**Supplementary Table** **5**.Analysis of PTR metabolic pathway enrichment

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Pathway Name | Match Status | -log(p) | Holm p | FDR | Impact | Details |
| Taurine and hypotaurine metabolism | 2/8 | 6.8401 | 5.7805E-6 | 2.964E-6 | 0.0 | KEGG SMP |
| Primary bile acid biosynthesis | 4/46 | 6.8291 | 5.7805E-6 | 2.964E-6 | 0.06417 | KEGG SMP |
| Tryptophan metabolism | 3/41 | 3.7534 | 0.0067052 | 0.0021579 | 0.0139 | KEGG SMP |
| Riboflavin metabolism | 1/4 | 3.666 | 0.0079842 | 0.0021579 | 0.0 | KEGG SMP |
| Glutathione metabolism | 2/28 | 3.3235 | 0.017091 | 0.0027412 | 0.02698 | KEGG SMP |
| beta-Alanine metabolism | 1/21 | 3.319 | 0.017091 | 0.0027412 | 0.05597 | KEGG SMP |
| Arginine and proline metabolism | 1/38 | 3.319 | 0.017091 | 0.0027412 | 0.0 | KEGG SMP |
| Glycerolipid metabolism | 1/16 | 2.7966 | 0.052718 | 0.0071 | 0.01246 | KEGG SMP |
| Phosphatidylinositol signaling system | 1/28 | 2.7966 | 0.052718 | 0.0071 | 0.00152 | KEGG |
| Glycine, serine and threonine metabolism | 1/34 | 2.5244 | 0.092684 | 0.011959 | 0.0 | KEGG SMP |
| Purine metabolism | 3/66 | 1.7577 | 0.52415 | 0.059558 | 0.13284 | KEGG SMP |
| Metabolism of xenobiotics by cytochrome P450 | 1/64 | 1.7479 | 0.52415 | 0.059558 | 0.0 | KEGG |
| Glycolysis / Gluconeogenesis | 2/26 | 1.5236 | 0.83852 | 0.085352 | 0.04443 | KEGG SMP SMP |
| Steroid hormone biosynthesis | 7/77 | 1.4957 | 0.86229 | 0.085352 | 0.10964 | KEGG |
| Ascorbate and aldarate metabolism | 1/10 | 1.4948 | 0.86229 | 0.085352 | 0.0 | KEGG |
| Galactose metabolism | 1/27 | 1.1258 | 1.0 | 0.18714 | 0.03577 | KEGG SMP |
| Caffeine metabolism | 1/12 | 1.0081 | 1.0 | 0.23096 | 0.0 | KEGG SMP |
| Sphingolipid metabolism | 3/21 | 0.80391 | 1.0 | 0.34904 | 0.0 | KEGG SMP |
| Folate biosynthesis | 1/27 | 0.70755 | 1.0 | 0.35187 | 0.0 | KEGG |
| Glycerophospholipid metabolism | 3/36 | 0.69438 | 1.0 | 0.35187 | 0.33882 | KEGG |
| Arachidonic acid metabolism | 4/36 | 0.69396 | 1.0 | 0.35187 | 0.0424 | KEGG SMP |
| Linoleic acid metabolism | 3/5 | 0.69395 | 1.0 | 0.35187 | 0.0 | KEGG |
| alpha-Linolenic acid metabolism | 2/13 | 0.69395 | 1.0 | 0.35187 | 0.0 | KEGG |
| Glycosylphosphatidylinositol (GPI)-anchor biosynthesis | 1/14 | 0.65376 | 1.0 | 0.3699 | 0.00399 | KEGG |
| Biosynthesis of unsaturated fatty acids | 1/36 | 0.63577 | 1.0 | 0.37012 | 0.0 | KEGG |
| Pyrimidine metabolism | 3/39 | 0.4317 | 1.0 | 0.5538 | 0.26541 | KEGG SMP |
| Steroid biosynthesis | 1/42 | 0.42554 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Fatty acid biosynthesis | 1/47 | 0.34339 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Fatty acid degradation | 1/39 | 0.30867 | 1.0 | 0.5538 | 0.02355 | KEGG SMP |
| Fatty acid elongation | 1/39 | 0.30867 | 1.0 | 0.5538 | 0.01148 | KEGG SMP |
| Valine, leucine and isoleucine degradation | 1/40 | 0.29304 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Valine, leucine and isoleucine biosynthesis | 1/8 | 0.29304 | 1.0 | 0.5538 | 0.0 | KEGG |
| Pantothenate and CoA biosynthesis | 1/19 | 0.29304 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Aminoacyl-tRNA biosynthesis | 1/48 | 0.29304 | 1.0 | 0.5538 | 0.0 | KEGG |
| Citrate cycle (TCA cycle) | 1/20 | 0.27893 | 1.0 | 0.5538 | 0.03273 | KEGG |
| Alanine, aspartate and glutamate metabolism | 1/28 | 0.27893 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Propanoate metabolism | 1/23 | 0.27893 | 1.0 | 0.5538 | 0.0 | KEGG SMP |
| Butanoate metabolism | 1/15 | 0.27893 | 1.0 | 0.5538 | 0.0 | KEGG |
| Amino sugar and nucleotide sugar metabolism | 1/37 | 0.21709 | 1.0 | 0.62216 | 0.0 | KEGG SMP SMP |
| Retinol metabolism | 1/16 | 0.092641 | 1.0 | 0.8079 | 0.0 | KEGG SMP |