

Supplemental Table 2. GO terms enriched in up- and down-regulated genes

| UP-REGULATED | Ontology ID | Ontology Name | Ontology Type | No. Changed | No. Measured | No. in Ontolog | % Changed | % Present | Z Score | Permute P | Adjusted P |
|--------------|----------------|--|----------------|-------------|--------------|-------------------|-----------------|----------------|------------|-----------|------------|
| | GO:0030554 | adenyl nucleotide binding | molecular_fun | 25 | 850 | 867 | 2.94 | 98.04 | 2.05083803 | 0.0595 | 1 |
| | GO:0032559 | adenyl ribonucleotide binding | molecular_fun | 25 | 849 | 866 | 2.94 | 98.04 | 2.05704183 | 0.0595 | 1 |
| | GO:0040812 | aminoadipate lyase activity | molecular_fun | 4 | 68 | 68 | 5.55 | 98.55 | 2.20859005 | 0.01875 | 1 |
| | GO:0005524 | ATP binding | molecular_fun | 25 | 847 | 864 | 2.95 | 98.03 | 2.06947206 | 0.062 | 1 |
| | GO:0043190 | ATP-binding cassette (ABC) transporter | cellular_comp | 3 | 43 | 43 | 6.98 | 100.00 | 2.33981471 | 0.0355 | 1 |
| | GO:0022403 | cell cycle phase | biological_pro | 13 | 222 | 222 | 5.86 | 100.00 | 4.15391262 | 0 | 0.32425 |
| | GO:0022402 | cell cycle process | biological_pro | 19 | 222 | 222 | 5.86 | 99.62 | 2.75117252 | 0.0025 | 0.60796874 |
| | GO:0000267 | cell fraction | cellular_comp | 7 | 118 | 118 | 5.93 | 100.00 | 3.07366599 | 0.0015 | 0.486375 |
| | GO:0044464 | cell part | cellular_comp | 136 | 6053 | 6530 | 2.25 | 92.70 | 2.07343074 | 0.82125 | 1 |
| | GO:0071842 | cellular component organization at cell junction | cellular_comp | 37 | 1349 | 1468 | 2.74 | 91.89 | 2.09309422 | 0.075 | 1 |
| | GO:0044255 | cellular lipid metabolic process | biological_pro | 10 | 197 | 198 | 5.08 | 99.49 | 3.11902121 | 0.00125 | 0.46321429 |
| | GO:0044427 | chromosomal part | cellular_comp | 11 | 267 | 377 | 4.12 | 70.82 | 2.51192043 | 0.0025 | 0.60796875 |
| | GO:0051276 | chromosome organization | biological_pro | 11 | 297 | 406 | 3.70 | 73.15 | 2.13318484 | 0.014 | 1 |
| | GO:0000781 | chromosome, telomeric region | cellular_comp | 3 | 11 | 11 | 27.27 | 100.00 | 5.99694947 | 0.00075 | 0.38975 |
| | GO:0008234 | cysteine-type peptidase activity | molecular_fun | 4 | 77 | 78 | 5.19 | 98.72 | 2.01402121 | 0.03425 | 1 |
| | GO:0015036 | disulfide oxidoreductase activity | molecular_fun | 3 | 29 | 29 | 10.34 | 100.00 | 3.21881951 | 0.007 | 1 |
| | GO:0006259 | DNA metabolic process | biological_pro | 10 | 250 | 251 | 4.00 | 99.50 | 2.29168345 | 0.0095 | 1 |
| | GO:0008094 | DNA-dependent ATPase activity | molecular_fun | 3 | 37 | 37 | 8.11 | 100.00 | 2.66271272 | 0.02025 | 1 |
| | GO:0004519 | endonuclease activity | molecular_fun | 3 | 49 | 50 | 6.12 | 98.00 | 2.06989569 | 0.041 | 1 |
| | GO:0005789 | endoplasmic reticulum membrane | cellular_comp | 7 | 145 | 145 | 4.83 | 100.00 | 2.45411219 | 0.00575 | 1 |
| | GO:0031012 | extracellular matrix | cellular_comp | 4 | 51 | 84 | 5.84 | 100.00 | 2.99251915 | 0.01375 | 1 |
| | GO:0044421 | extracellular region part | cellular_comp | 9 | 166 | 178 | 5.42 | 93.26 | 3.1797714 | 0.00125 | 0.46321429 |
| | GO:0030718 | germ-line stem cell maintenance | biological_pro | 3 | 36 | 36 | 8.33 | 100.00 | 2.72314119 | 0.018 | 1 |
| | GO:0046486 | glycerolipid metabolic process | biological_pro | 4 | 36 | 36 | 6.98 | 98.36 | 2.59384088 | 0.02025 | 1 |
| | GO:0006650 | glycerophospholipid metabolic process | biological_pro | 4 | 53 | 54 | 7.55 | 98.15 | 2.89648329 | 0.011 | 1 |
| | GO:0006055 | GPI anchor metabolic process | biological_pro | 3 | 25 | 25 | 12.00 | 100.00 | 3.58043554 | 0.0065 | 1 |
| | GO:0004553 | hydrolase activity, hydrolyzing O-glycosyl | molecular_fun | 5 | 103 | 108 | 4.85 | 95.37 | 2.08203576 | 0.019 | 1 |
| | GO:0015103 | inorganic anion transmembrane transport | molecular_fun | 3 | 44 | 44 | 6.82 | 100.00 | 2.92162236 | 0.03475 | 1 |
| | GO:0005626 | insoluble fraction | cellular_comp | 6 | 113 | 113 | 5.31 | 100.00 | 2.53162386 | 0.00575 | 1 |
| | GO:0008299 | isoprenoid biosynthetic process | biological_pro | 3 | 15 | 15 | 20.00 | 100.00 | 4.98892955 | 0.001 | 0.40957895 |
| | GO:0006720 | isoprenoid metabolic process | biological_pro | 3 | 15 | 15 | 20.00 | 100.00 | 5.90740055 | 0.002 | 0.60796875 |
| | GO:0000776 | kinetochore | cellular_comp | 5 | 29 | 29 | 17.24 | 100.00 | 5.87767728 | 0 | 0.32425 |
| | GO:0016876 | ligase activity, forming aminoacyl-tRNA | molecular_fun | 4 | 68 | 69 | 5.88 | 98.55 | 2.29850005 | 0.01875 | 1 |
| | GO:0016875 | ligase activity, forming carbon-oxygen | molecular_fun | 4 | 68 | 68 | 5.88 | 98.55 | 2.29850005 | 0.01875 | 1 |
| | GO:0009057 | macromolecule catabolic process | biological_pro | 8 | 199 | 202 | 4.02 | 98.51 | 2.060271 | 0.01225 | 1 |
| | GO:0005624 | membrane fraction | cellular_comp | 6 | 109 | 109 | 5.50 | 100.00 | 2.63213043 | 0.00475 | 0.97275 |
| | GO:0004222 | metalloendopeptidase activity | molecular_fun | 5 | 82 | 82 | 6.10 | 100.00 | 2.66551503 | 0.011 | 1 |
| | GO:0007552 | metastasis | cellular_comp | 3 | 27 | 27 | 11.11 | 96.43 | 3.39059555 | 0.0105 | 1 |
| | GO:0005792 | microsome | cellular_comp | 5 | 88 | 88 | 5.68 | 100.00 | 2.48210813 | 0.00875 | 1 |
| | GO:0031023 | microtubule organizing center organization | biological_pro | 3 | 48 | 48 | 6.25 | 100.00 | 2.11189276 | 0.0425 | 1 |
| | GO:0007067 | mitosis | biological_pro | 3 | 138 | 138 | 8.00 | 100.00 | 3.2128063 | 0.002 | 0.53669966 |
| | GO:0007094 | mitotic cell cycle spindle assembly | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 5.70086451 | 0.00025 | 0.32425 |
| | GO:0071174 | mitotic cell cycle spindle checkpoint | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 5.70086451 | 0.00025 | 0.32425 |
| | GO:0004497 | monooxygenase activity | molecular_fun | 6 | 116 | 117 | 5.17 | 99.15 | 2.45905722 | 0.01 | 1 |
| | GO:0004572 | negative regulation of cell cycle | biological_pro | 3 | 39 | 39 | 7.69 | 100.00 | 2.54799254 | 0.02425 | 1 |
| | GO:0010948 | negative regulation of cell cycle | biological_pro | 3 | 29 | 29 | 18.34 | 100.00 | 3.21881951 | 0.0085 | 1 |
| | GO:0045839 | negative regulation of mitosis | biological_pro | 3 | 16 | 16 | 10.75 | 100.00 | 4.79502808 | 0.001 | 0.40957895 |
| | GO:0045841 | negative regulation of mitotic metaphase | biological_pro | 3 | 14 | 14 | 14.43 | 100.00 | 5.20196131 | 0.0075 | 0.38975 |
| | GO:0051784 | negative regulation of nuclear division | biological_pro | 3 | 16 | 16 | 18.75 | 100.00 | 4.79502808 | 0.001 | 0.40957895 |
| | GO:0010639 | negative regulation of organelle organization | biological_pro | 3 | 40 | 40 | 7.50 | 100.00 | 2.49345246 | 0.02075 | 1 |
| | GO:0000280 | nuclear division | biological_pro | 8 | 141 | 141 | 5.67 | 100.00 | 3.14259575 | 0.002 | 0.53669966 |
| | GO:0048285 | organelle fission | biological_pro | 8 | 146 | 146 | 5.68 | 100.00 | 3.02957936 | 0.0075 | 0.62942647 |
| | GO:0006996 | organelle organization | biological_pro | 31 | 974 | 1091 | 3.18 | 89.28 | 2.77321697 | 0.00575 | 1 |
| | GO:0016667 | oxidoreductase activity, acting on a | molecular_fun | 3 | 41 | 41 | 7.32 | 100.00 | 2.44664116 | 0.01825 | 1 |
| | GO:0046488 | phosphatidylinositol metabolic process | biological_pro | 4 | 44 | 44 | 6.09 | 95.78 | 2.31645511 | 0.0075 | 1 |
| | GO:0046148 | pigment biosynthetic process | biological_pro | 4 | 51 | 51 | 7.84 | 100.00 | 2.99251915 | 0.0065 | 1 |
| | GO:0042440 | pigment metabolic process | biological_pro | 4 | 69 | 69 | 5.80 | 100.00 | 2.26466333 | 0.024 | 1 |
| | GO:0006779 | porphyrin biosynthetic process | biological_pro | 3 | 11 | 11 | 27.27 | 100.00 | 5.99694947 | 0.0015 | 0.486375 |
| | GO:0005778 | porphyria | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 5.70086451 | 0.0015 | 0.486375 |
| | GO:0007088 | regulation of mitosis | biological_pro | 4 | 46 | 46 | 6.72 | 100.00 | 3.25566561 | 0.00725 | 1 |
| | GO:0030071 | regulation of mitotic metaphase/anaphase | biological_pro | 4 | 24 | 24 | 16.70 | 100.00 | 5.14429492 | 0.001 | 0.40957895 |
| | GO:0051783 | regulation of nuclear division | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 3.25566561 | 0.00725 | 1 |
| | GO:0005819 | spindle | cellular_comp | 4 | 43 | 43 | 9.30 | 100.00 | 3.43227416 | 0.00375 | 0.83378571 |
| | GO:0071173 | spindle assembly checkpoint | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 5.70086451 | 0.00025 | 0.32425 |
| | GO:0031577 | spindle checkpoint | biological_pro | 3 | 12 | 12 | 25.00 | 100.00 | 5.70086451 | 0.00025 | 0.32425 |
| | GO:0019827 | stem cell maintenance | cellular_comp | 3 | 47 | 47 | 3.98 | 100.00 | 1.55003981 | 0.0425 | 1 |
| | GO:0044456 | synapse part | cellular_comp | 6 | 125 | 126 | 4.80 | 99.21 | 2.25432652 | 0.04325 | 1 |
| | GO:0033014 | tetrapyrrole biosynthetic process | biological_pro | 3 | 13 | 13 | 23.08 | 100.00 | 5.43768722 | 0.00175 | 0.50438889 |
| | GO:0033013 | tetrapyrrole biosynthetic process | biological_pro | 3 | 14 | 14 | 24.29 | 100.00 | 5.20196131 | 0.00175 | 0.50438889 |
| | GO:0000151 | ubiquitin ligase complex | cellular_comp | 3 | 14 | 14 | 48.25 | 100.00 | 2.11189276 | 0.037 | 1 |
| | GO:0042598 | vesicular fraction | cellular_comp | 5 | 88 | 88 | 5.68 | 100.00 | 2.48210813 | 0.00875 | 1 |
| | DOWN-REGULATED | | | | | | | | | | |
| | Ontology ID | Ontology Name | Ontology Type | Number | Meas. | Number in Ontolog | Percent Changed | Percent Preser | Z Score | PermuteP | AdjustedP |
| | GO:0022804 | active transmembrane transporter | molecular_fun | 12 | 372 | 377 | 3.23 | 98.67 | 2.85693886 | 0.003 | 1 |
| | GO:0046154 | alcohol dehydrogenase activity | molecular_fun | 3 | 51 | 51 | 5.88 | 100.00 | 2.62121722 | 0.0325 | 1 |
| | GO:0005275 | amine transmembrane transporter | molecular_fun | 4 | 59 | 59 | 6.78 | 100.00 | 3.39410121 | 0.007 | 1 |
| | GO:0015837 | amine transport | biological_pro | 3 | 44 | 44 | 6.82 | 100.00 | 2.95032707 | 0.02025 | 1 |
| | GO:0015171 | amino acid transmembrane transporter | molecular_fun | 4 | 54 | 54 | 7.41 | 100.00 | 3.63031984 | 0.0045 | 1 |
| | GO:0006865 | amino acid transport | biological_pro | 4 | 40 | 40 | 5.90 | 100.00 | 1.71211036 | 0.01375 | 1 |
| | GO:0006022 | aminoglycan metabolic process | biological_pro | 5 | 140 | 150 | 3.57 | 93.33 | 2.07566587 | 0.0175 | 1 |
| | GO:0006820 | anion transport | biological_pro | 3 | 53 | 54 | 5.66 | 98.15 | 2.53781528 | 0.024 | 1 |
| | GO:0043492 | ATPase activity, coupled to movement of | molecular_fun | 6 | 147 | 151 | 4.08 | 97.35 | 2.64466965 | 0.00875 | 1 |
| | GO:0042426 | ATPase activity, coupled to transmembrane | molecular_fun | 6 | 147 | 151 | 4.08 | 97.35 | 2.64466965 | 0.00875 | 1 |
| | GO:0043190 | ATP-binding cassette (ABC) transporter | cellular_comp | 3 | 43 | 43 | 6.98 | 100.00 | 3.00297625 | 0.01475 | 1 |
| | GO:0005509 | calcium ion binding | molecular_fun | 8 | 231 | 236 | 3.46 | 97.88 | 2.53838397 | 0.01075 | 1 |
| | GO:0016052 | carbohydrate catabolic process | biological_pro | 13 | 406 | 413 | 6.82 | 98.84 | 3.38915012 | 0.0025 | 0.38975 |
| | GO:0005975 | carbohydrate metabolic process | biological_pro | 13 | 408 | 422 | 3.19 | 96.68 | 2.92947458 | 0.002 | 1 |
| | GO:0046943 | carboxylic acid transmembrane transporter | molecular_fun | 7 | 86 | 87 | 8.14 | 98.85 | 5.15399915 | 0.00025 | 0.38975 |
| | GO:0046942 | carboxylic acid transport | biological_pro | 5 | 76 | 76 | 8.14 | 98.18 | 4.76289919 | 0.00025 | 0.38975 |
| | GO:0044275 | cellular carbohydrate catabolic process | biological_pro | 4 | 51 | 51 | 7.84 | 100.00 | 3.78652351 | 0.00275 | 1 |
| | GO:0044262 | cellular carbohydrate metabolic process | biological_pro | 6 | 184 | 188 | 3.26 | 97.87 | 2.03167306 | 0.032 | 1 |
| | GO:0008061 | chitin binding | molecular_fun | 4 | 99 | 107 | 4.04 | 92.52 | 2.13138702 | 0.02625 | 1 |
| | GO:0006030 | chitin metabolic process | biological_pro | 4 | 113 | 121 | 4.92 | 93.39 | 2.61066867 | 0.0085 | 1 |
| | GO:0048512 | circadian behavior | biological_pro | 4 | 45 | 45 | 8.89 | 100.00 | 4.13950999 | 0.0075 | 1 |