

**Supplementary Table S1.** 115 single-copy core genes found across the genomes of 37 *P. insidiosum* and 4 related oomycetes.

| Gene cluster ID  | Gene length (bp) | Gene product description  |
|------------------|------------------|---|
| p-cluster594855  | 10837            | Elongation factor 3, putative   |
| p-cluster682933  | 10071            | ABC transporter lipid export ABC Family                               |
| p-cluster312751* | 7015             | Hypothetical protein  |
| p-cluster539815  | 5833             | Pleiotropic drug resistance protein ABC superfamily                   |
| p-cluster454010  | 5716             | Calcium-translocating p-type ATPase, pmca-type                        |
| p-cluster510208* | 5687             | Hypothetical protein  |
| p-cluster099966  | 5560             | Phospholipid-transporting ATPase, putative, partial                   |
| p-cluster597669* | 5463             | Hypothetical protein  |
| p-cluster412135  | 5305             | Glucose transporter   |
| p-cluster095503  | 5168             | Myosin-like protein   |
| p-cluster421014  | 4840             | Intraflagellar transport protein 122                                  |
| p-cluster361620  | 4820             | Structural maintenance of chromosomes protein                         |
| p-cluster597184  | 4683             | Arf-gap with GTPase, ank repeat and ph domain-containing protein 9    |
| p-cluster306513  | 4594             | Transmembrane protein   |
| p-cluster316612  | 4496             | Elicitor-like transglutaminase  |
| p-cluster141083  | 4319             | Glycolate oxidase, subunit glcd, partial                              |
| p-cluster477503* | 4192             | Hypothetical protein  |
| p-cluster464758  | 4049             | Exportin-2-like protein   |
| p-cluster449940* | 3978             | Hypothetical protein  |
| p-cluster193710* | 3912             | Hypothetical protein  |
| p-cluster532599  | 3869             | Periodic tryptophan protein 2   |
| p-cluster065379* | 3730             | Hypothetical protein  |
| p-cluster434954  | 3539             | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit |
| p-cluster008242  | 3525             | Luminal-binding protein   |
| p-cluster644157* | 3499             | Hypothetical protein  |
| p-cluster359933* | 3432             | Hypothetical protein  |
| p-cluster709453  | 3418             | Long-chain-fatty-acid-CoA ligase                                      |
| p-cluster464826  | 3304             | Pre-rRNA-processing protein tsr1                                      |
| p-cluster709189  | 3232             | Peroxisome assembly factor  |
| p-cluster196014* | 3143             | Hypothetical protein  |
| p-cluster356030* | 3049             | Hypothetical protein  |
| p-cluster432958* | 3049             | Hypothetical protein  |
| p-cluster357833* | 2988             | Hypothetical protein  |
| p-cluster536025  | 2948             | Polypyrimidine tract-binding protein                                  |
| p-cluster054118  | 2947             | Calcineurin-like phosphoesterase                                      |
| p-cluster194771* | 2945             | Hypothetical protein  |
| p-cluster662691  | 2844             | ABC transporter-like protein, partial                                 |
| p-cluster554166  | 2765             | Glucose transporter   |
| p-cluster189931* | 2723             | Hypothetical protein  |
| p-cluster458608* | 2720             | Hypothetical protein  |
| p-cluster055747* | 2685             | Hypothetical protein  |
| p-cluster575357  | 2643             | Adenylate cyclase, putative   |
| p-cluster579716  | 2639             | Tigger transposable element-derived protein 6                         |
| p-cluster082612  | 2610             | 2-isopropylmalate synthase  |
| p-cluster729567* | 2603             | Hypothetical protein  |
| p-cluster386600  | 2559             | Threonine-tRNA ligase   |
| p-cluster540880  | 2503             | Lysosomal pro-x carboxypeptidase                                      |
| p-cluster054458  | 2422             | Radial spoke head 10 family protein                                   |
| p-cluster472248  | 2393             | Cytosol aminopeptidase  |
| p-cluster361606  | 2314             | 2,4-dienoyl-coa reductase   |
| p-cluster071300  | 2274             | Translocation protein sec63   |
| p-cluster524538  | 2271             | T-complex protein 1, theta subunit                                    |
| p-cluster476051* | 2270             | Hypothetical protein  |
| p-cluster324713* | 2160             | Hypothetical protein  |
| p-cluster590582  | 2143             | Exopolysaccharide phosphotransferase                                  |
| p-cluster197205  | 2135             | Glucose-6-phosphate isomerase   |
| p-cluster362721* | 2123             | Hypothetical protein  |
| p-cluster092525  | 2093             | Fact complex subunit ssrp1  |
| p-cluster198537* | 2055             | Hypothetical protein  |
| p-cluster190165  | 2039             | Cystathionine beta-lyase  |

|                  |      |   |
|------------------|------|---|
| p-cluster556727  | 2037 | Phosphoglycerate kinase   |
| p-cluster476199  | 2018 | ATP-dependent protease hslvu, ATPase subunit                      |
| p-cluster474688  | 1955 | Aldehyde dehydrogenase  |
| p-cluster397427  | 1954 | Actin-like protein  |
| p-cluster458607  | 1947 | Cyclin-y-like protein, partial                                    |
| p-cluster238230  | 1917 | Acyl-CoA dehydrogenase family member 9, mitochondrial precursor   |
| p-cluster331766* | 1910 | Hypothetical protein  |
| p-cluster508816  | 1888 | Dihydrolipoyl dehydrogenase 1, mitochondrial precursor            |
| p-cluster190599* | 1886 | Hypothetical protein  |
| p-cluster160158  | 1858 | 6-phosphogluconate dehydrogenase                                  |
| p-cluster125186  | 1842 | Pyruvate dehydrogenase e1 component subunit beta, mitochondrial   |
| p-cluster227751  | 1791 | Glutathione-dependent formaldehyde dehydrogenase                  |
| p-cluster190378  | 1773 | Pyruvate dehydrogenase e1 alpha subunit                           |
| p-cluster055980  | 1761 | Rna 3'-terminal phosphate cyclase                                 |
| p-cluster072639  | 1731 | Aminotransferase  |
| p-cluster408676* | 1697 | Hypothetical protein  |
| p-cluster309873* | 1575 | Hypothetical protein  |
| p-cluster578941  | 1568 | 60s ribosomal protein   |
| p-cluster646099  | 1555 | Serine/threonine-protein phosphatase ppe1                         |
| p-cluster539607  | 1551 | Asparagine-trna ligase  |
| p-cluster598164  | 1525 | Enoyl-coa hydratase, mitochondrial precursor                      |
| p-cluster063940  | 1523 | Protein phosphatase 2c  |
| p-cluster196735  | 1480 | Bifunctional fold protein   |
| p-cluster617622  | 1428 | Phosphoserine phosphatase   |
| p-cluster012729  | 1398 | S-adenosylmethionine synthase 2                                   |
| p-cluster423633* | 1371 | Hypothetical protein  |
| p-cluster192633  | 1361 | Acyl-CoA desaturase   |
| p-cluster412337  | 1361 | Sporangia induced 28 kDa inner dynein arm light chain             |
| p-cluster676979  | 1359 | Purine nucleoside phosphorylase i, inosine and guanosine-specific |
| p-cluster349235  | 1357 | 14-3-3 protein epsilon  |
| p-cluster083401  | 1247 | Voltage-dependent anion-selective channel protein                 |
| p-cluster556722* | 1237 | Hypothetical protein  |
| p-cluster149186* | 1235 | Hypothetical protein  |
| p-cluster173431  | 1212 | Myosin-like protein   |
| p-cluster053234* | 1110 | Hypothetical protein  |
| p-cluster000460  | 1106 | Vesicle-associated membrane protein, putative, partial            |
| p-cluster410772* | 1068 | Hypothetical protein  |
| p-cluster474440* | 1060 | Hypothetical protein  |
| p-cluster453101  | 1040 | Putative methyltransferase  |
| p-cluster476353* | 904  | Hypothetical protein  |
| p-cluster452444* | 768  | Hypothetical protein  |
| p-cluster263392  | 741  | Gtp-binding protein parf  |
| p-cluster450789* | 732  | Hypothetical protein  |
| p-cluster124244* | 685  | Hypothetical protein  |
| p-cluster270302  | 679  | Translation elongation factor ef5a                                |
| p-cluster193243  | 549  | Ribosomal protein l23   |
| p-cluster452513  | 547  | Eukaryotic translation initiation factor 1b                       |
| p-cluster452369  | 435  | Ribosomal protein l11   |
| p-cluster044680  | 429  | Mitochondrial/chloroplast ribosomal protein l13                   |
| p-cluster452752  | 398  | 60s ribosomal protein l44   |
| p-cluster236498* | 390  | Hypothetical protein  |
| p-cluster012383  | 387  | 13 kDa ribonucleoprotein-associated protein                       |
| p-cluster261767* | 383  | Hypothetical protein  |
| p-cluster005452  | 351  | Cytochrome c  |
| p-cluster056982  | 285  | U6 snrna-associated smlike protein lsm3                           |

**Footnote:**

\*Hypothetical protein

**Supplementary Table S2.** 112 *P. insidiosum*-specific (Core-2) genes that matched microbial virulence proteins and toxins deposited in the MvirDB database.

| Query Gene ID   | Hit VFID | Hit Gene Description [Microorganism]                          | Query Gene Length (bp) | Hit Gene Length (bp) | Alignment Identify (%) | Query Length Alignment Coverage (%) |
|-----------------|----------|---|------------------------|----------------------|------------------------|-------------------------------------|
| p-cluster695607 | 2428     | 30K adhesin-related protein [Mycoplasma pneumoniae]           | 296                    | 274                  | 47.7                   | 29.1                                |
| p-cluster397479 | 2478     | Mycocerosic acid synthase [Mycobacterium tuberculosis]        | 772                    | 2111                 | 33.1                   | 20.3                                |
| p-cluster474142 | 2575     | Hemoglobin-binding protein [Haemophilus influenzae]           | 1043                   | 1084                 | 32.9                   | 7.3                                 |
| p-cluster538005 | 2911     | Phosphatase   | 737                    | 171                  | 41.5                   | 7.2                                 |
| p-cluster087850 | 4404     | Alpha-latroinsectotoxin                                       | 490                    | 1411                 | 31.8                   | 25.9                                |
| p-cluster410852 | 4404     | Alpha-latroinsectotoxin                                       | 564                    | 1411                 | 26.3                   | 25.7                                |
| p-cluster712810 | 4404     | Alpha-latroinsectotoxin-Lt1a                                  | 143                    | 1411                 | 28.9                   | 79.7                                |
| p-cluster337533 | 5926     | Tryptophan repeat gene family protein                         | 264                    | 297                  | 48.8                   | 16.3                                |
| p-cluster376328 | 6974     | Cyclin D homolog  | 283                    | 254                  | 32.0                   | 61.5                                |
| p-cluster146673 | 7247     | 2,3-dihydroxybenzoate-2,3-dehydrogenase [Shigella flexneri]   | 453                    | 248                  | 26.2                   | 38.6                                |
| p-cluster709624 | 7458     | Chaperone DnAJ [Bacteroides thetaiotaomicron]                 | 247                    | 321                  | 30.7                   | 55.1                                |
| p-cluster608871 | 7464     | Oxidoreductase [Bacteroides thetaiotaomicron]                 | 717                    | 245                  | 28.3                   | 24.7                                |
| p-cluster501203 | 7841     | Filamentous hemagglutinin/adhesin [Bordetella pertussis]      | 288                    | 3590                 | 29.8                   | 34.4                                |
| p-cluster534263 | 7841     | Filamentous hemagglutinin/adhesin [Bordetella pertussis]      | 672                    | 3590                 | 34.0                   | 27.2                                |
| p-cluster404363 | 7938     | Pneumococcal surface protein A [Streptococcus pneumoniae]     | 181                    | 744                  | 43.3                   | 32.6                                |
| p-cluster187984 | 7988     | Phosphatidate cytidyltransferase [Enterococcus faecalis]      | 477                    | 266                  | 42.3                   | 26.2                                |
| p-cluster495776 | 8167     | Internalin A [Listeria monocytogenes]                         | 1149                   | 800                  | 33.3                   | 11.0                                |
| p-cluster721089 | 8434     | Hypothetical protein lpg2490 [Legionella pneumophila]         | 5018                   | 1294                 | 22.0                   | 11.3                                |
| p-cluster574646 | 9543     | Zinc finger and BTB domain-containing protein 7C              | 739                    | 619                  | 32.7                   | 18.9                                |
| p-cluster578127 | 9543     | Zinc finger and BTB domain-containing protein 7C              | 1019                   | 619                  | 34.9                   | 10.7                                |
| p-cluster199836 | 10373    | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase               | 236                    | 261                  | 33.3                   | 39.4                                |
| p-cluster322171 | 13372    | Pyruvate kinase [Salmonella typhimurium]                      | 151                    | 470                  | 46.2                   | 60.3                                |
| p-cluster357085 | 13763    | Helicase [Vibrio cholerae]                                    | 1242                   | 940                  | 24.0                   | 23.7                                |
| p-cluster706532 | 14026    | Lysyl-tRNA synthetase LysU [Escherichia coli]                 | 700                    | 498                  | 38.5                   | 67.1                                |
| p-cluster187093 | 14152    | Serine/threonine protein kinase PpkA [Pseudomonas aeruginosa] | 710                    | 1032                 | 32.4                   | 31.1                                |
| p-cluster460671 | 14152    | Serine/threonine protein kinase PpkA [Pseudomonas aeruginosa] | 849                    | 1032                 | 30.6                   | 25.1                                |
| p-cluster534559 | 14152    | Serine/threonine protein kinase PpkA [Pseudomonas aeruginosa] | 1378                   | 1032                 | 27.7                   | 16.1                                |
| p-cluster566997 | 14152    | Serine/threonine protein kinase PpkA [Pseudomonas aeruginosa] | 485                    | 1032                 | 32.2                   | 36.5                                |
| p-cluster598855 | 14152    | Serine/threonine protein kinase PpkA [Pseudomonas aeruginosa] | 923                    | 1032                 | 27.7                   | 30.8                                |
| p-cluster298495 | 14529    | Astacin-like metalloprotease toxin                            | 1593                   | 264                  | 25.6                   | 13.5                                |
| p-cluster475982 | 15449    | Hypothetical protein bll8085 [Bradyrhizobium japonicum]       | 548                    | 669                  | 30.4                   | 20.1                                |
| p-cluster507512 | 15953    | Hypothetical protein BT_2630 [Bacteroides thetaiotaomicron]   | 763                    | 316                  | 28.0                   | 29.1                                |
| p-cluster356795 | 16229    | Hypothetical protein [Escherichia coli]                       | 1108                   | 504                  | 30.9                   | 13.3                                |
| p-cluster570708 | 16240    | Transacylase [Escherichia coli]                               | 630                    | 422                  | 27.9                   | 45.2                                |
| p-cluster694284 | 16244    | 3-hydroxyacyl-CoA dehydrogenase [Escherichia coli]            | 330                    | 289                  | 28.2                   | 51.8                                |
| p-cluster348793 | 16625    | Ornithine carbamoyltransferase 2 [Escherichia coli]           | 1278                   | 334                  | 37.1                   | 21.5                                |
| p-cluster572952 | 16625    | Ornithine carbamoyltransferase 2 [Escherichia coli]           | 140                    | 334                  | 32.6                   | 67.9                                |

|                 |       |   |      |      |      |      |
|-----------------|-------|---|------|------|------|------|
| p-cluster546828 | 17975 | Ortho-methyltransferase [Mesorhizobium loti]                            | 176  | 344  | 28.8 | 79.0 |
| p-cluster394933 | 18009 | Hypothetical protein mlr8090 [Mesorhizobium loti]                       | 1531 | 274  | 33.3 | 12.9 |
| p-cluster099653 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 715  | 1526 | 34.0 | 20.4 |
| p-cluster104690 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 1012 | 1526 | 24.3 | 27.7 |
| p-cluster460953 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 768  | 1526 | 31.3 | 37.0 |
| p-cluster509407 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 729  | 1526 | 26.8 | 29.2 |
| p-cluster628984 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 478  | 1526 | 28.6 | 74.1 |
| p-cluster651543 | 18169 | WD-40 repeat-containing protein [Nostoc sp.]                            | 962  | 1526 | 26.6 | 32.0 |
| p-cluster278739 | 18492 | tRNA pseudouridine synthase A [Streptococcus agalactiae]                | 641  | 258  | 31.5 | 31.7 |
| p-cluster051977 | 18783 | Phosphomethylpyrimidine kinase [Streptococcus agalactiae]               | 1008 | 252  | 26.2 | 27.0 |
| p-cluster321888 | 18794 | Pyridine nucleotide-disulfide oxidoreductase [Streptococcus agalactiae] | 305  | 439  | 30.3 | 65.9 |
| p-cluster271256 | 18887 | Hypothetical protein gbs0204 [Streptococcus agalactiae]                 | 327  | 249  | 29.8 | 71.9 |
| p-cluster153820 | 19086 | Oxidoreductase [Streptomyces coelicolor]                                | 128  | 259  | 29.4 | 93.0 |
| p-cluster508567 | 19086 | Oxidoreductase [Streptomyces coelicolor]                                | 1256 | 259  | 31.8 | 11.7 |
| p-cluster520923 | 19524 | AAA family ATPase [Shewanella oneidensis]                               | 785  | 680  | 28.2 | 19.6 |
| p-cluster366095 | 20413 | Sialic acid transporter [Salmonella enterica]                           | 190  | 426  | 36.6 | 58.9 |
| p-cluster589962 | 20551 | Metallothionein SmtA [Salmonella enterica]                              | 307  | 267  | 29.5 | 44.6 |
| p-cluster139276 | 20945 | Oxidoreductase [Xylella fastidiosa]                                     | 887  | 247  | 29.7 | 20.9 |
| p-cluster132374 | 23568 | Dimethyltransferase [Photorhabdus luminescens]                          | 637  | 272  | 32.9 | 36.7 |
| p-cluster556115 | 25250 | TetT [Enterococcus faecalis]  | 850  | 651  | 27.0 | 21.2 |
| p-cluster299054 | 25899 | CRISP-PHI1 [Philodryas olfersii]  | 910  | 232  | 31.5 | 18.5 |
| p-cluster444101 | 25936 | Alpha-latrotoxin precursor [Latrodectus tredecimguttatus]               | 68   | 1401 | 36.7 | 88.2 |
| p-cluster217227 | 26380 | ATP-binding cassette protein [Cryptosporidium parvum]                   | 843  | 1431 | 44.6 | 10.9 |
| p-cluster282246 | 26380 | ATP-binding cassette protein [Cryptosporidium parvum]                   | 2290 | 1431 | 23.2 | 13.8 |
| p-cluster051071 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 1115 | 994  | 34.6 | 18.2 |
| p-cluster098355 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 461  | 994  | 35.6 | 35.1 |
| p-cluster160648 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 796  | 994  | 32.9 | 24.2 |
| p-cluster320677 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 473  | 994  | 31.5 | 34.7 |
| p-cluster456679 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 1377 | 994  | 38.6 | 16.9 |
| p-cluster461715 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 479  | 994  | 29.2 | 59.5 |
| p-cluster510105 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 1707 | 994  | 34.3 | 17.4 |
| p-cluster526470 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 1069 | 994  | 33.1 | 12.1 |
| p-cluster615580 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 1136 | 994  | 31.2 | 16.3 |
| p-cluster643963 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 412  | 994  | 37.1 | 28.2 |
| p-cluster697518 | 26400 | cGMP dependent protein kinase [Toxoplasma gondii]                       | 2273 | 994  | 26.8 | 11.2 |
| p-cluster605319 | 26433 | Regulator of chromosome condensation 1 [Toxoplasma gondii]              | 774  | 1155 | 31.4 | 25.8 |
| p-cluster117786 | 26467 | Aspartyl proteinase eimepsin [Eimeria tenella]                          | 303  | 468  | 34.6 | 42.9 |
| p-cluster191433 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                         | 143  | 1003 | 32.8 | 94.4 |
| p-cluster197376 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                         | 785  | 1003 | 41.5 | 36.4 |
| p-cluster285589 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                         | 543  | 1003 | 31.0 | 40.0 |
| p-cluster308454 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                         | 808  | 1003 | 37.1 | 34.5 |
| p-cluster446407 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                         | 595  | 1003 | 43.0 | 13.3 |

|                 |       |  |      |      |      |      |
|-----------------|-------|--|------|------|------|------|
| p-cluster460500 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                  | 830  | 1003 | 36.8 | 24.1 |
| p-cluster503872 | 26470 | cGMP-dependent protein kinase [Eimeria tenella]                  | 504  | 1003 | 31.0 | 43.7 |
| p-cluster058799 | 26605 | CTRP [Plasmodium falciparum]                                     | 244  | 2114 | 40.9 | 25.4 |
| p-cluster318682 | 26605 | CTRP [Plasmodium falciparum]                                     | 419  | 2114 | 44.1 | 13.6 |
| p-cluster543319 | 26605 | CTRP [Plasmodium falciparum]                                     | 176  | 2114 | 36.7 | 27.8 |
| p-cluster200695 | 26643 | Reticulocyte binding protein 2 homolog a [Plasmodium falciparum] | 984  | 3130 | 19.5 | 22.0 |
| p-cluster208509 | 26643 | Reticulocyte binding protein 2 homolog a [Plasmodium falciparum] | 607  | 3130 | 32.1 | 21.9 |
| p-cluster126489 | 26643 | Reticulocyte binding protein 2 homolog a [Plasmodium falciparum] | 2366 | 3130 | 36.5 | 6.9  |
| p-cluster534610 | 26643 | Reticulocyte binding protein 2 homolog a [Plasmodium falciparum] | 495  | 3130 | 33.3 | 20.8 |
| p-cluster644124 | 26643 | Reticulocyte binding protein 2 homolog a [Plasmodium falciparum] | 658  | 3130 | 29.4 | 21.0 |
| p-cluster139183 | 26985 | Adhesin protein AP51-3 [Trichomonas vaginalis]                   | 110  | 405  | 46.8 | 70.9 |
| p-cluster591236 | 26985 | Adhesin protein AP51-3 [Trichomonas vaginalis]                   | 131  | 405  | 50.0 | 80.2 |
| p-cluster721070 | 27018 | LPG2 [Leishmania donovani]                                       | 435  | 341  | 29.8 | 73.8 |
| p-cluster538689 | 27170 | Cathepsin B-like cysteine protease [Trypanosoma brucei]          | 1742 | 340  | 32.0 | 15.1 |
| p-cluster098089 | 27222 | Calcineurin B subunit [Trypanosoma cruzi]                        | 742  | 176  | 29.9 | 16.8 |
| p-cluster173714 | 27247 | Trans-sialidase [Trypanosoma cruzi]                              | 1638 | 1446 | 29.3 | 32.0 |
| p-cluster688261 | 27940 | Trans-sialidase [Trypanosoma cruzi]                              | 182  | 373  | 44.5 | 60.4 |
| p-cluster060553 | 27997 | Small GTPase Rab5 [Entamoeba histolytica]                        | 123  | 195  | 38.7 | 61.0 |
| p-cluster542461 | 27997 | Small GTPase Rab5 [Entamoeba histolytica]                        | 332  | 195  | 32.0 | 46.1 |
| p-cluster563931 | 28000 | Small GTPase Rab11B [Entamoeba histolytica]                      | 187  | 211  | 43.1 | 38.5 |
| p-cluster621238 | 28000 | Small GTPase Rab11B [Entamoeba histolytica]                      | 295  | 211  | 41.1 | 59.0 |
| p-cluster681597 | 28000 | Small GTPase Rab11B [Entamoeba histolytica]                      | 779  | 211  | 38.2 | 25.5 |
| p-cluster457390 | 28063 | Cyst wall protein 2 [Giardia lamblia]                            | 710  | 362  | 34.0 | 26.3 |
| p-cluster593714 | 28065 | Dynamin-like protein [Giardia intestinalis]                      | 1537 | 732  | 31.5 | 20.4 |
| p-cluster094690 | 28068 | GLP [Giardia lamblia]  | 2087 | 445  | 39.6 | 2.5  |
| p-cluster479841 | 28073 | Cruzipain [Trypanosoma cruzi]                                    | 1836 | 383  | 35.5 | 11.1 |
| p-cluster198255 | 28596 | Mitogen-activated protein kinase 13                              | 204  | 365  | 44.3 | 38.7 |
| p-cluster240502 | 28596 | Mitogen-activated protein kinase 13                              | 540  | 365  | 30.1 | 34.6 |
| p-cluster291907 | 28596 | Mitogen-activated protein kinase 13                              | 544  | 365  | 34.2 | 20.2 |
| p-cluster069608 | 30732 | Calglandulin   | 164  | 156  | 33.1 | 89.6 |
| p-cluster508880 | 30773 | Venom serine protease or Allergen                                | 1403 | 277  | 30.3 | 11.6 |
| p-cluster496872 | 31481 | Venom prothrombin activator                                      | 1149 | 467  | 28.8 | 19.0 |
| p-cluster707160 | 31481 | Venom prothrombin activator                                      | 591  | 467  | 32.4 | 32.3 |