**Supplementary Table 3.** Median abundance of KEGG pathways from PiCRUSt analysis in CLD and control subjects.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **KEGG\_Pathways** | **CLD** | **Control** | **p value** | **Higher abundance** |
| Environmental Information Processing; Signalling Molecules and Interaction; Bacterial toxins | 0.176 | 0.164 | \*\* | CLD |
| Metabolism; Amino Acid Metabolism; Valine, leucine and isoleucine biosynthesis | 0.791 | 0.764 | \* | CLD |
| Metabolism; Carbohydrate Metabolism; Amino sugar and nucleotide sugar metabolism | 1.692 | 1.623 | \* | CLD |
| Metabolism; Carbohydrate Metabolism; Galactose metabolism | 0.863 | 0.783 | \* | CLD |
| Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis | 1.240 | 1.224 | \* | CLD |
| Metabolism; Carbohydrate Metabolism; Propanoate metabolism | 0.518 | 0.500 | \* | CLD |
| Metabolism; Carbohydrate Metabolism; Pyruvate metabolism | 1.088 | 1.063 | \* | CLD |
| Metabolism; Glycan Biosynthesis and Metabolism; Glycosyltransferases | 0.500 | 0.492 | \* | CLD |
| Metabolism; Glycan Biosynthesis and Metabolism; Other glycan degradation | 0.234 | 0.223 | \* | CLD |
| Unclassified; Metabolism; Carbohydrate metabolism | 0.159 | 0.145 | \* | CLD |
| Metabolism; Amino Acid Metabolism; Amino acid related enzymes | 1.601 | 1.617 | \* | Control |
| Metabolism; Amino Acid Metabolism; Phenylalanine metabolism | 0.082 | 0.091 | \* | Control |
| Metabolism; Carbohydrate Metabolism; Citrate cycle (TCA cycle) | 0.565 | 0.602 | \* | Control |
| Metabolism; Carbohydrate Metabolism; Glyoxylate and dicarboxylate metabolism | 0.316 | 0.346 | \* | Control |
| Metabolism; Glycan Biosynthesis and Metabolism; Lipopolysaccharide biosynthesis | 0.304 | 0.355 | \* | Control |
| Metabolism; Glycan Biosynthesis and Metabolism; Lipopolysaccharide biosynthesis proteins | 0.430 | 0.483 | \* | Control |
| Metabolism; Amino Acid Metabolism; Alanine, aspartate and glutamate metabolism | 0.879 | 0.888 | NS |  |
| Metabolism; Amino Acid Metabolism; Cysteine and methionine metabolism | 0.994 | 0.996 | NS |  |
| Metabolism; Amino Acid Metabolism; Glycine, serine and threonine metabolism | 0.831 | 0.831 | NS |  |
| Metabolism; Amino Acid Metabolism; Histidine metabolism | 0.369 | 0.377 | NS |  |
| Metabolism; Amino Acid Metabolism; Lysine biosynthesis | 0.712 | 0.718 | NS |  |
| Metabolism; Amino Acid Metabolism; Lysine degradation | 0.116 | 0.115 | NS |  |
| Metabolism; Amino Acid Metabolism; Phenylalanine, tyrosine and tryptophan biosynthesis | 0.836 | 0.828 | NS |  |
| Metabolism; Amino Acid Metabolism; Tryptophan metabolism | 0.140 | 0.138 | NS |  |
| Metabolism; Amino Acid Metabolism; Tyrosine metabolism | 0.330 | 0.330 | NS |  |
| Metabolism; Amino Acid Metabolism; Valine, leucine and isoleucine degradation | 0.248 | 0.253 | NS |  |
| Metabolism; Carbohydrate Metabolism; Ascorbate and aldarate metabolism | 0.114 | 0.121 | NS |  |
| Metabolism; Carbohydrate Metabolism; Butanoate metabolism | 0.570 | 0.565 | NS |  |
| Metabolism; Carbohydrate Metabolism; C5-Branched dibasic acid metabolism | 0.307 | 0.300 | NS |  |
| Metabolism; Carbohydrate Metabolism; Fructose and mannose metabolism | 0.893 | 0.843 | NS |  |
| Metabolism; Carbohydrate Metabolism; Inositol phosphate metabolism | 0.123 | 0.124 | NS |  |
| Metabolism; Carbohydrate Metabolism; Pentose and glucuronate interconversions | 0.263 | 0.267 | NS |  |
| Metabolism; Carbohydrate Metabolism; Pentose phosphate pathway | 0.812 | 0.816 | NS |  |
| Metabolism; Carbohydrate Metabolism; Starch and sucrose metabolism | 0.870 | 0.855 | NS |  |
| Metabolism; Lipid Metabolism; Primary bile acid biosynthesis | 0.000 | 0.001 | NS |  |
| Metabolism; Lipid Metabolism; Secondary bile acid biosynthesis | 0.000 | 0.001 | NS |  |
| Metabolism; Nucleotide Metabolism; Purine metabolism | 2.791 | 2.805 | NS |  |
| Metabolism; Nucleotide Metabolism; Pyrimidine metabolism | 2.266 | 2.263 | NS |  |
| Unclassified; Metabolism; Amino acid metabolism | 0.166 | 0.166 | NS |  |

\* <0.05, \*\*<0.01, using Mann Whitney U test.

Pathways relevant to bacteria functions were evaluated, after the pathways related to human genomic functions were filtered from the raw data.

Abbreviations: CLD, chronic liver disease; KEGG, Kyoto Encyclopedia of Genes and Genomes; PICRUSt, Phylogenetic Investigation of Communities by Reconstruction of Unobserved States; NS, not significant.