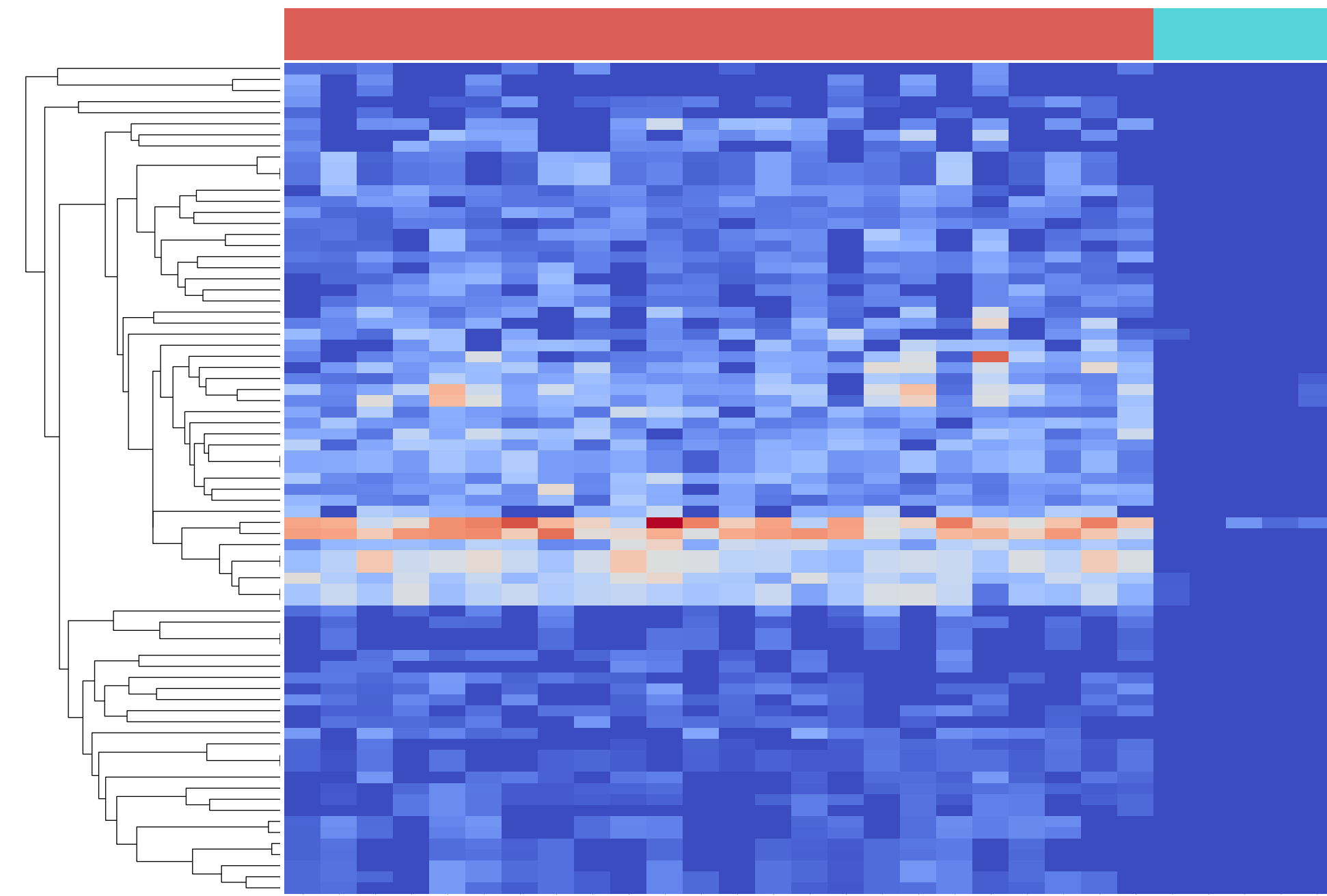


depletion no.depletion



20
25
36
41
46
47
66
69
76
86
95
100
114
117
127
135
154
158
176

P1.with.dep
P2.with.dep
P3.with.dep
P4.with.dep
P5.with.dep
P1.no.dep
P2.no.dep
P3.no.dep
P4.no.dep
P5.no.dep

PWY-7357: thiamin formation from pyrithiamine and oxythiamine (yeast) |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-7429: superpathway of adenosine nucleotides de novo biosynthesis II |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-6136: superpathway of adenosine nucleotides de novo biosynthesis II |g_Bacteroides.s_Bacteroides_vulgatus
 COA-PWY-1: coenzyme A biosynthesis II (mammalian) |g_Eubacterium.s_Eubacterium_rectale
 PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis II |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-1042: glycolysis IV (plant cytosol) |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6609: adenine and adenosine salvage III |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Bacteroides.s_Bacteroides_massiliensis
 PANTO-PWY: phosphopantothenate biosynthesis II |g_Bacteroides.s_Bacteroides_vulgatus
 SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis II |g_Eubacterium.s_Eubacterium_siraeum
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Eubacterium.s_Eubacterium_siraeum
 GLUCUROCAT-PWY: superpathway of β-D-glucuronide and D-glucuronate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 GALACT-GLUCUROCAT-PWY: superpathway of hexuronide and hexuronate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 DTPRHAMSYN-PWY: dTDP-L-rhamnose biosynthesis II |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-01296: purine ribonucleosides degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-7221: guanosine ribonucleotides de novo biosynthesis |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Bacteroides.s_Bacteroides_uniformis
 PWY-621: sucrose degradation III (sucrose invertase) |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-5177: glutaryl-CoA degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6737: starch degradation VI |g_Eubacterium.s_Eubacterium_rectale
 NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch) |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-6737: starch degradation VI |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 GLCMANNANAUT-PWY: superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-7242: D-fructuronate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6507: 4-deoxy-L-threo-hex-4-enopyranuronate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 GALACTUROCAT-PWY: D-galacturonate degradation |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-5695: urate biosynthesis/inosine 5'-phosphate degradation |g_Bacteroides.s_Bacteroides_vulgatus
 METHANOGENESIS-PWY: methanogenesis from H2 and CO2 |g_Methanobrevibacter.s_Methanobrevibacter_smithii
 CER-GLYSYN-PWY: Calvin-Benson-Bassham cycle |g_Ruminococcus.s_Ruminococcus_bromii
 SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis II |g_Ruminococcus.s_Ruminococcus_bromii
 VALSYN-PWY: L-valine biosynthesis |g_Eubacterium.s_Eubacterium_rectale
 PWY-7111: pyruvate fermentation to isobutanol (engineered) |g_Eubacterium.s_Eubacterium_rectale
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Eubacterium.s_Eubacterium_rectale
 PWY-2942: L-lysine biosynthesis III |g_Bacteroides.s_Bacteroides_vulgatus
 DTPRHAMSYN-PWY: dTDP-L-rhamnose biosynthesis II |g_Eubacterium.s_Eubacterium_rectale
 PWY-1042: glycolysis IV (plant cytosol) |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-7219: adenosine ribonucleotides de novo biosynthesis |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-7221: guanosine ribonucleotides de novo biosynthesis |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-7111: pyruvate fermentation to isobutanol (engineered) |g_Bacteroides.s_Bacteroides_vulgatus
 VALSYN-PWY: L-valine biosynthesis |g_Bacteroides.s_Bacteroides_vulgatus
 GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose) |g_Eubacterium.s_Eubacterium_rectale
 PWY-7111: pyruvate fermentation to isobutanol (engineered) |g_Ruminococcus.s_Ruminococcus_bromii
 VALSYN-PWY: L-valine biosynthesis |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-6737: starch degradation VI |g_Roseburia.s_Roseburia_inulinivorans
 PWY-5737: guanosine ribonucleotides de novo biosynthesis |g_Bacteroides.s_Bacteroides_massiliensis
 PWY-5667: CDP-diacylglycerol biosynthesis II |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-01319: CDP-diacylglycerol biosynthesis II |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-5097: L-lysine biosynthesis VI |g_Eubacterium.s_Eubacterium_rectale
 PWY-6700: queuosine biosynthesis |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-5686: UMP biosynthesis |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-6737: starch degradation VI |g_Ruminococcus.s_Ruminococcus_bromii
 PWY-66422: D-galactose degradation V (Leloir pathway) |g_Eubacterium.s_Eubacterium_rectale
 GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose) |g_Eubacterium.s_Eubacterium_siraeum
 PWY-7221: guanosine ribonucleotides de novo biosynthesis |g_Eubacterium.s_Eubacterium_rectale
 PWY-3841: folate transformations II |g_Bacteroides.s_Bacteroides_vulgatus
 PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II |g_Eubacterium.s_Eubacterium_siraeum
 PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II |g_Eubacterium.s_Eubacterium_siraeum
 PWY-6274: superpathway of 5-aminoimidazole ribonucleotide biosynthesis |g_Eubacterium.s_Eubacterium_siraeum
 PWY-6114: inosine 5'-phosphate biosynthesis II |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6114: pyruvate fermentation to isobutanol (engineered) |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 VALSYN-PWY: L-valine biosynthesis |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine) |g_Faecalibacterium.s_Faecalibacterium_prausnitzii
 PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) |g_Eubacterium.s_Eubacterium_rectale
 PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) |g_Eubacterium.s_Eubacterium_rectale
 BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched amino acid biosynthesis |g_Eubacterium.s_Eubacterium_siraeum
 PWY-5103: L-isoleucine biosynthesis III |g_Eubacterium.s_Eubacterium_siraeum
 ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine) |g_Eubacterium.s_Eubacterium_siraeum
 VALSYN-PWY: L-valine biosynthesis |g_Eubacterium.s_Eubacterium_siraeum
 PWY-7111: pyruvate fermentation to isobutanol (engineered) |g_Eubacterium.s_Eubacterium_siraeum

Taxon