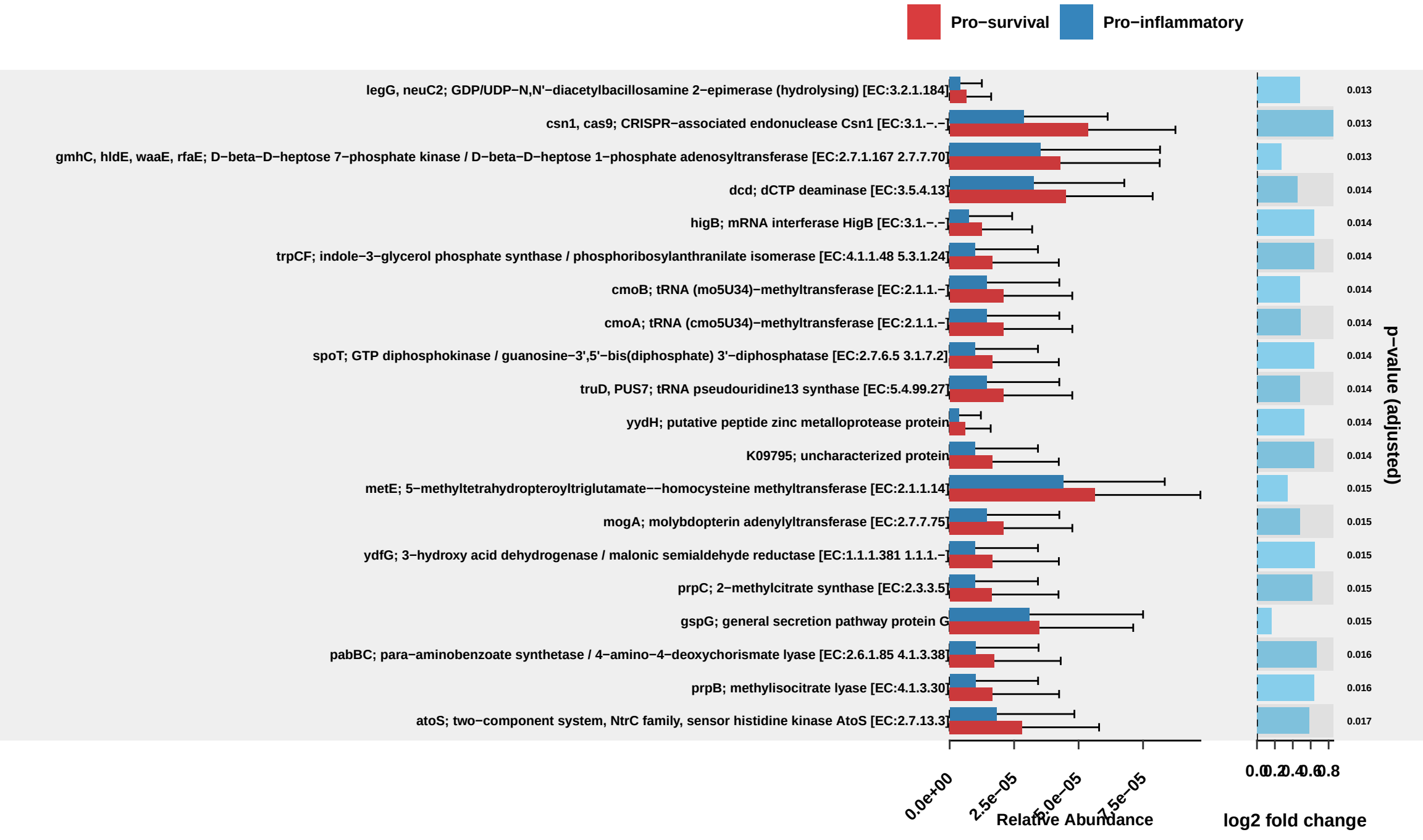
Pro−survival
Pro−inflammatory
legG, neuC2; GDP/UDP−N,N'−diacetylbacillosamine 2−epimerase (hydrolysing) [EC:3.2.1.184]
csn1, cas9; CRISPR−associated endonuclease Csn1 [EC:3.1.−.−]
gmhC, hldE, waaE, rfaE; D−beta−D−heptose 7−phosphate kinase / D−beta−D−heptose 1−phosphate adenosyltransferase [EC:2.7.1.167 2.7.7.70]
dcd; dCTP deaminase [EC:3.5.4.13]
higB; mRNA interferase HigB [EC:3.1.−.−]
trpCF; indole−3−glycerol phosphate synthase / phosphoribosylanthranilate isomerase [EC:4.1.1.48 5.3.1.24]
cmoB; tRNA (mo5U34)−methyltransferase [EC:2.1.1.−]
cmoA; tRNA (cmo5U34)−methyltransferase [EC:2.1.1.−]
spoT; GTP diphosphokinase / guanosine−3',5'−bis(diphosphate) 3'−diphosphatase [EC:2.7.6.5 3.1.7.2]
truD, PUS7; tRNA pseudouridine13 synthase [EC:5.4.99.27]
yydH; putative peptide zinc metalloprotease protein
K09795; uncharacterized protein
metE; 5−methyltetrahydropteroyltriglutamate−−homocysteine methyltransferase [EC:2.1.1.14]
mogA; molybdopterin adenylyltransferase [EC:2.7.7.75]
ydfG; 3−hydroxy acid dehydrogenase / malonic semialdehyde reductase [EC:1.1.1.381 1.1.1.−]
prpC; 2−methylcitrate synthase [EC:2.3.3.5]
gspG; general secretion pathway protein G
pabBC; para−aminobenzoate synthetase / 4−amino−4−deoxychorismate lyase [EC:2.6.1.85 4.1.3.38]
prpB; methylisocitrate lyase [EC:4.1.3.30]
atoS; two−component system, NtrC family, sensor histidine kinase AtoS [EC:2.7.13.3]
0.013
0.013
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0.015
0.016
0.016
0.017
p−value (adjusted)
0.0e+00
2.5e−05
5.0e−05
7.5e−05
Relative Abundance
0.0
0.2
0.4
0.6
0.8
log2 fold change