

Table S2: Percentages of KEGG orthologs that belong to gene families at levels 1, 2, and 3.

| Functional gene categories | Median (min-max) *in percent | | |
|--|------------------------------|-----------------|---------|
| | Healthy | Acute Diarrhea | p-value |
| Level 1 | | | |
| Cellular Processes | 1.7(1.4-1.8) | 1.5(1.3-3.6) | 0.9112 |
| Environmental Information Processing | 15.3(14.7-16.4) | 15.1(12.5-17.1) | 0.9559 |
| Genetic Information Processing | 19.7(19.1-20.4) | 19.8(19.0-22.1) | 0.7718 |
| Human Diseases | 0.6(0.6-0.7) | 0.7(0.4-0.8) | 0.7452 |
| Metabolism | 49.3(47.5-49.5) | 48.7(46.1-49.5) | 0.9672 |
| None | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Organismal Systems | 0.6(0.5-0.9) | 0.6(0.5-0.8) | 0.9339 |
| Unclassified | 13.2(12.8-13.6) | 13.5(12.7-14.0) | 0.9224 |
| Level 2 | | | |
| Cellular Processes Cell Growth and Death | 0.5(0.4-0.9) | 0.5(0.5-0.7) | 0.9659 |
| Cellular Processes Cell Motility | 0.8(0.6-1.2) | 0.9(0.7-2.4) | 0.8924 |
| Cellular Processes Transport and Catabolism | 0.2(0.0-0.2) | 0.1(0.1-0.2) | 0.9229 |
| Environmental Information Processing Membrane Transport | 14.1(13.6-15.0) | 13.7(10.9-16.2) | 0.9041 |
| Environmental Information Processing Signal Transduction | 1.3(0.9-1.6) | 1.2(1.0-1.6) | 0.9694 |
| Environmental Information Processing Signaling Molecules and Interaction | 0.1(0.1-0.2) | 0.1(0.0-0.2) | 0.9114 |
| Genetic Information Processing Folding, Sorting and Degradation | 2.3(2.1-2.6) | 2.4(2.2-2.7) | 1.0000 |
| Genetic Information Processing Replication and Repair | 9.0(7.9-9.5) | 9.0(8.5-10.0) | 0.9158 |
| Genetic Information Processing Transcription | 3.1(2.8-3.3) | 3.0(2.7-3.3) | 0.9874 |
| Genetic Information Processing Translation | 5.9(5.0-6.3) | 5.7(5.0-6.2) | 0.8403 |
| Human Diseases Cancers | 0.0(0.0-0.2) | 0.1(0.0-0.1) | 0.8960 |
| Human Diseases Immune System Diseases | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 0.8633 |
| Human Diseases Infectious Diseases | 0.3(0.2-0.4) | 0.3(0.2-0.5) | 0.9429 |
| Human Diseases Metabolic Diseases | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 0.9756 |
| Human Diseases Neurodegenerative Diseases | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Amino Acid Metabolism | 10.0(9.2-10.8) | 10.6(9.2-11.8) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites | 1.0(0.8-1.4) | 1.0(0.8-1.3) | 1.0000 |
| Metabolism Carbohydrate Metabolism | 11.6(11.1-13.0) | 11.3(10.1-12.7) | 1.0000 |

| | | | |
|--|--------------|--------------|--------|
| Metabolism Energy Metabolism | 6.3(5.4-6.8) | 5.8(5.4-6.6) | 1.0000 |
| Metabolism Enzyme Families | 2.1(1.8-2.3) | 2.0(1.7-2.4) | 0.8880 |
| Metabolism Glycan Biosynthesis and Metabolism | 1.4(1.1-1.7) | 1.3(1.1-1.9) | 0.9670 |
| Metabolism Lipid Metabolism | 2.6(2.3-2.9) | 2.6(2.1-3.2) | 0.9521 |
| Metabolism Metabolism of Cofactors and Vitamins | 4.5(3.6-4.7) | 4.3(4.0-4.8) | 0.9600 |
| Metabolism Metabolism of Other Amino Acids | 1.4(1.1-1.6) | 1.3(1.0-1.4) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides | 1.6(1.3-1.8) | 1.6(1.1-1.8) | 0.9391 |
| Metabolism Nucleotide Metabolism | 3.9(3.4-4.6) | 3.9(3.5-4.7) | 0.8899 |
| Metabolism Xenobiotics Biodegradation and Metabolism | 2.1(1.6-2.3) | 2.3(1.8-2.6) | 1.0000 |
| Organismal Systems Digestive System | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.8897 |
| Organismal Systems Endocrine System | 0.2(0.2-0.3) | 0.2(0.1-0.4) | 0.9532 |
| Organismal Systems Environmental Adaptation | 0.2(0.1-0.3) | 0.2(0.1-0.2) | 0.9722 |
| Organismal Systems Excretory System | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 0.8999 |
| Organismal Systems Immune System | 0.1(0.0-0.2) | 0.1(0.1-0.2) | 1.0000 |
| Organismal Systems Nervous System | 0.1(0.1-0.1) | 0.1(0.0-0.2) | 0.8637 |
| Unclassified Cellular Processes and Signaling | 3.9(3.5-4.4) | 4.0(3.6-4.6) | 0.8395 |
| Unclassified Genetic Information Processing | 2.4(2.1-3.0) | 2.3(2.2-3.1) | 0.9808 |
| Unclassified Metabolism | 2.9(2.3-3.2) | 2.7(2.2-3.0) | 0.8914 |
| Unclassified Poorly Characterized | 4.2(3.9-4.8) | 4.3(4.0-4.9) | 0.9386 |
| Level 3 | | | |
| Cellular Processes Cell Growth and Death Cell cycle - Caulobacter | 0.6(0.3-0.9) | 0.5(0.4-0.8) | 0.9767 |
| Cellular Processes Cell Motility Bacterial chemotaxis | 0.3(0.2-0.4) | 0.2(0.1-0.6) | 1.0000 |
| Cellular Processes Cell Motility Bacterial motility proteins | 0.2(0.0-0.2) | 0.2(0.0-1.0) | 1.0000 |
| Cellular Processes Cell Motility Cytoskeleton proteins | 0.4(0.2-0.5) | 0.4(0.3-0.6) | 0.9815 |
| Cellular Processes Cell Motility Flagellar assembly | 0.1(0.1-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Cellular Processes Transport and Catabolism Lysosome | 4.2(3.4-4.4) | 4.3(2.6-4.9) | 1.0000 |
| Cellular Processes Transport and Catabolism Peroxisome | 0.5(0.4-0.6) | 0.4(0.2-0.7) | 1.0000 |
| Environmental Information Processing Membrane Transport ABC transporters | 0.4(0.2-2.3) | 0.4(0.2-1.3) | 0.9768 |
| Environmental Information Processing Membrane Transport Bacterial secretion system | 0.8(0.7-1.0) | 0.9(0.8-1.1) | 0.9647 |
| Environmental Information Processing Membrane Transport Phosphotransferase system (PTS) | 7.9(7.4-8.7) | 8.1(6.0-8.9) | 1.0000 |
| Environmental Information Processing Membrane Transport Secretion system | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Environmental Information Processing Membrane Transport Transporters | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Environmental Information Processing Signal Transduction MAPK signaling pathway - yeast | 1.1(0.7-1.4) | 1.1(0.8-1.5) | 1.0000 |
| Environmental Information Processing Signal Transduction Phosphatidylinositol signaling system | 0.1(0.1-0.2) | 0.1(0.1-0.2) | 1.0000 |
| Environmental Information Processing Signal Transduction Two-component system | 0.9(0.6-1.1) | 0.9(0.7-1.2) | 1.0000 |

| | | | |
|---|--------------|--------------|--------|
| Environmental Information Processing Signaling Molecules and Interaction Bacterial toxins | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Environmental Information Processing Signaling Molecules and Interaction Cellular antigens | 0.5(0.4-0.7) | 0.5(0.3-0.7) | 0.9894 |
| Environmental Information Processing Signaling Molecules and Interaction Ion channels | 0.1(0.0-0.1) | 0.0(0.0-0.1) | 0.9715 |
| Genetic Information Processing Folding, Sorting and Degradation Chaperones and folding catalysts | 0.4(0.2-0.5) | 0.5(0.2-0.7) | 0.9839 |
| Genetic Information Processing Folding, Sorting and Degradation Proteasome | 0.2(0.2-0.4) | 0.3(0.3-0.5) | 0.9914 |
| Genetic Information Processing Folding, Sorting and Degradation Protein export | 0.5(0.3-0.6) | 0.5(0.4-0.6) | 1.0000 |
| Genetic Information Processing Folding, Sorting and Degradation Protein processing in endoplasmic reticulum | 1.5(1.4-1.7) | 1.5(1.3-1.9) | 1.0000 |
| Genetic Information Processing Folding, Sorting and Degradation RNA degradation | 3.0(2.7-3.3) | 2.8(2.6-3.4) | 1.0000 |
| Genetic Information Processing Folding, Sorting and Degradation Sulfur relay system | 0.7(0.5-0.8) | 0.7(0.5-0.8) | 0.8572 |
| Genetic Information Processing Replication and Repair Base excision repair | 1.2(0.9-1.5) | 1.3(1.0-1.7) | 1.0000 |
| Genetic Information Processing Replication and Repair Chromosome | 1.0(0.7-1.2) | 1.0(0.7-1.2) | 1.0000 |
| Genetic Information Processing Replication and Repair DNA repair and recombination proteins | 0.8(0.7-1.0) | 0.8(0.7-1.0) | 1.0000 |
| Genetic Information Processing Replication and Repair DNA replication | 0.4(0.2-0.5) | 0.4(0.2-0.5) | 1.0000 |
| Genetic Information Processing Replication and Repair DNA replication proteins | 0.2(0.1-0.2) | 0.2(0.0-0.2) | 0.9929 |
| Genetic Information Processing Replication and Repair Homologous recombination | 2.1(1.4-2.3) | 2.1(1.7-2.3) | 1.0000 |
| Genetic Information Processing Replication and Repair Mismatch repair | 1.0(0.8-1.2) | 1.0(0.9-1.1) | 1.0000 |
| Genetic Information Processing Replication and Repair Non-homologous end-joining | 1.2(1.0-1.5) | 1.1(0.8-1.6) | 1.0000 |
| Genetic Information Processing Replication and Repair Nucleotide excision repair | 0.2(0.1-0.2) | 0.2(0.0-0.2) | 1.0000 |
| Genetic Information Processing Transcription Basal transcription factors | 2.2(2.0-2.6) | 2.3(1.7-2.6) | 1.0000 |
| Genetic Information Processing Transcription RNA polymerase | 1.4(1.1-1.7) | 1.3(1.0-1.6) | 0.9686 |
| Genetic Information Processing Transcription Transcription factors | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Genetic Information Processing Transcription Transcription machinery | 0.6(0.5-0.7) | 0.5(0.4-0.9) | 1.0000 |
| Genetic Information Processing Translation Aminoacyl-tRNA biosynthesis | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Genetic Information Processing Translation Ribosome | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Genetic Information Processing Translation Ribosome Biogenesis | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 0.9752 |
| Genetic Information Processing Translation Ribosome biogenesis in eukaryotes | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Genetic Information Processing Translation RNA transport | 0.1(0.1-0.2) | 0.1(0.1-0.2) | 1.0000 |
| Genetic Information Processing Translation Translation factors | 0.1(0.0-0.1) | 0.1(0.0-0.2) | 1.0000 |
| Human Diseases Cancers Pathways in cancer | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Human Diseases Cancers Prostate cancer | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Human Diseases Immune System Diseases Primary immunodeficiency | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 0.9922 |
| Human Diseases Infectious Diseases Epithelial cell signaling in Helicobacter pylori infection | 1.2(0.9-1.3) | 1.1(0.9-1.5) | 1.0000 |
| Human Diseases Infectious Diseases Pertussis | 1.4(1.2-1.6) | 1.5(1.3-1.6) | 1.0000 |
| Human Diseases Infectious Diseases Staphylococcus aureus infection | 1.3(1.1-1.5) | 1.3(1.2-1.5) | 1.0000 |
| Human Diseases Infectious Diseases Tuberculosis | 0.9(0.6-1.2) | 1.0(0.8-1.3) | 0.9814 |

| | | | |
|---|--------------|--------------|--------|
| Human Diseases Infectious Diseases Vibrio cholerae pathogenic cycle | 0.9(0.8-1.0) | 0.9(0.7-1.1) | 1.0000 |
| Human Diseases Metabolic Diseases Type I diabetes mellitus | 0.8(0.6-1.0) | 0.7(0.5-1.0) | 1.0000 |
| Human Diseases Metabolic Diseases Type II diabetes mellitus | 0.8(0.7-1.0) | 0.9(0.7-1.1) | 0.9702 |
| Human Diseases Neurodegenerative Diseases Alzheimer's disease | 0.1(0.0-0.2) | 0.1(0.1-0.2) | 0.9802 |
| Human Diseases Neurodegenerative Diseases Huntington's disease | 0.2(0.1-0.3) | 0.2(0.1-0.3) | 1.0000 |
| Human Diseases Neurodegenerative Diseases Parkinson's disease | 0.9(0.8-1.2) | 0.9(0.7-1.2) | 1.0000 |
| Metabolism Amino Acid Metabolism Alanine, aspartate and glutamate metabolism | 0.1(0.1-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Amino Acid Metabolism Amino acid related enzymes | 0.5(0.3-0.6) | 0.6(0.3-0.7) | 1.0000 |
| Metabolism Amino Acid Metabolism Arginine and proline metabolism | 0.7(0.5-1.0) | 0.7(0.6-0.9) | 1.0000 |
| Metabolism Amino Acid Metabolism Cysteine and methionine metabolism | 0.2(0.1-0.2) | 0.2(0.1-0.2) | 0.9975 |
| Metabolism Amino Acid Metabolism Glycine, serine and threonine metabolism | 0.1(0.1-0.1) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Amino Acid Metabolism Histidine metabolism | 0.1(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Amino Acid Metabolism Lysine biosynthesis | 0.2(0.2-0.3) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Amino Acid Metabolism Lysine degradation | 0.1(0.1-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Amino Acid Metabolism Phenylalanine metabolism | 0.3(0.2-0.5) | 0.2(0.1-0.4) | 1.0000 |
| Metabolism Amino Acid Metabolism Phenylalanine, tyrosine and tryptophan biosynthesis | 0.2(0.1-0.3) | 0.2(0.0-0.3) | 1.0000 |
| Metabolism Amino Acid Metabolism Tryptophan metabolism | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 0.9861 |
| Metabolism Amino Acid Metabolism Tyrosine metabolism | 1.4(0.9-2.2) | 1.3(1.0-1.7) | 1.0000 |
| Metabolism Amino Acid Metabolism Valine, leucine and isoleucine biosynthesis | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Amino Acid Metabolism Valine, leucine and isoleucine degradation | 0.7(0.5-0.9) | 0.7(0.5-0.8) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites beta-Lactam resistance | 0.4(0.2-0.6) | 0.4(0.3-0.7) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Butirosin and neomycin biosynthesis | 0.5(0.4-0.8) | 0.6(0.1-0.8) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Flavone and flavonol biosynthesis | 1.3(1.0-1.8) | 1.2(1.0-1.5) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Isoquinoline alkaloid biosynthesis | 0.7(0.6-0.9) | 0.7(0.5-0.9) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Novobiocin biosynthesis | 1.3(1.1-1.5) | 1.3(1.1-1.6) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Phenylpropanoid biosynthesis | 0.5(0.4-0.7) | 0.5(0.4-0.8) | 0.9982 |
| Metabolism Biosynthesis of Other Secondary Metabolites Stilbenoid, diarylheptanoid and gingerol biosynthesis | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 0.9984 |
| Metabolism Biosynthesis of Other Secondary Metabolites Streptomycin biosynthesis | 0.6(0.5-0.7) | 0.6(0.2-0.7) | 1.0000 |
| Metabolism Biosynthesis of Other Secondary Metabolites Tropane, piperidine and pyridine alkaloid biosynthesis | 1.0(0.9-1.4) | 1.2(0.9-1.3) | 1.0000 |
| Metabolism Carbohydrate Metabolism Amino sugar and nucleotide sugar metabolism | 0.5(0.4-0.8) | 0.6(0.4-0.8) | 1.0000 |
| Metabolism Carbohydrate Metabolism Ascorbate and aldarate metabolism | 1.1(0.9-1.3) | 1.1(0.8-1.3) | 1.0000 |
| Metabolism Carbohydrate Metabolism Butanoate metabolism | 1.2(1.0-1.5) | 1.2(0.9-1.3) | 0.9757 |
| Metabolism Carbohydrate Metabolism C5-Branched dibasic acid metabolism | 0.8(0.5-1.0) | 0.7(0.6-0.9) | 1.0000 |
| Metabolism Carbohydrate Metabolism Citrate cycle (TCA cycle) | 0.9(0.8-1.2) | 1.0(0.7-1.1) | 1.0000 |
| Metabolism Carbohydrate Metabolism Fructose and mannose metabolism | 1.5(1.3-1.9) | 1.5(1.2-2.2) | 1.0000 |

| | | | |
|---|--------------|--------------|--------|
| Metabolism Carbohydrate Metabolism Galactose metabolism | 0.6(0.5-0.9) | 0.7(0.4-0.8) | 0.9982 |
| Metabolism Carbohydrate Metabolism Glycolysis / Gluconeogenesis | 1.2(0.9-1.5) | 1.3(0.8-1.4) | 1.0000 |
| Metabolism Carbohydrate Metabolism Glyoxylate and dicarboxylate metabolism | 0.5(0.4-0.7) | 0.4(0.3-0.6) | 1.0000 |
| Metabolism Carbohydrate Metabolism Inositol phosphate metabolism | 0.4(0.2-0.6) | 0.4(0.2-0.6) | 1.0000 |
| Metabolism Carbohydrate Metabolism Pentose and glucuronate interconversions | 0.2(0.1-0.4) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Carbohydrate Metabolism Pentose phosphate pathway | 1.9(1.6-2.1) | 1.7(1.4-2.1) | 1.0000 |
| Metabolism Carbohydrate Metabolism Propanoate metabolism | 0.2(0.2-0.4) | 0.3(0.1-0.5) | 1.0000 |
| Metabolism Carbohydrate Metabolism Pyruvate metabolism | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Carbohydrate Metabolism Starch and sucrose metabolism | 0.3(0.2-0.4) | 0.2(0.1-0.5) | 1.0000 |
| Metabolism Energy Metabolism Carbon fixation in photosynthetic organisms | 0.1(0.0-0.1) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Energy Metabolism Carbon fixation pathways in prokaryotes | 0.1(0.0-0.1) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Energy Metabolism Methane metabolism | 1.0(0.8-1.1) | 0.8(0.7-1.2) | 1.0000 |
| Metabolism Energy Metabolism Nitrogen metabolism | 0.1(0.1-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Energy Metabolism Oxidative phosphorylation | 0.5(0.3-0.7) | 0.6(0.3-0.8) | 1.0000 |
| Metabolism Energy Metabolism Photosynthesis | 0.2(0.2-0.4) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Energy Metabolism Photosynthesis proteins | 0.4(0.4-0.7) | 0.5(0.3-0.8) | 1.0000 |
| Metabolism Energy Metabolism Sulfur metabolism | 0.5(0.4-0.7) | 0.5(0.4-0.6) | 1.0000 |
| Metabolism Enzyme Families Peptidases | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 0.9820 |
| Metabolism Enzyme Families Protein kinases | 0.5(0.3-0.7) | 0.5(0.3-0.6) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Glycosaminoglycan degradation | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Glycosphingolipid biosynthesis - ganglio series | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 0.9729 |
| Metabolism Glycan Biosynthesis and Metabolism Glycosphingolipid biosynthesis - globo series | 0.1(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Glycosyltransferases | 0.1(0.1-0.3) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Lipopolysaccharide biosynthesis | 0.4(0.3-0.6) | 0.4(0.2-0.5) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Lipopolysaccharide biosynthesis proteins | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism N-Glycan biosynthesis | 0.4(0.4-0.6) | 0.4(0.2-0.7) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Other glycan degradation | 0.6(0.5-0.6) | 0.6(0.4-0.7) | 1.0000 |
| Metabolism Glycan Biosynthesis and Metabolism Peptidoglycan biosynthesis | 0.5(0.4-0.7) | 0.6(0.3-0.7) | 1.0000 |
| Metabolism Lipid Metabolism Arachidonic acid metabolism | 1.0(0.7-1.5) | 1.2(1.0-1.4) | 1.0000 |
| Metabolism Lipid Metabolism Biosynthesis of unsaturated fatty acids | 0.1(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Lipid Metabolism Ether lipid metabolism | 0.2(0.1-0.4) | 0.3(0.2-0.5) | 1.0000 |
| Metabolism Lipid Metabolism Fatty acid biosynthesis | 0.5(0.3-0.7) | 0.5(0.3-0.7) | 1.0000 |
| Metabolism Lipid Metabolism Fatty acid metabolism | 0.2(0.1-0.2) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Lipid Metabolism Glycerolipid metabolism | 0.2(0.2-0.4) | 0.2(0.1-0.4) | 0.9843 |
| Metabolism Lipid Metabolism Glycerophospholipid metabolism | 0.1(0.0-0.2) | 0.1(0.1-0.2) | 1.0000 |

| | | | |
|---|--------------|--------------|--------|
| Metabolism Lipid Metabolism Linoleic acid metabolism | 0.1(0.0-0.2) | 0.1(0.1-0.3) | 1.0000 |
| Metabolism Lipid Metabolism Lipid biosynthesis proteins | 0.1(0.0-0.2) | 0.1(0.1-0.4) | 0.9710 |
| Metabolism Lipid Metabolism Primary bile acid biosynthesis | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Lipid Metabolism Secondary bile acid biosynthesis | 0.2(0.1-0.3) | 0.2(0.2-0.4) | 1.0000 |
| Metabolism Lipid Metabolism Sphingolipid metabolism | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Lipid Metabolism Steroid hormone biosynthesis | 0.2(0.2-0.3) | 0.2(0.1-0.5) | 0.9884 |
| Metabolism Lipid Metabolism Synthesis and degradation of ketone bodies | 0.1(0.0-0.2) | 0.1(0.1-0.2) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Biotin metabolism | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Folate biosynthesis | 0.2(0.0-0.3) | 0.2(0.0-0.3) | 0.9897 |
| Metabolism Metabolism of Cofactors and Vitamins Lipoic acid metabolism | 0.1(0.0-0.3) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Nicotinate and nicotinamide metabolism | 0.2(0.1-0.4) | 0.2(0.1-0.4) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins One carbon pool by folate | 0.5(0.4-0.7) | 0.5(0.4-0.7) | 0.9807 |
| Metabolism Metabolism of Cofactors and Vitamins Pantothenate and CoA biosynthesis | 0.2(0.1-0.2) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Porphyrin and chlorophyll metabolism | 0.1(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Retinol metabolism | 2.1(1.8-2.5) | 2.2(2.0-2.5) | 0.9969 |
| Metabolism Metabolism of Cofactors and Vitamins Riboflavin metabolism | 1.8(1.6-2.3) | 1.9(1.6-2.3) | 1.0000 |
| Metabolism Metabolism of Cofactors and Vitamins Thiamine metabolism | 0.2(0.0-0.2) | 0.2(0.1-0.2) | 0.9916 |
| Metabolism Metabolism of Cofactors and Vitamins Ubiquinone and other terpenoid-quinone biosynthesis | 0.2(0.1-0.4) | 0.3(0.2-0.4) | 0.9956 |
| Metabolism Metabolism of Cofactors and Vitamins Vitamin B6 metabolism | 0.1(0.0-0.2) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids beta-Alanine metabolism | 0.4(0.2-0.6) | 0.4(0.2-0.6) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids Cyanoamino acid metabolism | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids D-Alanine metabolism | 0.1(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids D-Arginine and D-ornithine metabolism | 0.4(0.3-0.4) | 0.3(0.2-0.4) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids D-Glutamine and D-glutamate metabolism | 0.1(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids Glutathione metabolism | 0.1(0.0-0.2) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids Phosphonate and phosphinate metabolism | 0.3(0.2-0.4) | 0.3(0.2-0.4) | 1.0000 |
| Metabolism Metabolism of Other Amino Acids Selenocompound metabolism | 0.1(0.0-0.2) | 0.1(0.1-0.2) | 0.9915 |
| Metabolism Metabolism of Other Amino Acids Taurine and hypotaurine metabolism | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 0.9984 |
| Metabolism Metabolism of Terpenoids and Polyketides Biosynthesis of ansamycins | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Biosynthesis of siderophore group nonribosomal peptides | 0.1(0.0-0.1) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Biosynthesis of vancomycin group antibiotics | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Geraniol degradation | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Limonene and pinene degradation | 0.2(0.1-0.2) | 0.2(0.1-0.4) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Polyketide sugar unit biosynthesis | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Prenyltransferases | 0.1(0.0-0.1) | 0.0(0.0-0.1) | 0.9940 |

| | | | |
|--|--------------|--------------|--------|
| Metabolism Metabolism of Terpenoids and Polyketides Terpenoid backbone biosynthesis | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Tetracycline biosynthesis | 0.1(0.1-0.3) | 0.1(0.1-0.2) | 1.0000 |
| Metabolism Metabolism of Terpenoids and Polyketides Zeatin biosynthesis | 0.1(0.0-0.2) | 0.1(0.0-0.2) | 1.0000 |
| Metabolism Nucleotide Metabolism Purine metabolism | 0.1(0.0-0.1) | 0.1(0.0-0.2) | 0.9852 |
| Metabolism Nucleotide Metabolism Pyrimidine metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Aminobenzoate degradation | 0.2(0.1-0.2) | 0.2(0.1-0.2) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Atrazine degradation | 0.4(0.2-0.5) | 0.3(0.1-0.5) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Benzoate degradation | 1.0(0.9-1.3) | 1.1(0.9-1.2) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Bisphenol degradation | 0.1(0.1-0.3) | 0.2(0.2-0.4) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Caprolactam degradation | 0.1(0.1-0.2) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Chlороалкane and chloroalkene degradation | 0.5(0.2-0.6) | 0.5(0.3-0.7) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Chlorocyclohexane and chlorobenzene degradation | 1.2(1.0-1.5) | 1.3(1.0-1.6) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Dioxin degradation | 0.7(0.5-0.8) | 0.6(0.4-1.0) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Drug metabolism - cytochrome P450 | 0.8(0.5-1.1) | 0.7(0.6-1.0) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Drug metabolism - other enzymes | 0.2(0.1-0.4) | 0.1(0.1-0.2) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Ethylbenzene degradation | 1.0(0.7-1.1) | 0.8(0.7-1.1) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Metabolism of xenobiotics by cytochrome P450 | 0.4(0.3-0.5) | 0.3(0.2-0.6) | 0.9868 |
| Metabolism Xenobiotics Biodegradation and Metabolism Naphthalene degradation | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Nitrotoluene degradation | 0.1(0.1-0.3) | 0.2(0.1-0.3) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Polycyclic aromatic hydrocarbon degradation | 0.8(0.7-1.0) | 0.8(0.5-1.1) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Styrene degradation | 0.1(0.0-0.2) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Toluene degradation | 0.0(0.0-0.1) | 0.1(0.0-0.1) | 1.0000 |
| Metabolism Xenobiotics Biodegradation and Metabolism Xylene degradation | 1.3(1.1-1.6) | 1.3(1.0-1.5) | 1.0000 |
| Organismal Systems Digestive System Bile secretion | 1.1(0.8-1.2) | 1.0(0.8-1.3) | 0.9786 |
| Organismal Systems Digestive System Carbohydrate digestion and absorption | 3.3(2.7-3.8) | 3.2(3.0-3.6) | 1.0000 |
| Organismal Systems Digestive System Mineral absorption | 0.0(0.0-0.1) | 0.0(0.0-0.6) | 1.0000 |
| Organismal Systems Endocrine System Adipocytokine signaling pathway | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Organismal Systems Endocrine System Insulin signaling pathway | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Organismal Systems Endocrine System PPAR signaling pathway | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Organismal Systems Endocrine System Progesterone-mediated oocyte maturation | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Organismal Systems Environmental Adaptation Plant-pathogen interaction | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.9939 |
| Organismal Systems Excretory System Proximal tubule bicarbonate reclamation | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Organismal Systems Immune System Antigen processing and presentation | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Organismal Systems Immune System NOD-like receptor signaling pathway | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 0.9857 |
| Organismal Systems Immune System RIG-I-like receptor signaling pathway | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.9865 |

| | | | |
|---|--------------|--------------|--------|
| Organismal Systems Nervous System Glutamatergic synapse | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Cellular Processes and Signaling Cell division | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Cellular Processes and Signaling Cell motility and secretion | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Cellular Processes and Signaling Electron transfer carriers | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Cellular Processes and Signaling Germination | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Cellular Processes and Signaling Inorganic ion transport and metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Cellular Processes and Signaling Membrane and intracellular structural molecules | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Cellular Processes and Signaling Other ion-coupled transporters | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Cellular Processes and Signaling Other transporters | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Cellular Processes and Signaling Pores ion channels | 0.0(0.0-0.0) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Cellular Processes and Signaling Signal transduction mechanisms | 0.0(0.0-0.1) | 0.0(0.0-0.2) | 1.0000 |
| Unclassified Cellular Processes and Signaling Sporulation | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Genetic Information Processing Protein folding and associated processing | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Genetic Information Processing Replication, recombination and repair proteins | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Genetic Information Processing Restriction enzyme | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.6076 |
| Unclassified Genetic Information Processing Translation proteins | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Metabolism Amino acid metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.9975 |
| Unclassified Metabolism Biosynthesis and biodegradation of secondary metabolites | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Metabolism Carbohydrate metabolism | 0.0(0.0-0.1) | 0.0(0.0-0.1) | 1.0000 |
| Unclassified Metabolism Energy metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Metabolism Glycan biosynthesis and metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Metabolism Lipid metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.9842 |
| Unclassified Metabolism Metabolism of cofactors and vitamins | 0.0(0.0-0.1) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Metabolism Nucleotide metabolism | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 0.9711 |
| Unclassified Metabolism Others | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Poorly Characterized Function unknown | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |
| Unclassified Poorly Characterized General function prediction only | 0.0(0.0-0.0) | 0.0(0.0-0.0) | 1.0000 |

P-value adjusted based on the Benjamini and Hochberg false discovery rate.