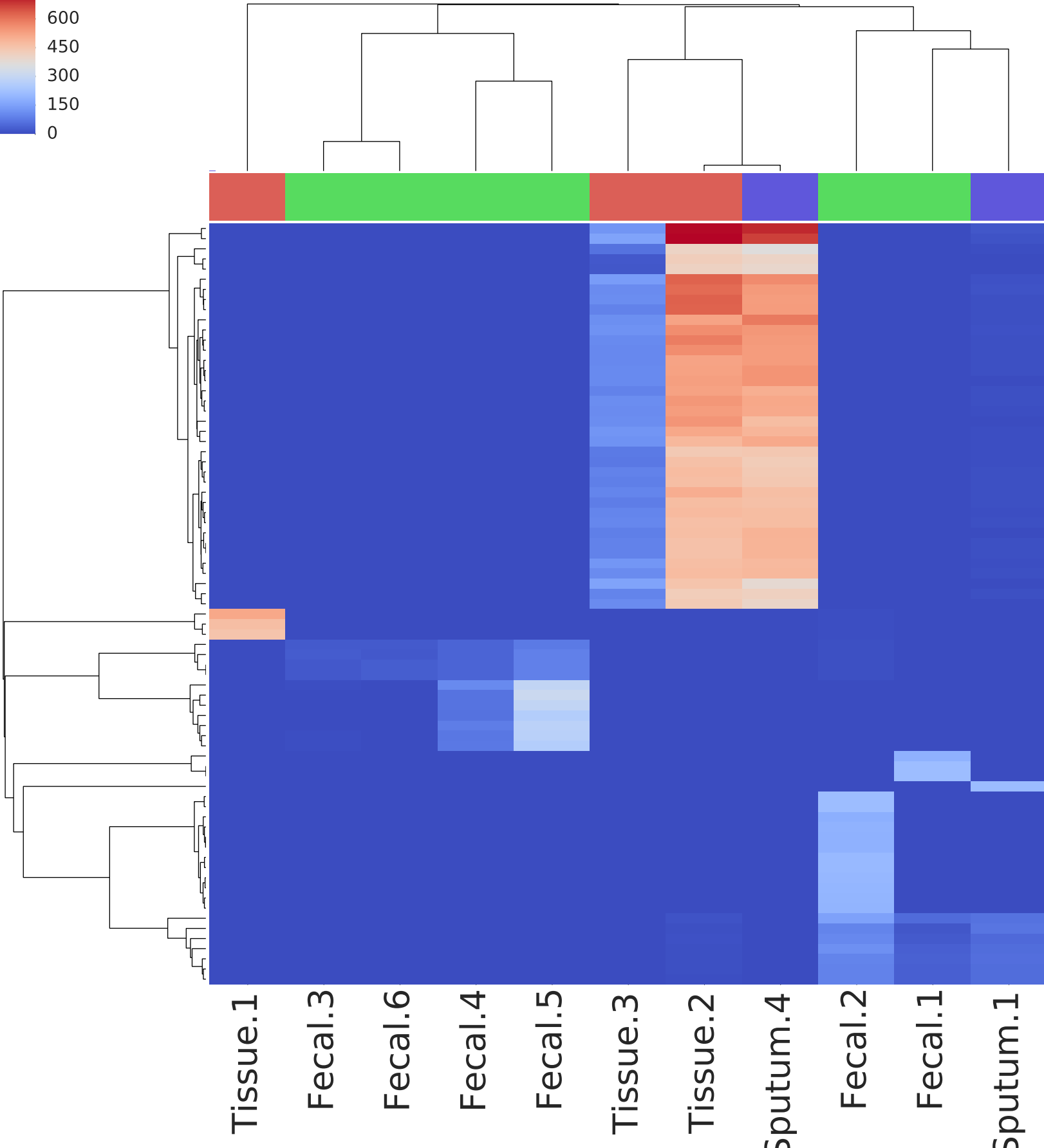


Tissue Fecal Sputum



- PWY-1042: glycolysis IV (plant cytosol)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-4981: L-proline biosynthesis II (from arginine)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7298: superpathway of guanosine nucleotides de novo biosynthesis Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6123: inosine 5'-phosphate biosynthesis Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6124: inosine 5'-phosphate biosynthesis IIlg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7219: adenosine ribonucleotides de novo biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- LACTOSECAT-PWY: lactose and galactose degradation Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- UDPNAAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-66-400: glycolysis VI (metazoan)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- CALVIN-PWY: Calvin-Benson-Bassham cyclelg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-5100: pyruvate fermentation to acetate and lactate IIlg\_Staphylococcus.s\_Staphylococcus\_aureus
- ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-5484: glycolysis II (from fructose 6-phosphate)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-4984: urea cyclelg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6936: seleno-amino acid biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- HISDEG-PWY: L-histidine degradation Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7208: superpathway of pyrimidine nucleobases salvage Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7111: pyruvate fermentation to isobutanol (engineered)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PANTO-PWY: phosphopantothenate biosynthesis Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-5188: tetrapyrrole biosynthesis I (from glutamate)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6897: thiamin salvage Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7197: pyrimidine deoxyribonucleotide phosphorylationlg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7221: guanosine ribonucleotides de novo biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-5265: peptidoglycan biosynthesis II (staphylococci)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-7357: thiamin formation from pyrithiamine and oxythiamine (yeast)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-3841: folate transformations IIIlg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- VALSYN-PWY: L-valine biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis IIlg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6700: queuosine biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6151: S-adenosyl-L-methionine cycle Ilg\_Staphylococcus.s\_Staphylococcus\_aureus
- COA-PWY-1: coenzyme A biosynthesis II (mammalian)lg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-5686: UMP biosynthesislg\_Staphylococcus.s\_Staphylococcus\_aureus
- PWY-6163: chorismate biosynthesis from 3-dehydroquinatelg\_Staphylococcus.s\_Staphylococcus\_aureus
- HISDEG-PWY: L-histidine degradation Ilg\_Corynebacterium.s\_Corynebacterium\_tuberculoostearicum
- VALSYN-PWY: L-valine biosynthesislg\_Corynebacterium.s\_Corynebacterium\_tuberculoostearicum
- HISDEG-PWY: L-histidine degradation IIlg\_Corynebacterium.s\_Corynebacterium\_pseudogenitulum
- PWY-7219: adenosine ribonucleotides de novo biosynthesislg\_Faecalibacterium.s\_Faecalibacterium\_prausnitzii
- PWY-7111: pyruvate fermentation to isobutanol (engineered)lg\_Faecalibacterium.s\_Faecalibacterium\_prausnitzii
- ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)lg\_Faecalibacterium.s\_Faecalibacterium\_prausnitzii
- VALSYN-PWY: L-valine biosynthesislg\_Faecalibacterium.s\_Faecalibacterium\_prausnitzii
- PWY-7219: adenosine ribonucleotides de novo biosynthesislg\_Prevotella.s\_Prevotella\_copri
- PWY-6151: S-adenosyl-L-methionine cycle Ilg\_Prevotella.s\_Prevotella\_copri
- PWY-5686: UMP biosynthesislg\_Prevotella.s\_Prevotella\_copri
- PWY-7221: guanosine ribonucleotides de novo biosynthesislg\_Prevotella.s\_Prevotella\_copri
- PWY-5097: L-lysine biosynthesis VIIlg\_Prevotella.s\_Prevotella\_copri
- PWY-2942: L-lysine biosynthesis IIIlg\_Prevotella.s\_Prevotella\_copri
- BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched amino acid biosynthesislg\_Brevibacterium.s\_Brevibacterium\_mcbrellneri
- VALSYN-PWY: L-valine biosynthesislg\_Brevibacterium.s\_Brevibacterium\_mcbrellneri
- ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)lg\_Brevibacterium.s\_Brevibacterium\_mcbrellneri
- NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)lg\_Anaerococcus.s\_Anaerococcus\_hydrogenalis
- COA-PWY: coenzyme A biosynthesis Ilg\_Prevotella.s\_Prevotella\_disiens
- PWY-6700: queuosine biosynthesislg\_Prevotella.s\_Prevotella\_disiens
- PWY-6609: adenine and adenosine salvage IIIlg\_Fusobacterium.s\_Fusobacterium\_gondiaformans
- PWY-6703: preO0 biosynthesislg\_Fusobacterium.s\_Fusobacterium\_gondiaformans
- PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis Ilg\_Prevotella.s\_Prevotella\_disiens
- PWY-7663: gondoate biosynthesis (anaerobic)lg\_Prevotella.s\_Prevotella\_disiens
- COA-PWY-1: coenzyme A biosynthesis II (mammalian)lg\_Prevotella.s\_Prevotella\_disiens
- PWY-6163: chorismate biosynthesis from 3-dehydroquinatelg\_Prevotella.s\_Prevotella\_disiens
- PWY-7219: adenosine ribonucleotides de novo biosynthesislg\_Prevotella.s\_Prevotella\_disiens
- PWY-6151: S-adenosyl-L-methionine cycle Ilg\_Prevotella.s\_Prevotella\_disiens
- PWY-7221: guanosine ribonucleotides de novo biosynthesislg\_Prevotella.s\_Prevotella\_disiens
- PWY-5973: cis-vaccenate biosynthesislg\_Prevotella.s\_Prevotella\_disiens
- PWY-7147: adenosine ribonucleotides de novo biosynthesislg\_Finegoldia.s\_Finegoldia\_magna
- PWY-6151: S-adenosyl-L-methionine cycle Ilg\_Finegoldia.s\_Finegoldia\_magna
- NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch)lg\_Finegoldia.s\_Finegoldia\_magna
- PWY-7221: guanosine ribonucleotides de novo biosynthesislg\_Finegoldia.s\_Finegoldia\_magna
- PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)lg\_Finegoldia.s\_Finegoldia\_magna
- PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)lg\_Finegoldia.s\_Finegoldia\_magna
- PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)lg\_Finegoldia.s\_Finegoldia\_magna

Taxon