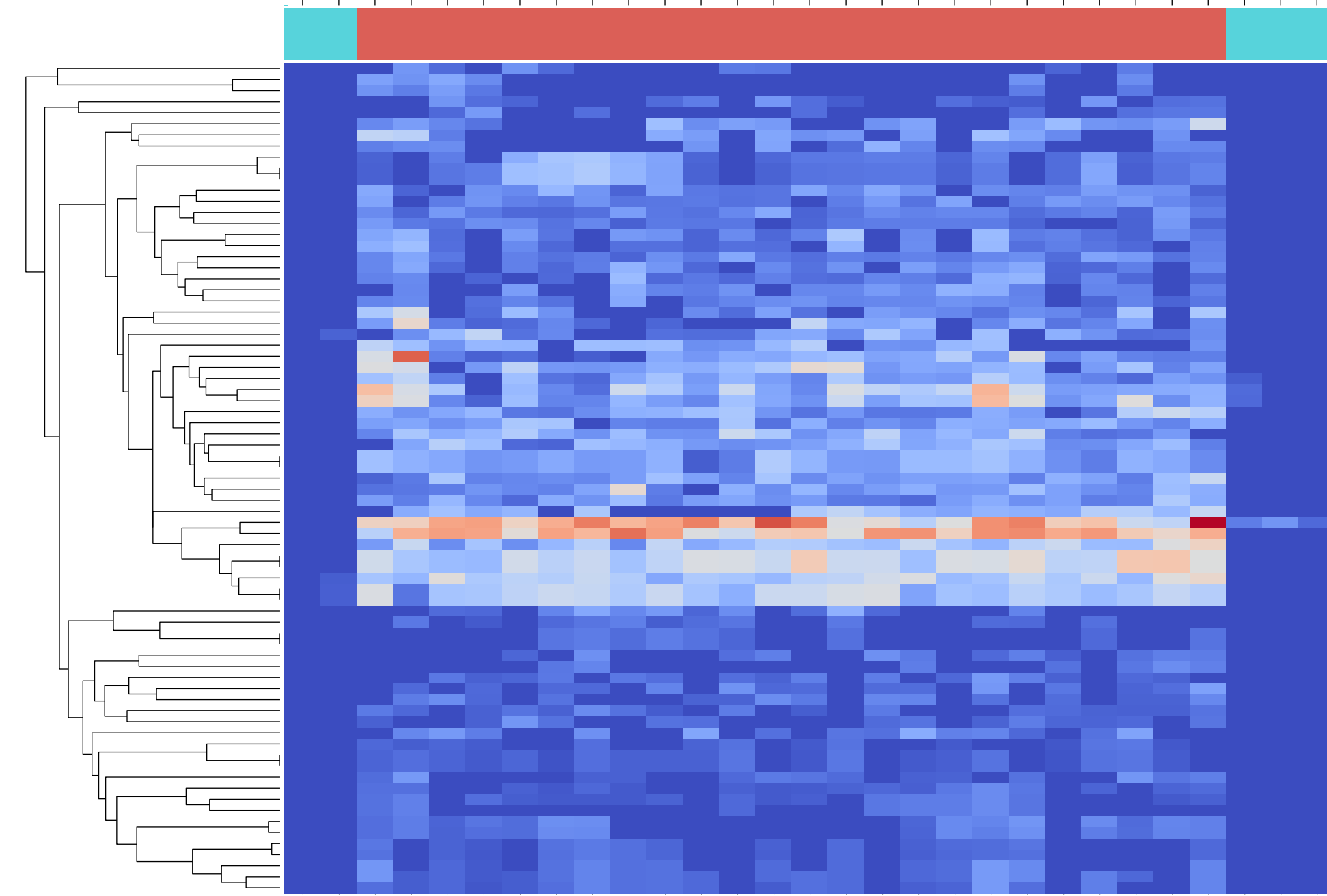




depletion no.depletion



P2.no.dep  
P1.no.dep  
158  
P1.with.dep  
20  
135  
76  
25  
176  
69  
117  
100  
P5.with.dep  
66  
P4.with.dep  
154  
41  
127  
P2.with.dep  
46  
47  
114  
P3.with.dep  
36  
86  
95  
P5.no.dep  
P3.no.dep  
P4.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 |lg\_Bacteroides.s\_Bacteroides\_vulgatus  
PWY-6136: superpathway of adenosine nucleotides de novo biosynthesis |lg\_Bacteroides.s\_Bacteroides\_vulgatus  
COA-PWY-1: coenzyme A biosynthesis II (mammal) |g\_Eubacterium.s\_Eubacterium\_rectale  
PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis |lg\_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 |lg\_Ruminococcus.s\_Ruminococcus\_bromii  
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis |lg\_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 |lg\_Bacteroides.s\_Bacteroides\_vulgatus  
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis |g\_Eubacterium.s\_Eubacterium\_siraeum  
PWY-7219: adenosine ribonucleotides de novo biosynthesis |g\_Eubacterium.s\_Eubacterium\_siraeum  
GLUCUROCAT-PWY: superpathway of &beta;-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 |lg\_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 VIg\_Eubacterium.s\_Eubacterium\_rectale  
NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch) |g\_Ruminococcus.s\_Ruminococcus\_bromii  
PWY-6737: starch degradation VIg\_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 |lg\_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 |lg\_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 VIg\_Roseburia.s\_Roseburia\_inulinivorans  
PWY-5667: CDP-diacylglycerol biosynthesis |lg\_Bacteroides.s\_Bacteroides\_vulgatus  
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 VIg\_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 |lg\_Eubacterium.s\_Eubacterium\_siraeum  
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis |lg\_Eubacterium.s\_Eubacterium\_siraeum  
PWY-6274: superpathway of 5-aminoimidazole ribonucleotide biosynthesis |g\_Eubacterium.s\_Eubacterium\_siraeum  
PWY-6114: inosine 5'-phosphate biosynthesis |lg\_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