**Suppl. Table 3. GO pathway for negatively correlated genes.**

|  |  |  |  |
| --- | --- | --- | --- |
| **GO biological process complete** | **Fold Enrichment** | **raw P-value** | **FDR** |
| regulation of catalytic activity (GO:0050790) | 1.9 | 5.56E-05 | 8.71E-01 |
| renal absorption (GO:0070293) | 22.34 | 5.67E-05 | 4.45E-01 |
| regulation of molecular function (GO:0065009) | 1.74 | 6.67E-05 | 3.48E-01 |
| microtubule nucleation (GO:0007020) | 16.33 | 1.67E-04 | 6.54E-01 |
| regulation of hydrolase activity (GO:0051336) | 2.33 | 2.92E-04 | 9.14E-01 |
| response to inorganic substance (GO:0010035) | 2.89 | 4.59E-04 | 1.00E+00 |
| renal system process (GO:0003014) | 6.18 | 5.59E-04 | 1.00E+00 |
| microtubule polymerization (GO:0046785) | 11.47 | 5.69E-04 | 1.00E+00 |
| negative regulation of JNK cascade (GO:0046329) | 11.47 | 5.69E-04 | 9.91E-01 |
| cellular response to cadmium ion (GO:0071276) | 11.17 | 6.24E-04 | 9.79E-01 |
| regulation of plasma membrane bounded cell projection assembly (GO:0120032) | 4.38 | 6.39E-04 | 9.10E-01 |
| response to metal ion (GO:0010038) | 3.3 | 6.65E-04 | 8.69E-01 |
| regulation of cell projection assembly (GO:0060491) | 4.33 | 6.81E-04 | 8.21E-01 |
| prostaglandin metabolic process (GO:0006693) | 10.89 | 6.83E-04 | 7.65E-01 |
| prostanoid metabolic process (GO:0006692) | 10.89 | 6.83E-04 | 7.14E-01 |
| detoxification of copper ion (GO:0010273) | 19.9 | 6.95E-04 | 6.81E-01 |
| stress response to copper ion (GO:1990169) | 19.9 | 6.95E-04 | 6.41E-01 |
| positive regulation of catalytic activity (GO:0043085) | 2.15 | 7.01E-04 | 6.11E-01 |
| icosanoid metabolic process (GO:0006690) | 5.74 | 8.12E-04 | 6.70E-01 |
| detoxification of inorganic compound (GO:0061687) | 16.76 | 1.08E-03 | 8.48E-01 |
| stress response to metal ion (GO:0097501) | 15.92 | 1.24E-03 | 9.22E-01 |
| negative regulation of stress-activated MAPK cascade (GO:0032873) | 8.84 | 1.40E-03 | 1.00E+00 |
| negative regulation of stress-activated protein kinase signaling cascade (GO:0070303) | 8.84 | 1.40E-03 | 9.57E-01 |
| lipid metabolic process (GO:0006629) | 2.01 | 1.84E-03 | 1.00E+00 |
| response to toxic substance (GO:0009636) | 3.64 | 1.97E-03 | 1.00E+00 |
| response to zinc ion (GO:0010043) | 7.86 | 2.11E-03 | 1.00E+00 |
| microtubule polymerization or depolymerization (GO:0031109) | 7.86 | 2.11E-03 | 1.00E+00 |
| gene expression (GO:0010467) | 0.37 | 2.11E-03 | 1.00E+00 |
| cellular response to zinc ion (GO:0071294) | 12.74 | 2.21E-03 | 1.00E+00 |
| purine ribonucleoside diphosphate catabolic process (GO:0009181) | 35.38 | 2.34E-03 | 1.00E+00 |
| purine nucleoside diphosphate catabolic process (GO:0009137) | 35.38 | 2.34E-03 | 1.00E+00 |
| regulation of plasma membrane bounded cell projection organization (GO:0120035) | 2.4 | 2.60E-03 | 1.00E+00 |
| regulation of cellular component biogenesis (GO:0044087) | 2.13 | 2.78E-03 | 1.00E+00 |
| cellular aldehyde metabolic process (GO:0006081) | 7.2 | 2.85E-03 | 1.00E+00 |
| cellular response to copper ion (GO:0071280) | 11.37 | 2.97E-03 | 1.00E+00 |
| oligosaccharide biosynthetic process (GO:0009312) | 11.37 | 2.97E-03 | 1.00E+00 |
| ERBB2 signaling pathway (GO:0038128) | 30.32 | 2.99E-03 | 1.00E+00 |
| response to cadmium ion (GO:0046686) | 7.08 | 3.02E-03 | 1.00E+00 |
| response to calcium ion (GO:0051592) | 4.36 | 3.08E-03 | 1.00E+00 |
| unsaturated fatty acid metabolic process (GO:0033559) | 5.15 | 3.45E-03 | 1.00E+00 |
| positive regulation of hydrolase activity (GO:0051345) | 2.4 | 3.68E-03 | 1.00E+00 |
| centrosome separation (GO:0051299) | 26.53 | 3.71E-03 | 1.00E+00 |
| ribonucleoside diphosphate catabolic process (GO:0009191) | 26.53 | 3.71E-03 | 1.00E+00 |
| regulation of ruffle assembly (GO:1900027) | 10.27 | 3.87E-03 | 1.00E+00 |
| regulation of peptidase activity (GO:0052547) | 2.61 | 4.02E-03 | 1.00E+00 |
| adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway (GO:0007196) | 23.58 | 4.51E-03 | 1.00E+00 |
| response to bacterium (GO:0009617) | 2.19 | 5.01E-03 | 1.00E+00 |
| activation of GTPase activity (GO:0090630) | 4.65 | 5.21E-03 | 1.00E+00 |
| regulation of cell projection organization (GO:0031344) | 2.34 | 5.29E-03 | 1.00E+00 |
| positive regulation of axon regeneration (GO:0048680) | 21.23 | 5.38E-03 | 1.00E+00 |
| RNA processing (GO:0006396) | 0.12 | 5.38E-03 | 1.00E+00 |
| cellular zinc ion homeostasis (GO:0006882) | 8.84 | 5.72E-03 | 1.00E+00 |
| cellular response to inorganic substance (GO:0071241) | 3.35 | 5.83E-03 | 1.00E+00 |
| nucleotide catabolic process (GO:0009166) | 5.82 | 5.86E-03 | 1.00E+00 |
| negative regulation of MAPK cascade (GO:0043409) | 3.79 | 5.94E-03 | 1.00E+00 |
| microtubule bundle formation (GO:0001578) | 4.46 | 6.19E-03 | 1.00E+00 |
| positive regulation of neuron projection regeneration (GO:0070572) | 19.3 | 6.32E-03 | 1.00E+00 |
| regulation of transferase activity (GO:0051338) | 2.03 | 6.59E-03 | 1.00E+00 |
| zinc ion homeostasis (GO:0055069) | 8.16 | 7.04E-03 | 1.00E+00 |
| regulation of endopeptidase activity (GO:0052548) | 2.53 | 7.23E-03 | 1.00E+00 |
| p38MAPK cascade (GO:0038066) | 17.69 | 7.33E-03 | 1.00E+00 |
| amide transport (GO:0042886) | 4.25 | 7.53E-03 | 1.00E+00 |
| cytoskeleton organization (GO:0007010) | 1.87 | 7.88E-03 | 1.00E+00 |
| purine ribonucleotide catabolic process (GO:0009154) | 7.77 | 8.01E-03 | 1.00E+00 |
| epithelial cilium movement involved in extracellular fluid movement (GO:0003351) | 7.77 | 8.01E-03 | 1.00E+00 |
| positive regulation of molecular function (GO:0044093) | 1.74 | 8.15E-03 | 1.00E+00 |
| negative regulation of sodium ion transmembrane transporter activity (GO:2000650) | 16.33 | 8.40E-03 | 1.00E+00 |
| nucleoside diphosphate catabolic process (GO:0009134) | 16.33 | 8.40E-03 | 1.00E+00 |
| response to copper ion (GO:0046688) | 7.58 | 8.52E-03 | 1.00E+00 |
| nucleoside phosphate catabolic process (GO:1901292) | 5.11 | 8.97E-03 | 1.00E+00 |
| peptide transport (GO:0015833) | 5.05 | 9.33E-03 | 1.00E+00 |
| oligopeptide transport (GO:0006857) | 15.16 | 9.54E-03 | 1.00E+00 |
| negative regulation of sodium ion transmembrane transport (GO:1902306) | 15.16 | 9.54E-03 | 1.00E+00 |
| actin crosslink formation (GO:0051764) | 15.16 | 9.54E-03 | 1.00E+00 |
| extracellular transport (GO:0006858) | 7.24 | 9.61E-03 | 1.00E+00 |
| activation of protein kinase activity (GO:0032147) | 3.99 | 9.61E-03 | 1.00E+00 |
| negative regulation of endopeptidase activity (GO:0010951) | 3.02 | 9.83E-03 | 1.00E+00 |
| purine nucleotide catabolic process (GO:0006195) | 7.08 | 1.02E-02 | 1.00E+00 |
| central nervous system development (GO:0007417) | 1.92 | 1.05E-02 | 1.00E+00 |
| detoxification (GO:0098754) | 3.9 | 1.05E-02 | 1.00E+00 |
| regulation of protein kinase activity (GO:0045859) | 2.15 | 1.06E-02 | 1.00E+00 |
| G protein-coupled glutamate receptor signaling pathway (GO:0007216) | 14.15 | 1.08E-02 | 1.00E+00 |
| positive regulation of ruffle assembly (GO:1900029) | 14.15 | 1.08E-02 | 1.00E+00 |
| response to pH (GO:0009268) | 6.92 | 1.08E-02 | 1.00E+00 |
| sensory perception of chemical stimulus (GO:0007606) | < 0.01 | 1.08E-02 | 1.00E+00 |
| cellular response to metal ion (GO:0071248) | 3.3 | 1.11E-02 | 1.00E+00 |
| locomotory behavior (GO:0007626) | 3.3 | 1.11E-02 | 1.00E+00 |
| intracellular signal transduction (GO:0035556) | 1.72 | 1.12E-02 | 1.00E+00 |
| regulation of sodium ion transport (GO:0002028) | 4.77 | 1.13E-02 | 1.00E+00 |
| detection of stimulus involved in sensory perception (GO:0050906) | < 0.01 | 1.14E-02 | 1.00E+00 |
| ribonucleotide catabolic process (GO:0009261) | 6.77 | 1.14E-02 | 1.00E+00 |
| negative regulation of peptidase activity (GO:0010466) | 2.91 | 1.17E-02 | 1.00E+00 |
| DNA-dependent DNA replication maintenance of fidelity (GO:0045005) | 6.63 | 1.20E-02 | 1.00E+00 |
| cellular response to acidic pH (GO:0071468) | 13.27 | 1.20E-02 | 1.00E+00 |
| negative regulation of biological process (GO:0048519) | 1.32 | 1.28E-02 | 1.00E+00 |
| maintenance of location in cell (GO:0051651) | 4.56 | 1.30E-02 | 1.00E+00 |
| regulation of MAPK cascade (GO:0043408) | 2.07 | 1.32E-02 | 1.00E+00 |
| purine-containing compound catabolic process (GO:0072523) | 6.37 | 1.33E-02 | 1.00E+00 |
| fucosylation (GO:0036065) | 12.49 | 1.34E-02 | 1.00E+00 |
| membrane depolarization during cardiac muscle cell action potential (GO:0086012) | 12.49 | 1.34E-02 | 1.00E+00 |
| 3'-UTR-mediated mRNA destabilization (GO:0061158) | 12.49 | 1.34E-02 | 1.00E+00 |
| olefinic compound metabolic process (GO:0120254) | 3.66 | 1.34E-02 | 1.00E+00 |
| positive regulation of protein polymerization (GO:0032273) | 4.52 | 1.35E-02 | 1.00E+00 |
| protein polymerization (GO:0051258) | 4.52 | 1.35E-02 | 1.00E+00 |
| regulation of protein polymerization (GO:0032271) | 3.15 | 1.36E-02 | 1.00E+00 |
| regulation of organelle assembly (GO:1902115) | 3.12 | 1.42E-02 | 1.00E+00 |
| RNA metabolic process (GO:0016070) | 0.38 | 1.42E-02 | 1.00E+00 |
| activation of NF-kappaB-inducing kinase activity (GO:0007250) | 11.79 | 1.47E-02 | 1.00E+00 |
| Unclassified (UNCLASSIFIED) | 0.57 | 1.51E-02 | 1.00E+00 |
| biological\_process (GO:0008150) | 1.07 | 1.51E-02 | 1.00E+00 |
| membrane depolarization (GO:0051899) | 6.01 | 1.55E-02 | 1.00E+00 |
| detection of chemical stimulus involved in sensory perception (GO:0050907) | < 0.01 | 1.60E-02 | 1.00E+00 |
| organophosphate catabolic process (GO:0046434) | 3.49 | 1.61E-02 | 1.00E+00 |
| mRNA stabilization (GO:0048255) | 5.9 | 1.62E-02 | 1.00E+00 |
| retinal metabolic process (GO:0042574) | 11.17 | 1.62E-02 | 1.00E+00 |
| negative regulation of sodium ion transport (GO:0010766) | 11.17 | 1.62E-02 | 1.00E+00 |
| regulation of hydrogen peroxide metabolic process (GO:0010310) | 11.17 | 1.62E-02 | 1.00E+00 |
| regulation of organelle organization (GO:0033043) | 1.78 | 1.65E-02 | 1.00E+00 |
| 3'-UTR-mediated mRNA stabilization (GO:0070935) | 10.61 | 1.77E-02 | 1.00E+00 |
| retrograde axonal transport (GO:0008090) | 10.61 | 1.77E-02 | 1.00E+00 |
| cellular chemical homeostasis (GO:0055082) | 2 | 1.79E-02 | 1.00E+00 |
| ERBB signaling pathway (GO:0038127) | 5.59 | 1.86E-02 | 1.00E+00 |
| antibacterial humoral response (GO:0019731) | 5.59 | 1.86E-02 | 1.00E+00 |