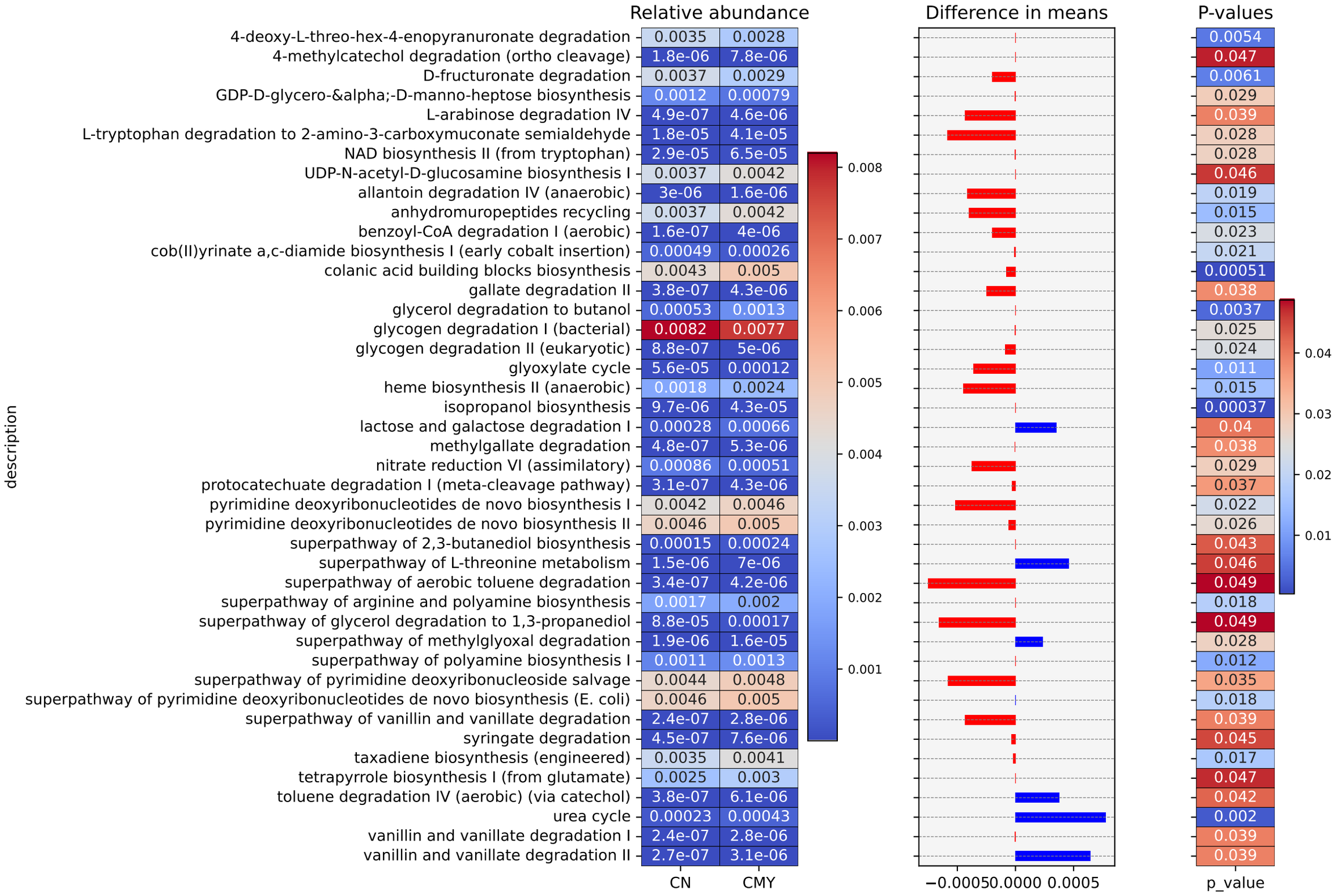
Relative abundance
Difference in means
P-values
description
4-deoxy-L-threo-hex-4-enopyranuronate degradation 0.0035 0.0028 0.0054
4-methylcatechol degradation (ortho cleavage) 1.8e-06 7.8e-06 0.047
D-fructuronate degradation 0.0037 0.0029 0.0061
GDP-D-glycero-α-D-manno-heptose biosynthesis 0.0012 0.00079 0.029
L-arabinose degradation IV 4.9e-07 4.6e-06 0.039
L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde 1.8e-05 4.1e-05 0.028
NAD biosynthesis II (from tryptophan) 2.9e-05 6.5e-05 0.028
UDP-N-acetyl-D-glucosamine biosynthesis I 0.0037 0.0042 0.046
allantoin degradation IV (anaerobic) 3e-06 1.6e-06 0.019
anhydromuropeptides recycling 0.0037 0.0042 0.015
benzoyl-CoA degradation I (aerobic) 1.6e-07 4e-06 0.023
cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) 0.00049 0.00026 0.021
colanic acid building blocks biosynthesis 0.0043 0.005 0.00051
gallate degradation II 3.8e-07 4.3e-06 0.038
glycerol degradation to butanol 0.00053 0.0013 0.0037
glycogen degradation I (bacterial) 0.0082 0.0077 0.025
glycogen degradation II (eukaryotic) 8.8e-07 5e-06 0.024
glyoxylate cycle 5.6e-05 0.00012 0.011
heme biosynthesis II (anaerobic) 0.0018 0.0024 0.015
isopropanol biosynthesis 9.7e-06 4.3e-05 0.00037
lactose and galactose degradation I 0.00028 0.00066 0.04
methylgallate degradation 4.8e-07 5.3e-06 0.038
nitrate reduction VI (assimilatory) 0.00086 0.00051 0.029
protocatechuate degradation I (meta-cleavage pathway) 3.1e-07 4.3e-06 0.037
pyrimidine deoxyribonucleotides de novo biosynthesis I 0.0042 0.0046 0.022
pyrimidine deoxyribonucleotides de novo biosynthesis II 0.0046 0.005 0.026
superpathway of 2,3-butanediol biosynthesis 0.00015 0.00024 0.043
superpathway of L-threonine metabolism 1.5e-06 7e-06 0.046
superpathway of aerobic toluene degradation 3.4e-07 4.2e-06 0.049
superpathway of arginine and polyamine biosynthesis 0.0017 0.002 0.018
superpathway of glycerol degradation to 1,3-propanediol 8.8e-05 0.00017 0.049
superpathway of methylglyoxal degradation 1.9e-06 1.6e-05 0.028
superpathway of polyamine biosynthesis I 0.0011 0.0013 0.012
superpathway of pyrimidine deoxyribonucleoside salvage 0.0044 0.0048 0.035
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) 0.0046 0.005 0.018
superpathway of vanillin and vanillate degradation 2.4e-07 2.8e-06 0.039
syringate degradation 4.5e-07 7.6e-06 0.045
taxadiene biosynthesis (engineered) 0.0035 0.0041 0.017
tetrapyrrole biosynthesis I (from glutamate) 0.0025 0.003 0.047
toluene degradation IV (aerobic) (via catechol) 3.8e-07 6.1e-06 0.042
urea cycle 0.00023 0.00043 0.002
vanillin and vanillate degradation I 2.4e-07 2.8e-06 0.039
vanillin and vanillate degradation II 2.7e-07 3.1e-06 0.039
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.04
0.03
0.02
0.01
CN
CMY
−0.0005 0.0000 0.0005
p_value