|  |
| --- |
| **Table S1 Enriched KEGG pathway** |
| # | KEGG Pathway | DEGs genes with pathway annotation (Gene Number) | All genes with pathway annotation (Background number) | P-Value | Pathway ID |
| 1 | Carbohydrate digestion and absorption | 5 | 116 | 0.004451214 | ko04973 |
| 2 | Pentose and glucuronate interconversions | 4 | 111 | 0.019656025 | ko00040 |
| 3 | Estrogen signaling pathway | 6 | 216 | 0.015236596 | ko04915 |
| 4 | Antigen processing and presentation | 7 | 262 | 0.010990207 | ko04612 |
| 5 | Endocytosis | 8 | 394 | 0.030073798 | ko04144 |
| 6 | Protein processing in endoplasmic reticulum | 10 | 605 | 0.054181144 | ko04141 |
| 7 | RNA degradation | 4 | 159 | 0.060311891 | ko03018 |
| 8 | Starch and sucrose metabolism | 6 | 309 | 0.067496952 | ko00500 |
| 9 | Biosynthesis of ansamycins | 1 | 8 | 0.071778099 | ko01051 |
| 10 | Apoptosis | 5 | 362 | 0.245015214 | ko04210 |
| 11 | Cell cycle | 1 | 144 | 0.740170047 | ko04110 |
| 12 | Necroptosis | 3 | 234 | 0.36927766 | ko04217 |
| 13 | Oocyte meiosis | 1 | 166 | 0.788799668 | ko04114 |
| 14 | Regulation of actin cytoskeleton | 3 | 370 | 0.670768255 | ko04810 |
| 15 | Adherens junction | 2 | 245 | 0.666316347 | ko04520 |
| 16 | Focal adhesion | 3 | 352 | 0.63740108 | ko04510 |
| 17 | Gap junction | 3 | 162 | 0.18999664 | ko04540 |
| 18 | Tight junction | 4 | 471 | 0.639691151 | ko04530 |
| 19 | Lysosome | 7 | 433 | 0.107414375 | ko04142 |
| 20 | Phagosome | 7 | 463 | 0.138351022 | ko04145 |
| 21 | Calcium signaling pathway | 2 | 184 | 0.510766129 | ko04020 |
| 22 | cAMP signaling pathway | 2 | 301 | 0.771948459 | ko04024 |
| 23 | cGMP - PKG signaling pathway | 3 | 322 | 0.576818658 | ko04022 |
| 24 | Hippo signaling pathway -fly | 2 | 262 | 0.701959924 | ko04391 |
| 25 | Hippo signaling pathway | 2 | 285 | 0.745137818 | ko04390 |
| 26 | MAPK signaling pathway - fly | 2 | 257 | 0.691814018 | ko04013 |
| 27 | MAPK signaling pathway | 4 | 250 | 0.201931613 | ko04010 |
| 28 | MAPK signaling pathway - yeast | 1 | 102 | 0.614456126 | ko04011 |
| 29 | Phospholipase D signaling pathway | 2 | 116 | 0.291937095 | ko04072 |
| 30 | PI3K-Akt signaling pathway | 3 | 329 | 0.591497681 | ko04151 |
| 31 | Protein export | 1 | 74 | 0.498786236 | ko03060 |
| 32 | Basal transcription factors | 1 | 46 | 0.348780147 | ko03022 |
| 33 | Spliceosome | 3 | 284 | 0.491811402 | ko03040 |
| 34 | Ribosome biogenesis in eukaryotes | 1 | 95 | 0.588296949 | ko03008 |
| 35 | Ribosome | 3 | 440 | 0.779207045 | ko03010 |
| 36 | RNA transport | 5 | 358 | 0.238122212 | ko03013 |
| 37 | Arginine and proline metabolism | 3 | 116 | 0.09287874 | ko00330 |
| 38 | Glycine, serine and threonine metabolism | 1 | 83 | 0.539294725 | ko00260 |
| 39 | Lysine degradation | 1 | 115 | 0.658739981 | ko00310 |
| 40 | Tryptophan metabolism | 1 | 88 | 0.560378391 | ko00380 |
| 41 | Flavone and flavonol biosynthesis | 1 | 14 | 0.122236126 | ko00944 |
| 42 | Streptomycin biosynthesis | 1 | 42 | 0.32399291 | ko00521 |
| 43 | Amino sugar and nucleotide sugar metabolism | 1 | 167 | 0.790781397 | ko00520 |
| 44 | Citrate cycle (TCA cycle) | 1 | 110 | 0.642338795 | ko00020 |
| 45 | Fructose and mannose metabolism | 2 | 112 | 0.278199659 | ko00051 |
| 46 | Galactose metabolism | 2 | 105 | 0.254135415 | ko00052 |
| 47 | Glycolysis / Gluconeogenesis | 3 | 178 | 0.22833776 | ko00010 |
| 48 | Inositol phosphate metabolism | 1 | 91 | 0.572566272 | ko00562 |
| 49 | Pentose phosphate pathway | 1 | 63 | 0.44445176 | ko00030 |
| 50 | Pyruvate metabolism | 1 | 107 | 0.632125296 | ko00620 |
| 51 | Carbon fixation in photosynthetic organisms | 2 | 93 | 0.213082065 | ko00710 |
| 52 | Methane metabolism | 1 | 79 | 0.521708254 | ko00680 |
| 53 | Oxidative phosphorylation | 3 | 342 | 0.617888056 | ko00190 |
| 54 | Glycosaminoglycan degradation | 1 | 40 | 0.311250656 | ko00531 |
| 55 | N-Glycan biosynthesis | 2 | 84 | 0.182771865 | ko00510 |
| 56 | Various types of N-glycan biosynthesis | 1 | 72 | 0.4893153 | ko00513 |
| 57 | Ether lipid metabolism | 1 | 30 | 0.243877218 | ko00565 |
| 58 | Glycerolipid metabolism | 1 | 82 | 0.534959177 | ko00561 |
| 59 | Porphyrin and chlorophyll metabolism | 1 | 90 | 0.568541349 | ko00860 |
| 60 | Glutathione metabolism | 1 | 131 | 0.70637293 | ko00480 |
| 61 | Selenocompound metabolism | 1 | 38 | 0.298270225 | ko00450 |
| 62 | Insect hormone biosynthesis | 1 | 56 | 0.406874171 | ko00981 |
| 63 | Purine metabolism | 3 | 297 | 0.521849456 | ko00230 |
| 64 | Biosynthesis of amino acids | 4 | 249 | 0.200025715 | ko01230 |
| 65 | Carbon metabolism | 5 | 365 | 0.250220246 | ko01200 |
| 66 | Drug metabolism - other enzymes | 1 | 106 | 0.628656926 | ko00983 |
| 67 | Longevity regulating pathway - multiple species | 3 | 150 | 0.162478482 | ko04213 |
| 68 | Adrenergic signaling in cardiomyocytes | 2 | 309 | 0.784417638 | ko04261 |
| 69 | Cardiac muscle contraction | 2 | 262 | 0.701959924 | ko04260 |
| 70 | Dorso-ventral axis formation | 1 | 56 | 0.406874171 | ko04320 |
| 71 | Bile secretion | 1 | 158 | 0.772260899 | ko04976 |
| 72 | Gastric acid secretion | 1 | 113 | 0.652270992 | ko04971 |
| 73 | Mineral absorption | 1 | 97 | 0.595945585 | ko04978 |
| 74 | Protein digestion and absorption | 1 | 141 | 0.732730517 | ko04974 |
| 75 | Salivary secretion | 4 | 184 | 0.091613621 | ko04970 |
| 76 | Glucagon signaling pathway | 2 | 188 | 0.522292533 | ko04922 |
| 77 | Insulin secretion | 1 | 129 | 0.700799953 | ko04911 |
| 78 | PPAR signaling pathway | 3 | 282 | 0.487109792 | ko03320 |
| 79 | Progesterone-mediated oocyte maturation | 2 | 135 | 0.356499306 | ko04914 |
| 80 | Renin secretion | 1 | 146 | 0.745015254 | ko04924 |
| 81 | Thyroid hormone signaling pathway | 2 | 314 | 0.791906365 | ko04919 |
| 82 | Thyroid hormone synthesis | 3 | 174 | 0.218605502 | ko04918 |
| 83 | Plant-pathogen interaction | 2 | 111 | 0.274762339 | ko04626 |
| 84 | Aldosterone-regulated sodium reabsorption | 1 | 99 | 0.603453267 | ko04960 |
| 85 | Collecting duct acid secretion | 2 | 66 | 0.124758284 | ko04966 |
| 86 | Endocrine and other factor-regulated calcium reabsorption | 2 | 154 | 0.418905964 | ko04961 |
| 87 | Proximal tubule bicarbonate reclamation | 1 | 89 | 0.564478837 | ko04964 |
| 88 | IL-17 signaling pathway | 2 | 110 | 0.27132439 | ko04657 |
| 89 | Leukocyte transendothelial migration | 2 | 242 | 0.659684995 | ko04670 |
| 90 | NOD-like receptor signaling pathway | 3 | 223 | 0.341407707 | ko04621 |
| 91 | Th17 cell differentiation | 2 | 101 | 0.240403581 | ko04659 |
| 92 | Toll and Imd signaling pathway | 1 | 75 | 0.503456167 | ko04624 |
| 93 | Retrograde endocannabinoid signaling | 1 | 152 | 0.759019677 | ko04723 |
| 94 | Synaptic vesicle cycle | 3 | 175 | 0.221030364 | ko04721 |
| 95 | Phototransduction - fly | 1 | 163 | 0.782742091 | ko04745 |
| 96 | Rap1 signaling pathway | 2 | 333 | 0.818325446 | ko04015 |
| 97 | Neurotrophin signaling pathway | 1 | 191 | 0.833182313 | ko04722 |
| 98 | mTOR signaling pathway | 1 | 201 | 0.848223142 | ko04150 |
| 99 | Autophagy - animal | 1 | 246 | 0.900883306 | ko04140 |
| 100 | Peroxisome | 1 | 253 | 0.907252608 | ko04146 |
| 101 | Longevity regulating pathway - worm | 1 | 240 | 0.895079903 | ko04212 |
| 102 | Pancreatic secretion | 1 | 258 | 0.911551912 | ko04972 |
| 103 | Platelet activation | 1 | 228 | 0.882443164 | ko04611 |
| 104 | Oxytocin signaling pathway | 1 | 299 | 0.940109695 | ko04921 |