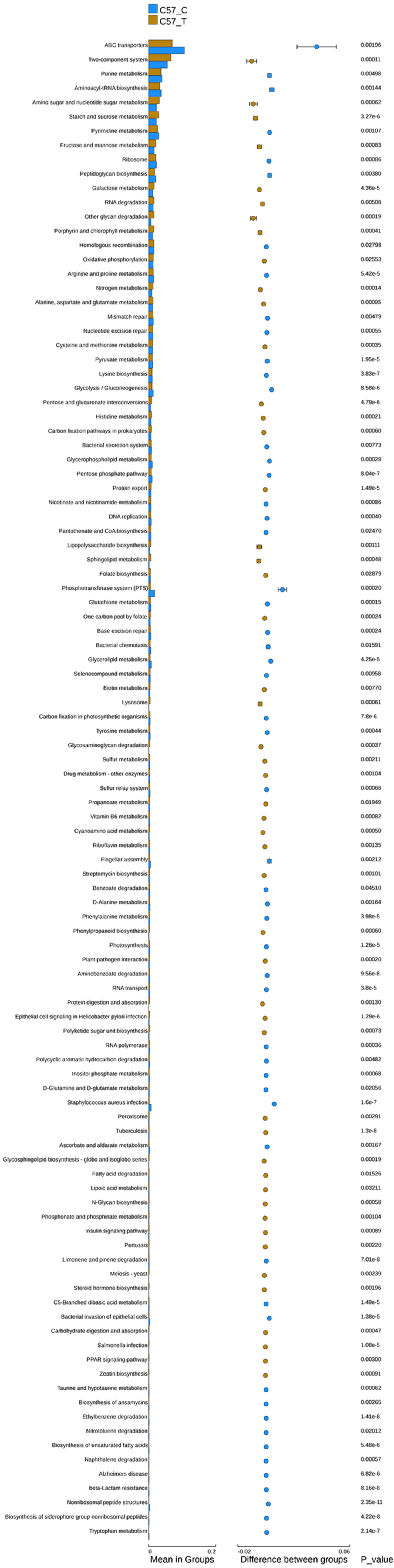
C57_C
C57_T
ABC transporters 0.00196
Two-component system 0.00011
Purine metabolism 0.00498
Aminoacyl-tRNA biosynthesis 0.00144
Amino sugar and nucleotide sugar metabolism 0.00062
Starch and sucrose metabolism 3.27e-6
Pyrimidine metabolism 0.00107
Fructose and mannose metabolism 0.00083
Ribosome 0.00086
Peptidoglycan biosynthesis 0.00380
Galactose metabolism 4.36e-5
RNA degradation 0.00508
Other glycan degradation 0.00019
Porphyrin and chlorophyll metabolism 0.00041
Homologous recombination 0.02798
Oxidative phosphorylation 0.02553
Arginine and proline metabolism 5.42e-5
Nitrogen metabolism 0.00014
Alanine, aspartate and glutamate metabolism 0.00095
Mismatch repair 0.00479
Nucleotide excision repair 0.00055
Cysteine and methionine metabolism 0.00035
Pyruvate metabolism 1.95e-5
Lysine biosynthesis 3.83e-7
Glycolysis / Gluconeogenesis 8.58e-6
Pentose and glucuronate interconversions 4.79e-6
Histidine metabolism 0.00021
Carbon fixation pathways in prokaryotes 0.00060
Bacterial secretion system 0.00773
Glycerophospholipid metabolism 0.00028
Pentose phosphate pathway 8.04e-7
Protein export 1.49e-5
Nicotinate and nicotinamide metabolism 0.00086
DNA replication 0.00040
Pantothenate and CoA biosynthesis 0.02470
Lipopolysaccharide biosynthesis 0.00111
Sphingolipid metabolism 0.00048
Folate biosynthesis 0.02879
Phosphotransferase system (PTS) 0.00020
Glutathione metabolism 0.00015
One carbon pool by folate 0.00024
Base excision repair 0.00024
Bacterial chemotaxis 0.01591
Glycerolipid metabolism 4.25e-5
Selenocompound metabolism 0.00958
Biotin metabolism 0.00770
Lysosome 0.00061
Carbon fixation in photosynthetic organisms 7.8e-6
Tyrosine metabolism 0.00044
Glycosaminoglycan degradation 0.00037
Sulfur metabolism 0.00211
Drug metabolism - other enzymes 0.00104
Sulfur relay system 0.00066
Propanoate metabolism 0.01949
Vitamin B6 metabolism 0.00082
Cyanoamino acid metabolism 0.00050
Riboflavin metabolism 0.00135
Flagellar assembly 0.00212
Streptomycin biosynthesis 0.00101
Benzoate degradation 0.04510
D-Alanine metabolism 0.00164
Phenylalanine metabolism 3.98e-5
Phenylpropanoid biosynthesis 0.00060
Photosynthesis 1.26e-5
Plant-pathogen interaction 0.00020
Aminobenzoate degradation 9.56e-8
RNA transport 3.8e-5
Protein digestion and absorption 0.00130
Epithelial cell signaling in Helicobacter pylori infection 1.29e-6
Polyketide sugar unit biosynthesis 0.00073
RNA polymerase 0.00036
Polycyclic aromatic hydrocarbon degradation 0.00482
Inositol phosphate metabolism 0.00068
D-Glutamine and D-glutamate metabolism 0.02056
Staphylococcus aureus infection 1.6e-7
Peroxisome 0.00291
Tuberculosis 1.3e-8
Ascorbate and aldarate metabolism 0.00167
Glycosphingolipid biosynthesis - globo and isoglobo series 0.00019
Fatty acid degradation 0.01526
Lipoic acid metabolism 0.03211
N-Glycan biosynthesis 0.00058
Phosphonate and phosphinate metabolism 0.00104
Insulin signaling pathway 0.00089
Pertussis 0.00220
Limonene and pinene degradation 7.01e-8
Meiosis - yeast 0.00239
Steroid hormone biosynthesis 0.00196
C5-Branched dibasic acid metabolism 1.49e-5
Bacterial invasion of epithelial cells 1.38e-5
Carbohydrate digestion and absorption 0.00047
Salmonella infection 1.08e-5
PPAR signaling pathway 0.00300
Zeatin biosynthesis 0.00091
Taurine and hypotaurine metabolism 0.00062
Biosynthesis of ansamycins 0.00265
Ethylbenzene degradation 1.41e-8
Nitrotoluene degradation 0.02012
Biosynthesis of unsaturated fatty acids 5.48e-6
Naphthalene degradation 0.00057
Alzheimers disease 6.82e-6
beta-Lactam resistance 8.16e-8
Nonribosomal peptide structures 2.35e-11
Biosynthesis of siderophore group nonribosomal peptides 4.22e-8
Tryptophan metabolism 2.14e-7
0
0.2
Mean in Groups
-0.02
0.06
Difference between groups
P_value