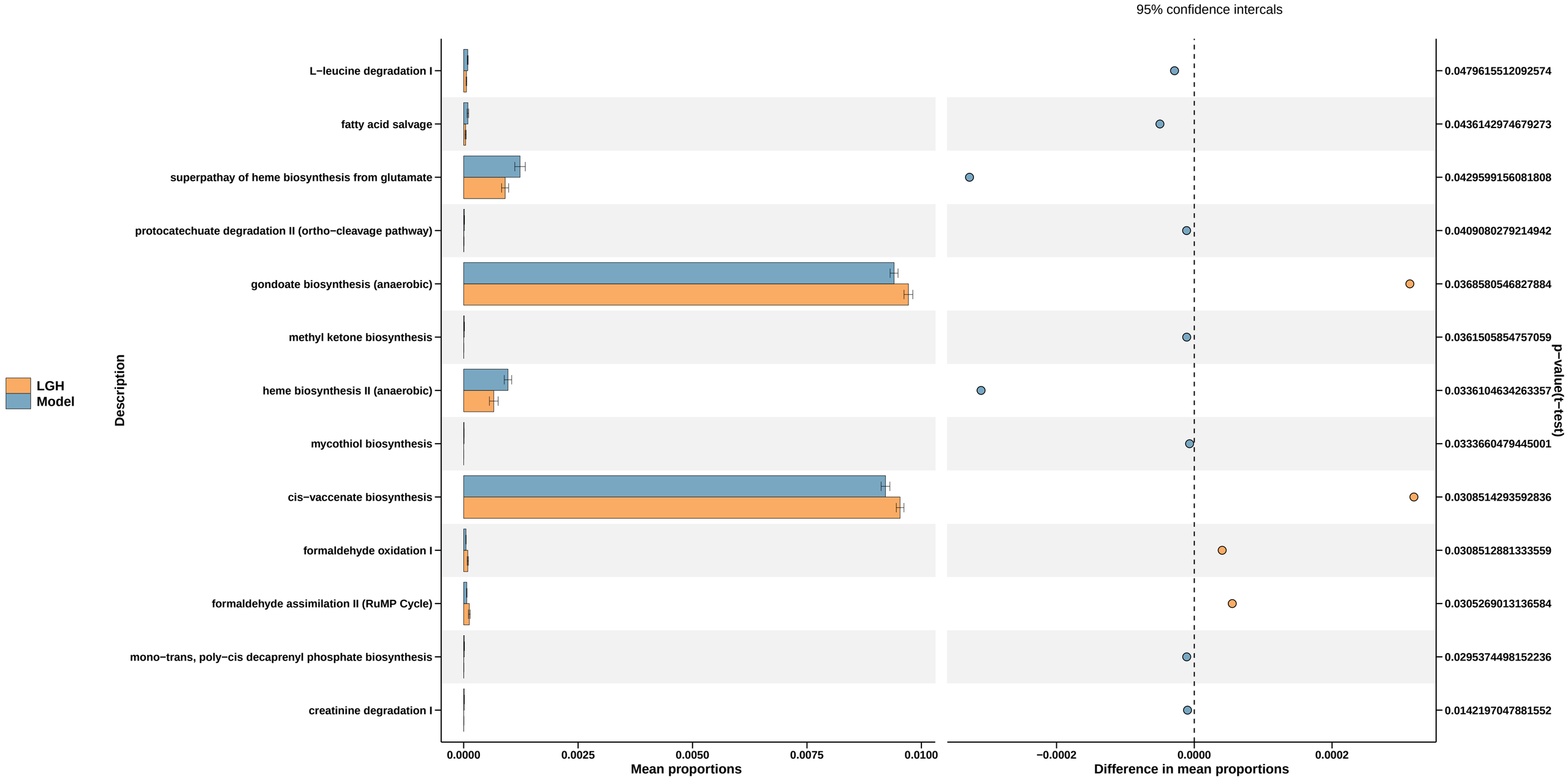
95% confidence intercals
LGH
Model
Description
L−leucine degradation I
fatty acid salvage
superpathay of heme biosynthesis from glutamate
protocatechuate degradation II (ortho−cleavage pathway)
gondoate biosynthesis (anaerobic)
methyl ketone biosynthesis
heme biosynthesis II (anaerobic)
mycothiol biosynthesis
cis−vaccenate biosynthesis
formaldehyde oxidation I
formaldehyde assimilation II (RuMP Cycle)
mono−trans, poly−cis decaprenyl phosphate biosynthesis
creatinine degradation I
0.0000
0.0025
0.0050
0.0075
0.0100
Mean proportions
−0.0002
0.0000
0.0002
Difference in mean proportions
0.0479615512092574
0.0436142974679273
0.0429599156081808
0.0409080279214942
0.0368580546827884
0.0361505854757059
0.0336104634263357
0.0333660479445001
0.0308514293592836
0.0308512881333559
0.0305269013136584
0.0295374498152236
0.0142197047881552
p−value(t−test)