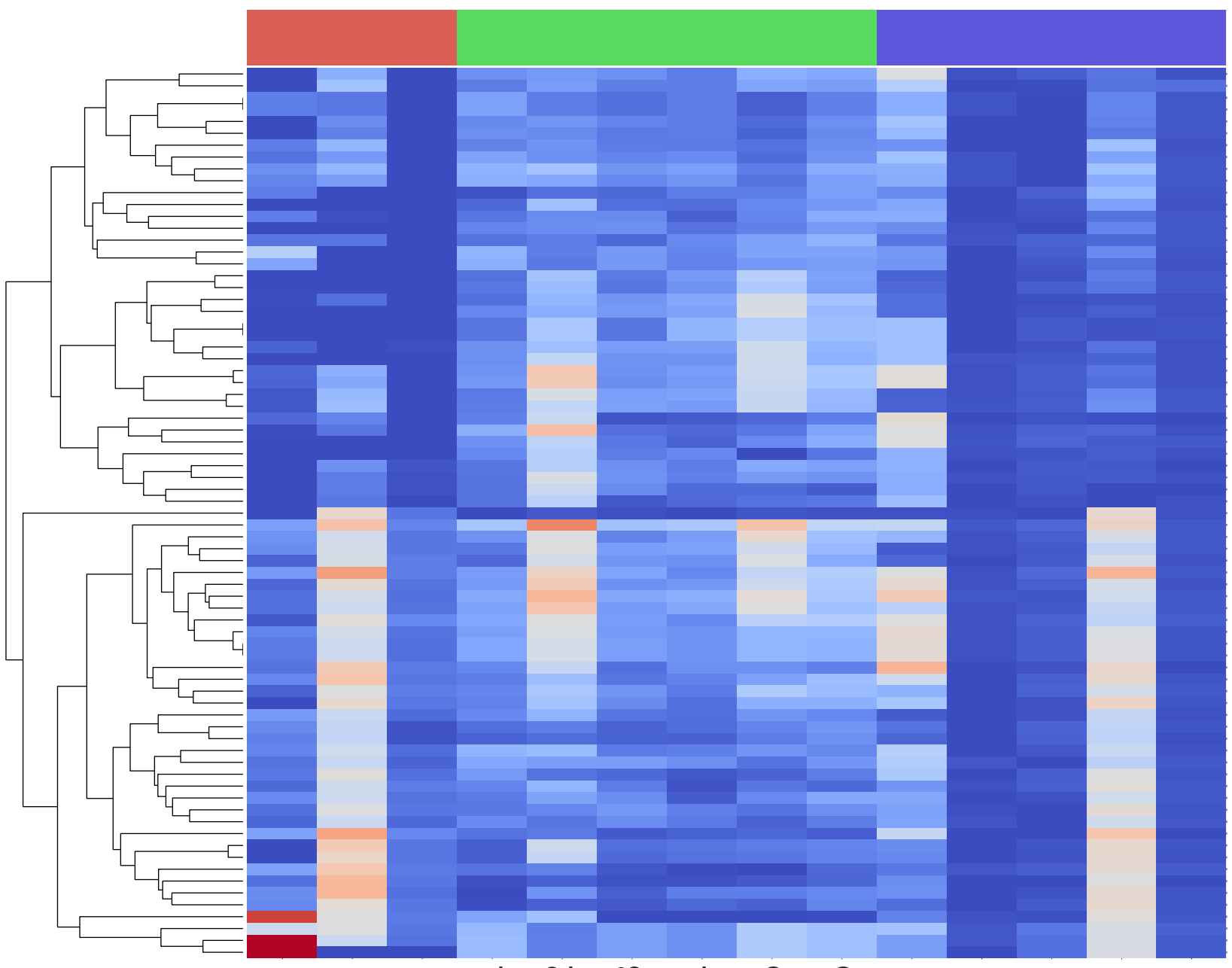


Tissue Fecal Sputum



- PWY-6385: peptidoglycan biosynthesis III (mycobacteria)
- NONOXIPEN-PWY: pentose phosphate pathway (non-oxidative branch)
- PWY-7227: guanosine deoxyribonucleotides de novo biosynthesis II
- PWY-0160: adenosine deoxyribonucleotides de novo biosynthesis II
- PWY-7184: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)
- PWY-8414: pyrimidine deoxyribonucleotides de novo biosynthesis I
- PWY-8415: superpathway of purine nucleotides de novo biosynthesis I
- PWY-6228: superpathway of guanosine nucleotides de novo biosynthesis II
- PWY-6178: superpathway of adenosine nucleotides de novo biosynthesis II
- PWY-6100: superpathway of adenosine nucleotides de novo biosynthesis II
- PWY-6100: L-arginine biosynthesis IV (archaeobacteria)
- ANAEROBUTIC-PWY: homolactic fermentation
- TCME12-PWY: N10-formyl-tetrahydrofolate biosynthesis
- PWY-0192: superpathway of pyrimidine ribonucleotides de novo biosynthesis
- PWY-0196: purine ribonucleosides degradation
- BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched amino acid biosynthesis
- PWY-5103: L-isoleucine biosynthesis III
- PWY-2093: cis-vaccenate biosynthesis
- PWY-7663: gondopate biosynthesis (anaerobic)
- PWY-2993: starch degradation
- PWY-2094: L-lysine biosynthesis VI
- PWY-01319: CDP-diacylglycerol biosynthesis II
- PWY-5624: CDP-diacylglycerol biosynthesis I
- PWY-2894: L-lysine biosynthesis II
- NONMEVIPP-PWY: mevalonate phosphate pathway I
- PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)
- ARO-PWY: chorismate biosynthesis
- COMPLETE-ARO-PWY: superpathway of aromatic amino acid biosynthesis
- PWY-7199: pyrimidine deoxyribonucleosides salvage
- PWY-6609: adenine and adenosine salvage II
- PWY-2995: urate biosynthesis/inosine 5'-phosphate degradation
- PWY-2970: pyrene biosynthesis I
- PANTOSYN-PWY: pantoic acid and coenzyme A biosynthesis I
- COA-PWY: coenzyme A biosynthesis I
- PWY-4242: benzothienate and coenzyme A biosynthesis III
- PHISNARA-PWY: superpathway of thiamin diphosphate biosynthesis III (eukaryotes)
- PWY-4984: urea cycle
- PWY-7219: adenosine ribonucleotides de novo biosynthesis
- PWY-6151: S-adenosyl-methionine cycle I
- PWY-8424: chorismate biosynthesis from 3-dehydroquinate
- PWY-8400: dicyclopentane biosynthesis
- PWY-0047: glycolysis IV (plant cytosol)
- PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
- PWY-6386: guanosine ribonucleotides de novo biosynthesis
- PWY-5686: UMP biosynthesis
- COA-PWY-1: coenzyme A biosynthesis II (mammalian)
- PWY-6121: 5-aminimidazole ribonucleotide biosynthesis I
- PWY-8422: 5-aminimidazole ribonucleotide biosynthesis II
- PWY-8277: superpathway of 5-aminimidazole ribonucleotide biosynthesis
- PWY-5100: pyruvate fermentation to acetate and lactate II
- ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)
- PANTO-PWY: phosphopantothenate biosynthesis I
- CALVIN-PWY: Calvin-Benson-Bassham cycle
- PWY-6897: thiamin salvage II
- PWY-8123: inosine-5'-phosphate biosynthesis I
- PWY-8122: inosine-5'-phosphate biosynthesis II
- PWY-7357: thiamin formation from pyriothiamine and oxythiamine (yeast)
- PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis I
- PWY-6936: seleno-amino acid biosynthesis
- PWY-5188: tetrapyrrole biosynthesis I (from glutamate)
- PWY-3849: folate transformations II
- PWY-7208: superpathway of pyrimidine nucleobases salvage
- PWY-7195: pyrimidine deoxyribonucleotide phosphorylation
- PWY-4981: L-proline biosynthesis II (from arginine)
- GLYCOLYSIS: glycolysis (from glucose 6-phosphate)
- PWY-5484: glycolysis II (from fructose 6-phosphate)
- UDPNAAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis I
- LACTOSECAT-PWY: lactose and galactose degradation I
- PWY-66-400: glycolysis VI (metazoan)
- ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)
- DISDEG-PWY: L-histidine degradation I
- PWY-7111: pyruvate fermentation to isobutanol (engineered)
- VALSYN-PWY: L-valine biosynthesis
- ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)

Taxon