Table S6: Functional pathways predicted by Tax4Fun analyses altered by diet in ileum of growing pigs provided inulin

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| --- | --- | --- | --- |
| Tax4Fun-based Pathways | | Inu Relative to Con | |
| Fold Difference3 | *P*4 |
| ko04213 | Longevity regulating pathway - multiple species | -0.14 | <0.05 |
| ko00400 | Phenylalanine, tyrosine and tryptophan biosynthesis | 0.21 | <0.05 |
| ko00941 | Flavonoid biosynthesis | 0.96 | <0.01 |
| ko00945 | Stilbenoid, diarylheptanoid and gingerol biosynthesis | 0.96 | <0.01 |
| ko00966 | Glucosinolate biosynthesis | 0.54 | <0.05 |
| ko05231 | Choline metabolism in cancer | 0.55 | <0.05 |
| ko05230 | Central carbon metabolism in cancer | -0.23 | <0.05 |
| ko05206 | MicroRNAs in cancer | -0.57 | <0.05 |
| ko05215 | Prostate cancer | 0.62 | <0.01 |
| ko04112 | Cell cycle - Caulobacter | 0.22 | <0.05 |
| ko04214 | Apoptosis | 0.55 | <0.05 |
| ko04261 | Adrenergic signaling in cardiomyocytes | -0.95 | <0.05 |
| ko04970 | Salivary secretion | -0.95 | <0.05 |
| ko04971 | Gastric acid secretion | -0.95 | <0.05 |
| ko04972 | Pancreatic secretion | -0.95 | <0.05 |
| ko04974 | Protein digestion and absorption | -0.62 | <0.05 |
| ko04976 | Bile secretion | -0.76 | <0.05 |
| ko04940 | Type I diabetes mellitus | -0.13 | <0.05 |
| ko04914 | Progesterone-mediated oocyte maturation | 0.62 | <0.01 |
| ko04915 | Estrogen signaling pathway | 0.62 | <0.01 |
| ko04911 | Insulin secretion | -0.95 | <0.05 |
| ko04925 | Aldosterone synthesis and secretion | -0.95 | <0.05 |
| ko04918 | Thyroid hormone synthesis | -0.29 | <0.05 |
| ko04964 | Proximal tubule bicarbonate reclamation | -0.58 | <0.01 |
| ko04960 | Aldosterone-regulated sodium reabsorption | -0.95 | <0.05 |
| ko04961 | Endocrine and other factor-regulated calcium reabsorption | -0.95 | <0.05 |
| ko00510 | N-Glycan biosynthesis | 0.92 | <0.01 |
| ko04612 | Antigen processing and presentation | 0.62 | <0.01 |
| ko04657 | IL-17 signaling pathway | 0.62 | <0.01 |
| ko04659 | Th17 cell differentiation | 0.62 | <0.01 |
| ko04621 | NOD-like receptor signaling pathway | 0.22 | <0.05 |
| ko05120 | Epithelial cell signaling in Helicobacter pylori infection | 0.62 | <0.01 |
| ko05150 | Staphylococcus aureus infection | -0.55 | <0.05 |
| ko00860 | Porphyrin and chlorophyll metabolism | 0.23 | <0.05 |
| ko00473 | D-Alanine metabolism | -0.25 | <0.01 |
| ko00906 | Carotenoid biosynthesis | 0.86 | <0.05 |
| ko04151 | PI3K-Akt signaling pathway | 0.56 | <0.01 |
| ko04016 | MAPK signaling pathway - plant | -0.33 | <0.01 |
| ko04072 | Phospholipase D signaling pathway | 0.55 | <0.05 |
| ko04022 | cGMP-PKG signaling pathway | -0.95 | <0.05 |
| ko04024 | cAMP signaling pathway | -0.91 | <0.05 |
| ko03022 | Basal transcription factors | 0.87 | <0.01 |

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.