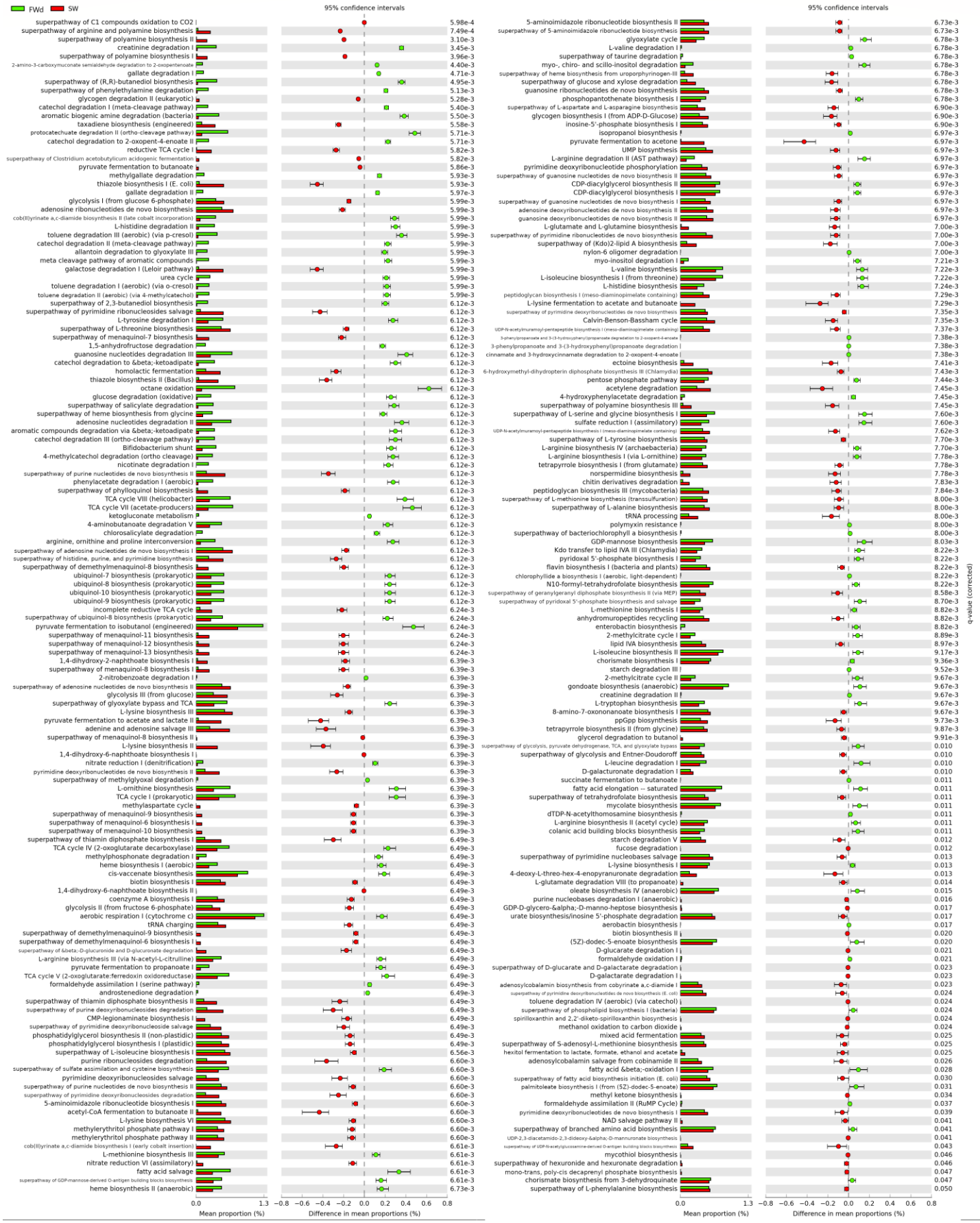
FWd
SW
95% confidence intervals
superpathway of C1 compounds oxidation to CO2 5.98e-4
superpathway of arginine and polyamine biosynthesis 7.49e-4
superpathway of polyamine biosynthesis II 3.10e-3
creatinine degradation I 3.45e-3
superpathway of polyamine biosynthesis I 3.96e-3
2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate 4.40e-3
gallate degradation I 4.71e-3
superpathway of (R,R)-butanediol biosynthesis 4.95e-3
superpathway of phenylethylamine degradation 5.13e-3
glycogen degradation II (eukaryotic) 5.28e-3
catechol degradation I (meta-cleavage pathway) 5.40e-3
aromatic biogenic amine degradation (bacteria) 5.50e-3
taxadiene biosynthesis (engineered) 5.58e-3
protocatechuate degradation II (ortho-cleavage pathway) 5.71e-3
catechol degradation to 2-oxopent-4-enoate II 5.71e-3
reductive TCA cycle I 5.82e-3
superpathway of Clostridium acetobutylicum acidogenic fermentation 5.82e-3
pyruvate fermentation to butanoate 5.86e-3
methylgallate degradation 5.93e-3
thiazole biosynthesis I (E. coli) 5.93e-3
gallate degradation II 5.97e-3
glycolysis I (from glucose 6-phosphate) 5.99e-3
adenosine ribonucleotides de novo biosynthesis 5.99e-3
cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) 5.99e-3
L-histidine degradation II 5.99e-3
toluene degradation III (aerobic) (via p-cresol) 5.99e-3
catechol degradation II (meta-cleavage pathway) 5.99e-3
allantoin degradation to glyoxylate III 5.99e-3
meta cleavage pathway of aromatic compounds 5.99e-3
galactose degradation I (Leloir pathway) 5.99e-3
urea cycle 5.99e-3
toluene degradation I (aerobic) (via o-cresol) 5.99e-3
toluene degradation II (aerobic) (via 4-methylcatechol) 5.99e-3
superpathway of 2,3-butanediol biosynthesis 6.12e-3
superpathway of pyrimidine ribonucleosides salvage 6.12e-3
L-tyrosine degradation I 6.12e-3
superpathway of L-threonine biosynthesis 6.12e-3
superpathway of menaquinol-7 biosynthesis 6.12e-3
1,5-anhydrofructose degradation 6.12e-3
guanosine nucleotides degradation III 6.12e-3
catechol degradation to β-ketoadipate 6.12e-3
homolactic fermentation 6.12e-3
thiazole biosynthesis II (Bacillus) 6.12e-3
octane oxidation 6.12e-3
glucose degradation (oxidative) 6.12e-3
superpathway of salicylate degradation 6.12e-3
superpathway of heme biosynthesis from glycine 6.12e-3
adenosine nucleotides degradation II 6.12e-3
aromatic compounds degradation via β-ketoadipate 6.12e-3
catechol degradation III (ortho-cleavage pathway) 6.12e-3
Bifidobacterium shunt 6.12e-3
4-methylcatechol degradation (ortho cleavage) 6.12e-3
nicotinate degradation I 6.12e-3
superpathway of purine nucleotides de novo biosynthesis II 6.12e-3
phenylacetate degradation I (aerobic) 6.12e-3
superpathway of phylloquinol biosynthesis 6.12e-3
TCA cycle VIII (helicobacter) 6.12e-3
TCA cycle VII (acetate-producers) 6.12e-3
ketogluconate metabolism 6.12e-3
4-aminobutanoate degradation V 6.12e-3
chlorosalicylate degradation 6.12e-3
arginine, ornithine and proline interconversion 6.12e-3
superpathway of adenosine nucleotides de novo biosynthesis I 6.12e-3
superpathway of histidine, purine, and pyrimidine biosynthesis 6.12e-3
superpathway of demethylmenaquinol-8 biosynthesis 6.12e-3
ubiquinol-7 biosynthesis (prokaryotic) 6.12e-3
ubiquinol-8 biosynthesis (prokaryotic) 6.12e-3
ubiquinol-10 biosynthesis (prokaryotic) 6.12e-3
ubiquinol-9 biosynthesis (prokaryotic) 6.12e-3
incomplete reductive TCA cycle 6.24e-3
superpathway of ubiquinol-8 biosynthesis (prokaryotic) 6.24e-3
pyruvate fermentation to isobutanol (engineered) 6.24e-3
superpathway of menaquinol-11 biosynthesis 6.24e-3
superpathway of menaquinol-12 biosynthesis 6.24e-3
superpathway of menaquinol-13 biosynthesis 6.24e-3
1,4-dihydroxy-2-naphthoate biosynthesis I 6.39e-3
superpathway of menaquinol-8 biosynthesis I 6.39e-3
2-nitrobenzoate degradation I 6.39e-3
superpathway of adenosine nucleotides de novo biosynthesis II 6.39e-3
glycolysis III (from glucose) 6.39e-3
superpathway of glyoxylate bypass and TCA 6.39e-3
L-lysine biosynthesis III 6.39e-3
pyruvate fermentation to acetate and lactate II 6.39e-3
adenine and adenosine salvage III 6.39e-3
superpathway of menaquinol-8 biosynthesis II 6.39e-3
L-lysine biosynthesis II 6.39e-3
1,4-dihydroxy-6-naphthoate biosynthesis I 6.39e-3
nitrate reduction I (denitrification) 6.39e-3
pyrimidine deoxyribonucleotides de novo biosynthesis II 6.39e-3
superpathway of methylglyoxal degradation 6.39e-3
L-ornithine biosynthesis I 6.39e-3
TCA cycle I (prokaryotic) 6.39e-3
methylaspartate cycle 6.39e-3
superpathway of menaquinol-9 biosynthesis 6.39e-3
superpathway of menaquinol-6 biosynthesis I 6.39e-3
superpathway of menaquinol-10 biosynthesis 6.39e-3
superpathway of thiamin diphosphate biosynthesis I 6.49e-3
TCA cycle IV (2-oxoglutarate decarboxylase) 6.49e-3
methylphosphonate degradation I 6.49e-3
heme biosynthesis I (aerobic) 6.49e-3
cis-vaccenate biosynthesis 6.49e-3
biotin biosynthesis I 6.49e-3
1,4-dihydroxy-6-naphthoate biosynthesis II 6.49e-3
coenzyme A biosynthesis I 6.49e-3
glycolysis II (from fructose 6-phosphate) 6.49e-3
aerobic respiration I (cytochrome c) 6.49e-3
tRNA charging 6.49e-3
superpathway of demethylmenaquinol-9 biosynthesis 6.49e-3
superpathway of demethylmenaquinol-6 biosynthesis I 6.49e-3
superpathway of β-D-glucuronide and D-glucuronate degradation 6.49e-3
L-arginine biosynthesis III (via N-acetyl-L-citrulline) 6.49e-3
pyruvate fermentation to propanoate I 6.49e-3
TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) 6.49e-3
formaldehyde assimilation I (serine pathway) 6.49e-3
androstenedione degradation I 6.49e-3
superpathway of thiamin diphosphate biosynthesis II 6.49e-3
superpathway of purine deoxyribonucleosides degradation 6.49e-3
CMP-legionaminate biosynthesis I 6.49e-3
superpathway of pyrimidine deoxyribonucleoside salvage 6.49e-3
phosphatidylglycerol biosynthesis II (non-plastidic) 6.49e-3
phosphatidylglycerol biosynthesis I (plastidic) 6.49e-3
superpathway of L-isoleucine biosynthesis I 6.56e-3
purine ribonucleosides degradation 6.60e-3
superpathway of sulfate assimilation and cysteine biosynthesis 6.60e-3
pyrimidine deoxyribonucleosides salvage 6.60e-3
superpathway of purine nucleotides de novo biosynthesis II 6.60e-3
superpathway of pyrimidine deoxyribonucleosides degradation 6.60e-3
5-aminoimidazole ribonucleotide biosynthesis I 6.60e-3
acetyl-CoA fermentation to butanoate II 6.60e-3
L-lysine biosynthesis VI 6.60e-3
methylerythritol phosphate pathway I 6.60e-3
methylerythritol phosphate pathway II 6.60e-3
cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) 6.61e-3
L-methionine biosynthesis III 6.61e-3
nitrate reduction VI (assimilatory) 6.61e-3
fatty acid salvage 6.61e-3
superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis 6.61e-3
heme biosynthesis II (anaerobic) 6.73e-3
0.0 1.3
Mean proportion (%)
−0.8 −0.6 −0.4 −0.2 0.0 0.2 0.4 0.6 0.8
Difference in mean proportions (%)
95% confidence intervals
5-aminoimidazole ribonucleotide biosynthesis II 6.73e-3
superpathway of 5-aminoimidazole ribonucleotide biosynthesis 6.73e-3
glyoxylate cycle 6.78e-3
L-valine degradation I 6.78e-3
superpathway of taurine degradation I 6.78e-3
myo-, chiro- and scillo-inositol degradation 6.78e-3
superpathway of heme biosynthesis from uroporphyrinogen-III 6.78e-3
superpathway of glucose and xylose degradation 6.78e-3
guanosine ribonucleotides de novo biosynthesis 6.78e-3
phosphopantothenate biosynthesis I 6.78e-3
superpathway of L-aspartate and L-asparagine biosynthesis 6.90e-3
glycogen biosynthesis I (from ADP-D-Glucose) 6.90e-3
inosine-5'-phosphate biosynthesis I 6.90e-3
isopropanol biosynthesis I 6.97e-3
pyruvate fermentation to acetone 6.97e-3
UMP biosynthesis 6.97e-3
L-arginine degradation II (AST pathway) 6.97e-3
pyrimidine deoxyribonucleotide phosphorylation 6.97e-3
superpathway of guanosine nucleotides de novo biosynthesis II 6.97e-3
CDP-diacylglycerol biosynthesis II 6.97e-3
CDP-diacylglycerol biosynthesis I 6.97e-3
superpathway of guanosine nucleotides de novo biosynthesis I 6.97e-3
adenosine deoxyribonucleotides de novo biosynthesis II 6.97e-3
guanosine deoxyribonucleotides de novo biosynthesis II 6.97e-3
L-glutamate and L-glutamine biosynthesis 7.00e-3
superpathway of pyrimidine ribonucleotides de novo biosynthesis 7.00e-3
superpathway of (Kdo)2-lipid A biosynthesis 7.00e-3
nylon-6 oligomer degradation I 7.00e-3
myo-inositol degradation I 7.21e-3
L-valine biosynthesis 7.22e-3
L-isoleucine biosynthesis I (from threonine) 7.22e-3
L-histidine biosynthesis 7.24e-3
peptidoglycan biosynthesis I (meso-diaminopimelate containing) 7.29e-3
L-lysine fermentation to acetate and butanoate 7.29e-3
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis 7.35e-3
Calvin-Benson-Bassham cycle 7.35e-3
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) 7.37e-3
3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate 7.38e-3
3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation I 7.38e-3
cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate 7.38e-3
ectoine biosynthesis 7.41e-3
6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) 7.43e-3
pentose phosphate pathway 7.44e-3
acetylene degradation 7.45e-3
4-hydroxyphenylacetate degradation 7.45e-3
superpathway of polyamine biosynthesis III 7.45e-3
superpathway of L-serine and glycine biosynthesis I 7.60e-3
sulfate reduction I (assimilatory) 7.60e-3
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) 7.62e-3
superpathway of L-tyrosine biosynthesis 7.70e-3
L-arginine biosynthesis IV (archaebacteria) 7.70e-3
L-arginine biosynthesis I (via L-ornithine) 7.78e-3
tetrapyrrole biosynthesis I (from glutamate) 7.78e-3
norspermidine biosynthesis 7.78e-3
chitin derivatives degradation 7.83e-3
peptidoglycan biosynthesis III (mycobacteria) 7.84e-3
superpathway of L-methionine biosynthesis (transsulfuration) 8.00e-3
superpathway of L-alanine biosynthesis 8.00e-3
tRNA processing 8.00e-3
polymyxin resistance 8.00e-3
superpathway of bacteriochlorophyll a biosynthesis I 8.00e-3
GDP-mannose biosynthesis 8.03e-3
Kdo transfer to lipid IVA III (Chlamydia) 8.22e-3
pyridoxal 5'-phosphate biosynthesis I 8.22e-3
flavin biosynthesis I (bacteria and plants) 8.22e-3
chlorophyllide a biosynthesis I (aerobic, light-dependent) 8.22e-3
N10-formyl-tetrahydrofolate biosynthesis 8.22e-3
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) 8.58e-3
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage 8.70e-3
L-methionine biosynthesis I 8.82e-3
anhydromuropeptides recycling 8.82e-3
enterobactin biosynthesis I 8.82e-3
2-methylcitrate cycle I 8.89e-3
lipid IVA biosynthesis 8.97e-3
L-isoleucine biosynthesis II 9.17e-3
chorismate biosynthesis I 9.36e-3
starch degradation III 9.52e-3
2-methylcitrate cycle II 9.67e-3
gondoate biosynthesis (anaerobic) 9.67e-3
creatinine degradation II I 9.67e-3
L-tryptophan biosynthesis 9.67e-3
8-amino-7-oxononanoate biosynthesis I 9.67e-3
ppGpp biosynthesis 9.73e-3
tetrapyrrole biosynthesis II (from glycine) 9.87e-3
glycerol degradation to butanol 9.91e-3
superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass 0.010
superpathway of glycolysis and Entner-Doudoroff 0.010
L-leucine degradation I 0.010
D-galacturonate degradation I 0.010
succinate fermentation to butanoate 0.011
fatty acid elongation -- saturated 0.011
superpathway of tetrahydrofolate biosynthesis 0.011
mycolate biosynthesis 0.011
dTDP-N-acetylthomosamine biosynthesis 0.011
L-arginine biosynthesis II (acetyl cycle) 0.011
colanic acid building blocks biosynthesis 0.011
starch degradation V 0.012
fucose degradation I 0.012
superpathway of pyrimidine nucleobases salvage 0.013
L-lysine biosynthesis I 0.013
4-deoxy-L-threo-hex-4-enopyranuronate degradation 0.013
L-glutamate degradation VIII (to propanoate) 0.014
oleate biosynthesis IV (anaerobic) 0.015
purine nucleobases degradation I (anaerobic) 0.016
GDP-D-glycero-α-D-manno-heptose biosynthesis 0.017
urate biosynthesis/inosine 5'-phosphate degradation 0.017
aerobactin biosynthesis I 0.017
biotin biosynthesis II 0.020
(5Z)-dodec-5-enoate biosynthesis 0.020
D-glucarate degradation I 0.021
formaldehyde oxidation I 0.021
superpathway of D-glucarate and D-galactarate degradation I 0.023
D-galactarate degradation I 0.023
adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I 0.023
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) 0.024
toluene degradation IV (aerobic) (via catechol) 0.024
superpathway of phospholipid biosynthesis I (bacteria) 0.024
spirilloxanthin and 2,2'-diketo-spirilloxanthin biosynthesis 0.024
methanol oxidation to carbon dioxide 0.024
mixed acid fermentation 0.025
superpathway of S-adenosyl-L-methionine biosynthesis 0.025
hexitol fermentation to lactate, formate, ethanol and acetate 0.025
adenosylcobalamin salvage from cobinamide II 0.026
fatty acid β-oxidation I 0.028
superpathway of fatty acid biosynthesis initiation (E. coli) 0.030
palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) 0.031
methyl ketone biosynthesis 0.034
formaldehyde assimilation II (RuMP Cycle) 0.037
pyrimidine deoxyribonucleotides de novo biosynthesis I 0.039
NAD salvage pathway II 0.041
superpathway of branched amino acid biosynthesis 0.041
UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronate biosynthesis 0.041
superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis 0.043
mycothiol biosynthesis I 0.046
superpathway of hexuronide and hexuronate degradation 0.046
mono-trans, poly-cis decaprenyl phosphate biosynthesis 0.047
chorismate biosynthesis from 3-dehydroquinate 0.047
superpathway of L-phenylalanine biosynthesis 0.050
0.0 1.3
Mean proportion (%)
−0.8 −0.6 −0.4 −0.2 0.0 0.2 0.4 0.6 0.8
Difference in mean proportions (%)
q-value (corrected)