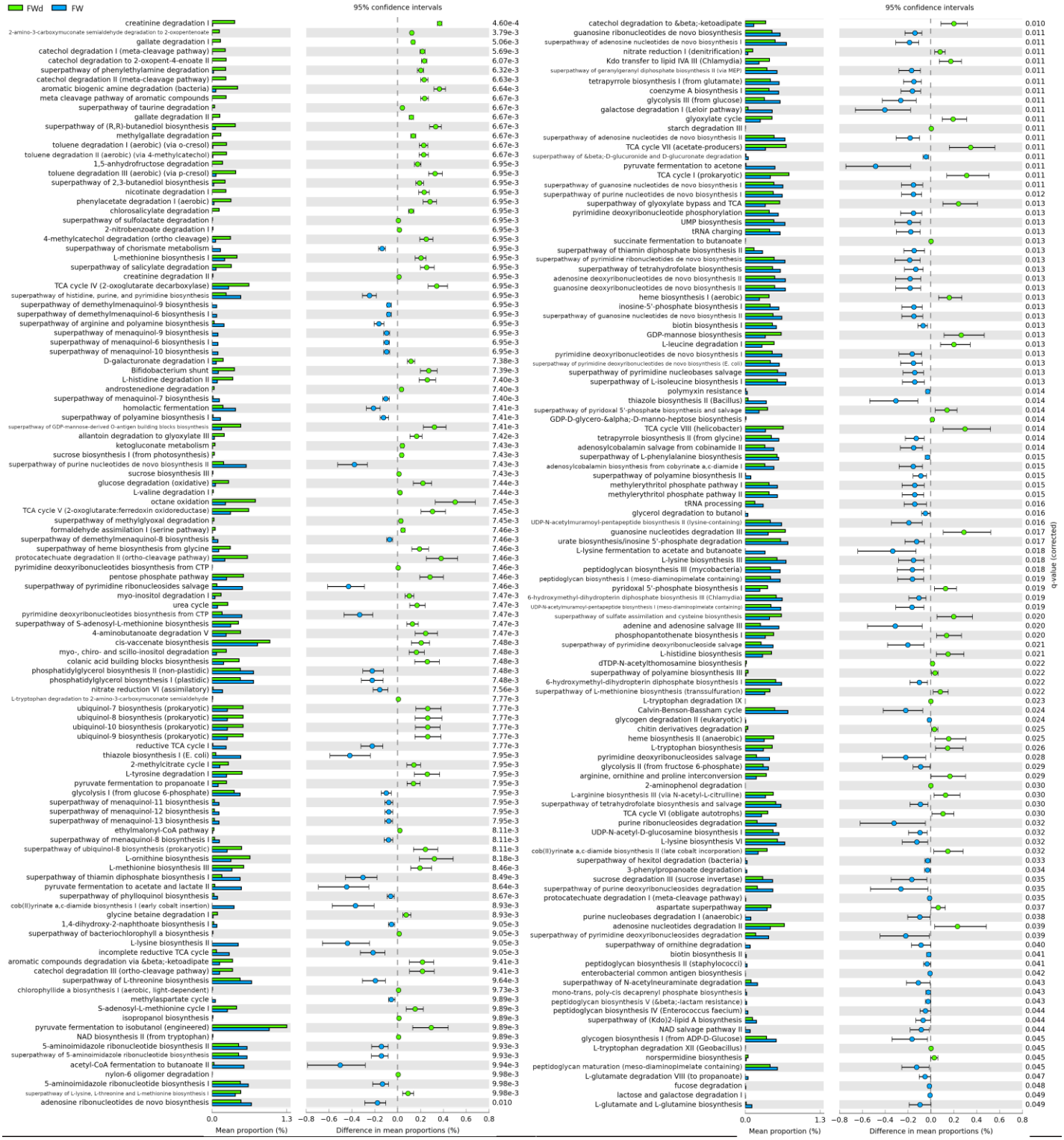
FWd
FW
95% confidence intervals
creatinine degradation I 4.60e-4
2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate 3.79e-3
gallate degradation I 5.06e-3
catechol degradation I (meta-cleavage pathway) 5.69e-3
catechol degradation to 2-oxopent-4-enoate II 6.07e-3
superpathway of phenylethylamine degradation 6.32e-3
catechol degradation II (meta-cleavage pathway) 6.63e-3
aromatic biogenic amine degradation (bacteria) 6.64e-3
meta cleavage pathway of aromatic compounds 6.67e-3
superpathway of taurine degradation 6.67e-3
gallate degradation II 6.67e-3
superpathway of (R,R)-butanediol biosynthesis 6.67e-3
methylgallate degradation 6.67e-3
toluene degradation I (aerobic) (via o-cresol) 6.67e-3
toluene degradation II (aerobic) (via 4-methylcatechol) 6.67e-3
1,5-anhydrofructose degradation 6.95e-3
toluene degradation III (aerobic) (via p-cresol) 6.95e-3
superpathway of 2,3-butanediol biosynthesis 6.95e-3
nicotinate degradation I 6.95e-3
phenylacetate degradation I (aerobic) 6.95e-3
chlorosalicylate degradation 6.95e-3
superpathway of sulfolactate degradation 6.95e-3
2-nitrobenzoate degradation I 6.95e-3
4-methylcatechol degradation (ortho cleavage) 6.95e-3
superpathway of chorismate metabolism 6.95e-3
L-methionine biosynthesis I 6.95e-3
superpathway of salicylate degradation 6.95e-3
creatinine degradation II 6.95e-3
TCA cycle IV (2-oxoglutarate decarboxylase) 6.95e-3
superpathway of histidine, purine, and pyrimidine biosynthesis 6.95e-3
superpathway of demethylmenaquinol-9 biosynthesis 6.95e-3
superpathway of demethylmenaquinol-6 biosynthesis I 6.95e-3
superpathway of arginine and polyamine biosynthesis 6.95e-3
superpathway of menaquinol-9 biosynthesis 6.95e-3
superpathway of menaquinol-6 biosynthesis I 6.95e-3
superpathway of menaquinol-10 biosynthesis 6.95e-3
D-galacturonate degradation I 7.38e-3
Bifidobacterium shunt 7.39e-3
L-histidine degradation II 7.40e-3
androstenedione degradation 7.40e-3
superpathway of menaquinol-7 biosynthesis 7.40e-3
homolactic fermentation 7.41e-3
superpathway of polyamine biosynthesis I 7.41e-3
superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis 7.41e-3
allantoin degradation to glyoxylate III 7.42e-3
ketogluconate metabolism 7.43e-3
sucrose biosynthesis I (from photosynthesis) 7.43e-3
superpathway of purine nucleotides de novo biosynthesis II 7.43e-3
sucrose biosynthesis III 7.43e-3
glucose degradation (oxidative) 7.44e-3
L-valine degradation I 7.44e-3
octane oxidation 7.45e-3
TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) 7.45e-3
superpathway of methylglyoxal degradation 7.45e-3
formaldehyde assimilation I (serine pathway) 7.46e-3
superpathway of demethylmenaquinol-8 biosynthesis 7.46e-3
superpathway of heme biosynthesis from glycine 7.46e-3
protocatechuate degradation II (ortho-cleavage pathway) 7.46e-3
pyrimidine deoxyribonucleotides biosynthesis from CTP 7.46e-3
pentose phosphate pathway 7.46e-3
superpathway of pyrimidine ribonucleosides salvage 7.46e-3
myo-inositol degradation I 7.47e-3
urea cycle 7.47e-3
pyrimidine deoxyribonucleotides biosynthesis from CTP 7.47e-3
superpathway of S-adenosyl-L-methionine biosynthesis 7.47e-3
4-aminobutanoate degradation V 7.47e-3
cis-vaccenate biosynthesis 7.48e-3
myo-, chiro- and scillo-inositol degradation 7.48e-3
colanic acid building blocks biosynthesis 7.48e-3
phosphatidylglycerol biosynthesis II (non-plastidic) 7.48e-3
phosphatidylglycerol biosynthesis I (plastidic) 7.48e-3
nitrate reduction VI (assimilatory) 7.56e-3
L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde 7.77e-3
ubiquinol-7 biosynthesis (prokaryotic) 7.77e-3
ubiquinol-8 biosynthesis (prokaryotic) 7.77e-3
ubiquinol-10 biosynthesis (prokaryotic) 7.77e-3
ubiquinol-9 biosynthesis (prokaryotic) 7.77e-3
reductive TCA cycle I 7.77e-3
thiazole biosynthesis I (E. coli) 7.95e-3
2-methylcitrate cycle I 7.95e-3
L-tyrosine degradation I 7.95e-3
pyruvate fermentation to propanoate I 7.95e-3
glycolysis I (from glucose 6-phosphate) 7.95e-3
superpathway of menaquinol-11 biosynthesis 7.95e-3
superpathway of menaquinol-12 biosynthesis 7.95e-3
superpathway of menaquinol-13 biosynthesis 7.95e-3
ethylmalonyl-CoA pathway 8.11e-3
superpathway of menaquinol-8 biosynthesis I 8.11e-3
superpathway of ubiquinol-8 biosynthesis (prokaryotic) 8.11e-3
L-ornithine biosynthesis 8.18e-3
L-methionine biosynthesis III 8.46e-3
superpathway of thiamin diphosphate biosynthesis I 8.49e-3
pyruvate fermentation to acetate and lactate II 8.64e-3
superpathway of phylloquinol biosynthesis 8.67e-3
cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) 8.93e-3
glycine betaine degradation I 8.93e-3
1,4-dihydroxy-2-naphthoate biosynthesis I 9.05e-3
superpathway of bacteriochlorophyll a biosynthesis I 9.05e-3
L-lysine biosynthesis II 9.05e-3
incomplete reductive TCA cycle 9.05e-3
aromatic compounds degradation via β-ketoadipate 9.41e-3
catechol degradation III (ortho-cleavage pathway) 9.41e-3
superpathway of L-threonine biosynthesis 9.64e-3
chlorophyllide a biosynthesis I (aerobic, light-dependent) 9.73e-3
methylaspartate cycle 9.89e-3
S-adenosyl-L-methionine cycle I 9.89e-3
isopropanol biosynthesis I 9.89e-3
pyruvate fermentation to isobutanol (engineered) 9.89e-3
NAD biosynthesis II (from tryptophan) 9.89e-3
5-aminoimidazole ribonucleotide biosynthesis II 9.93e-3
superpathway of 5-aminoimidazole ribonucleotide biosynthesis 9.93e-3
acetyl-CoA fermentation to butanoate II 9.94e-3
nylon-6 oligomer degradation 9.98e-3
5-aminoimidazole ribonucleotide biosynthesis I 9.98e-3
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I 9.98e-3
adenosine ribonucleotides de novo biosynthesis 0.010
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
catechol degradation to β-ketoadipate 0.010
guanosine ribonucleotides de novo biosynthesis 0.011
superpathway of adenosine nucleotides de novo biosynthesis I 0.011
nitrate reduction I (denitrification) 0.011
Kdo transfer to lipid IVA III (Chlamydia) 0.011
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) 0.011
tetrapyrrole biosynthesis I (from glutamate) 0.011
coenzyme A biosynthesis I 0.011
glycolysis III (from glucose) 0.011
galactose degradation I (Leloir pathway) 0.011
glyoxylate cycle 0.011
starch degradation III 0.011
superpathway of adenosine nucleotides de novo biosynthesis II 0.011
TCA cycle VII (acetate-producers) 0.011
superpathway of β-D-glucuronide and D-glucuronate degradation 0.011
pyruvate fermentation to acetone 0.011
TCA cycle I (prokaryotic) 0.011
superpathway of guanosine nucleotides de novo biosynthesis I 0.011
superpathway of purine nucleotides de novo biosynthesis I 0.012
superpathway of glyoxylate bypass and TCA 0.013
pyrimidine deoxyribonucleotide phosphorylation 0.013
UMP biosynthesis 0.013
tRNA charging 0.013
succinate fermentation to butanoate 0.013
superpathway of thiamin diphosphate biosynthesis II 0.013
superpathway of pyrimidine ribonucleotides de novo biosynthesis 0.013
superpathway of tetrahydrofolate biosynthesis 0.013
adenosine deoxyribonucleotides de novo biosynthesis II 0.013
guanosine deoxyribonucleotides de novo biosynthesis II 0.013
heme biosynthesis I (aerobic) 0.013
inosine-5'-phosphate biosynthesis I 0.013
superpathway of guanosine nucleotides de novo biosynthesis II 0.013
biotin biosynthesis I 0.013
GDP-mannose biosynthesis 0.013
L-leucine degradation I 0.013
pyrimidine deoxyribonucleotides de novo biosynthesis I 0.013
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) 0.013
superpathway of pyrimidine nucleobases salvage 0.013
superpathway of L-isoleucine biosynthesis I 0.013
polymyxin resistance I 0.014
thiazole biosynthesis II (Bacillus) 0.014
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage 0.014
GDP-D-glycero-α-D-manno-heptose biosynthesis I 0.014
TCA cycle VIII (helicobacter) 0.014
tetrapyrrole biosynthesis II (from glycine) 0.014
adenosylcobalamin salvage from cobinamide II 0.014
superpathway of L-phenylalanine biosynthesis 0.015
adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I 0.015
superpathway of polyamine biosynthesis II 0.015
methylerythritol phosphate pathway I 0.015
methylerythritol phosphate pathway II 0.015
tRNA processing 0.016
glycerol degradation to butanol 0.016
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) 0.016
guanosine nucleotides degradation III 0.017
urate biosynthesis/inosine 5'-phosphate degradation 0.017
L-lysine fermentation to acetate and butanoate 0.018
L-lysine biosynthesis III 0.018
peptidoglycan biosynthesis III (mycobacteria) 0.018
peptidoglycan biosynthesis I (meso-diaminopimelate containing) 0.019
pyridoxal 5'-phosphate biosynthesis I 0.019
6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) 0.019
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) 0.019
superpathway of sulfate assimilation and cysteine biosynthesis 0.020
adenine and adenosine salvage III 0.020
phosphopantothenate biosynthesis I 0.020
superpathway of pyrimidine deoxyribonucleoside salvage 0.021
L-histidine biosynthesis 0.021
dTDP-N-acetylthomosamine biosynthesis I 0.022
superpathway of polyamine biosynthesis III 0.022
6-hydroxymethyl-dihydropterin diphosphate biosynthesis I 0.022
superpathway of L-methionine biosynthesis (transsulfuration) 0.022
L-tryptophan degradation IX 0.023
Calvin-Benson-Bassham cycle 0.024
glycogen degradation II (eukaryotic) 0.024
chitin derivatives degradation 0.025
heme biosynthesis II (anaerobic) 0.025
L-tryptophan biosynthesis 0.026
pyrimidine deoxyribonucleosides salvage 0.028
glycolysis II (from fructose 6-phosphate) 0.029
arginine, ornithine and proline interconversion 0.029
2-aminophenol degradation 0.030
L-arginine biosynthesis III (via N-acetyl-L-citrulline) 0.030
superpathway of tetrahydrofolate biosynthesis and salvage 0.030
TCA cycle VI (obligate autotrophs) 0.030
purine ribonucleosides degradation 0.032
UDP-N-acetyl-D-glucosamine biosynthesis I 0.032
L-lysine biosynthesis VI 0.032
cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) 0.032
superpathway of hexitol degradation (bacteria) 0.033
3-phenylpropanoate degradation 0.034
sucrose degradation III (sucrose invertase) 0.035
superpathway of purine deoxyribonucleosides degradation 0.035
protocatechuate degradation I (meta-cleavage pathway) 0.035
aspartate superpathway 0.037
purine nucleobases degradation I (anaerobic) 0.038
adenosine nucleotides degradation II 0.039
superpathway of pyrimidine deoxyribonucleosides degradation 0.039
superpathway of ornithine degradation 0.040
biotin biosynthesis II 0.041
peptidoglycan biosynthesis II (staphylococci) 0.041
enterobacterial common antigen biosynthesis 0.042
superpathway of N-acetylneuraminate degradation 0.043
mono-trans, poly-cis decaprenyl phosphate biosynthesis 0.043
peptidoglycan biosynthesis V (β-lactam resistance) 0.043
peptidoglycan biosynthesis IV (Enterococcus faecium) 0.044
superpathway of (Kdo)2-lipid A biosynthesis 0.044
NAD salvage pathway II 0.044
glycogen biosynthesis I (from ADP-D-Glucose) 0.045
L-tryptophan degradation XII (Geobacillus) 0.045
norspermidine biosynthesis 0.045
peptidoglycan maturation (meso-diaminopimelate containing) 0.045
L-glutamate degradation VIII (to propanoate) 0.047
fucose degradation 0.048
lactose and galactose degradation I 0.049
L-glutamate and L-glutamine biosynthesis 0.049
q-value (corrected)
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 (%)