Table S3.

Comparison of predicted microbial function with Kruskal-Wallis H test among groups based on KEGG level-3

KEGG pathway	**p value**
Caprolactam degradation	0.020
Geraniol degradation	0.026
Ethylbenzene degradation	0.033
Antigen processing and presentation	0.034
Progesterone-mediated oocyte maturation	0.034
Prostate cancer	0.045
Type II diabetes mellitus	0.010
NOD-like receptor signaling pathway	0.047
Alzheimer's disease	0.021
Ribosome biogenesis in eukaryotes	0.031
Pathways in cancer	0.018
Primary immunodeficiency	0.016
Zeatin biosynthesis	0.006
Isoquinoline alkaloid biosynthesis	＜0.001
Protein processing in endoplasmic reticulum	0.003
Biosynthesis of vancomycin group antibiotics	0.038
Toluene degradation	0.022
Vibrio cholerae pathogenic cycle	0.002
Aminobenzoate degradation	0.001
Cell division	0.030
Ascorbate and aldarate metabolism	0.030
Taurine and hypotaurine metabolism	0.038
Lysine degradation	0.044
Epithelial cell signaling in Helicobacter pylori infection	0.041
D-Alanine metabolism	0.018
Tropane, piperidine and pyridine alkaloid biosynthesis	0.009
Metabolism of cofactors and vitamins	0.013
Novobiocin biosynthesis	0.044
Glycosphingolipid biosynthesis - globo series	0.033
Peroxisome	0.047
Ubiquinone and other terpenoid-quinone biosynthesis	0.014
Phenylalanine metabolism	0.045
D-Glutamine and D-glutamate metabolism	0.025
RNA polymerase	0.022
Cell motility and secretion	0.002
Valine, leucine and isoleucine degradation	0.003
beta-Alanine metabolism	0.013
Glutathione metabolism	0.001
Vitamin B6 metabolism	0.008
Lipopolysaccharide biosynthesis	0.030

Riboflavin metabolism	0.004
Prenyltransferases	0.001
Pores ion channels	0.003
Lipopolysaccharide biosynthesis proteins	0.003
Drug metabolism - other enzymes	0.008
Glycosyltransferases	0.003
Folate biosynthesis	0.001
Nucleotide excision repair	0.020
Base excision repair	0.050
Nicotinate and nicotinamide metabolism	0.048
RNA degradation	0.028
Citrate cycle (TCA cycle)	＜0.001
Membrane and intracellular structural molecules	0.004
Bacterial secretion system	0.029
Cell cycle - Caulobacter	0.013
Translation factors	0.018
Terpenoid backbone biosynthesis	0.011
Protein export	0.027
Protein folding and associated processing	0.015
Carbon fixation in photosynthetic organisms	0.024
One carbon pool by folate	0.005
DNA replication	0.009
Glycine, serine and threonine metabolism	0.039
Energy metabolism	0.033
Peptidoglycan biosynthesis	0.047
Mismatch repair	0.013
Carbon fixation pathways in prokaryotes	0.003
Translation proteins	0.037
Homologous recombination	0.014
Cysteine and methionine metabolism	0.040
Chaperones and folding catalysts	0.015
Oxidative phosphorylation	0.018
DNA replication proteins	0.015
Other ion-coupled transporters	0.030
Amino acid related enzymes	0.036
Chromosome	0.027
Pyrimidine metabolism	0.012
Peptidases	0.034
Purine metabolism	0.016
Ribosome	0.017
DNA repair and recombination proteins	0.023
General function prediction only	0.046

KEGG: Kyoto Encyclopedia of Genes and Genomes