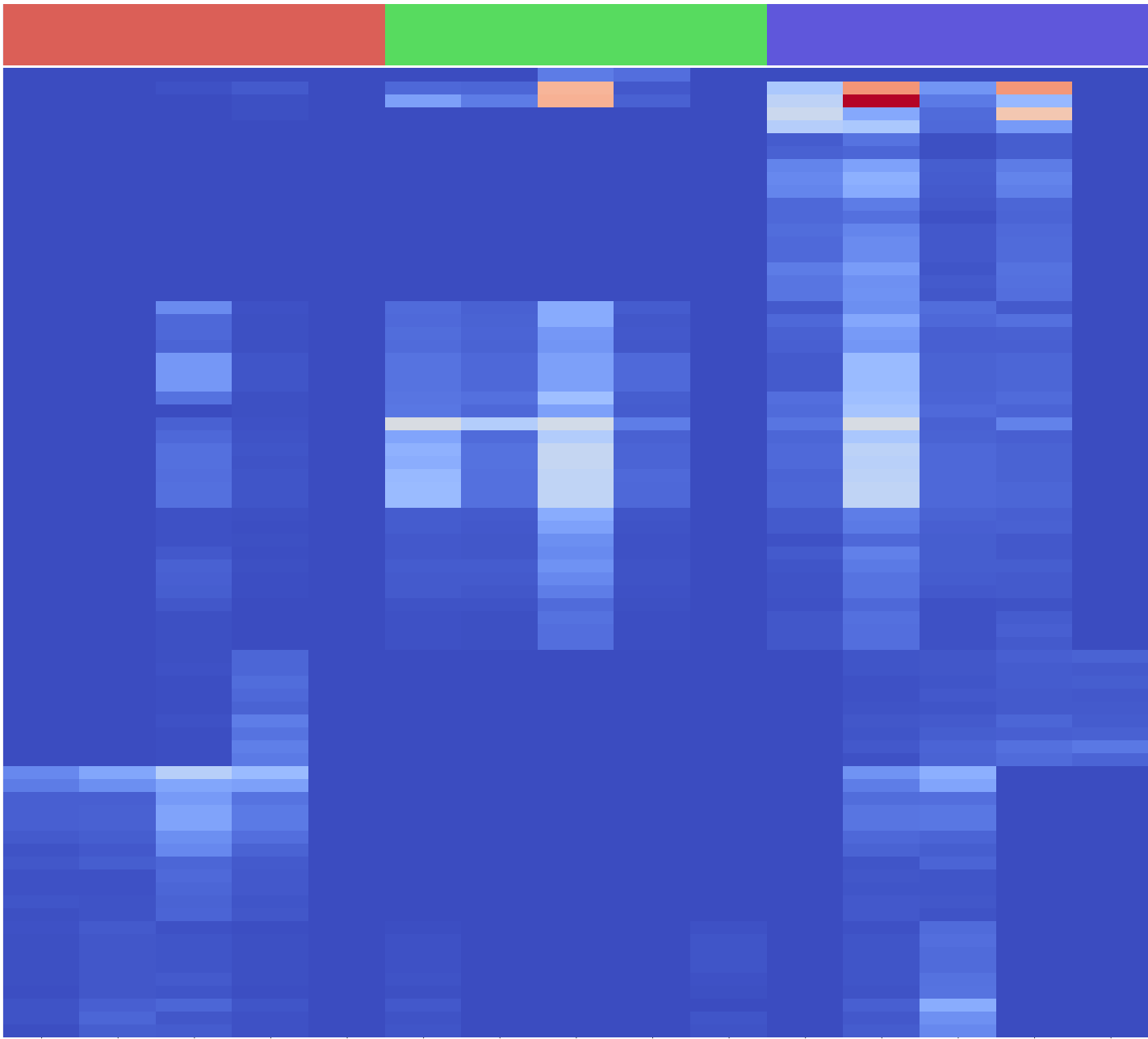
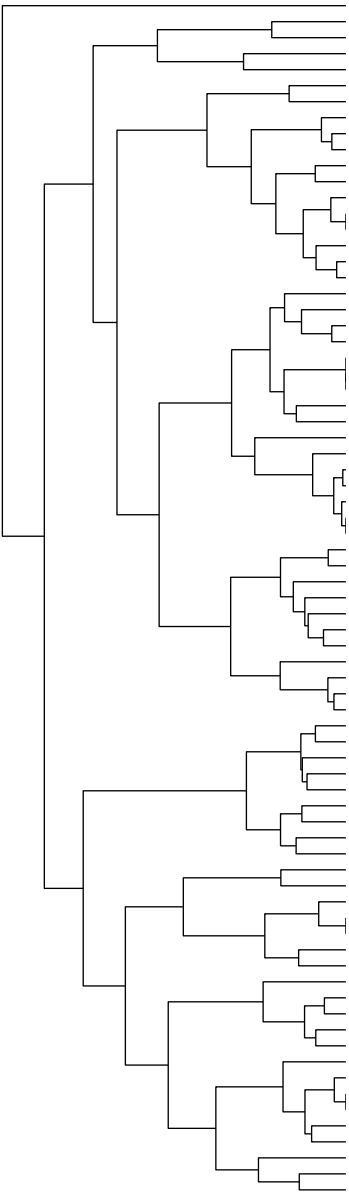


Young Old Treatment



PWY-7238: sucrose biosynthesis II[g_Faecalibaculum.s_Faecalibaculum_rodentium
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)[g_Lactobacillus.s_Lactobacillus_murinus
PWY0-1296: purine ribonucleosides degradation[g_Lactobacillus.s_Lactobacillus_murinus
LACTOFECAI-PWY: lactose and galactose degradation II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-5100: pyruvate fermentation to acetate and lactate II[g_Helicobacter.s_Helicobacter_typhlonius
GLUCONEO-PWY: gluconeogenesis II[g_Helicobacter.s_Helicobacter_typhlonius
PWY-6126: superpathway of adenosine nucleotides de novo biosynthesis II[g_Helicobacter.s_Helicobacter_typhlonius
VALSYN-PWY: L-valine biosynthesis[g_Helicobacter.s_Helicobacter_typhlonius
PWY-5973: cis-vaccenate biosynthesis[g_Helicobacter.s_Helicobacter_typhlonius
PWY-7663: gondoate biosynthesis (anaerobic)[g_Helicobacter.s_Helicobacter_typhlonius
PWY-7111: pyruvate fermentation to isobutanol (engineered)[g_Helicobacter.s_Helicobacter_typhlonius
ASPASN-PWY: superpathway of L-aspartate and L-asparagine biosynthesis[g_Helicobacter.s_Helicobacter_typhlonius
PWY-5103: L-isoleucine biosynthesis III[g_Helicobacter.s_Helicobacter_typhlonius
PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II[g_Helicobacter.s_Helicobacter_typhlonius
PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis II[g_Helicobacter.s_Helicobacter_typhlonius
PWY66-429: fatty acid biosynthesis initiation (mitochondria)[g_Helicobacter.s_Helicobacter_typhlonius
LEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)[g_Helicobacter.s_Helicobacter_typhlonius
BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched chain amino acid biosynthesis[g_Helicobacter.s_Helicobacter_typhlonius
PWY-7221: guanosine ribonucleotides de novo biosynthesis[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6151: S-adenosyl-L-methionine salvage II[g_Lactobacillus.s_Lactobacillus_murinus
OANTIGEN-PWY: O-antigen building blocks biosynthesis (E. coli)[g_Lactobacillus.s_Lactobacillus_murinus
UDPNAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-7790: UMP biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-5686: UMP biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-7791: UMP biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6609: adenine and adenosine salvage III[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6527: stachyose degradation[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6124: inosine 5'-phosphate biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6123: inosine 5'-phosphate biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-7234: inosine 5'-phosphate biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-2942: L-lysine biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-2941: L-lysine biosynthesis II[g_Lactobacillus.s_Lactobacillus_murinus
PWY-5097: L-lysine biosynthesis VI[g_Lactobacillus.s_Lactobacillus_murinus
PWY-3841: folate transformations II (plants)[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)[g_Lactobacillus.s_Lactobacillus_murinus
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)[g_Lactobacillus.s_Lactobacillus_murinus
PWY-6700: queuosine biosynthesis I (de novo)[g_Lactobacillus.s_Lactobacillus_murinus
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)[g_Lactobacillus.s_Lactobacillus_murinus
COA-PWY: coenzyme A biosynthesis I (prokaryotic)[g_Lactobacillus.s_Lactobacillus_murinus
PWY-7851: coenzyme A biosynthesis II (eukaryotic)[g_Lactobacillus.s_Lactobacillus_murinus
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-7221: guanosine ribonucleotides de novo biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
COA-PWY: coenzyme A biosynthesis I (prokaryotic)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-6527: stachyose degradation[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-7238: sucrose biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-6609: adenine and adenosine salvage III[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-6317: D-galactose degradation I (Lefoir pathway)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY0-1296: purine ribonucleosides degradation[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_28_4
PWY-7238: sucrose biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
VALSYN-PWY: L-valine biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6609: adenine and adenosine salvage III[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
ARGSYN-PWY: L-arginine biosynthesis I (via L-ornithine)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6151: S-adenosyl-L-methionine salvage II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
GLUTORN-PWY: L-ornithine biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A4
PWY-6151: S-adenosyl-L-methionine salvage II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-7238: sucrose biosynthesis II[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-7221: guanosine ribonucleotides de novo biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
PWY-1042: glycolysis IV[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis[g_Lachnospiraceae_unclassified.s_Lachnospiraceae_bacterium_A2

Taxon