| KO | symbol | gene name | log2FC | p-value | adj. p-value |
|---|---|---|---|---|---|
| K08906 | petJ | cytochrome c6 | -12.37 | 2.96E-14 | 3.82E-11 |
| K02636 | petC | cytochrome b6-f complex iron-sulfur subunit [EC:1.10.9.1] | -13.56 | 1.96E-13 | 1.26E-10 |
| K00218 | E1.3.1.33, por | protochlorophyllide reductase [EC:1.3.1.33] | -11.21 | 1.68E-07 | 5.43E-05 |
| K03428 | E2.1.1.11, chlM, bchM | magnesium-protoporphyrin O-methyltransferase [EC:2.1.1.11] | -11.24 | 1.65E-07 | 5.43E-05 |
| K00463 | INDO | indoleamine 2,3-dioxygenase [EC:1.13.11.52] | 8.56 | 3.46E-07 | 8.92E-05 |
| K01768 | E4.6.1.1 | adenylate cyclase [EC:4.6.1.1] | -10.36 | 1.47E-06 | 3.16E-04 |
| K09839 | VDE, NPQ1 | violaxanthin de-epoxidase [EC:1.10.99.3] | -8.86 | 3.31E-06 | 6.10E-04 |
| K15634 | gpmB | probable phosphoglycerate mutase [EC:5.4.2.12] | 8.22 | 4.10E-06 | 6.61E-04 |
| K11150 | RDH8 | retinol dehydrogenase 8 [EC:1.1.1.-] | -10.29 | 4.82E-06 | 6.91E-04 |
| K03002 | RPA2, POLR1B | DNA-directed RNA polymerase I subunit RPA2 [EC:2.7.7.6] | 8.24 | 5.76E-06 | 7.44E-04 |
| K14424 | SMO2 | 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase [EC:1.14.13.72] | 8.17 | 1.05E-05 | 1.18E-03 |
| K09838 | ZEP, ABA1 | zeaxanthin epoxidase [EC:1.14.13.90] | -8.66 | 1.09E-05 | 1.18E-03 |
| K00284 | E1.4.7.1 | glutamate synthase (ferredoxin) [EC:1.4.7.1] | -8.82 | 1.19E-05 | 1.18E-03 |
| K10259 | MET30 | F-box and WD-40 domain protein MET30 | -9.28 | 3.64E-05 | 3.36E-03 |
| K02690 | psaB | photosystem I P700 chlorophyll a apoprotein A2 | -7.45 | 4.72E-05 | 3.83E-03 |
| K02257 | COX10 | protoheme IX farnesyltransferase [EC:2.5.1.-] | 8.18 | 4.79E-05 | 3.83E-03 |
| K01275 | CTSC | cathepsin C [EC:3.4.14.1] | -9.13 | 5.05E-05 | 3.83E-03 |
| K07253 | MIF | phenylpyruvate tautomerase [EC:5.3.2.1] | -9.03 | 6.91E-05 | 4.96E-03 |
| K09565 | PPIF | peptidyl-prolyl isomerase F (cyclophilin D) [EC:5.2.1.8] | 7.60 | 1.48E-04 | 8.29E-03 |
| K00616 | E2.2.1.2, talA, talB | transaldolase [EC:2.2.1.2] | 6.83 | 1.42E-04 | 8.29E-03 |
| K03527 | ispH, lytB | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.17.1.2] | -7.54 | 1.32E-04 | 8.29E-03 |
| K02720 | psbV | photosystem II cytochrome c550 | -8.62 | 1.38E-04 | 8.29E-03 |
| K17705 | KRIT1 | Krev interaction trapped protein 1 | -8.63 | 1.34E-04 | 8.29E-03 |
| K00223 | ERG4 | delta24(24(1))-sterol reductase [EC:1.3.1.71] | 7.41 | 1.62E-04 | 8.71E-03 |
| K16054 | DEP1 | methylthioribulose 1-phosphate dehydratase / enolase-phosphatase E1 [EC:4.2.1.109 3.1.3.77] | 7.04 | 1.84E-04 | 8.84E-03 |
| K03938 | NDUFS5 | NADH dehydrogenase (ubiquinone) Fe-S protein 5 | 6.87 | 1.78E-04 | 8.84E-03 |
| K15744 | Z-ISO | zeta-carotene isomerase [EC:5.2.1.12] | -8.54 | 1.85E-04 | 8.84E-03 |
| K00927 | PGK, pgk | phosphoglycerate kinase [EC:2.7.2.3] | -5.16 | 2.90E-04 | 1.34E-02 |
| K11927 | rhlE | ATP-dependent RNA helicase RhlE [EC:3.6.4.13] | 7.04 | 3.12E-04 | 1.39E-02 |
| K00134 | GAPDH, gapA | glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] | -5.21 | 3.83E-04 | 1.65E-02 |

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| K02293 | PDS, crtP | 15-cis-phytoene desaturase [EC:1.3.5.5] | -6.81 | 3.99E-04 | 1.66E-02 |
| K02707 | psbE | photosystem II cytochrome b559 subunit alpha | -6.87 | 5.50E-04 | 2.22E-02 |
| K08681 | pdxT, pdx2 | 5'-phosphate synthase pdxT subunit [EC:4.3.3.6] | -6.33 | 7.42E-04 | 2.90E-02 |
| K00031 | IDH1, IDH2, icd | isocitrate dehydrogenase [EC:1.1.1.42] | 5.13 | 7.67E-04 | 2.91E-02 |
| K00416 | QCR6, UQCRH | ubiquinol-cytochrome c reductase subunit 6 | -6.52 | 7.93E-04 | 2.92E-02 |
| K10257 | FAD8, desB | omega-3 fatty acid desaturase (delta-15 desaturase) [EC:1.14.19.-] | 7.06 | 9.11E-04 | 3.27E-02 |
| K11827 | AP2S1 | AP-2 complex subunit sigma-1 | 6.40 | 9.88E-04 | 3.45E-02 |
| K02132 | ATPeF1A, ATP5A1, ATP1 | F-type H+-transporting ATPase subunit alpha | 3.74 | 1.30E-03 | 4.21E-02 |
| K03100 | lepB | signal peptidase I [EC:3.4.21.89] | 6.47 | 1.34E-03 | 4.21E-02 |
| K08239 | GNPTAB | UDP-N-acetylglucosamine-lysosomal-enzyme [EC:2.7.8.17] | 6.29 | 1.25E-03 | 4.21E-02 |
| K08901 | psbQ | photosystem II oxygen-evolving enhancer protein 3 | -6.50 | 1.30E-03 | 4.21E-02 |
| K08334 | BECN1, VPS30, ATG6 | beclin 1 | 6.52 | 1.56E-03 | 4.80E-02 |
| K10144 | RCHY1, PIRH2 | RING finger and CHY zinc finger domain-containing protein 1 [EC:6.3.2.19] | 6.37 | 1.64E-03 | 4.94E-02 |
| K03404 | chlD, bchD | magnesium chelatase subunit D [EC:6.6.1.1] | -7.03 | 1.88E-03 | 5.51E-02 |
| K13953 | adhP | alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1] | -6.03 | 1.93E-03 | 5.54E-02 |
| K06134 | COQ7 | ubiquinone biosynthesis monooxygenase Coq7 [EC:1.14.13.-] | 6.30 | 1.97E-03 | 5.54E-02 |
| K03130 | TAF5 | transcription initiation factor TFIID subunit 5 | 6.39 | 2.48E-03 | 6.16E-02 |
| K07366 | GRAP2, GADS | GRB2-related adaptor protein 2 | 6.48 | 2.45E-03 | 6.16E-02 |
| K05641 | ABCA1 | ATP-binding cassette, subfamily A (ABC1), member 1 | -5.38 | 2.40E-03 | 6.16E-02 |
| K09518 | DNAJB12 | DnaJ homolog subfamily B member 12 | 5.43 | 2.48E-03 | 6.16E-02 |
| K11129 | NHP2, NOLA2 | H/ACA ribonucleoprotein complex subunit 2 | 5.32 | 2.26E-03 | 6.16E-02 |
| K11094 | SNRPB2 | U2 small nuclear ribonucleoprotein B" | -6.91 | 2.31E-03 | 6.16E-02 |
| K14157 | AASS | alpha-aminoadipic semialdehyde synthase [EC:1.5.1.8 1.5.1.9] | 6.32 | 2.56E-03 | 6.25E-02 |
| K03952 | NDUFA8 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8 | 6.00 | 2.81E-03 | 6.43E-02 |
| K02113 | ATPF1D, atpH | F-type H+-transporting ATPase subunit delta | 6.27 | 2.83E-03 | 6.43E-02 |
| K13998 | DHFR-TS | dihydrofolate reductase / thymidylate synthase [EC:1.5.1.3 2.1.1.45] | 5.98 | 2.84E-03 | 6.43E-02 |
| K12948 | SPCS3, SPC3 | signal peptidase complex subunit 3 [EC:3.4.-.-] | 5.98 | 2.78E-03 | 6.43E-02 |
| K00365 | E1.7.3.3 | urate oxidase [EC:1.7.3.3] | 6.26 | 3.56E-03 | 7.79E-02 |
| K02974 | RP-S24e, RPS24 | small subunit ribosomal protein S24e | 4.70 | 3.53E-03 | 7.79E-02 |

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| K01581 | E4.1.1.17,<br>ODC1,<br>speC,<br>speF | ornithine decarboxylase [EC:4.1.1.17] | 4.59 | 3.87E-03 | 8.18E-02 |
| K02716 | psbO | photosystem II oxygen-evolving enhancer protein 1 | -5.98 | 3.81E-03 | 8.18E-02 |
| K01809 | manA,<br>MPI | mannose-6-phosphate isomerase [EC:5.3.1.8] | -5.67 | 4.21E-03 | 8.76E-02 |
| K10413 | DYNC1H | dynein heavy chain 1, cytosolic | -4.91 | 4.74E-03 | 9.71E-02 |
| K04077 | groEL,<br>HSPD1 | chaperonin GroEL | -3.80 | 4.87E-03 | 9.83E-02 |
| K13025 | EIF4A3,<br>FAL1 | ATP-dependent RNA helicase [EC:3.6.4.13] | -3.39 | 5.16E-03 | 9.94E-02 |
| K02897 | RP-L25,<br>rplY | large subunit ribosomal protein L25 | 5.92 | 5.10E-03 | 9.94E-02 |
| K06066 | CIR | CBF1 interacting corepressor | 5.52 | 5.15E-03 | 9.94E-02 |