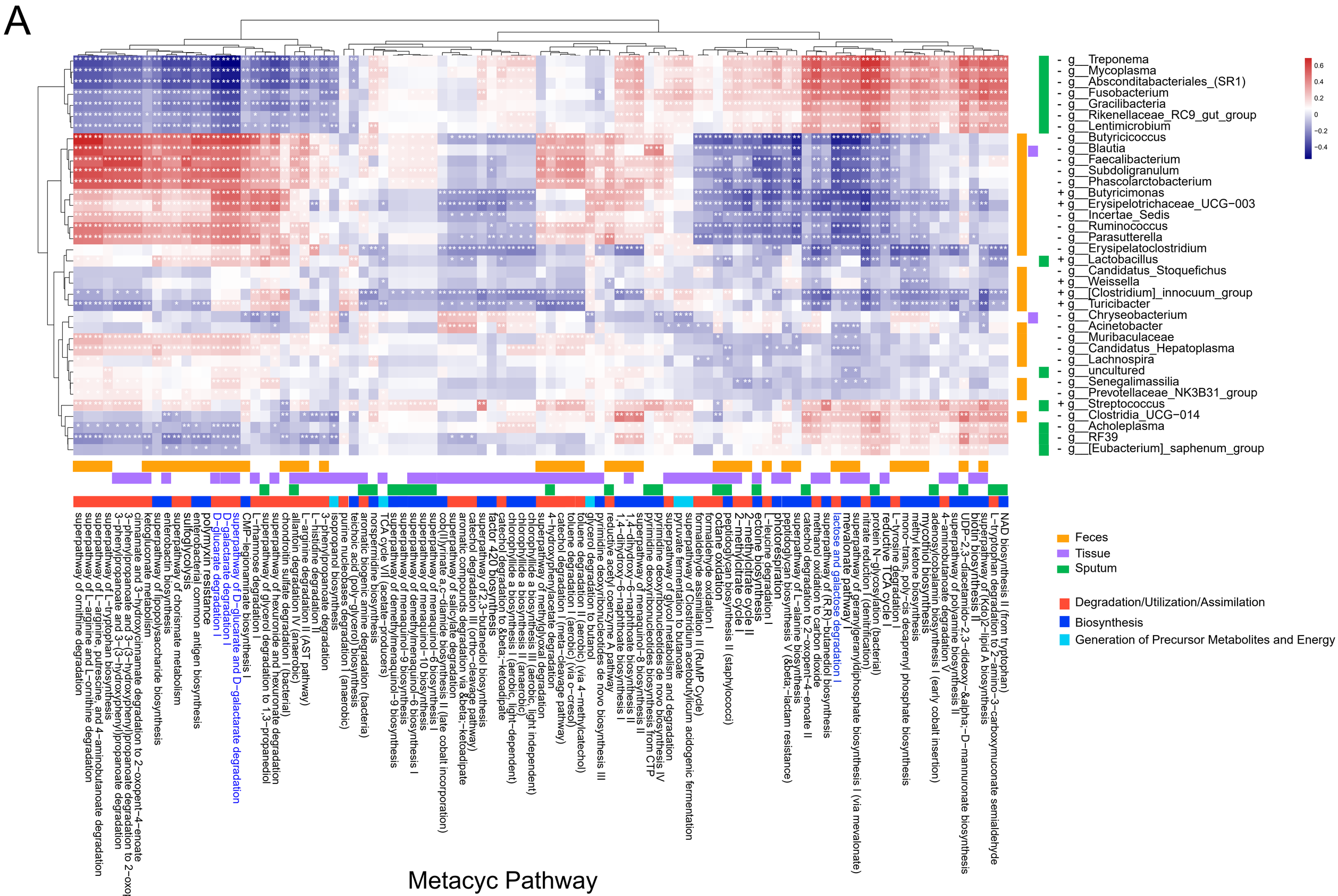
A
- g__Treponema
- g__Mycoplasma
- g__Absconditabacteriales_(SR1)
- g__Fusobacterium
- g__Gracilibacteria
- g__Rikenellaceae_RC9_gut_group
- g__Lentimicrobium
- g__Butyricicoccus
- g__Blautia
- g__Faecalibacterium
- g__Subdoligranulum
- g__Phascolarctobacterium
+ g__Butyricimonas
+ g__Erysipelotrichaceae_UCG−003
- g__Incertae_Sedis
- g__Ruminococcus
- g__Parasutterella
- g__Erysipelatoclostridium
+ g__Lactobacillus
- g__Candidatus_Stoquefichus
+ g__Weissella
+ g__[Clostridium]_innocuum_group
+ g__Turicibacter
- g__Chryseobacterium
- g__Acinetobacter
- g__Muribaculaceae
- g__Candidatus_Hepatoplasma
- g__Lachnospira
- g__uncultured
- g__Senegalimassilia
- g__Prevotellaceae_NK3B31_group
+ g__Streptococcus
- g__Clostridia_UCG−014
- g__Acholeplasma
- g__RF39
- g__[Eubacterium]_saphenum_group
0.6
0.4
0.2
0
−0.2
−0.4
NAD biosynthesis II (from tryptophan)
L−tryptophan degradation to 2−amino−3−carboxymuconate semialdehyde
superpathway of (Kdo)2−lipid A biosynthesis
biotin biosynthesis II
UDP−2,3−diacetamido−2,3−dideoxy−α−D−mannuronate biosynthesis
superpathway of polyamine biosynthesis II
4−aminobutanoate degradation V
adenosylcobalamin biosynthesis I (early cobalt insertion)
mycothiol biosynthesis
methyl ketone biosynthesis
mono−trans, poly−cis decaprenyl phosphate biosynthesis
L−tyrosine degradation I
reductive TCA cycle I
protein N−glycosylation (bacterial)
nitrate reduction I (denitrification)
superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)
mevalonate pathway I
lactose and galactose degradation I
superpathway of (R,R)−butanediol biosynthesis
methanol oxidation to carbon dioxide
catechol degradation to 2−oxopent−4−enoate II
superpathway of L−alanine biosynthesis
peptidoglycan biosynthesis V (β−lactam resistance)
photorespiration
L−leucine degradation I
ectoine biosynthesis
2−methylcitrate cycle II
2−methylcitrate cycle I
peptidoglycan biosynthesis II (staphylococci)
octane oxidation
formaldehyde oxidation I
formaldehyde assimilation II (RuMP Cycle)
superpathway of Clostridium acetobutylicum acidogenic fermentation
pyruvate fermentation to butanoate
superpathway of glycol metabolism and degradation
pyrimidine deoxyribonucleotides de novo biosynthesis IV
pyrimidine deoxyribonucleotides biosynthesis from CTP
superpathway of menaquinol−8 biosynthesis II
1,4−dihydroxy−6−naphthoate biosynthesis II
1,4−dihydroxy−6−naphthoate biosynthesis I
reductive acetyl coenzyme A pathway
pyrimidine deoxyribonucleotides de novo biosynthesis III
glycerol degradation to butanol
toluene degradation II (aerobic) (via 4−methylcatechol)
toluene degradation I (aerobic) (via o−cresol)
catechol degradation I (meta−cleavage pathway)
4−hydroxyphenylacetate degradation
superpathway of methylglyoxal degradation
chlorophyllide a biosynthesis III (aerobic, light independent)
chlorophyllide a biosynthesis II (anaerobic)
chlorophyllide a biosynthesis I (aerobic, light−dependent)
catechol degradation to β−ketoadipate
factor 420 biosynthesis
superpathway of 2,3−butanediol biosynthesis
catechol degradation III (ortho−cleavage pathway)
aromatic compounds degradation via β−ketoadipate
superpathway of salicylate degradation
cob(II)yrinate a,c−diamide biosynthesis II (late cobalt incorporation)
superpathway of menaquinol−6 biosynthesis I
superpathway of menaquinol−10 biosynthesis
superpathway of demethylmenaquinol−6 biosynthesis I
superpathway of menaquinol−9 biosynthesis
superpathway of demethylmenaquinol−9 biosynthesis
TCA cycle VII (acetate−producers)
norspermidine biosynthesis
aromatic biogenic amine degradation (bacteria)
teichoic acid (poly−glycerol) biosynthesis
purine nucleobases degradation I (anaerobic)
isopropanol biosynthesis
3−phenylpropanoate degradation
L−histidine degradation II
L−arginine degradation II (AST pathway)
allantoin degradation IV (anaerobic)
chondroitin sulfate degradation I (bacterial)
superpathway of hexuronide and hexuronate degradation
superpathway of glycerol degradation to 1,3−propanediol
L−rhamnose degradation I
CMP−legionaminate biosynthesis I
superpathway of D−glucarate and D−galactarate degradation
D−galactarate degradation I
D−glucarate degradation I
polymyxin resistance
enterobacterial common antigen biosynthesis
sulfoglycolysis
superpathway of chorismate metabolism
enterobactin biosynthesis
superpathway of lipopolysaccharide biosynthesis
ketogluconate metabolism
cinnamate and 3−hydroxycinnamate degradation to 2−oxopent−4−enoate
3−phenylpropanoate and 3−(3−hydroxyphenyl)propanoate degradation to 2−oxopent−4−enoate
3−phenylpropanoate and 3−(3−hydroxyphenyl)propanoate degradation
superpathway of L−tryptophan biosynthesis
superpathway of L−arginine, putrescine, and 4−aminobutanoate degradation
superpathway of L−arginine and L−ornithine degradation
superpathway of ornithine degradation
Metacyc Pathway
Feces
Tissue
Sputum
Degradation/Utilization/Assimilation
Biosynthesis
Generation of Precursor Metabolites and Energy