Supplementary Information

Human follicular mites: Ectoparasites become symbionts

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Contents

1 Supplementary Figures and Table 3

Fig. S1 Demodex is maternally inherited 3
Fig. S2 Functions of rapidly evolving gene families of Demodex and Acariformes 4
Fig. S3 Mitochondrial genome has polycistrons 5
Fig. S4 Distribution of the RELAX parameter K across significant selection tests 6
Fig. S5 Host association determines extent of AT-bias of invertebrate and vertebrate animals 7
Tab. S1 Intergenic distances and introns 8
Fig. S6 Endopolyploidy in Demodex 9

2 Supplementary Items (SI) 10

Fig. SI 1 Benchmarking Universal Single Copy Orthologs 10
Fig. SI 2 Length distribution of proteins in parasitic/endosymbiotic Demodex and free-living/plant-parasitic Tetranychus 11
Tab. SI 1 Probably pseudogenes of Demodex arranged according to Demodex AA length 12
Tab. SI 2 Orthogroups of Demodex rapidly expanding 14
Tab. SI 3 Minimal genome sizes and number of coding genes per taxonomic clade in the Pan-Arthropoda 15
Tab. SI 4 Species used in genome analysis 18
Tab. SI 5 Repeat content of mite genomes 20
Tab. SI 6 Intergenic distances and introns 21
Fig. SI 3 Host association determines extent of AT-bias of Acariformes 23
Fig. SI 4 Genome-wide codon usage bias in Acariformes 25
Fig. SI 5 Mutation spectrum for Demodex demonstrates an AT-mutational bias 27
Tab. SI 7 Orthogroups (OGs) of arthropod species 28
Tab. SI 8 Computational analysis of gene family evolution model parameters 30
Fig. SI 6 Computational Analysis of Gene Family Evolution Ihtest histogram 32
Fig. SI 7 Alternative IQtree topologies 33
Tab. SI 9 Gene families showing rapid contraction in Demodex 34
Tab. SI 10 Gene families showing rapid contraction in the Acariformes 38
Tab. SI 11 Gene families showing rapid expansion in the Acariformes 42
| Table   | Title                                                      | Page |
|---------|------------------------------------------------------------|------|
| Tab. SI 12 | Gene family loss in Demodex                              | 46   |
| Tab. SI 13 | Gene family loss in the Acariformes                      | 50   |
| Tab. SI 14 | RELAX test significant orthogroups                        | 54   |
| Tab. SI 15 | Relaxed selection enrichment                              | 58   |
| Tab. SI 16 | Intensified selection enrichment                          | 62   |
| Tab. SI 17 | Counting of nuclei in *Drosophila melanogaster*           | 66   |
| Tab. SI 18 | Histidine pathway genes                                   | 67   |
|          | References                                                 | 68   |
Supplementary Figures and Table

Demodex is maternally inherited

Figure S1. Demodex is predominantly maternally inherited. Cladogram of partial mtDNA of *D. folliculorum*. Six maternal relationships highlighted in yellow. Relationships: F: female, M: male, D: daughter, S: son, GD: granddaughter, GS: grandson; female and male couples: F1, M1: female 1 with male 1, GD9a is the daughter of D9a who is the daughter of F9. For horizontal transmission, it is expected that couples carry similar lineages of mites. Female and male couples do not carry similar mite lineages with the exception of F1 (green background). For vertical transmission, it is expected that offspring clusters with maternal lineage (yellow background). Without exception, this is the case for all six families analysed. F10 (mother) clusters daughter D10 and granddaughter GD10 and grandson GS10. F7 (mother) clusters with her two daughters D7a and D7b. F8 (mother) clusters with her son S8 as is the case for F5 (mother) and son S5; mother F6 (mother) and her daughter D6; and F9 (mother) and her two daughters D9a and D9b and her granddaughter D9.
**Functions of rapidly evolving gene families in Demodex and Acariformes**

**Figure S2.** Functions of rapidly evolving gene families. **A** Contracting gene families in Demodex. **B** Contracting gene families Acariformes. **C** Expanding gene families in Acariformes. Eight cryptic orthogroups expanding in Demodex are listed Tab. SI 2.
Mitochondrial genome has polycistrons

Figure S3. Polycistrons in the mitochondrial genome of the human follicle mite, *D. folliculorum*. A: Mitochondrial genome annotated with protein coding (orange) and non-coding (green) genes. B: Linear view of the mitochondrial genome with transcript-based evidence for polycistronic expression (red: labelled “Poly” for each polycistronic unit). Transcripts were assembled from RNA-sequencing data and mapped to the mitochondrial reference.
Distribution of the RELAX parameter K across significant selection tests

**Figure S4.** Relaxed selection is more common than intensified (purifying) selection in Acariformes compared to spiders and scorpions. Distribution of the RELAX parameter K across significant selection tests (adjusted $p < 0.1$; red bars), and all tests (blue bars, inset). The density plot of omega values (non-synonymous/synonymous substitutions: dN/dS) for genes showing relaxation of selection ($K < 1$; main) and intensified selection ($K > 1$; inset) in Acariformes and Functions of genes under relaxed selection in Acariformes are depicted in Fig. 2 of the main paper.
Host association determines the extend of AT-bias in 85 species of invertebrates and vertebrate animals based on the *Srp54K* gene, green host-associated, red free-living. 

**B.** Same analysis detailed for acariformes. 

**C.** Genome-wide codon usage bias seen in acariformes is more likely due to mutational bias leading to a higher frequency of codons containing adenine or thymine in the second and/or third position. ENCprime was used to calculate NC, the number of effective codons across coding sequence sets, as well as Ncp (Nc prime or Nc'), a measure of codon use corrected by the background mutation pattern. Corrections were performed using the nucleotide frequency of the third codon position for each respective gene under study. 

**D.** Mutation spectrum for Demodex demonstrates an AT-mutational bias. Frequency is for all mutation types discovered in RNA-sequencing data.
### Table S6. Acariformes have reduced their intergenic and intronic content compared to most arachnids, and a little more than Drosophila too.

Intron numbers are lower in Acariformes, except for Demodex. Intron length is shorter on average in Acariformes as well, even when compared to *Galendromus occidentalis* and Drosophila. Intergenic distance is also lower in Acariformes than all else, though melanogaster is close. *D. melanogaster* sometimes is close to Acariformes based on median, but not mean, suggesting wider variation in metrics in *D. melanogaster*.
Endopolyploidy in *D. folliculorum* female

**Figure S7.** Ploidy distribution of nuclei in different body regions of *D. folliculorum* females. Abscissa: ploidy of nuclei, ordinate: number of nuclei per body region. 2C means diploid, 2C− indicates underreplication. The highest level of polyploidy observed was decaploid. The levels of polyploidy deviate from a geometric progression.

2C− presents underreplication where a premature stall takes place with less than one complete cycle of replication, unlike underreplication in nuclei of follicle cells and cells of salivary glands. In *D. folliculorum*, around 20% of the diploid nuclei (some 222 nuclei) of adult females showed an 11% deficiency in fluorescent intensity or nuclear content; these nuclei are called diploid infer.

The higher ploidy levels of *D. folliculorum* are mostly restricted to the gnathosomal and podosomal regions, with very little in the opisthosoma. These polyploid cells are mainly located in the internal organs as compared to the peripheral nuclei and the integument. Within the gnathosomal and podosomal regions, lower level polyploid nuclei are more prominent in the internal structures of the legs whereas the higher levels of polyploid nuclei such as hexaploid are standing out in the internal organs of the main body of the gnathosoma and podosoma.
2 Supplementary Items (SI)

Benchmarking Universal Single Copy Orthologs

A BUSCO Assessment Results

Figure SI 1. The *Demodex* genome is quite complete and well annotated. BUSCO results for genomes compared in this study. BUSCO was run for both eukaryote (A) and arthropod (B) sets of single copy orthologs, on released curated protein sets for each genome, filtered for longest isoform per gene where isoforms were annotated.
Length distribution of proteins in parasitic/endosymbiotic Demodex and free-living/plant-parasitic Tetranychus

![Length distribution of proteins](image)

**Figure SI 2.** Zoomed-in length distribution of proteins in parasitic/endosymbiotic Demodex and free-living/plant-parasitic Tetranychus. The amino acid length of 4,582 one-to-one orthologues of Demodex was divided by the amino acid length of Tetranychus. All values on the abscissa below 1 represent proteins that are shorter in Demodex compared to Tetranychus and vice versa. The biggest problem here is that in fact two parasitic species are compared with each other. Sequences of closely related free-living species are still missing.

Assuming in a first approximation that pseudogenes will have lost 50% or more of their protein length, only 50 Demodex proteins (1.1%) meet this criterion, whereas 214 Tetranychus proteins (4.7%) would qualify as pseudogenes.

The Asian long-horn beetle, *Anoplophora glabripennis*, has a large genome with 22,253 protein-coding genes and 66 pseudogenes, which represent 0.3% (McKenna et al. 2016; Li et al. 2019).
### Table SI 1

Probably pseudogenes of Demodex arranged according to Demodex AA length

| ID               | Dem. AA | Tet. AA | Function                                           |
|------------------|---------|---------|---------------------------------------------------|
| DMDXFOLL_001444  | 110     | 988     | ataxin-2 homolog                                  |
| DMDXFOLL_008670  | 253     | 1,456   | matricellular osteonectin sparc bm-40            |
| DMDXFOLL_000412  | 134     | 735     | glycerol-3-phosphate mitochondrial               |
| DMDXFOLL_006536  | 72      | 361     | large proline-rich BAG6                          |
| DMDXFOLL_002943  | 285     | 1,301   | endothelial PAS domain-containing 1-like         |
| DMDXFOLL_001752  | 208     | 912     | WD repeat-containing 43-like                     |
| DMDXFOLL_003669  | 244     | 1,029   | mediator of RNA polymerase II transcription subunit 8 isoform X2 |
| DMDXFOLL_009322  | 121     | 497     | GTP-binding RAD-like                             |
| DMDXFOLL_005420  | 559     | 2,239   | multiple PDZ domain                               |
| DMDXFOLL_006675  | 391     | 1,469   | arrestin domain-containing 3-like                |
| DMDXFOLL_005513  | 147     | 475     | spaetzle 4                                       |
| DMDXFOLL_005099  | 125     | 395     | steroid receptor seven- isoforms b c             |
| DMDXFOLL_002884  | 203     | 616     | 5-hydroxytryptamine receptor 2A isoform X1       |
| DMDXFOLL_006689  | 124     | 365     | thromboxane-A synthase-like                      |
| DMDXFOLL_001855  | 149     | 438     | targeting for Xklp2-B-like                       |
| DMDXFOLL_008375  | 146     | 429     | tachykinin-like peptides receptor 99D            |
| DMDXFOLL_006396  | 248     | 723     | ataxin-3-like isoform X2                         |
| DMDXFOLL_005292  | 407     | 1,145   | TBC1 domain family member 1 isoform X9           |
| DMDXFOLL_010085  | 370     | 1,014   | glutamate receptor delta-1-like                  |
| DMDXFOLL_004532  | 294     | 770     | DNA helicase MCM8-like                           |
| DMDXFOLL_000519  | 130     | 339     | RNA-binding motif X-linked 2                     |
| DMDXFOLL_004346  | 258     | 670     | suppressor of lurcher 1                          |
| DMDXFOLL_001802  | 463     | 1,185   | von Willebrand factor type EGF and pentraxin domain-containing 1 |
| DMDXFOLL_005387  | 154     | 391     | CCAAT enhancer-binding gamma-like                |
| DMDXFOLL_002434  | 149     | 378     | iron-sulfur cluster assembly 2 mitochondrial     |
| DMDXFOLL_000594  | 242     | 593     | alkylated DNA repair alkB homolog 8              |
| DMDXFOLL_005803  | 178     | 436     | tachykinin-like peptides receptor 99D            |
| DMDXFOLL_010004  | 657     | 1,601   | hepatocyte nuclear factor 6 isoform X3           |
| DMDXFOLL_002872  | 321     | 779     | sarcalumenin-like isoform X2                     |
| DMDXFOLL_007387  | 194     | 457     | class A basic helix-loop-helix 15-like           |
| DMDXFOLL_005646  | 127     | 293     | NA                                                |
| DMDXFOLL_006282  | 98      | 226     | zinc finger CCCH domain-containing 41-like        |
| DMDXFOLL_009539  | 188     | 422     | potassium voltage-gated channel subfamily KQT member 2 isoform X1 |
| DMDXFOLL_007218  | 775     | 1,739   | low-density lipo                                 |
| DMDXFOLL_010102  | 280     | 624     | neuronal acetylcholine receptor subunit alpha-7 isoform X1 |
| DMDXFOLL_009219  | 332     | 730     | C-ets-1-like isoform X1                          |
| DMDXFOLL_004796  | 509     | 1,109   | Shroom2 isoform X2                               |
| DMDXFOLL_008193  | 147     | 320     | uncharacterized serine-rich -like                |
| DMDXFOLL_006964  | 497     | 1,080   | homeobox ceh-9                                   |
| DMDXFOLL_000555  | 96      | 205     | NA                                                |
| DMDXFOLL_003743  | 229     | 488     | lin-28 homolog                                   |
| Gene ID              | Start | End   | Description                                      |
|---------------------|-------|-------|--------------------------------------------------|
| DMDXFOLL_008558     | 370   | 787   | histone acetyltransferase KAT6A-like             |
| DMDXFOLL_009331     | 230   | 481   | forkhead box F1                                 |
| DMDXFOLL_003624     | 107   | 222   | serum response factor homolog B-like            |
| DMDXFOLL_006709     | 217   | 450   | von Willebrand factor C and EGF domain-containing |
| DMDXFOLL_002777     | 590   | 1,220 | tRNA-dihydouridine(47) synthase [NAD(P)(+)]-like |
| DMDXFOLL_008265     | 277   | 565   | galactosamine (N-acetyl)-6-sulfate sulfatase     |
| DMDXFOLL_003162     | 219   | 446   | serine threonine-phosphatase 2A 55 kDa regulatory subunit B delta isoform isoform X3 |
| DMDXFOLL_007010     | 411   | 837   | homeobox HMX3                                   |
### Tab. SI 2  Orthogroups of Demodex rapidly expanding

| Orthogroup ID | Consensus KEGG K number | KEGG K title |
|---------------|-------------------------|--------------|
| OG0000063     | NA                      | NA           |
| OG0000064     | NA                      | NA           |
| OG0000121     | NA                      | NA           |
| OG0000129     | NA                      | NA           |
| OG0000132     | NA                      | NA           |
| OG0000256     | K08592                  | SENP1; sentrin-specific protease 1 [EC:3.4.22.68] |
| OG0000283     | K06704                  | ADAM10, CD156c; disintegrin and metalloproteinase domain-containing protein 10 [EC:3.4.24.81] |
| OG0000428     | K15695                  | RNF103, KF1; E3 ubiquitin-protein ligase RNF103 [EC:2.3.2.27] |

KEGG analysis of orthogroups expanding in Demodex compared to Acari.
### Table SI 3

Minimal genome sizes and number of coding genes per taxonomic clade in the Pan-Arthropoda

| Taxonomic Clade | Organism | Species | Genome Size | Coding Genes |
|-----------------|----------|---------|-------------|--------------|
| **Arthropoda**  |          |         |             |              |
| Chelicerata     |          |         |             |              |
| Arachnida       |          |         |             |              |
| Acari           |          |         |             |              |
| Acariformes     |          |         |             |              |
| Sarcoptiformes  |          |         |             |              |
| Astigmata       |          |         |             |              |
| *Sarcoptes scabiei* | scabies mite | GCA_000828355.1 | 56.3 | 10,473 |
| Oribatida       |          |         |             |              |
| *Steganacarus magnus* | predatory mite | GenBank median | 426.5 | 13,305 |
| **Endeostigmata** |          |         |             |              |
| Eriophycoidea   |          |         |             |              |
| *Aculops lycopersici* | tomato russet mite | GCA_015350385.1 | 32.5 | 10,263 |
| **Trombidiformes** |          |         |             |              |
| Prostigmata     |          |         |             |              |
| *Brevipalpus yothersi* | false spider mite | GCA_003956705.1 | 71.2 | ~16,000 |
| **Parasitiformes** |          |         |             |              |
| Ixodida, Ixodoidea |       |         |             |              |
| *Ixodes scapularis* | black-legged tick | Randall et al. (2018) | 1,760.0 | 20,467 |
| Mesostigmata, Monogynaspida |          |         |             |              |
| *Galendromus occidentalis* | western predatory mite | GCA_000255335.1 | 151.7 | 11,944 |
| Kingdom   | Class               | Order                  | Species                                      | Genus/Species                     | GCA Accession     | Length (bp) | Nucleotides | Name                  |
|-----------|---------------------|------------------------|----------------------------------------------|-----------------------------------|-------------------|-------------|-------------|-----------------------|
| Araneae   |                     |                        | *Latrodectus hesperus*                       | western black widow               | GCA_000697925.2   | 1,234.0     | ?           |                       |
|           |                     |                        | *Cordylochernes scorpioides*                 | pseudoscorpion                    | QEEW00000000.1    | 2,807.1     | ?           |                       |
| Scorpiones|                     |                        | *Centruroides sculpturatus*                  | bark scorpion                     | GCA_000671375.2   | 925.5       | 35,529      |                       |
| Merostomata|                   |                        | *Carcinoscorpius rotundicauedes*             | mangrove horseshoe crab           | GCA_011833715.1   | 1,669.0     | 25,985      |                       |
|           |                     |                        |                                             |                                   |                   |             |             |                       |
| Myriapoda |                     |                        | *Strigamia maritima*                         | centipede                         | GCA_000239455.1   | 176.2       | 13,233      |                       |
| Pancrustacea|                 |                        |                                             |                                   |                   |             |             |                       |
|           |                     |                        |                                             |                                   |                   |             |             |                       |
| Crustacea |                     |                        |                                             |                                   |                   |             |             |                       |
|           |                     |                        |                                             |                                   |                   |             |             |                       |
| Branchiopoda|                 |                        | *Lepidurus arcticus*                        | tadpole shrimp                    | GCA_003724045.1   | 73.1        | 10,718      |                       |
|           |                     |                        |                                             |                                   |                   |             |             |                       |
| Multicrustacea|               |                        | *Oithona nana*                              | copepod                           | GCA_900157175.1   | 85.0        | ?           |                       |
| Hexapoda  |                     |                        |                                             |                                   |                   |             |             |                       |
| Collembola|                     |                        | *Pseudachorutes palmiensis*                 | springtail                        | VNWY00000000.1    | 77.1        | ?           |                       |
|           |                     |                        |                                             |                                   |                   |             |             |                       |
| Diplura   |                     |                        | *Catajapyx aquilonaris*                     | earwig-like entroph               | JYFJ00000000.2    | 285.6       | ?           |                       |
| Insecta   |                     |                        | *Clunio marinus*                            | marine midge                      | GCA_900005825.1   | 85.5        | 22,620      |                       |
| Onychophora|                   |                        | *Euperipatoides rowelli*                    | velvet worm                       | PXIH00000000.1    | 1,745.2     | ?           |                       |
| Tartigrada|                     |                        |                                             |                                   |                   |             |             |                       |
| *Ramazzottius varieornatus* | water bear | GCA_001949185.1 | 55.8 | 22,994 |

Smallest genome size per taxonomic clade in Mbp based on assembly length, not on genome size estimates; vernacular name, and number of coding genes, where known; GenBank or INSDC code as of May 2021. The placement of the Eriophycoidea follows hypothesis 4 of Klimov et al. (2018) and is supported by Arribas et al. (2020) and Greenhalgh et al. (2020).
| Species                  | Vernacular name            | Accession/genome version)       | Total assembly length (Mb) |
|-------------------------|----------------------------|---------------------------------|---------------------------|
| *Demodex folliculorum*  | Human follicle mite        | D_folliculorum_v1.1assembly_v02_annotations | 51.5                      |
| *Sarcoptes scabiei*     | Itch mite                  | GCA_000828355.1_SarSca1.0       | 56.3                      |
| *Tetranychus urticae*   | Two spotted spider mite    | 20160622                        | 90.8                      |
| *Ixodes scapularis*     | Black-legged tick          | IscaW1.4                        | 1,765                     |
| *Galendromus occidentalis* | Western predatory mite  | GCF_000255335.1_Mocc_1.0       | 152                       |
| *Dermatophagoides farinae* | American house dust mite | Dfarinae1.0                     | 53.5                      |
| *Parasteatoda tepidariorum* | Common house spider      | GCF_000365465.2_v2.0            | 1,445.4                   |
| *Tropilaelaps mercedesae* | Asian bee mite            | T._mercedesae_v01               | 352.5                     |
| *Stegodyphus mimosarum* | Spider                     | GCA_000611955.2                 | 2,738.7                   |
| *Centruroides sculpturatus* | Bark scorpion             | GCA_000671375.2_Cexi_2.0       | 925.5                     |
| *Varroa jacobsoni*      | Bee mite                   | GCA_002532875.1_vjacob_1.0     | 365.6                     |
| *Daphnia pulex*         | Water flea                 | GCA_000187875.1_V1.0           | 197.2                     |
| *Tribolium castaneum*   | Red flour beetle           | GCF_000002335.3_Tcas5.2        | 165.9                     |
| *Drosophila melanogaster* | Fruit fly, vinegar fly    | GCF_000001215.4_Release_6      | 143.7                     |
| *Limulus polyphemus*    | Atlantic horseshoe crab    | GCF_000517525.1                 | 1,828.3                   |
| Species                     | No. scaffolds | No. proteins (longest isoform) | Scaffold N50 (Kb) | Scaffold L50 | GC content | Data source                      |
|-----------------------------|---------------|--------------------------------|-------------------|--------------|------------|----------------------------------|
| *Demodex folliculorum*      | 241           | 9,707                          | 488               | 31           | 31.3       | Current study                    |
| *Sarcoptes scabiei*         | 18,861        | 10,473                         | 11.6              | 972          | 33.3       | NCBI                             |
| *Tetranychus urticae*       | 640           | 19,104                         | 2,993             | 10           | 32.3       | bioinformatics.psb.ugent.be/gdb/tetranychus/ |
| *Ixodes scapularis*         | 369,492       | 20,486                         | 76.2              | 3,623        | 45.2       | Vectorbase                       |
| *Galendromus occidentalis*  | 2,211         | 11,710                         | 896.8             | 52           | 51.6       | NCBI                             |
| *Dermatophagoides farinae*  | 515           | 16,376                         | 186.3             | 85           | 30.6       | Personal communication           |
| *Parasteatoda tepidariorum* | 16,533        | 18,601                         | 4,055.4           | 94           | 32.9       | NCBI                             |
| *Tropilaelaps mercedesae*   | 33,764        | 14,303                         | 28.9              | 3,629        | 40.9       | NCBI                             |
| *Stegodyphus mimosarum*     | 68,653        | 27,135                         | 480.6             | 1,734        | 33.8       | NCBI                             |
| *Centruroides sculpturatus* | 8,338         | 24,591                         | 537.5             | 523          | 31.4       | NCBI                             |
| *Varroa jacobsoni*          | 4,881         | 10,739                         | 233.8             | 482          | 40.9       | NCBI                             |
| *Daphnia pulex*             | 5,186         | 30,590                         | 642.1             | 75           | 42.4       | NCBI                             |
| *Tribolium castaneum*       | 2,149         | 12,873                         | 4.5               | 12           | 35.2       | NCBI                             |
| *Drosophila melanogaster*   | 1,870         | 13,929                         | 25.3              | 3            | 42.1       | NCBI                             |
| *Limulus polyphemus*        | 286,793       | 22,873                         | 254.1             | 1,712        | 34.5       | NCBI                             |
**Table SI 5**

Repeat content of mite genomes

|                          | No. RepeatModeler families | Percent total repeats | Taxonomy   |
|--------------------------|-----------------------------|-----------------------|------------|
| *Aculops lycopersici*    | 13                          | 2.1 %                 | Acariforme |
| *Demodex folliculorum*   | 164                         | 7.2 %                 | Acariforme |
| *Sarcoptes scabiei*      | 49                          | 9.3 %                 | Acariforme |
| *Tetranychus urticae*    | 484                         | 12.5 %                | Acariforme |
| *Dermatophagoides farinae* | 40                     | 11.0 %                | Acariforme |
| *Metaseiulus occidentalis* | 593                  | 9.3 %                 | Parasitiforme |
| *Ixodes scapularis*      | 3,497                       | 41.7 %                | Parasitiforme |
| *Drosophila melanogaster*| 808                         | 22.6 %                | Insect     |
### Table SI 6

**Intergenic distances and introns**

| Species* | *Demodex folliculorum* | *Aculops lycopersici* | *Tetranychus urticae* | *Dermatophagoides farinae* | *Sarcoptes scabiei* | *Ixodes scapularis* | *Galendromus occidentalis* | *Parasteatoda tepidariorum* | *Drosophila melanogaster* |
|----------|------------------------|-----------------------|-----------------------|---------------------------|-------------------|-------------------|---------------------------|---------------------------|--------------------------|
| mean intron length (bp) | 514 | 502 | 693 | 147 | 2,920 | 625 | 4,324 | 1,067 |
| median intron length (bp) | 79 | 170 | 94 | 95 | 69 | 1,602 | 133 | 1,850 | 69 |
| mean intron count per gene | 2.83 | 0.30 | 2.35 | 1.93 | 2.03 | 3.33 | 4.61 | 6.2 | 2.94 |
| mean exon length (bp) | 383 | 319 | 456 | 367 | 197 | 266 | 198 | 400 |
| median exon length (bp) | 180 | 156 | 279 | 203 | 143 | 171 | 129 | 215 |
| mean distance between CDS (bp) * | 2,429 | 2,630 | 1,850 | 1,526 | 2,6615 | 8,028 | 44,743 | 5,668 |
| median distance between CDS (bp) § | 1,293 | 538 | 1,313 | 630 | 749 | 9,236 | 2,890 | 14,217 | 1,197 |

*Data is for coding sequences only and is for one CDS per gene. No filtering on raw numbers has been performed, so annotation quality may play a role in differences.

§ Distance between CDS annotations does not include distance between last CDS and scaffold ends.

Acariformes have reduced their intergenic and intronic content compared to most arachnids, and a little more than Drosophila too. Intron numbers are lower in Acariformes, except for Demodex. Intron length is shorter on average in Acariformes as well even when compared to *Galendromus occidentalis* and Drosophila. Intergenic distance is also lower in Acariformes than all else, though Melanogaster is close. *D. melanogaster* sometimes is close to Acariformes based on median, but not mean, suggesting wider variation in metrics in *D. melanogaster*. 

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*Table S16*
Within Acariformes, there is phylogenetic divergence: the Sarcoptiformes, *Sarcoptes scabiei*, have much shorter distances between CDSs; and slightly longer exons.
Host association determines the extent of AT-bias in Acariformes.
Fig. SI 3. Host association determines the extent of AT-bias in Acariformes based on the Srp54K gene, green host-associated, red free-living. Demodex is at a derived position at around 1 o’clock.
Genome-wide codon usage bias in Acariformes

![Graph showing the relationship between genome-wide GC content and effective number of codons. The graph includes two lines: one for Nc and another for Ncp. The x-axis represents genome-wide GC content, ranging from 30 to 50, and the y-axis represents effective number of codons, ranging from 45 to 60.](image-url)
**Fig. SI 4.** Genome-wide codon usage bias seen in acariformes is more likely due to mutational bias leading to a higher frequency of codons containing adenine or thymine in the second and/or third position. ENCprime was used to calculate NC, the number of effective codons across coding sequence sets, as well as Ncp (Nc prime or Nc’), a measure of codon use corrected by the background mutation pattern. Corrections were performed using the nucleotide frequency of the third codon position for each respective gene under study.
Mutation spectrum for Demodex demonstrates an AT-mutational bias.

Fig. SI 5. Mutation spectrum for Demodex demonstrates an AT-mutational bias. Frequency is for all mutation types discovered in RNA-sequencing data.
| Species                         | # genes | # genes in OGs | # unassigned genes | % genes in OGs | % unassigned genes | # OGs containing species | % OGs containing species | # genes in species-specific OG | % genes in species-specific OGs |
|--------------------------------|---------|----------------|-------------------|---------------|-------------------|--------------------------|--------------------------|-----------------------------|-----------------------------|
| Demodex folliculorum           | 9,707   | 8,131          | 1,576             | 83.8          | 16.2              | 6,237                    | 44.3                     | 6                           | 46                          | 0.5                         |
| Sarcoptes scabiei              | 10,473  | 8,440          | 2,033             | 80.6          | 19.4              | 6,279                    | 44.6                     | 7                           | 24                          | 0.2                         |
| Tetranychusurticae             | 19,104  | 11,939         | 7,165             | 62.5          | 37.5              | 6,254                    | 44.6                     | 55                          | 1,111                       | 5.8                         |
| Ixodes scapularis              | 20,486  | 14,054         | 6,432             | 68.6          | 31.4              | 7,730                    | 54.9                     | 19                          | 95                          | 0.5                         |
| Galendromusoccidentalis        | 11,710  | 10,851         | 859               | 92.7          | 7.3               | 6,975                    | 49.6                     | 6                           | 27                          | 0.2                         |
| Dermatophagoidesfarinae        | 16,376  | 9,413          | 6,963             | 57.5          | 42.5              | 6,547                    | 46.5                     | 19                          | 66                          | 0.4                         |
| Parasteatodatepidariorum       | 18,601  | 17,049         | 1,552             | 91.7          | 8.3               | 8,396                    | 59.7                     | 17                          | 82                          | 0.4                         |
| Tropilaelapsmercedesae         | 14,303  | 11,695         | 2,608             | 81.8          | 18.2              | 7,602                    | 54                       | 5                           | 12                          | 0.1                         |
| Stegodyphusmosimarum           | 27,135  | 20,921         | 6,214             | 77.1          | 22.9              | 8,842                    | 62.8                     | 13                          | 61                          | 0.2                         |
| Centruroidessculpturatus       | 24,591  | 21,700         | 2,891             | 88.2          | 11.8              | 8,498                    | 60.4                     | 13                          | 102                         | 0.4                         |
| Varroajacobsoni                | 10,739  | 9,899          | 840               | 92.2          | 7.8               | 7,484                    | 53.2                     | 2                           | 4                           | 0                           |
| Daphniapulex                   | 30,590  | 17,221         | 13,369            | 56.3          | 43.7              | 7,335                    | 52.1                     | 120                         | 972                         | 3.2                         |
| Triboliumpastaneum             | 12,873  | 11,182         | 1,691             | 86.9          | 13.1              | 7,313                    | 52                       | 27                          | 177                         | 1.4                         |
| Drosophilamelanogaster         | 13,929  | 10,729         | 3,200             | 77.0          | 23.0              | 6,957                    | 49.4                     | 29                          | 179                         | 1.3                         |
| Limuluspolyphemus              | 22,873  | 21,165         | 1,708             | 92.5          | 7.5               | 8,500                    | 60.4                     | 12                          | 47                          | 0.2                         |
|            | Cscu   | Demo2 | Derm  | Dmel2 | Dpul2 | IxSc2 | Lpol2 | Gale2 | Ptep2 | Sarc2 |
|------------|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| # genes    | 24591  | 9707  | 16376 | 13929 | 30590 | 20486 | 22873 | 11710 | 18601 | 10473 |
| # genes in orthogroups | 21700  | 8131  | 9413  | 10729 | 17221 | 14054 | 21165 | 10851 | 17049 | 8440  |
| # unassigned genes | 2891   | 1576  | 6963  | 3200  | 13369 | 6432  | 1708  | 859   | 1552  | 2033  |
| % genes in orthogroups | 88.2   | 83.8  | 57.5  | 77    | 56.3  | 68.6  | 92.5  | 92.7  | 91.7  | 80.6  |
| % unassigned genes | 11.8   | 16.2  | 42.5  | 23    | 43.7  | 31.4  | 7.5   | 7.3   | 8.3   | 19.4  |
| # orthogroups containing species | 8498   | 6237  | 6547  | 6957  | 7335  | 7730  | 8500  | 6975  | 8396  | 6279  |
| % orthogroups containing species | 60.4   | 44.3  | 46.5  | 49.4  | 52.1  | 54.9  | 60.4  | 49.6  | 59.7  | 44.6  |
| # species-specific orthogroups | 13     | 6     | 19    | 29    | 120   | 19    | 12    | 6     | 17    | 7     |
| # in species-specific orthogroups | 102    | 46    | 66    | 179   | 972   | 95    | 47    | 27    | 82    | 24    |
| % genes in species-specific orthogroups | 0.4    | 0.5   | 0.4   | 1.3   | 3.2   | 0.5   | 0.2   | 0.2   | 0.4   | 0.2   |

|            | Smim2 | Tcas2 | Tetr2 | Tmer2 | Vjac |
|------------|-------|-------|-------|-------|------|
| # genes    | 27135 | 12873 | 19104 | 14303 | 10739|
| # genes in orthogroups | 20921  | 11182 | 11939 | 11695 | 9899 |
| # unassigned genes | 6214   | 1691  | 7165  | 2608  | 840  |
| % genes in orthogroups | 77.1   | 86.9  | 62.5  | 81.8  | 92.2 |
| % unassigned genes | 22.9   | 13.1  | 37.5  | 18.2  | 7.8  |
| # orthogroups containing species | 8842   | 7313  | 6254  | 7602  | 7484 |
| % orthogroups containing species | 62.8   | 52    | 44.4  | 54    | 53.2 |
| # species-specific orthogroups | 13     | 27    | 55    | 5     | 2    |
| # in species-specific orthogroups | 61     | 177   | 1111  | 12    | 4    |
| % genes in species-specific orthogroups | 0.2    | 1.4   | 5.8   | 0.1   | 0    |
Table SI 8

Computational analysis of gene family evolution model parameters

| Replicate | Topology type | Run parameters | Lambda estimate (All, Acariformes, Parasitiformes) | Mu estimate (All, Acariformes, Parasitiformes) | Log-Likelihood |
|-----------|---------------|----------------|----------------------------------------------------|------------------------------------------------|----------------|
| 1         | unconstrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009987,0.0005362,0.0006846 | 0.0003055,0.0006493,0.0005634 | -129584 |
| 2         | unconstrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009987,0.0005362,0.0006846 | 0.0003055,0.0006493,0.0005634 | -129584 |
| 3         | unconstrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009987,0.0005362,0.0006846 | 0.0003055,0.0006493,0.0005634 | -129584 |
| 4         | unconstrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009987,0.0005362,0.0006846 | 0.0003055,0.0006493,0.0005634 | -129584 |
| 5         | unconstrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009987,0.0005362,0.0006846 | 0.0003055,0.0006493,0.0005634 | -129584 |
| 1         | unconstrained | Multi-lamdamu All/Acariformes | 0.0009329,0.0005435 | 0.0003671,0.0006394 | -130372 |
| 2         | unconstrained | Multi-lamdamu All/Acariformes | 0.0009329,0.0005434 | 0.0003671,0.0006394 | -130372 |
| 3         | unconstrained | Multi-lamdamu All/Acariformes | 0.0009329,0.0005434 | 0.0003671,0.0006394 | -130372 |
| 4         | unconstrained | Multi-lamdamu All/Acariformes | 0.0009329,0.0005435 | 0.0003671,0.0006394 | -130372 |
| 5         | unconstrained | Multi-lamdamu All/Acariformes | 0.0009329,0.0005435 | 0.0003671,0.0006394 | -130372 |
| 1         | unconstrained | Single lambdamu | 0.0008591 | 0.0004289 | -131605 |
| 2         | unconstrained | Single lambdamu | 0.000859 | 0.0004289 | -131605 |
| 3         | unconstrained | Single lambdamu | 0.0008591 | 0.0004289 | -131605 |
| 4         | unconstrained | Single lambdamu | 0.000859 | 0.0004289 | -131605 |
| 5         | unconstrained | Single lambdamu | 0.0008636 | 0.0004273 | -131606 |
| 1         | unconstrained | Single lambda | 0.0006764 | NA | -133563 |
| 2         | unconstrained | Single lambda | 0.0006764 | NA | -133563 |
| 3         | unconstrained | Single lambda | 0.0006764 | NA | -133563 |
| 4         | unconstrained | Single lambda | 0.0006764 | NA | -133563 |
| 5         | unconstrained | Single lambda | 0.0006764 | NA | -133563 |
| 1         | constrained | Multi-lamdamu All/Acariformes/Parasitiformes | 0.0009399,0.0008018,0.0008803 | 0.0002468,0.0013128,0.0008238 | -129336 |
Constraint and unconstrained trees were used to examine gene family evolution with the program CAFE (Computational Analysis of Gene Family Evolution) v4.0 (De Bie et al. 2006). Several models of gene family evolution, testing different parameter combinations for the birth (Lambda) and death (Mu) probabilities of genes, were investigated. Each model run demonstrated consistent parameter estimates and log-likelihood values across replicates, suggesting the models successfully converged.
Figure SI 6. Selection was more frequently relaxed than intensified during Acariformes evolution. Constraint and unconstrained trees were used to examine gene family evolution with the program CAFE v4.0. A likelihood ratio comparison of a global-lambda model versus multi-lambda model (different birth and death parameters across the tree) demonstrated significant improvement in likelihood when the Acariforme and Parasitiforme branches were allowed separate parameter values (the test likelihood ratio fell in the far tail of the null distribution. For the computational analysis of gene family evolution model parameters, see Tab. SI 8.
Alternative IQtree topologies

Figure SI 7. Alternative IQtree topologies: A: unconstrained, B: Outgroup constrained, C: Acariformes and Parasitiformes monophyletic, D: Spiders/scorpions and Acariformes monophyletic, and E: Spiders/scorpions and Parasitiformes monophyletic. Phylogenetic reconstruction using several different data sets of concatenated, unpartitioned loci, and partitioned single copy orthologs, including the slowest evolving sites and genes, respectively. However, like Sharma et al., every species tree recovered had the same topology, with Acariformes located at the base of arachnids, and with the horse shoe crab (*Limulus polyphemus*) grouped with spiders and scorpions (Sharma et al. 2014). Several different constrained topologies were tested against our data, with the most likely constraint tree, where *L. polyphemus* was constrained as outgroup to arachnids, resulting in a topology where Acariformes and Parasitiformes were monophyletic, and spiders and scorpions basal. Alternative topologies were significantly less likely compared to this one ($p << 0.05$; see below). Both the constraint tree and unconstrained tree were used to examine gene family evolution with the program CAFE. For values of individual trees, see corresponding table in Supplementary file.
| ontology                  | node_id     | node_name                        | raw_p_overrep | FWER_overrep | qvalue  |
|---------------------------|-------------|----------------------------------|---------------|--------------|---------|
| biological_process        | GO:0000003  | reproduction                     | 0.000245058   | 0.003        | 0.02725491 |
| biological_process        | GO:0006950  | response to stress               | 0.000332377   | 0.003        | 0.02725491 |
| biological_process        | GO:0002376  | immune system process            | 0.00066175    | 0.012        | 0.03124041 |
| biological_process        | GO:0006629  | lipid metabolic process          | 0.000761961   | 0.021        | 0.03124041 |
| biological_process        | GO:0009056  | catabolic process                | 0.006247036   | 0.167        | 0.20393705 |
| biological_process        | GO:0006790  | sulfur compound metabolic process| 0.007679403   | 0.19         | 0.20393705 |
| biological_process        | GO:0007568  | aging                            | 0.009022401   | 0.242        | 0.20393705 |
| biological_process        | GO:0048856  | anatomical structure development | 0.010106617   | 0.263        | 0.20393705 |
| biological_process        | GO:0042592  | homeostatic process              | 0.012847617   | 0.29         | 0.20393705 |
| biological_process        | GO:00065008 | regulation of biological quality | 0.012847617   | 0.29         | 0.20393705 |
| biological_process        | GO:0032502  | developmental process            | 0.015663056   | 0.33         | 0.20393705 |
| biological_process        | GO:0051179  | localization                     | 0.016923338   | 0.362        | 0.20393705 |
| biological_process        | GO:0019748  | secondary metabolic process       | 0.017470317   | 0.382        | 0.20393705 |
| biological_process        | GO:0006810  | transport                         | 0.022870499   | 0.47         | 0.20393705 |
| biological_process        | GO:0005134  | establishment of localization     | 0.024870372   | 0.51         | 0.20393705 |
| biological_process        | GO:0044403  | symbiont process                  | 0.024870372   | 0.51         | 0.20393705 |
| biological_process        | GO:0044419  | interspecies interaction between organisms | 0.024870372 | 0.51         | 0.20393705 |
| biological_process        | GO:0051704  | multi-organism process            | 0.024870372   | 0.51         | 0.20393705 |
| biological_process        | GO:0050896  | response to stimulus              | 0.027503143   | 0.535        | 0.21478645 |
| biological_process        | GO:0044281  | small molecule metabolic process  | 0.047013759   | 0.681        | 0.3504662 |
| biological_process        | GO:0071554  | cell wall organization or biogenesis | 0.06273701   | 0.789        | 0.44734216 |
| biological_process        | GO:0006928  | movement of cell or subcellular component | 0.073181626 | 0.85         | 0.46160718 |
| biological_process        | GO:0048870  | cell motility                     | 0.073181626   | 0.85         | 0.46160718 |
| biological_process        | GO:0051674  | localization of cell              | 0.073181626   | 0.85         | 0.46160718 |
| biological_process        | GO:0008152  | metabolic process                 | 0.078813623   | 0.864        | 0.47871978 |
| biological_process        | GO:0030154  | cell differentiation              | 0.093264571   | 0.874        | 0.54626392 |
| biological_process        | GO:0048869  | cellular developmental process     | 0.102771437   | 0.889        | 0.56260801 |
| biological_process        | GO:0016192  | vesicle-mediated transport        | 0.1029161     | 0.897        | 0.56260801 |
| biological_process        | GO:0007155  | cell adhesion                     | 0.117409573   | 0.917        | 0.60172406 |
| biological_process        | GO:0022610  | biological adhesion               | 0.117409573   | 0.917        | 0.60172406 |
| biological_process        | GO:0007005  | mitochondrion organization        | 0.127290235   | 0.93         | 0.6325939 |
| biological_process        | GO:0034330  | cell junction organization        | 0.199451925   | 0.985        | 0.90304936 |
| biological_process        | GO:0065007  | biological regulation             | 0.200081845   | 0.985        | 0.90304936 |
| biological_process        | GO:0022607  | cellular component assembly       | 0.202729973   | 0.986        | 0.90304936 |
| biological_process        | GO:0051186  | cofactor metabolic process        | 0.203736745   | 0.987        | 0.90304936 |
| biological_process        | GO:0051604  | protein maturation                | 0.217343088   | 0.993        | 0.93800701 |
| biological_process        | GO:0034641  | cellular nitrogen compound metabolic process | 0.262660078 | 0.996        | 1 |
| biological_process        | GO:0006913  | nucleocytoplasmic transport       | 0.302944918   | 0.999        | 1 |
| biological_process        | GO:0051189  | nuclear transport                 | 0.302944918   | 0.999        | 1 |
| ontology         | node_id    | node_name                                           | raw_p_overrep | FWER_overrep | qvalue |
|------------------|------------|-----------------------------------------------------|---------------|--------------|--------|
| biological_process | GO:0044238 | primary metabolic process                           | 0.309201542   | 0.999        | 1      |
| biological_process | GO:0071704 | organic substance metabolic process                 | 0.309201542   | 0.999        | 1      |
| biological_process | GO:0005975 | carbohydrate metabolic process                      | 0.318049044   | 0.999        | 1      |
| biological_process | GO:0008283 | cell proliferation                                  | 0.331043814   | 0.999        | 1      |
| biological_process | GO:0007154 | cell communication                                  | 0.342388669   | 0.999        | 1      |
| biological_process | GO:0023052 | signaling                                           | 0.342388669   | 0.999        | 1      |
| biological_process | GO:0044085 | cellular component biogenesis                       | 0.351129691   | 0.999        | 1      |
| biological_process | GO:0006259 | DNA metabolic process                               | 0.371485078   | 1            | 1      |
| biological_process | GO:0008219 | cell death                                          | 0.380568189   | 1            | 1      |
| biological_process | GO:0061914 | autophagy                                           | 0.422077586   | 1            | 1      |
| biological_process | GO:0061914 | process utilizing autophagic mechanism              | 0.422077586   | 1            | 1      |
| biological_process | GO:016043 | cell component organization                         | 0.434496275   | 1            | 1      |
| biological_process | GO:0090304 | nucleic acid metabolic process                      | 0.43986963    | 1            | 1      |
| biological_process | GO:0048646 | anatomical structure formation involved in morphogenesis | 0.445251545   | 1            | 1      |
| biological_process | GO:0021700 | developmental maturation                            | 0.46593427    | 1            | 1      |
| biological_process | GO:0044237 | cellular metabolic process                          | 0.480261342   | 1            | 1      |
| biological_process | GO:0000902 | cell morphogenesis                                  | 0.501535874   | 1            | 1      |
| biological_process | GO:0032989 | cellular component morphogenesis                    | 0.501535874   | 1            | 1      |
| biological_process | GO:0061024 | membrane organization                               | 0.506579824   | 1            | 1      |
| biological_process | GO:0006914 | autophagy                                           | 0.523973308   | 1            | 1      |
| biological_process | GO:0061024 | generation of precursor metabolites and energy      | 0.512850603   | 1            | 1      |
| biological_process | GO:0009653 | nucleobase-containing compound metabolic process    | 0.513956066   | 1            | 1      |
| biological_process | GO:009987  | cellular process                                    | 0.523973308   | 1            | 1      |
| biological_process | GO:007267  | cell-cell signaling                                 | 0.548995919   | 1            | 1      |
| biological_process | GO:0006139 | nucleobase-containing compound metabolic process    | 0.55642788    | 1            | 1      |
| biological_process | GO:0006725 | nucleobase-containing compound metabolic process    | 0.55642788    | 1            | 1      |
| biological_process | GO:0046483 | heterocyclic metabolic process                      | 0.55642788    | 1            | 1      |
| biological_process | GO:1901360 | organic cyclic compound metabolic process            | 0.55642788    | 1            | 1      |
| biological_process | GO:0071840 | cellular component organization or biogenesis       | 0.557358456   | 1            | 1      |
| biological_process | GO:0007165 | signal transduction                                 | 0.556280129   | 1            | 1      |
| biological_process | GO:0050789 | regulation of biological process                    | 0.566280129   | 1            | 1      |
| biological_process | GO:0050794 | regulation of cellular process                      | 0.566280129   | 1            | 1      |
| biological_process | GO:0051716 | cellular response to stimulus                       | 0.566280129   | 1            | 1      |
| biological_process | GO:006396  | RNA processing                                      | 0.569277826   | 1            | 1      |
| biological_process | GO:0006397 | mRNA processing                                     | 0.569277826   | 1            | 1      |
| biological_process | GO:0016071 | mRNA metabolic process                              | 0.569277826   | 1            | 1      |
| biological_process | GO:0006807 | nitrogen compound metabolic process                 | 0.575412062   | 1            | 1      |
| biological_process | GO:0046907 | intracellular transport                             | 0.606402652   | 1            | 1      |
| biological_process | GO:0051614 | cellular localization                              | 0.606402652   | 1            | 1      |
| biological_process | GO:0051649 | establishment of localization in cell              | 0.606402652   | 1            | 1      |
| biological_process | GO:0006996 | organelle organization                             | 0.703884896   | 1            | 1      |
| biological_process | GO:0044248 | cellular catabolic process                          | 0.708703423   | 1            | 1      |
| biological_process | GO:0006082 | organic acid metabolic process                      | 0.713230583   | 1            | 1      |
| ontology               | node_id         | node_name                                           | raw_p_overrep | FWER_overrep | qvalue | node_id         | node_name                                           | raw_p_overrep | FWER_overrep | qvalue |
|-----------------------|-----------------|-----------------------------------------------------|---------------|--------------|--------|-----------------|-----------------------------------------------------|---------------|--------------|--------|
| biological_process    | GO:0006520      | cellular amino acid metabolic process                | 0.713230583   | 1            | 1      | biological_process    | GO:0019752      | carboxylic acid metabolic process                    | 0.713230583   | 1            | 1      |
| biological_process    | GO:0043436      | oxoacid metabolic process                           | 0.713230583   | 1            | 1      | biological_process    | GO:0016070      | RNA metabolic process                                 | 0.716211023   | 1            | 1      |
| biological_process    | GO:0050877      | nervous system process                              | 0.783465346   | 1            | 1      | biological_process    | GO:0007010      | cytoskeleton organization                            | 0.796695486   | 1            | 1      |
| biological_process    | GO:0003008      | system process                                      | 0.813299838   | 1            | 1      | biological_process    | GO:0043933      | protein-containing complex subunit organization      | 0.814286624   | 1            | 1      |
| biological_process    | GO:0065003      | protein-containing complex assembly                 | 0.814286624   | 1            | 1      | biological_process    | GO:0007275      | multicellular organism development                   | 0.817709874   | 1            | 1      |
| biological_process    | GO:0009790      | embryo development                                  | 0.817709874   | 1            | 1      | biological_process    | GO:0032501      | multicellular organismal process                     | 0.818071026   | 1            | 1      |
| biological_process    | GO:0009058      | biosynthetic process                                | 0.830778115   | 1            | 1      | biological_process    | GO:0000038      | cellular protein modification process                 | 0.830778115   | 1            | 1      |
| biological_process    | GO:0010467      | gene expression                                     | 0.906486839   | 1            | 1      | biological_process    | GO:0095491      | cell cycle                                          | 0.90925124    | 1            | 1      |
| biological_process    | GO:0043170      | macromolecule metabolic process                     | 0.948710932   | 1            | 1      | biological_process    | GO:1901564      | organonitrogen compound metabolic process           | 0.951827599   | 1            | 1      |
| biological_process    | GO:0044260      | cellular macromolecule metabolic process            | 0.963070644   | 1            | 1      | biological_process    | GO:0019538      | protein metabolic process                            | 0.980979132   | 1            | 1      |
| biological_process    | GO:0006464      | cellular protein modification process                | 0.987889042   | 1            | 1      | biological_process    | GO:0036211      | protein modification process                         | 0.987889042   | 1            | 1      |
| biological_process    | GO:0043412      | macromolecule modification process                  | 0.987889042   | 1            | 1      | biological_process    | GO:0044267      | cellular protein metabolic process                    | 0.99702158    | 1            | 1      |
| biological_process    | GO:0008150      | biological_process                                  | 1             | 1            | 1      | biological_process    | GO:0017334      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0007194      | nitrogen cycle metabolic process                     | 1             | 1            | 1      | biological_process    | GO:1901564      | organonitrogen compound metabolic process           | 1             | 1            | 1      |
| biological_process    | GO:0008150      | biological_process                                  | 1             | 1            | 1      | biological_process    | GO:1901564      | organonitrogen compound metabolic process           | 1             | 1            | 1      |
| biological_process    | GO:0007010      | cytoskeleton organization                            | 1             | 1            | 1      | biological_process    | GO:0043436      | extracellular structure organization                  | 1             | 1            | 1      |
| biological_process    | GO:0007034      | vacuolar transport                                  | 1             | 1            | 1      | biological_process    | GO:0043412      | macromolecule modification process                   | 1             | 1            | 1      |
| biological_process    | GO:0043436      | extracellular structure organization                 | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0030313      | circulatory system process                           | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0030705      | cytoskeleton-dependent intracellular transport       | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0043473      | pigmentation                                        | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0006457      | protein folding                                     | 1             | 1            | 1      | biological_process    | GO:0043436      | extracellular structure organization                  | 1             | 1            | 1      |
| biological_process    | GO:0006605      | protein targeting                                   | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0006886      | intracellular protein transport                      | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0008104      | protein localization                                | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0015031      | protein transport                                   | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0015833      | peptide transport                                   | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0033036      | macromolecule localization                          | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0034613      | cellular protein localization                       | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| biological_process    | GO:0042886      | amide transport                                     | 1             | 1            | 1      | biological_process    | GO:0030198      | extracellular matrix organization                    | 1             | 1            | 1      |
| ontology          | node_id      | node_name                                      | raw_p_overrep | FWER_overrep | qvalue |
|-------------------|--------------|-----------------------------------------------|---------------|--------------|--------|
| biological_process| GO:0045184   | establishment of protein localization         | 1             | 1            | 1      |
| biological_process| GO:0070727   | cellular macromolecule localization            | 1             | 1            | 1      |
| biological_process| GO:0071702   | organic substance transport                     | 1             | 1            | 1      |
| biological_process| GO:0071705   | nitrogen compound transport                     | 1             | 1            | 1      |
| biological_process| GO:0022618   | ribonucleoprotein complex assembly             | 1             | 1            | 1      |
| biological_process| GO:0034622   | cellular protein-containing complex assembly    | 1             | 1            | 1      |
| biological_process| GO:0071826   | ribonucleoprotein complex subunit organization | 1             | 1            | 1      |
| biological_process| GO:0006399   | tRNA metabolic process                          | 1             | 1            | 1      |
| biological_process| GO:0034660   | ncRNA metabolic process                         | 1             | 1            | 1      |
| biological_process| GO:000280    | nuclear division                                | 1             | 1            | 1      |
| biological_process| GO:0022402   | cell cycle process                              | 1             | 1            | 1      |
| biological_process| GO:0048285   | organelle fission                               | 1             | 1            | 1      |
| biological_process| GO:0140014   | mitogenic nuclear division                      | 1             | 1            | 1      |
| biological_process| GO:1903047   | mitotic cell cycle process                       | 1             | 1            | 1      |
| biological_process| GO:0007059   | chromosome segregation                          | 1             | 1            | 1      |
| biological_process| GO:0019439   | aromatic compound catabolic process             | 1             | 1            | 1      |
| biological_process| GO:0034655   | nucleobase-containing compound catabolic process| 1             | 1            | 1      |
| biological_process| GO:0044270   | cellular nitrogen compound catabolic process    | 1             | 1            | 1      |
| biological_process| GO:0046700   | heterocycle catabolic process                   | 1             | 1            | 1      |
| biological_process| GO:1901361   | organic cyclic compound catabolic process       | 1             | 1            | 1      |
| biological_process| GO:1901575   | organic substance catabolic process             | 1             | 1            | 1      |
| biological_process| GO:0051301   | cell division                                   | 1             | 1            | 1      |
| biological_process| GO:0042254   | ribosome biogenesis                             | 1             | 1            | 1      |
| biological_process| GO:0022613   | ribonucleoprotein complex biogenesis            | 1             | 1            | 1      |
| biological_process| GO:0006412   | translation                                     | 1             | 1            | 1      |
| biological_process| GO:0006518   | peptide metabolic process                        | 1             | 1            | 1      |
| biological_process| GO:009059    | macromolecule biosynthetic process              | 1             | 1            | 1      |
| biological_process| GO:0034645   | cellular macromolecule biosynthetic process     | 1             | 1            | 1      |
| biological_process| GO:0043043   | peptide biosynthetic process                    | 1             | 1            | 1      |
| biological_process| GO:0043603   | cellular amide metabolic process                | 1             | 1            | 1      |
| biological_process| GO:0043604   | amide biosynthetic process                      | 1             | 1            | 1      |
| biological_process| GO:0044249   | cellular biosynthetic process                   | 1             | 1            | 1      |
| biological_process| GO:0044271   | cellular nitrogen compound biosynthetic process | 1             | 1            | 1      |
| biological_process| GO:1901566   | organonitrogen compound biosynthetic process    | 1             | 1            | 1      |
| biological_process| GO:1901576   | organic substance biosynthetic process growth   | 1             | 1            | 1      |
| biological_process| GO:0040007   | mitotic cell cycle                              | 1             | 1            | 1      |
| biological_process| GO:0000278   | mitotic cell                                    | 1             | 1            | 1      |
| biological_process| GO:0051276   | chromosome organization                         | 1             | 1            | 1      |
Table SI 10
Gene families showing rapid contraction in the Acariformes

| ontology                             | node_id    | node_name                                         | raw_p_overrep | FWER_overrep | qvalue   |
|--------------------------------------|------------|---------------------------------------------------|---------------|--------------|----------|
| biological_process                   | GO:0000003 | reproduction                                      | 0.00075246    | 0.026        | 0.110618425 |
| biological_process                   | GO:0040011 | locomotion                                        | 0.002161383   | 0.068        | 0.110618425 |
| biological_process                   | GO:0051179 | localization                                      | 0.003618482   | 0.114        | 0.110618425 |
| biological_process                   | GO:0032502 | developmental process                             | 0.005302367   | 0.164        | 0.110618425 |
| biological_process                   | GO:0006790 | sulfur compound metabolic process                 | 0.006286359   | 0.206        | 0.110618425 |
| biological_process                   | GO:0002376 | immune system process                             | 0.006397885   | 0.208        | 0.110618425 |
| biological_process                   | GO:0048856 | anatomical structure development                  | 0.006549997   | 0.212        | 0.110618425 |
| biological_process                   | GO:0055085 | transmembrane transport                           | 0.007086009   | 0.224        | 0.110618425 |
| biological_process                   | GO:007568  | aging                                             | 0.007715849   | 0.245        | 0.110618425 |
| biological_process                   | GO:0006928 | movement of cell or subcellular component        | 0.008094031   | 0.266        | 0.110618425 |
| biological_process                   | GO:0048870 | cell motility                                     | 0.008094031   | 0.266        | 0.110618425 |
| biological_process                   | GO:0051674 | localization of cell                              | 0.008094031   | 0.266        | 0.110618425 |
| biological_process                   | GO:0006950 | response to stress                                | 0.008844222   | 0.293        | 0.111573268 |
| biological_process                   | GO:0006810 | transport                                         | 0.016701402   | 0.384        | 0.182601993 |
| biological_process                   | GO:0051234 | establishment of localization                     | 0.016701402   | 0.384        | 0.182601993 |
| biological_process                   | GO:0030154 | cell differentiation                              | 0.019485944   | 0.429        | 0.199730922 |
| biological_process                   | GO:0048869 | cellular developmental process                    | 0.02328447    | 0.504        | 0.216975628 |
| biological_process                   | GO:0006629 | lipid metabolic process                            | 0.023814398   | 0.511        | 0.216975628 |
| biological_process                   | GO:0007267 | cell-cell signaling                               | 0.042436087   | 0.73         | 0.34443338 |
| biological_process                   | GO:0042592 | homeostatic process                               | 0.044104274   | 0.738        | 0.34443338 |
| biological_process                   | GO:0065008 | regulation of biological quality                  | 0.044104274   | 0.738        | 0.34443338 |
| biological_process                   | GO:0019748 | secondary metabolic process                       | 0.052304225   | 0.788        | 0.38990422 |
| biological_process                   | GO:0051604 | protein maturation                                | 0.071581325   | 0.867        | 0.459538925 |
| biological_process                   | GO:0044403 | symbiont process                                  | 0.072853732   | 0.874        | 0.459538925 |
| biological_process                   | GO:0044419 | interspecies interaction between organisms        | 0.072853732   | 0.874        | 0.459538925 |
| biological_process                   | GO:0051704 | multi-organism process                            | 0.072853732   | 0.874        | 0.459538925 |
| biological_process                   | GO:0008219 | cell death                                        | 0.086779075   | 0.913        | 0.514498092 |
| biological_process                   | GO:0007155 | cell adhesion                                     | 0.090978321   | 0.919        | 0.514498092 |
| biological_process                   | GO:0022610 | biological adhesion                               | 0.090978321   | 0.919        | 0.514498092 |
| biological_process                   | GO:0032196 | transposition                                     | 0.102562725   | 0.939        | 0.556515136 |
| biological_process                   | GO:0050896 | response to stimulus                              | 0.105194934   | 0.941        | 0.556515136 |
| biological_process                   | GO:0071554 | cell wall organization or biogenesis              | 0.110629151    | 0.953        | 0.566974397 |
| biological_process                   | GO:0048646 | anatomical structure formation involved in morphogenesis | 0.130916311   | 0.97        | 0.650614396 |
| biological_process                   | GO:0009056 | catabolic process                                 | 0.154669718   | 0.979        | 0.746053932 |
| biological_process                   | GO:006259 | DNA metabolic process                             | 0.202384132   | 0.991        | 0.946668035 |
| biological_process                   | GO:009653 | anatomical structure morphogenesis               | 0.209021269   | 0.991        | 0.946668035 |
| biological_process                   | GO:007154 | cell communication                                | 0.219349911   | 0.993        | 0.946668035 |
| biological_process                   | GO:0023052 | signaling                                         | 0.219349911   | 0.993        | 0.946668035 |
| biological_process                   | GO:0016192 | vesicle-mediated transport                        | 0.226951806   | 0.997        | 0.954361442 |
| biological_process                   | GO:0008152 | metabolic process                                 | 0.264042327   | 0.998        | 1        |
| ontology              | node_id    | node_name                                         | raw_p_overrep       | FWER_overrep | qvalue |
|----------------------|------------|---------------------------------------------------|---------------------|--------------|--------|
| biological_process   | GO:0044281 | small molecule metabolic process                  | 0.276655906         | 0.998        | 1      |
| biological_process   | GO:0050877 | nervous system process                            | 0.279767473         | 0.998        | 1      |
| biological_process   | GO:0021700 | developmental maturation                          | 0.30849507          | 1            | 1      |
| biological_process   | GO:0007005 | mitochondrion organization                        | 0.310156903         | 1            | 1      |
| biological_process   | GO:0034330 | cell junction organization                        | 0.331938287         | 1            | 1      |
| biological_process   | GO:003008  | system process                                    | 0.33449441          | 1            | 1      |
| biological_process   | GO:0065007 | biological regulation                             | 0.33904724          | 1            | 1      |
| biological_process   | GO:0005975 | carbohydrate metabolic process                    | 0.341866703         | 1            | 1      |
| biological_process   | GO:0022607 | cellular component assembly                       | 0.345528291         | 1            | 1      |
| biological_process   | GO:0000902 | cell morphogenesis                                | 0.35074755          | 1            | 1      |
| biological_process   | GO:0032989 | cellular component morphogenesis                  | 0.35074755          | 1            | 1      |
| biological_process   | GO:0034441 | cellular nitrogen compound metabolic process      | 0.373643909         | 1            | 1      |
| biological_process   | GO:0044373 | pigmentation                                      | 0.447726767         | 1            | 1      |
| biological_process   | GO:0051186 | cofactor metabolic process                        | 0.45015205          | 1            | 1      |
| biological_process   | GO:0090304 | nucleic acid metabolic process                    | 0.451635461         | 1            | 1      |
| biological_process   | GO:0016043 | cellular component organization                   | 0.45512102          | 1            | 1      |
| biological_process   | GO:006913  | nucleocytoplasmic transport                       | 0.479539532         | 1            | 1      |
| biological_process   | GO:0051169 | nuclear transport                                 | 0.479539532         | 1            | 1      |
| biological_process   | GO:004085  | cellular component biogenesis                     | 0.53706885          | 1            | 1      |
| biological_process   | GO:0007275 | multicellular organism development                | 0.578845652         | 1            | 1      |
| biological_process   | GO:0009790 | embryo development                                | 0.578845652         | 1            | 1      |
| biological_process   | GO:006139  | nucleobase-containing compound metabolic process  | 0.600457204         | 1            | 1      |
| biological_process   | GO:0006725 | cellular aromatic compound metabolic process      | 0.600457204         | 1            | 1      |
| biological_process   | GO:0046483 | heterocycle metabolic process                     | 0.600457204         | 1            | 1      |
| biological_process   | GO:1901360 | organic cyclic compound metabolic process         | 0.600457204         | 1            | 1      |
| biological_process   | GO:0071840 | cellular component organization or biogenesis     | 0.61796777          | 1            | 1      |
| biological_process   | GO:0044327 | cellular metabolic process                         | 0.624727844         | 1            | 1      |
| biological_process   | GO:0006914 | autophagy                                         | 0.629238041         | 1            | 1      |
| biological_process   | GO:0061919 | process utilizing autophagic mechanism             | 0.629238041         | 1            | 1      |
| biological_process   | GO:0032501 | multicellular organismal process                  | 0.642699034         | 1            | 1      |
| biological_process   | GO:0007059 | chromosome segregation                            | 0.64915975          | 1            | 1      |
| biological_process   | GO:0044238 | primary metabolic process                         | 0.65416095          | 1            | 1      |
| biological_process   | GO:0071704 | organic substance metabolic process               | 0.65416095          | 1            | 1      |
| biological_process   | GO:0006807 | nitrogen compound metabolic process growth        | 0.657432121         | 1            | 1      |
| biological_process   | GO:0040007 | signal transduction                               | 0.692047958         | 1            | 1      |
| biological_process   | GO:0007165 | regulation of biological process                  | 0.692122475         | 1            | 1      |
| biological_process   | GO:0050789 | regulation of cellular process                    | 0.692122475         | 1            | 1      |
| biological_process   | GO:0050794 | cellular response to stimulus                     | 0.692122475         | 1            | 1      |
| biological_process   | GO:0061024 | membrane organization                             | 0.721474951         | 1            | 1      |
| biological_process   | GO:0006091 | generation of precursor metabolites and energy    | 0.727847321         | 1            | 1      |
| ontology                  | node_id      | node_name                          | raw_p_overrep | FWER_overrep | qvalue |
|---------------------------|--------------|------------------------------------|---------------|--------------|--------|
| biological_process        | GO:0007010   | cytoskeleton organization          | 0.775744055  | 1            | 1      |
| biological_process        | GO:0009987   | cellular process                   | 0.779030697  | 1            | 1      |
| biological_process        | GO:0006996   | organelle organization             | 0.781866266  | 1            | 1      |
| biological_process        | GO:0006396   | RNA processing                     | 0.782196866  | 1            | 1      |
| biological_process        | GO:0006397   | mRNA processing                    | 0.782196866  | 1            | 1      |
| biological_process        | GO:0016071   | mRNA metabolic process             | 0.782196866  | 1            | 1      |
| biological_process        | GO:0009058   | biosynthetic process               | 0.795244716  | 1            | 1      |
| biological_process        | GO:0007049   | cell cycle                         | 0.79549112   | 1            | 1      |
| biological_process        | GO:0006503   | protein-containing complex subunit organization | 0.802546635 | 1            | 1      |
| biological_process        | GO:0006608   | organic acid metabolic process     | 0.895678378  | 1            | 1      |
| biological_process        | GO:0006520   | cellular amino acid metabolic process | 0.895678378 | 1            | 1      |
| biological_process        | GO:0006608   | protein metabolic process          | 0.895678378  | 1            | 1      |
| biological_process        | GO:0006608   | gene expression                    | 0.924471813  | 1            | 1      |
| biological_process        | GO:0006608   | establishment of localization in cell | 0.958266433  | 1            | 1      |
| biological_process        | GO:0006608   | chromosome organization            | 0.958266433  | 1            | 1      |
| biological_process        | GO:0006608   | macromolecule metabolic process    | 0.962591317  | 1            | 1      |
| biological_process        | GO:0006608   | cellular macromolecule metabolic process | 0.978828947  | 1            | 1      |
| biological_process        | GO:0006608   | oxoacid metabolic process          | 0.9873187    | 1            | 1      |
| biological_process        | GO:0006608   | organonitrogen compound metabolic process | 0.992942032  | 1            | 1      |
| biological_process        | GO:0006608   | protein folding                    | 0.996694521  | 1            | 1      |
| biological_process        | GO:0006608   | protein targeting                  | 0.996694521  | 1            | 1      |
| biological_process        | GO:0006608   | intracellular matrix organization   | 0.999655784  | 1            | 1      |
| biological_process        | GO:0006608   | extracellular structure organization | 1             | 1            | 1      |
| biological_process        | GO:0006608   | extracellular matrix organization  | 1             | 1            | 1      |
| biological_process        | GO:0006608   | circulatory system process         | 1             | 1            | 1      |
| biological_process        | GO:0006608   | cytokinetic-dependent intracellular transport | 1             | 1            | 1      |
| biological_process        | GO:0006608   | protein folding                    | 1             | 1            | 1      |
| biological_process        | GO:0006608   | protein targeting                  | 1             | 1            | 1      |
| biological_process        | GO:0006608   | intracellular protein transport     | 1             | 1            | 1      |
| biological_process        | GO:0006608   | protein localization               | 1             | 1            | 1      |
| ontology         | node_id        | node_name                      | raw_p_overrep | FWER_overrep | qvalue |
|------------------|----------------|--------------------------------|---------------|--------------|--------|
| biological_process | GO:0015031    | protein transport              | 1             | 1            | 1      |
| biological_process | GO:0015833    | peptide transport              | 1             | 1            | 1      |
| biological_process | GO:0033036    | macromolecule localization     | 1             | 1            | 1      |
| biological_process | GO:0034613    | cellular protein localization  | 1             | 1            | 1      |
| biological_process | GO:0042886    | amide transport                | 1             | 1            | 1      |
| biological_process | GO:0045184    | establishment of protein       | 1             | 1            | 1      |
| biological_process | GO:0070727    | cellular macromolecule         | 1             | 1            | 1      |
| biological_process | GO:0071702    | organic substance transport    | 1             | 1            | 1      |
| biological_process | GO:0071705    | nitrogen compound transport    | 1             | 1            | 1      |
| biological_process | GO:0022618    | ribonucleoprotein complex      | 1             | 1            | 1      |
| biological_process | GO:0034622    | cellular protein-containing    | 1             | 1            | 1      |
| biological_process | GO:0071826    | complex assembly               | 1             | 1            | 1      |
| biological_process | GO:0006399    | tRNA metabolic process         | 1             | 1            | 1      |
| biological_process | GO:0034660    | ncRNA metabolic process        | 1             | 1            | 1      |
| biological_process | GO:0000280    | nuclear division               | 1             | 1            | 1      |
| biological_process | GO:0022402    | cell cycle process             | 1             | 1            | 1      |
| biological_process | GO:0048285    | organelle fission              | 1             | 1            | 1      |
| biological_process | GO:0140014    | mitotic nuclear division       | 1             | 1            | 1      |
| biological_process | GO:1903047    | mitotic cell cycle process     | 1             | 1            | 1      |
| biological_process | GO:0019439    | aromatic compound catabolic    | 1             | 1            | 1      |
| biological_process | GO:0034655    | nucleobase-containing          | 1             | 1            | 1      |
| biological_process | GO:004270     | compound catabolic process     | 1             | 1            | 1      |
| biological_process | GO:0046700    | heterocycle catabolic process  | 1             | 1            | 1      |
| biological_process | GO:1901361    | organic cyclic compound        | 1             | 1            | 1      |
| biological_process | GO:1901575    | organic substance catabolic    | 1             | 1            | 1      |
| biological_process | GO:0051301    | cell division                  | 1             | 1            | 1      |
| biological_process | GO:0042254    | ribosome biogenesis            | 1             | 1            | 1      |
| biological_process | GO:0022613    | ribonucleoprotein complex      | 1             | 1            | 1      |
| biological_process | GO:0006412    | translation                    | 1             | 1            | 1      |
| biological_process | GO:0006518    | peptide metabolic process      | 1             | 1            | 1      |
| biological_process | GO:0009059    | macromolecule biosynthetic     | 1             | 1            | 1      |
| biological_process | GO:0034645    | cellular macromolecule         | 1             | 1            | 1      |
| biological_process | GO:0043043    | peptide biosynthetic process   | 1             | 1            | 1      |
| biological_process | GO:0043603    | cellular amide metabolic process| 1            | 1            | 1      |
| biological_process | GO:0043604    | amide biosynthetic process     | 1             | 1            | 1      |
| biological_process | GO:0044249    | cellular biosynthetic process  | 1             | 1            | 1      |
| biological_process | GO:0044271    | cellular nitrogen compound     | 1             | 1            | 1      |
| biological_process | GO:1901566    | organonitrogen compound        | 1             | 1            | 1      |
| biological_process | GO:1901576    | organic substance biosynthetic | 1             | 1            | 1      |
| biological_process | GO:0000278    | mitotic cell cycle             | 1             | 1            | 1      |
Table S1 11

Gene families showing rapid expansion in the Acariformes

| ontology               | node_id   | node_name                          | raw_p_overrep | FWER_overrep | qvalue   |
|------------------------|-----------|------------------------------------|---------------|--------------|----------|
| biological_process     | GO:0030154| cell differentiation               | 0.000758826   | 0.026        | 0.075680876 |
| biological_process     | GO:0048869| cellular developmental process     | 0.000922938   | 0.028        | 0.075680876 |
| biological_process     | GO:0048856| anatomical structure development   | 0.001987254   | 0.067        | 0.108636548 |
| biological_process     | GO:0032502| developmental process              | 0.003344292   | 0.092        | 0.112633924 |
| biological_process     | GO:0006629| lipid metabolic process            | 0.003438321   | 0.093        | 0.112633924 |
| biological_process     | GO:0005975| carbohdrate metabolic process      | 0.004120753   | 0.121        | 0.112633924 |
| biological_process     | GO:0006259| DNA metabolic process              | 0.006809496   | 0.179        | 0.112633924 |
| biological_process     | GO:0044238| primary metabolic process          | 0.011757261   | 0.268        | 0.214243415 |
| biological_process     | GO:0071704| organic substance metabolic process| 0.011757261   | 0.268        | 0.214243415 |
| biological_process     | GO:0009987| cellular process                   | 0.024478493   | 0.487        | 0.401447277 |
| biological_process     | GO:0000003| reproduction                        | 0.039277058   | 0.629        | 0.58558523  |
| biological_process     | GO:0002376| immune system process              | 0.059950675   | 0.785        | 0.711049681 |
| biological_process     | GO:0071554| cell wall organization or biogenesis| 0.060395654   | 0.8          | 0.711049681 |
| biological_process     | GO:0007568| aging                              | 0.06495895    | 0.832        | 0.711049681 |
| biological_process     | GO:0008152| metabolic process                   | 0.108006837   | 0.897        | 0.728374061 |
| biological_process     | GO:0009653| metabolic process                   | 0.108619193   | 0.901        | 0.728374061 |
| biological_process     | GO:0007155| metabolic process                   | 0.109559465   | 0.903        | 0.728374061 |
| biological_process     | GO:0007155| cell adhesion                       | 0.109959986   | 0.909        | 0.728374061 |
| biological_process     | GO:0022610| biological adhesion                 | 0.109959986   | 0.909        | 0.728374061 |
| biological_process     | GO:0044260| cellular macromolecule metabolic process| 0.111350058   | 0.911        | 0.728374061 |
| biological_process     | GO:0006950| response to stress                  | 0.117627012   | 0.918        | 0.728374061 |
| biological_process     | GO:0021700| developmental maturation            | 0.118511666   | 0.922        | 0.728374061 |
| biological_process     | GO:0006139| nucleobase-containing compound metabolic process| 0.132667593   | 0.946        | 0.728374061 |
| biological_process     | GO:0006725| cellular aromatic compound metabolic process| 0.132667593   | 0.946        | 0.728374061 |
| biological_process     | GO:0046483| heterocycle metabolic process       | 0.132667593   | 0.946        | 0.728374061 |
| biological_process     | GO:0006950| metabolic process                   | 0.132667593   | 0.946        | 0.728374061 |
| biological_process     | GO:0013620| organic cyclic compound metabolic process| 0.132667593   | 0.946        | 0.728374061 |
| biological_process     | GO:0009056| catabolic process                   | 0.144100466   | 0.96         | 0.728374061 |
| biological_process     | GO:0023610| generation of precursor metabolites and energy| 0.147603293   | 0.965        | 0.728374061 |
| biological_process     | GO:0042592| homeostatic process                 | 0.158670502   | 0.97         | 0.728374061 |
| biological_process     | GO:0065008| regulation of biological quality    | 0.158670502   | 0.97         | 0.728374061 |
| biological_process     | GO:0007154| cell communication                  | 0.165799716   | 0.972        | 0.728374061 |
| biological_process     | GO:0023052| signaling                           | 0.165799716   | 0.972        | 0.728374061 |
| biological_process     | GO:0065007| biological regulation               | 0.169451082   | 0.975        | 0.728374061 |
| biological_process     | GO:0007165| signal transduction                 | 0.182041445   | 0.986        | 0.728374061 |
| biological_process     | GO:0050789| regulation of biological process    | 0.182041445   | 0.986        | 0.728374061 |
| biological_process     | GO:0050794| regulation of cellular process      | 0.182041445   | 0.986        | 0.728374061 |
| biological_process     | GO:0051716| cellular response to stimulus       | 0.182041445   | 0.986        | 0.728374061 |
| ontology               | node_id         | node_name                              | raw_p_overrep | FWER_overrep | qvalue |
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| biological_process     | GO:0034330      | cell junction organization              | 0.192564658  | 0.994        | 0.728374061 |
| biological_process     | GO:0040011      | locomotion                              | 0.20200589    | 0.995        | 0.728374061 |
| biological_process     | GO:0044400      | symbiont process                        | 0.21182876    | 0.997        | 0.728374061 |
| biological_process     | GO:0044419      | interspecies interaction between organisms | 0.21182876    | 0.997        | 0.728374061 |
| biological_process     | GO:0051704      | multi-organism process                  | 0.21182876    | 0.997        | 0.728374061 |
| biological_process     | GO:0000902      | cell morphogenesis                      | 0.212033514   | 0.997        | 0.728374061 |
| biological_process     | GO:0032989      | cellular component morphogenesis         | 0.212033514   | 0.997        | 0.728374061 |
| biological_process     | GO:0044203      | macromolecule metabolic process         | 0.213182652   | 0.998        | 0.728374061 |
| biological_process     | GO:0044281      | small molecule metabolic process        | 0.228160739   | 0.998        | 0.763640025 |
| biological_process     | GO:0006928      | movement of cell or subcellular component | 0.243221961   | 0.998        | 0.767084645 |
| biological_process     | GO:0006970      | cell motility                           | 0.243221961   | 0.998        | 0.767084645 |
| biological_process     | GO:0006970      | localization of cell                    | 0.243221961   | 0.998        | 0.767084645 |
| biological_process     | GO:0006970      | nucleocytoplasmic transport             | 0.293190212   | 0.998        | 0.890429532 |
| biological_process     | GO:0006970      | nuclear transport                       | 0.293190212   | 0.998        | 0.890429532 |
| biological_process     | GO:0006970      | localization                           | 0.308825213   | 0.998        | 0.920860636 |
| biological_process     | GO:0006970      | transport                              | 0.381950437   | 1            | 1       |
| biological_process     | GO:0006970      | establishment of localization           | 0.381950437   | 1            | 1       |
| biological_process     | GO:0006970      | cellular component organization         | 0.390362777   | 1            | 1       |
| biological_process     | GO:0006970      | autophagy                              | 0.409745256   | 1            | 1       |
| biological_process     | GO:0006970      | process utilizing autophagic mechanism  | 0.409745256   | 1            | 1       |
| biological_process     | GO:0006970      | anatomical structure formation          | 0.425276384   | 1            | 1       |
| biological_process     | GO:0006970      | involved in morphogenesis               | 0.454216394   | 1            | 1       |
| biological_process     | GO:0006970      | transmembrane transport                 | 0.457817797   | 1            | 1       |
| biological_process     | GO:0006970      | membrane organization                   | 0.492973595   | 1            | 1       |
| biological_process     | GO:0006970      | cellular component organization or biogenesis | 0.510470477   | 1            | 1       |
| biological_process     | GO:0006970      | cell-cell signaling                     | 0.527526553   | 1            | 1       |
| biological_process     | GO:0006970      | cofactor metabolic process              | 0.55945645    | 1            | 1       |
| biological_process     | GO:0006970      | cellular protein modification process    | 0.562011557   | 1            | 1       |
| biological_process     | GO:0006970      | protein modification process            | 0.562011557   | 1            | 1       |
| biological_process     | GO:0006970      | macromolecule modification              | 0.562011557   | 1            | 1       |
| biological_process     | GO:0006970      | cellular metabolic process              | 0.569726955   | 1            | 1       |
| biological_process     | GO:0006970      | intracellular transport                 | 0.59201324    | 1            | 1       |
| biological_process     | GO:0006970      | cellular localization                   | 0.59201324    | 1            | 1       |
| biological_process     | GO:0006970      | establishment of localization in cell    | 0.59201324    | 1            | 1       |
| biological_process     | GO:0006970      | cellular component assembly             | 0.601595032   | 1            | 1       |
| biological_process     | GO:0006970      | cell cycle                              | 0.65957998    | 1            | 1       |
| biological_process     | GO:0006970      | organelle organization                  | 0.677643051   | 1            | 1       |
| biological_process     | GO:0006970      | cell proliferation                      | 0.686775765   | 1            | 1       |
| biological_process     | GO:0006970      | cellular catabolic process              | 0.695323821   | 1            | 1       |
| biological_process     | GO:0006970      | cellular nitrogen compound metabolic process | 0.695739754   | 1            | 1       |
| biological_process     | GO:0006970      | organic acid metabolic process          | 0.699099749   | 1            | 1       |
| biological_process     | GO:0006970      | cellular amino acid metabolic process   | 0.699099749   | 1            | 1       |
| biological_process     | GO:0006970      | carboxylic acid metabolic process       | 0.699099749   | 1            | 1       |
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| biological_process        | GO:0043436   | o xoacid metabolic process      | 0.699099749   | 1            | 1       |
| biological_process        | GO:0006412   | translation                    | 0.723064429   | 1            | 1       |
| biological_process        | GO:0006518   | peptide metabolic process      | 0.723064429   | 1            | 1       |
| biological_process        | GO:0009059   | macromolecule biosynthetic      | 0.723064429   | 1            | 1       |
| biological_process        | GO:0034645   | cellular macromolecule         | 0.723064429   | 1            | 1       |
| biological_process        | GO:0043043   | peptide biosynthetic process   | 0.723064429   | 1            | 1       |
| biological_process        | GO:0043603   | cellular amide metabolic       | 0.723064429   | 1            | 1       |
| biological_process        | GO:0043604   | amide biosynthetic process     | 0.723064429   | 1            | 1       |
| biological_process        | GO:0044249   | cellular biosynthetic process  | 0.723064429   | 1            | 1       |
| biological_process        | GO:0044271   | cellular nitrogen compound     | 0.723064429   | 1            | 1       |
| biological_process        | GO:0044271   | organonitrogen compound        | 0.723064429   | 1            | 1       |
| biological_process        | GO:0008219   | cell death                     | 0.726531627   | 1            | 1       |
| biological_process        | GO:0044085   | cellular component biogenesis  | 0.747897987   | 1            | 1       |
| biological_process        | GO:0044267   | cellular protein metabolic     | 0.767112945   | 1            | 1       |
| biological_process        | GO:0050877   | nervous system process         | 0.770324023   | 1            | 1       |
| biological_process        | GO:0007010   | cytoskeleton organization      | 0.782810667   | 1            | 1       |
| biological_process        | GO:0019538   | protein metabolic process      | 0.788793063   | 1            | 1       |
| biological_process        | GO:0006807   | nitrogen compound metabolic    | 0.79948347    | 1            | 1       |
| biological_process        | GO:0032501   | multicellular organismal       | 0.80046482    | 1            | 1       |
| biological_process        | GO:0030008   | system process                 | 0.800835345   | 1            | 1       |
| biological_process        | GO:0043933   | protein-containing complex     | 0.801849627   | 1            | 1       |
| biological_process        | GO:0065003   | protein-containing complex     | 0.801849627   | 1            | 1       |
| biological_process        | GO:009058    | biosynthetic process           | 0.802577982   | 1            | 1       |
| biological_process        | GO:007275    | multicellular organism         | 0.805360706   | 1            | 1       |
| biological_process        | GO:0009790   | embryo development             | 0.805360706   | 1            | 1       |
| biological_process        | GO:0051276   | chromosome organization        | 0.815066347   | 1            | 1       |
| biological_process        | GO:0016192   | vesicle-mediated transport     | 0.83567729    | 1            | 1       |
| biological_process        | GO:0030705   | protein maturation             | 0.897551836   | 1            | 1       |
| biological_process        | GO:0008150   | biological_process             | 1             | 1            | 1       |
| biological_process        | GO:0071941   | nitrogen cycle metabolic       | 1             | 1            | 1       |
| biological_process        | GO:0032196   | transposition                  | 1             | 1            | 1       |
| biological_process        | GO:0007034   | vacuolar transport             | 1             | 1            | 1       |
| biological_process        | GO:0030198   | extracellular matrix           | 1             | 1            | 1       |
| biological_process        | GO:0043062   | extracellular structure        | 1             | 1            | 1       |
| biological_process        | GO:0003013   | circulatory system             | 1             | 1            | 1       |
| biological_process        | GO:0019748   | secondary metabolic process    | 1             | 1            | 1       |
| biological_process        | GO:0030705   | cytoskeleton-dependent         | 1             | 1            | 1       |
| biological_process        | GO:0051604   | protein maturation             | 1             | 1            | 1       |
| biological_process        | GO:0043473   | pigmentation                   | 1             | 1            | 1       |
| biological_process        | GO:0006457   | protein folding                | 1             | 1            | 1       |
| biological_process        | GO:0006605   | protein targeting              | 1             | 1            | 1       |
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| biological_process        | GO:0006886   | intracellular protein transport                     | 1             | 1            | 1      |
| biological_process        | GO:0008104   | protein localization                                | 1             | 1            | 1      |
| biological_process        | GO:0015031   | protein transport                                   | 1             | 1            | 1      |
| biological_process        | GO:0015833   | peptide transport                                   | 1             | 1            | 1      |
| biological_process        | GO:0033036   | macromolecule localization                          | 1             | 1            | 1      |
| biological_process        | GO:0034613   | cellular protein localization                       | 1             | 1            | 1      |
| biological_process        | GO:0042886   | amide transport                                     | 1             | 1            | 1      |
| biological_process        | GO:0045184   | establishment of protein localization               | 1             | 1            | 1      |
| biological_process        | GO:0070727   | cellular macromolecule localization                | 1             | 1            | 1      |
| biological_process        | GO:0071702   | organic substance transport                         | 1             | 1            | 1      |
| biological_process        | GO:0071705   | nitrogen compound transport                         | 1             | 1            | 1      |
| biological_process        | GO:0022618   | ribonucleoprotein complex assembly                 | 1             | 1            | 1      |
| biological_process        | GO:0034622   | cellular protein-containing complex assembly        | 1             | 1            | 1      |
| biological_process        | GO:0071826   | ribonucleoprotein complex subunit organization      | 1             | 1            | 1      |
| biological_process        | GO:0006790   | sulfur compound metabolic process                   | 1             | 1            | 1      |
| biological_process        | GO:0006399   | tRNA metabolic process                              | 1             | 1            | 1      |
| biological_process        | GO:0034660   | ncRNA metabolic process                             | 1             | 1            | 1      |
| biological_process        | GO:0000280   | nuclear division                                    | 1             | 1            | 1      |
| biological_process        | GO:0022402   | cell cycle process                                  | 1             | 1            | 1      |
| biological_process        | GO:0048285   | organelle fission                                   | 1             | 1            | 1      |
| biological_process        | GO:0140014   | mitotic nuclear division                            | 1             | 1            | 1      |
| biological_process        | GO:1903047   | mitotic cell cycle process                          | 1             | 1            | 1      |
| biological_process        | GO:007059    | chromosome segregation                              | 1             | 1            | 1      |
| biological_process        | GO:0019439   | aromatic compound catabolic process                 | 1             | 1            | 1      |
| biological_process        | GO:0034655   | nucleobase-containing compound catabolic process    | 1             | 1            | 1      |
| biological_process        | GO:0044270   | cellular nitrogen compound catabolic process        | 1             | 1            | 1      |
| biological_process        | GO:0046700   | heterocycle catabolic process                       | 1             | 1            | 1      |
| biological_process        | GO:1901361   | organic cyclic compound catabolic process           | 1             | 1            | 1      |
| biological_process        | GO:1901575   | organic substance catabolic process                 | 1             | 1            | 1      |
| biological_process        | GO:0006396   | RNA processing                                      | 1             | 1            | 1      |
| biological_process        | GO:0006397   | mRNA processing                                     | 1             | 1            | 1      |
| biological_process        | GO:0016071   | mRNA metabolic process                              | 1             | 1            | 1      |
| biological_process        | GO:0051301   | cell division                                       | 1             | 1            | 1      |
| biological_process        | GO:0042254   | ribosome biogenesis                                 | 1             | 1            | 1      |
| biological_process        | GO:0022613   | ribonucleoprotein complex biogenesis                | 1             | 1            | 1      |
| biological_process        | GO:0016070   | RNA metabolic process                               | 1             | 1            | 1      |
| biological_process        | GO:0040007   | growth                                              | 1             | 1            | 1      |
| biological_process        | GO:0000278   | mitotic cell cycle                                  | 1             | 1            | 1      |
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| biological_process        | GO:0071840  | cellular component organization or biogenesis| 1.06E-05      | 0            | 0.001741165|
| biological_process        | GO:0009987  | cellular process                              | 0.001053662   | 0.042        | 0.064736089|
| biological_process        | GO:0022613  | ribonucleoprotein complex biogenesis          | 0.001349684    | 0.048        | 0.064736089|
| biological_process        | GO:0042254  | ribosome biogenesis                           | 0.001578929    | 0.06         | 0.064736089|
| biological_process        | GO:0044085  | cellular component biogenesis                 | 0.00245798     | 0.095        | 0.080621753|
| biological_process        | GO:0016043  | cellular component organization               | 0.003418112    | 0.13         | 0.083263927|
| biological_process        | GO:000902   | cell morphogenesis                            | 0.00604121     | 0.221        | 0.083263927|
| biological_process        | GO:0032989  | cellular component morphogenesis              | 0.00604121     | 0.221        | 0.083263927|
| biological_process        | GO:0006124  | translation                                   | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0006518  | peptide metabolic process                     | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0009059  | macromolecule biosynthetic process            | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0034645  | cellular macromolecule biosynthetic process   | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0043043  | peptide biosynthetic process                  | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0043603  | cellular amide metabolic process              | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0043604  | amide biosynthetic process                    | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0044249  | cellular biosynthetic process                 | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0044271  | cellular nitrogen compound biosynthetic process| 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:1901566  | organonitrogen compound biosynthetic process | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:1901576  | organic substance biosynthetic process        | 0.009646431    | 0.335        | 0.083263927|
| biological_process        | GO:0009058  | biosynthetic process                          | 0.013939565    | 0.425        | 0.114304434|
| biological_process        | GO:0010467  | gene expression                               | 0.014676231    | 0.456        | 0.114614376|
| biological_process        | GO:0008152  | metabolic process                             | 0.024770389    | 0.609        | 0.179443035|
| biological_process        | GO:0006790  | sulfur compound metabolic process             | 0.025165791    | 0.62         | 0.179443035|
| biological_process        | GO:1901564  | organonitrogen compound metabolic process     | 0.043934443    | 0.771        | 0.300218694|
| biological_process        | GO:0044281  | small molecule metabolic process              | 0.053966828    | 0.816        | 0.354022393|
| biological_process        | GO:006810   | transport                                     | 0.066392058    | 0.874        | 0.396157912|
| biological_process        | GO:0051234  | establishment of localization                 | 0.066392058    | 0.874        | 0.396157912|
| biological_process        | GO:0051186  | cofactor metabolic process                    | 0.069859781    | 0.891        | 0.396157912|
| biological_process        | GO:0051179  | localization                                  | 0.072176341    | 0.902        | 0.396157912|
| biological_process        | GO:0044238  | primary metabolic process                     | 0.074883508    | 0.911        | 0.396157912|
| biological_process        | GO:0071704  | organic substance metabolic process           | 0.074883508    | 0.911        | 0.396157912|
| biological_process        | GO:0044267  | cellular protein metabolic process            | 0.095434595    | 0.952        | 0.4891023   |
| cardiovascular_process    | GO:0040011  | locomotion                                    | 0.103200534    | 0.965        | 0.512875382|
| biological_process        | GO:0009653  | anatomical structure morphogenesis            | 0.12812015     | 0.984        | 0.574452123|
| biological_process        | GO:0007267  | cell-cell signaling                           | 0.131590292    | 0.984        | 0.574452123|
| biological_process        | GO:0019538  | protein metabolic process                     | 0.135767357    | 0.985        | 0.574452123|
| biological_process        | GO:006629   | lipid metabolic process                       | 0.152574468    | 0.992        | 0.574452123|
| biological_process        | GO:0022607  | cellular component assembly                   | 0.159648252    | 0.992        | 0.574452123|
| biological_process        | GO:0048869  | cellular developmental process                | 0.168998263    | 0.993        | 0.574452123|
| biological_process        | GO:0003013  | circulatory system process                    | 0.17122575     | 0.995        | 0.574452123|
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| biological_process | GO:0005975 | carbohydrate metabolic process                         | 0.178265402   | 0.995        | 0.574452123 |
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| biological_process | GO:0007010 | cytoskeleton organization                              | 0.190082851   | 0.995        | 0.574452123 |
| biological_process | GO:004237 | cellular metabolic process                             | 0.19362453    | 0.995        | 0.574452123 |
| biological_process | GO:0006996 | organelle organization                                 | 0.198360394   | 0.998        | 0.574452123 |
| biological_process | GO:0034330 | cell junction organization                              | 0.201938732   | 0.999        | 0.574452123 |
| biological_process | GO:0006807 | nitrogen compound metabolic process                    | 0.203797937   | 0.999        | 0.574452123 |
| biological_process | GO:0006457 | protein folding                                        | 0.212263833   | 0.999        | 0.574452123 |
| biological_process | GO:0055085 | transmembrane transport                                | 0.224126734   | 0.999        | 0.574452123 |
| biological_process | GO:0006091 | generation of precursor metabolites and energy         | 0.228412211   | 0.999        | 0.574452123 |
| biological_process | GO:0006082 | organic acid metabolic process                         | 0.234093385   | 0.999        | 0.574452123 |
| biological_process | GO:0006520 | cellular amino acid metabolic process                  | 0.234093385   | 0.999        | 0.574452123 |
| biological_process | GO:0019752 | carboxylic acid metabolic process                      | 0.234093385   | 0.999        | 0.574452123 |
| biological_process | GO:0043436 | o xoacid metabolic process                              | 0.234093385   | 0.999        | 0.574452123 |
| biological_process | GO:0007155 | cell adhesion                                          | 0.234479675   | 0.999        | 0.574452123 |
| biological_process | GO:0022610 | biological adhesion                                    | 0.234479675   | 0.999        | 0.574452123 |
| biological_process | GO:0006605 | protein targeting                                      | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0006886 | intracellular protein transport                        | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0008104 | protein localization                                   | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0015031 | protein transport                                      | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0015833 | peptide transport                                     | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0033036 | macromolecule localization                             | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0034613 | cellular protein localization                          | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0042886 | amide transport                                        | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0045184 | establishment of protein localization                  | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0070727 | cellular macromolecule localization                    | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0071702 | organic substance transport                            | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0071705 | nitrogen compound transport                            | 0.238187465   | 0.999        | 0.574452123 |
| biological_process | GO:0032502 | developmental process                                  | 0.25451468    | 1            | 0.604933443 |
| biological_process | GO:0048856 | anatomical structure development                       | 0.27600911    | 1            | 0.646630705 |
| biological_process | GO:0034641 | cellular nitrogen compound metabolic process growth    | 0.299472113    | 1            | 0.691738401 |
| biological_process | GO:0040007 |                                     | 0.308640182    | 1            | 0.703013748 |
| biological_process | GO:0044260 | cellular macromolecule metabolic process              | 0.315591782    | 1            | 0.709000715 |
| biological_process | GO:0043170 | macromolecule metabolic process                        | 0.348286904    | 1            | 0.733597838 |
| biological_process | GO:0043933 | protein-containing complex subunit organization       | 0.352569703    | 1            | 0.733597838 |
| biological_process | GO:0065003 | protein-containing complex assembly                    | 0.352569703    | 1            | 0.733597838 |
| biological_process | GO:0006396 | RNA processing                                        | 0.359854261    | 1            | 0.733597838 |
| biological_process | GO:0006397 | mRNA processing                                       | 0.359854261    | 1            | 0.733597838 |
| biological_process | GO:0016071 | mRNA metabolic process                                | 0.359854261    | 1            | 0.733597838 |
| biological_process | GO:0061024 | membrane organization                                 | 0.361092246    | 1            | 0.733597838 |
| biological_process | GO:0007568 | aging                                                 | 0.363030875    | 1            | 0.733597838 |
| biological_process | GO:0071554 | cell wall organization or biogenesis                  | 0.366798919    | 1            | 0.733597838 |
| biological_process | GO:0016192 | vesicle-mediated transport                            | 0.388735272    | 1            | 0.746392249 |
| biological_process | GO:0007154 | cell communication                                    | 0.39152288     | 1            | 0.746392249 |

47
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| biological_process        | GO:0043412| macromolecule modification                     | 0.400503158   | 1            | 0.746392249 |
| biological_process        | GO:0042592| homeostatic process                            | 0.428903071   | 1            | 0.777220411 |
| biological_process        | GO:0065008| regulation of biological quality               | 0.428903071   | 1            | 0.777220411 |
| biological_process        | GO:0030705| cytoskeleton-dependent intracellular transport | 0.431262545   | 1            | 0.777220411 |
| biological_process        | GO:0007275| multicellular organism development             | 0.485004615   | 1            | 0.851787083 |
| biological_process        | GO:0009790| embryo development                             | 0.485004615   | 1            | 0.851787083 |
| biological_process        | GO:0051604| protein maturation                             | 0.511338541   | 1            | 0.851787083 |
| biological_process        | GO:0022618| ribonucleoprotein complex assembly             | 0.512766771   | 1            | 0.851787083 |
| biological_process        | GO:0034622| cellular protein-containing complex assembly    | 0.512766771   | 1            | 0.851787083 |
| biological_process        | GO:0071826| ribonucleoprotein complex subunit organization  | 0.512766771   | 1            | 0.851787083 |
| biological_process        | GO:0051276| chromosome organization                        | 0.527423946   | 1            | 0.851787083 |
| biological_process        | GO:0069194| autophagy                                      | 0.528298514   | 1            | 0.851787083 |
| biological_process        | GO:0061919| process utilizing autophagic mechanism          | 0.528298514   | 1            | 0.851787083 |
| biological_process        | GO:006928 | movement of cell or subcellular component      | 0.534963839   | 1            | 0.851787083 |
| biological_process        | GO:0048870| cell motility                                  | 0.534963839   | 1            | 0.851787083 |
| biological_process        | GO:0051974| localization of cell                           | 0.534963839   | 1            | 0.851787083 |
| biological_process        | GO:0051301| cell division                                  | 0.556106096   | 1            | 0.876936537 |
| biological_process        | GO:006950 | response to stress                             | 0.616557136   | 1            | 0.924210792 |
| biological_process        | GO:0065007| biological regulation                          | 0.619234404   | 1            | 0.924210792 |
| biological_process        | GO:0007034| vacuolar transport                             | 0.620165163   | 1            | 0.924210792 |
| biological_process        | GO:0046907| intracellular transport                        | 0.622360589   | 1            | 0.924210792 |
| biological_process        | GO:0051641| cellular localization                          | 0.622360589   | 1            | 0.924210792 |
| biological_process        | GO:0051649| establishment of localization in cell          | 0.622360589   | 1            | 0.924210792 |
| biological_process        | GO:0016070| RNA metabolic process                          | 0.633448753   | 1            | 0.924210792 |
| biological_process        | GO:0021700| developmental maturation                       | 0.633665138   | 1            | 0.924210792 |
| biological_process        | GO:0007005| mitochondrion organization                     | 0.636803778   | 1            | 0.924210792 |
| biological_process        | GO:0050896| response to stimulus                           | 0.661702481   | 1            | 0.947510784 |
| biological_process        | GO:0048473| pigmentation                                   | 0.668893693   | 1            | 0.947510784 |
| biological_process        | GO:0030198| extracellular matrix organization              | 0.67596806    | 1            | 0.947510784 |
| biological_process        | GO:0043062| extracellular structure organization            | 0.67596806    | 1            | 0.947510784 |
| biological_process        | GO:0007165| signal transduction                            | 0.715783728   | 1            | 0.970153151 |
| biological_process        | GO:0050789| regulation of biological process               | 0.715783728   | 1            | 0.970153151 |
| biological_process        | GO:0050794| regulation of cellular process                 | 0.715783728   | 1            | 0.970153151 |
| biological_process        | GO:0051716| cellular response to stimulus                  | 0.715783728   | 1            | 0.970153151 |
| biological_process        | GO:0006259| DNA metabolic process                          | 0.803769892   | 1            | 1         |
| biological_process        | GO:0090304| nucleic acid metabolic process                 | 0.815500516   | 1            | 1         |
| biological_process        | GO:008219 | cell death                                     | 0.819185541   | 1            | 1         |
| biological_process        | GO:0044403| symbiont process                               | 0.825557148   | 1            | 1         |
| biological_process        | GO:0044419| interspecies interaction between organisms      | 0.825557148   | 1            | 1         |
| biological_process        | GO:0051704| multi-organism process                         | 0.825557148   | 1            | 1         |
| biological_process        | GO:0000003| reproduction                                   | 0.847166808   | 1            | 1         |
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| biological_process | GO:0032501         | multicellular organismal process                          | 0.85244846    | 1            | 1      |
| biological_process | GO:0002376         | immune system process                                     | 0.863456662   | 1            | 1      |
| biological_process | GO:0048646         | anatomical structure formation involved in morphogenesis  | 0.904945927   | 1            | 1      |
| biological_process | GO:0007059         | chromosome segregation                                    | 0.912899052   | 1            | 1      |
| biological_process | GO:0009056         | catabolic process                                         | 0.92837298    | 1            | 1      |
| biological_process | GO:0006139         | nucleobase-containing compound metabolic process          | 0.946192676   | 1            | 1      |
| biological_process | GO:0007225         | cellular aromatic compound metabolic process              | 0.946192676   | 1            | 1      |
| biological_process | GO:0046483         | heterocycle metabolic process                             | 0.946192676   | 1            | 1      |
| biological_process | GO:1901360         | organic cyclic compound metabolic process                 | 0.946192676   | 1            | 1      |
| biological_process | GO:0006399         | tRNA metabolic process                                    | 0.949763075   | 1            | 1      |
| biological_process | GO:0034660         | ncRNA metabolic process                                   | 0.949763075   | 1            | 1      |
| biological_process | GO:0007049         | cell cycle                                               | 0.964901836   | 1            | 1      |
| biological_process | GO:0044248         | cellular catabolic process                                | 0.971927658   | 1            | 1      |
| biological_process | GO:0003008         | system process                                           | 0.974387194   | 1            | 1      |
| biological_process | GO:0008283         | cell proliferation                                       | 0.990351413   | 1            | 1      |
| biological_process | GO:000278          | mitotic cell cycle                                       | 0.996615052   | 1            | 1      |
| biological_process | GO:0050877         | nervous system process                                   | 0.998464955   | 1            | 1      |
| biological_process | GO:0008150         | biological_process                                       | 1             | 1            | 1      |
| biological_process | GO:0071941         | nitrogen cycle metabolic process                          | 1             | 1            | 1      |
| biological_process | GO:0032196         | transposition                                            | 1             | 1            | 1      |
| biological_process | GO:0007049         | plasma membrane organization                             | 1             | 1            | 1      |
| biological_process | GO:0010256         | endomembrane system organization                         | 1             | 1            | 1      |
| biological_process | GO:0019748         | secondary metabolic process                               | 1             | 1            | 1      |
| biological_process | GO:0006913         | nucleocytoplasmic transport                              | 1             | 1            | 1      |
| biological_process | GO:0051169         | nuclear transport                                        | 1             | 1            | 1      |
| biological_process | GO:0000280         | nuclear division                                         | 1             | 1            | 1      |
| biological_process | GO:0022402         | cell cycle process                                       | 1             | 1            | 1      |
| biological_process | GO:0048285         | organelle fission                                        | 1             | 1            | 1      |
| biological_process | GO:0140014         | mitotic nuclear division                                 | 1             | 1            | 1      |
| biological_process | GO:1903047         | mitotic cell cycle process                                | 1             | 1            | 1      |
| biological_process | GO:0019439         | aromatic compound catabolic process                      | 1             | 1            | 1      |
| biological_process | GO:0034655         | nucleobase-containing compound catabolic process          | 1             | 1            | 1      |
| biological_process | GO:0044270         | cellular nitrogen compound catabolic process             | 1             | 1            | 1      |
| biological_process | GO:0046700         | heterocycle catabolic process                            | 1             | 1            | 1      |
| biological_process | GO:1901361         | organic cyclic compound catabolic process                 | 1             | 1            | 1      |
| biological_process | GO:1901575         | organic substance catabolic process                       | 1             | 1            | 1      |
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| biological_process        | GO:0071941  | nitrogen cycle metabolic process                              | 0.004596994   | 0.19         | 0.38951373 |
| biological_process        | GO:0006259  | DNA metabolic process                                         | 0.011963106   | 0.411        | 0.38951373 |
| biological_process        | GO:0044260  | cellular macromolecule metabolic process                     | 0.012425921   | 0.42         | 0.38951373 |
| biological_process        | GO:006464   | cellular protein modification process                         | 0.014250502   | 0.462        | 0.38951373 |
| biological_process        | GO:0036211  | protein modification process                                  | 0.014250502   | 0.462        | 0.38951373 |
| biological_process        | GO:0043412  | macromolecule modification                                   | 0.014250502   | 0.462        | 0.38951373 |
| biological_process        | GO:0051276  | chromosome organization                                       | 0.020695666   | 0.562        | 0.4848699  |
| biological_process        | GO:0009987  | cellular process                                              | 0.021059341   | 0.975        | 0.94424454 |
| biological_process        | GO:0000280  | nuclear division                                              | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0022402  | cell cycle process                                            | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0048285  | organelle fission                                             | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0140014  | mitotic nuclear division                                      | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:1901564  | organonitrogen compound metabolic process                     | 0.119146254   | 0.987        | 0.94424454 |
| biological_process        | GO:0044287  | cellular protein metabolic process                            | 0.105159341   | 0.975        | 0.94424454 |
| biological_process        | GO:000280   | metabolic process                                             | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0022402  | cell cycle process                                            | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0048285  | organelle fission                                             | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0009056  | catabolic process                                             | 0.113419842   | 0.979        | 0.94424454 |
| biological_process        | GO:0000679  | catabolic process                                             | 0.291524051   | 1            | 1          |
| biological_process        | GO:0090304  | nucleic acid metabolic process                                | 0.304837486   | 1            | 1          |
| biological_process        | GO:0022618  | ribonucleoprotein complex assembly                            | 0.308203039   | 1            | 1          |
| biological_process        | GO:0034622  | cellular protein-containing complex assembly                 | 0.308203039   | 1            | 1          |
| biological_process        | GO:0071826  | ribonucleoprotein complex subunit organization               | 0.308203039   | 1            | 1          |
| biological_process        | GO:006996   | organelle organization                                       | 0.323962456   | 1            | 1          |
| biological_process        | GO:006139   | nucleobase-containing compound metabolic process             | 0.32488387    | 1            | 1          |
| biological_process        | GO:006725   | cellular aromatic compound metabolic process                 | 0.32488387    | 1            | 1          |
| biological_process        | GO:006483   | heterocycle metabolic process                                | 0.32488387    | 1            | 1          |
| biological_process        | GO:1901360  | organic cyclic compound metabolic process                    | 0.32488387    | 1            | 1          |
| biological_process        | GO:016043   | cellular component organization                              | 0.330666898   | 1            | 1          |
| biological_process        | GO:006790   | sulfur compound metabolic process                             | 0.344946803   | 1            | 1          |
| biological_process        | GO:005089   | response to stimulus                                         | 0.375493445   | 1            | 1          |
| biological_process        | GO:000278   | mitotic cell cycle                                           | 0.390477332   | 1            | 1          |
| biological_process        | GO:007049   | cell cycle                                                   | 0.39040683    | 1            | 1          |
| biological_process        | GO:0071840  | cellular component organization or biogenesis               | 0.391468641   | 1            | 1          |
| biological_process        | GO:0007009  | plasma membrane organization                                 | 0.420109841   | 1            | 1          |
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| biological_process  | GO:0010256 | endomembrane system organization      | 0.420109841   | 1            | 1      |
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| biological_process  | GO:002610  | biological adhesion                   | 0.426379461   | 1            | 1      |
| biological_process  | GO:0006457 | protein folding                       | 0.443671225   | 1            | 1      |
| biological_process  | GO:0034330 | cell junction organization             | 0.477563339   | 1            | 1      |
| biological_process  | GO:0051604 | protein maturation                    | 0.52873914    | 1            | 1      |
| biological_process  | GO:0019439 | aromatic compound catabolic process    | 0.543377088   | 1            | 1      |
| biological_process  | GO:0034655 | nucleobase-containing compound catabolic process | 0.543377088   | 1            | 1      |
| biological_process  | GO:0044270 | cellular nitrogen compound catabolic process | 0.543377088   | 1            | 1      |
| biological_process  | GO:0046700 | heterocycle catabolic process          | 0.543377088   | 1            | 1      |
| biological_process  | GO:1901361 | organic cyclic compound catabolic process | 0.543377088   | 1            | 1      |
| biological_process  | GO:1901575 | organic substance catabolic process    | 0.543377088   | 1            | 1      |
| biological_process  | GO:0000902 | cell morphogenesis                    | 0.544063053   | 1            | 1      |
| biological_process  | GO:0032989 | cellular component morphogenesis       | 0.544063053   | 1            | 1      |
| biological_process  | GO:0016192 | vesicle-mediated transport             | 0.551638793   | 1            | 1      |
| biological_process  | GO:0006500 | biological regulation                 | 0.57083738    | 1            | 1      |
| biological_process  | GO:0002376 | immune system process                 | 0.58218119    | 1            | 1      |
| biological_process  | GO:0006950 | response to stress                    | 0.600011394   | 1            | 1      |
| biological_process  | GO:0022613 | ribonucleoprotein complex biogenesis  | 0.611317973   | 1            | 1      |
| biological_process  | GO:0008283 | cell proliferation                     | 0.623292303   | 1            | 1      |
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| biological_process  | GO:0048646 | involved in morphogenesis             | 0.645575671   | 1            | 1      |
| biological_process  | GO:0044248 | cellular catabolic process             | 0.646753605   | 1            | 1      |
| biological_process  | GO:0007165 | signal transduction                   | 0.654188707   | 1            | 1      |
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| biological_process  | GO:0051716 | cellular response to stimulus          | 0.654188707   | 1            | 1      |
| biological_process  | GO:0009653 | anatomical structure formation         | 0.673885968   | 1            | 1      |
| biological_process  | GO:0007154 | cell communication                    | 0.691186605   | 1            | 1      |
| biological_process  | GO:0023052 | signaling                             | 0.691186605   | 1            | 1      |
| biological_process  | GO:0051186 | cofactor metabolic process             | 0.729432783   | 1            | 1      |
| biological_process  | GO:0006913 | nucleocytoplasmic transport           | 0.735289987   | 1            | 1      |
| biological_process  | GO:0051169 | nuclear transport                     | 0.735289987   | 1            | 1      |
| biological_process  | GO:0030154 | cell differentiation                  | 0.735695164   | 1            | 1      |
| biological_process  | GO:0008219 | cell death                            | 0.739428246   | 1            | 1      |
| biological_process  | GO:0043933 | protein-containing complex subunit     | 0.747869356   | 1            | 1      |
| biological_process  | GO:0065003 | protein-containing complex assembly    | 0.747869356   | 1            | 1      |
| biological_process  | GO:006914  | protein-containing complex autophagy   | 0.755431047   | 1            | 1      |
| biological_process  | GO:0061919 | process utilizing autophagic mechanism | 0.755431047   | 1            | 1      |
| biological_process  | GO:0003013 | circulatory system process             | 0.775346593   | 1            | 1      |
| biological_process  | GO:0048869 | cellular developmental process         | 0.778557326   | 1            | 1      |
| biological_process  | GO:0042254 | ribosome biogenesis                   | 0.782503945   | 1            | 1      |
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| biological_process        | GO:0006399  | tRNA metabolic process              | 0.811500514   | 1            | 1      |
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| biological_process        | GO:0042592  | homeostatic process                 | 0.825763053   | 1            | 1      |
| biological_process        | GO:0065008  | regulation of biological quality    | 0.825763053   | 1            | 1      |
| biological_process        | GO:007568   | aging                              | 0.826622932   | 1            | 1      |
| biological_process        | GO:0021700  | developmental maturation            | 0.829596269   | 1            | 1      |
| biological_process        | GO:0007005  | mitochondrion organization          | 0.831632086   | 1            | 1      |
| biological_process        | GO:0040007  | growth                             | 0.840847148   | 1            | 1      |
| biological_process        | GO:0034641  | cellular nitrogen compound          | 0.855455086   | 1            | 1      |
| biological_process        | GO:0061024  | membrane organization               | 0.883703358   | 1            | 1      |
| biological_process        | GO:0022607  | cellular component assembly         | 0.890133706   | 1            | 1      |
| biological_process        | GO:0032502  | developmental process               | 0.89887734    | 1            | 1      |
| biological_process        | GO:0006810  | transport                          | 0.905196187   | 1            | 1      |
| biological_process        | GO:0051234  | establishment of localization       | 0.905196187   | 1            | 1      |
| biological_process        | GO:0003008  | system process                      | 0.90769941    | 1            | 1      |
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| biological_process        | GO:0005975  | carbohydrate metabolic process      | 0.921327947   | 1            | 1      |
| biological_process        | GO:0006629  | lipid metabolic process             | 0.949040387   | 1            | 1      |
| biological_process        | GO:0040011  | locomotion                          | 0.953150599   | 1            | 1      |
| biological_process        | GO:0007267  | cell-cell signaling                 | 0.955444497   | 1            | 1      |
| biological_process        | GO:0007275  | multicellular organism development  | 0.957872507   | 1            | 1      |
| biological_process        | GO:0009790  | embryo development                  | 0.957872507   | 1            | 1      |
| biological_process        | GO:0006412  | translation                         | 0.962000821   | 1            | 1      |
| biological_process        | GO:0006518  | peptide metabolic process           | 0.962000821   | 1            | 1      |
| biological_process        | GO:0009059  | macromolecule biosynthetic process  | 0.962000821   | 1            | 1      |
| biological_process        | GO:0034645  | cellular macromolecule biosynthetic process | 0.962000821 | 1 | 1 |
| biological_process        | GO:0043043  | peptide biosynthetic process        | 0.962000821   | 1            | 1      |
| biological_process        | GO:0043603  | cellular amide metabolic process    | 0.962000821   | 1            | 1      |
| biological_process        | GO:0043604  | amide biosynthetic process          | 0.962000821   | 1            | 1      |
| biological_process        | GO:0044249  | cellular biosynthetic process       | 0.962000821   | 1            | 1      |
| biological_process        | GO:0044271  | cellular nitrogen compound          | 0.962000821   | 1            | 1      |
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| biological_process        | GO:1901576  | organic substance biosynthetic process localization | 0.962000821 | 1 | 1 |
| biological_process        | GO:0051179  | small molecule metabolic process    | 0.970255898    | 1            | 1      |
| biological_process        | GO:0044281  | multicytoplasmal metabolism         | 0.975433312    | 1            | 1      |
| biological_process        | GO:0006082  | organic acid metabolic process      | 0.978816461   | 1            | 1      |
| biological_process        | GO:0006520  | cellular amino acid metabolic process | 0.978816461 | 1 | 1 |
| biological_process        | GO:0019752  | carboxylic acid metabolic process   | 0.978816461   | 1            | 1      |
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| biological_process  | GO:0051301      | cell division                                                             | 0.986811841   | 1            | 1      |
| biological_process  | GO:0046907      | intracellular transport                                                   | 0.991070368   | 1            | 1      |
| biological_process  | GO:0051641      | cellular localization                                                     | 0.991070368   | 1            | 1      |
| biological_process  | GO:0051649      | establishment of localization in cell                                     | 0.991070368   | 1            | 1      |
| biological_process  | GO:0010467      | gene expression                                                           | 0.994152793   | 1            | 1      |
| biological_process  | GO:0006928      | movement of cell or subcellular component                                  | 0.994270882   | 1            | 1      |
| biological_process  | GO:0048870      | cell motility                                                             | 0.994270882   | 1            | 1      |
| biological_process  | GO:0051674      | localization of cell                                                      | 0.994270882   | 1            | 1      |
| biological_process  | GO:0016070      | RNA metabolic process                                                     | 0.994305797   | 1            | 1      |
| biological_process  | GO:0055085      | transmembrane transport                                                   | 0.99744064    | 1            | 1      |
| biological_process  | GO:0006396      | RNA processing                                                            | 0.997842852   | 1            | 1      |
| biological_process  | GO:0006397      | mRNA processing                                                           | 0.997842852   | 1            | 1      |
| biological_process  | GO:0016071      | mRNA metabolic process                                                    | 0.997842852   | 1            | 1      |
| biological_process  | GO:0008150      | biological_process                                                        | 1             | 1            | 1      |
| biological_process  | GO:0032196      | transposition                                                             | 1             | 1            | 1      |
| biological_process  | GO:0071554      | cell wall organization or biogenesis                                       | 1             | 1            | 1      |
| biological_process  | GO:0030198      | extracellular matrix organization                                         | 1             | 1            | 1      |
| biological_process  | GO:0043062      | extracellular structure organization                                       | 1             | 1            | 1      |
| biological_process  | GO:0019748      | secondary metabolic process                                               | 1             | 1            | 1      |
| biological_process  | GO:0030705      | cytoskeleton-dependent intracellular transport                             | 1             | 1            | 1      |
| biological_process  | GO:0044403      | symbiont process                                                          | 1             | 1            | 1      |
| biological_process  | GO:0044419      | interspecies interaction between organisms                                 | 1             | 1            | 1      |
| biological_process  | GO:0051704      | multi-organism process                                                    | 1             | 1            | 1      |
| biological_process  | GO:0043473      | pigmentation                                                              | 1             | 1            | 1      |
| biological_process  | GO:0006605      | protein targeting                                                         | 1             | 1            | 1      |
| biological_process  | GO:0006886      | intracellular protein transport                                           | 1             | 1            | 1      |
| biological_process  | GO:0008104      | protein localization                                                      | 1             | 1            | 1      |
| biological_process  | GO:0015031      | protein transport                                                         | 1             | 1            | 1      |
| biological_process  | GO:0015833      | peptide transport                                                         | 1             | 1            | 1      |
| biological_process  | GO:0033036      | macromolecule localization                                                | 1             | 1            | 1      |
| biological_process  | GO:0034613      | cellular protein localization                                             | 1             | 1            | 1      |
| biological_process  | GO:0042886      | amide transport                                                           | 1             | 1            | 1      |
| biological_process  | GO:0045184      | establishment of protein localization                                     | 1             | 1            | 1      |
| biological_process  | GO:0070727      | cellular macromolecule localization                                       | 1             | 1            | 1      |
| biological_process  | GO:0071702      | organic substance transport                                               | 1             | 1            | 1      |
| biological_process  | GO:0071705      | nitrogen compound transport                                               | 1             | 1            | 1      |
| biological_process  | GO:0006091      | generation of precursor metabolites and energy                             | 1             | 1            | 1      |
| Orthogroup | No. codons | omega spiders/scorpions | omega Acariformes | RELAX null log-likelihood | RELAX alternative log-likelihood | RELAX K parameter | p-value | SGoF adjusted p-value |
|------------|------------|-------------------------|------------------|--------------------------|-------------------------------|-----------------|---------|----------------------|
| OG0002034  | 428        | 0.017                   | 0.1167           | -13259.34                | -13249.87                    | 0.2             | 0       | 0.0016               |
| OG0002407  | 218        | 0.0119                  | 0.015            | -4187.74                 | -4161.53                     | 7.06            | 0       | 0.0016               |
| OG0003444  | 788        | 0.0052                  | 0.0085           | -17427.94                | -17419.58                    | 0.61            | 0       | 0.0016               |
| OG0004159  | 314        | 0.0217                  | 0.0095           | -7561.59                 | -7552.82                     | 1.06            | 0       | 0.0016               |
| OG0004254  | 309        | 0.0098                  | 0.0539           | -6969.44                 | -6958                         | 0.18            | 0       | 0.0016               |
| OG0004266  | 327        | 0.0478                  | 0.0565           | -8694.06                 | -8572.65                     | 0.83            | 0       | 0.0016               |
| OG0004288  | 430        | 0.0156                  | 0.0136           | -11033.26                | -11003.13                    | 1.04            | 0       | 0.0016               |
| OG0004689  | 1081       | 0.0076                  | 0.0264           | -24156.75                | -24139.02                    | 0.23            | 0       | 0.0016               |
| OG0004728  | 321        | 0.0376                  | 0.0319           | -10692.35                | -10594.26                    | 0.8             | 0       | 0.0016               |
| OG0005109  | 377        | 0.0114                  | 0.0363           | -15384.38                | -15147.02                    | 0.94            | 0       | 0.0016               |
| OG0005307  | 424        | 0.034                   | 0.0499           | -12364.88                | -12345.49                    | 0.89            | 0       | 0.0016               |
| OG0005333  | 150        | 0.0519                  | 0.0095           | -4480.29                 | -4466                        | 0.95            | 0       | 0.0016               |
| OG0005379  | 2046       | 0.0029                  | 0.0133           | -43386.9                 | -43362.39                    | 0.12            | 0       | 0.0016               |
| OG0005399  | 1044       | 0.0065                  | 0.0348           | -24099.55                | -24072.93                    | 0.59            | 0       | 0.0016               |
| OG0005576  | 215        | 0.029                   | 0.0378           | -5198.53                 | -5185.13                     | 1.3             | 0       | 0.0016               |
| OG0004832  | 286        | 4.00E-04                | 0.0163           | -6682.25                 | -6674.83                     | 0.28            | 1.00E-04 | 0.0022               |
| OG0004978  | 351        | 0.0153                  | 0.0332           | -9854.15                 | -9846.65                     | 0.19            | 1.00E-04 | 0.0022               |
| OG0005329  | 277        | 0.0081                  | 0.0449           | -6422.48                 | -6414.41                     | 0.33            | 1.00E-04 | 0.0022               |
| OG0003260  | 167        | 0.0171                  | 0.0631           | -6243.69                 | -6236.97                     | 0.98            | 2.00E-04 | 0.0027               |
| OG0005149  | 142        | 0.0018                  | 0.0399           | -3207.27                 | -3200.3                      | 0.11            | 2.00E-04 | 0.0027               |
| OG0005207  | 453        | 0.0036                  | 0.0367           | -13138.53                | -13132.09                    | 0.26            | 3.00E-04 | 0.0029               |
| OG0004223  | 567        | 0.0572                  | 0.0851           | -17248.81                | -17242.59                    | 0.57            | 4.00E-04 | 0.003                |
| OG0005045  | 188        | 0.0221                  | 0.0989           | -6137.99                 | -6132.18                     | 0.37            | 6.00E-04 | 0.0038               |
| OG0005391  | 371        | 0.0113                  | 0.0463           | -9145.95                 | -9140.01                     | 0.17            | 6.00E-04 | 0.0038               |
| OG0005680  | 88         | 0.0546                  | 0.1453           | -3014.85                 | -3009.11                     | 0.27            | 7.00E-04 | 0.0041               |
| Orthogroup | No. codons | omega spiders/scorpions | omega Acariformes | RELAX null log-likelihood | RELAX alternative log-likelihood | RELAX K parameter | p-value | SGoF adjusted p-value |
|------------|------------|-------------------------|------------------|--------------------------|-------------------------------|-------------------|--------|---------------------|
| OG0002809 | 149        | 0                       | 0.0366           | -2594.95                | -2594.95                      | 0.3               | 8.00E-04 | 0.0046              |
| OG0004780 | 100        | 0.0925                  | 0.0369           | -3582.18                | -3576.68                      | 7.82              | 9.00E-04 | 0.0046              |
| OG0004758 | 330        | 0.0271                  | 0.0695           | -10269.7                | -10264.39                     | 0.42              | 0.0011 | 0.0054              |
| OG0006117 | 163        | 0.044                   | 0.109            | -5221.8                 | -5216.49                      | 0.35              | 0.0011 | 0.0054              |
| OG0005638 | 350        | 0.0402                  | 0.0956           | -12133.98               | -12128.93                     | 0.51              | 0.0015 | 0.006               |
| OG0004759 | 259        | 0.0396                  | 0.1112           | -8633.59                | -8628.62                      | 0.28              | 0.0016 | 0.0061              |
| OG0003950 | 61         | 0.0153                  | 0.0751           | -1353.06                | -1348.12                      | 0                | 0.0017 | 0.0062              |
| OG0004588 | 469        | 0.0436                  | 0.0713           | -15374.31               | -15369.55                     | 0.49              | 0.002   | 0.007               |
| OG0005213 | 561        | 0.0107                  | 0.0281           | -14909.26               | -14904.47                     | 0.53              | 0.002   | 0.007               |
| OG0004162 | 173        | 0.041                   | 0.0341           | -5110.09                | -5105.41                      | 0.87              | 0.0022 | 0.008               |
| OG0004440 | 412        | 0.0638                  | 0.0198           | -14186.21               | -14181.71                     | 1.39              | 0.0027 | 0.0093              |
| OG0005766 | 134        | 0.0053                  | 0.0516           | -2915.81                | -2911.31                      | 0.59              | 0.0027 | 0.0093              |
| OG0004091 | 192        | 0.3278                  | 0.0372           | -7325.68                | -7321.24                      | 1.71              | 0.0029 | 0.0096              |
| OG0004892 | 224        | 0.0147                  | 0.0782           | -6261.06                | -6256.67                      | 0.3               | 0.003   | 0.01                |
| OG0003839 | 391        | 0.0372                  | 0.0207           | -10347.54               | -10343.18                     | 1.56              | 0.0031 | 0.01                |
| OG0005016 | 407        | 0.0576                  | 0.0659           | -12817.98               | -12813.72                     | 0.52              | 0.0035 | 0.0101              |
| OG0005234 | 190        | 0.0108                  | 0.0426           | -4713.81                | -4709.62                      | 0.07              | 0.0038 | 0.0115              |
| OG0004861 | 364        | 0.0607                  | 0.0299           | -13706.89               | -13702.76                     | 1.62              | 0.0041 | 0.0115              |
| OG0004043 | 415        | 0.0643                  | 0.1034           | -11885.11               | -11881.08                     | 0.44              | 0.0046 | 0.0126              |
| OG0004413 | 334        | 0.019                   | 0.0313           | -9566.34                | -9562.33                      | 0.56              | 0.0046 | 0.0126              |
| OG0004641 | 233        | 0.0499                  | 0.0169           | -7040.75                | -7036.74                      | 1.98              | 0.0046 | 0.0126              |
| OG0005182 | 271        | 0.0313                  | 0.0954           | -8352.15                | -8348.24                      | 0.9               | 0.0051 | 0.0137              |
| OG0004547 | 172        | 0.016                   | 0.029            | -3908.68                | -3904.81                      | 0.9               | 0.0054 | 0.014               |
| OG0002024 | 654        | 0.0375                  | 0.0088           | -16432.61               | -16428.84                     | 1.33              | 0.006  | 0.0169              |
| OG0003505 | 467        | 0.0166                  | 0.0419           | -10210.75               | -10206.99                     | 0.82              | 0.0061 | 0.0193              |
| OG0005256 | 1094       | 0.0251                  | 0.0353           | -31883                  | -31879.26                     | 0.57              | 0.0062 | 0.0204              |
| OG0004635 | 476        | 0.0542                  | 0.0117           | -16775.59               | -16771.94                     | 1.62              | 0.0069 | 0.0206              |
| OG0004378 | 173        | 0.0256                  | 0.1063           | -4524.58                | -4520.95                      | 0                | 0.007  | 0.022               |
| Orthogroup | No. codons | omega spiders/scorpions | omega Acariformes | RELAX null log-likelihood | RELAX alternative log-likelihood | RELAX K parameter | p-value | SGoF adjusted p-value |
|------------|------------|-------------------------|----------------|--------------------------|-------------------------------|-----------------|--------|----------------------|
| OG0005676  | 179        | 0.0098                  | 0.1094         | -6101.36                 | -6097.73                      | 0.58            | 0.007  | 0.022                |
| OG0005186  | 378        | 0.0495                  | 0.044          | -15037.93                | -15034.41                     | 1.45            | 0.008  | 0.023                |
| OG0004017  | 291        | 0.0229                  | 0.0677         | -7364.79                 | -7361.34                      | 0.76            | 0.0086 | 0.024                |
| OG0004305  | 429        | 0.1203                  | 0.0438         | -14437.74                | -14434.36                     | 2.42            | 0.0093 | 0.0239               |
| OG0003924  | 506        | 0.0206                  | 0.0127         | -12512.16                | -12508.78                     | 0.98            | 0.0094 | 0.026                |
| OG0004300  | 145        | 0.0135                  | 0.0217         | -3740.42                 | -3737.07                      | 0.61            | 0.0096 | 0.0265               |
| OG0004837  | 313        | 0.0399                  | 0.0669         | -8870.3                  | -8866.98                      | 0.19            | 0.01   | 0.0265               |
| OG0005898  | 552        | 0.0138                  | 0.0324         | -13351.42                | -13348.1                      | 0.84            | 0.01   | 0.0265               |
| OG0005894  | 470        | 0.0199                  | 0.0275         | -15476.05                | -15472.74                     | 0.26            | 0.0101 | 0.0272               |
| OG0005904  | 74         | 0.0989                  | 0.0082         | -2537.15                 | -2533.92                      | 3.2             | 0.011  | 0.0272               |
| OG0005073  | 311        | 0.023                   | 0.0559         | -9021.01                 | -9017.82                      | 0.35            | 0.0115 | 0.0367               |
| OG0005740  | 275        | 0.0309                  | 0.017          | -8375.01                 | -8371.81                      | 0.49            | 0.0115 | 0.0367               |
| OG0004516  | 162        | 0.005                   | 0.0309         | -4862.79                 | -4859.65                      | 0.62            | 0.0121 | 0.0426               |
| OG0006208  | 300        | 0.0523                  | 0.0107         | -9970.54                 | -9967.39                      | 1.99            | 0.0121 | 0.0426               |
| OG0005140  | 95         | 0.0108                  | 0.02           | -2004.77                 | -2001.65                      | 0.12            | 0.0126 | 0.0438               |
| OG0005335  | 306        | 0.0245                  | 0.0602         | -10288.85                | -10285.77                     | 0.3             | 0.0131 | 0.0446               |
| OG0002859  | 541        | 0.0375                  | 0.0728         | -15211.26                | -15208.22                     | 0.55            | 0.0137 | 0.0455               |
| OG0004385  | 151        | 0.0016                  | 0.0375         | -3452.5                  | -3449.48                      | 0.27            | 0.014  | 0.0458               |
| OG0004517  | 206        | 0.0083                  | 0.0263         | -4885.33                 | -4882.48                      | 0.51            | 0.0168 | 0.0458               |
| OG0004679  | 254        | 0.0069                  | 0.038          | -6848.1                  | -6845.25                      | 0.3             | 0.0169 | 0.0469               |
| OG0003752  | 407        | 0.0146                  | 0.0258         | -11245.13                | -11242.37                     | 0.67            | 0.0187 | 0.0483               |
| OG0004023  | 272        | 0.0524                  | 0.0115         | -8241.39                 | -8238.66                      | 1.55            | 0.0193 | 0.0552               |
| OG0004820  | 176        | 0.0043                  | 0.0151         | -4046.9                  | -4044.21                      | 0.55            | 0.0204 | 0.0559               |
| OG0004904  | 348        | 0.0281                  | 0.0191         | -12900.59                | -12897.91                     | 1.58            | 0.0206 | 0.0575               |
| OG0004476  | 161        | 0.0071                  | 0.0348         | -4747.48                 | -4744.8                       | 0.41            | 0.0207 | 0.0579               |
| OG0003594  | 266        | 0.0663                  | 0.0509         | -8150.71                 | -8148.05                      | 1.56            | 0.021  | 0.059                |
| OG0005293  | 303        | 0.033                   | 0.0475         | -9740.18                 | -9737.55                      | 0.48            | 0.022  | 0.0598               |
| OG0003623  | 429        | 0.0359                  | 0.0605         | -12515.04                | -12512.43                     | 0.39            | 0.0223 | 0.06     |
| Orthogroup     | No. codons | omega spiders/scorpions | omega Acariformes | RELAX null log-likelihood | RELAX alternative log-likelihood | RELAX K parameter | p-value | SGoF adjusted p-value |
|---------------|------------|-------------------------|-------------------|--------------------------|-------------------------------|------------------|---------|----------------------|
| OG0004344    | 251        | 0.0421                  | 0.0642            | -7706.79                 | -7704.18                      | 0.49             | 0.0224             | 0.0624               |
| OG0004032    | 166        | 0.0092                  | 0.0205            | -4373.66                 | -4371.09                      | 0.69             | 0.0236             | 0.0644               |
| OG0005080    | 222        | 0.0971                  | 0.0548            | -7666.12                 | -7663.57                      | 1.85             | 0.0239             | 0.0644               |
| OG0004875    | 203        | 0.0467                  | 0.0296            | -7117.15                 | -7114.64                      | 1.02             | 0.025              | 0.0646               |
| OG0003328    | 303        | 0.0065                  | 0.0332            | -8417.42                 | -8414.94                      | 0.59             | 0.026              | 0.0667               |
| OG0004207    | 308        | 0.0287                  | 0.0554            | -8614.88                 | -8612.42                      | 0.43             | 0.0265             | 0.0738               |
| OG0004610    | 160        | 0.0321                  | 0.0148            | -4714.14                 | -4711.68                      | 1.67             | 0.0265             | 0.0738               |
| OG0005091    | 665        | 0.0296                  | 0.0478            | -22186.84                | -22184.38                     | 0.67             | 0.0265             | 0.0738               |
| OG0005220    | 82         | 0.008                   | 0.0286            | -1989.11                 | -1986.66                      | 0.64             | 0.0271             | 0.074                |
| OG0004808    | 202        | 0.0258                  | 0.0211            | -7541.21                 | -7538.77                      | 0.92             | 0.0272             | 0.0767               |
| OG0005302    | 162        | 0.0482                  | 0.1364            | -5435.11                 | -5432.73                      | 0.5              | 0.029              | 0.0771               |
| OG0004568    | 240        | 0.0519                  | 0.0126            | -8080.54                 | -8078.22                      | 1.44             | 0.0312             | 0.0771               |
| OG0004646    | 194        | 0.0316                  | 0.0657            | -5612.66                 | -5610.42                      | 0.52             | 0.0342             | 0.0775               |
| OG0003453    | 555        | 0.0226                  | 0.0461            | -16930.38                | -16928.17                     | 0.52             | 0.0355             | 0.078                |
| OG0003205    | 609        | 0.0134                  | 0.0319            | -13237.18                | -13234.98                     | 0.73             | 0.0358             | 0.0822               |
| OG0004080    | 248        | 0.0265                  | 0.068             | -8774.73                 | -8772.55                      | 0.53             | 0.0367             | 0.083                |
| OG0005101    | 231        | 0.0483                  | 0.0253            | -8426.44                 | -8424.26                      | 1.35             | 0.0372             | 0.0848               |
### Table SI 15

| ontology          | node_id     | node_name                              | raw_p_overrep | FWER_overrep | qvalue     |
|-------------------|-------------|----------------------------------------|---------------|--------------|------------|
| biological_process| GO:0006396  | RNA processing                         | 0.000296311   | 0.008        | 0.009493355 |
| biological_process| GO:0006397  | mRNA processing                        | 0.000296311   | 0.008        | 0.009493355 |
| biological_process| GO:0016071  | mRNA metabolic process                 | 0.000296311   | 0.008        | 0.009493355 |
| biological_process| GO:0006464  | cellular protein modification process   | 0.00035379     | 0.012        | 0.009493355 |
| biological_process| GO:0036211  | protein modification process           | 0.00035379     | 0.012        | 0.009493355 |
| biological_process| GO:0043412  | macromolecule modification             | 0.00035379     | 0.012        | 0.009493355 |
| biological_process| GO:0044238  | primary metabolic process              | 0.001296222    | 0.058        | 0.024522172 |
| biological_process| GO:0071704  | organic substance metabolic process     | 0.001296222    | 0.058        | 0.024522172 |
| biological_process| GO:0016070  | RNA metabolic process                  | 0.00183788     | 0.076        | 0.024522172 |
| biological_process| GO:0006139  | nucleobase-containing compound metabolic process | 0.001980051 | 0.083 | 0.024522172 |
| biological_process| GO:0006725  | cellular aromatic compound metabolic process | 0.001980051 | 0.083 | 0.024522172 |
| biological_process| GO:0046483  | heterocyclic metabolic process          | 0.001980051    | 0.083        | 0.024522172 |
| biological_process| GO:1901360  | organic cyclic compound metabolic process | 0.003465608 | 0.143 | 0.039754306 |
| biological_process| GO:0043170  | macromolecule metabolic process         | 0.003703817    | 0.173        | 0.039754306 |
| biological_process| GO:0093034  | nucleic acid metabolic process          | 0.007359904    | 0.26         | 0.074059033 |
| biological_process| GO:1901564  | organonitrogen compound metabolic process | 0.010752663 | 0.332 | 0.08655894 |
| biological_process| GO:0006082  | organic acid metabolic process          | 0.010752663    | 0.332        | 0.08655894 |
| biological_process| GO:0006520  | cellular amino acid metabolic process   | 0.010752663    | 0.332        | 0.08655894 |
| biological_process| GO:0019752  | carboxylic acid metabolic process       | 0.010752663    | 0.332        | 0.08655894 |
| biological_process| GO:0043436  | oxoacid metabolic process               | 0.010752663    | 0.332        | 0.08655894 |
| biological_process| GO:0044267  | cellular protein metabolic process       | 0.012801893    | 0.36         | 0.098147845 |
| biological_process| GO:0044237  | cellular metabolic process              | 0.020337019    | 0.528        | 0.144624503 |
| biological_process| GO:0006807  | nitrogen compound metabolic process     | 0.020660643    | 0.529        | 0.144624503 |
| biological_process| GO:0019538  | protein metabolic process               | 0.024635519    | 0.555        | 0.16526327 |
| biological_process| GO:0008152  | metabolic process                       | 0.040286324    | 0.76         | 0.259443924 |
| biological_process| GO:0044260  | cellular macromolecule metabolic process | 0.048049138 | 0.807 | 0.297535048 |
| biological_process| GO:0032502  | developmental process                   | 0.06846904     | 0.896        | 0.408278352 |
| biological_process| GO:0010467  | gene expression                         | 0.083934988    | 0.932        | 0.482626179 |
| biological_process| GO:0048856  | anatomical structure development        | 0.094648458    | 0.943        | 0.507946725 |
| biological_process| GO:0050896  | response to stimulus                   | 0.094648458    | 0.943        | 0.507946725 |
| biological_process| GO:0019439  | aromatic compound catabolic process     | 0.121575745    | 0.98         | 0.518187958 |
| biological_process| GO:0034655  | nucleobase-containing compound catabolic process | 0.121575745 | 0.98 | 0.518187958 |
| biological_process| GO:0044270  | cellular nitrogen compound catabolic process | 0.121575745 | 0.98 | 0.518187958 |
| biological_process| GO:0046700  | heterocyclic catabolic process          | 0.121575745    | 0.98         | 0.518187958 |
| biological_process| GO:1901361  | organic cyclic compound catabolic process | 0.121575745 | 0.98 | 0.518187958 |
| biological_process| GO:1901575  | organic substance catabolic process     | 0.121575745    | 0.98         | 0.518187958 |
| biological_process| GO:007154   | cell communication                     | 0.12264475     | 0.98         | 0.518187958 |
| biological_process| GO:0023052  | signaling                              | 0.12264475     | 0.98         | 0.518187958 |
| biological_process| GO:0046907  | intracellular transport                 | 0.132893482    | 0.986        | 0.518187958 |
| biological_process| GO:0051641  | cellular localization                  | 0.132893482    | 0.986        | 0.518187958 |
| ontology          | node_id     | node_name                                   | raw_p_overrep | FWER_overrep | qvalue     |
|-------------------|-------------|---------------------------------------------|---------------|--------------|------------|
| biological_process | GO:0051649  | establishment of localization in cell       | 0.132893482   | 0.986        | 0.516187958 |
| biological_process | GO:0003008  | system process                              | 0.138398026   | 0.989        | 0.518187958 |
| biological_process | GO:0050877  | nervous system process                       | 0.138398026   | 0.989        | 0.518187958 |
| biological_process | GO:0003013  | circulatory system process                   | 0.16          | 0.996        | 0.51995079  |
| biological_process | GO:0006629  | lipid metabolic process                      | 0.168673263   | 0.996        | 0.51995079  |
| biological_process | GO:0007165  | signal transduction                          | 0.169675612   | 0.996        | 0.51995079  |
| biological_process | GO:0022607  | cellular component assembly                  | 0.169675612   | 0.996        | 0.51995079  |
| biological_process | GO:0050789  | regulation of biological process             | 0.169675612   | 0.996        | 0.51995079  |
| biological_process | GO:0050794  | regulation of cellular process               | 0.169675612   | 0.996        | 0.51995079  |
| biological_process | GO:0051716  | cellular response to stimulus                | 0.169675612   | 0.996        | 0.51995079  |
| biological_process | GO:0007267  | cell-cell signaling                          | 0.169762992   | 0.996        | 0.51995079  |
| biological_process | GO:0006913  | nucleocytoplasmic transport                  | 0.171163925   | 0.996        | 0.51995079  |
| biological_process | GO:0051169  | nuclear transport                            | 0.171163925   | 0.996        | 0.51995079  |
| biological_process | GO:0009056  | catabolic process                            | 0.208281416   | 0.998        | 0.617204168 |
| biological_process | GO:0009987  | cellular process                             | 0.218865963   | 0.999        | 0.617204168 |
| biological_process | GO:0022618  | ribonucleoprotein complex assembly           | 0.222346843   | 0.999        | 0.617204168 |
| biological_process | GO:0034622  | ribonucleoprotein complex subunit organization | 0.222346843   | 0.999        | 0.617204168 |
| biological_process | GO:0006950  | response to stress                           | 0.229712924   | 0.999        | 0.626843742 |
| biological_process | GO:0006259  | DNA metabolic process                         | 0.24781934    | 1           | 0.664981896 |
| biological_process | GO:0032196  | transposition                                | 0.294699332   | 1           | 0.690037679 |
| biological_process | GO:0021700  | developmental maturation                     | 0.298026763   | 1           | 0.690037679 |
| biological_process | GO:0008219  | cell death                                   | 0.311665952   | 1           | 0.690037679 |
| biological_process | GO:0006605  | protein targeting                            | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0006886  | intracellular protein transport               | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0008104  | protein localization                          | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0015031  | protein transport                            | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0015833  | peptide transport                            | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0033036  | macromolecule localization                   | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0034613  | cellular protein localization                 | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0042886  | amide transport                              | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0045184  | establishment of protein localization        | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0070727  | cellular macromolecule localization          | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0071702  | organic substance transport                   | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0071705  | nitrogen compound transport                   | 0.321446124   | 1           | 0.690037679 |
| biological_process | GO:0007010  | cytoskeleton organization                    | 0.342899315   | 1           | 0.704966797 |
| biological_process | GO:0006928  | movement of cell or subcellular component    | 0.345915385    | 1           | 0.704966797 |
| biological_process | GO:0048870  | cell motility                                | 0.345915385    | 1           | 0.704966797 |
| biological_process | GO:0051674  | localization of cell                         | 0.345915385    | 1           | 0.704966797 |
| biological_process | GO:0016043  | cellular component organization              | 0.37086114     | 1           | 0.735241846 |
| biological_process | GO:004248   | cellular catabolic process                   | 0.378971723    | 1           | 0.735241846 |
| biological_process | GO:0043933  | protein-containing complex subunit organization | 0.379037722   | 1           | 0.735241846 |
| biological_process | GO:0065003  | protein-containing complex assembly          | 0.379037722    | 1           | 0.735241846 |
| biological_process | GO:0034330  | cell junction organization                   | 0.408051225    | 1           | 0.779464522 |
| ontology                   | node_id | node_name                                           | raw_p_overrep | FWER_overrep | qvalue  |
|----------------------------|---------|-----------------------------------------------------|---------------|--------------|---------|
| biological_process         | GO:0032501 | multcellular organism process                       | 0.493778689  | 1            | 0.855877206 |
| biological_process         | GO:0051186 | cofactor metabolic process                          | 0.500302061  | 1            | 0.855877206 |
| biological_process         | GO:0051179 | localization                                        | 0.506067352  | 1            | 0.855877206 |
| biological_process         | GO:0006810 | transport                                           | 0.510336719  | 1            | 0.855877206 |
| biological_process         | GO:0051234 | establishment of localization                       | 0.510336719  | 1            | 0.855877206 |
| biological_process         | GO:0008283 | cell proliferation                                  | 0.540928159  | 1            | 0.897829212 |
| biological_process         | GO:0005975 | carbohydrate metabolic process                      | 0.571096925  | 1            | 0.928753585 |
| biological_process         | GO:0040011 | locomotion                                          | 0.571096925  | 1            | 0.928753585 |
| biological_process         | GO:006790  | sulfur compound metabolic process                   | 0.597672708  | 1            | 0.952725801 |
| biological_process         | GO:0051604 | protein maturation                                  | 0.597672708  | 1            | 0.952725801 |
| biological_process         | GO:0007049 | cell cycle                                          | 0.605884081  | 1            | 0.954201271 |
| biological_process         | GO:0044085 | cellular component biogenesis                       | 0.616658575  | 1            | 0.954201271 |
| biological_process         | GO:0009002 | cell morphogenesis                                  | 0.622305176  | 1            | 0.954201271 |
| biological_process         | GO:0032989 | cellular component morphogenesis                    | 0.622305176  | 1            | 0.954201271 |
| biological_process         | GO:030705  | cytoskeleton-dependent intracellular transport       | 0.650945344  | 1            | 0.979459817 |
| biological_process         | GO:0043473 | pigmentation                                        | 0.650945344  | 1            | 0.979459817 |
| biological_process         | GO:006457  | protein folding                                     | 0.685092082  | 1            | 0.989918624 |
| biological_process         | GO:0044403 | symbiont process                                    | 0.685092082  | 1            | 0.989918624 |
| biological_process         | GO:0044419 | interspecies interaction between organisms          | 0.685092082  | 1            | 0.989918624 |
| biological_process         | GO:0051704 | multi-organism process                              | 0.685092082  | 1            | 0.989918624 |
| biological_process         | GO:000278  | mitotic cell cycle                                  | 0.688639043  | 1            | 0.989918624 |
| biological_process         | GO:0066091 | generation of precursor metabolites and energy      | 0.714111747  | 1            | 1           |
| biological_process         | GO:0071840 | cellular component organization or biogenesis       | 0.726857231  | 1            | 1           |
| biological_process         | GO:007275  | multicellular organism development                  | 0.738620981  | 1            | 1           |
| biological_process         | GO:0009790 | embryo development                                  | 0.738620981  | 1            | 1           |
| biological_process         | GO:0040007 | growth                                              | 0.743213786  | 1            | 1           |
| biological_process         | GO:0061024 | membrane organization                               | 0.743213786  | 1            | 1           |
| biological_process         | GO:007155  | cell adhesion                                       | 0.755080374  | 1            | 1           |
| biological_process         | GO:0022610 | biological adhesion                                 | 0.755080374  | 1            | 1           |
| biological_process         | GO:006996  | organelle organization                              | 0.781982111  | 1            | 1           |
| biological_process         | GO:007968  | aging                                               | 0.794976783  | 1            | 1           |
| biological_process         | GO:009653  | anatomical structure morphogenesis                  | 0.798641316  | 1            | 1           |
| biological_process         | GO:0022613 | ribonucleoprotein complex biogenesis                | 0.818260447  | 1            | 1           |
| biological_process         | GO:016192  | vesicle-mediated transport                          | 0.830541998  | 1            | 1           |
| biological_process         | GO:0051301 | cell division                                       | 0.856452885  | 1            | 1           |
| biological_process         | GO:006399  | tRNA metabolic process                              | 0.856521786  | 1            | 1           |
| biological_process         | GO:0034660 | ncRNA metabolic process                             | 0.856521786  | 1            | 1           |
| ontology            | node_id      | node_name                                          | raw_p_overrep | FWER_overrep | qvalue |
|---------------------|--------------|----------------------------------------------------|---------------|--------------|--------|
| biological_process  | GO:0000003   | reproduction                                       | 0.856817158   | 1            | 1      |
| biological_process  | GO:0048646   | anatomical structure formation involved in morphogenesis | 0.875159595   | 1            | 1      |
| biological_process  | GO:0006914   | autophagy                                          | 0.893953811   | 1            | 1      |
| biological_process  | GO:0007005   | mitochondrion organization                        | 0.893953811   | 1            | 1      |
| biological_process  | GO:0061919   | process utilizing autophagic mechanism             | 0.893953811   | 1            | 1      |
| biological_process  | GO:0006412   | translation                                        | 0.917917395   | 1            | 1      |
| biological_process  | GO:0006518   | peptide metabolic process                          | 0.917917395   | 1            | 1      |
| biological_process  | GO:0009059   | macromolecule biosynthetic process                 | 0.917917395   | 1            | 1      |
| biological_process  | GO:0034645   | cellular macromolecule biosynthetic process        | 0.917917395   | 1            | 1      |
| biological_process  | GO:0043043   | peptide biosynthetic process                       | 0.917917395   | 1            | 1      |
| biological_process  | GO:0043603   | cellular amide metabolic process                   | 0.917917395   | 1            | 1      |
| biological_process  | GO:0043604   | amide biosynthetic process                         | 0.917917395   | 1            | 1      |
| biological_process  | GO:0044249   | cellular biosynthetic process                      | 0.917917395   | 1            | 1      |
| biological_process  | GO:0044271   | cellular nitrogen compound biosynthetic process    | 0.917917395   | 1            | 1      |
| biological_process  | GO:1901566   | organonitrogen compound biosynthetic process       | 0.917917395   | 1            | 1      |
| biological_process  | GO:1901576   | organic substance biosynthetic process             | 0.917917395   | 1            | 1      |
| biological_process  | GO:0000280   | nuclear division                                   | 0.930109073   | 1            | 1      |
| biological_process  | GO:0022402   | cell cycle process                                 | 0.930109073   | 1            | 1      |
| biological_process  | GO:0048285   | organelle fission                                  | 0.930109073   | 1            | 1      |
| biological_process  | GO:0140014   | mitotic nuclear division                           | 0.930109073   | 1            | 1      |
| biological_process  | GO:1903047   | mitotic cell cycle process                         | 0.930109073   | 1            | 1      |
| biological_process  | GO:0051276   | chromosome organization                            | 0.938812565   | 1            | 1      |
| biological_process  | GO:0055085   | transmembrane transport                            | 0.97651662    | 1            | 1      |
| biological_process  | GO:0042254   | ribosome biogenesis                                | 0.979812934   | 1            | 1      |
| biological_process  | GO:0042592   | homeostatic process                                | 0.990690553   | 1            | 1      |
| biological_process  | GO:0065008   | regulation of biological quality                   | 0.990690553   | 1            | 1      |
| biological_process  | GO:0008150   | biological_process                                 | 1             | 1            | 1      |
| biological_process  | GO:0007009   | plasma membrane organization                       | 1             | 1            | 1      |
| biological_process  | GO:0010256   | endomembrane system organization                   | 1             | 1            | 1      |
| biological_process  | GO:0030198   | extracellular matrix organization                  | 1             | 1            | 1      |
| biological_process  | GO:0043062   | extracellular structure organization                | 1             | 1            | 1      |
| biological_process  | GO:0007034   | vacuolar transport                                 | 1             | 1            | 1      |
| biological_process  | GO:0007059   | chromosome segregation                             | 1             | 1            | 1      |
### Table SI 16

| ontology                  | node_id                  | node_name                                             | raw_p_overrep | FWER_overrep | qvalue |
|---------------------------|--------------------------|-------------------------------------------------------|---------------|--------------|--------|
| biological_process        | GO:0044281               | small molecule metabolic process                      | 0.011067621   | 0.254        | 1      |
| biological_process        | GO:0006629               | lipid metabolic process                               | 0.027846065   | 0.514        | 1      |
| biological_process        | GO:0019439               | aromatic compound catabolic process                   | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:0034685               | nucleobase-containing compound catabolic process      | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:0044270               | cellular nitrogen compound catabolic process          | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:0046700               | heterocycle catabolic process                         | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:1901361               | organic cyclic compound catabolic process             | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:1901575               | organic substance catabolic process                   | 0.09492738    | 0.904        | 1      |
| biological_process        | GO:0006091               | generation of precursor metabolites and energy        | 0.101687021   | 0.931        | 1      |
| biological_process        | GO:0044248               | cellular catabolic process                            | 0.167118394   | 0.993        | 1      |
| biological_process        | GO:0046700               | heterocycle catabolic process                         | 0.261725275   | 0.998        | 1      |
| biological_process        | GO:00051186              | cofactor metabolic process                            | 0.261725275   | 0.998        | 1      |
| biological_process        | GO:0040007               | growth                                                | 0.331309947   | 1            | 1      |
| biological_process        | GO:0007287               | cell-cell signaling                                   | 0.3353463     | 1            | 1      |
| biological_process        | GO:0009056               | catabolic process                                     | 0.344198198   | 1            | 1      |
| biological_process        | GO:0025020               | developmental process                                 | 0.344986113   | 1            | 1      |
| biological_process        | GO:0009058               | biosynthetic process                                  | 0.261725275   | 0.998        | 1      |
| biological_process        | GO:0007568               | aging                                                 | 0.379070546   | 1            | 1      |
| biological_process        | GO:0051276               | chromosome organization                               | 0.379934885   | 1            | 1      |
| biological_process        | GO:0006790               | sulfur compound metabolic process                     | 0.471442619   | 1            | 1      |
| biological_process        | GO:0006412               | translation                                           | 0.505179796   | 1            | 1      |
| biological_process        | GO:0005181               | peptide metabolic process                             | 0.505179796   | 1            | 1      |
| biological_process        | GO:0009059               | macromolecule biosynthetic process                    | 0.505179796   | 1            | 1      |
| biological_process        | GO:0034645               | cellular macromolecule biosynthetic process           | 0.505179796   | 1            | 1      |
| biological_process        | GO:0043043               | peptide biosynthetic process                          | 0.505179796   | 1            | 1      |
| biological_process        | GO:0043603               | cellular amide metabolic process                      | 0.505179796   | 1            | 1      |
| biological_process        | GO:0043604               | amide biosynthetic process                            | 0.505179796   | 1            | 1      |
| biological_process        | GO:0044249               | cellular biosynthetic process                         | 0.505179796   | 1            | 1      |
| biological_process        | GO:0044271               | cellular nitrogen compound biosynthetic process       | 0.505179796   | 1            | 1      |
| biological_process        | GO:1901566               | organonitrogen compound biosynthetic process          | 0.505179796   | 1            | 1      |
| biological_process        | GO:1901576               | organic substance biosynthetic process                | 0.505179796   | 1            | 1      |
| biological_process        | GO:0006082               | organic acid metabolic process                         | 0.532810481   | 1            | 1      |
| biological_process        | GO:0006520               | cellular amino acid metabolic process                 | 0.532810481   | 1            | 1      |
| biological_process        | GO:0019752               | carboxylic acid metabolic process                     | 0.532810481   | 1            | 1      |
| biological_process        | GO:0043436               | oxoacid metabolic process                             | 0.532810481   | 1            | 1      |
| ontology                  | node_id  | node_name                                                                 | raw_p_overrep | FWER_overrep | qvalue |
|---------------------------|----------|----------------------------------------------------------------------------|---------------|--------------|--------|
| biological_process        | GO:0022613 | ribonucleoprotein complex biogenesis                                      | 0.56433647    | 1            | 1      |
| biological_process        | GO:0048646 | anatomical structure formation involved in morphogenesis                  | 0.580974516   | 1            | 1      |
| biological_process        | GO:0008152 | metabolic process                                                          | 0.595379374   | 1            | 1      |
| biological_process        | GO:0040011 | locomotion                                                                 | 0.618315427   | 1            | 1      |
| biological_process        | GO:0000003 | reproduction                                                               | 0.672156468   | 1            | 1      |
| biological_process        | GO:0055085 | transmembrane transport                                                    | 0.676217767   | 1            | 1      |
| biological_process        | GO:0034641 | cellular nitrogen compound metabolic process                              | 0.678136068   | 1            | 1      |
| biological_process        | GO:0002376 | cellular component biogenesis                                              | 0.693576721   | 1            | 1      |
| biological_process        | GO:0006914 | autophagy                                                                  | 0.693576721   | 1            | 1      |
| biological_process        | GO:0007005 | mitochondrion organization                                                 | 0.693576721   | 1            | 1      |
| biological_process        | GO:0061919 | process utilizing autophagic mechanism                                     | 0.693576721   | 1            | 1      |
| biological_process        | GO:0061024 | membrane organization                                                      | 0.710043392   | 1            | 1      |
| biological_process        | GO:0044085 | cellular component biogenesis                                              | 0.737513994   | 1            | 1      |
| biological_process        | GO:0044237 | cellular metabolic process                                                 | 0.743553821   | 1            | 1      |
| biological_process        | GO:0006139 | nucleobase-containing compound metabolic process                          | 0.748949908   | 1            | 1      |
| biological_process        | GO:0006725 | cellular aromatic compound metabolic process                              | 0.748949908   | 1            | 1      |
| biological_process        | GO:0046483 | heterocycle metabolic process                                              | 0.748949908   | 1            | 1      |
| biological_process        | GO:1901360 | organic cyclic compound metabolic process                                  | 0.748949908   | 1            | 1      |
| biological_process        | GO:0009653 | organic cyclic compound metabolic process                                  | 0.784949908   | 1            | 1      |
| biological_process        | GO:0030154 | cell differentiation                                                       | 0.813402776   | 1            | 1      |
| biological_process        | GO:0007275 | multicellular organism development                                         | 0.839111243   | 1            | 1      |
| biological_process        | GO:0009790 | embryo development                                                         | 0.863971013   | 1            | 1      |
| biological_process        | GO:0016192 | vesicle-mediated transport                                                 | 0.86799866    | 1            | 1      |
| biological_process        | GO:0048869 | cellular developmental process                                             | 0.870925271   | 1            | 1      |
| biological_process        | GO:0006810 | transport                                                                  | 0.872496499   | 1            | 1      |
| biological_process        | GO:0051234 | establishment of localization                                              | 0.873150409   | 1            | 1      |
| biological_process        | GO:0006996 | organelle organization                                                     | 0.87543095    | 1            | 1      |
| biological_process        | GO:1901564 | organonitrogen compound metabolic process                                 | 0.875920169   | 1            | 1      |
| biological_process        | GO:0006950 | response to stress                                                         | 0.883303182   | 1            | 1      |
| biological_process        | GO:0051179 | localization                                                               | 0.883303182   | 1            | 1      |
| biological_process        | GO:0044238 | primary metabolic process                                                  | 0.883591263   | 1            | 1      |
| biological_process        | GO:0071704 | organic substance metabolic process                                        | 0.890794287   | 1            | 1      |
| biological_process        | GO:0044267 | cellular protein metabolic process                                         | 0.895195592   | 1            | 1      |
| biological_process        | GO:0006259 | DNA metabolic process                                                      | 0.914633112   | 1            | 1      |
| biological_process        | GO:0071840 | cellular component organization or biogenesis                             | 0.9153289     | 1            | 1      |
| ontology            | node_id   | node_name                                  | raw_p_overrep | FWER_overrep | qvalue |
|---------------------|-----------|--------------------------------------------|---------------|--------------|--------|
| biological_process  | GO:0007154| cell communication                          | 0.949016686  | 1            | 1      |
| biological_process  | GO:0023052| signaling                                   | 0.949016686  | 1            | 1      |
| biological_process  | GO:0022607| cellular component assembly                 | 0.952593999  | 1            | 1      |
| biological_process  | GO:0006464| cellular protein modification process        | 0.963660717  | 1            | 1      |
| biological_process  | GO:0036211| protein modification process                 | 0.963660717  | 1            | 1      |
| biological_process  | GO:0043412| macromolecule modification                  | 0.963660717  | 1            | 1      |
| biological_process  | GO:0016043| cellular component organization             | 0.978677687  | 1            | 1      |
| biological_process  | GO:0043170| macromolecule metabolic process             | 0.979157815  | 1            | 1      |
| biological_process  | GO:0009987| cellular process                            | 0.988392955  | 1            | 1      |
| biological_process  | GO:0003013| circulatory system process                  | 1             | 1            | 1      |
| biological_process  | GO:0007009| plasma membrane organization                | 1             | 1            | 1      |
| biological_process  | GO:0010256| endomembrane system organization            | 1             | 1            | 1      |
| biological_process  | GO:0030198| extracellular matrix organization           | 1             | 1            | 1      |
| biological_process  | GO:0032196| transposition                               | 1             | 1            | 1      |
| biological_process  | GO:0043062| extracellular structure organization         | 1             | 1            | 1      |
| biological_process  | GO:0034330| cell junction organization                   | 1             | 1            | 1      |
| biological_process  | GO:0007155| cell adhesion                               | 1             | 1            | 1      |
| biological_process  | GO:0007092| plasma membrane organization                | 1             | 1            | 1      |
| biological_process  | GO:0006399| tRNA metabolic process                      | 1             | 1            | 1      |
| biological_process  | GO:0034690| ncRNA metabolic process                     | 1             | 1            | 1      |
| biological_process  | GO:0021700| developmental maturation                    | 1             | 1            | 1      |
| biological_process  | GO:0051604| protein maturation                          | 1             | 1            | 1      |
| biological_process  | GO:0003008| system process                              | 1             | 1            | 1      |
| biological_process  | GO:0006928| movement of cell or subcellular component   | 1             | 1            | 1      |
| biological_process  | GO:0048870| cell motility                               | 1             | 1            | 1      |
| biological_process  | GO:0050877| nervous system process                      | 1             | 1            | 1      |
| biological_process  | GO:0051674| localization of cell                        | 1             | 1            | 1      |
| biological_process  | GO:0006457| protein folding                             | 1             | 1            | 1      |
| biological_process  | GO:0006913| nucleocytoplasmic transport                 | 1             | 1            | 1      |
| biological_process  | GO:0044403| symbiont process                            | 1             | 1            | 1      |
| biological_process  | GO:0044419| interspecies interaction between organisms   | 1             | 1            | 1      |
| biological_process  | GO:0051169| nuclear transport                           | 1             | 1            | 1      |
| biological_process  | GO:0051704| multi-organism process                      | 1             | 1            | 1      |
| biological_process  | GO:000280 | nuclear division                            | 1             | 1            | 1      |
| biological_process  | GO:0022402| cell cycle process                          | 1             | 1            | 1      |
| biological_process  | GO:0048285| organelle fission                           | 1             | 1            | 1      |
| biological_process  | GO:0140014| mitotic nuclear division                    | 1             | 1            | 1      |
| biological_process  | GO:1903047| mitotic cell cycle process                   | 1             | 1            | 1      |
| biological_process  | GO:0007059| chromosome segregation                      | 1             | 1            | 1      |
| biological_process  | GO:0006605| protein targeting                           | 1             | 1            | 1      |
| ontology          | node_id     | node_name                                    | raw_p_overrep | FWER_overrep | qvalue |
|-------------------|-------------|----------------------------------------------|---------------|--------------|--------|
| biological_process | GO:0006886  | intracellular protein transport              | 1             | 1            | 1      |
| biological_process | GO:0008104  | protein localization                         | 1             | 1            | 1      |
| biological_process | GO:0015031  | protein transport                            | 1             | 1            | 1      |
| biological_process | GO:0015833  | peptide transport                            | 1             | 1            | 1      |
| biological_process | GO:0033036  | macromolecule localization                   | 1             | 1            | 1      |
| biological_process | GO:0034613  | cellular protein localization                | 1             | 1            | 1      |
| biological_process | GO:0042886  | amide transport                              | 1             | 1            | 1      |
| biological_process | GO:0045184  | establishment of protein localization        | 1             | 1            | 1      |
| biological_process | GO:0070727  | cellular macromolecule localization          | 1             | 1            | 1      |
| biological_process | GO:0071702  | organic substance transport                   | 1             | 1            | 1      |
| biological_process | GO:0071705  | nitrogen compound transport                   | 1             | 1            | 1      |
| biological_process | GO:0000902  | cell morphogenesis                           | 1             | 1            | 1      |
| biological_process | GO:0022618  | ribonucleoprotein complex assembly           | 1             | 1            | 1      |
| biological_process | GO:0032989  | cellular component morphogenesis              | 1             | 1            | 1      |
| biological_process | GO:0034622  | cellular protein-containing complex assembly  | 1             | 1            | 1      |
| biological_process | GO:0071826  | ribonucleoprotein complex subunit organization | 1          | 1            | 1      |
| biological_process | GO:0051301  | cell division                                | 1             | 1            | 1      |
| biological_process | GO:0008219  | cell death                                   | 1             | 1            | 1      |
| biological_process | GO:0007010  | cytoskeleton organization                     | 1             | 1            | 1      |
| biological_process | GO:0008283  | cell proliferation                            | 1             | 1            | 1      |
| biological_process | GO:0000278  | mitotic cell cycle                            | 1             | 1            | 1      |
| biological_process | GO:0046907  | intracellular transport                       | 1             | 1            | 1      |
| biological_process | GO:0051641  | cellular localization                         | 1             | 1            | 1      |
| biological_process | GO:0051649  | establishment of localization in cell         | 1             | 1            | 1      |
| biological_process | GO:0006396  | RNA processing                                | 1             | 1            | 1      |
| biological_process | GO:0006397  | mRNA processing                               | 1             | 1            | 1      |
| biological_process | GO:0016071  | mRNA metabolic process                        | 1             | 1            | 1      |
| biological_process | GO:0016070  | RNA metabolic process                         | 1             | 1            | 1      |
| biological_process | GO:0007049  | cell cycle                                   | 1             | 1            | 1      |
| biological_process | GO:0007165  | signal transduction                          | 1             | 1            | 1      |
| biological_process | GO:0050789  | regulation of biological process              | 1             | 1            | 1      |
| biological_process | GO:0050794  | regulation of cellular process                | 1             | 1            | 1      |
| biological_process | GO:0051716  | cellular response to stimulus                 | 1             | 1            | 1      |
**Table SI 17**

Counting of nuclei in *Drosophila melanogaster*

| Developmental stage                                      | Estimated number of cells |
|----------------------------------------------------------|---------------------------|
| Stage 13 embryo                                          | ~ 107,912                 |
| Stage 16 embryo/begin 1st instar larval stage            | ≥ 140,000                 |
| End 1st instar larval stage                              | ≥ 200,000                 |
| End 2nd instar larval stage                              | ≥ 370,000                 |
| End 3rd instar larval stage                              | ≥ 400,000                 |

Cell number estimates based on manual counting nuclei in 24 confocal planes of half a body.
Table SI 18

Histidine pathway genes

| Species                        | hutH  | hutU  | hutI  | FTCD  |
|-------------------------------|-------|-------|-------|-------|
|                               | OG0005325 | OG0004955 | OG0006789 | OG0005056 |
| Demodex folliculorum          | 0     | 0     | 0     | 0     |
| Dermatophagoides farinae      | 1     | 2     | 1     | 1     |
| Ixodes scapularis             | 1     | 1     | 2     | 2     |
| Metaseiulus occidentalis      | 1     | 1     | 1     | 1     |
| Sarcoptes scabiei             | 1     | 1     | 1     | 1     |
| Tetranychus urticae           | 1     | 0     | 0     | 0     |
| Drosophila melanogaster       | 0     | 0     | 0     | 0     |
| Parasteatoda tepidariorum     | 1     | 1     | 1     | 1     |
| Limulus polyphemus            | 2     | 2     | 1     | 3     |
| Stegodyphus mimosarum         | 2     | 1     | 1     | 1     |
| Daphnia pulex                 | 1     | 1     | 1     | 1     |
| Tribolium castaneum           | 1     | 0     | 0     | 0     |
| Tropilaelaps mercedesae       | 1     | 2     | 0     | 1     |
| Centruroides sculpturatus     | 1     | 2     | 1     | 2     |
| Varroa jacobsoni              | 1     | 1     | 1     | 1     |
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