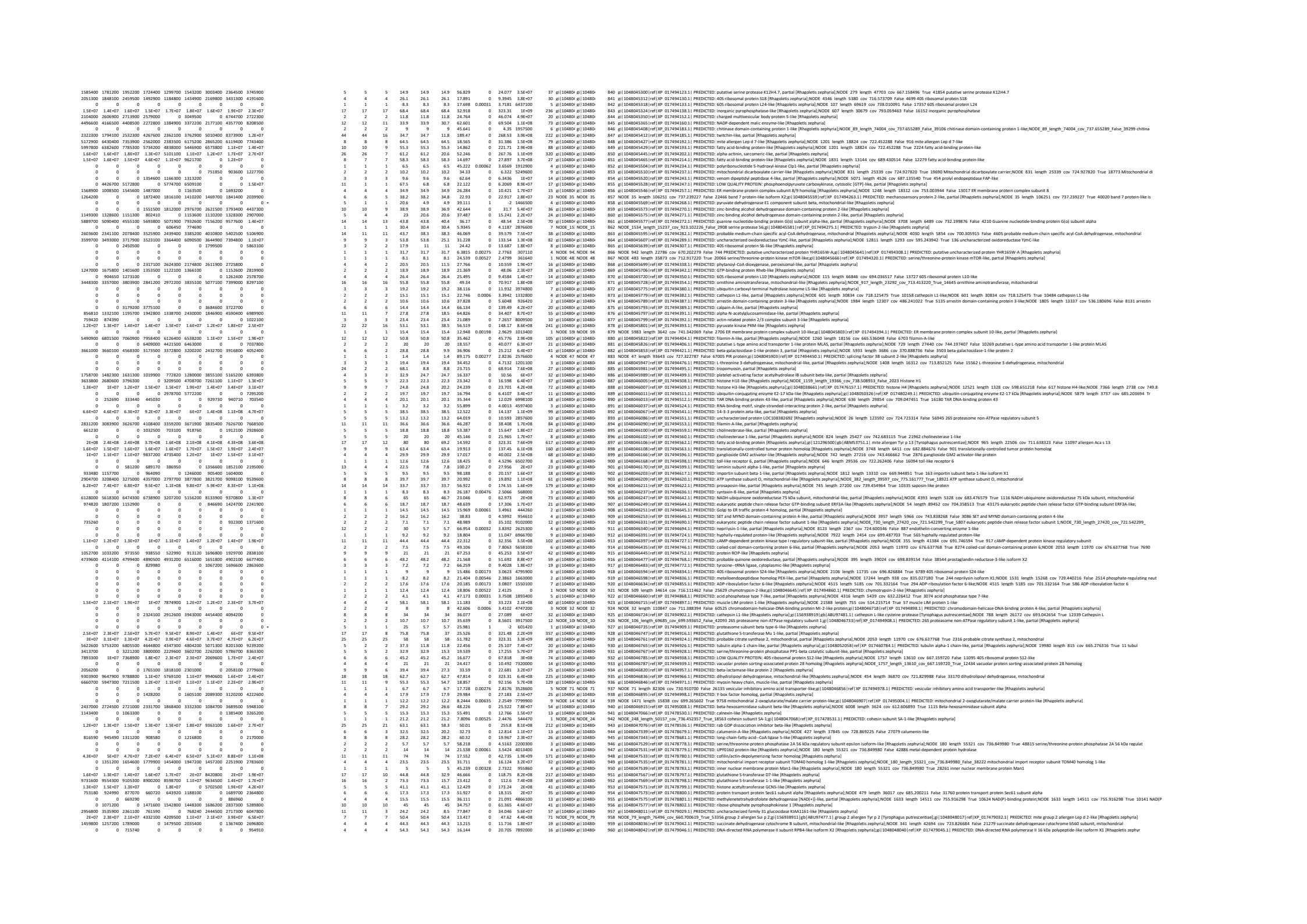


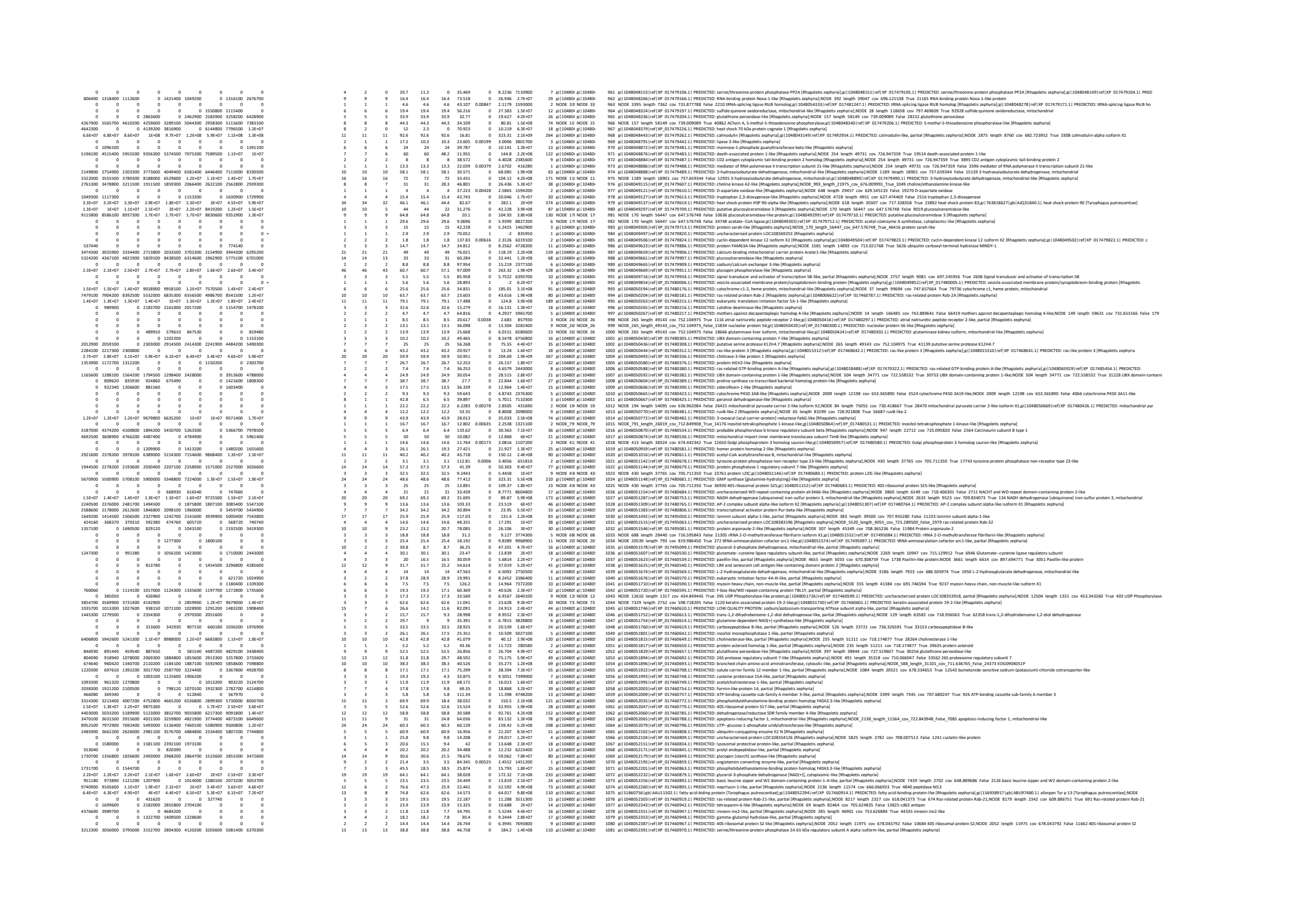


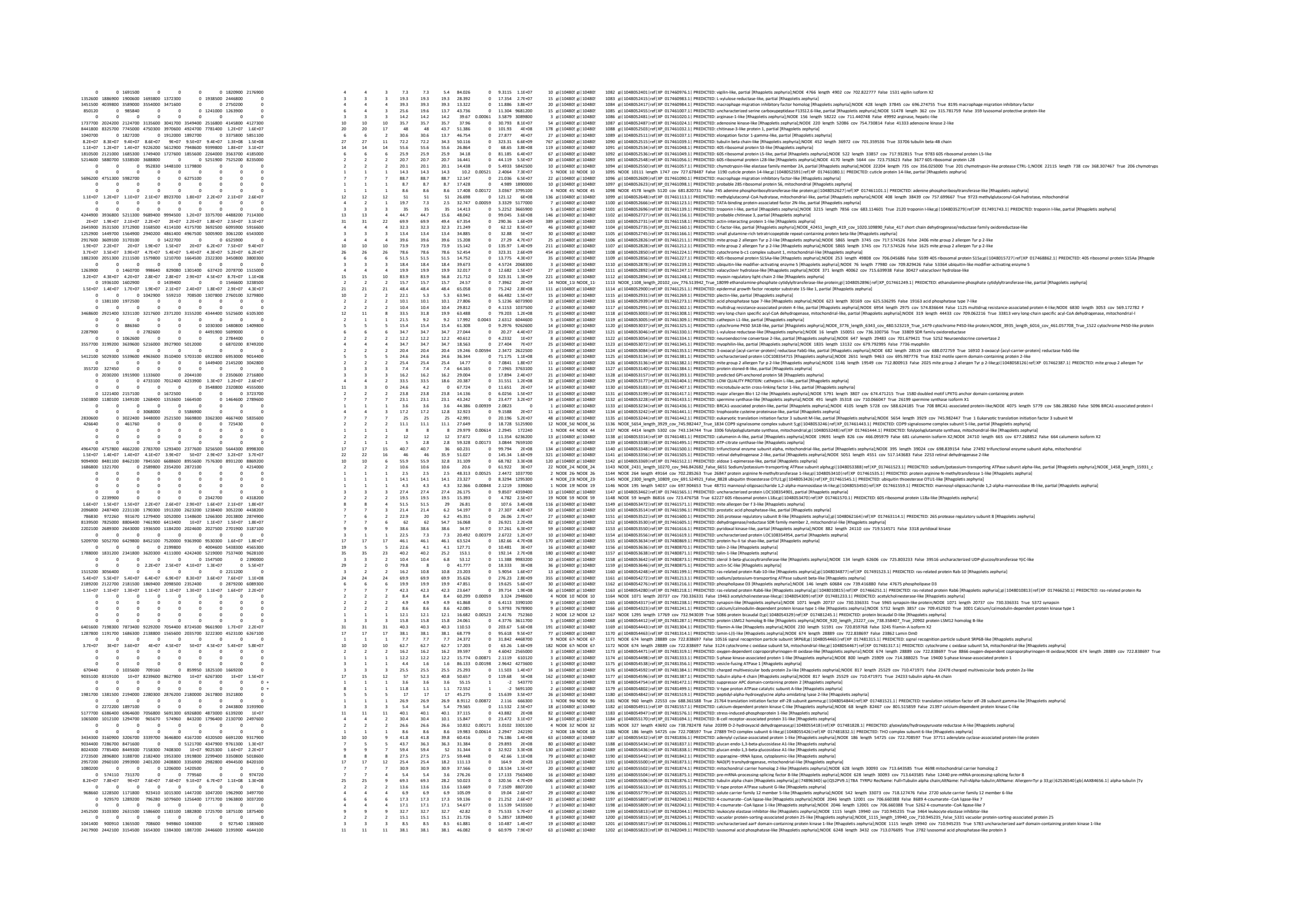


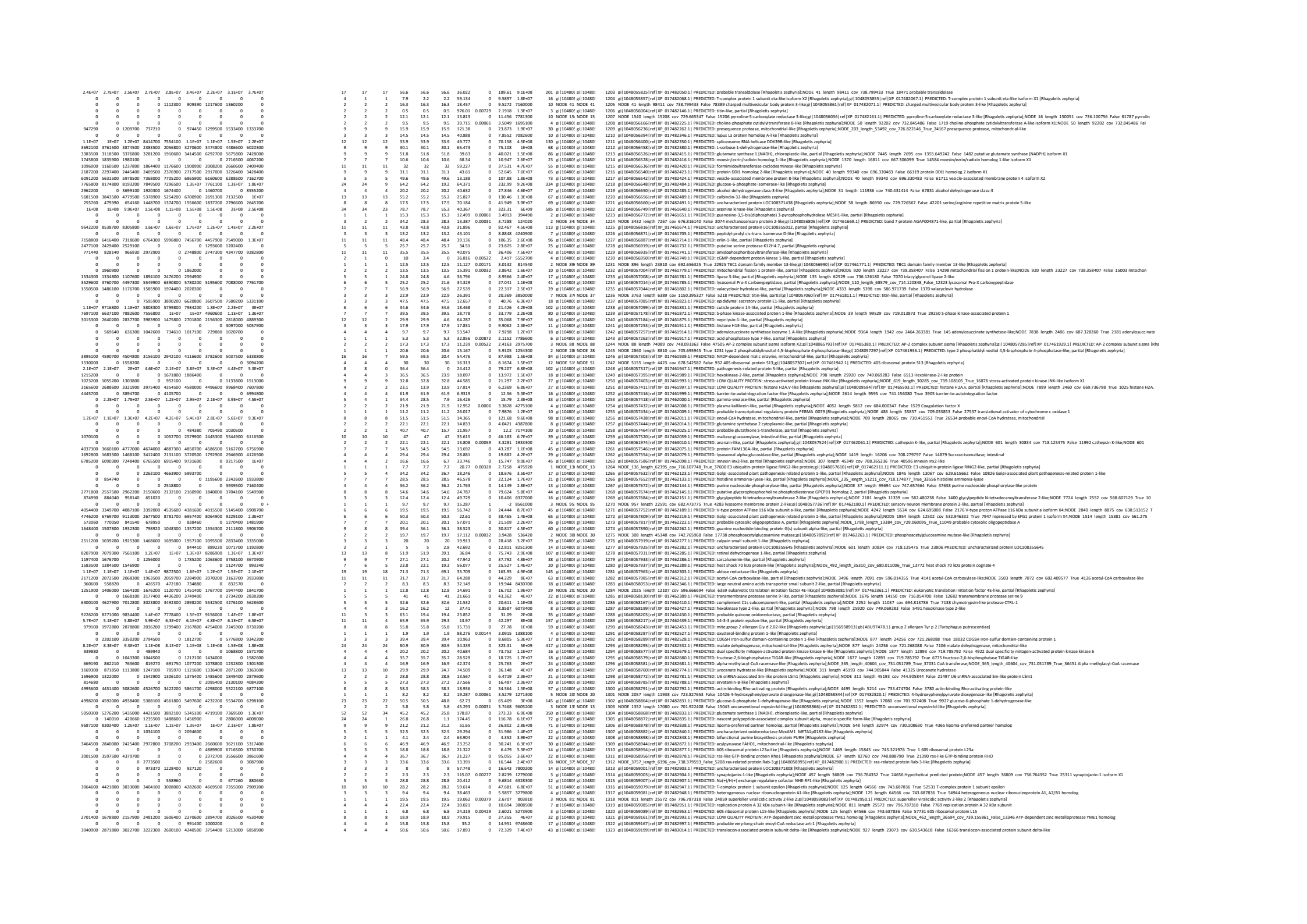


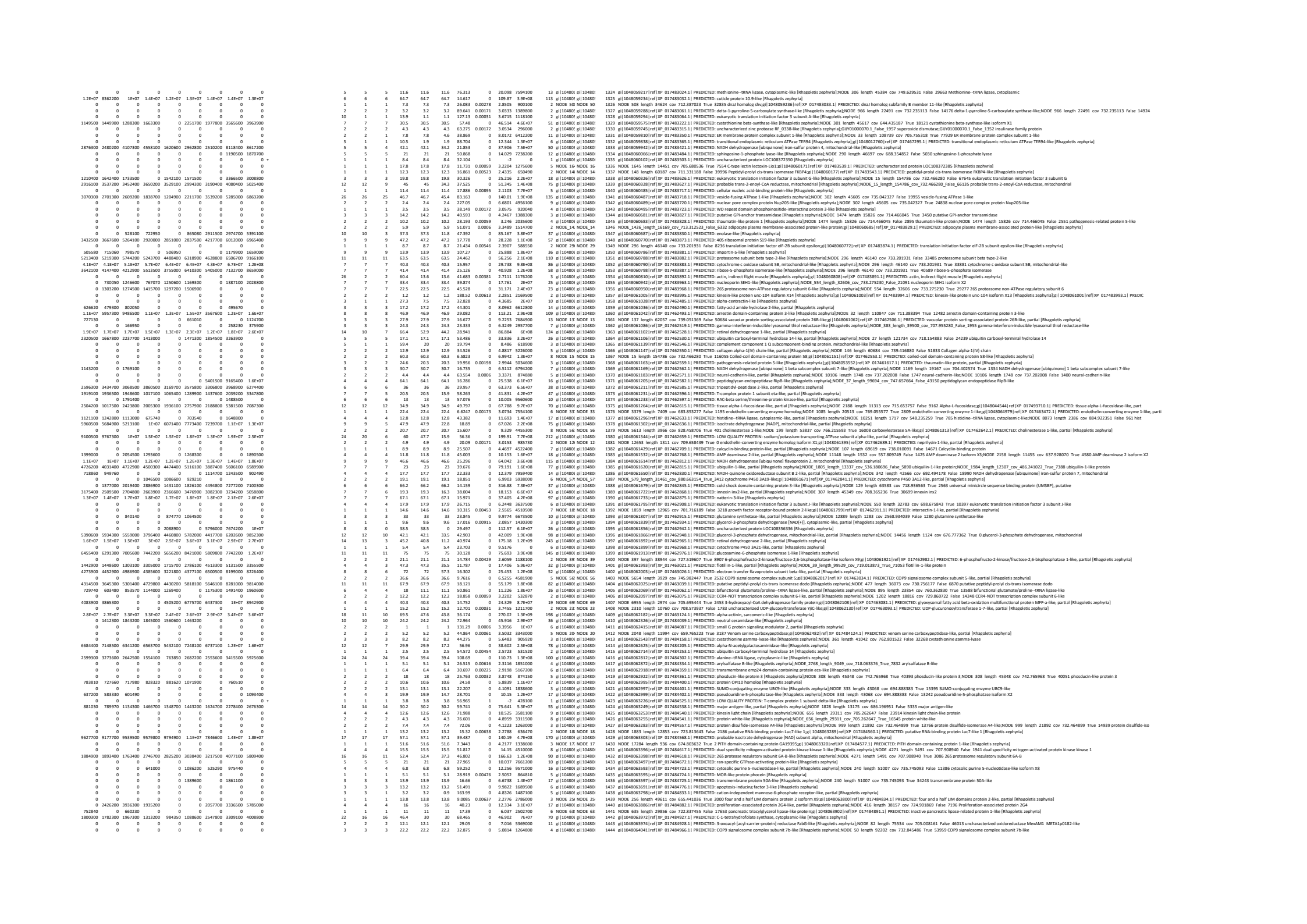


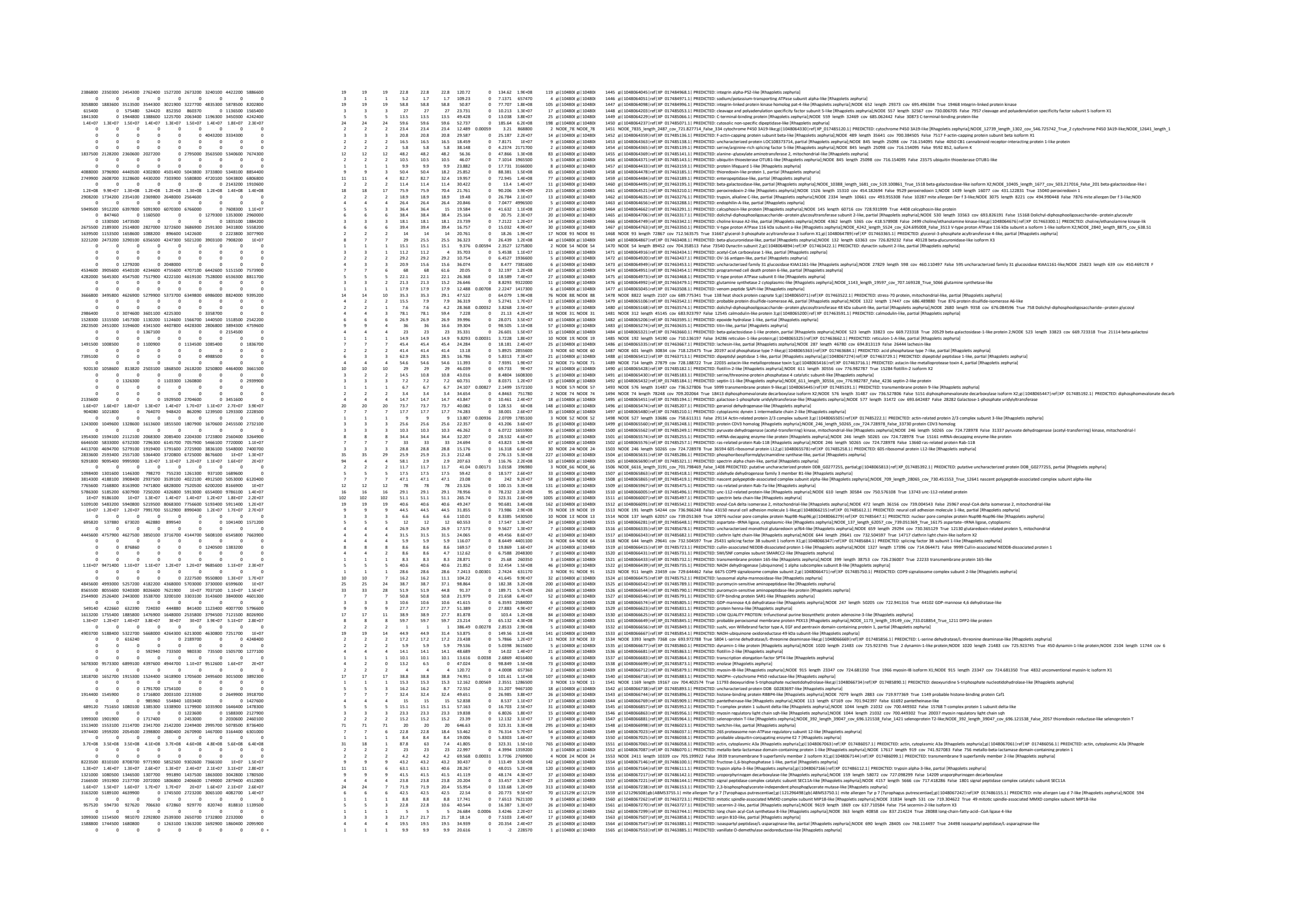




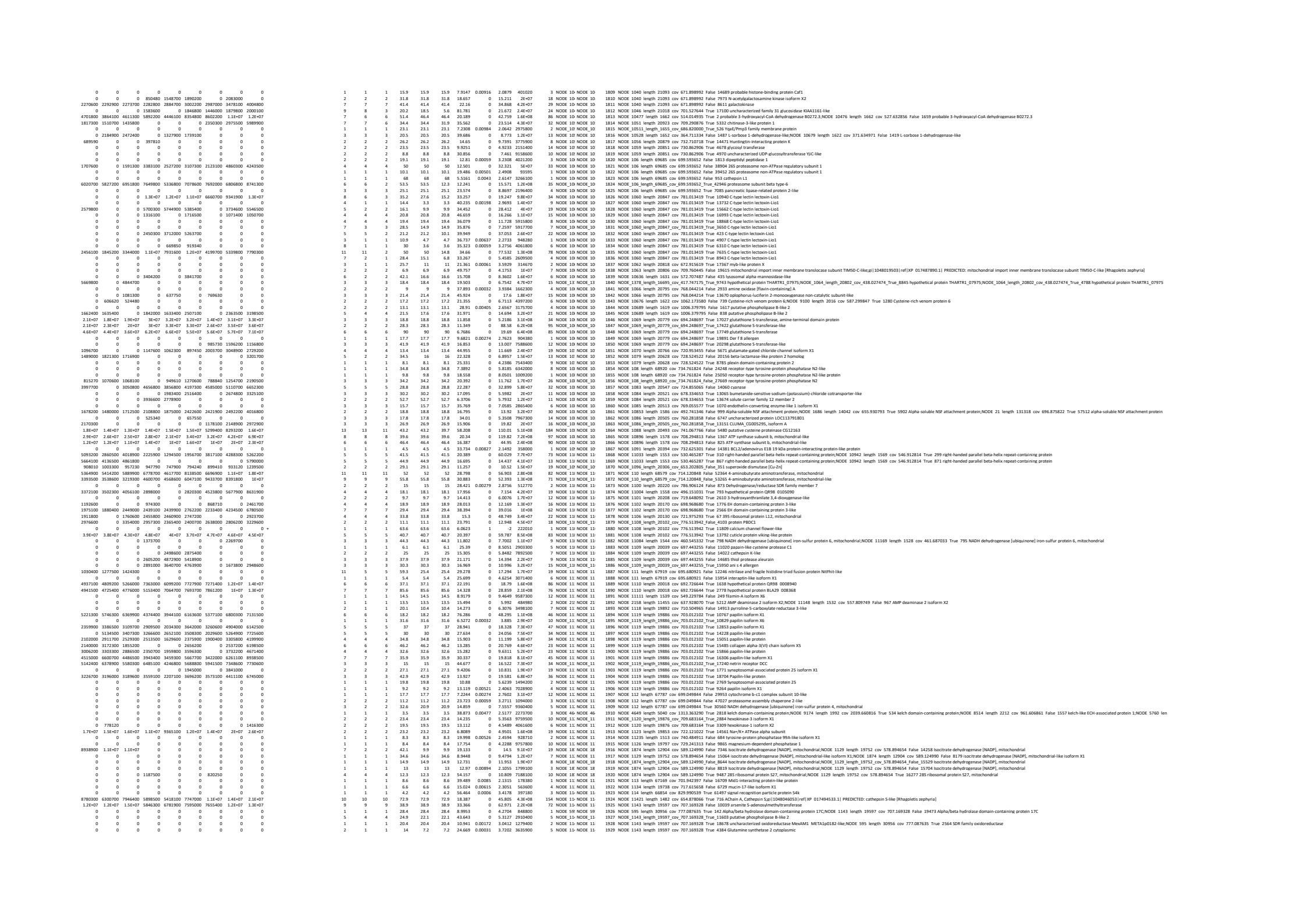


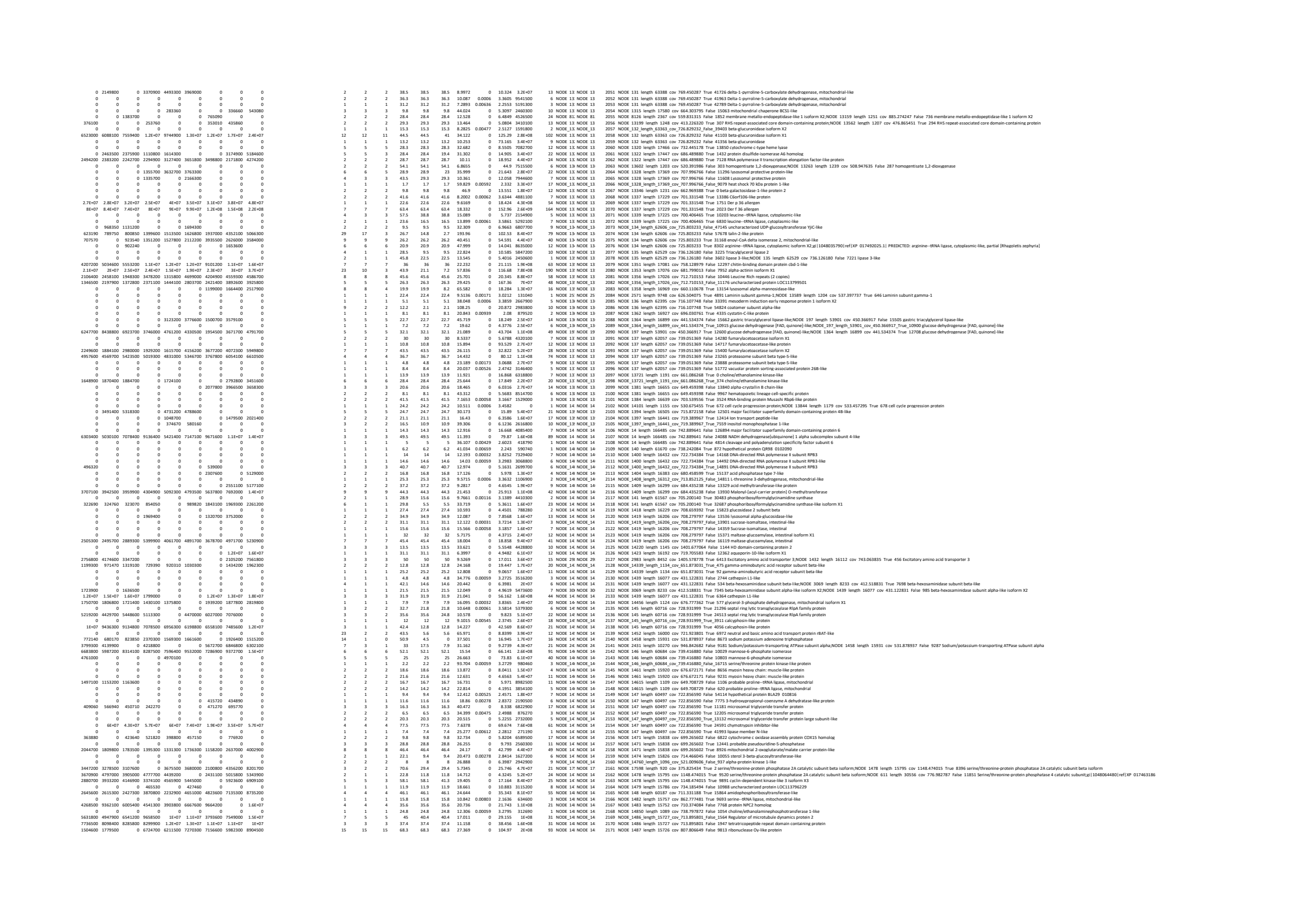




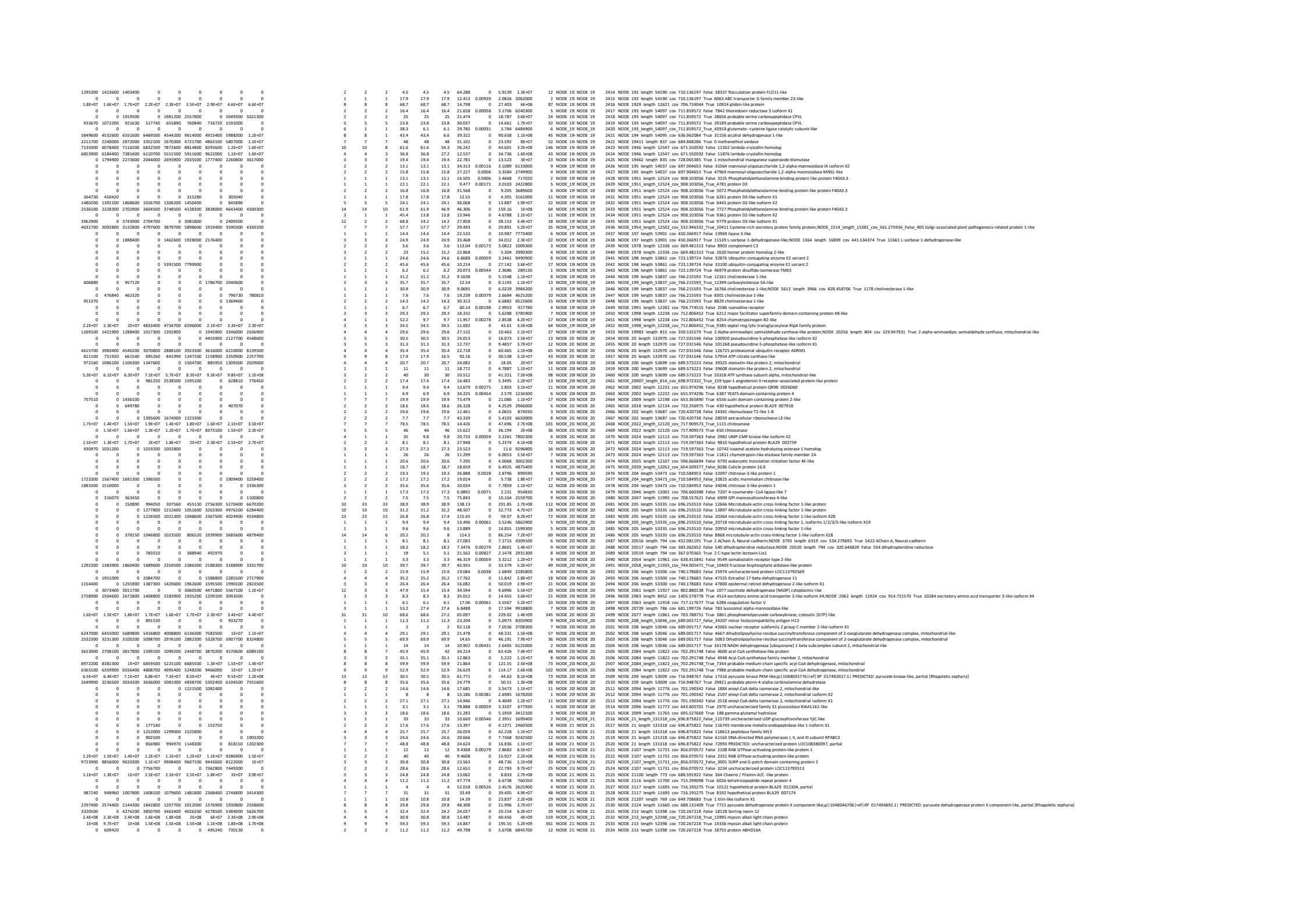


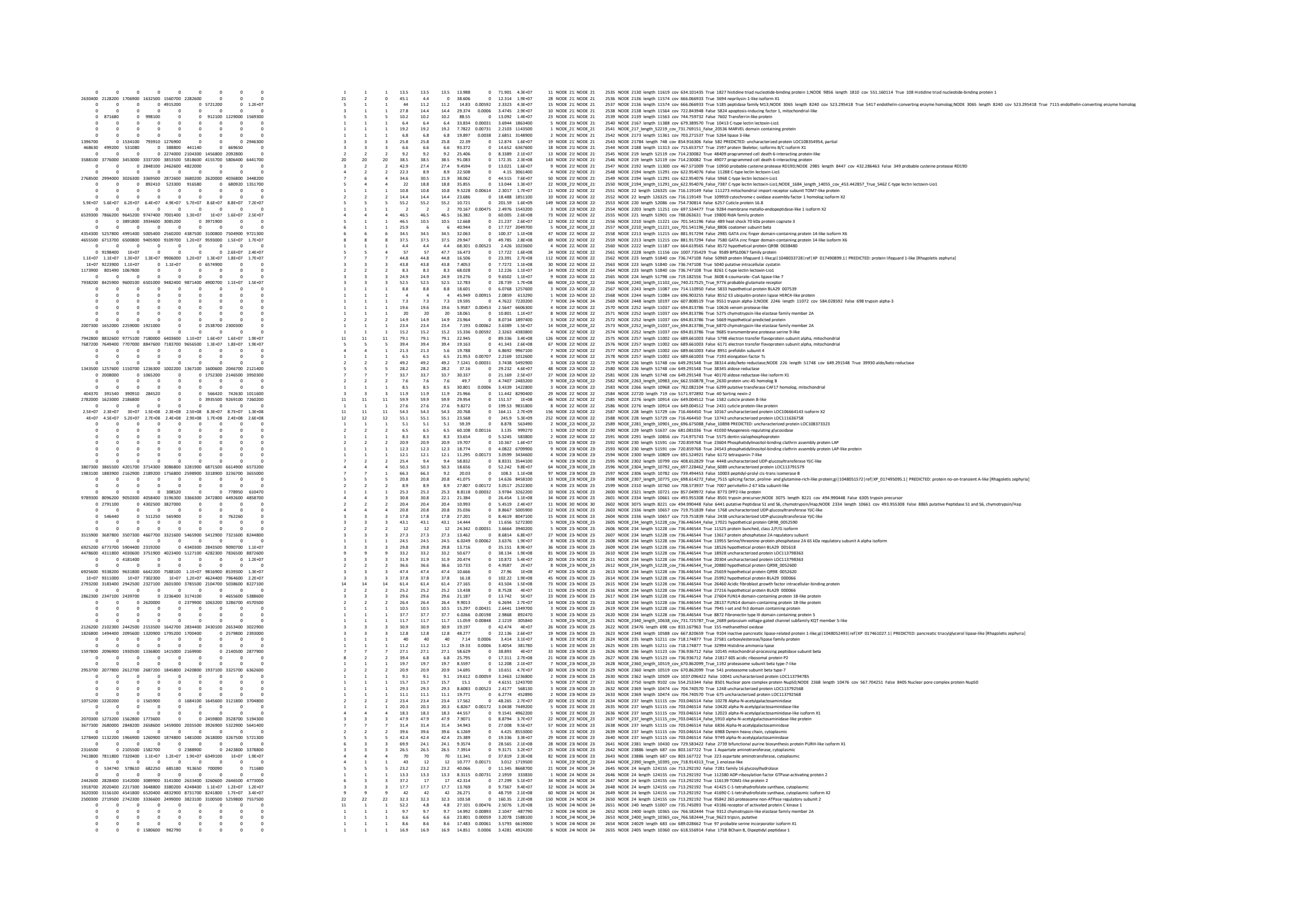
2610600	3255700	3126100	3325200	3106600	4180300	4113700	4366400	6664400	10	10	4	47.3	47.3	21.1	32.926	0	59.491	1.2E+08	75	gi|104806	gi|104806	1566	gi|1048067611|ref|XP 017463917.1| PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial-like, partial [Rhagoletis zephyria]
4871100	0	3131300	3198700	4313500	3752200	3288100	3793600	4266400	8	8	3	35	35	15.9	34.939	0	36.619	8E+07	40	gi|104806	gi|104806	1567	gi|1048067742|ref|XP 017463991.1| PREDICTED: deoxyribose-phosphate aldolase-like [Rhagoletis zephyria]
1366900	0	1778300	0	802440	1411000	0	1985000	3327400	5	5	5	32.6	32.6	32.6	25.648	0	19.293	2.3E+07	27	gi|104806	gi|104806	1568	gi|1048067780|ref|XP 017464013.1| PREDICTED: neutral alpha-glucosidase AB-like [Rhagoletis zephyria];NODE 1655 length 14391 cov 793.435268 True 13688 neutral alpha-glucosidase AB
0	0	0	0	0	0	0	0	0	7	1	1	62.1	14.5	14.5	16.675	0	4.7066	1052800	4	gi|104806	gi|104806	1569	gi|1048067801|ref|XP 017464025.1| PREDICTED: soma ferritin-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	14	14	14	15.486	0.00061	3.5497	1064800	2	gi|104806	gi|104806	1570	gi|1048067803|ref|XP 017464026.1| PREDICTED: C-type lectin lectoxin-Lio2-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	1	1	29.4	19.3	19.3	13.574	0.0006	3.3545	474990	1	gi|104806	gi|104806	1571	gi|1048067864|ref|XP 017464060.1| PREDICTED: calmodulin-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	26.9	26.9	26.9	8.824	0.00224	2.8966	1810300	3	gi|104806	gi|104806	1572	gi|1048067878|ref|XP 017464069.1| PREDICTED: cdc42 homolog, partial [Rhagoletis zephyria];NODE 6483 length 3281 cov 679.274954 False 2639 cdc42 homolog
2729600	2493800	2631800	3625800	2833900	5959000	2036800	0	3856700	7	2	2	82.8	34.4	34.4	13.564	0	19.27	5.4E+07	28	gi|104806	gi|104806	1573	gi|1048067933|ref|XP 017464100.1| PREDICTED: aldehyde dehydrogenase, cytosolic 2-like, partial [Rhagoletis zephyria]
2621000	2401500	1835300	2445300	2228400	3804300	1212800	3548200	4664400	2	1	1	15.8	9.9	9.9	19.448	0	179.18	4.7E+07	24	gi|104806	gi|104806	1574	gi|1048067960|ref|XP 017464117.1| PREDICTED: innexin inx2-like, partial [Rhagoletis zephyria];NODE 307 length 45349 cov 708.365236 True 31488 Innexin inx2
1.1E+07	1.3E+07	1.3E+07	1E+07	1.2E+07	1.4E+07	5546600	1.2E+07	1.9E+07	13	13	1	68.3	68.3	3.4	30.807	0	66.806	4.7E+08	149	gi|104806	gi|104806	1575	gi|1048068055|ref|XP 017464170.1| PREDICTED: sorbitol dehydrogenase-like [Rhagoletis zephyria]
1291200	913150	1199000	1770800	0	1426500	1732500	1910100	1344400	3	3	3	13.9	13.9	13.9	35.846	0	27.96	1.9E+07	21	gi|104806	gi|104806	1576	gi|1048068107|ref|XP 017486182.1| PREDICTED: ubiquitin-like-conjugating enzyme ATG3 [Rhagoletis zephyria];NODE 2423 length 10300 cov 730.958224 False 2844 ubiquitin-like-conjugating enzyme ATG3
3601700	3099300	3867100	3765000	4145700	4947800	2308900	3819900	6855200	11	11	11	43.7	43.7	43.7	34.942	0	47.411	1.1E+08	62	gi|104806	gi|104806	1577	gi|1048068111|ref|XP 017486185.1| PREDICTED: ester hydrolase C11orf54 homolog [Rhagoletis zephyria];NODE 4257 length 5503 cov 763.142438 True 709 ester hydrolase C11orf54 homolog
3918000	3264200	3480100	4642100	4614900	5704900	1850600	3425100	5279700	8	8	8	51.6	51.6	51.6	24.265	0	70.036	1.4E+08	78	gi|104806	gi|104806	1578	gi|1048068113|ref|XP 017486186.1| PREDICTED: methylthioribulose-1-phosphate dehydratase-like [Rhagoletis zephyria];NODE 8621 length 2172 cov 743.175720 True 407 methylthioribulose-1-phosphate dehydratase
0	0	0	0	0	0	0	0	0	1	1	1	12.1	12.1	12.1	11.343	0.00613	2.2846	1.3E+07	8	NODE 57	NODE 57	1579	NODE 574 length 31621 cov 726.726478 False 5297 40S ribosomal protein S14;gi|1048068117|ref|XP 017486188.1| PREDICTED: 40S ribosomal protein S14 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	9.2	9.2	9.2	15.638	0.00058	3.18	1408100	4	NODE 9 |	NODE 9 |	1580	NODE 9 length 186394 cov 717.866013 False 63208 long-chain fatty acid transport protein 1-like;gi|1048068245|ref|XP 017486259.1| PREDICTED: long-chain fatty acid transport protein 1-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	2	2	6.3	6.3	6.3	54.879	0	7.0723	6520000	10	gi|104806	gi|104806	1581	gi|1048068265|ref|XP 017486269.1| PREDICTED: transmembrane protein 184B-like [Rhagoletis zephyria];NODE 175 length 55635 cov 670.799532 False 6659 transmembrane protein 184B isoform X1
8737300	6426800	7684900	7523000	8163000	8183300	8816200	1E+07	1.3E+07	11	11	11	56.2	56.2	56.2	38.605	0	177.25	4.1E+08	134	gi|104806	gi|104806	1582	gi|1048068267|ref|XP 017486270.1| PREDICTED: eukaryotic translation initiation factor 3 subunit I-like [Rhagoletis zephyria]
1419200	1359500	1082100	1476100	629690	1845600	1052900	1151700	1387800	10	10	6	8.3	8.3	4.5	241.74	0	39.513	2.7E+07	50	gi|104806	gi|104806	1583	gi|1048068303|ref|XP 017486290.1| PREDICTED: CAD protein-like [Rhagoletis zephyria]
8362200	7435600	9308700	1.2E+07	8549000	1.3E+07	2.2E+07	2.9E+07	3.7E+07	11	11	11	48.5	48.5	48.5	41.277	0	97.094	5.2E+08	128	gi|104806	gi|104806	1584	gi|1048068369|ref|XP 017486328.1| PREDICTED: phosphoserine aminotransferase-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	3.7	3.7	3.7	78.679	0	4.3311	577880	3	NODE 37	NODE 37	1585	NODE 374 length 39911 cov 715.537008 True 20055 hepatocyte growth factor-regulated tyrosine kinase substrate;gi|1048068438|ref|XP 017486367.1| PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate-like [Rhagoletis zephyria]
0	0	90767	102700	104460	1687300	4448100	5607400	8467100	40	40	3	26.5	26.5	1.5	278.8	0	231.53	1.9E+08	132	gi|104806	gi|104806	1586	gi|1048068440|ref|XP 017486368.1| PREDICTED: fatty acid synthase-like [Rhagoletis zephyria]
809040	0	1187700	1499100	1293900	0	2223300	0	2100400	5	5	5	30.5	30.5	30.5	30.196	0	15.77	2.3E+07	16	gi|104806	gi|104806	1587	gi|1048068467|ref|XP 017486382.1| PREDICTED: palmitoyl-protein thioesterase 1-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	10.6	10.6	10.6	12.294	0.00198	2.9774	0	1	gi|104806	gi|104806	1588	gi|1048068479|ref|XP 017486388.1| PREDICTED: enhancer of rudimentary homolog [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	4.6	4.6	4.6	27.157	0.00544	2.3686	8307700	7	NODE 37	NODE 37	1589	NODE 370 length 40098 cov 734.626352 True 15321 mannosyl-oligosaccharide alpha-1,2-mannosidase IA-like;gi|1048068481|ref|XP 017486389.1| PREDICTED: mannosyl-oligosaccharide alpha-1,2-mannosidase IA-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	4.9	4.9	4.9	46.093	0.00225	2.9427	370600	1	gi|104806	gi|104806	1590	gi|1048068529|ref|XP 017486415.1| PREDICTED: drebrin-like protein B [Rhagoletis zephyria]
1.1E+07	9457100	1.3E+07	1.4E+07	1.5E+07	1.5E+07	1.1E+07	1.3E+07	1.8E+07	9	9	9	50.5	50.5	50.5	34.006	0	85.511	3.8E+08	122	gi|104806	gi|104806	1591	gi|1048068537|ref|XP 017486420.1| PREDICTED: glycogenin-1-like [Rhagoletis zephyria]
1694200	1966400	1891400	1421600	0	0	0	3406400	4676200	4	4	4	18.1	18.1	18.1	30.23	0	19.784	3E+07	20	gi|104806	gi|104806	1592	gi|1048068545|ref|XP 017486426.1| PREDICTED: 60S ribosomal protein L7a-like [Rhagoletis zephyria];NODE 442 length 37388 cov 750.421557 False 10896 ribosomal protein L7a
0	0	0	0	0	0	0	0	0	1	1	1	19.7	19.7	19.7	8.6619	0	93.403	9436300	11	NODE 26	NODE 26	1593	NODE 2690 length 9320 cov 654.022882 False 2424 charged multivesicular body protein 1b;gi|1048068677|ref|XP 017486493.1| PREDICTED: charged multivesicular body protein 1b-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	4	4	4	5.7	5.7	5.7	107.14	0	8.7005	3625200	8	gi|104806	gi|104806	1594	gi|1048068687|ref|XP 017486499.1| PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Rhagoletis zephyria];gi|1048068685|ref|XP 017486498.1| PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Rhagoletis zephyria];NODE 284
2451900	2332200	2694900	3157600	2146000	2742800	3478900	4661700	5311700	16	16	16	47.9	47.9	47.9	48.423	0	81.684	9.7E+07	85	gi|104806	gi|104806	1595	gi|1048068703|ref|XP 017486507.1| PREDICTED: elongation factor Tu-like [Rhagoletis zephyria];NODE 2908 length 8648 cov 604.671360 False 8233 elongation factor Tu, mitochondrial
0	1250900	2132800	1226700	2101800	2157300	1339400	2392200	2826800	6	6	3	41.7	41.7	23.6	28.117	0	16.937	2.7E+07	28	gi|104806	gi|104806	1596	gi|1048068705|ref|XP 017486508.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial-like [Rhagoletis zephyria]
1853600	0	1942700	0	0	0	0	0	0	2	2	2	10	10	10	26.807	0.00031	3.8135	1.3E+07	13	gi|104806	gi|104806	1597	gi|1048068764|ref|XP 017486540.1| PREDICTED: superoxide dismutase [Cu-Zn]-like, partial [Rhagoletis zephyria];NODE 3545 length 6954 cov 644.510654 False 6917 Superoxide dismutase [Cu-Zn]
0	0	0	0	0	0	0	0	0	1	1	1	5.9	5.9	5.9	27.515	0.00381	2.7101	798300	2	NODE 55	NODE 55	1598	NODE 557 length 32567 cov 730.006705 False 16269 tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit wdr4;gi|1048068833|ref|XP 017486575.1| PREDICTED: tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit wdr4-like [Rhagoletis zephyria]
0	0	747880	0	0	1070000	0	0	0	3	3	3	7.7	7.7	7.7	47.933	0	4.611	3815600	11	gi|104806	gi|104806	1599	gi|1048068835|ref|XP 017486576.1| PREDICTED: heat shock factor protein-like [Rhagoletis zephyria]
5993300	6331900	6377400	6667300	6284900	7491600	4609500	7199900	9485400	20	20	20	52.6	52.6	52.6	55.934	0	146.24	4.7E+08	195	gi|104806	gi|104806	1600	gi|1048068837|ref|XP 017486577.1| PREDICTED: xaa-Pro dipeptidase-like [Rhagoletis zephyria];NODE 557 length 32567 cov 730.006705 False 30618 xaa-Pro dipeptidase
1E+07	1.1E+07	1.1E+07	1.2E+07	1E+07	1E+07	1E+07	1.4E+07	2E+07	39	39	34	65.2	65.2	56.1	89.066	0	323.31	8.1E+08	290	gi|104806	gi|104806	1601	gi|1048068952|ref|XP 017486639.1| PREDICTED: transitional endoplasmic reticulum ATPase-like [Rhagoletis zephyria];NODE 391 length 39090 cov 734.817548 True 3569 Transitional endoplasmic reticulum ATPase TER94
1.3E+07	1.2E+07	1.4E+07	1.4E+07	9559700	1.3E+07	1.5E+07	2.3E+07	3.2E+07	11	11	11	59.7	59.7	59.7	20.867	0	115.31	7.8E+08	178	gi|104806	gi|104806	1602	gi|1048068994|ref|XP 017486661.1| PREDICTED: ATP synthase subunit d, mitochondrial-like [Rhagoletis zephyria];NODE 336 length 42956 cov 721.378966 True 26720 ATP synthase subunit d, mitochondrial-like
0	0	0	0	0	0	0	0	0	1	1	1	22.4	22.4	22.4	9.9655	0.00525	2.4548	1748300	1	NODE 33	NODE 33	1603	NODE 336 length 42956 cov 721.378966 False 35544 ER lumen protein-retaining receptor;gi|1048068996|ref|XP 017486662.1| PREDICTED: ER lumen protein-retaining receptor 1-B-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	2	2	4.2	4.2	4.2	109.3	0	4.6633	3318400	7	gi|104806	gi|104806	1604	gi|1048069000|ref|XP 017486665.1| PREDICTED: exocyst complex component 2-like [Rhagoletis zephyria];NODE 827 length 25396 cov 716.219171 True 16642 exocyst complex component 2
0	0	2302200	2596600	0	0	0	5786100	6321600	5	5	5	19.1	19.1	19.1	44.098	0	15.129	2.7E+07	16	gi|104806	gi|104806	1605	gi|1048069010|ref|XP 017486670.1| PREDICTED: carboxypeptidase B-like [Rhagoletis zephyria];NODE 565 length 32137 cov 736.652671 True 11478 carboxypeptidase B-like
1E+07	9793800	1E+07	3.7E+07	3.3E+07	4E+07	1.2E+07	1.9E+07	3E+07	43	43	35	61.1	61.1	50.7	95.906	0	323.31	2.4E+09	549	gi|104806	gi|104806	1606	gi|1048069056|ref|XP 017486696.1| PREDICTED: sucrase-isomaltase, intestinal-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	14.3	14.3	14.3	21.572	0.00731	2.1968	638860	2	NODE 79	NODE 79	1607	NODE 793 length 25978 cov 712.349497 True 16358 atypical protein kinase C-like isoform X1;gi|1048069083|ref|XP 017486712.1| PREDICTED: atypical protein kinase C-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	5.5	5.5	5.5	28.883	0.0006	3.3569	617600	4	NODE 79	NODE 79	1608	NODE 793 length 25978 cov 712.349497 False 8974 cytoplasmic FMR1-interacting protein 2-like;gi|1048069085|ref|XP 017486713.1| PREDICTED: cytoplasmic FMR1-interacting protein [Rhagoletis zephyria]
3126100	3642500	3550600	3434200	2204000	4723000	5025600	4635000	6149000	24	24	24	38.4	38.4	38.4	97.324	0	61.166	9.4E+07	80	gi|104806	gi|104806	1609	gi|1048069087|ref|XP 017486714.1| PREDICTED: ubiquitin carboxyl-terminal hydrolase 5-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	3.7	3.7	3.7	68.446	0.00731	2.2039	695400	2	NODE 87	NODE 87	1610	NODE 876 length 24266 cov 715.666722 False 11628 phospholipase DDHD2 isoform X2;gi|1048069107|ref|XP 017486725.1| PREDICTED: phospholipase DDHD2-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	4	2	2	15.4	8.1	8.1	47.422	0	18.433	3550300	10	gi|104806	gi|104806	1611	gi|1048069186|ref|XP 017486767.1| PREDICTED: calphotin-like, partial [Rhagoletis zephyria]
914430	1129100	1149400	1523300	995780	1789700	2250400	2819600	3342000	8	8	8	32.9	32.9	32.9	33.661	0	18.744	3E+07	37	gi|104806	gi|104806	1612	gi|1048069192|ref|XP 017486770.1| PREDICTED: hydroxymethylglutaryl-CoA lyase, mitochondrial-like, partial [Rhagoletis zephyria];NODE 4132 length 5699 cov 722.413182 False 1258 Hydroxymethylglutaryl-CoA lyase, mitochondrial
1493100	2635100	2229200	1918500	2014700	2207100	0	1809800	2184200	5	5	5	20.3	20.3	20.3	35.105	0	12.611	5E+07	38	gi|104806	gi|104806	1613	gi|1048069241|ref|XP 017486795.1| PREDICTED: histidine-rich glycoprotein-like [Rhagoletis zephyria];NODE 4451 length 5256 cov 674.763507 True 4062 adhesion G- coupled receptor G7-like protein
683940	721750	742750	581180	400030	703000	729970	976000	997180	8	7	7	12.8	11.8	11.8	110	0	23.746	1.9E+07	39	gi|104806	gi|104806	1614	gi|1048069253|ref|XP 017486801.1| PREDICTED: 116 kDa U5 small nuclear ribonucleoprotein component-like [Rhagoletis zephyria]
0	0	8375700	6831900	0	5882700	1.2E+07	1.4E+07	0	8	1	0	17.2	3.7	0	71.364	0	20.433	6.5E+07	21	gi|104806	gi|104806	1615	gi|1048069293|ref|XP 017486823.1| PREDICTED: heat shock 70 kDa protein cognate 4 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	3	1	1	7.2	2.8	2.8	46.199	0.00172	3.0361	8233700	7	gi|104806	gi|104806	1616	gi|1048069309|ref|XP 017486830.1| PREDICTED: enolase-like [Rhagoletis zephyria]
5142300	5175100	4948400	7606400	6469200	7988900	7452800	9041000	1.1E+07	18	18	17	50.5	50.5	48.6	45.822	0	114.24	3.6E+08	147	gi|104806	gi|104806	1617	gi|1048069315|ref|XP 017486833.1| PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like [Rhagoletis zephyria]
4913000	4741700	4594500	4891600	4482700	6645900	8719600	9522400	9700900	8	8	8	57	57	57	23.496	0	37.764	1.6E+08	54	gi|104806	gi|104806	1618	gi|1048069385|ref|XP 017486868.1| PREDICTED: 5-formyltetrahydrofolate cyclo-ligase-like [Rhagoletis zephyria];NODE 15 length 154786 cov 732.466280 True 101983 5-formyltetrahydrofolate cyclo-ligase
1904000	1621600	1608800	2203700	0	2085000	2837700	2890600	4863400	8	8	8	27.1	27.1	27.1	50.704	0	34.503	5.6E+07	35	gi|104806	gi|104806	1619	gi|1048069393|ref|XP 017486874.1| PREDICTED: eukaryotic translation initiation factor 2 subunit 3-like [Rhagoletis zephyria];NODE 15 length 154786 cov 732.466280 True 88876 eukaryotic translation initiation factor 2 subunit 3-like
873230	678570	1030600	916280	0	998640	0	921720	1504500	6	6	6	51.4	51.4	51.4	21.109	0	16.891	2.2E+07	23	gi|104806	gi|104806	1620	gi|1048069395|ref|XP 017486875.1| PREDICTED: uncharacterized protein LOC108375287 [Rhagoletis zephyria];NODE 15 length 154786 cov 732.466280 False 88354 PREDICTED: uncharacterized protein LOC108375287
0	0	0	0	0	0	0	0	0	1	1	1	3.6	3.6	3.6	61.149	0.00032	3.9114	1609800	8	gi|104806	gi|104806	1621	gi|1048069397|ref|XP 017486876.1| PREDICTED: NCK-interacting protein with SH3 domain-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	7.1	7.1	7.1	39.17	0	5.9373	4437800	7	gi|104806	gi|104806	1622	gi|1048069399|ref|XP 017486877.1| PREDICTED: dimethylaniline monooxygenase [N-oxide-forming] 5-like, partial [Rhagoletis zephyria]
2608500	2527400	2638400	2526900	2963400	3833000	2821100	3448100	5248800	13	13	2	32.8	32.8	5.5	65.353	0	92.968	1.6E+08	126	gi|104806	gi|104806	1623	gi|1048069401|ref|XP 017486878.1| PREDICTED: UDP-glucose 4-epimerase-like [Rhagoletis zephyria]
1071700	0	1342300	1289000	1521100	1663300	1547600	1703100	3379200	10	10	10	13.2	13.2	13.2	110.4	0	56.084	4.1E+07	47	gi|104806	gi|104806	1624	gi|1048069421|ref|XP 017486889.1| PREDICTED: sodium/calcium exchanger 3-like [Rhagoletis zephyria];NODE 60 length 86167 cov 723.652151 False 41093 sodium/calcium exchanger 3-like
0	0	0	0	0	0	0	0	0	1	1	1	21.7	21.7	21.7	10.005	0	6.9717	7572300	7	gi|104806	gi|104806	1625	gi|1048069427|ref|XP 017486893.1| PREDICTED: U6 snRNA-associated Sm-like protein LSm5 [Rhagoletis zephyria]
3581800	3978100	4234500	2792600	2521200	3885700	3457400	5106200	6944500	17	17	17	42.2	42.2	42.2	71.815	0	169.83	1.8E+08	137	gi|104806	gi|104806	1626	gi|1048069443|ref|XP 017486901.1| PREDICTED: plastin-2-like [Rhagoletis zephyria]
592020	546180	675420	1155300	747520	1058400	2128200	3320300	2469400	17	17	17	27.1	27.1	27.1	106.2	0	96.755	6.2E+07	76	gi|104806	gi|104806	1627	gi|1048069492|ref|XP 017486928.1| PREDICTED: vinculin-like [Rhagoletis zephyria]
1.3E+07	1.5E+07	1.4E+07	1.7E+07	7168200	1.9E+07	1.7E+07	2.2E+07	3.2E+07	24	24	24	83	83	83	41.973	0	323.31	1.2E+09	304	gi|104806	gi|104806	1628	gi|1048069494|ref|XP 017486930.1| PREDICTED: 3-ketoacyl-CoA thiolase, mitochondrial-like [Rhagoletis zephyria]
1094900	0	0	1794100	0	1928900	0	2481500	4522000	5	5	4	24.9	24.9	20.7	32.471	0	14.136	2.5E+07	25	gi|104806	gi|104806	1629	gi|1048069498|ref|XP 017486932.1| PREDICTED: pyrroline-5-carboxylate reductase 3-like [Rhagoletis zephyria];NODE 464 length 36455 cov 743.745495 True 35895 pyrroline-5-carboxylate reductase 3-like;NODE 1118 length 19892 cov 710.504965 False 14479 pyrroline
7780900	7931600	8282100	8541600	8888000	8708100	7703100	9834500	1.3E+07	15	15	15	58.2	58.2	58.2	33.969	0	111.71	3.7E+08	203	NODE 65	NODE 65	1630	NODE 654 length 29324 cov 725.602822 True 4078 Proteasome subunit alpha type-1;gi|1048069506|ref|XP 017486937.1| PREDICTED: proteasome subunit alpha type-1-like [Rhagoletis zephyria]
0	1065900	1178400	857760	0	0	0	0	0	4	4	4	17.5	17.5	17.5	30.601	0	12.951	1.3E+07	15	gi|104806	gi|104806	1631	gi|1048069516|ref|XP 017486944.1| PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member B-like, partial [Rhagoletis zephyria]
1.5E+07	9727800	1.3E+07	0	1.4E+07	9654200	0	1.1E+07	1.4E+07	3	3	3	16.3	16.3	16.3	20.786	0	11.174	1.1E+08	46	gi|104806	gi|104806	1632	gi|1048069560|ref|XP 017486969.1| PREDICTED: acyl carrier protein, mitochondrial-like [Rhagoletis zephyria];NODE 2186 length 11317 cov 676.711863 False 9993 acyl carrier protein, mitochondrial isoform X1
0	0	0	0	0	0	0	0	0	2	2	2	12.2	12.2	12.2	24.927	0	4.47	3414900	3	gi|104806	gi|104806	1633	gi|1048069591|ref|XP 017486986.1| PREDICTED: 60S ribosomal protein L10a-2-like [Rhagoletis zephyria];NODE 3321 length 7549 cov 709.206165 True 5041 60S ribosomal protein L10a
0	0	0	0	0	1075400	618470	1369600	0	2	2	2	28	28	28	18.757	0	10.443	5824200	8	gi|104806	gi|104806	1634	gi|1048069695|ref|XP 017487040.1| PREDICTED: ubiquitin-conjugating enzyme E2 A [Rhagoletis zephyria];NODE 162 length 57653 cov 710.035105 False 22418 ubiquitin-conjugating enzyme E2 A
0	0	0	0	0	0	0	0	0	2	2	2	12.9	12.9	12.9	23.457	0	4.272	6739900	8	gi|104806	gi|104806	1635	gi|1048069721|ref|XP 017487056.1| PREDICTED: high mobility group protein DSP1-like [Rhagoletis zephyria];NODE 99 length 71160 cov 740.022825 True 3020 high mobility group protein DSP1-like;NODE 99 length 71160 cov 740.022825 True 3277 High mobility group p
4792200	4473900	4340900	4854800	4718800	5976700	7020600	5992500	8198800	6	6	3	56.4	56.4	28.2	17.984	0	24.601	7.9E+07	46	gi|104806	gi|104806	1636	gi|1048069729|ref|XP 017487060.1| PREDICTED: UMP-CMP kinase-like, partial [Rhagoletis zephyria]
1806900	1610400	2909500	0	0	1562400	0	2053200	0	5	4	3	27.2	21.6	16.4	29.864	0	53.799	1.9E+07	24	gi|104806	gi|104806	1637	gi|1048069758|ref|XP 017487077.1| PREDICTED: tubulin alpha chain-like [Rhagoletis zephyria];NODE 895 length 23854 cov 760.362830 True 7148 Tubulin alpha-1A chain
8420000	8666800	8717400	8396100	7535000	7640000	3734700	8080200	1.4E+07	5	5	1	56.4	56.4	8.5	10.513	0	103.31	2E+08	119	gi|104806	gi|104806	1638	gi|1048069848|ref|XP 017464209.1| PREDICTED: adenosine kinase-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	56.9	56.9	56.9	7.0925	0	13.765	437920	2	NODE 63	NODE 63	1639	NODE 636 length 29854 cov 709.047451 False 21365 charged multivesicular body protein 6-A-like;gi|1048069913|ref|XP 017464246.1| PREDICTED: charged multivesicular body protein 6-A-like, partial [Rhagoletis zephyria]
4331600	4522600	5898200	5680300	3636100	5375800	3058400	6987100	1.1E+07	9	9	4	62.7	62.7	27.4	23.515	0	86.256	1.5E+08	87	gi|104806	gi|104806	1640	gi|1048069921|ref|XP 017464250.1| PREDICTED: probable chitinase 2, partial [Rhagoletis zephyria]
1236800	812320	1463700	1536100	0	0	1661500	4214500	4437500	6	2	2	39.2	15.3	15.3	23.705	0	26.42	3E+07	22	gi|104806	gi|104806	1641	gi|1048069938|ref|XP 017464259.1| PREDICTED: laminin-like protein lam-2, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	2	2	13.9	13.9	13.9	17.803	0	4.6355	928330	4	gi|104806	gi|104806	1642	gi|1048069964|ref|XP 017464274.1| PREDICTED: neprilysin-1-like, partial [Rhagoletis zephyria];NODE 1085 length 20513 cov 769.055577 True 500 neprilysin-like isoform X1
0	0	0	0	0	0	0	0	0	2	2	2	12.4	12.4	12.4	39.133	0	7.2288	1850000	5	gi|104806	gi|104806	1643	gi|1048069982|ref|XP 017464285.1| PREDICTED: dynamin-like 120 kDa protein, mitochondrial, partial [Rhagoletis zephyria];NODE 342 length 42566 cov 692.494178 True 24487 dynamin-like 120 kDa protein, mitochondrial isoform X1
0	1243800	1007900	781770	735040	0	1023500	1573200	2429900	2	2	1	14.7	14.7	8.8	15.842	0	5.3288	1.8E+07	17	gi|104807	gi|104807	1644	gi|1048070034|ref|XP 017464316.1| PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit 3-like, partial [Rhagoletis zephyria];NODE 1708 length 13844 cov 702.977518 False 8198 phosphatase 2B at 14D-like protein
0	0	0	0	0	0	0	0	0	4	1	1	28.8	7.3	7.3	19.414	0.00031	3.6677	4.1E+07	15	gi|104807	gi|104807	1645	gi|1048070100|ref|XP 017464356.1| PREDICTED: heat shock-related 70 kDa protein 2-like, partial [Rhagoletis zephyria]
3946100	3600200	4608000	4516500	4985400	5691400	2302200	7358100	6999000	6	6	6	61.5	61.5	61.5	13.616	0	29.002	8.8E+07	49	gi|104807	gi|104807	1646	gi|1048070334|ref|XP 017487117.1| PREDICTED: V-type proton ATPase subunit F-like [Rhagoletis zephyria];NODE 848 length 24957 cov 661.678379 True 19078 V-type proton ATPase subunit F
3137800	3316300	3832800	2389900	3414300	5740600	2390500	3848900	4379100	10	10	10	60	60	60	31.393	0	29.531	9.1E+07	47	gi|104807	gi|104807	1647	gi|1048070474|ref|XP 017487189.1| PREDICTED: putative hydroxypyruvate isomerase [Rhagoletis zephyria];NODE 149 length 59631 cov 731.653166 False 30880 hydroxypyruvate isomerase-like protein
0	0	0	407900	0	516020	733630	869280	1259900	11	11	11	7.1	7.1	7.1	303.06	0	39.003	1.6E+07	31	gi|104807	gi|104807	1648	gi|1048070484|ref|XP 017487195.1| PREDICTED: dmX-like protein 2 [Rhagoletis zephyria];NODE 441 length 37407 cov 693.046129 True 21250 dmX-like protein 2
0	0	0	0	0	0	0	0	0	1	1	1	25.8	25.8	25.8	7.2609	0.00428	2.5885	2099600	6	NODE 13	NODE 13	1649	NODE 137 length 62057 cov 739.051369 False 35346 RING finger protein 11-like;gi|1048070504|ref|XP 017487206.1| PREDICTED: RING finger protein 11-like [Rhagoletis zephyria]
2257700	2620700	2207600	2895000	0	2455700	3114900	4294200	6887000	9	9	9	32.6	32.6	32.6	44.004	0	37.43	7.2E+07	51	gi|104807	gi|104807	1650	gi|1048070510|ref|XP 017487209.1| PREDICTED: adenylyltransferase and sulfurtransferase MOCS3-like [Rhagoletis zephyria];NODE 97 length 71692 cov 706.114005 False 41118 adenylyltransferase and sulfurtransferase MOCS3
0	0	0	0	0	0	0	0	0	1	1	1	14.3	14.3	14.3	12.84	0.00543	2.3683	453380	2	gi|104807	gi|104807	1651	gi|1048070514|ref|XP 017487212.1| PREDICTED: succinate dehydrogenase assembly factor 2-B, mitochondrial-like [Rhagoletis zephyria]
1.2E+07	1.4E+07	1.3E+07	2.3E+07	2E+07	2.6E+07	2.7E+07	3.6E+07	5E+07	14	14	12	65.8	65.8	59.6	35.295	0	130.29	8.5E+08	236	gi|104807	gi|104807	1652	gi|1048070516|ref|XP 017487213.1| PREDICTED: delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial-like [Rhagoletis zephyria];NODE 97 length 71692 cov 706.114005 False 32414 delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
0	0	0	0	0	0	0	0	0	6	4	4	14.2	9.9	9.9	66.571	0	5.9966	5188900	5	gi|104807	gi|104807	1653	gi|1048070560|ref|XP 017487236.1| PREDICTED: trifunctional enzyme subunit alpha, mitochondrial, partial [Rhagoletis zephyria];NODE 395 length 39024 cov 698.839154 False 23424 trifunctional enzyme subunit alpha, mitochondrial
3918900	3370400	3481500	3701000	2722400	3554200	2591600	3544000	3039100	6	5	5	35.8	32.5	32.5	27.166	0	16.605	6E+07	37	gi|104807	gi|104807	1654	gi|1048070580|ref|XP 017487247.1| PREDICTED: peroxiredoxin-4-like [Rhagoletis zephyria];NODE 327 length 43692 cov 738.782478 True 41028 peroxiredoxin-4-like protein
1.2E+07	1.2E+07	1.3E+07	1.4E+07	1.3E+07	1.5E+07	1.5E+07	2E+07	2.3E+07	36	36	27	69.2	69.2	53.5	68.108	0	323.31	1.3E+09	437	gi|104807	gi|104807	1655	gi|1048070586|ref|XP 017487251.1| PREDICTED: V-type proton ATPase catalytic subunit A-like [Rhagoletis zephyria]
0	0	478950	0	0	0	0	0	835820	1	1	1	5.9	5.9	5.9	24.443	0.0006	3.4729	5165900	13	NODE 10	NODE 10	1656	NODE 108 length 68920 cov 734.761824 False 33395 pancreatic triacylglycerol lipase-like;gi|1048070613|ref|XP 017487266.1| PREDICTED: pancreatic lipase-related protein 2-like, partial [Rhagoletis zephyria]
905740	931210	1240400	1242000	0	0	1968000	2373300	2949800	9	9	9	19.7	19.7	19.7	69.123	0	47.293	3.4E+07	31	gi|104807	gi|104807	1657	gi|1048070619|ref|XP 017487269.1| PREDICTED: polyadenylate-binding protein 4-like [Rhagoletis zephyria];NODE 108 length 68920 cov 734.761824 False 42599 polyadenylate-binding protein 4-like
0	0	0	0	0	0	0	0	0 +	1	1	1	2.5	2.5	2.5	53.723	1	-2	9885600	1	gi|104807	gi|104807	1658	gi|1048070691|ref|XP 017487306.1| PREDICTED: tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform X2 [Rhagoletis zephyria];gi|1048070689|ref|XP 017487305.1| PREDICTED: tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform X1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	4	4	4	3.3	3.3	3.3	247.3	0	14.657	3397600	7	gi|104807	gi|104807	1659	gi|1048070711|ref|XP 017487318.1| PREDICTED: fatty acid synthase-like [Rhagoletis zephyria];NODE 96 length 71730 cov 732.300886 False 19906 fatty acid synthase-like
1895000	0	1784100	1233000	0	0	1504600	0	0	6	6	6	20.8	20.8	20.8	68.708	0	28.603	1.7E+07	17	gi|104807	gi|104807	1660	gi|1048070713|ref|XP 017487319.1| PREDICTED: glucose dehydrogenase [FAD, quinone]-like [Rhagoletis zephyria];NODE 96 length 71730 cov 732.300886 False 24499 glucose dehydrogenase [FAD, quinone]-like
0	0	0	0	0	0	1503900	2248400	3250100	4	4	4	19.9	19.9	19.9	28.279	0	14.445	1.4E+07	17	gi|104807	gi|104807	1661	gi|1048070715|ref|XP 017487320.1| PREDICTED: 7-alpha-hydroxysteroid dehydrogenase-like [Rhagoletis zephyria]
9046300	8730400	1.1E+07	8454900	7202300	1.2E+07	1.1E+07	1.6E+07	1.9E+07	16	16	16	83.1	83.1	83.1	25.513	0	141.97	6.4E+08	209	gi|104807	gi|104807	1662	gi|1048070717|ref|XP 017487321.1| PREDICTED: dehydrogenase/reductase SDR family member 4-like [Rhagoletis zephyria]
2096100	2252600	2010000	2000700	1518800	1686800	1735400	2256000	2799900	12	12	12	25.4	25.4	25.4	82.453	0	42.608	4.8E+07	55	gi|104807	gi|104807	1663	gi|1048070719|ref|XP 017487322.1| PREDICTED: acylamino-acid-releasing enzyme-like [Rhagoletis zephyria];NODE 96 length 71730 cov 732.300886 True 31092 acylamino-acid-releasing enzyme-like
2016100	2248900	1876400	2053600	2342700	2221700	1805100	2383700	2561300	9	9	5	37.2	37.2	23.7	37.77	0	78.601	4.9E+07	64	gi|104807	gi|104807	1664	gi|1048070751|ref|XP 017487339.1| PREDICTED: eukaryotic translation initiation factor 3 subunit H-like [Rhagoletis zephyria]
3001700	2954400	3311900	2247300	1967300	2671100	1496100	3589800	4800300	12	12	2	13.7	13.7	1.7	124.07	0	38.045	9.6E+07	72	gi|104807	gi|104807	1665	gi|1048070767|ref|XP 017487345.1| PREDICTED: glycine--tRNA ligase-like [Rhagoletis zephyria]
643540	564730	0	0	0	0	503680	547520	807520	7	7	7	5.3	5.3	5.3	249.69	0	19.626	6368300	19	gi|104807	gi|104807	1666	gi|1048070769|ref|XP 017487346.1| PREDICTED: eIF-2-alpha kinase activator GCN1-like [Rhagoletis zephyria];NODE 725 length 27459 cov 727.364180 False 15016 eIF-2-alpha kinase activator GCN1
0	0	1401100	0	0	0	1305400	1426300	0	1	1	1	27	27	27	8.8267	0	57.807	1.2E+07	15	NODE 72	NODE 72	1667	NODE 725 length 27459 cov 727.364180 False 7833 transmembrane protein 120 homolog;gi|1048070771|ref|XP 017487348.1| PREDICTED: transmembrane protein 120 homolog [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	4.7	4.7	4.7	39.827	0.00569	2.3551	987290	2	gi|104807	gi|104807	1668	gi|1048070773|ref|XP 017487349.1| PREDICTED: protein spinster homolog 1-like [Rhagoletis zephyria];NODE 725 length 27459 cov 727.364180 True 4513 protein spinster isoform X1
1239100	1595200	1276300	2079700	0	1219600	2225800	2384100	2051600	5	5	5	38.2	38.2	38.2	21.77	0	16.392	2.9E+07	24	gi|104807	gi|104807	1669	gi|1048070799|ref|XP 017487363.1| PREDICTED: prefoldin subunit 3-like [Rhagoletis zephyria];NODE 354 length 41421 cov 723.963376 False 23810 Prefoldin subunit 3
5930800	6273300	6286000	7373800	7803500	8494000	6643000	9145900	1E+07	11	11	11	44.3	44.3	44.3	39.855	0	66.385	2.2E+08	68	gi|104807	gi|104807	1670	gi|1048070813|ref|XP 017487371.1| PREDICTED: V-type proton ATPase subunit d 1-like [Rhagoletis zephyria];NODE 1483 length 15752 cov 710.374084 True 9201 vacuolar ATP synthase subunit ac39
0	0	0	0	0	0	0	0	0	2	2	2	13.5	13.5	13.5	30.414	0	7.8837	1.1E+07	7	gi|104807	gi|104807	1671	gi|1048070821|ref|XP 017487376.1| PREDICTED: uncharacterized protein LOC108375741, partial [Rhagoletis zephyria];NODE 3039 length 8327 cov 710.941731 False 6199 early nodulin-75-like;NODE 3039 length 8327 cov 710.941731 False 5618 PREDICTED: uncharacterize
6185900	5591900	6155800	6662200	6745000	8034200	6465700	7462600	8968000	25	25	25	51.2	51.2	51.2	79.257	0	89.375	4E+08	195	gi|104807	gi|104807	1672	gi|1048070837|ref|XP 017487385.1| PREDICTED: 1,4-alpha-glucan-branching enzyme-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	566170	701340	4	4	4	14.4	14.4	14.4	45.039	0	10.985	5228200	10	gi|104807	gi|104807	1673	gi|1048070843|ref|XP 017487389.1| PREDICTED: hexokinase-2-like, partial [Rhagoletis zephyria];NODE 14 length 166485 cov 742.889641 False 10634 hexokinase type 2-like
2100800	2038300	2040500	2974200	2140500	2315700	3214700	5302400	4985700	12	12	12	17.1	17.1	17.1	95.858	0	62.438	5.8E+07	55	gi|104807	gi|104807	1674	gi|1048070845|ref|XP 017487390.1| PREDICTED: protein-methionine sulfoxide oxidase MICAL3-like, partial [Rhagoletis zephyria]
0	562280	589680	0	747180	841640	0	821660	1404000	2	2	2	35.1	35.1	35.1	10.768	0	10.911	9382600	15	NODE 69	NODE 69	1675	NODE 690 length 28405 cov 748.114497 True 13547 derlin-1-like;gi|1048070870|ref|XP 017487404.1| PREDICTED: derlin-1-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	18.6	18.6	18.6	12.898	0.00638	2.2778	1698700	2	NODE 69	NODE 69	1676	NODE 690 length 28405 cov 748.114497 False 19156 divalent-cation tolerance protein CutA;gi|1048070872|ref|XP 017487405.1| PREDICTED: uncharacterized protein LOC108375769 [Rhagoletis zephyria]
4.2E+07	4.5E+07	5.1E+07	6.7E+07	4E+07	5.8E+07	7.9E+07	9.6E+07	1.1E+08	11	11	11	73.3	73.3	73.3	17.748	0	72.558	1.1E+09	149	gi|104807	gi|104807	1677	gi|1048070874|ref|XP 017487406.1| PREDICTED: peptidyl-prolyl cis-trans isomerase-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	146.72	0.00847	2.1201	3.9E+07	9	gi|104807	gi|104807	1678	gi|1048070924|ref|XP 017487434.1| PREDICTED: putative elongator complex protein 1 [Rhagoletis zephyria]
2E+07	2.1E+07	2.2E+07	1.7E+07	2.1E+07	2E+07	1.3E+07	2.4E+07	2.9E+07	23	23	23	66.8	66.8	66.8	29.597	0	181.59	1E+09	205	gi|104807	gi|104807	1679	gi|1048070966|ref|XP 017487454.1| PREDICTED: tropomyosin-1, isoforms 9A/A/B-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	11.2	11.2	11.2	12.3	0.00617	2.3211	6161700	7	NODE 49	NODE 49	1680	NODE 4934 length 4684 cov 707.006697 False 1732 pyroglutamyl-peptidase 1-like protein isoform X1;gi|1048070972|ref|XP 017487458.1| PREDICTED: pyroglutamyl-peptidase 1-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	618780	850110	3	2	2	8.2	6.4	6.4	74.991	0	12.571	3438800	6	NODE 19	NODE 19	1681	NODE 1913 length 12700 cov 930.144326 False 5415 uncharacterized family 31 glucosidase KIAA1161-like;gi|1048070981|ref|XP 017487462.1| PREDICTED: uncharacterized family 31 glucosidase KIAA1161-like [Rhagoletis zephyria]
6.7E+07	6.4E+07	7.1E+07	9.8E+07	1E+08	1.1E+08	7.1E+07	1.1E+08	1.4E+08	46	46	37	52.4	52.4	42.7	113.05	0	323.31	8.5E+09	1078	gi|104807	gi|104807	1682	gi|1048070983|ref|XP 017487463.1| PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Rhagoletis zephyria]
1.7E+09	1.7E+09	1.7E+09	2E+09	1.8E+09	2.2E+09	1.7E+09	2.5E+09	2.9E+09	36	36	4	93.1	93.1	12.8	41.568	0	323.31	1.2E+11	3523	gi|104807	gi|104807	1683	gi|1048070985|ref|XP 017487464.1| PREDICTED: actin-4-like [Rhagoletis zephyria];NODE 1123 length 19853 cov 722.121022 True 4026 CRE-ACT-2 protein
0	0	0	0	0	0	0	0	0	1	1	1	6	6	6	20.398	0.00378	2.6594	3102000	2	gi|104807	gi|104807	1684	gi|1048071034|ref|XP 017487494.1| PREDICTED: peptidyl-prolyl cis-trans isomerase H-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	2	2	3.6	3.6	3.6	80.571	0.00525	2.4554	1461400	2	gi|104807	gi|104807	1685	gi|1048071048|ref|XP 017487502.1| PREDICTED: apoptotic chromatin condensation inducer in the nucleus-like [Rhagoletis zephyria];NODE 14 length 166485 cov 742.889641 False 138492 apoptotic chromatin condensation inducer in the nucleus-like
1.1E+07	1.1E+07	1.2E+07	1.4E+07	1.5E+07	1.7E+07	1.2E+07	1.7E+07	1.9E+07	6	6	6	71.2	71.2	71.2	12.001	0	104.07	3E+08	92	gi|104807	gi|104807	1686	gi|1048071050|ref|XP 017487503.1| PREDICTED: cytochrome b5-like [Rhagoletis zephyria]



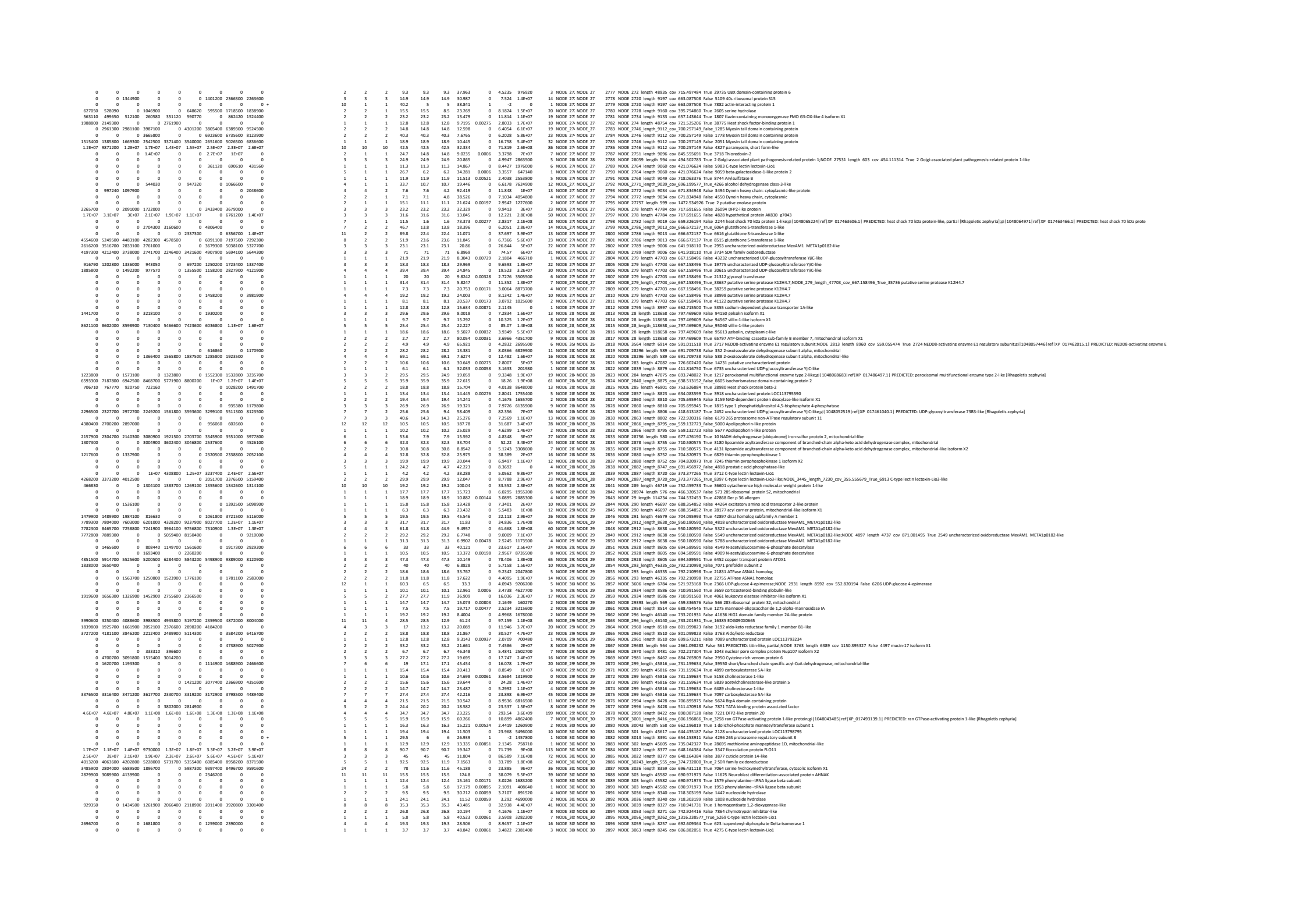


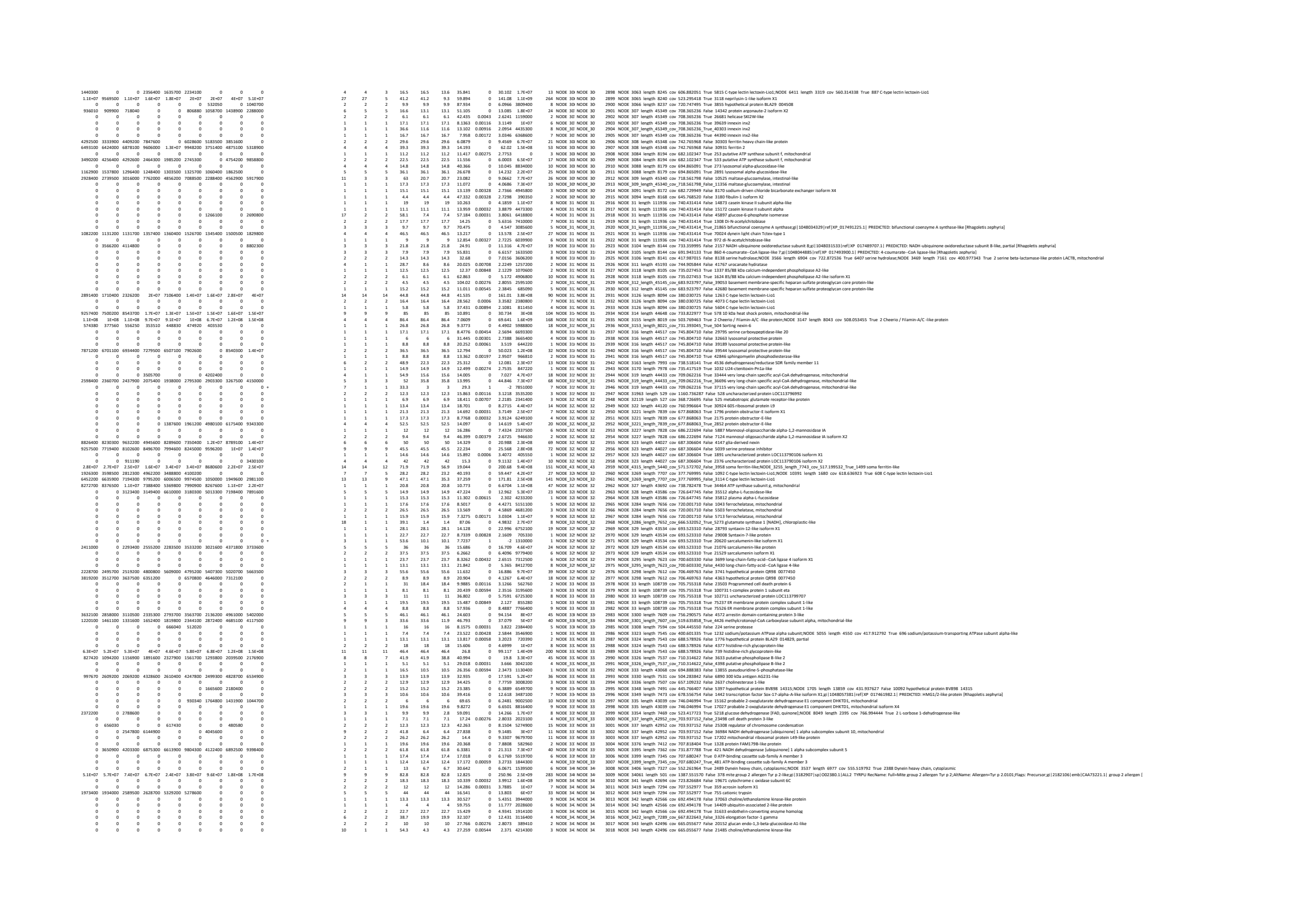
3352800	2777400	3458600	5776100	5267700	5201600	5712200	5859700	6804000		4	4	4	51	51	51	11.548	0	27.368	5.6E+07	33	NODE 14	NODE 14	2172	NODE 149 length 59631 cov 731.653166 False 9973 mitochondrial import inner membrane translocase subunit Tim13
7094200	6645400	7422700	4342300	4739800	5953800	4450500	1.5E+07	1.3E+07		11	11	9	52.8	52.8	52.8	24.518	0	37.899	2.7E+08	102	NODE 14	NODE 14	2173	NODE 1494 length 15655 cov 740.940385 True 11991 uncharacterized protein LOC113792410
0	0	0	0	0	0	0	0	0		1	1	1	30.7	30.7	30.7	10.175	0	5.53	626050	1	NODE 14	NODE 14	2174	NODE 1496 length 15610 cov 719.073995 False 4493 uncharacterized UDP-glucosyltransferase YjiC-like
744070	0	754940	488630	358500	684550	1276100	1021700	1603800		4	4	4	16.5	16.5	16.5	42.306	0	12.144	1.4E+07	28	NODE 14	NODE 14	2175	NODE 1496 length 15610 cov 719.073995 False 5675 uncharacterized UDP-glucosyltransferase YjiC-like
0	0	0	0	0	0	0	0	0		2	2	2	14.4	14.4	14.4	23.755	0	4.6764	600560	4	NODE 14	NODE 14	2176	NODE 1498 length 15554 cov 729.517324 False 8889 hypothetical protein BLA29 013531, partial
0	0	0	0	0	0	0	0	0		4	1	1	24	6	6	22.502	0.00545	2.3739	452130	1	NODE 15	NODE 15	2177	NODE 15 length 154786 cov 732.466280 False 65558 probable trans-2-enoyl-CoA reductase, mitochondrial
2300700	2281200	2474900	3784400	2983800	3042400	1842200	3384400	4162000		2	2	2	29.4	29.4	29.4	11.583	0	12.382	4.7E+07	20	NODE 15	NODE 15	2178	NODE 15 length 154786 cov 732.466280 True 57128 Beta-galactosidase
0	0	0	0	0	0	0	0	0		2	2	2	24.8	24.8	24.8	16.757	0	4.5457	1E+07	6	NODE 15	NODE 15	2179	NODE 15 length 154786 cov 732.466280 True 58520 beta-galactosidase-like protein
1994400	1576600	1737900	2661300	1864200	2097900	1244600	2332100	2601800		4	4	4	26.1	26.1	26.1	18.124	0	47.432	3.5E+07	24	NODE 15	NODE 15	2180	NODE 15 length 154786 cov 732.466280 True 58957 Beta-galactosidase
0	525860	425160	316570	391750	448450	0	0	532230		1	1	1	14.5	14.5	14.5	7.1133	0.00432	2.6518	4688600	13	NODE 15	NODE 15	2181	NODE 15 length 154786 cov 732.466280 True 66408 cytochrome c oxidase copper chaperone
6114700	5351300	5092000	6217300	6127400	7627300	5139600	5666100	7389800		13	13	13	33.4	33.4	33.4	44.507	0	88.265	2.4E+08	106	NODE 15	NODE 15	2182	NODE 1513 length 15415 cov 944.342969 False 11446 uncharacterized protein LOC113793556
1403000	0	0	2557400	0	0	0	0	0		8	3	3	37.6	15.8	15.8	30.372	0	7.1503	2E+07	11	NODE 15	NODE 15	2183	NODE 1513 length 15415 cov 944.342969 False 12993 deoxyribose-phosphate aldolase-like
1897500	1346900	981490	2274400	1397800	1809200	3537800	3240700	1879800		6	5	5	30.9	26.7	26.7	29.46	0	33.207	3.5E+07	30	NODE 15	NODE 15	2184	NODE 1513 length 15415 cov 944.342969 True 13807 pseudouridine-5-phosphatase isoform X1
0	0	0	0	0	0	0	0	0		3	3	3	17.4	17.4	17.4	29.59	0	11.154	1.1E+07	7	NODE 19	NODE 19	2185	NODE 1954 length 12502 cov 532.946332 True 1079 Golgi-associated plant pathogenesis-related protein 1-like;NODE 1514 length 15381 cov 561.275936 False 10143 Golgi-associated plant pathogenesis-related protein 1-like
0	0	0	0	0	0	0	0	0		2	2	2	14.9	14.9	14.9	22.012	0	5.1867	3817300	5	NODE 53	NODE 53	2186	NODE 5308 length 4280 cov 656.388402 False 780 Golgi-associated plant pathogenesis-related protein 1;NODE 1514 length 15381 cov 561.275936 False 11881 Golgi-associated plant pathogenesis-related protein 1
3611400	3551500	4769700	4867100	1.1E+07	8616500	5334500	4637800	6528800		6	6	6	43.9	43.9	43.9	25.054	0	37.853	1.1E+08	45	NODE 53	NODE 53	2187	NODE 5308 length 4280 cov 656.388402 False 2686 secretion protein;NODE 1514 length 15381 cov 561.275936 False 13787 cysteine-rich secretory protein family protein
0	0	0	1.2E+07	0	9642100	1.1E+07	0	0		4	4	2	39.9	39.9	22.8	18.235	0	11.107	9.4E+07	18	NODE 15	NODE 15	2188	NODE 1514 length 15381 cov 561.275936 False 15380 Golgi-associated plant pathogenesis-related protein 1-like;NODE 5308 length 4280 cov 656.388402 False 4279 cysteine-rich secretory protein family protein
0	0	0	0	0	0	0	0	0		2	2	2	16	16	16	16.951	0.00172	3.0415	1847000	3	NODE 19	NODE 19	2189	NODE 1954 length 12502 cov 532.946332 True 9098 Golgi-associated plant pathogenesis-related protein 1-like;NODE 1514 length 15381 cov 561.275936 False 1741 Golgi-associated plant pathogenesis-related protein 1-like
0	0	0	0	0	0	0	0	0		1	1	1	26.5	26.5	26.5	10.793	0	6.7949	4.8E+07	9	NODE 19	NODE 19	2190	NODE 1954 length 12502 cov 532.946332 True 10114 Golgi-associated plant pathogenesis-related protein 1-like;NODE 1514 length 15381 cov 561.275936 False 732 Golgi-associated plant pathogenesis-related protein 1-like
0	0	0	0	0	0	0	0	0	+	13	1	1	42	5	5	39.644	1	-2	3249100	4	NODE 15	NODE 15	2191	NODE 1518 length 15375 cov 690.165731 False 14770 Tubulin beta-1 chain
896560	0	1164500	1665800	1235400	0	0	1174300	2893200		6	2	0	20.6	7.4	0	37.251	0	5.9333	1.5E+07	18	NODE 15	NODE 15	2192	NODE 1521 length 15333 cov 691.807043 True 13868 adenylyl cyclase-associated protein 1
0	0	0	0	0	0	0	0	0		5	3	3	19.6	14.1	14.1	37.053	0	7.2408	3185600	4	NODE 15	NODE 15	2193	NODE 1529 length 15284 cov 725.027710 True 2850 C-type lectin lectoxin-Lio1
0	0	0	4266200	5725500	7428900	7879200	8480800	1.2E+07		5	5	4	23.8	23.8	20.6	36.389	0	30.497	1E+08	31	NODE 15	NODE 15	2194	NODE 1529 length 15284 cov 725.027710 True 4384 C-type lectin lectoxin-Lio1
1796900	1750100	2182000	5818100	5331700	9816600	8027600	8517100	1.2E+07		9	9	9	61.8	61.8	61.8	25.972	0	58.202	1.6E+08	81	NODE 15	NODE 15	2195	NODE 1529 length 15284 cov 725.027710 True 8683 3-hydroxyacyl-CoA dehydrogenase type-2-like
1272400	1198600	1391800	1299100	1103600	0	1514800	1830200	1928100		2	2	2	18.5	18.5	18.5	16.796	0	7.0989	1.7E+07	19	NODE 15	NODE 15	2196	NODE 1532 length 15247 cov 701.355911 False 1890 proteasome inhibitor PI31 subunit
0	0	0	0	0	0	0	0	0		1	1	1	4.8	4.8	4.8	23.344	0.00895	2.1098	4068900	9	NODE 15	NODE 15	2197	NODE 1532 length 15247 cov 701.355911 False 2486 Proteasome inhibitor PI31 subunit
1E+07	8937400	9875100	2E+07	2.2E+07	2E+07	1.5E+07	1.4E+07	1.8E+07		4	4	4	27.9	27.9	27.9	18.218	0	17.642	3.9E+08	57	NODE 15	NODE 15	2198	NODE 1534 length 15237 cov 923.102226 False 3463 fibrinolytic enzyme, isozyme C-like
0	0	0	0	0	0	0	0	0		1	1	1	4.6	4.6	4.6	37.752	0	6.0791	5040000	5	NODE 15	NODE 15	2199	NODE 1539 length 15211 cov 639.331156 True 4881 myb-like protein AA
0	0	0	0	0	0	0	0	0		1	1	1	6.6	6.6	6.6	27.153	0	4.5295	877770	5	NODE 15	NODE 15	2200	NODE 1539 length 15211 cov 639.331156 True 6237 myb-like protein AA
0	0	0	0	0	0	0	0	0		1	1	1	3.3	3.3	3.3	104.14	0	4.1932	2987000	8	NODE 15	NODE 15	2201	NODE 1540 length 15208 cov 729.665347 True 2341 dystroglycan isoform X2
0	0	0	0	0	0	0	0	0		2	2	2	13	13	13	24.654	0.00031	3.8096	611330	2	NODE 15	NODE 15	2202	NODE 1540 length 15208 cov 729.665347 True 5225 Dystroglycan-like protein
1969200	2799900	1783000	1367000	1402800	2081000	0	2059000	3389600		8	3	3	33.1	14.2	14.2	34.284	0	15.234	2.6E+07	34	NODE 15	NODE 15	2203	NODE 1542 length 15201 cov 732.203420 False 3942 puromycin-sensitive aminopeptidase-like protein
0	1679400	0	1265300	1011300	1528300	0	2018000	0		2	1	1	14.1	7.3	7.3	23.492	0	31.523	1.7E+07	21	NODE 15	NODE 15	2204	NODE 1542 length 15201 cov 732.203420 True 6889 puromycin-sensitive aminopeptidase-like protein
1584900	1710300	1652800	3083300	2327100	3202800	2212300	4651900	5580400		6	6	6	36.2	36.2	36.2	24.292	0	18.902	7E+07	39	NODE 15	NODE 15	2205	NODE 1544 length 15179 cov 789.976131 False 12511 adenylate kinase isoenzyme 1-like isoform X2
0	0	0	0	0	0	0	0	0		2	2	2	32	32	32	13.817	0	6.5046	2871600	5	NODE 15	NODE 15	2206	NODE 15595 length 1036 cov 711.191641 True 668 secretion protein
5268900	5468300	5039200	1387700	3530700	4787000	1830400	5089700	5257000		10	8	4	77.4	59.1	27	15.667	0	37.222	1.2E+08	62	NODE 15	NODE 15	2207	NODE 1560 length 15075 cov 772.720306 False 5858 ferritin;NODE 3754 length 6402 cov 714.289271 False 6003 ferritin-like protein;gi|1048056941|ref|XP 017461745.1| PREDICTED: soma ferritin-like [Rhagoletis zephyria]
2060300	1496300	2021200	2275000	1482000	2065600	3604100	2799200	4444600		5	5	4	41.1	41.1	33.7	19.61	0	19.796	4.3E+07	27	NODE 15	NODE 15	2208	NODE 15628 length 1034 cov 348.511747 False 1031 AMP-binding protein;NODE 15875 length 1018 cov 315.841121 False 1015 AMP-binding protein
0	0	0	0	0	0	0	0	0		1	1	1	7.5	7.5	7.5	21.428	0.00937	2.0732	0	3	NODE 15	NODE 15	2209	NODE 1570 length 14978 cov 701.000536 True 582 uncharacterized protein LOC113793589
0	0	387540	431660	0	0	828520	700930	805340		2	2	2	10.1	10.1	10.1	39.927	0	8.5469	6011500	17	NODE 15	NODE 15	2210	NODE 1572 length 14960 cov 729.614358 True 4762 putative mediator of RNA polymerase II transcription subunit 26
1.4E+07	1.4E+07	1.5E+07	7902500	1E+07	1.1E+07	0	1.3E+07	2.9E+07		2	2	2	26.1	26.1	26.1	13.178	0	41.133	1.4E+08	32	NODE 15	NODE 15	2211	NODE 1573 length 14949 cov 743.084464 False 357 protein D2-like isoform X2
7255500	0	8863100	7361900	5032300	9897800	1.2E+07	1.1E+07	1.4E+07		1	1	1	54.2	54.2	54.2	8.1181	0	21.595	1E+08	34	NODE 15	NODE 15	2212	NODE 1573 length 14949 cov 743.084464 False 485 Phosphatidylethanolamine-binding protein 1
0	0	0	0	0	0	0	0	0		2	2	2	15.5	15.5	15.5	6.5887	0.00032	3.8285	1.4E+07	4	NODE 15	NODE 15	2213	NODE 1573 length 14949 cov 743.084464 False 794 protein D3-like
0	0	0	0	0	0	0	0	0		1	1	1	9.4	9.4	9.4	13.802	0.0085	2.131	6837300	4	NODE 15	NODE 15	2214	NODE 158 length 58128 cov 721.164500 True 26007 tripeptidyl-peptidase 2-like
1171400	1287600	1269200	0	0	0	0	0	2653400		4	4	4	15.8	15.8	15.8	35.907	0	9.2749	2.1E+07	15	NODE 15	NODE 15	2215	NODE 158 length 58128 cov 721.164500 True 26356 tripeptidyl-peptidase 2
0	925120	884080	692550	0	924600	844220	1192500	1740500		3	3	3	22.4	22.4	22.4	19.232	0	5.815	1.5E+07	26	NODE 15	NODE 15	2216	NODE 158 length 58128 cov 721.164500 True 27523 tripeptidyl-peptidase 2 isoform X2
2160200	0	2493700	0	2899200	3619300	0	3985700	4736000		3	3	3	10.8	10.8	10.8	37.474	0	7.19	3E+07	16	NODE 15	NODE 15	2217	NODE 158 length 58128 cov 721.164500 True 28271 tripeptidyl-peptidase 2 isoform X1
0	0	0	0	0	0	0	0	0		2	2	2	8.5	8.5	8.5	18.742	0.00451	2.5279	1879500	2	NODE 15	NODE 15	2218	NODE 158 length 58128 cov 721.164500 True 29343 tripeptidyl-peptidase 2-like
0	0	0	0	0	0	0	0	0		2	2	2	20.9	20.9	20.9	14.948	0.00058	3.162	3378600	5	NODE 15	NODE 15	2219	NODE 158 length 58128 cov 721.164500 True 47863 putative gamma-glutamylcyclotransferase CG2811 isoform X4
0	0	0	0	0	0	0	0	0		1	1	1	17.9	17.9	17.9	12.25	0.0006	3.3778	1327400	4	NODE 15	NODE 15	2220	NODE 15849 length 1019 cov 722.298755 True 0 neuronal acetylcholine receptor subunit alpha-5-like
0	0	0	0	0	0	0	0	0		1	1	1	5	5	5	29.603	0	5.0875	9713000	9	NODE 15	NODE 15	2221	NODE 1587 length 14867 cov 718.180664 True 5471 thioredoxin reductase 1, cytoplasmic-like
0	0	0	0	0	0	0	1477700	4112100		3	3	3	49.6	49.6	49.6	13.053	0	12.249	2.2E+07	12	NODE 15	NODE 15	2222	NODE 1587 length 14867 cov 718.180664 True 6371 thioredoxin reductase 1, cytoplasmic-like
0	0	0	0	0	0	0	0	0		2	1	1	22.5	14	14	14.374	0	4.8619	2E+07	8	NODE 15	NODE 15	2223	NODE 1587 length 14867 cov 718.180664 True 6751 thioredoxin reductase 1, cytoplasmic-like
1939600	1614700	1969400	0	0	1648400	0	0	2700900		6	4	4	36.8	28.7	28.7	22.878	0	55.554	2.1E+07	18	NODE 15	NODE 15	2224	NODE 1587 length 14867 cov 718.180664 True 7160 thioredoxin reductase 1, cytoplasmic-like
0	0	0	0	0	0	0	0	0		1	1	1	24.2	24.2	24.2	10.485	0	19.141	1.9E+07	12	NODE 15	NODE 15	2225	NODE 1587 length 14867 cov 718.180664 True 7827 Thioredoxin reductase 1, cytoplasmic
1564400	1925000	0	0	0	0	0	0	0		2	2	2	7.1	7.1	7.1	38.59	0	4.4384	4917500	5	NODE 15	NODE 15	2226	NODE 15870 length 1018 cov 689.937695 False 1016 Apolipophorin-like protein
0	0	0	0	0	0	0	0	0		1	1	1	18.2	18.2	18.2	6.08	0.00475	2.4934	6589200	3	NODE 15	NODE 15	2227	NODE 159 length 58072 cov 727.098299 True 20427 Proteasome subunit alpha type-4
0	1534900	1226200	1805000	0	0	0	2122200	3554900		3	3	3	18.7	18.7	18.7	28.402	0	8.1537	2.1E+07	18	NODE 15	NODE 15	2228	NODE 159 length 58072 cov 727.098299 True 20640 Proteasome subunit alpha type-4
0	0	0	0	0	0	0	0	0		2	2	2	3.7	3.7	3.7	140.44	0	4.2106	1050400	2	NODE 15	NODE 15	2229	NODE 1593 length 14850 cov 779.116053 True 916 serine-rich adhesin for platelets-like;gi|1048052357|ref|XP 017460950.1| PREDICTED: mucin-2-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+	5	1	1	83.3	16.7	16.7	7.1741	1	-2	118780	0	NODE 15	NODE 15	2230	NODE 15943 length 1012 cov 1052.582027 False 198 heat shock 70 kDa cognate protein
2906200	2412700	2561400	2474700	0	3107400	3870800	4648700	5455100		5	3	3	58.3	36.1	36.1	7.959	0	9.0009	5.6E+07	25	NODE 15	NODE 15	2231	NODE 15943 length 1012 cov 1052.582027 False 446 heat shock cognate 71 kDa protein-like
0	0	0	0	0	0	0	0	0		6	2	2	35.1	13.9	13.9	21.705	0	4.889	1.2E+07	6	NODE 15	NODE 15	2232	NODE 1596 length 14813 cov 444.379862 True 11980 secretion protein
1766200	1632500	2512000	988470	1264000	1126400	4590800	5521900	6045800		3	3	3	31.1	31.1	31.1	20.763	0	38.154	8.1E+07	61	NODE 15	NODE 15	2233	NODE 1596 length 14813 cov 444.379862 True 13999 PR-1-like protein
0	0	0	0	0	0	0	0	0		1	1	1	2.1	2.1	2.1	91.358	0.0085	2.1322	0	1	NODE 18	NODE 18	2234	NODE 1882 length 12869 cov 517.153114 False 9605 pre-mRNA-processing factor 6;NODE 1596 length 14813 cov 444.379862 True 3252 pre-mRNA-processing factor 6
0	0	0	0	0	0	0	0	0		1	1	1	41.2	41.2	41.2	7.7067	0.00613	2.2849	1504600	1	NODE 15	NODE 15	2235	NODE 15962 length 1011 cov 362.367155 True 2 uncharacterized UDP-glucosyltransferase YjiC-like
0	0	0	0	0	0	0	0	0		5	1	1	27.2	6.7	6.7	28.568	0	11.175	2.6E+07	8	NODE 16	NODE 16	2236	NODE 16 length 150051 cov 736.100756 True 131310 endoplasmic reticulum resident protein 29
594540	0	0	0	0	0	600760	0	0		3	3	3	7.7	7.7	7.7	76.15	0	11.678	7375400	10	NODE 16	NODE 16	2237	NODE 16 length 150051 cov 736.100756 True 139337 Methylmalonyl-CoA mutase, mitochondrial;gi|1048019749|ref|XP 017488025.1| PREDICTED: methylmalonyl-CoA mutase, mitochondrial-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		3	3	3	42.9	42.9	42.9	8.5026	0	9.5332	2.9E+07	13	NODE 16	NODE 16	2238	NODE 160 length 58023 cov 721.874655 True 1652 bolA-like protein 2
0	0	0	0	0	0	8000800	9692900	8552600		1	1	1	21.5	21.5	21.5	8.0853	0	5.22	4.2E+07	14	NODE 16	NODE 16	2239	NODE 160 length 58023 cov 721.874655 True 55448 cuticle protein 64-like
2680800	2193700	3026800	3659600	0	4969800	1.2E+07	1.2E+07	1.3E+07		3	3	3	27.8	27.8	27.8	11.25	0	5.7071	9.8E+07	30	NODE 16	NODE 16	2240	NODE 160 length 58023 cov 721.874655 True 55684 pleckstrin homology-like domain family A member 1
0	0	0	0	0	0	0	0	0		1	1	1	7.9	7.9	7.9	28.626	0.00171	3.0086	5285600	8	NODE 16	NODE 16	2241	NODE 1629 length 14565 cov 710.083873 True 3218 uncharacterized protein LOC113793316
0	0	0	0	0	0	0	0	0		1	1	1	8.1	8.1	8.1	20.006	0	4.0514	1474700	2	NODE 16	NODE 16	2242	NODE 1629 length 14565 cov 710.083873 True 3904 hypothetical protein QR98 0088340
0	0	0	0	0	137850	0	168990	0		4	4	4	3	3	3	214.09	0	8.8971	943040	8	NODE 16	NODE 16	2243	NODE 163 length 57499 cov 688.371858 False 21438 Ankyrin repeat-containing domain,Ankyrin repeat
0	0	0	340220	0	0	463570	529940	0		2	2	2	37.3	37.3	37.3	11.122	0	8.0923	4501200	10	NODE 16	NODE 16	2244	NODE 1634 length 14506 cov 767.025327 True 13403 polyadenylate-binding protein-interacting protein 1-like
0	0	0	0	0	0	0	0	0		1	1	1	9.6	9.6	9.6	12.853	0.00327	2.7209	1.1E+07	8	NODE 16	NODE 16	2245	NODE 1640 length 14480 cov 724.370953 True 1105 phytanoyl-CoA dioxygenase, peroxisomal-like
0	0	0	0	0	0	0	0	0		1	1	1	17.5	17.5	17.5	16.022	0	6.0347	1.2E+07	10	NODE 16	NODE 16	2246	NODE 1640 length 14480 cov 724.370953 True 1585 phytanoyl-CoA dioxygenase, peroxisomal
0	0	0	0	0	0	0	0	0		4	4	4	20.9	20.9	20.9	18.07	0	10.53	1.7E+07	5	NODE 16	NODE 16	2247	NODE 1640 length 14480 cov 724.370953 True 3382 phytanoyl-CoA dioxygenase, peroxisomal
0	0	0	0	0	0	3860100	2937600	7635100		6	6	6	45.6	45.6	45.6	23.316	0	24.432	3.9E+07	15	NODE 16	NODE 16	2248	NODE 1640 length 14480 cov 724.370953 True 3994 phytanoyl-CoA dioxygenase, peroxisomal-like
2692700	2023300	2465000	2594200	0	2888900	4007000	3501200	5133400		2	2	2	6.4	6.4	6.4	25.36	0	39.897	3.8E+07	20	NODE 16	NODE 16	2249	NODE 1654 length 14401 cov 860.040917 False 13438 thioredoxin-like protein 1
0	0	0	0	1246500	0	0	0	1907100		3	3	3	20.8	20.8	20.8	16.068	0	5.8911	1.1E+07	11	NODE 16	NODE 16	2250	NODE 1654 length 14401 cov 860.040917 False 7339 thioredoxin-like protein 1
654500	0	856450	0	0	0	0	1060600	1972200		6	6	6	19.7	19.7	19.7	57.391	0	8.9451	1.2E+07	16	NODE 16	NODE 16	2251	NODE 1655 length 14391 cov 793.435268 True 11163 neutral alpha-glucosidase AB-like isoform X1;NODE 1655 length 14391 cov 793.435268 True 5020 neutral alpha-glucosidase AB-like
0	0	0	0	0	0	0	0	0		1	1	1	13.5	13.5	13.5	17.181	0.00172	3.045	2931000	3	NODE 16	NODE 16	2252	NODE 1655 length 14391 cov 793.435268 True 6575 neutral alpha-glucosidase AB;NODE 1655 length 14391 cov 793.435268 True 12794 neutral alpha-glucosidase AB
0	0	0	0	0	0	0	0	0		1	1	1	20.4	20.4	20.4	11.034	0	4.41	5939400	3	NODE 16	NODE 16	2253	NODE 166 length 56776 cov 684.232612 False 35389 Der f 36 allergen
0	0	0	1274900	0	2830300	0	0	969260		2	2	2	44.6	44.6	44.6	6.1582	0	6.0517	1.3E+07	15	NODE 16	NODE 16	2254	NODE 166 length 56776 cov 684.232612 False 35584 Der p 36 allergen
0	0	0	0	0	0	0	0	0		1	1	1	7.1	7.1	7.1	22.012	0	8.7255	9766300	4	NODE 16	NODE 16	2255	NODE 166 length 56776 cov 684.232612 False 36029 Der p 36 allergen
0	0	0	0	0	0	0	0	0		2	2	2	13.8	13.8	13.8	19.007	0.00354	2.7156	2030500	3	NODE 16	NODE 16	2256	NODE 166 length 56776 cov 684.232612 False 53095 Mitochondrial enolase superfamily member 1
0	0	0	1083800	0	0	1828100	1548100	0		3	3	3	37	37	37	15.729	0	7.4973	8549500	11	NODE 16	NODE 16	2257	NODE 166 length 56776 cov 684.232612 False 53521 fuconate dehydratase
0	0	0	0	0	0	0	0	0		1	1	1	14.9	14.9	14.9	7.801	0.00454	2.5808	3182100	6	NODE 28	NODE 28	2258	NODE 288 length 46733 cov 654.383457 False 23374 copine-like protein;NODE 166 length 56776 cov 684.232612 True 34434 copine-8-like
1129100	1736500	0	0	0	0	0	0	4062300		2	2	2	22.2	22.2	22.2	13.498	0	11.681	2E+07	13	NODE 16	NODE 16	2259	NODE 1662 length 14272 cov 698.188014 False 1283 dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial
0	0	0	0	0	0	0	0	0		2	2	2	17.1	17.1	17.1	12.081	0.00032	3.8911	2.1E+07	11	NODE 16	NODE 16	2260	NODE 1662 length 14272 cov 698.188014 False 1619 dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial-like
6058100	5400400	5171900	6502700	5296300	7408500	6676500	6753600	9319100		3	3	3	26.9	26.9	26.9	19.869	0	15.623	8.2E+07	32	NODE 16	NODE 16	2261	NODE 1662 length 14272 cov 698.188014 False 2245 dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial-like
4558100	8294200	6140300	4040700	8841100	0	3765900	1.4E+07	0		2	2	2	22	22	22	13.283	0	10.176	6.8E+07	26	NODE 16	NODE 16	2262	NODE 1662 length 14272 cov 698.188014 False 2609 dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;gi|1048065162|ref|XP 017463571.1| PREDICTED: dihydrolipoyllysine-residue acetyltransferase component o
0	0	0	0	0	0	0	0	0		2	2	2	28.6	28.6	28.6	7.027	0.00172	3.0512	8539400	6	NODE 16	NODE 16	2263	NODE 1676 length 14150 cov 716.054700 False 11939 putative serine protease 47
0	0	0	0	0	0	0	0	0		2	2	2	17.2	17.2	17.2	19.751	0	6.6244	8104400	12	NODE 16	NODE 16	2264	NODE 16768 length 963 cov 749.549559 True 373 glycerophosphocholine phosphodiesterase GPCPD1-like isoform X2
0	0	0	0	0	0	0	0	0		7	3	3	24.2	11.1	11.1	45.922	0	4.0011	2673800	3	NODE 16	NODE 16	2265	NODE 1679 length 14095 cov 728.328561 True 4419 alpha-N-acetylglucosaminidase
0	0	0	0	0	0	0	0	0		2	2	2	21.9	21.9	21.9	14.899	0	7.7932	1E+07	5	NODE 16	NODE 16	2266	NODE 1679 length 14095 cov 728.328561 True 5628 alpha-N-acetylglucosaminidase
0	0	4765200	4346700	4267800	0	6329200	0	0		1	1	1	29.4	29.4	29.4	10.069	0	6.0568	3.6E+07	20	NODE 16	NODE 16	2267	NODE 1679 length 14095 cov 728.328561 True 6642 hypothetical protein BLA29 013675, partial
1.8E+07	1.5E+07	1.6E+07	1.8E+07	1E+07	1.5E+07	1.6E+07	2.4E+07	3E+07		3	3	3	47.1	47.1	47.1	8.2403	0	28.462	2.4E+08	56	NODE 16	NODE 16	2268	NODE 1679 length 14095 cov 728.328561 True 6900 uncharacterized protein LOC113788571
0	1212800	1552100	2908100	0	2765900	0	0	0		3	3	3	10.7	10.7	10.7	38.182	0	7.2966	1.6E+07	11	NODE 16	NODE 16	2269	NODE 1684 length 14055 cov 453.442857 True 4130 C-type lectin lectoxin-Lio1;NODE 2194 length 11291 cov 622.954076 False 8730 C-type lectin lectoxin-Lio1
0	0	0	8193600	0	9630700	0	4749400	0		4	4	2	35.3	35.3	20.1	15.029	0	31.087	3.8E+07	11	NODE 16	NODE 16	2270	NODE 16840 length 959 cov 321.561947 True 68 cystatin-like
8832000	8108100	9871000	9520900	9384000	1.1E+07	9279000	1.2E+07	1.2E+07		13	13	13	55.2	55.2	55.2	29.302	0	111.86	4.3E+08	176	NODE 16	NODE 16	2271	NODE 16948 length 953 cov 754.871938 True 0 glutamate receptor kainate-like protein
0	0	0	0	0	0	0	0	0		3	3	3	10.5	10.5	10.5	58.896	0	42.647	7106900	11	NODE 16	NODE 16	2272	NODE 1697 length 13935 cov 664.990490 False 10355 inositol hexakisphosphate kinase 3
3074300	3563600	3550600	66219	0	75003	3779300	4277800	4323000		33	33	33	32.4	32.4	32.4	197.76	0	169.42	1.8E+08	170	NODE 17	NODE 17	2273	NODE 17 length 144846 cov 702.126168 False 128883 vitellogenin-like protein
3034300	3463000	2556200	818240	0	0	3315900	2407400	3233500		7	7	7	26.5	26.5	26.5	45.151	0	31.576	5.9E+07	38	NODE 17	NODE 17	2274	NODE 17 length 144846 cov 702.126168 False 130141 vitellogenin-like protein
0	0	0	0	0	0	0	0	0		2	2	2	8.4	8.4	8.4	36.285	0	14.85	445950	3	NODE 17	NODE 17	2275	NODE 17 length 144846 cov 702.126168 True 12889 uncharacterized protein LOC113799427
2533600	2592500	2626400	0	0	0	0	0	0		11	11	11	19.5	19.5	19.5	97.692	0	102.58	3.8E+07	29	NODE 17	NODE 17	2276	NODE 17 length 144846 cov 702.126168 True 13913 uncharacterized protein LOC113799427
4743000	5843700	4547400	0	0	0	917020	1098700	754750		13	13	13	24.6	24.6	24.6	94.047	0	65.886	6.9E+07	49	NODE 17	NODE 17	2277	NODE 17 length 144846 cov 702.126168 True 16715 uncharacterized protein LOC113799427
0	0	0	0	0	0	0	0	0		2	2	2	8.6	8.6	8.6	41.359	0.00032	3.9001	568210	2	NODE 17	NODE 17	2278	NODE 17 length 144846 cov 702.126168 True 26792 phosphatidylinositol 3-kinase 1-like
0	0	0	0	0	0	0	0	0		1	1	1	6	6	6	40.891	0.00031	3.7568	663080	1	NODE 17	NODE 17	2279	NODE 17 length 144846 cov 702.126168 True 32589 Rho GTPase-activating protein 100F
0	0	0	0	0	0	0	0	0		1	1	1	7.1	7.1	7.1	21.29	0	7.4627	4150000	5	NODE 17	NODE 17	2280	NODE 17 length 144846 cov 702.126168 True 87417 ethylmalonyl-CoA decarboxylase-like
0	0	0	0	0	0	0	0	0		2	2	2	15.4	15.4	15.4	26.552	0	22.639	1.1E+07	9	NODE 17	NODE 17	2281	NODE 17 length 144846 cov 702.126168 True 8755 beta-1,3-glucan-binding protein precursor
7960500	9098100	7951200	794940	0	860770	2848800	2982100	1419600		24	24	24	31.2	31.2	31.2	130.86	0	131.2	1.7E+08	122	NODE 17	NODE 17	2282	NODE 17 length 144846 cov 702.126168 True 9404 apolipophorins-like protein
1197000	998860	674750	0	0	0	0	0	0		2	2	2	7.5	7.5	7.5	52.29	0	5.6096	4431300	7	NODE 17	NODE 17	2283	NODE 170 length 56447 cov 647.576748 False 17777 protein PFF0380w-like
907130	689020	720010	2536200	1399100	1612500	1524200	2086100	2811200		8	3	3	39.9	13.6	13.6	26.685	0	5.7645	3E+07	36	NODE 17	NODE 17	2284	NODE 170 length 56447 cov 647.576748 False 9933 putative glucosylceramidase 3
0	0	1336400	0	0	0	734750	1740800	0		3	3	3	25.6	25.6	25.6	27.561	0	13.02	1.5E+07	14	NODE 17	NODE 17	2285	NODE 1704 length 13861 cov 740.135955 True 10911 Phenazine biosynthesis-like domain-containing protein
0	0	0	0	0	0	0	0	0		2	2	2	17.3	17.3	17.3	29.471	0.00116	3.1148	345310	4	NODE 17	NODE 17	2286	NODE 1706 length 13851 cov 697.366990 False 5372 putative cysteine proteinase;gi|1048030256|ref|XP 017489023.1| PREDICTED: cysteine proteinase 15A-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		2	2	2	10	10	10	30.397	0	5.5548	1E+07	5	NODE 17	NODE 17	2287	NODE 1706 length 13851 cov 697.366990 False 9428 cathepsin L1-like
0	0	0	0	0	0	0	0	0		1	1	1	22.7	22.7	22.7	7.5206	0	24.024	1.1E+07	8	NODE 17	NODE 17	2288	NODE 171 length 55957 cov 721.538550 True 54664 calpain-9 isoform X1
0	0	0	0	0	0	0	0	0		1	1	1	7.9	7.9	7.9	25.957	0	11.624	4634700	8	NODE 17	NODE 17	2289	NODE 1712 length 13825 cov 711.553377 False 6028 cytochrome b561-like isoform X1
3197900	5484700	4485800	0	2210100	0	3464500	3355500	4699300		4	4	4	21.6	21.6	21.6	40.633	0	24.873	3.9E+07	28	NODE 17	NODE 17	2290	NODE 1714 length 13820 cov 542.759535 True 4159 glucose dehydrogenase [FAD, quinone]-like isoform X4;NODE 4687 length 4998 cov 502.644548 True 4193 glucose dehydrogenase [FAD, quinone]-like isoform X4
0	0	3278700	2145600	0	0	2188000	3209800	0		2	2	2	20	20	20	24.736	0	19.78	2E+07	14	NODE 17	NODE 17	2291	NODE 1714 length 13820 cov 542.759535 True 5166 glucose dehydrogenase [FAD, quinone]-like
0	0	0	0	0	0	0	0	0		1	1	1	18.6	18.6	18.6	10.246	0	7.6987	3326300	9	NODE 17	NODE 17	2292	NODE 17654 length 917 cov 506.967517 True 306 CD151 antigen-like;NODE 17145 length 943 cov 494.540541 False 631 CD151 antigen-like

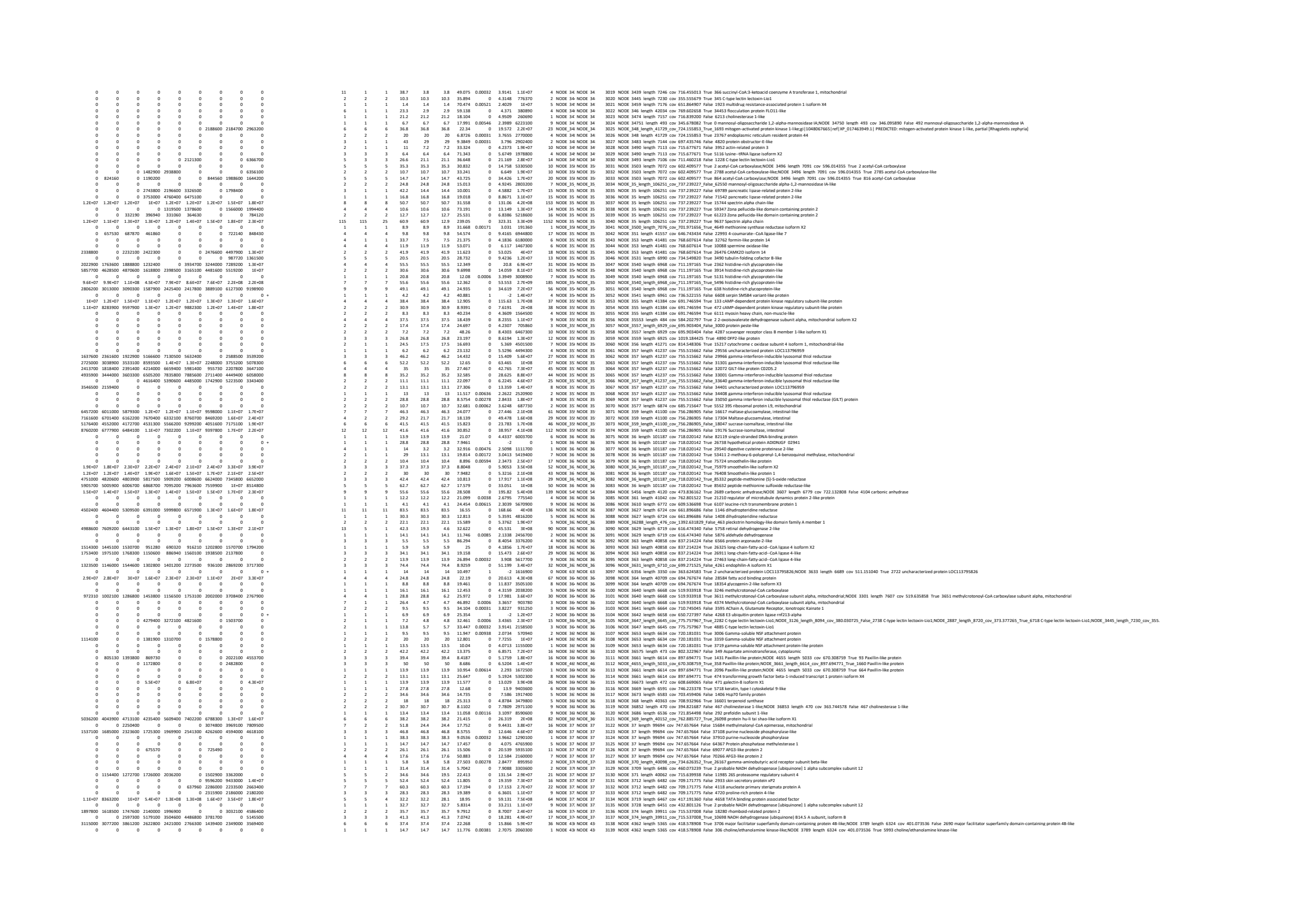


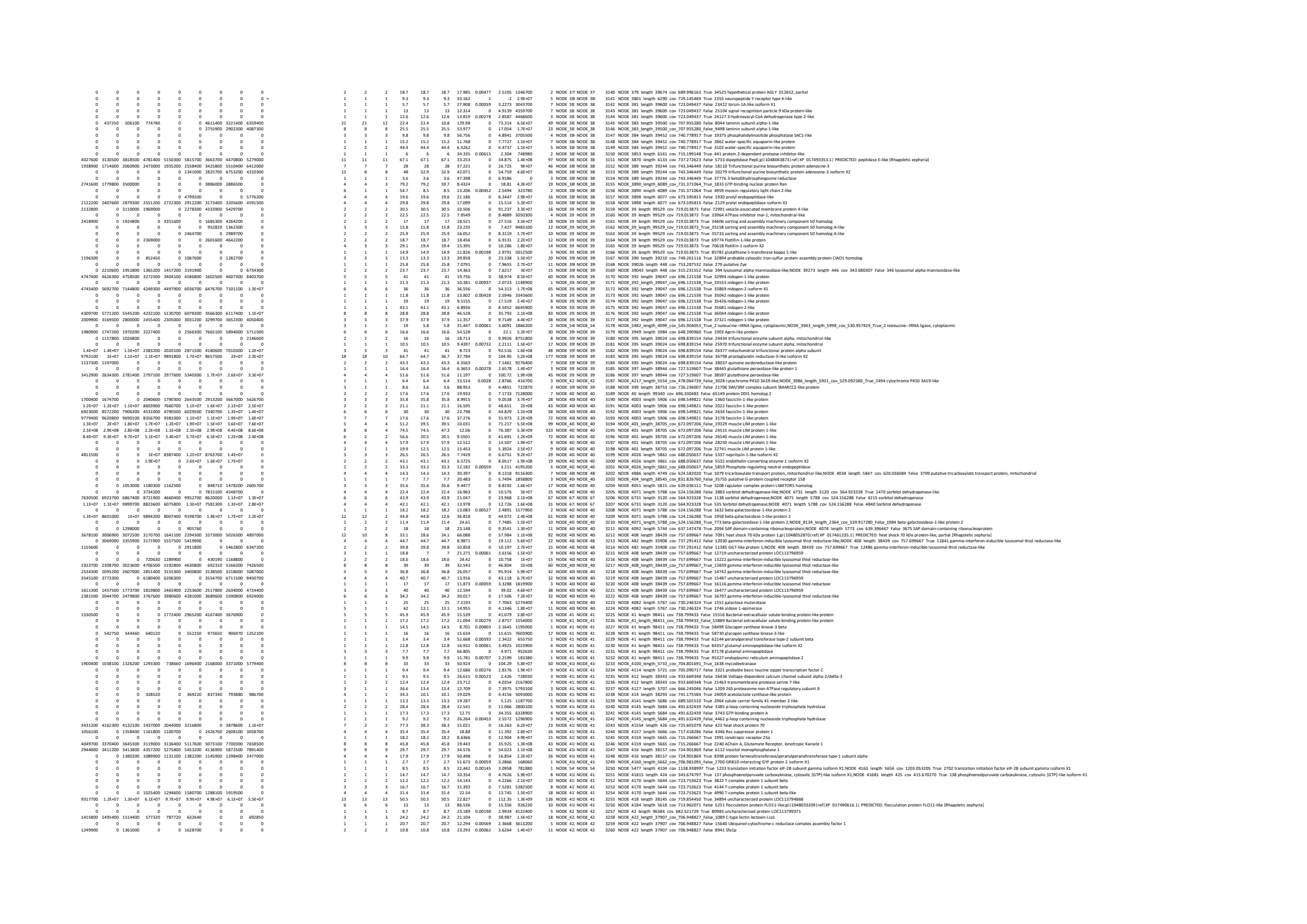


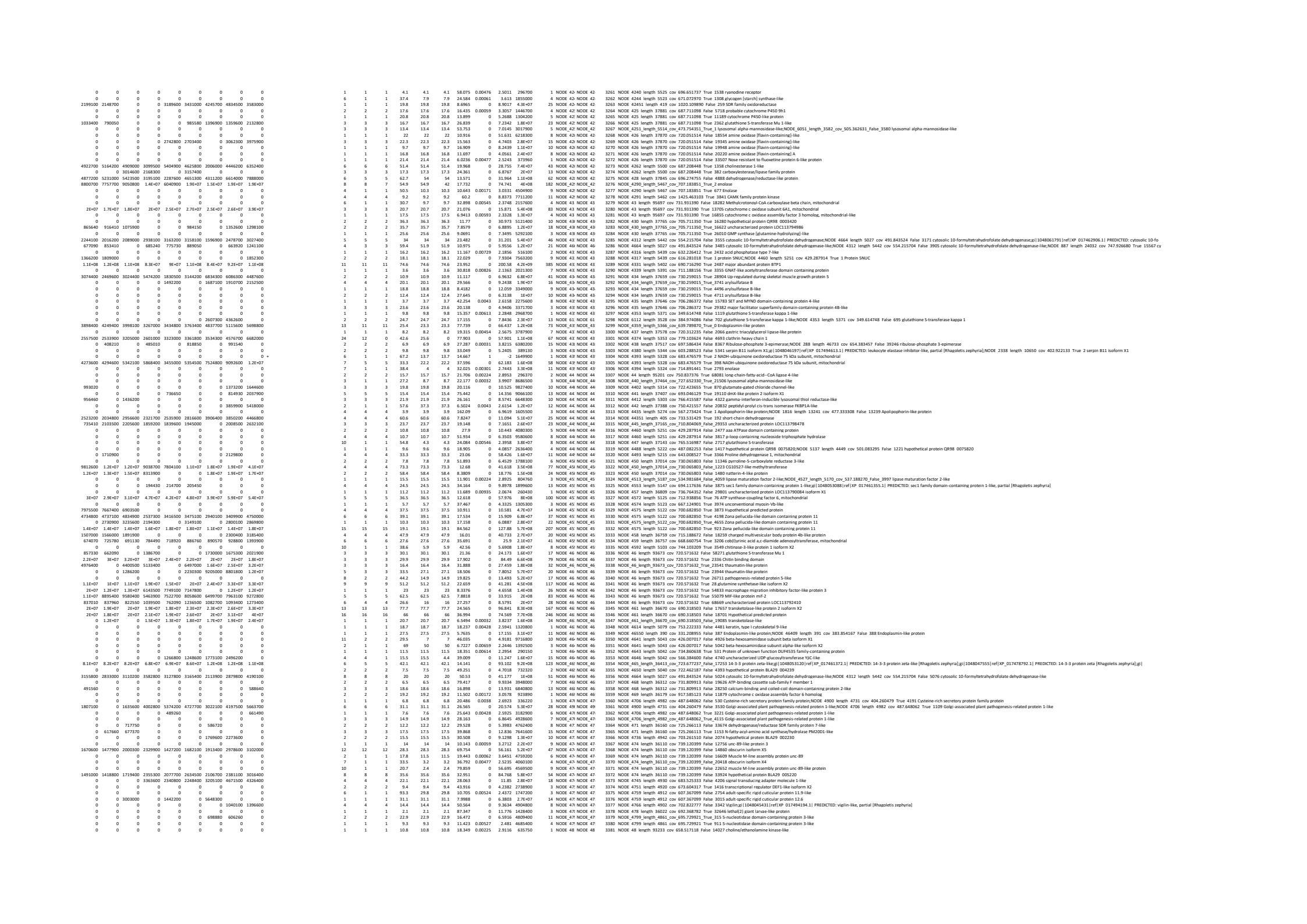
0	0	0	0	0	0	0	0	0	1	1	1	6.1	6.1	6.1	32.023	0	16.527	2.6E+07	17	NODE 24	NODE 24	2656 NODE 2405 length 10360 cov 618.556914 False 2552 dipeptidyl peptidase 1
0	0	0	0	0	0	0	0	0	13	1	1	37.6	2.8	2.8	50.75	0	6.46	5307600	3	NODE 24	NODE 24	2657 NODE 241 length 50966 cov 691.966746 True 27719 C-1-tetrahydrofolate synthase, cytoplasmic
0	0	899030	1255200	1188400	1367900	819300	1331900	1435000	2	2	2	26.5	26.5	26.5	16.441	0	7.2658	1.6E+07	20	NODE 24	NODE 24	2658 NODE 2415 length 10322 cov 715.276614 False 7329 gamma-glutamyltranspeptidase 1 isoform X4
0	0	0	2500400	0	0	0	2310200	0	3	3	3	9.7	9.7	9.7	43.391	0	11.173	1.8E+07	13	NODE 24	NODE 24	2659 NODE 2415 length 10322 cov 715.276614 False 8611 glutathione hydrolase 1 proenzyme
0	0	0	0	0	0	0	0	0	1	1	1	4.8	4.8	4.8	20.88	0.00635	2.2506	1.5E+07	11	NODE 24	NODE 24	2660 NODE 24188 length 678 cov 699.455859 False 565 lipase maturation factor 2-like
1E+08	7.9E+07	8.9E+07	7.9E+07	8.4E+07	8.2E+07	7.9E+07	8.1E+07	1.3E+08	6	6	6	62.9	62.9	62.9	13.403	0	89.023	1.7E+09	90	NODE 24	NODE 24	2661 NODE 2421 length 10313 cov 762.084129 True 51 60S acidic ribosomal protein P1
0	0	0	0	0	0	0	2236000	1888500	3	3	3	16.3	16.3	16.3	24.028	0	6.7569	9302100	7	NODE 24	NODE 24	2662 NODE 2422 length 10303 cov 691.733411 False 4377 15.2 antigen
0	0	0	0	0	0	0	0	0	2	2	2	11.9	11.9	11.9	26.166	0	4.8033	8220400	7	NODE 24	NODE 24	2663 NODE 2423 length 10300 cov 730.958224 False 6458 actin-related protein 2/3 complex subunit 5
0	0	0	0	0	0	0	0	0	13	1	1	51.2	4.2	4.2	37.19	0.00224	2.9073	1.2E+07	6	NODE 24	NODE 24	2664 NODE 2431 length 10270 cov 946.842682 False 8570 sodium potassium adenosine triphosphatase
0	0	0	0	0	0	0	0	0	6	2	2	27.5	13.3	13.3	26.221	0	4.2379	2905200	5	NODE 24	NODE 24	2665 NODE 2439 length 10250 cov 728.884453 True 4441 phosphoglucomutase-2 isoform X1
5576200	5357000	5185700	3801700	2848300	3389600	1E+07	1.3E+07	1.9E+07	6	3	2	51.6	32.8	23	13.718	0	63.974	1.6E+08	37	NODE 24	NODE 24	2666 NODE 2439 length 10250 cov 728.884453 True 7937 GDSL family lipase
4090100	4109700	4127700	5026700	3269500	4860400	7388800	1.1E+07	1.1E+07	8	8	6	35.3	35.3	29.1	29.146	0	43.51	1.5E+08	78	NODE 24	NODE 24	2667 NODE 2439 length 10250 cov 728.884453 True 9132 GDSL family lipase
0	0	0	0	0	0	0	0	0	4	4	4	9	9	9	94.677	0	10.86	4545100	13	NODE 24	NODE 24	2668 NODE 2449 length 10193 cov 719.894358 False 2627 CD109 antigen-like
0	0	0	0	570970	598100	0	0	0	2	2	2	17.8	17.8	17.8	17.787	0	4.2868	4327000	9	NODE 24	NODE 24	2669 NODE 2449 length 10193 cov 719.894358 False 3759 CD109 antigen
0	0	0	0	0	0	0	0	0	2	2	2	13.5	13.5	13.5	24.762	0.00032	3.9567	2362800	7	NODE 24	NODE 24	2670 NODE 2449 length 10193 cov 719.894358 False 5378 CD109 antigen
0	0	0	0	0	0	0	0	0	1	1	1	25	25	25	7.1493	0	23.726	2.9E+07	8	NODE 30	NODE 30	2671 NODE 3002 length 8415 cov 500.440670 False 6116 xaa-Pro aminopeptidase 1-like;NODE 2453 length 10174 cov 476.683862 False 9037 xaa-Pro aminopeptidase 1-like
0	0	0	2098800	2143100	0	2179400	2424400	0	3	3	3	16.6	16.6	16.6	27.091	0	13.299	2.4E+07	16	NODE 24	NODE 24	2672 NODE 2453 length 10174 cov 476.683862 False 9758 xaa-Pro aminopeptidase 1-like protein;NODE 3002 length 8415 cov 500.440670 False 6843 xaa-Pro aminopeptidase 1-like protein
0	0	0	0	0	0	0	0	0	2	1	1	26.5	13.2	13.2	7.3344	0.00637	2.2734	2.8E+07	6	NODE 24	NODE 24	2673 NODE 24589 length 668 cov 334.500816 False 378 trypsin-like serine protease
0	0	0	244280	0	0	343600	0	0	2	1	1	44.4	31.9	31.9	7.5727	0	4.3191	1768000	8	NODE 24	NODE 24	2674 NODE 24589 length 668 cov 334.500816 False 665 trypsin
3979800	3566900	5508500	5885300	5509200	6763700	2721300	7165500	6799700	11	11	11	52.5	52.5	52.5	21.184	0	48.638	1.9E+08	93	NODE 24	NODE 24	2675 NODE 2459 length 10140 cov 692.746356 True 630 protein lethal(2)essential for life-like
1050500	1948500	1938000	4562600	922230	4382500	5033300	6388900	8084600	14	14	10	44.7	44.7	32.1	55.348	0	44.828	1.3E+08	69	NODE 24	NODE 24	2676 NODE 246 length 50265 cov 724.728978 False 38986 dihydropyrimidinase-like isoform X1
1747700	1425400	1899000	2024700	1554300	1958000	1728000	2703500	0	3	3	2	48.2	48.2	29.5	12.79	0	25.185	2.8E+07	22	NODE 24	NODE 24	2677 NODE 2462 length 10129 cov 1362.663887 True 8398 cGMP-dependent protein kinase, isozyme 2 forms cD4/T1/T3A/T3B-like isoform X1
0	0	0	0	0	0	0	0	0	1	1	1	7	7	7	15.802	0.00635	2.2531	5524500	7	NODE 24	NODE 24	2678 NODE 247 length 50205 cov 722.941316 True 38913 hypothetical protein A2647 03500
0	0	0	0	0	0	0	0	0	1	1	1	16.5	16.5	16.5	9.6402	0	4.8474	7418300	8	NODE 24	NODE 24	2679 NODE 247 length 50205 cov 722.941316 True 39292 DUF333 domain-containing protein
0	0	0	0	0	0	0	0	0	1	1	1	8.8	8.8	8.8	13.475	0.00544	2.3731	2587000	2	NODE 24	NODE 24	2680 NODE 2474 length 10093 cov 697.731122 False 9560 mitogen-activated protein kinase 1
0	5777300	7042700	6234200	8758400	1E+07	0	0	9707200	8	8	4	53.2	53.2	29.4	25.405	0	42.822	1E+08	39	NODE 24	NODE 24	2681 NODE 2476 length 10091 cov 568.891391 True 6309 secretion protein
0	0	1312800	1565000	0	1432400	0	0	0	2	2	2	36.3	36.3	36.3	10.016	0	6.4794	9112600	11	NODE 24	NODE 24	2682 NODE 248 length 50157 cov 736.452357 False 11102 MICOS complex subunit MIC27
0	0	0	0	0	0	0	0	0	3	3	3	43.2	43.2	43.2	8.2456	0	10.015	3.4E+07	12	NODE 24	NODE 24	2683 NODE 248 length 50157 cov 736.452357 False 11327 hypothetical protein QR98 0019020, partial
2187600	2506700	2588800	5959500	2680300	6075500	3700800	5150400	7166800	5	5	5	37.5	37.5	37.5	13.781	0	24.631	1.2E+08	57	NODE 28	NODE 28	2684 NODE 2839 length 8879 cov 411.816750 True 3082 group 2 allergen Ale o 2;NODE 2482 length 10062 cov 440.063556 False 7491 group 2 allergen Sui p 2
0	0	0	0	0	0	0	0	0	10	1	1	68.6	3.4	3.4	31.963	0.00381	2.7006	2504800	5	NODE 24	NODE 24	2685 NODE 2487 length 10046 cov 673.957562 True 1155 NADP-dependent malic enzyme, mitochondrial-like
0	0	0	0	1026100	1176100	0	0	0	1	1	1	21.9	21.9	21.9	8.2364	0.0006	3.4201	4217300	9	NODE 25	NODE 25	2686 NODE 25 length 123598 cov 740.273686 False 39658 lysosomal acid glucosylceramidase
0	0	0	0	0	0	0	0	0	1	1	1	3.6	3.6	3.6	52.173	0	10.598	1414600	6	NODE 25	NODE 25	2687 NODE 250 length 50133 cov 784.987539 False 39802 PREDICTED: nucleolin-like, partial
0	0	0	0	0	0	0	0	0	12	12	8	12.9	12.9	8.6	142.82	0	28.182	5820600	19	NODE 25	NODE 25	2688 NODE 250 length 50133 cov 784.987539 False 43544 nucleoprotein TPR;gi|1048052607|ref|XP 017461089.1| PREDICTED: restin homolog, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	1	1	1	12.5	12.5	12.5	12.524	0.00275	2.7984	4553800	9	NODE 25	NODE 25	2689 NODE 250 length 50133 cov 784.987539 True 32567 peptidyl-prolyl cis-trans isomerase FKBP8
0	0	0	0	0	0	0	0	0	1	1	1	18.8	18.8	18.8	9.8125	0	6.2046	9520900	6	NODE 25	NODE 25	2690 NODE 2529 length 9905 cov 692.614518 False 3090 protein kinase C and casein kinase substrate in neurons protein 1 isoform X1
0	0	0	0	0	0	0	0	0	1	1	1	5.2	5.2	5.2	26.7	0.00224	2.8917	904400	2	NODE 25	NODE 25	2691 NODE 2529 length 9905 cov 692.614518 False 5551 protein kinase C and casein kinase substrate in neurons protein 1 isoform X1
0	0	0	0	0	0	1E+07	0	2E+07	13	2	2	41.1	4	4	46.138	0	5.5889	9.6E+07	12	NODE 25	NODE 25	2692 NODE 253 length 49808 cov 706.045686 True 1542 methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial
0	0	0	0	0	0	0	0	0	2	2	2	24.3	24.3	24.3	12.485	0	8.5257	7416100	9	NODE 25	NODE 25	2693 NODE 253 length 49808 cov 706.045686 True 54 laminin subunit alpha
661230	0	0	608800	620710	671500	763400	1005600	0	4	4	4	25.2	25.2	25.2	32.59	0	10.238	1.1E+07	21	NODE 25	NODE 25	2694 NODE 2554 length 9803 cov 619.312987 True 3504 dihydroorotate dehydrogenase (quinone), mitochondrial;gi|1048057006|ref|XP 017461780.1| PREDICTED: dihydroorotate dehydrogenase (quinone)-like, partial [Rhagoletis zephyria];NODE 2197 length 11274 cov 611.7294
458850	331570	672840	518930	301630	0	826850	2513400	6640700	13	13	13	30.8	30.8	30.8	65.756	0	83.433	5.2E+07	50	NODE 25	NODE 25	2695 NODE 2555 length 9800 cov 647.075013 True 2978 twitchin-like isoform X2
3428300	3010200	2730100	5193200	3058000	3767000	4804300	9296600	1.3E+07	23	13	13	44.8	26.4	26.4	86.194	0	190.49	1.4E+08	68	NODE 25	NODE 25	2696 NODE 2555 length 9800 cov 647.075013 True 4786 twitchin-like protein
1823200	1790400	1816900	2997500	3093200	3344000	1806000	2055600	0	2	2	2	30.8	30.8	30.8	10.541	0	10.045	2.9E+07	21	NODE 25	NODE 25	2697 NODE 256 length 49611 cov 655.441036 True 21192 probable serine carboxypeptidase CPVL;NODE 819 length 25504 cov 658.534324 False 23565 probable serine carboxypeptidase CPVL
2230500	0	0	0	2796300	2694700	0	0	1929500	4	4	4	16.6	16.6	16.6	43.674	0	10.127	2.1E+07	17	NODE 25	NODE 25	2698 NODE 256 length 49611 cov 655.441036 True 21513 probable serine carboxypeptidase CPVL
0	0	0	0	0	0	0	0	0	1	1	1	17.9	17.9	17.9	9.0432	0.0006	3.4213	6169200	8	NODE 25	NODE 25	2699 NODE 256 length 49611 cov 655.441036 True 33799 putative sulfite oxidase-like protein
0	0	0	0	0	0	0	0	0	2	2	2	5.4	5.4	5.4	53.379	0	4.4166	1097600	5	NODE 25	NODE 25	2700 NODE 2566 length 9766 cov 784.698795 False 5306 histone deacetylase 6 isoform X1
0	0	0	0	0	0	0	0	0	1	1	1	5	5	5	20.57	0.00429	2.6034	955240	3	NODE 25	NODE 25	2701 NODE 257 length 49482 cov 699.031521 True 26061 uncharacterized protein LOC111621116
1185000	1227400	1465300	2039300	910780	1810400	1922200	3041800	3913700	8	8	4	33.3	33.3	19.3	39.301	0	90.314	6.7E+07	62	NODE 25	NODE 25	2702 NODE 2571 length 9748 cov 626.504075 True 2599 laminin subunit gamma-1-like
5095800	4925600	5663000	7385000	2949600	5552100	1E+07	1.4E+07	1.9E+07	7	7	7	41.1	41.1	41.1	33.408	0	52.432	2E+08	77	NODE 25	NODE 25	2703 NODE 2571 length 9748 cov 626.504075 True 5557 laminin subunit gamma-1
3897900	4238100	4603200	6070500	3293900	4884100	7734100	1.2E+07	1.7E+07	29	29	29	45.4	45.4	45.4	84.161	0	260.52	4.2E+08	179	NODE 25	NODE 25	2704 NODE 2571 length 9748 cov 626.504075 True 6978 laminin subunit gamma-1-like
2752000	0	0	0	0	0	0	0	9443000	3	3	3	29.7	29.7	29.7	10.635	0	4.9368	2.8E+07	10	NODE 25	NODE 25	2705 NODE 2571 length 9748 cov 626.504075 True 9309 laminin subunit gamma-1
0	0	0	0	0	0	0	0	0	3	3	3	5.7	5.7	5.7	65.324	0	4.6603	1747400	5	NODE 25	NODE 25	2706 NODE 2586 length 9699 cov 665.511510 True 5526 UDP-glucose:glycoprotein glucosyltransferase 1-like
0	0	0	0	0	0	0	0	0	2	2	2	26.9	26.9	26.9	11.787	0	5.2019	2E+07	8	NODE 25	NODE 25	2707 NODE 259 length 49338 cov 704.441511 True 31968 cardiomyopathy-associated protein 5 isoform X1
0	0	0	0	0	0	0	0	0	1	1	1	15.7	15.7	15.7	9.9002	0.00031	3.6763	6842300	4	NODE 25	NODE 25	2708 NODE 2592 length 9686 cov 684.322604 False 3492 titin
0	0	0	942880	0	0	1004000	1502400	0	2	2	2	24.2	24.2	24.2	19.357	0	7.0288	1E+07	11	NODE 25	NODE 25	2709 NODE 2592 length 9686 cov 684.322604 False 4062 titin-like isoform X1
2560900	2019600	2699600	2769000	2977800	2981000	3341900	3277100	4258700	13	13	13	43.3	43.3	43.3	52.388	0	114.36	1.4E+08	120	NODE 25	NODE 25	2710 NODE 2592 length 9686 cov 684.322604 False 5783 titin isoform X1
3252800	3139800	4010400	3752600	4360400	4974900	3092700	5081800	5737900	20	20	20	34.4	34.4	34.4	91.318	0	106.53	2.7E+08	171	NODE 25	NODE 25	2711 NODE 2592 length 9686 cov 684.322604 False 8253 titin
2140600	1716800	2544700	3040400	3642000	2773800	2310200	3350800	3017200	8	6	6	36.3	28.2	28.2	36.494	0	27.225	6E+07	50	NODE 25	NODE 25	2712 NODE 2592 length 9686 cov 684.322604 False 9255 titin-like isoform X1
1312300	1681800	1495700	1395800	1316900	2280100	1048100	0	2534100	2	2	2	12.3	12.3	12.3	28.671	0	7.8267	2.5E+07	20	NODE 25	NODE 25	2713 NODE 2593 length 9684 cov 656.201579 False 1012 CD109 antigen-like
0	0	0	0	0	0	0	0	0	2	2	2	22.9	22.9	22.9	17.335	0.00058	3.1857	7583400	8	NODE 25	NODE 25	2714 NODE 2596 length 9678 cov 490.836641 False 459 serine/threonine-protein phosphatase CPPED1-like;NODE 1906 length 12749 cov 491.330314 True 10099 serine/threonine-protein phosphatase CPPED1-like
0	0	0	0	0	0	0	0	0	2	2	2	18.9	18.9	18.9	33.812	0	6.6182	1417500	3	NODE 26	NODE 26	2715 NODE 26 length 123592 cov 724.723314 False 10473 Down syndrome cell adhesion molecule-like protein 1
0	0	0	0	0	0	0	0	0	1	1	1	9.3	9.3	9.3	18.145	0.00059	3.2596	8300500	10	NODE 26	NODE 26	2716 NODE 26 length 123592 cov 724.723314 False 14025 pro-neuregulin-1, membrane-bound isoform-like
0	0	0	0	0	0	0	0	0	2	2	2	25.5	25.5	25.5	10.531	0	7.0017	1914700	2	NODE 26	NODE 26	2717 NODE 26 length 123592 cov 724.723314 False 1973 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	1	1	1	13.6	13.6	13.6	12.228	0	6.5875	1.2E+07	5	NODE 26	NODE 26	2718 NODE 26 length 123592 cov 724.723314 False 2311 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	2	2	2	43.3	43.3	43.3	7.1533	0	4.5584	2033000	3	NODE 26	NODE 26	2719 NODE 26 length 123592 cov 724.723314 False 2735 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	1	1	1	10.7	10.7	10.7	17.241	0.00058	3.1768	4251600	4	NODE 26	NODE 26	2720 NODE 26 length 123592 cov 724.723314 False 3000 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	1	1	1	23.2	23.2	23.2	7.5967	0.0006	3.3357	2215800	4	NODE 26	NODE 26	2721 NODE 26 length 123592 cov 724.723314 False 3086 acyl-CoA dehydrogenase family member 11-like isoform X1
960470	1123100	1564200	0	0	0	1666500	2562100	0	4	4	4	41.1	41.1	41.1	21.548	0	14.753	1.8E+07	17	NODE 26	NODE 26	2722 NODE 26 length 123592 cov 724.723314 False 3709 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	1	1	1	27.4	27.4	27.4	10.718	0	5.5506	4964400	5	NODE 26	NODE 26	2723 NODE 26 length 123592 cov 724.723314 False 3983 acyl-CoA dehydrogenase family member 11-like
0	0	0	0	0	0	0	0	0	1	1	1	5.7	5.7	5.7	34.198	0	4.8281	6650600	4	NODE 26	NODE 26	2724 NODE 26 length 123592 cov 724.723314 True 93944 hypothetical protein AK812 SmicGene3514
0	0	0	0	0	0	0	0	0	1	1	1	8.6	8.6	8.6	23.642	0.00225	2.9157	3225600	1	NODE 26	NODE 26	2725 NODE 26100 length 633 cov 333.821799 True 2 ryanodine receptor-like;NODE 26099 length 633 cov 362.951557 False 630 ryanodine receptor-like
0	0	0	0	0	0	0	0	0	2	2	2	13.4	13.4	13.4	20.969	0	6.9047	1E+07	7	NODE 26	NODE 26	2726 NODE 261 length 49252 cov 741.843568 False 21102 uncharacterized protein LOC113790559
0	2084500	1737700	4800100	2621400	3590800	2838000	0	6956300	5	2	2	25.6	10.1	10.1	14.015	0	5.4742	4.3E+07	18	NODE 26	NODE 26	2727 NODE 261 length 49252 cov 741.843568 False 4032 flocculation protein FLO11-like
1869800	2327700	1989600	2605200	4201500	3022600	0	0	4325100	2	2	2	32.8	32.8	32.8	6.8808	0	7.2706	4.1E+07	26	NODE 26	NODE 26	2728 NODE 2614 length 9595 cov 741.156080 True 4332 Barrier-to-autointegration factor
0	0	0	0	0	0	0	0	0	1	1	1	20.7	20.7	20.7	12.822	0	4.3258	1489600	1	NODE 26	NODE 26	2729 NODE 26173 length 631 cov 670.781250 True 281 L-sorbose 1-dehydrogenase-like
0	0	0	0	0	0	0	0	0	1	1	1	11.6	11.6	11.6	19.539	0.00116	3.1067	1496100	3	NODE 26	NODE 26	2730 NODE 26222 length 630 cov 733.768696 False 570 uncharacterized protein LOC110855663
7071200	6186600	7315300	8639900	7973000	1.1E+07	5853700	1.1E+07	1.4E+07	8	8	8	41.5	41.5	41.5	29.808	0	31.096	1.9E+08	90	NODE 26	NODE 26	2731 NODE 2627 length 9547 cov 657.998420 True 6017 arrestin domain-containing protein 3-like
0	0	0	0	0	0	0	0	0	1	1	1	8.1	8.1	8.1	13.349	0.00707	2.2182	2621800	5	NODE 26	NODE 26	2732 NODE 2638 length 9512 cov 554.060167 True 2022 uncharacterized protein LOC113791874
0	0	0	0	0	0	1184400	1013100	0	3	3	3	17.7	17.7	17.7	35.091	0	8.2239	8927300	10	NODE 26	NODE 26	2733 NODE 264 length 49164 cov 702.285263 True 21758 nicalin-like protein
0	0	0	0	0	0	0	0	0	3	3	3	9.9	9.9	9.9	37.171	0	4.434	2766400	4	NODE 26	NODE 26	2734 NODE 264 length 49164 cov 702.285263 True 22927 nicalin isoform X4
0	0	0	0	0	0	0	0	0	2	2	2	27.6	27.6	27.6	21.256	0.00171	3.0294	952770	5	NODE 26	NODE 26	2735 NODE 2640 length 9506 cov 689.761401 True 8928 probable glutamine--tRNA ligase;NODE 140 length 61670 cov 738.242084 False 339 glutamine--tRNA ligase-like;NODE 28 length 118658 cov 797.469609 True 77853 glutamine--tRNA ligase-like
0	0	0	767020	654240	748110	0	1597100	2653700	19	2	2	65.3	5.8	5.8	48.838	0	5.0915	1.2E+07	14	NODE 26	NODE 26	2736 NODE 2642 length 9501 cov 677.173407 True 7796 2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like
593420	673080	805660	646840	501760	779510	706840	1313400	1793300	6	6	6	21.2	21.2	21.2	56.19	0	20.665	1.6E+07	27	NODE 26	NODE 26	2737 NODE 265 length 49143 cov 752.104975 False 21136 pre-mRNA-processing factor 19
0	0	0	0	0	0	0	0	0	1	1	1	5	5	5	49.058	0.00526	2.472	1168200	2	NODE 26	NODE 26	2738 NODE 2651 length 9463 cov 695.987776 False 3959 neuroglian
0	0	0	0	0	0	0	1809800	2990600	5	5	5	33.1	33.1	33.1	35.459	0	18.55	1.5E+07	16	NODE 26	NODE 26	2739 NODE 2651 length 9463 cov 695.987776 True 5450 Beta-hexosaminidase subunit beta;gi|1048044268|ref|XP 017493563.1| PREDICTED: beta-hexosaminidase subunit beta-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	2	2	2	8.8	8.8	8.8	34.965	0.00428	2.5832	1672600	2	NODE 26	NODE 26	2740 NODE 2651 length 9463 cov 695.987776 True 6322 beta-hexosaminidase subunit beta
2986800	2090200	2698800	2585100	2384500	3419800	4162300	2973600	4699300	2	2	2	20.2	20.2	20.2	19.132	0	27.463	4.8E+07	21	NODE 26	NODE 26	2741 NODE 2656 length 9447 cov 689.033007 True 7929 hypothetical protein BLA29 000024
0	0	1611200	0	0	0	0	2559300	0	3	3	3	18.6	18.6	18.6	13.988	0	5.5324	2.5E+07	11	NODE 26	NODE 26	2742 NODE 2656 length 9447 cov 689.033007 True 8540 uncharacterized protein LOC113798905
0	0	0	0	0	0	0	0	0	1	1	1	8	8	8	20.699	0.00521	2.403	1429300	1	NODE 26	NODE 26	2743 NODE 266 length 49117 cov 749.185500 True 28946 delta-aminolevulinic acid dehydratase
2115100	0	0	0	0	0	2570200	3293100	0	2	2	2	41.4	41.4	41.4	10.543	0	5.2635	1E+07	9	NODE 26	NODE 26	2744 NODE 266 length 49117 cov 749.185500 True 29410 porphobilinogen synthase
0	0	0	0	0	0	0	0	0	2	2	2	13.6	13.6	13.6	14.439	0	4.296	551840	3	NODE 26	NODE 26	2745 NODE 266 length 49117 cov 749.185500 True 29719 delta-aminolevulinic acid dehydratase-like
0	0	0	0	0	0	0	0	0	1	1	1	10.7	10.7	10.7	16.238	0.00173	3.0608	959190	2	NODE 26	NODE 26	2746 NODE 266 length 49117 cov 749.185500 True 5907 FGGY-family carbohydrate kinase
324350	361800	362170	0	0	0	0	0	653800	2	2	2	7.3	7.3	7.3	40.274	0	6.9446	3924100	11	NODE 26	NODE 26	2747 NODE 2660 length 9434 cov 690.235846 True 5907 FAS-associated factor 2-like
0	0	0	0	0	0	0	0	0	1	1	1	23.1	23.1	23.1	10.545	0	4.663	1.4E+07	6	NODE 26	NODE 26	2748 NODE 2664 length 9424 cov 489.860711 True 3947 Kynurenine--oxoglutarate transaminase 3;NODE 2702 length 9276 cov 490.649496 False 5409 Kynurenine--oxoglutarate transaminase 3
1949400	0	2004100	1485900	0	1564100	0	1502100	2558100	4	4	3	54.8	54.8	44.4	13.787	0	11.003	1.7E+07	21	NODE 27	NODE 27	2749 NODE 2702 length 9276 cov 490.649496 False 5053 kynurenine--oxoglutarate transaminase 3 isoform X2;NODE 2664 length 9424 cov 489.860711 True 4252 kynurenine--oxoglutarate transaminase 3 isoform X2
3845700	2799500	3715300	4794800	3623100	4715000	1.1E+07	1.5E+07	1.7E+07	8	7	7	40.8	36.5	36.5	27.035	0	24.411	1.9E+08	56	NODE 27	NODE 27	2750 NODE 2702 length 9276 cov 490.649496 False 2093 lysosomal alpha-mannosidase-like protein;NODE 2664 length 9424 cov 489.860711 True 7327 lysosomal alpha-mannosidase-like protein
4121300	3258700	3374100	4798400	3685800	5684900	1.3E+07	1.5E+07	2.3E+07	10	10	10	49.8	49.8	49.8	35.098	0	61.026	3.5E+08	105	NODE 26	NODE 26	2751 NODE 2664 length 9424 cov 489.860711 True 7895 Lysosomal alpha-mannosidase;NODE 2702 length 9276 cov 490.649496 False 1531 Lysosomal alpha-mannosidase
2310800	2334400	0	4756600	3060200	5595800	0	0	6802500	8	1	1	66.8	8.8	8.8	21.733	0	11.026	3.5E+07	14	NODE 26	NODE 26	2752 NODE 2664 length 9424 cov 489.860711 True 8844 lysosomal alpha-mannosidase-like
2189400	0	0	0	0	0	1549800	0	0	7	3	3	24.1	13	13	58.579	0	13.071	1.8E+07	13	NODE 26	NODE 26	2753 NODE 2675 length 9381 cov 706.250161 True 5913 glycogen debranching enzyme-like
1276700	948220	1122800	1843900	2185800	1932600	1711400	3186800	4725200	4	4	4	17.5	17.5	17.5	29.633	0	45.369	4.8E+07	46	NODE 26	NODE 26	2754 NODE 2679 length 9365 cov 871.565091 True 7314 glycoside hydrolase family 25 protein
0	0	0	0	0	0	0	0	0	2	2	2	13.2	13.2	13.2	29.197	0	5.8097	6121600	6	NODE 26	NODE 26	2755 NODE 2684 length 9344 cov 721.054150 False 8687 synaptobrevin homolog YKT6
0	0	0	0	0	0	0	0	0	1	1	1	13	13	13	20.619	0	14.144	3410300	4	NODE 26	NODE 26	2756 NODE 2684 length 9344 cov 721.054150 True 1664 carboxypeptidase Q-like
1563200	2395100	3200100	1902500	1611800	0	0	0	0	4	4	4	28.2	28.2	28.2	17.947	0	8.2392	2.6E+07	16	NODE 26	NODE 26	2757 NODE 2684 length 9344 cov 721.054150 True 2239 carboxypeptidase Q-like
0	0	0	0	0	0	0	0	0	1	1	1	12.1	12.1	12.1	13.756	0.00452	2.5462	8773400	1	NODE 26	NODE 26	2758 NODE 2684 length 9344 cov 721.054150 True 3243 carboxypeptidase Q-like
0	0	0	4251300	4226900	4061700	0	1.7E+07	0	1	1	1	9.8	9.8	9.8	15.709	0.00032	3.9659	5.3E+07	13	NODE 26	NODE 26	2759 NODE 2685 length 9335 cov 644.982543 True 5868 hypothetical protein QR98 0021510
2403700	2295000	2786800	2002000	2175000	2884600	3481900	4559400	4641400	8	8	8	24	24	24	51.507	0	50.406	5.8E+07	36	NODE 26	NODE 26	2760 NODE 269 length 48981 cov 643.294118 False 39288 neuroglian isoform X1
6625600	5729800	7277300	4345000	4712600	7052400	6363900	7180700	6143400	5	4	4	45.7	33.3	33.3	20.373	0	13.101	1.1E+08	42	NODE 26	NODE 26	2761 NODE 269 length 48981 cov 643.294118 True 32941 probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial
7391900	7243100	9603600	1E+07	1E+07	1E+07	1E+07	1.3E+07	1.4E+07	4	4	4	63.9	63.9	63.9	9.1032	0	9.9928	1.3E+08	36	NODE 26	NODE 26	2762 NODE 269 length 48981 cov 643.294118 True 33519 probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial
0	0	0	0	0	0	0	0	0 +	1	1	1	25.6	25.6	25.6	9.5653	1	-2	5.2E+07	4	NODE 26	NODE 26	2763 NODE 2691 length 9311 cov 639.996219 False 5202 hypothetical protein BWX45 00848
0	0	0	0	0	0	0	0	0	2	2	2	16.3	16.3	16.3	40.187	0	4.8189	835130	3	NODE 26	NODE 26	2764 NODE 2691 length 9311 cov 639.996219 True 4205 UDP-glucose 6-dehydrogenase-like;gi|1048043250|ref|XP 017493009.1| PREDICTED: UDP-glucose 6-dehydrogenase-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	4	4	3	10.3	10.3	7.5	67.232	0	11.363	9867500	12	NODE 26	NODE 26	2765 NODE 2692 length 9309 cov 695.011995 False 5938 myogenesis-regulating glycosidase-like
0	1278900	0	0	1391000	0	2062100	0	2594900	2	2	2	20.2	20.2	20.2	26.434	0	9.4664	1.9E+07	13	NODE 27	NODE 27	2766 NODE 27 length 121734 cov 718.154883 False 70699 Ubiquinol-cytochrome-c reductase complex assembly factor 2
2087600	0	2650500	0	0	4557500	0	0	0	2	2	2	17.7	17.7	17.7	22.514	0	5.4122	1.6E+07	9	NODE 27	NODE 27	2767 NODE 27 length 121734 cov 718.154883 True 42559 OCIA domain-containing protein 1-like
1483500	1642100	1510100	2111700	0	2128400	1343200	2483200	0	2	2	2	12.9	12.9	12.9	28.116	0	13.763	2.1E+07	21	NODE 27	NODE 27	2768 NODE 27 length 121734 cov 718.154883 True 44889 OCIA domain-containing protein 1-like
2878800	0	3121700	4735400	4701700	6193300	1779900	0	0	6	3	3	34.4	18.8	18.8	24.183	0	13.592	4E+07	25	NODE 27	NODE 27	2769 NODE 27 length 121734 cov 718.154883 True 9005 regucalcin-like
0	0	0	0	0	0	0	1031300	1511100	5	5	5	10.1	10.1	10.1	83.933	0	12.47	6044900	11	NODE 27	NODE 27	2770 NODE 270 length 48948 cov 721.556153 False 13123 heparinase II/III family protein
0	0	0	0	0	0	1.2E+07	1.6E+07	2.5E+07	6	6	6	24.6	24.6	24.6	35.116	0	16.724	1.2E+08	26	NODE 27	NODE 27	2771 NODE 2702 length 9276 cov 490.649496 False 2824 lysosomal alpha-mannosidase;NODE 2664 length 9424 cov 489.860711 True 6559 lysosomal alpha-mannosidase
2288600	2394700	2958100	4209400	2605100	4120300	2.2E+07	1.8E+07	2E+07	9	9	2	70.1	70.1	16.8	20.814	0	109.07	2.5E+08	72	NODE 27	NODE 27	2772 NODE 2702 length 9276 cov 490.649496 False 552 lysosomal alpha-mannosidase-like
0	0	0	0	0	0	0	1352300	2435600	4	4	4	24.7	24.7	24.7	22.053	0	7.6892	6452600	8	NODE 27	NODE 27	2773 NODE 2715 length 9209 cov 1218.285340 True 6228 C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8;NODE 2708 length 9231 cov 1212.624455 True 6257 C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8
3320400	3420200	4624800	0	0	0	3627600	0	6127900	3	3	3	15.2	15.2	15.2	44.904	0	10.786	3.6E+07	18	NODE 27	NODE 27	2774 NODE 2709 length 9231 cov 581.508173 True 2062 succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial isoform X2
0	0	0	0	0	0	0	0	0	1	1	1	10.9	10.9	10.9	12.73	0.00453	2.5559	3127200	3	NODE 27	NODE 27	2775 NODE 2709 length 9231 cov 581.508173 True 3350 succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial-like
0	0	0	0	0	0	0	0	0	1	1	1	14.2	14.2	14.2	15.476	0.00709	2.2299	645500	2	NODE 27	NODE 27	2776 NODE 272 length 48935 cov 715.497484 True 29279 UBX domain-containing protein 6-like

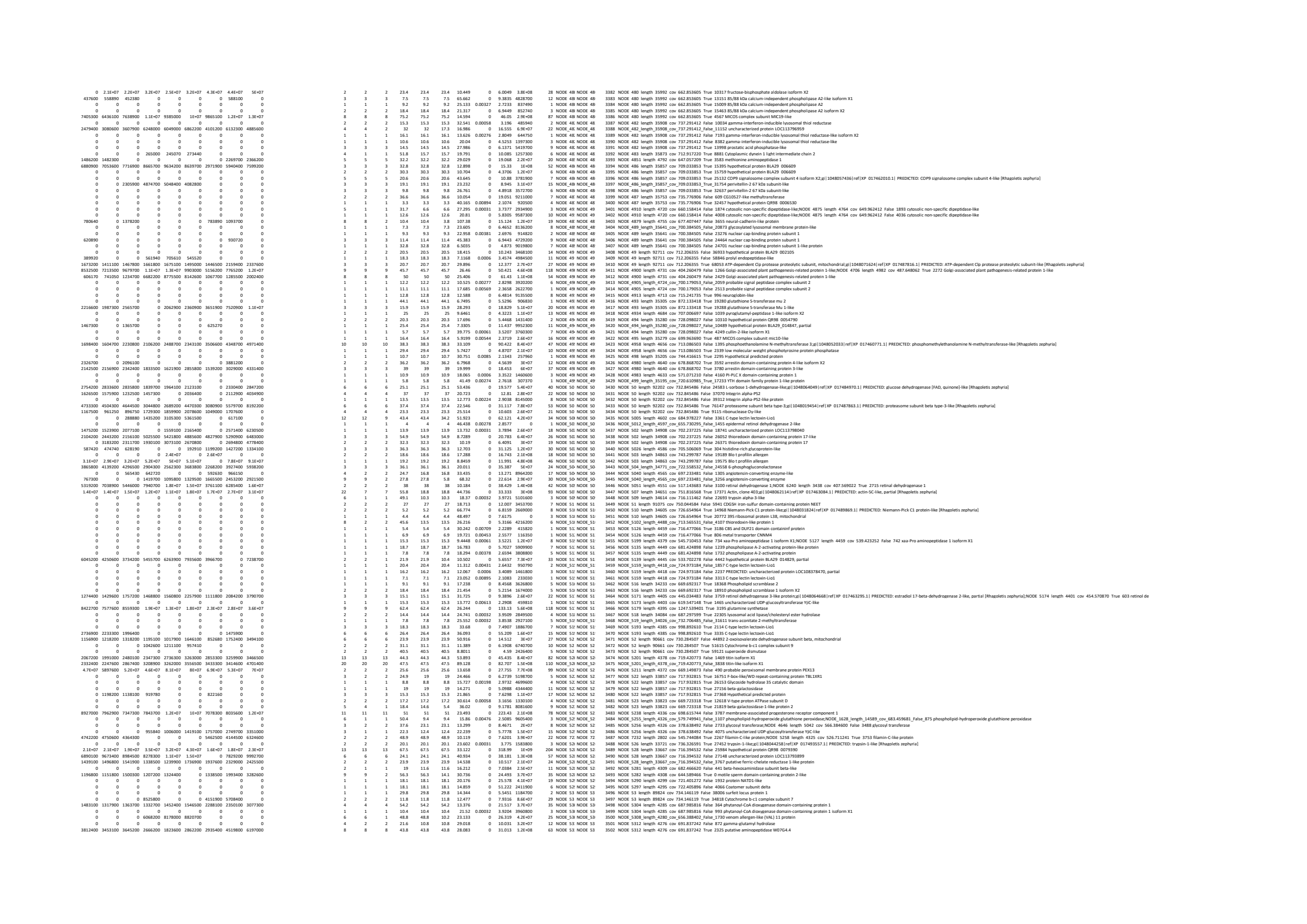


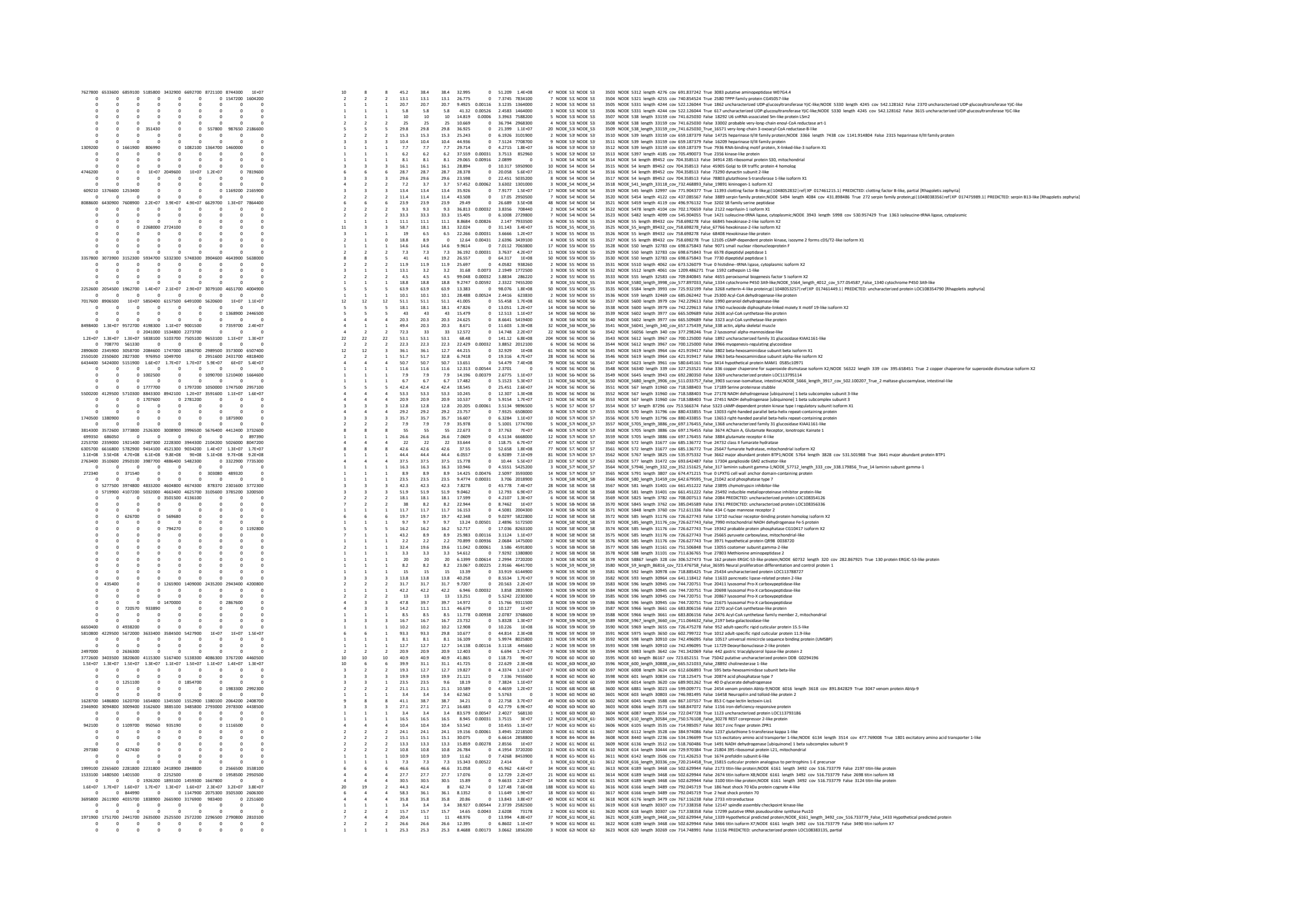


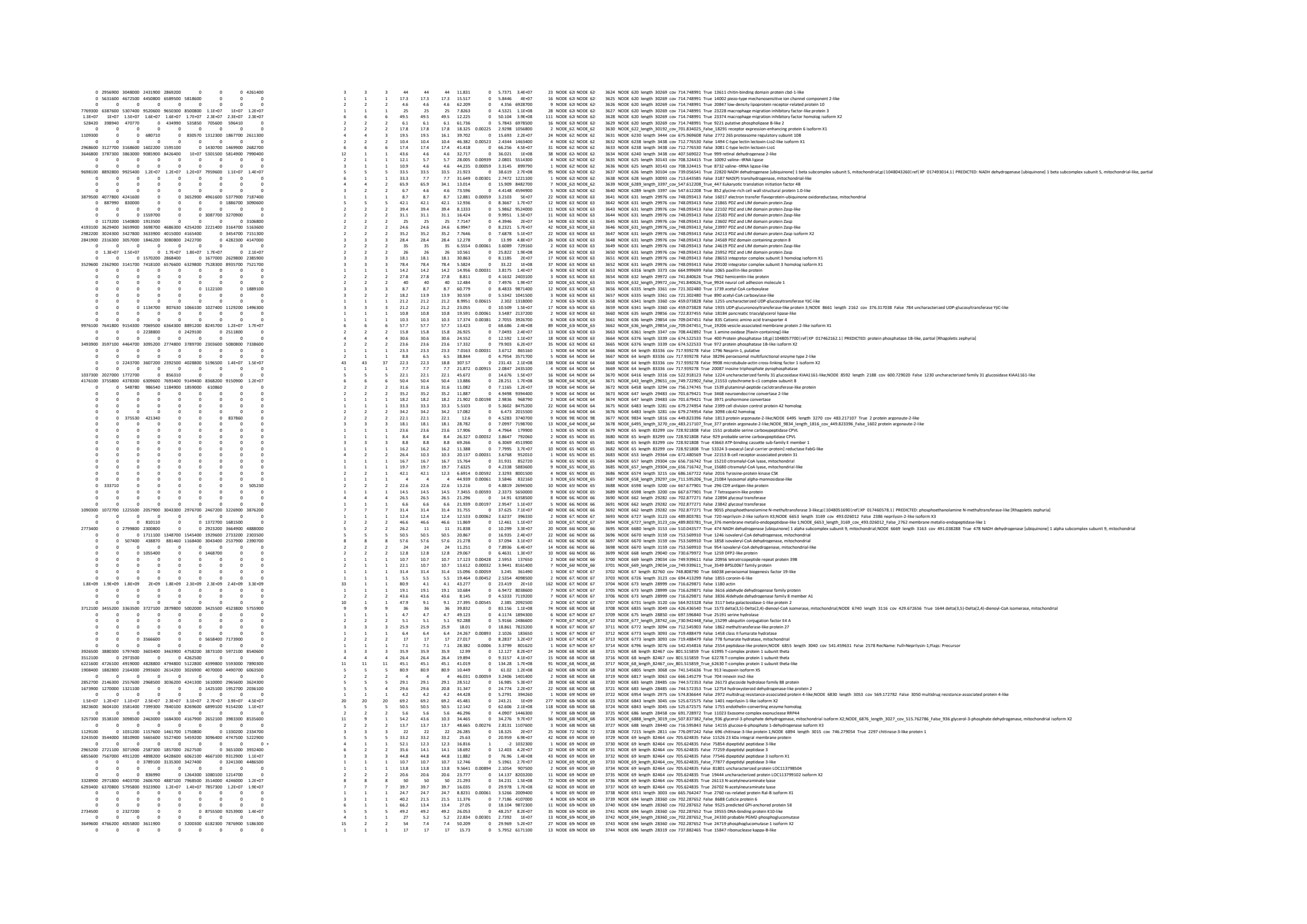






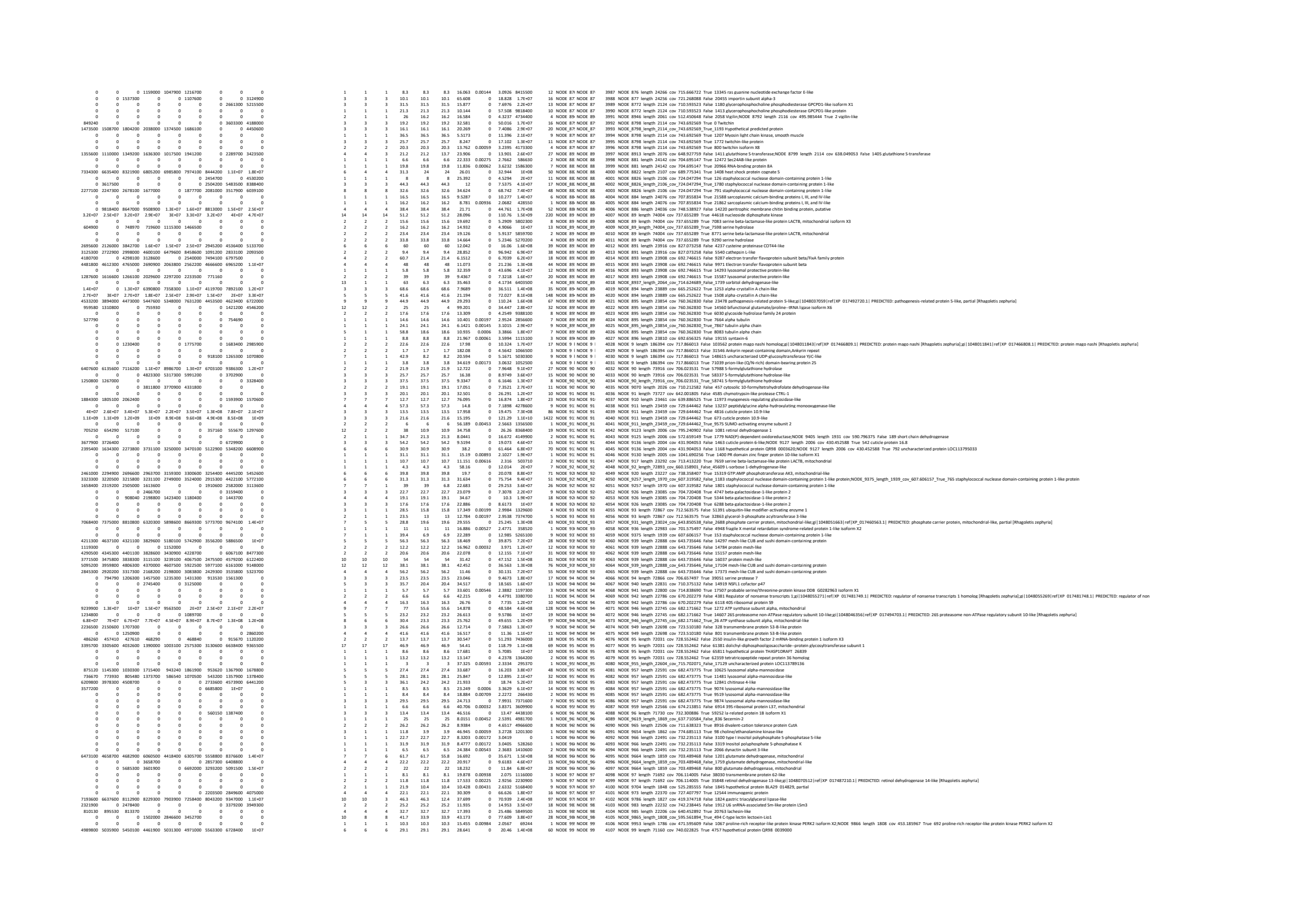






589500	566940	0	0	0	0	0	0	1711200		3	3	3	24.7	24.7	24.7	30.424	0	5.2581	5639300	8	NODE 70	NODE 70	3745	NODE 7005 length 2939 cov 555.137656 True 2137 tyrosine-protein phosphatase 99A-like protein;NODE 6961 length 2966 cov 527.171075 True 2158 tyrosine-protein phosphatase 99A-like protein
0	0	0	0	0	0	0	0	0		1	1	1	3.8	3.8	3.8	35.551	0.00708	2.2247	1065900	2	NODE 69	NODE 69	3746	NODE 699 length 28301 cov 716.224244 True 0 mannosyl-oligosaccharide alpha-1,2-mannosidase IA-like
0	0	0	0	0	0	0	0	0		2	2	2	11.8	11.8	11.8	33.692	0	6.2823	5769500	7	NODE 70	NODE 70	3747	NODE 7007 length 2937 cov 697.642956 False 2470 retinol dehydrogenase 12-like
3.5E+07	3.3E+07	3.7E+07	5.5E+07	6.3E+07	5.5E+07	6.3E+07	1.1E+08	9.3E+07		1	1	1	33.8	33.8	33.8	7.7286	0	6.9349	6.2E+08	43	NODE 70	NODE 70	3748	NODE 7040 length 2912 cov 709.845992 True 0 DFP2-like protein
0	0	0	0	0	0	0	0	0		2	2	2	17.3	17.3	17.3	19.03	0	8.7864	1.3E+07	7	NODE 70	NODE 70	3749	NODE 7043 length 2908 cov 655.887136 True 830 PREDICTED: kininogen-1-like
0	0	0	0	0	0	0	0	0		1	1	1	18.6	18.6	18.6	11.439	0.00637	2.2754	379230	4	NODE 70	NODE 70	3750	NODE 7048 length 2904 cov 689.312741 True 2613 E3 ubiquitin-protein ligase BRE1B isoform X2
0	0	0	3148500	3743300	4292100	1.1E+07	7114700	0		7	7	6	38.5	38.5	38.5	16.987	0	24.026	6.1E+07	28	NODE 70	NODE 70	3751	NODE 7057 length 2898 cov 728.828350 True 30 platelet-activating factor acetylhydrolase IB subunit beta-like
1.2E+07	9496000	1E+07	1.3E+07	9214800	1.6E+07	1.6E+07	2.4E+07	4.1E+07		7	5	4	61.4	49.2	43.9	15.248	0	16.146	5.1E+08	67	NODE 70	NODE 70	3752	NODE 7057 length 2898 cov 728.828350 True 473 GDSL family lipase
0	0	0	0	0	0	0	0	0		1	1	1	16.5	16.5	16.5	11.267	0.00173	3.0644	1091500	2	NODE 70	NODE 70	3753	NODE 706 length 28139 cov 712.670310 True 25597 biogenesis of lysosome-related organelles complex 1 subunit 2-like protein
0	0	0	943720	1281100	1361700	0	0	0		4	4	2	20.1	20.1	11.8	45.168	0	9.9356	7.8E+08	15	NODE 70	NODE 70	3754	NODE 7060 length 2896 cov 615.091165 False 1527 choline/ethanolamine kinase-like;NODE 7017 length 2931 cov 614.876912 False 1540 choline/ethanolamine kinase-like
0	0	0	0	0	0	0	0	0		1	1	1	15.4	15.4	15.4	7.4007	0.00429	2.607	1448500	6	NODE 70	NODE 70	3755	NODE 708 length 28097 cov 721.280579 False 26063 NDRG3-like protein
1303700	861190	988630	1303200	0	1364600	1707900	2165300	2018200		5	5	5	27.9	27.9	27.9	29.527	0	15.412	1.8E+07	25	NODE 70	NODE 70	3756	NODE 708 length 28097 cov 721.280579 False 26975 NDRG3-like protein
0	0	0	0	0	0	0	0	0		1	1	1	2.2	2.2	2.2	57.363	0.00937	2.0717	318690	1	NODE 70	NODE 70	3757	NODE 709 length 28065 cov 730.451553 True 17074 paired amphipathic helix protein Sin3a isoform X1
1.7E+07	1.5E+07	1.8E+07	4E+07	3.4E+07	4.6E+07	4.9E+07	5.2E+07	6.2E+07		4	4	4	54.3	54.3	54.3	12.218	0	93.296	9E+08	163	NODE 70	NODE 70	3758	NODE 709 length 28065 cov 730.451553 True 26995 Enoyl-CoA hydratase, mitochondrial
0	0	0	0	0	0	0	0	0		1	1	1	3.3	3.3	3.3	51.936	0.00593	2.3383	371360	1	NODE 70	NODE 70	3759	NODE 7095 length 2875 cov 669.389007 False 1444 replication protein A 70 kDa DNA-binding subunit
0	0	0	0	0	0	0	0	0		1	1	1	9.6	9.6	9.6	15.225	0.00452	2.5327	1331500	5	NODE 71	NODE 71	3760	NODE 712 length 27917 cov 719.098019 True 14717 LYR motif-containing protein 4
0	0	0	0	0	0	0	0	0		1	1	1	18.7	18.7	18.7	8.5678	0.00594	2.3465	2293000	5	NODE 71	NODE 71	3761	NODE 712 length 27917 cov 719.098019 True 21201 BTB/POZ domain-containing protein 6-B-like protein
0	0	0	0	0	0	0	0	0		1	1	1	39.7	39.7	39.7	8.2379	0.00452	2.5491	2786200	3	NODE 71	NODE 71	3762	NODE 713 length 27902 cov 720.192552 True 23322 reticulocalbin-2-like isoform X2
1738600	1455900	1912000	1470800	1219500	1593800	1307300	2374800	4146300		4	4	4	14.9	14.9	14.9	35.506	0	32.975	3.3E+07	31	NODE 71	NODE 71	3763	NODE 7135 length 2856 cov 1167.133524 False 1058 Sorting nexin-2
0	0	0	0	0	0	0	0	0		1	1	1	4.5	4.5	4.5	29.538	0.00328	2.7289	392750	1	NODE 71	NODE 71	3764	NODE 714 length 27879 cov 728.188722 False 13383 LOW QUALITY PROTEIN: uncharacterized protein LOC117223387
0	0	0	0	0	0	0	0	0		2	2	2	27.7	27.7	27.7	10.652	0	4.7107	1.6E+07	9	NODE 71	NODE 71	3765	NODE 714 length 27879 cov 728.188722 True 25023 chymotrypsin inhibitor-like
0	0	0	0	0	0	0	0	0		1	1	1	7.1	7.1	7.1	38.754	0.00634	2.2474	1289500	1	NODE 71	NODE 71	3766	NODE 7144 length 2851 cov 700.453147 True 1751 DnaJ protein
1100500	0	1409000	0	0	0	0	2633800	3688400		2	2	2	16	16	16	36.295	0	4.9644	1.5E+07	11	NODE 71	NODE 71	3767	NODE 7144 length 2851 cov 700.453147 True 270 DnaJ protein
0	0	0	0	0	0	0	0	0		1	1	1	2.1	2.1	2.1	104.2	0.00545	2.3792	279040	2	NODE 71	NODE 71	3768	NODE 717 length 27740 cov 745.140365 False 7196 WD repeat-containing protein 44
0	1383900	1390400	805590	732350	877210	0	0	2332000		5	4	4	29	24.4	24.4	33.908	0	12.901	1.9E+07	19	NODE 72	NODE 72	3769	NODE 721 length 27587 cov 716.399353 False 22375 contactin-like
0	0	0	0	0	0	0	0	0		2	2	2	20.8	20.8	20.8	16.039	0	5.1354	6780900	7	NODE 72	NODE 72	3770	NODE 7232 length 2802 cov 545.744084 True 1788 filamin repeat containing protein 2;NODE 5258 length 4325 cov 526.711241 True 3263 filamin repeat containing protein 2
4909500	5165700	5616000	5557300	4758400	5933000	8705100	1.6E+07	1.7E+07		7	7	7	46.3	46.3	46.3	15.323	0	33.155	1.6E+08	53	NODE 72	NODE 72	3771	NODE 725 length 27459 cov 727.364180 True 1208 4-hydroxyphenylpyruvate dioxygenase
0	0	3714100	0	0	0	7682500	1.4E+07	1.6E+07		3	3	3	32.7	32.7	32.7	12.879	0	15.96	1E+08	24	NODE 72	NODE 72	3772	NODE 725 length 27459 cov 727.364180 True 1636 4-hydroxyphenylpyruvate dioxygenase-like
0	0	0	0	0	0	0	0	0		11	1	1	20.1	1.9	1.9	82	0	5.8116	1.6E+07	9	NODE 72	NODE 72	3773	NODE 725 length 27459 cov 727.364180 True 19179 glycine--tRNA ligase
0	0	0	0	0	0	0	0	0		1	1	1	25.9	25.9	25.9	6.6967	0.00031	3.7771	4.1E+07	16	NODE 72	NODE 72	3774	NODE 725 length 27459 cov 727.364180 True 646 4-hydroxyphenylpyruvate dioxygenase-like
3786900	4465400	5003900	6345700	5213800	7079300	8951600	1.9E+07	2.2E+07		4	4	4	36.7	36.7	36.7	16.254	0	14.584	1.7E+08	53	NODE 72	NODE 72	3775	NODE 725 length 27459 cov 727.364180 True 823 4-hydroxyphenylpyruvate dioxygenase
0	0	0	0	0	0	0	0	0		1	1	1	11.9	11.9	11.9	12.942	0.00826	2.1422	2009100	3	NODE 72	NODE 72	3776	NODE 726 length 27453 cov 726.322067 False 19461 long-chain-fatty-acid--CoA ligase 5 isoform X1
0	0	0	0	0	0	0	0	0		1	1	1	8.3	8.3	8.3	29.633	0	5.1164	2289800	8	NODE 72	NODE 72	3777	NODE 726 length 27453 cov 726.322067 False 9832 RNA-binding protein cabeza-like
0	0	0	0	0	0	0	0	0		1	1	1	5.7	5.7	5.7	57.12	0.00059	3.3332	579850	1	NODE 72	NODE 72	3778	NODE 727 length 27452 cov 735.546994 False 9739 lysosomal alpha-mannosidase-like protein
0	0	0	0	0	0	0	0	0		1	1	1	19.2	19.2	19.2	11.796	0	25.218	1E+07	12	NODE 72	NODE 72	3779	NODE 729 length 27440 cov 744.197407 True 18574 leucine carboxyl methyltransferase 1
0	0	0	0	0	0	0	0	0		3	3	3	15.7	15.7	15.7	26.278	0	6.2349	4096200	8	NODE 72	NODE 72	3780	NODE 729 length 27440 cov 744.197407 True 18923 leucine carboxyl methyltransferase 1
869870	807700	735520	1237400	1835200	1755400	0	1567100	2485900		2	2	2	16.7	16.7	16.7	17.994	0	8.0524	2.8E+07	34	NODE 72	NODE 72	3781	NODE 729 length 27440 cov 744.197407 True 19959 nodal modulator-like protein
1085900	885950	1121800	1784100	1300800	1811600	1613700	2791200	2493000		3	3	3	22.8	22.8	22.8	11.199	0	7.2411	2.1E+07	22	NODE 72	NODE 72	3782	NODE 729 length 27440 cov 744.197407 True 20448 nodal modulator-like protein
2439000	2170500	2086300	3442500	3836300	3705100	3320100	3520100	4933200		6	6	6	34.9	34.9	34.9	27.457	0	26.037	7.5E+07	35	NODE 72	NODE 72	3783	NODE 729 length 27440 cov 744.197407 True 20734 MICOS complex subunit MIC60-like
800370	867910	839920	895000	752050	965850	0	1519600	3003200		8	8	8	13.7	13.7	13.7	108.22	0	39.148	2E+07	38	NODE 72	NODE 72	3784	NODE 729 length 27440 cov 744.197407 True 22279 nodal modulator 1
0	0	0	0	0	0	0	0	0	+	1	1	1	15.5	15.5	15.5	11.189	1	-2	864590	1	NODE 73	NODE 73	3785	NODE 731 length 27401 cov 690.298801 False 15974 chitinase-3-like protein 1
0	0	0	0	0	0	2695600	1586500	3612700		3	3	3	20.3	20.3	20.3	19.318	0	12.757	1.9E+07	16	NODE 73	NODE 73	3786	NODE 731 length 27401 cov 690.298801 False 16514 chitinase-3-like protein 1
0	0	0	3632400	0	0	2358500	0	0		2	2	2	11	11	11	12.405	0	4.6604	2.7E+07	14	NODE 73	NODE 73	3787	NODE 731 length 27401 cov 690.298801 False 16844 acidic mammalian chitinase-like
4643100	3619800	4963800	1.1E+07	9612100	7637100	1.6E+07	1.1E+07	1.5E+07		7	6	6	55.4	46.8	46.8	15.393	0	33.187	1.7E+08	48	NODE 73	NODE 73	3788	NODE 731 length 27401 cov 690.298801 False 4407 myosin heavy chain, muscle-like
0	0	0	0	0	0	0	0	0		1	1	1	8.1	8.1	8.1	17.898	0.00277	2.8323	1828400	6	NODE 73	NODE 73	3789	NODE 732 length 27398 cov 758.612076 False 2411 prostatic acid phosphatase-like
0	0	0	0	0	0	0	0	0	+	1	1	1	5.6	5.6	5.6	47.276	1	-2	151280	1	NODE 73	NODE 73	3790	NODE 732 length 27398 cov 758.612076 True 12046 uncharacterized protein LOC113788365
0	0	0	0	0	0	0	0	0		10	3	3	44	10.5	10.5	30.414	0	6.7129	4.1E+07	13	NODE 73	NODE 73	3791	NODE 733 length 27384 cov 723.071536 True 16995 serine protease, putative
0	0	0	0	0	0	0	0	0		5	1	1	48.6	7.7	7.7	15.912	0.00524	2.4455	2779700	3	NODE 73	NODE 73	3792	NODE 737 length 27299 cov 674.945970 False 7605 glucose phosphate dehydrogenase
0	1E+07	8245100	7637700	7305300	7826300	9278400	8745800	1.3E+07		3	3	3	24	24	24	16.372	0	8.994	1.1E+08	20	NODE 73	NODE 73	3793	NODE 737 length 27299 cov 674.945970 False 8983 glucose-6-phosphate 1-dehydrogenase-like
0	0	0	0	0	0	0	0	0		1	1	1	10.5	10.5	10.5	19.506	0.00984	2.0632	0	1	NODE 73	NODE 73	3794	NODE 7381 length 2730 cov 744.036636 False 896 TBC1 domain containing protein
0	0	0	0	0	0	0	0	0		2	2	2	33.3	33.3	33.3	10.737	0	4.711	2754300	5	NODE 73	NODE 73	3795	NODE 739 length 27272 cov 671.282801 False 2038 AP-2 complex subunit mu
0	785170	818370	0	0	0	0	1351200	1851200		3	3	3	18.3	18.3	18.3	21.054	0	9.2739	1.1E+07	16	NODE 73	NODE 73	3796	NODE 739 length 27272 cov 671.282801 False 2642 AP-2 complex subunit mu;gi|1048064843|ref|XP 017463394.1| PREDICTED: AP-2 complex subunit mu-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	1548500	2576400	0		3	3	3	20.8	20.8	20.8	18.373	0	6.5793	1.4E+07	16	NODE 73	NODE 73	3797	NODE 739 length 27272 cov 671.282801 False 5401 sodium/potassium-transporting ATPase subunit beta-like
3819000	1691000	2280000	1.3E+07	9035900	1.3E+07	2.6E+07	3.1E+07	4.6E+07		11	10	3	48.9	46.1	16.2	40.768	0	42.289	4.4E+08	80	NODE 74	NODE 74	3798	NODE 74 length 78248 cov 709.202064 False 29074 beta-galactosidase-1-like protein 2
0	0	0	0	0	0	0	0	0		4	1	1	62.5	11.5	11.5	12.071	0.00031	3.7203	2234900	1	NODE 74	NODE 74	3799	NODE 74 length 78248 cov 709.202064 False 32536 beta-galactosidase-1-like protein 2
0	0	0	0	0	0	0	0	0		1	1	1	1.9	1.9	1.9	99.741	0.00061	3.4847	360530	2	NODE 74	NODE 74	3800	NODE 74 length 78248 cov 709.202064 True 69477 PorP/SprF family type IX secretion system membrane protein
0	0	0	0	0	0	0	0	0		2	2	2	16.1	16.1	16.1	31.765	0	8.0019	2834200	5	NODE 74	NODE 74	3801	NODE 741 length 27244 cov 688.223252 True 23689 putative stoned B-like protein
0	0	0	0	0	0	0	0	0		1	1	1	5.8	5.8	5.8	25.189	0.00058	3.1537	3794800	4	NODE 74	NODE 74	3802	NODE 7414 length 2714 cov 519.340730 True 2 serine protease-like protein 2
0	0	0	0	0	0	0	0	0		1	1	1	7.2	7.2	7.2	18.668	0.00031	3.7352	7820600	5	NODE 74	NODE 74	3803	NODE 7429 length 2707 cov 526.438914 True 195 chymotrypsin-like protease CTRL-1
0	0	0	0	0	0	0	0	0		1	1	1	28.7	28.7	28.7	10.3	0	8.9111	4259600	3	NODE 74	NODE 74	3804	NODE 7429 length 2707 cov 526.438914 True 2 granzyme A-like
0	0	0	1596000	4741200	5234400	0	0	0		2	2	2	70.9	70.9	70.9	6.0507	0	8.9342	2.1E+07	9	NODE 74	NODE 74	3805	NODE 7429 length 2707 cov 526.438914 True 691 complement C1r-A subcomponent-like
7035300	6362400	7174600	5128900	3970400	6797100	6424000	1E+07	1.5E+07		11	11	10	66.7	66.7	61.6	30.303	0	75.438	1.9E+08	85	NODE 74	NODE 74	3806	NODE 7445 length 2695 cov 1355.649242 False 2692 putative glutamate synthase [NADPH] isoform X3
0	0	0	0	0	0	0	0	0		1	1	1	12.6	12.6	12.6	10.144	0.00525	2.4466	1374000	1	NODE 74	NODE 74	3807	NODE 745 length 27200 cov 739.454964 False 25416 glutamate decarboxylase isoform X1
0	0	0	0	0	0	0	0	0		6	1	1	47.4	7.9	7.9	16.24	0.00172	3.0502	8.7E+07	15	NODE 74	NODE 74	3808	NODE 745 length 27200 cov 739.454964 False 5040 pyruvate kinase-like
0	0	0	0	0	0	0	0	0		2	1	1	24.8	11.2	11.2	14.163	0.00198	2.9684	3442900	7	NODE 74	NODE 74	3809	NODE 745 length 27200 cov 739.454964 False 6664 pyruvate kinase-like protein
0	0	0	2533600	2681300	3238100	2440700	5184900	6361200		7	7	7	47.7	47.7	47.7	23.741	0	33.901	7.3E+07	36	NODE 74	NODE 74	3810	NODE 746 length 27200 cov 732.525364 False 22888 sucrase-isomaltase, intestinal-like
0	0	0	0	0	0	0	3368300	3806100		2	2	2	28.6	28.6	28.6	17.727	0	13.247	1.8E+07	9	NODE 74	NODE 74	3811	NODE 746 length 27200 cov 732.525364 False 23383 sucrase-isomaltase, intestinal-like
0	0	0	0	0	0	0	0	0		1	1	1	8.4	8.4	8.4	22.111	0.00032	3.9641	1.1E+07	8	NODE 74	NODE 74	3812	NODE 746 length 27200 cov 732.525364 False 23621 maltase-glucoamylase, intestinal
0	0	0	0	0	1621900	0	2848200	6150400		4	4	4	28	28	28	17.734	0	16.583	2.9E+07	14	NODE 74	NODE 74	3813	NODE 746 length 27200 cov 732.525364 False 25693 maltase-glucoamylase, intestinal
1481200	1557900	1766800	0	0	0	0	0	0		4	4	4	13.6	13.6	13.6	37.008	0	66.888	9835100	10	NODE 74	NODE 74	3814	NODE 746 length 27200 cov 732.525364 True 20154 venom acid phosphatase Acph-1-like
2173000	2062600	3745200	960080	0	0	0	0	0		3	3	3	24.2	24.2	24.2	25.691	0	17.475	2.1E+07	13	NODE 74	NODE 74	3815	NODE 746 length 27200 cov 732.525364 True 21166 prostatic acid phosphatase-like
365470	577570	622820	0	0	0	0	0	0		1	1	1	18.4	18.4	18.4	10.968	0.0006	3.4495	3167100	8	NODE 74	NODE 74	3816	NODE 746 length 27200 cov 732.525364 True 21891 prostatic acid phosphatase-like
0	0	0	0	0	0	0	0	0		1	1	1	13.1	13.1	13.1	11.833	0.0006	3.3684	1342000	4	NODE 75	NODE 75	3817	NODE 75 length 78014 cov 690.976436 False 52364 putative cytochrome c oxidase assembly protein Cox19
5873400	8028500	8679900	5019400	5757200	8819900	1951900	6737200	1.5E+07		5	5	5	37.8	37.8	37.8	19.879	0	17.559	1.2E+08	33	NODE 75	NODE 75	3818	NODE 75 length 78014 cov 690.976436 False 71446 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13
0	0	0	0	0	0	2554200	4454500	0		4	4	4	23.1	23.1	23.1	23.681	0	7.6152	1.6E+07	9	NODE 75	NODE 75	3819	NODE 75 length 78014 cov 690.976436 True 16116 phosphoribosyl pyrophosphate synthase-associated protein 2
0	1296000	1567100	1328200	2008800	2529300	3207700	4093900	3211800		5	5	5	40.2	40.2	40.2	24.789	0	16.996	3.6E+07	23	NODE 75	NODE 75	3820	NODE 75 length 78014 cov 690.976436 True 16673 phosphoribosyl pyrophosphate synthase-associated protein 2 isoform X2
0	0	0	0	0	0	0	0	0		1	1	1	30.2	30.2	30.2	7.0705	0	8.5848	3875500	7	NODE 75	NODE 75	3821	NODE 75 length 78014 cov 690.976436 True 58779 DnaJ domain containing protein
0	0	0	950620	1187000	842070	1034800	1578000	2736600		7	7	7	23.7	23.7	23.7	52.393	0	34.484	2.3E+07	27	NODE 75	NODE 75	3822	NODE 75 length 78014 cov 690.976436 True 67199 Protein CBG13257
1.8E+07	1.8E+07	1.7E+07	1.6E+07	1.6E+07	2.5E+07	1.7E+07	2E+07	3E+07		14	12	3	57.6	55.1	24.8	34.08	0	48.901	7.5E+08	166	NODE 75	NODE 75	3823	NODE 7503 length 2670 cov 753.584321 False 2156 retinal dehydrogenase 1 isoform X2
6083200	5972700	6284900	4920200	4942100	7431000	8078700	8626600	1.5E+07		4	4	4	41.9	41.9	41.9	10.147	0	13.102	1.1E+08	34	NODE 75	NODE 75	3824	NODE 751 length 27076 cov 717.293883 True 3080 protein obstructor-E
0	0	0	0	0	0	0	0	0		1	1	1	29.1	29.1	29.1	9.7609	0	5.8491	6.4E+07	9	NODE 75	NODE 75	3825	NODE 751 length 27076 cov 717.293883 True 3387 Protein obstructor-E
3264000	3765400	3678000	2739700	3475100	3713500	5280500	6793700	8229500		4	4	4	64.5	64.5	64.5	7.1831	0	10.005	1.2E+08	48	NODE 75	NODE 75	3826	NODE 751 length 27076 cov 717.293883 True 3654 protein obstructor-E
0	0	0	0	0	0	0	0	0		2	2	2	41.6	41.6	41.6	8.7503	0.00032	3.8543	633740	4	NODE 75	NODE 75	3827	NODE 7597 length 2619 cov 583.884945 False 2374 keratin, type I cytoskeletal 9-like;NODE 7531 length 2659 cov 574.064900 True 218 keratin, type I cytoskeletal 9-like
987030	1152900	1122900	0	0	954980	0	0	1400800		3	3	3	8.3	8.3	8.3	65.356	0	12.656	1.1E+07	16	NODE 75	NODE 75	3828	NODE 7534 length 2657 cov 718.792083 True 958 exportin-2-like;gi|1048067576|ref|XP 017463898.1| PREDICTED: exportin-2-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		3	1	1	51.4	15.7	15.7	7.95	0.00031	3.7431	6709900	10	NODE 75	NODE 75	3829	NODE 756 length 27029 cov 715.836250 False 2631 glyceraldehyde-3-phosphate dehydrogenase
0	0	0	0	0	0	4191100	4994100	7122600		8	8	3	28.3	28.3	7.5	44.008	0	27.628	4.3E+07	29	NODE 75	NODE 75	3830	NODE 758 length 26962 cov 675.952800 True 2887 p-loop containing nucleoside triphosphate hydrolase
0	0	0	0	0	0	0	0	0		1	1	1	12	12	12	18.576	0.00275	2.7991	419040	3	NODE 76	NODE 76	3831	NODE 76 length 77980 cov 709.829426 False 12050 histone deacetylase 2
0	0	0	0	0	0	0	0	0		1	1	1	33.9	33.9	33.9	6.6504	0	7.7002	0	1	NODE 76	NODE 76	3832	NODE 76 length 77980 cov 709.829426 False 12159 histone deacetylase 2
0	0	0	0	0	0	0	0	0		1	1	1	21	21	21	8.5218	0.00199	2.9992	418170	1	NODE 76	NODE 76	3833	NODE 76 length 77980 cov 709.829426 False 12405 Histone deacetylase 1
0	0	0	0	0	0	0	0	0		1	1	1	8.5	8.5	8.5	23.895	0.00059	3.2081	6169600	7	NODE 76	NODE 76	3834	NODE 76 length 77980 cov 709.829426 False 13043 histone deacetylase
0	0	0	0	0	0	0	0	0		1	1	1	19.1	19.1	19.1	7.8902	0.00849	2.1299	5490700	6	NODE 76	NODE 76	3835	NODE 76 length 77980 cov 709.829426 False 13317 histone deacetylase 2
4.3E+07	3.7E+07	4E+07	9.3E+07	7E+07	7.3E+07	3.1E+07	3.8E+07	4.6E+07		12	12	7	61.8	61.8	36.7	22.924	0	100.19	1.9E+09	235	NODE 76	NODE 76	3836	NODE 76 length 77980 cov 709.829426 False 25058 protein lethal(2)essential for life-like;gi|1048033876|ref|XP 017490976.1| PREDICTED: alpha-crystallin A chain-like [Rhagoletis zephyria]
4513400	5537900	6643700	3253400	3944200	4763300	4708700	6471500	1E+07		6	6	6	30.6	30.6	30.6	26.294	0	29.204	7.9E+07	28	NODE 76	NODE 76	3837	NODE 76 length 77980 cov 709.829426 False 54887 40S ribosomal protein S3a;gi|1048052876|ref|XP 017461238.1| PREDICTED: 40S ribosomal protein S3a-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		2	2	2	19.7	19.7	19.7	8.3669	0.00279	2.8593	4561400	6	NODE 76	NODE 76	3838	NODE 76 length 77980 cov 709.829426 False 55118 Rps1ap
0	0	0	0	0	0	0	0	0		13	1	1	42.4	3	3	47.541	0.00031	3.774	5E+07	6	NODE 76	NODE 76	3839	NODE 760 length 26909 cov 677.370857 True 11355 ATP synthase subunit gamma, mitochondrial-like
5947400	7105000	4800400	6958500	6226300	9007000	9800200	1.2E+07	1.8E+07		9	9	9	46.4	46.4	46.4	26.917	0	34.12	3.1E+08	106	NODE 76	NODE 76	3840	NODE 760 length 26909 cov 677.370857 True 3946 Platelet-activating factor acetylhydrolase IB subunit gamma
2911700	2473600	2492900	2449600	1819800	3470800	3713000	5655200	1E+07		6	6	6	67.5	67.5	67.5	14.269	0	84.389	1.3E+08	80	NODE 76	NODE 76	3841	NODE 760 length 26909 cov 677.370857 True 4632 GDSL family lipase
0	0	0	0	0	0	0	0	0		4	3	2	20	16.4	10.3	21.916	0	6.7389	3384400	5	NODE 76	NODE 76	3842	NODE 7622 length 2605 cov 519.444314 False 2603 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	0	0		2	2	2	51.5	51.5	51.5	10.955	0.00526	2.472	1102100	2	NODE 76	NODE 76	3843	NODE 7638 length 2598 cov 474.999214 True 254 keratin, type I cytoskeletal 9-like;NODE 17773 length 911 cov 355.942757 True 257 keratin, type I cytoskeletal 9-like
3934100	3906400	3900400	6438500	6549400	7873100	3242400	9645900	1.5E+07		2	2	2	43.3	43.3	43.3	7.1382	0	11.644	1.4E+08	39	NODE 76	NODE 76	3844	NODE 765 length 26795 cov 715.856021 True 15292 glucosylceramidase-like protein
1749000	1620200	1578500	3261800	2259700	2436400	2010500	3841400	5061500		2	2	2	31.7	31.7	31.7	9.4945	0	5.861	5.3E+07	32	NODE 76	NODE 76	3845	NODE 765 length 26795 cov 715.856021 True 15575 glucosylceramidase-like
4092300	0	0	6838900	5453200	7135500	4772000	8224600	1.2E+07		6	6	6	53.1	53.1	53.1	14.74	0	12.308	9.8E+07	29	NODE 76	NODE 76	3846	NODE 765 length 26795 cov 715.856021 True 16000 glucosylceramidase-like
0	0	0	0	0	0	0	0	0		2	2	2	8	8	8	44.97	0	6.9182	1824200	3	NODE 76	NODE 76	3847	NODE 765 length 26795 cov 715.856021 True 20352 spectrin beta chain-like
0	0	0	0	0	0	0	0	0		17	1	0	45	2.4	0	45.113	0.00431	2.6322	3.3E+07	6	NODE 76	NODE 76	3848	NODE 7655 length 2589 cov 610.596685 True 1194 lysosomal alpha-mannosidase-like
1999600	2837400	2217000	6869900	6936900	5993200	2022500	4861600	8267700		10	10	10	46.9	46.9	46.9	31.97	0	62.907	1.2E+08	56	NODE 76	NODE 76	3849	NODE 769 length 26648 cov 711.626970 True 12907 cathepsin B;gi|1048064571|ref|XP 017463239.1| PREDICTED: cathepsin B-like, partial [Rhagoletis zephyria]
0	0	0	1201400	0	1455100	0	2038100	2579700		4	4	4	13	13	13	43.289	0	9.534	1.6E+07	15	NODE 76	NODE 76	3850	NODE 769 length 26648 cov 711.626970 True 1692 serpin family protein
0	0	0	2738300	2351400	2732800	0	0	0		8	8	8	28.4	28.4	28.4	47.502	0	42.175	2.9E+07	22	NODE 76	NODE 76	3851	NODE 769 length 26648 cov 711.626970 True 4786 serpin family protein
0	0	0	0	0	0	0	0	0		1	1	1	42	42	42	9.0203	0.0006	3.4418	135740	1	NODE 77	NODE 77	3852	NODE 770 length 26597 cov 711.175910 False 18568 trafficking protein particle complex subunit 11
4.1E+07	4.9E+07	4.1E+07	4.3E+07	6E+07	5.5E+07	1.5E+07	5.3E+07	8.1E+07		7	7	6	45.7	45.7	39.1	17.101	0	139.59	1.1E+09	279	NODE 77	NODE 77	3853	NODE 770 length 26597 cov 711.175910 False 3437 14-3-3 protein epsilon
0	0	0	0	0	0	0	0	0		9	2	2	63.2	23.7	23.7	12.89	0	11.673	2.6E+07	16	NODE 77	NODE 77	3854	NODE 770 length 26597 cov 711.175910 False 3786 14-3-3 protein epsilon
0	0	0	580800	1159100	0	1564300	2306400	3759400		4	4	4	44.2	44.2	44.2	13.83	0	15.325	2.3E+07	26	NODE 77	NODE 77	3855	NODE 770 length 26597 cov 711.175910 False 9344 Phosphoserine phosphatase
0	0	0	0	0	0	0	0	0		1	1	1	11.6	11.6	11.6	12.945	0.00225	2.9191	1624400	2	NODE 77	NODE 77	3856	NODE 770 length 26597 cov 711.175910 False 9683 phosphoserine phosphatase-like
0	0	0	0	0	0	0	0	0		2	2	2	8.4	8.4	8.4	39.952	0	5.112	1264600	2	NODE 77	NODE 77	3857	NODE 7716 length 2557 cov 596.066347 True 1002 long-chain-fatty-acid--CoA ligase 4-like;NODE 7712 length 2559 cov 602.753594 True 1004 long-chain-fatty-acid--CoA ligase 4-like
0	0	0	0	0	0	0	0	0		2	2	2	26.6	26.6	26.6	11.835	0.00059	3.2946	3224900	3	NODE 77	NODE 77	3858	NODE 7719 length 2554 cov 705.463786 True 1425 uncharacterized protein LOC113793237
0	0	0	0	0	0	0	0	0		3	3	3	11.9	11.9	11.9	40.043	0	5.6473	3787100	9	NODE 77	NODE 77	3859	NODE 773 length 26542 cov 726.870049 True 18367 Phosphoribosyl pyrophosphate synthase-associated protein 2
0	0	0	0	0	0	0	0	0		1	1	1	2.8	2.8	2.8	47.97	0.00328	2.726	436150	1	NODE 77	NODE 77	3860	NODE 774 length 26509 cov 662.681220 False 6607 adipocyte plasma membrane-associated protein-like
1.7E+07	1.9E+07	1.9E+07	7945500	2.4E+07	1.9E+07	1993500	1.1E+07	2.9E+07		6	6	4	37.4	37.4	35	35.948	0	46.841	3.3E+08	49	NODE 77	NODE 77	3861	NODE 775 length 26434 cov 710.296562 False 10267 PREDICTED: calphotin-like, partial
0	0	0	0	0	0	0	0	0		3	2	2	11.9	9.9	9.9	38.554	0	5.7174	2467800	4	NODE 77	NODE 77	3862	NODE 7767 length 2529 cov 723.088116 True 1364 C-type lectin lectoxin-Lio1
4616000	4123400	2939200	0	0	0	2341300	4460000	4406500		3	3	3	28.7	28.7	28.7	27.364	0	21.088	3.6E+07	18	NODE 77	NODE 77	3863	NODE 7767 length 2529 cov 723.088116 True 2 C-type lectin lectoxin-Lio1
0	0	0	342150	0	0	361430	0	692010		2	2	2	23.6	23.6	23.6	11.836	0.00032	3.9528	3356000	10	NODE 77	NODE 77	3864	NODE 7776 length 2524 cov 622.100041 False 1087 long-chain-fatty-acid--CoA ligase 4-like;NODE 7836 length 2487 cov 645.348684 False 1075 long-chain-fatty-acid--CoA ligase 4-like
0	0	0	0	0	0	0	0	0		1	1	1	26.8	26.8	26.8	6.5016	0.0028	2.88	1289600	3	NODE 77	NODE 77	3865	NODE 7776 length 2524 cov 622.100041 False 168 long-chain-fatty-acid--CoA ligase 4-like;NODE 7836 length 2487 cov 645.348684 False 177 long-chain-fatty-acid--CoA ligase 4-like

0	0	0	0	0	0	0	0	0		1	1	1	31.2	31.2	31.2	6.952	0	3.9967	7583600	7	NODE 77	NODE 77	3866	NODE 7776 length 2524 cov 622.100041 False 400 long-chain-fatty-acid--CoA ligase 4-like;NODE 7836 length 2487 cov 645.348684 False 394 long-chain-fatty-acid--CoA ligase 4-like
0	0	0	0	0	0	0	0	0		3	3	3	24.9	24.9	24.9	28.012	0	7.448	3468100	7	NODE 77	NODE 77	3867	NODE 7785 length 2517 cov 728.830219 True 1309 uncharacterized UDP-glucosyltransferase YjiC-like
0	0	1126400	1339300	1344600	1496900	0	0	0		1	1	1	30.8	30.8	30.8	12.331	0	19.977	1.1E+07	15	NODE 77	NODE 77	3868	NODE 779 length 26342 cov 635.046677 False 5734 NDRG3-like protein
0	0	0	0	0	0	0	0	0		2	2	2	8.1	8.1	8.1	37.958	0	4.2778	1103200	3	NODE 77	NODE 77	3869	NODE 7798 length 2511 cov 486.457655 False 1984 nucleoside hydrolase
1.9E+07	2E+07	2.2E+07	0	1.7E+07	0	1.5E+07	0	0		4	4	4	49.2	49.2	49.2	13.563	0	48.42	1.4E+08	30	NODE 78	NODE 78	3870	NODE 78 length 76615 cov 746.913009 False 71374 cuticle protein, putative
0	0	0	0	0	0	0	0	0		3	3	3	16.2	16.2	16.2	19.272	0	6.219	2936200	7	NODE 78	NODE 78	3871	NODE 7802 length 2509 cov 715.276284 True 1327 ras-related protein Ral-A-like
0	0	0	0	0	0	0	0	0		5	1	1	29.9	6	6	30.017	0.00522	2.417	1.5E+07	8	NODE 78	NODE 78	3872	NODE 781 length 26283 cov 731.082698 True 1 probable maleylacetoacetate isomerase 2
0	0	0	0	0	0	0	0	0		1	1	1	9.6	9.6	9.6	15.911	0	4.5882	2767300	9	NODE 78	NODE 78	3873	NODE 782 length 26261 cov 737.984240 False 19077 nuclear migration protein nudC
0	0	0	0	0	0	0	0	0		1	1	1	7.7	7.7	7.7	26.489	0.00172	3.0433	0	1	NODE 78	NODE 78	3874	NODE 782 length 26261 cov 737.984240 False 20057 nuclear migration protein nudC
0	0	0	0	0	0	0	0	0		1	1	1	11.3	11.3	11.3	15.146	0.00172	3.0408	2267100	4	NODE 78	NODE 78	3875	NODE 7828 length 2489 cov 570.668858 True 1448 transcription elongation factor SPT5-like
0	0	0	0	0	0	0	0	0		1	1	1	38.2	38.2	38.2	8.2325	0.00894	2.107	1639300	2	NODE 78	NODE 78	3876	NODE 785 length 26194 cov 718.893952 False 15313 Protein cornichon
0	0	0	0	0	0	0	0	0	+	1	1	1	2.3	2.3	2.3	44.979	1	-2	1628900	3	NODE 78	NODE 78	3877	NODE 7875 length 2470 cov 536.455901 True 82 uncharacterized protein LOC113795125
4172400	4981500	5576600	1950400	1529500	0	3184600	3254700	2893900		9	9	9	38.2	38.2	38.2	32.866	0	107.65	8.7E+07	56	NODE 78	NODE 78	3878	NODE 789 length 26146 cov 876.478173 False 20427 hypothetical protein QR98 0103690
0	0	1594800	0	2180000	0	1113200	2477200	0		4	4	4	16.5	16.5	16.5	26.578	0	8.4729	1.9E+07	24	NODE 78	NODE 78	3879	NODE 789 length 26146 cov 876.478173 False 25813 chromobox protein homolog 6 isoform X2
0	0	0	0	0	0	0	0	0		1	1	1	9.1	9.1	9.1	28.829	0.0006	3.4158	498940	1	NODE 78	NODE 78	3880	NODE 789 length 26146 cov 876.478173 True 3211 trypsin alpha-3-like
0	0	0	0	0	0	1301500	0	1840300		10	3	3	21.2	7.4	7.4	78.291	0	8.4561	7865100	10	NODE 79	NODE 79	3881	NODE 79 length 76496 cov 660.700619 False 26345 uncharacterized family 31 glucosidase KIAA1161-like
3988000	4602200	4561600	3192800	3826400	4007900	4296000	5295500	6497500		21	21	21	39.7	39.7	39.7	85.07	0	94.83	2.3E+08	128	NODE 79	NODE 79	3882	NODE 79 length 76496 cov 660.700619 False 41202 uncharacterized family 31 glucosidase KIAA1161-like
0	0	0	0	0	0	0	0	0		3	3	3	39.6	39.6	39.6	16.394	0	6.3946	5512400	9	NODE 79	NODE 79	3883	NODE 791 length 26019 cov 712.849908 False 2883 mitochondrial intermembrane space import and assembly protein 40;gi|1048066107|ref|XP 017485551.1| PREDICTED: mitochondrial intermembrane space import and assembly protein 40-like [Rhagoletis zephyria]
0	1945400	2602400	0	0	0	0	0	0		2	2	2	11.6	11.6	11.6	22.273	0.00276	2.8054	1.3E+07	7	NODE 79	NODE 79	3884	NODE 7945 length 2441 cov 705.491199 False 1514 neural cell adhesion molecule 1-like
0	0	0	0	0	0	488510	667910	829050		3	3	3	3.2	3.2	3.2	171.88	0	9.1656	3028600	10	NODE 79	NODE 79	3885	NODE 795 length 25951 cov 734.886392 False 23197 RING finger protein nhl-1-like
1655800	2132300	2130900	2585500	1984700	2724900	2139300	3116900	2758600		2	2	2	52.2	52.2	52.2	7.5317	0	39.389	4.2E+07	25	NODE 79	NODE 79	3886	NODE 7963 length 2433 cov 491.613120 True 1418 galactose mutarotase;NODE 8059 length 2392 cov 484.810441 True 1383 galactose mutarotase
0	0	0	0	0	0	0	0	0		2	2	2	17.7	17.7	17.7	13.951	0.00172	3.0475	1245600	3	NODE 79	NODE 79	3887	NODE 7969 length 2427 cov 398.588111 True 392 insulin-like growth factor-binding protein complex acid labile subunit;NODE 6803 length 3071 cov 391.564987 False 2659 insulin-like growth factor-binding protein complex acid labile subunit
3060700	3802100	0	5437300	7284000	5382100	3254500	3346800	6748100		3	3	3	30.9	30.9	30.9	6.283	0	30.686	5.9E+07	20	NODE 80	NODE 80	3888	NODE 80 length 76295 cov 746.454538 False 36443 cuticular protein, putative
3498500	3081000	3756700	4071800	4304000	4204500	3610600	6227800	7809200		3	3	2	9.7	9.7	4.1	29.735	0	59.159	7.9E+07	35	NODE 80	NODE 80	3889	NODE 80 length 76295 cov 746.454538 False 4430 ribosomal protein S6
0	0	0	0	0	0	0	0	0		2	1	1	46.1	23.7	23.7	8.7457	0	10.757	1.7E+07	6	NODE 80	NODE 80	3890	NODE 80 length 76295 cov 746.454538 False 75237 diaminopimelate decarboxylase
0	0	0	0	0	0	0	0	0		6	1	1	30	5.4	5.4	23.095	0.00116	3.125	1E+08	10	NODE 80	NODE 80	3891	NODE 80 length 76295 cov 746.454538 False 76196 diaminopimelate decarboxylase
0	3025700	2657900	4175200	3451400	4755000	6338900	7293200	6369400		5	5	5	21.1	21.1	21.1	38.331	0	23.254	7.1E+07	38	NODE 80	NODE 80	3892	NODE 80 length 76295 cov 746.454538 True 11890 succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial-like
7861700	8207800	7619600	7223300	7524200	1.1E+07	7148500	1.1E+07	1.9E+07		6	6	6	52.2	52.2	52.2	22.449	0	100.97	3.5E+08	100	NODE 80	NODE 80	3893	NODE 80 length 76295 cov 746.454538 True 12813 ADP-forming succinate--CoA ligase subunit beta;gi|1048052323|ref|XP 017460931.1| PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta-like [Rhagoletis zephyria]
723690	521040	0	0	0	0	0	0	0		3	3	3	11.4	11.4	11.4	52.852	0	8.7932	3560900	9	NODE 80	NODE 80	3894	NODE 80 length 76295 cov 746.454538 True 30188 complement C3-like
0	603220	0	0	0	0	0	0	1368600		3	3	3	7	7	7	76.925	0	5.4928	6150400	8	NODE 80	NODE 80	3895	NODE 80 length 76295 cov 746.454538 True 31735 Complement C3
3819600	4385100	6137400	6681800	6941300	7241300	7997800	4650900	1E+07		2	2	2	27.6	27.6	27.6	18.865	0	12.972	1E+08	29	NODE 80	NODE 80	3896	NODE 80 length 76295 cov 746.454538 True 43583 DFP2-like protein 25
1.3E+07	1.4E+07	1.6E+07	1.5E+07	1.4E+07	1.4E+07	1.2E+07	1.6E+07	1.5E+07		4	4	4	45.3	45.3	45.3	13.042	0	42.466	2E+08	53	NODE 80	NODE 80	3897	NODE 80 length 76295 cov 746.454538 True 49906 cuticular protein, putative
0	990960	1340200	0	0	0	0	0	0		3	3	3	21.8	21.8	21.8	25.023	0	10.515	8538800	11	NODE 80	NODE 80	3898	NODE 80 length 76295 cov 746.454538 True 66539 putative ferric-chelate reductase 1 homolog
0	0	0	0	0	0	0	0	0		1	1	1	15.2	15.2	15.2	7.7509	0.0043	2.6078	6300700	9	NODE 80	NODE 80	3899	NODE 8004 length 2413 cov 709.122986 True 2213 cyclase family protein
0	0	0	0	0	0	0	0	0		1	1	1	3	3	3	56.697	0.00848	2.1204	6979200	5	NODE 80	NODE 80	3900	NODE 8013 length 2409 cov 782.988530 True 153 serine/threonine-protein kinase SRK2A-like
0	0	0	0	0	0	0	0	0		1	1	1	9.5	9.5	9.5	23.882	0.00061	3.5787	2299100	6	NODE 80	NODE 80	3901	NODE 802 length 25891 cov 694.598158 True 6048 glutamine synthetase
0	0	0	0	0	0	0	0	0		2	2	2	13.3	13.3	13.3	22.613	0.00059	3.3027	1637100	4	NODE 80	NODE 80	3902	NODE 802 length 25891 cov 694.598158 True 6802 glutamine synthetase 2 cytoplasmic-like
0	0	0	0	0	0	0	0	0		1	1	1	7.7	7.7	7.7	33.331	0.00031	3.7175	709080	3	NODE 80	NODE 80	3903	NODE 8079 length 2385 cov 694.663948 False 2009 HRAS-like suppressor 3
0	0	0	0	0	0	0	0	0		2	2	2	19.1	19.1	19.1	15.523	0.00032	3.8895	1.1E+07	3	NODE 80	NODE 80	3904	NODE 808 length 25670 cov 703.024790 False 14899 globin isoform X3
6.4E+07	4.6E+07	5.1E+07	6E+07	5.3E+07	6.3E+07	9.8E+07	9.9E+07	7.9E+07		15	7	3	67.1	41.1	24	16.261	0	26.79	1.1E+09	111	NODE 80	NODE 80	3905	NODE 808 length 25670 cov 703.024790 False 18112 arginine kinase
9.7E+07	7.7E+07	8.9E+07	1.8E+08	1.3E+08	1.7E+08	1.2E+08	1.9E+08	2.4E+08		7	5	5	53.8	41.5	41.5	12.522	0	46.272	2E+09	69	NODE 80	NODE 80	3906	NODE 808 length 25670 cov 703.024790 False 18433 arginine kinase
0	0	0	0	0	0	0	0	0		1	1	1	26.5	26.5	26.5	10.693	0	7.9402	5E+08	28	NODE 80	NODE 80	3907	NODE 808 length 25670 cov 703.024790 False 18720 arginine kinase
0	0	0	0	0	0	0	0	0		1	1	1	8	8	8	12.39	0.00429	2.5979	628710	1	NODE 80	NODE 80	3908	NODE 808 length 25670 cov 703.024790 False 20204 AChain A, arginine kinase
0	0	0	2219000	0	2523700	2174500	3302000	5441500		3	3	3	17.2	17.2	17.2	29.709	0	9.0606	3.6E+07	16	NODE 80	NODE 80	3909	NODE 8088 length 2383 cov 602.454897 True 153 sodium-driven chloride bicarbonate exchanger isoform X4;NODE 8084 length 2384 cov 603.037355 False 2364 sodium-driven chloride bicarbonate exchanger isoform X4
0	0	0	0	0	0	0	0	0		2	2	2	10.3	10.3	10.3	22.857	0.00031	3.6726	5683900	2	NODE 80	NODE 80	3910	NODE 8084 length 2384 cov 603.037355 False 699 electrogenic sodium bicarbonate cotransporter 1 isoform X1;NODE 8088 length 2383 cov 602.454897 True 1674 electrogenic sodium bicarbonate cotransporter 1 isoform X1
0	0	0	0	0	0	0	0	0		1	1	1	29.6	29.6	29.6	6.2982	0	4.071	2.3E+07	9	NODE 80	NODE 80	3911	NODE 8092 length 2382 cov 813.718092 False 1386 32 kDa beta-galactoside-binding lectin-like
0	0	0	0	0	0	0	0	0		2	2	2	40.7	40.7	40.7	9.2965	0	5.4843	9460700	5	NODE 80	NODE 80	3912	NODE 8092 length 2382 cov 813.718092 False 1632 32 kDa beta-galactoside-binding lectin
0	0	0	0	0	0	0	0	0		2	2	2	8.7	8.7	8.7	31.902	0.00475	2.4955	2926400	4	NODE 81	NODE 81	3913	NODE 8108 length 2372 cov 480.155373 True 170 39S ribosomal protein L44, mitochondrial;NODE 8224 length 2325 cov 493.910573 True 168 mitochondrial 39S ribosomal protein L44
2623500	2522600	3940600	1153600	0	1197300	5852800	8569300	1.2E+07		3	3	3	14.2	14.2	14.2	30.697	0	58.127	5.3E+07	38	NODE 81	NODE 81	3914	NODE 812 length 25571 cov 748.469901 False 1801 hypothetical protein BLA29 012342
0	0	0	0	0	0	0	0	0		3	1	1	23.2	10.7	10.7	18.768	0	7.1731	3000100	3	NODE 81	NODE 81	3915	NODE 813 length 25564 cov 779.220432 False 15867 motile sperm domain-containing protein 2-like
0	0	0	0	0	0	0	0	0		1	1	1	4.4	4.4	4.4	36.073	0.00197	2.9449	916720	4	NODE 81	NODE 81	3916	NODE 813 length 25564 cov 779.220432 True 13103 motile sperm domain-containing protein 2-like
0	0	0	0	0	0	0	0	0		2	2	2	12.9	12.9	12.9	29.91	0	5.6562	4383300	5	NODE 81	NODE 81	3917	NODE 814 length 25551 cov 707.294674 False 17677 rhythmically expressed gene 2 protein
0	0	0	0	0	0	0	0	0		2	2	2	11.3	11.3	11.3	22.757	0	6.7161	1E+07	9	NODE 81	NODE 81	3918	NODE 815 length 25542 cov 678.028014 False 25539 protein SEC13 homolog;NODE 1183 length 18931 cov 785.934944 True 17036 protein SEC13 homolog
0	0	0	0	0	0	0	0	0		4	2	2	23.8	11.3	11.3	37.076	0	7.9404	4231500	4	NODE 81	NODE 81	3919	NODE 8155 length 2350 cov 401.035730 True 140 cholinesterase 1-like
0	0	0	0	0	0	0	0	0		1	1	1	15.6	15.6	15.6	14.765	0.00892	2.1003	4.8E+07	19	NODE 81	NODE 81	3920	NODE 8163 length 2348 cov 692.633668 True 0 cuticular protein-like protein
1671200	1554300	1728600	1878900	1692300	1826500	1780400	2088400	2667800		7	7	7	26.8	26.8	26.8	44.683	0	20.684	3.1E+07	33	NODE 81	NODE 81	3921	NODE 819 length 25504 cov 658.534324 False 16969 inactive pancreatic lipase-related protein 1-like;gi|1048067691|ref|XP 017463965.1| PREDICTED: inactive pancreatic lipase-related protein 1-like [Rhagoletis zephyria]
1.1E+07	9981000	7854600	5547000	3060000	1E+07	1.8E+07	1.8E+07	2.6E+07		3	2	2	40	33.3	33.3	17.693	0	82.332	2.1E+08	52	NODE 82	NODE 82	3922	NODE 82 length 75534 cov 705.008161 False 47003 Cuticle protein 14 isoform a
9707400	1.3E+07	1.4E+07	7561400	0	1.1E+07	1.4E+07	1.8E+07	2.5E+07		1	1	1	32.9	32.9	32.9	7.2771	0	36.426	1.3E+08	23	NODE 82	NODE 82	3923	NODE 82 length 75534 cov 705.008161 False 47260 adult-specific rigid cuticular protein 15.7-like
0	0	0	0	0	0	0	0	0		1	1	1	11.9	11.9	11.9	15.163	0	23.401	2E+07	11	NODE 82	NODE 82	3924	NODE 82 length 75534 cov 705.008161 True 58547 glutathione S-transferase-like
1.9E+07	1.5E+07	1.7E+07	1.7E+07	1.3E+07	1.8E+07	6922900	1.6E+07	1.4E+07		3	3	3	39.2	39.2	39.2	11.005	0	21.859	2.3E+08	46	NODE 82	NODE 82	3925	NODE 82 length 75534 cov 705.008161 True 59581 glutathione S-transferase Mu 1-like
0	0	0	0	3562600	4312500	0	0	0		2	2	2	18.2	18.2	18.2	9.8612	0.00032	3.8886	2.8E+07	10	NODE 82	NODE 82	3926	NODE 82 length 75534 cov 705.008161 True 59879 glutathione S-transferase Mu 5
0	0	0	0	0	0	0	0	0		1	1	1	22.6	22.6	22.6	7.4453	0.00915	2.0877	1148200	2	NODE 82	NODE 82	3927	NODE 8202 length 2332 cov 431.617918 False 948 cholinesterase 1-like
1041700	0	1297900	942600	0	0	1857700	1920700	0		2	2	2	38.7	38.7	38.7	11.98	0	6.5345	1.1E+07	13	NODE 82	NODE 82	3928	NODE 8222 length 2325 cov 717.951101 False 1162 peptidase S10, serine carboxypeptidase
0	0	0	0	0	0	0	0	0		1	1	1	3.5	3.5	3.5	31.533	0.00849	2.1267	673690	1	NODE 82	NODE 82	3929	NODE 8222 length 2325 cov 717.951101 False 2048 lysosomal protective protein-like
2199200	2598100	2180600	4175100	4843000	6470100	4897900	6562400	4437200		3	3	3	32.3	32.3	32.3	20.075	0	22.6	9E+07	42	NODE 82	NODE 82	3930	NODE 8237 length 2319 cov 702.685954 False 1657 DFP2-like protein
0	0	0	0	0	0	0	0	0		1	1	1	23.1	23.1	23.1	7.257	0	5.2269	8509200	3	NODE 82	NODE 82	3931	NODE 824 length 25427 cov 742.683115 True 21787 PREDICTED: cholinesterase-like, partial
0	0	0	0	0	0	0	2935100	4442000		3	3	3	29.4	29.4	29.4	18.176	0	11.482	1.7E+07	8	NODE 82	NODE 82	3932	NODE 824 length 25427 cov 742.683115 True 22930 cholinesterase 1-like
2781200	3279100	3215700	3087500	2964900	4149100	2928000	3230800	0		4	4	4	13.5	13.5	13.5	50.845	0	60.903	4E+07	25	NODE 82	NODE 82	3933	NODE 8253 length 2315 cov 723.318584 False 2314 CD109 antigen-like
0	1483800	1763800	3758000	1812600	2985300	2350000	3318200	4018500		4	4	4	39	39	39	19.055	0	18.958	2.8E+07	32	NODE 82	NODE 82	3934	NODE 8253 length 2315 cov 723.318584 False 532 CD109 antigen-like
0	0	0	0	0	0	0	0	0		2	2	2	13.6	13.6	13.6	14.739	0.00032	3.9566	3.1E+07	10	NODE 82	NODE 82	3935	NODE 8270 length 2310 cov 678.431042 True 1499 innexin inx2-like
0	3405400	3244900	4145300	2485400	4598000	0	0	0		2	2	2	13.6	13.6	13.6	20.873	0	21.588	3.2E+07	13	NODE 84	NODE 84	3936	NODE 8421 length 2245 cov 524.184018 True 888 CD109 antigen-like protein;NODE 8281 length 2306 cov 518.107508 True 918 CD109 antigen-like protein
0	0	0	0	0	0	0	0	0		1	1	1	4.9	4.9	4.9	31.584	0.00061	3.4777	4119600	10	NODE 83	NODE 83	3937	NODE 831 length 25339 cov 724.927820 True 15882 nucleoporin Nup37-like
0	221980	0	353410	0	0	0	676360	737560		1	1	1	14.4	14.4	14.4	12.377	0	4.3008	3939700	10	NODE 83	NODE 83	3938	NODE 832 length 25313 cov 715.847929 False 21520 vesicular glutamate transporter 1-like
0	0	0	0	0	0	0	0	0		1	1	1	4	4	4	46.777	0.00116	3.1243	2032900	3	NODE 83	NODE 83	3939	NODE 8348 length 2274 cov 685.782334 True 0 protein SGT1 homolog
0	0	0	0	0	0	0	0	0		2	2	2	14.1	14.1	14.1	24.543	0	5.4473	3466300	6	NODE 83	NODE 83	3940	NODE 8352 length 2273 cov 696.748873 True 942 glycosyl transferase;NODE 9107 length 2014 cov 340.008678 True 624 glycosyl transferase
0	0	0	0	0	0	1541400	0	2915100		1	1	1	8.3	8.3	8.3	17.99	0	5.5886	8037000	5	NODE 83	NODE 83	3941	NODE 8388 length 2256 cov 723.361654 True 710 putative glycine receptor subunit alpha-3-like
0	0	0	0	0	0	0	0	0		5	1	1	54.1	17.2	17.2	13.619	0.00225	2.9136	1065900	2	NODE 84	NODE 84	3942	NODE 84 length 75055 cov 730.418667 True 46184 adenosine kinase 2
2.6E+07	3.1E+07	2.8E+07	2.3E+07	1.2E+07	2.2E+07	2E+07	2.6E+07	5.6E+07		2	2	2	49.2	49.2	49.2	7.2182	0	91.479	3.8E+08	46	NODE 84	NODE 84	3943	NODE 84 length 75055 cov 730.418667 True 47353 adenosine kinase
0	0	0	0	0	0	0	0	0		2	2	2	30.7	30.7	30.7	19.358	0	5.4807	2129300	2	NODE 84	NODE 84	3944	NODE 8421 length 2245 cov 524.184018 True 1716 CD109 antigen-like protein;NODE 8281 length 2306 cov 518.107508 True 1843 CD109 antigen-like protein
0	0	0	0	0	0	0	0	0		1	1	1	12.9	12.9	12.9	10.56	0.00061	3.4921	8295800	3	NODE 84	NODE 84	3945	NODE 8426 length 2241 cov 706.111619 True 165 Golgi-associated plant pathogenesis-related protein 1-like
2E+07	2.2E+07	2.6E+07	2.9E+07	2.8E+07	2.6E+07	3.6E+07	4E+07	4.3E+07		2	2	2	25.8	25.8	25.8	9.886	0	8.5858	4.6E+08	38	NODE 84	NODE 84	3946	NODE 843 length 25132 cov 716.241656 False 2607 smoothelin-like protein
8196800	8478500	1.1E+07	1.5E+07	1.1E+07	1.2E+07	1.3E+07	1.7E+07	2.2E+07		4	4	4	50.7	50.7	50.7	7.1079	0	12.46	2.9E+08	49	NODE 84	NODE 84	3947	NODE 843 length 25132 cov 716.241656 False 3005 Smoothelin-like protein 1
0	0	0	2750200	0	0	3419300	0	0		3	3	3	10.6	10.6	10.6	23.749	0	5.2679	2.4E+07	11	NODE 84	NODE 84	3948	NODE 843 length 25132 cov 716.241656 False 3406 smoothelin-like protein
707310	0	0	775130	725960	872080	0	918700	1505700		1	1	1	28.6	28.6	28.6	6.6758	0.00061	3.5291	8986100	19	NODE 84	NODE 84	3949	NODE 843 length 25132 cov 716.241656 False 369 smoothelin-like protein
0	0	0	0	0	0	0	0	0		2	2	2	12.5	12.5	12.5	8.122	0.00301	2.7454	6E+07	20	NODE 84	NODE 84	3950	NODE 843 length 25132 cov 716.241656 False 635 smoothelin-like protein
0	0	0	0	0	0	0	0	0		1	1	1	22.2	22.2	22.2	6.0938	0.00116	3.105	2107700	1	NODE 84	NODE 84	3951	NODE 843 length 25132 cov 716.241656 False 790 smoothelin-like protein 2
0	1918400	0	2093000	1809400	1953500	2750200	2586900	3264900		3	3	3	17.5	17.5	17.5	30.02	0	16.351	2.7E+07	21	NODE 84	NODE 84	3952	NODE 848 length 24957 cov 661.678379 True 2926 synaptophysin-like protein
0	0	0	0	0	0	0	0	0		4	2	2	39.8	17	17	9.8491	0	4.2692	2.2E+08	16	NODE 88	NODE 88	3953	NODE 8819 length 2108 cov 562.800779 False 1664 glutamate dehydrogenase, mitochondrial-like;NODE 8493 length 2218 cov 886.702728 False 1748 glutamate dehydrogenase, mitochondrial-like
905920	938690	868220	0	0	0	0	0	1327600		2	2	2	12.1	12.1	12.1	23.836	0	5.1283	1.1E+07	17	NODE 89	NODE 89	3954	NODE 8977 length 2051 cov 393.142285 True 1276 transmembrane protein 79-like;NODE 8571 length 2194 cov 375.468911 True 1383 transmembrane protein 79-like;NODE 8377 length 2260 cov 1112.263039 True 65 transmembrane protein 79-like
0	0	0	0	0	0	0	0	0		2	2	2	20.3	20.3	20.3	17.231	0	4.4757	3581100	8	NODE 86	NODE 86	3955	NODE 86 length 74613 cov 706.678425 True 19119 beta-mannosidase
2333600	2351900	2662000	2353000	1818000	2537000	0	2770300	3101200		2	2	2	17.8	17.8	17.8	11.321	0	11.248	3.6E+07	26	NODE 86	NODE 86	3956	NODE 86 length 74613 cov 706.678425 True 36373 transmembrane emp24 domain-containing protein bai-like
0	0	0	0	0	0	0	0	0		1	1	1	17.9	17.9	17.9	6.4946	0.00526	2.4736	6298600	3	NODE 86	NODE 86	3957	NODE 86 length 74613 cov 706.678425 True 36933 transmembrane emp24 domain-containing protein 10
0	1385000	1836300	1837200	0	2249800	0	0	2984300		1	1	1	8.4	8.4	8.4	14.814	0.00059	3.2954	2.1E+07	14	NODE 86	NODE 86	3958	NODE 86 length 74613 cov 706.678425 True 46587 probable cathepsin C
0	0	0	0	0	0	0	0	0		3	2	2	14.1	11.6	11.6	37.009	0.00354	2.7139	7560000	6	NODE 86	NODE 86	3959	NODE 860 length 24747 cov 876.970152 True 2471 C-type lectin lectoxin-Lio1
0	0	0	0	0	0	0	0	0		2	1	1	18.9	13.9	13.9	22.884	0.00637	2.2655	3811000	5	NODE 86	NODE 86	3960	NODE 860 length 24747 cov 876.970152 True 3741 C-type lectin lectoxin-Lio1
0	0	0	837560	0	0	0	0	1608000		3	2	2	24.3	18.1	18.1	22.852	0	8.3883	6601400	10	NODE 86	NODE 86	3961	NODE 861 length 24746 cov 633.272569 True 12893 cathepsin L1-like
0	0	0	1273800	1181700	2438700	0	0	0		5	4	4	29.2	26.3	26.3	27.216	0	10.828	1.1E+07	7	NODE 86	NODE 86	3962	NODE 8615 length 2178 cov 676.451719 False 2177 C-type lectin lectoxin-Lio1
743130	803280	0	0	2177100	1039900	1810700	3413400	5467300		14	14	14	29.5	29.5	29.5	72.555	0	35.33	5E+07	42	NODE 86	NODE 86	3963	NODE 862 length 24674 cov 702.974654 False 24248 beta-glucuronidase-like isoform X3
0	0	0	913700	990290	1093300	1705300	2291000	0		4	4	4	11.5	11.5	11.5	47.929	0	11.329	1.7E+07	19	NODE 86	NODE 86	3964	NODE 862 length 24674 cov 702.974654 False 5876 tetratricopeptide repeat protein 38-like
1.2E+07	1.2E+07	1.2E+07	1.1E+07	1E+07	1.5E+07	6520700	1.2E+07	1.9E+07		6	6	6	30.4	30.4	30.4	36.406	0	30.635	2.4E+08	101	NODE 86	NODE 86	3965	NODE 864 length 24558 cov 756.378811 True 12927 Carbonic anhydrase 7-like protein
0	0	0	1384000	1739600	3790800	0	0	0		6	6	6	30.1	30.1	30.1	33.467	0	10.959	1.5E+07	11	NODE 86	NODE 86	3966	NODE 8652 length 2164 cov 482.280228 True 2 Group 1 mite allergen-like protein (Cysteine protease);NODE 8580 length 2191 cov 488.660581 True 177 cathepsin L1-like
0	0	0	0	0	0	0	0	0		2	2	2	20.3	20.3	20.3	24.79	0	16.47	1.2E+07	6	NODE 86	NODE 86	3967	NODE 866 length 24550 cov 659.120882 False 3450 IST1 homolog isoform X2
0	0	0	0	0	0	0	0	0		1	1	1	13.8	13.8	13.8	15.894	0	4.3199	379000	3	NODE 86	NODE 86	3968	NODE 866 length 24550 cov 659.120882 False 3875 IST1 homolog
0	0	0	0	0	0	0	0	0		5	5	1	33.5	33.5	4.8	21.45	0	11.148	4064300	11	NODE 86	NODE 86	3969	NODE 8661 length 2162 cov 376.317038 False 1314 uncharacterized UDP-glucosyltransferase YjiC-like
0	0	0	0	0	0	0	0	0		1	1	1	9.8	9.8	9.8	22.127	0.00729	2.1845	1377900	1	NODE 86	NODE 86	3970	NODE 8664 length 2161 cov 743.637702 True 99 60S ribosomal protein L21-like
0	0	0	0	0	0	0	0	0	+	1	1	1	6.9	6.9	6.9	16.088	1	-2	8341200	2	NODE 87	NODE 87	3971	NODE 87 length 74280 cov 726.260532 False 44209 UDP-N-acetylglucosamine transporter-like isoform X1
982340	1037300	1137700	930250	788310	0	1208200	1440800	0		5	5	5	28.9	28.9	28.9	26.066	0	15.204	1.8E+07	21	NODE 87	NODE 87	3972	NODE 87 length 74280 cov 726.260532 True 28370 Thymidylate kinase
0	0	0	0	0	0	0	0	0		1	1	1	19.1	19.1	19.1	7.2725	0.00061	3.6183	1741900	4	NODE 87	NODE 87	3973	NODE 870 length 24504 cov 718.990020 False 13632 aquaporin-11-like isoform X1
0	0	0	0	0	0	0	0	0		2	2	2	4.1	4.1	4.1	81.14	0	5.5376	1908100	4	NODE 87	NODE 87	3974	NODE 870 length 24504 cov 718.990020 False 17389 hypothetical protein QR98 0050420
0	0	0	0	0	0	0	0	0		4	4	4	5.5	5.5	5.5	100.16	0	6.0872	1653200	9	NODE 87	NODE 87	3975	NODE 870 length 24504 cov 718.990020 False 4484 protein scribble homolog;gi|1048046275|ref|XP 017494658.1| PREDICTED: protein lap4-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		2	2	2	14.9	14.9	14.9	22.478	0.00524	2.4381	477130	2	NODE 87	NODE 87	3976	NODE 871 length 24500 cov 650.181591 False 16919 nucleoside diphosphate-linked moiety X motif 6-like isoform X1
0	0	0	0	0	0	0	0	0	+	1	1	1	6.6	6.6	6.6	23.761	1	-2	8622000	3	NODE 87	NODE 87	3977	NODE 8723 length 2141 cov 741.098754 False 1944 splicing factor ESS-2 homolog
0	0	0	0	0	0	0	0	0		3	3	3	17.7	17.7	17.7	35.43	0	7.6899	6833000	6	NODE 87	NODE 87	3978	NODE 874 length 24332 cov 691.935659 False 5457 vacuolar protein sorting-associated protein 35
0	0	0	0	0	0	0	0	0		1	1	1	4.9	4.9	4.9	31.841	0	4.7255	4001200	10	NODE 87	NODE 87	3979	NODE 874 length 24332 cov 691.935659 False 6324 vacuolar protein sorting-associated protein 35 isoform X1
0	0	3000400	2815300	0	0	0	0	0		2	2	2	9.6	9.6	9.6	26.417	0	8.7928	1.9E+07	8	NODE 87	NODE 87	3980	NODE 874 length 24332 cov 691.935659 True 19120 N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase-like
3039500	0	0	1.7E+07	1.5E+07	1.7E+07	1E+07	8957600	1.6E+07		8	8	8	43.3	43.3	43.3	25.48	0	21.448	2.7E+08	64	NODE 87	NODE 87	3981	NODE 876 length 24266 cov 715.666722 False 6630 maltase-glucoamylase, intestinal-like
0	0	0	304950	562670	445560	0	0	0		1	1	1	7.8	7.8	7.8	18.793	0	4.2651	2488700	10	NODE 87	NODE 87	3982	NODE 876 length 24266 cov 715.666722 False 6737 maltase-glucoamylase, intestinal-like
7242100	6068300	6069200	1.3E+07	1.6E+07	2.7E+07	5315100	1.1E+07	2.3E+07		5	5	3	43.2	43.2	35.5	17.649	0	114.37	2.5E+08	55	NODE 87	NODE 87	3983	NODE 876 length 24266 cov 715.666722 False 7251 Sucrase-isomaltase, intestinal
2213900	1382300	1797800	1.4E+07	1.2E+07	1.6E+07	3459600	4469200	1.1E+07		5	5	5	25	25	25	16.744	0	24.327	1.7E+08	41	NODE 87	NODE 87	3984	NODE 876 length 24266 cov 715.666722 False 7990 sucrase-isomaltase, intestinal-like
0	0	0	0	0	0	0	0	0		1	1	1	15.3	15.3	15.3	11.215	0.00032	3.8872	2805200	5	NODE 87	NODE 87	3985	NODE 876 length 24266 cov 715.666722 False 8345 maltase-glucoamylase, intestinal
1902900	1397500	1336800	3.1E+07	2.3E+07	3.4E+07	9185900	9747200	1.4E+07		8	8	8	42.5	42.5	42.5	30.549	0	38.902	4.8E+08	95	NODE 87	NODE 87	3986	NODE 876 length 24266 cov 715.666722 False 9163 sucrase-isomaltase, intestinal isoform X2



4360100	4640400	5580200	4137200	5192600	5183400	6352000	6453200	7333800			7	7	7	29.8	29.8	29.8	28.687	0	28.873	1.3E+08	63	NODE	99	NODE	99	4108	NODE 99 length 71160 cov 740.022825 True 65417 tetratricopeptide repeat protein
0	0	0	0	0	0	0	0	0			1	1	1	8.9	8.9	8.9	33.155	0.0073	2.1944	424530	1	NODE	99	NODE	99	4109	NODE 992 length 22012 cov 665.666576 False 21410 C-type lectin lectoxin-Lio1
865520	0	760220	621030	605480	0	523130	911660	1921600			2	2	2	20.6	20.6	20.6	20.062	0	13.168	1.1E+07	18	NODE	99	NODE	99	4110	NODE 992 length 22012 cov 665.666576 True 17286 GA25341
3316400	2876200	3293400	4979200	4962600	4674600	6120500	6017300	5753800			9	2	2	51.8	10.7	10.7	31.416	0	53.593	7.6E+07	23	NODE	99	NODE	99	4111	NODE 9922 length 1795 cov 400.276437 False 1712 gastric triacylglycerol lipase-like
0	0	0	0	0	0	0	0	0			1	1	1	4.1	4.1	4.1	28.517	0.00892	2.1003	255880	1	NODE	99	NODE	99	4112	NODE 993 length 21975 cov 676.009991 False 2700 choline/ethanolamine kinase-like
0	0	0	0	0	0	0	0	0			1	1	1	14.3	14.3	14.3	15.244	0.00058	3.1613	1302800	2	NODE	99	NODE	99	4113	NODE 995 length 21948 cov 685.502489 False 18511 hypothetical protein QR98 0059340
545090	0	0	318120	448790	549810	475030	996690	968910			3	3	3	28.9	28.9	28.9	23.998	0	26.371	8738900	23	NODE	99	NODE	99	4114	NODE 9958 length 1784 cov 692.514748 False 753 probable 3-hydroxyacyl-CoA dehydrogenase B0272.3
0	0	0	0	0	0	0	0	0			1	1	1	45.2	45.2	45.2	6.936	0	7.5893	9609000	8	NODE	99	NODE	99	4115	NODE 9958 length 1784 cov 692.514748 False 948 probable 3-hydroxyacyl-CoA dehydrogenase B0272.3
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	978.53	0.00199	3.0017	1.1E+07	2	REV	gi|1	REV	gi|1	4116	gi|1048002959|ref|XP 017477803.1| PREDICTED: nesprin-1 isoform X4 [Rhagoletis zephyria];gi|1048002957|ref|XP 017477794.1| PREDICTED: nesprin-1 isoform X3 [Rhagoletis zephyria];gi|1048002955|ref|XP 017477784.1| PREDICTED: nesprin-1 isoform X2 [Rhagoletis ze
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	36.501	1	-2	305540	1	REV	gi|1	REV	gi|1	4117	gi|1048004182|ref|XP 017483781.1| PREDICTED: WD repeat-containing protein 61 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	81.132	0.00432	2.652	5905400	2	REV	gi|1	REV	gi|1	4118	gi|1048018991|ref|XP 017470580.1| PREDICTED: cilia- and flagella-associated protein 52 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	483.24	0.00594	2.3547	699650	2	REV	gi|1	REV	gi|1	4119	gi|1048027390|ref|XP 017474401.1| PREDICTED: spectrin beta chain, non-erythrocytic 5 isoform X2 [Rhagoletis zephyria];gi|1048027388|ref|XP 017474400.1| PREDICTED: spectrin beta chain, non-erythrocytic 5 isoform X1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	75.044	0.00638	2.2802	4E+07	8	REV	gi|1	REV	gi|1	4120	gi|1048029247|ref|XP 017475376.1| PREDICTED: TBC1 domain family member 15 isoform X2 [Rhagoletis zephyria];gi|1048029245|ref|XP 017475375.1| PREDICTED: TBC1 domain family member 15 isoform X2 [Rhagoletis zephyria];gi|1048029243|ref|XP 017475374.1| PREDICTE
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	78.445	1	-2	1.8E+08	1	REV	NOI	REV	NOI	4121	NODE 226 length 51748 cov 649.291548 False 45556 PREDICTED: uncharacterized protein LOC108377078;gi|1048029903|ref|XP 017488832.1| PREDICTED: uncharacterized protein LOC108377078 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	93.634	1	-2	4.8E+07	4	REV	gi|1	REV	gi|1	4122	gi|1048030159|ref|XP 017488972.1| PREDICTED: general vesicular transport factor p115 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	152.34	0.00478	2.5271	1E+07	3	REV	NOI	REV	NOI	4123	NODE 1541 length 15208 cov 693.122616 True 1262 fatty acid synthase;gi|1048035210|ref|XP 017491704.1| PREDICTED: fatty acid synthase-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	98.971	0.00062	3.6595	3.3E+07	5	REV	gi|1	REV	gi|1	4124	gi|1048036494|ref|XP 017492408.1| PREDICTED: uncharacterized protein LOC108380547 isoform X1 [Rhagoletis zephyria];gi|1048036496|ref|XP 017492410.1| PREDICTED: uncharacterized protein LOC108380547 isoform X2 [Rhagoletis zephyria];gi|1048036498|ref|XP 01749
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	140.01	0.00547	2.4029	1.1E+07	5	REV	gi|1	REV	gi|1	4125	gi|1048039790|ref|XP 017476753.1| PREDICTED: uncharacterized protein LOC108366790 isoform X4 [Rhagoletis zephyria];gi|1048039788|ref|XP 017476752.1| PREDICTED: uncharacterized protein LOC108366790 isoform X3 [Rhagoletis zephyria];gi|1048039786|ref|XP 01747
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	50.017	0.00896	2.1116	2476900	1	REV	gi|1	REV	gi|1	4126	gi|1048040776|ref|XP 017477276.1| PREDICTED: UBX domain-containing protein 6 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	376.28	1	-2	2.3E+07	4	REV	gi|1	REV	gi|1	4127	gi|1048041200|ref|XP 017477498.1| PREDICTED: serine/threonine-protein kinase Smg1 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	97.288	0.0096	2.0668	6015700	6	REV	gi|1	REV	gi|1	4128	gi|1048041334|ref|XP 017477568.1| PREDICTED: glutamate receptor ionotropic, kainate 2-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	59.105	0.00301	2.7506	1.6E+07	6	REV	gi|1	REV	gi|1	4129	gi|1048041370|ref|XP 017477588.1| PREDICTED: type-2 histone deacetylase 1-like isoform X3 [Rhagoletis zephyria];gi|1048041368|ref|XP 017477586.1| PREDICTED: type-2 histone deacetylase 1-like isoform X3 [Rhagoletis zephyria];gi|1048041366|ref|XP 017477585.1
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	31.101	0.00225	2.944	385640	2	REV	gi|1	REV	gi|1	4130	gi|1048043950|ref|XP 017493391.1| PREDICTED: protein scalloped-like, partial [Rhagoletis zephyria];gi|1048042821|ref|XP 017478366.1| PREDICTED: protein scalloped isoform X2 [Rhagoletis zephyria];gi|1048042819|ref|XP 017478365.1| PREDICTED: protein scallope
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	15.014	0.00454	2.5808	2.3E+08	18	REV	NOI	REV	NOI	4131	NODE 2257 length 11002 cov 689.661003 True 7726 elongation factor Ts, mitochondrial;gi|1048045915|ref|XP 017494457.1| PREDICTED: elongation factor Ts, mitochondrial-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	62.104	0.00917	2.0998	2E+07	6	REV	gi|1	REV	gi|1	4132	gi|1048047252|ref|XP 017478631.1| PREDICTED: lysosome membrane protein 2-like, partial [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	24.571	0.00732	2.216	4E+08	16	REV	gi|1	REV	gi|1	4133	gi|1048047612|ref|XP 017478819.1| PREDICTED: protein YIPF6 isoform X4 [Rhagoletis zephyria];gi|1048047610|ref|XP 017478818.1| PREDICTED: protein YIPF6 isoform X3 [Rhagoletis zephyria];gi|1048047608|ref|XP 017478817.1| PREDICTED: protein YIPF6 isoform X2 [R
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	36.247	0.00569	2.3675	2.2E+07	7	REV	NOI	REV	NOI	4134	NODE 25 length 123598 cov 740.273686 False 72852 glycogen phosphorylase;gi|1048049669|ref|XP 017479911.1| PREDICTED: glycogen phosphorylase-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	15.67	1	-2	1387400	2	REV	NOI	REV	NOI	4135	NODE 947 length 22712 cov 725.095820 True 18675 Annulin-like protein;gi|1048050876|ref|XP 017480538.1| PREDICTED: annulin-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	37.827	1	-2	3.8E+07	2	REV	gi|1	REV	gi|1	4136	gi|1048051708|ref|XP 017460588.1| PREDICTED: nuclear pore complex protein Nup93-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	86.047	0.00684	2.2409	7391000	5	REV	gi|1	REV	gi|1	4137	gi|1048051999|ref|XP 017460752.1| PREDICTED: uncharacterized protein LOC108354068 [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	82.009	0.00851	2.1347	6804900	5	REV	gi|1	REV	gi|1	4138	gi|1048054025|ref|XP 017481080.1| PREDICTED: mediator of RNA polymerase II transcription subunit 15-like [Rhagoletis zephyria];NODE 1446 length 16042 cov 672.935573 False 14505 mediator of RNA polymerase II transcription subunit 15 isoform X1
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	40.524	1	-2	4.6E+08	5	REV	gi|1	REV	gi|1	4139	gi|1048055934|ref|XP 017482110.1| PREDICTED: myc protein-like [Rhagoletis zephyria];gi|1048060692|ref|XP 017483832.1| PREDICTED: myc protein-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	34.077	0.00032	3.9947	1.5E+07	4	REV	gi|1	REV	gi|1	4140	gi|1048056553|ref|XP 017482430.1| PREDICTED: LOW QUALITY PROTEIN: surfeit locus protein 6 homolog [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	13.653	0.00501	2.4911	3219600	2	REV	NOI	REV	NOI	4141	NODE 767 length 26732 cov 718.808487 False 24024 60S ribosomal protein L38 isoform X1;gi|1048062557|ref|XP 017484166.1| PREDICTED: 60S ribosomal protein L38 [Rhagoletis zephyria];gi|1048030603|ref|XP 017489207.1| PREDICTED: 60S ribosomal protein L38 [Rhago
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	86.008	0.00116	3.1414	1.8E+07	2	REV	gi|1	REV	gi|1	4142	gi|1048066138|ref|XP 017485570.1| PREDICTED: activating signal cointegrator 1 complex subunit 2 homolog [Rhagoletis zephyria];NODE 1112 length 19987 cov 719.748144 False 6191 activating signal cointegrator 1 complex subunit 2 homolog;NODE 1112 length 19987
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	23.4	0.00355	2.7164	1.5E+08	8	REV	gi|1	REV	gi|1	4143	gi|1048067278|ref|XP 017463731.1| PREDICTED: 2-hydroxypropyl-CoM lyase-like [Rhagoletis zephyria]
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	249.69	0.00145	3.1044	6926200	3	REV	gi|1	REV	gi|1	4144	gi|1048070769|ref|XP 017487346.1| PREDICTED: eIF-2-alpha kinase activator GCN1-like [Rhagoletis zephyria];NODE 725 length 27459 cov 727.364180 False 15016 eIF-2-alpha kinase activator GCN1
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	28.06	0.00527	2.4893	9438200	5	REV	gi|1	REV	gi|1	4145	gi|1048071103|ref|XP 017487532.1| PREDICTED: SH3 domain-binding glutamic acid-rich protein homolog [Rhagoletis zephyria];NODE 334 length 43066 cov 659.215178 True 17983 SH3 domain-binding glutamic acid-rich protein homolog
0	0	0	0	0	0	0	0	0	+	+	1	1	1	0	0	0	33.92	1	-2	1911300	2	REV	GIJ\	REV	GIJ\	4146	GIJY01000013.1 False 1757 Uncharacterised protein
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	14.755	0.0066	2.2458	1083700	1	REV	GIJ\	REV	GIJ\	4147	GIJY01000052.1 True 5 ---NA---
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	5.8267	0.00617	2.3252	1.7E+07	7	REV	GIJ\	REV	GIJ\	4148	GIJY01000088.1 True 906 ---NA---
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	85.127	0.0071	2.2371	3946800	2	REV	GIJ\	REV	GIJ\	4149	GIJY01000106.1 False 2664 polyribonucleotide nucleotidyltransferase
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	6.4576	0.00328	2.7382	2989200	1	REV	NOI	REV	NOI	4150	NODE 133 length 62984 cov 725.151695 True 22990 hypothetical protein X777 13119
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	22.727	0.00173	3.0888	1.9E+08	28	REV	NOI	REV	NOI	4151	NODE 1727 length 13753 cov 716.367572 False 9218 NADH:flavin oxidoreductase/NADH oxidase
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	21.571	0.00087	3.1453	1.8E+08	11	REV	NOI	REV	NOI	4152	NODE 2361 length 10518 cov 686.166109 False 8069 allatostatin-A receptor-like
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	6.9165	0.00779	2.1718	767180	1	REV	NOI	REV	NOI	4153	NODE 2762 length 9065 cov 1244.131299 False 6867 histone-fold-containing protein
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	19.616	0.00804	2.1695	3.3E+07	5	REV	NOI	REV	NOI	4154	NODE 2888 length 8716 cov 721.382173 False 6229 glycine-rich protein 1-like
0	0	0	0	0	0	0	0	0		+	2	2	2	0	0	0	43.485	0.00382	2.7131	1445400	2	REV	NOI	REV	NOI	4155	NODE 3039 length 8327 cov 710.941731 True 1 homogentisate 1,2-dioxygenase-like
7608600	5653200	6322000	3782800	3635700	0	0	0	6309600		+	1	1	1	0	0	0	16.767	0.0028	2.8803	4.9E+07	32	REV	NOI	REV	NOI	4156	NODE 380 length 39631 cov 656.218061 True 930 membrane metallo-endopeptidase-like 1
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	31.851	0.00405	2.6568	1.6E+07	2	REV	NOI	REV	NOI	4157	NODE 432 length 37753 cov 732.480768 True 19382 nuclear factor NF-kappa-B p100 subunit isoform X1
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	13.322	0.00984	2.0649	5774000	2	REV	NOI	REV	NOI	4158	NODE 4880 length 4754 cov 679.201958 False 3479 diuretic hormone 31
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	50.81	0.00939	2.0838	1824000	1	REV	NOI	REV	NOI	4159	NODE 54 length 89452 cov 704.358513 False 35944 28S ribosomal protein S30, mitochondrial
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	101.86	0.00828	2.1617	373060	1	REV	NOI	REV	NOI	4160	NODE 605 length 30774 cov 719.823887 True 5339 uncharacterized protein LOC113790219
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	25.009	0.00872	2.1168	2696800	2	REV	NOI	REV	NOI	4161	NODE 668 length 29040 cov 730.679972 True 9389 Latrophilin-like protein LAT-2
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	34.674	0.00754	2.1763	2007600	2	REV	NOI	REV	NOI	4162	NODE 7971 length 2426 cov 422.249262 True 1543 cubilin-like protein
0	0	0	0	0	0	0	0	0		+	1	1	1	0	0	0	47.571	0.00252	2.8896	3.8E+07	12	REV	NOI	REV	NOI	4163	NODE 831 length 25339 cov 724.927820 True 6023 hypothetical protein BpHYR1 009354