Supplemental Table S6. *S. cerevisiae* pathways with significant over-enrichment of detected homologues.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Pathway** | **Number of Genes in Pathway** | **Number of Genes with detectable homologue** | **Detected Yeast:Human Homologues** | **P value (binomial test)** |
| glutamine biosynthesis | 1 | 1 | GLN1:GLUL | < 1 x 10-6 \*\*\* |
| glycerol degradation | 2 | 2 | GUT1:GK GUT2:GPD2 | < 1 x 10-6 \*\*\* |
| 2-ketoglutarate dehydrogenase complex | 3 | 3 | KGD1:OGDHL KGD1:OGDH KGD2:DBT KGD2:DLST LPD1:AIFM3 LPD1:DLD | < 1 x 10-6 \*\*\* |
| pyruvate dehydrogenase complex | 4 | 4 | LAT1:PDHX LAT1:DLAT LPD1:AIFM3 LPD1:DLD PDA1:PDHA1 PDB1:PDHB | < 1 x 10-6 \*\*\* |
| proline utilization | 2 | 2 | PUT1:PRODH PUT2:ALDH4A1 | < 1 x 10-6 \*\*\* |
| glycolysis | 14 | 11 | CDC19:PKM2 ENO1:ENO1 ENO1:ENO2 ENO1:ENO3 GPM1:PGAM1 PFK1:PFKP PFK2:PFKP PFK2:PFKM PFK2:PFKL PGI1:GPI PGK1:PGK1 PYK2:PKM2 TDH1:GAPDH TDH3:GAPDH TPI1:TPI1 | 0.0000002 \*\*\* |
| TCA cycle, aerobic respiration | 22 | 12 | ACO1:ACO2 CIT1:CS FUM1:FH IDH2:IDH3A KGD1:OGDHL KGD1:OGDH KGD2:DBT KGD2:DLST LPD1:AIFM3 LPD1:DLD LSC1:ACLY LSC1:SUCLG1 LSC2:SUCLA2 MDH1:MDH2 MDH3:LDHA MDH3:LDHB MDH3:MDH1 PYC2:PC PYC2:PCCA | 0.0000421 \*\* |