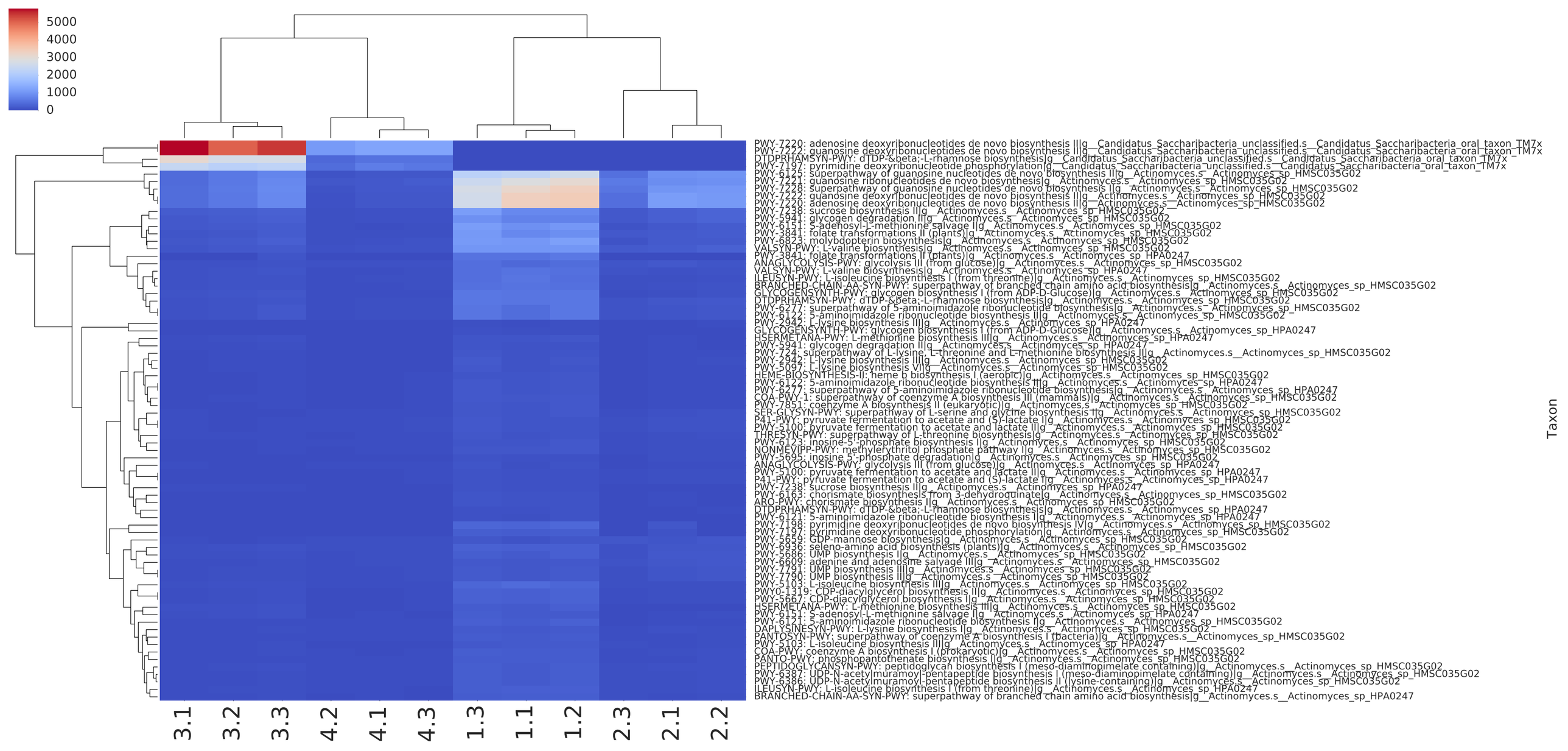

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4000
3000
2000
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PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis III|g__Candidatus_Saccharibacteria_unclassified.s__Candidatus_Saccharibacteria_oral_taxon_TM7x
PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II|g__Candidatus_Saccharibacteria_unclassified.s__Candidatus_Saccharibacteria_oral_taxon_TM7x
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis|g__Candidatus_Saccharibacteria_unclassified.s__Candidatus_Saccharibacteria_oral_taxon_TM7x
PWY-7197: pyrimidine deoxyribonucleotide phosphorylation|g__Candidatus_Saccharibacteria_unclassified.s__Candidatus_Saccharibacteria_oral_taxon_TM7x
PWY-6125: superpathway of guanosine nucleotides de novo biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7221: guanosine ribonucleotides de novo biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7238: sucrose biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5941: glycogen degradation II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6151: S-adenosyl-L-methionine salvage I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-3841: folate transformations II (plants)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6823: molybdopterin biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
VALSYN-PWY: L-valine biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-3841: folate transformations II (plants)|g__Actinomyces.s__Actinomyces_sp_HPA0247
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
VALSYN-PWY: L-valine biosynthesis|g__Actinomyces.s__Actinomyces_sp_HPA0247
ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched chain amino acid biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-2942: L-lysine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HPA0247
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)|g__Actinomyces.s__Actinomyces_sp_HPA0247
HSERMETANA-PWY: L-methionine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-5941: glycogen degradation II|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-724: superpathway of L-lysine, L-threonine and L-methionine biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-2942: L-lysine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5097: L-lysine biosynthesis VI|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
HEME-BIOSYNTHESIS-II: heme b biosynthesis I (aerobic)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis|g__Actinomyces.s__Actinomyces_sp_HPA0247
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7851: coenzyme A biosynthesis II (eukaryotic)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
P41-PWY: pyruvate fermentation to acetate and (S)-lactate I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5100: pyruvate fermentation to acetate and lactate II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
THRESYN-PWY: superpathway of L-threonine biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6123: inosine-5'-phosphate biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
NONMEVIPP-PWY: methylerythritol phosphate pathway I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5695: inosine 5'-phosphate degradation|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-5100: pyruvate fermentation to acetate and lactate II|g__Actinomyces.s__Actinomyces_sp_HPA0247
P41-PWY: pyruvate fermentation to acetate and (S)-lactate I|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-7238: sucrose biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-6163: chorismate biosynthesis from 3-dehydroquinate|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
ARO-PWY: chorismate biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-7198: pyrimidine deoxyribonucleotides de novo biosynthesis IV|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7197: pyrimidine deoxyribonucleotide phosphorylation|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5659: GDP-mannose biosynthesis|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6936: seleno-amino acid biosynthesis (plants)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5686: UMP biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6609: adenine and adenosine salvage III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7791: UMP biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-7790: UMP biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5103: L-isoleucine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY0-1319: CDP-diacylglycerol biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5667: CDP-diacylglycerol biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
HSERMETANA-PWY: L-methionine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6151: S-adenosyl-L-methionine salvage I|g__Actinomyces.s__Actinomyces_sp_HPA0247
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
DAPLYSINESYN-PWY: L-lysine biosynthesis I|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PANTOSYN-PWY: superpathway of coenzyme A biosynthesis I (bacteria)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-5103: L-isoleucine biosynthesis III|g__Actinomyces.s__Actinomyces_sp_HPA0247
COA-PWY: coenzyme A biosynthesis I (prokaryotic)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PANTO-PWY: phosphopantothenate biosynthesis II|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)|g__Actinomyces.s__Actinomyces_sp_HMSC035G02
ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)|g__Actinomyces.s__Actinomyces_sp_HPA0247
BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched chain amino acid biosynthesis|g__Actinomyces.s__Actinomyces_sp_HPA0247
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3.3
4.2
4.1
4.3
1.3
1.1
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2.3
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Taxon