Table S7: Functional pathways predicted by Tax4Fun analyses altered by diet in cecum of growing pigs provided inulin

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| --- | --- | --- | --- |
| Tax4Fun-based Pathways | | Inu Relative to Con | |
| Fold Difference3 | *P*4 |
| ko00620 | Pyruvate metabolism | -0.10 | <0.01 |
| ko00280 | Valine, leucine and isoleucine degradation | -0.23 | <0.05 |
| ko00500 | Starch and sucrose metabolism | 0.16 | 0.05 |
| ko00640 | Propanoate metabolism | -0.12 | <0.05 |
| ko00650 | Butanoate metabolism | -0.18 | <0.01 |
| ko01212 | Fatty acid metabolism | -0.10 | 0.05 |
| ko00310 | Lysine degradation | -0.27 | <0.05 |
| ko00052 | Galactose metabolism | 0.12 | <0.05 |
| ko00770 | Pantothenate and CoA biosynthesis | -0.10 | <0.05 |
| ko00380 | Tryptophan metabolism | -0.28 | <0.05 |
| ko02010 | ABC transporters | 0.07 | <0.05 |
| ko00525 | Acarbose and validamycin biosynthesis | -0.17 | <0.05 |
| ko00250 | Alanine, aspartate and glutamate metabolism | -<0.05 | <0.05 |
| ko05034 | Alcoholism | 0.98 | <0.01 |
| ko00520 | Amino sugar and nucleotide sugar metabolism | 0.07 | <0.05 |
| ko05031 | Amphetamine addiction | 0.98 | <0.01 |
| ko00965 | Betalain biosynthesis | -1.06 | <0.01 |
| ko01130 | Biosynthesis of antibiotics | -0.05 | <0.01 |
| ko01110 | Biosynthesis of secondary metabolites | -<0.05 | <0.05 |
| ko01056 | Biosynthesis of type II polyketide backbone | -0.97 | <0.05 |
| ko01057 | Biosynthesis of type II polyketide products | 0.77 | <0.01 |
| ko01055 | Biosynthesis of vancomycin group antibiotics | -0.18 | <0.05 |
| ko05219 | Bladder cancer | -0.43 | <0.01 |
| ko00930 | Caprolactam degradation | -0.39 | <0.05 |
| ko04973 | Carbohydrate digestion and absorption | 0.20 | <0.01 |
| ko00720 | Carbon fixation pathways in prokaryotes | -0.08 | <0.01 |
| ko01200 | Carbon metabolism | -0.08 | <0.01 |
| ko04979 | Cholesterol metabolism | 0.78 | <0.01 |
| ko05231 | Choline metabolism in cancer | 0.67 | <0.05 |
| ko00020 | Citrate cycle (TCA cycle) | -0.10 | <0.01 |
| ko05030 | Cocaine addiction | 0.98 | <0.01 |
| ko05210 | Colorectal cancer | 0.69 | <0.05 |
| ko00473 | D-Alanine metabolism | 0.17 | <0.05 |
| ko00472 | D-Arginine and D-ornithine metabolism | 1.04 | <0.01 |
| ko01220 | Degradation of aromatic compounds | 0.08 | <0.05 |
| ko04728 | Dopaminergic synapse | 0.98 | <0.01 |
| ko00062 | Fatty acid elongation | 0.57 | <0.05 |
| ko00941 | Flavonoid biosynthesis | 1.02 | <0.05 |
| ko00790 | Folate biosynthesis | -0.19 | <0.05 |
| ko04724 | Glutamatergic synapse | 0.11 | <0.05 |
| ko00564 | Glycerophospholipid metabolism | 0.14 | <0.01 |
| ko00604 | Glycosphingolipid biosynthesis - ganglio series | 0.88 | <0.05 |
| ko00630 | Glyoxylate and dicarboxylate metabolism | -0.17 | <0.05 |
| ko05161 | Hepatitis B | 0.69 | <0.05 |
| ko05160 | Hepatitis C | -0.82 | <0.01 |
| ko05168 | Herpes simplex infection | -0.72 | <0.05 |
| ko05166 | HTLV-I infection | 0.78 | <0.01 |
| ko05163 | Human cytomegalovirus infection | 0.69 | <0.05 |
| ko05165 | Human papillomavirus infection | -0.09 | <0.01 |
| ko05164 | Influenza A | -0.72 | <0.05 |
| ko05167 | Kaposi's sarcoma-associated herpesvirus infection | 0.69 | <0.05 |
| ko00540 | Lipopolysaccharide biosynthesis | -0.51 | <0.05 |
| ko05162 | Measles | -0.82 | <0.01 |
| ko01100 | Metabolic pathways | -<0.05 | <0.05 |
| ko00680 | Methane metabolism | -0.06 | <0.05 |
| ko01120 | Microbial metabolism in diverse environments | -0.08 | <0.05 |
| ko05206 | MicroRNAs in cancer | 0.41 | <0.05 |
| ko04080 | Neuroactive ligand-receptor interaction | 0.78 | <0.01 |
| ko00510 | N-Glycan biosynthesis | 0.34 | <0.05 |
| ko00633 | Nitrotoluene degradation | -0.40 | <0.05 |
| ko04932 | Non-alcoholic fatty liver disease (NAFLD) | -0.59 | 0.05 |
| ko03420 | Nucleotide excision repair | 0.09 | 0.05 |
| ko04115 | p53 signaling pathway | 0.69 | <0.05 |
| ko05012 | Parkinson's disease | 1.02 | <0.05 |
| ko00040 | Pentose and glucuronate interconversions | -0.22 | <0.05 |
| ko05133 | Pertussis | -0.46 | <0.05 |
| ko04070 | Phosphatidylinositol signaling system | 0.14 | <0.01 |
| ko04072 | Phospholipase D signaling pathway | 0.69 | <0.01 |
| ko03320 | PPAR signaling pathway | -0.25 | <0.05 |
| ko00120 | Primary bile acid biosynthesis | 0.40 | <0.05 |
| ko05340 | Primary immunodeficiency | 0.41 | <0.01 |
| ko03060 | Protein export | <0.05 | <0.05 |
| ko00121 | Secondary bile acid biosynthesis | 0.40 | <0.05 |
| ko04726 | Serotonergic synapse | 0.98 | <0.01 |
| ko05222 | Small cell lung cancer | 0.69 | <0.05 |
| ko00945 | Stilbenoid, diarylheptanoid and gingerol biosynthesis | 1.02 | <0.05 |
| ko00643 | Styrene degradation | -0.63 | <0.05 |
| ko00900 | Terpenoid backbone biosynthesis | 0.06 | <0.05 |
| ko00253 | Tetracycline biosynthesis | -0.96 | <0.05 |
| ko05145 | Toxoplasmosis | 0.69 | <0.05 |
| ko04930 | Type II diabetes mellitus | -0.21 | <0.01 |
| ko01502 | Vancomycin resistance | 0.18 | <0.01 |
| ko00513 | Various types of N-glycan biosynthesis | 0.90 | <0.05 |
| ko05110 | Vibrio cholerae infection | 0.82 | <0.01 |
| ko05203 | Viral carcinogenesis | -0.09 | <0.01 |
| ko05416 | Viral myocarditis | 0.69 | <0.05 |

1 Pairwise comparisons of diet group using Mann-Whitney U Test.

2 Functional pathway prediction based on Silva123 Database and showed at level 3.

3 Log2 fold differences.

4 Benjamini and Hochberg FDR correction.

5 The highlight were commons to both Tax4Fun and MetaboAnalyst pathway analyses.