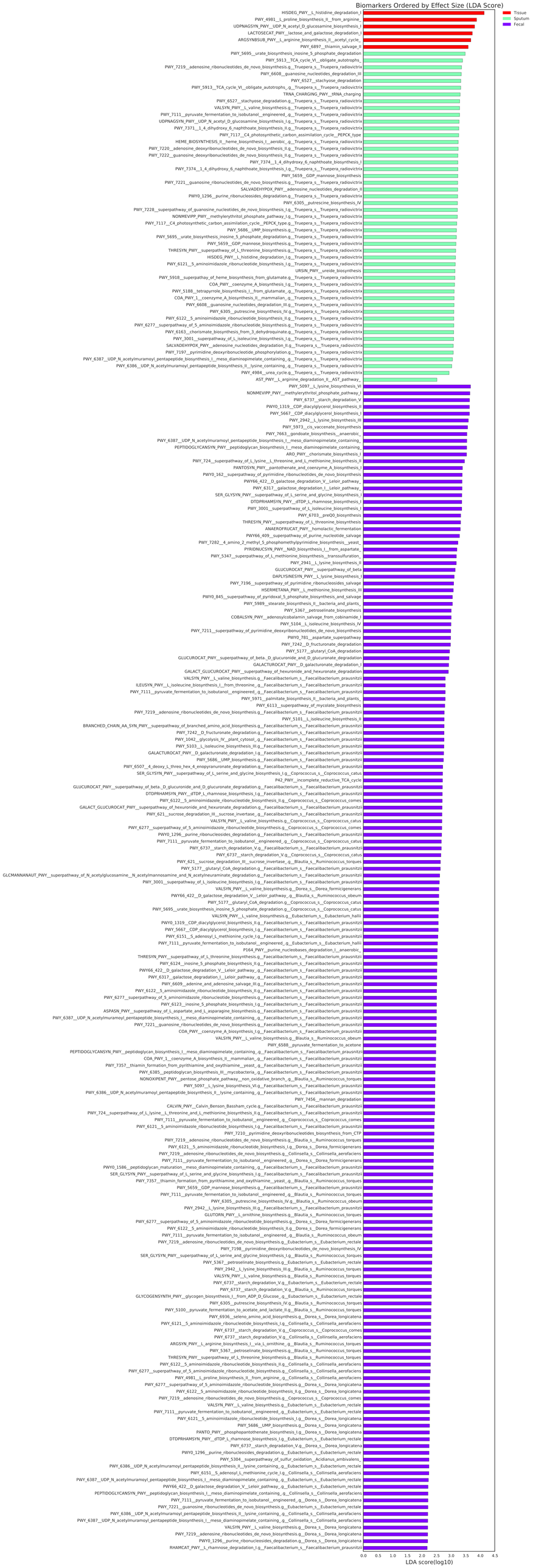
Biomarkers Ordered by Effect Size (LDA Score)
Tissue
Sputum
Fecal
HISDEG_PWY__L_histidine_degradation_I
PWY_4981__L_proline_biosynthesis_II__from_arginine_
UDPNAGSYN_PWY__UDP_N_acetyl_D_glucosamine_biosynthesis_I
LACTOSECAT_PWY__lactose_and_galactose_degradation_I
ARGSYNBSUB_PWY__L_arginine_biosynthesis_II__acetyl_cycle_
PWY_6897__thiamin_salvage_II
PWY_5695__urate_biosynthesis_inosine_5_phosphate_degradation
PWY_5913__TCA_cycle_VI__obligate_autotrophs_
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Truepera_s__Truepera_radiovictrix
PWY_6608__guanosine_nucleotides_degradation_III
PWY_6527__stachyose_degradation
PWY_5913__TCA_cycle_VI__obligate_autotrophs_,_g__Truepera_s__Truepera_radiovictrix
TRNA_CHARGING_PWY__tRNA_charging
PWY_6527__stachyose_degradation_g__Truepera_s__Truepera_radiovictrix
VALSYN_PWY__L_valine_biosynthesis_g__Truepera_s__Truepera_radiovictrix
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Truepera_s__Truepera_radiovictrix
UDPNAGSYN_PWY__UDP_N_acetyl_D_glucosamine_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
PWY_7371__1_4_dihydroxy_6_naphthoate_biosynthesis_II_g__Truepera_s__Truepera_radiovictrix
PWY_7117__C4_photosynthetic_carbon_assimilation_cycle__PEPCK_type
HEME_BIOSYNTHESIS_II__heme_biosynthesis_I_aerobic_,_g__Truepera_s__Truepera_radiovictrix
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II_g__Truepera_s__Truepera_radiovictrix
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II_g__Truepera_s__Truepera_radiovictrix
PWY_7374__1_4_dihydroxy_6_naphthoate_biosynthesis_I
PWY_7374__1_4_dihydroxy_6_naphthoate_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
PWY_5659__GDP_mannose_biosynthesis
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis_g__Truepera_s__Truepera_radiovictrix
SALVADEHYPOX_PWY__adenosine_nucleotides_degradation_II
PWY0_1296__purine_ribonucleosides_degradation_g__Truepera_s__Truepera_radiovictrix
PWY_6305__putrescine_biosynthesis_IV
PWY_7228__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I_g__Truepera_s__Truepera_radiovictrix
PWY_7117__C4_photosynthetic_carbon_assimilation_cycle__PEPCK_type_g__Truepera_s__Truepera_radiovictrix
PWY_5686__UMP_biosynthesis_g__Truepera_s__Truepera_radiovictrix
PWY_5695__urate_biosynthesis_inosine_5_phosphate_degradation_g__Truepera_s__Truepera_radiovictrix
PWY_5659__GDP_mannose_biosynthesis_g__Truepera_s__Truepera_radiovictrix
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis_g__Truepera_s__Truepera_radiovictrix
HISDEG_PWY__L_histidine_degradation_I_g__Truepera_s__Truepera_radiovictrix
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
URSIN_PWY__ureide_biosynthesis
PWY_5918__superpathway_of_heme_biosynthesis_from_glutamate_g__Truepera_s__Truepera_radiovictrix
COA_PWY__coenzyme_A_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_,_g__Truepera_s__Truepera_radiovictrix
COA_PWY_1__coenzyme_A_biosynthesis_II__mammalian_,_g__Truepera_s__Truepera_radiovictrix
PWY_6608__guanosine_nucleotides_degradation_III_g__Truepera_s__Truepera_radiovictrix
PWY_6305__putrescine_biosynthesis_IV_g__Truepera_s__Truepera_radiovictrix
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Truepera_s__Truepera_radiovictrix
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Truepera_s__Truepera_radiovictrix
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate_g__Truepera_s__Truepera_radiovictrix
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I_g__Truepera_s__Truepera_radiovictrix
SALVADEHYPOX_PWY__adenosine_nucleotides_degradation_II_g__Truepera_s__Truepera_radiovictrix
PWY_7197__pyrimidine_deoxyribonucleotide_phosphorylation_g__Truepera_s__Truepera_radiovictrix
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_,_g__Truepera_s__Truepera_radiovictrix
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_,_g__Truepera_s__Truepera_radiovictrix
PWY_4984__urea_cycle_g__Truepera_s__Truepera_radiovictrix
AST_PWY__L_arginine_degradation_II__AST_pathway_
PWY_5097__L_lysine_biosynthesis_VI
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I
PWY_6737__starch_degradation_V
PWY0_1319__CDP_diacylglycerol_biosynthesis_II
PWY_5667__CDP_diacylglycerol_biosynthesis_I
PWY_2942__L_lysine_biosynthesis_III
PWY_5973__cis_vaccenate_biosynthesis
PWY_7663__gondoate_biosynthesis__anaerobic_
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_
ARO_PWY__chorismate_biosynthesis_I
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II
PANTOSYN_PWY__pantothenate_and_coenzyme_A_biosynthesis_I
PWY0_162__superpathway_of_pyrimidine_ribonucleotides_de_novo_biosynthesis
PWY66_422__D_galactose_degradation_V__Leloir_pathway_
PWY_6317__galactose_degradation_I__Leloir_pathway_
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I
PWY_6703__preQ0_biosynthesis
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis
ANAEROFRUCAT_PWY__homolactic_fermentation
PWY66_409__superpathway_of_purine_nucleotide_salvage
PWY_7282__4_amino_2_methyl_5_phosphomethylpyrimidine_biosynthesis__yeast_
PYRIDNUCSYN_PWY__NAD_biosynthesis_I__from_aspartate_
PWY_5347__superpathway_of_L_methionine_biosynthesis__transsulfuration_
PWY_2941__L_lysine_biosynthesis_II
GLUCUROCAT_PWY__superpathway_of_beta
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I
PWY_7196__superpathway_of_pyrimidine_ribonucleosides_salvage
HSERMETANA_PWY__L_methionine_biosynthesis_III
PWY0_845__superpathway_of_pyridoxal_5_phosphate_biosynthesis_and_salvage
PWY_5989__stearate_biosynthesis_II__bacteria_and_plants_
PWY_5367__petroselinate_biosynthesis
COBALSYN_PWY__adenosylcobalamin_salvage_from_cobinamide_I
PWY_5104__L_isoleucine_biosynthesis_IV
PWY_7211__superpathway_of_pyrimidine_deoxyribonucleotides_de_novo_biosynthesis
PWY0_781__aspartate_superpathway
PWY_7242__D_fructuronate_degradation
PWY_5177__glutaryl_CoA_degradation
GLUCUROCAT_PWY__superpathway_of_beta_D_glucuronide_and_D_glucuronate_degradation
GALACTUROCAT_PWY__D_galacturonate_degradation_I
GALACT_GLUCUROCAT_PWY__superpathway_of_hexuronide_and_hexuronate_degradation
VALSYN_PWY__L_valine_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5971__palmitate_biosynthesis_II__bacteria_and_plants_
PWY_6113__superpathway_of_mycolate_biosynthesis
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5101__L_isoleucine_biosynthesis_II
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_amino_acid_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7242__D_fructuronate_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_1042__glycolysis_IV__plant_cytosol_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5103__L_isoleucine_biosynthesis_III_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
GALACTUROCAT_PWY__D_galacturonate_degradation_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5686__UMP_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6507__4_deoxy_L_threo_hex_4_enopyranuronate_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I_g__Coprococcus_s__Coprococcus_catus
P42_PWY__incomplete_reductive_TCA_cycle
GLUCUROCAT_PWY__superpathway_of_beta_D_glucuronide_and_D_glucuronate_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Coprococcus_s__Coprococcus_comes
GALACT_GLUCUROCAT_PWY__superpathway_of_hexuronide_and_hexuronate_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_621__sucrose_degradation_III__sucrose_invertase_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
VALSYN_PWY__L_valine_biosynthesis_g__Coprococcus_s__Coprococcus_catus
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Coprococcus_s__Coprococcus_comes
PWY0_1296__purine_ribonucleosides_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Coprococcus_s__Coprococcus_catus
PWY_6737__starch_degradation_V_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6737__starch_degradation_V_g__Coprococcus_s__Coprococcus_catus
PWY_621__sucrose_degradation_III__sucrose_invertase_,_g__Blautia_s__Ruminococcus_torques
PWY_5177__glutaryl_CoA_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
GLCMANNANAUT_PWY__superpathway_of_N_acetylglucosamine__N_acetylmannosamine_and_N_acetylneuraminate_degradation_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
VALSYN_PWY__L_valine_biosynthesis_g__Dorea_s__Dorea_formicigenerans
PWY66_422__D_galactose_degradation_V__Leloir_pathway_,_g__Blautia_s__Ruminococcus_obeum
PWY_5177__glutaryl_CoA_degradation_g__Coprococcus_s__Coprococcus_catus
PWY_5695__urate_biosynthesis_inosine_5_phosphate_degradation_g__Coprococcus_s__Coprococcus_catus
VALSYN_PWY__L_valine_biosynthesis_g__Eubacterium_s__Eubacterium_hallii
PWY0_1319__CDP_diacylglycerol_biosynthesis_II_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5667__CDP_diacylglycerol_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6151__S_adenosyl_L_methionine_cycle_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Eubacterium_s__Eubacterium_hallii
P164_PWY__purine_nucleobases_degradation_I__anaerobic_
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6124__inosine_5_phosphate_biosynthesis_II_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY66_422__D_galactose_degradation_V__Leloir_pathway_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6317__galactose_degradation_I__Leloir_pathway_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6609__adenine_and_adenosine_salvage_III_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6123__inosine_5_phosphate_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
ASPASN_PWY__superpathway_of_L_aspartate_and_L_asparagine_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
COA_PWY__coenzyme_A_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
VALSYN_PWY__L_valine_biosynthesis_g__Blautia_s__Ruminococcus_obeum
PWY_6588__pyruvate_fermentation_to_acetone
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
COA_PWY_1__coenzyme_A_biosynthesis_II__mammalian_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7357__thiamin_formation_from_pyrithiamine_and_oxythiamine__yeast_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6385__peptidoglycan_biosynthesis_III__mycobacteria_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
NONOXIPENT_PWY__pentose_phosphate_pathway__non_oxidative_branch_,_g__Blautia_s__Ruminococcus_torques
PWY_5097__L_lysine_biosynthesis_VI_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7456__mannan_degradation
CALVIN_PWY__Calvin_Benson_Bassham_cycle_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Coprococcus_s__Coprococcus_comes
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7210__pyrimidine_deoxyribonucleotides_biosynthesis_from_CTP
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Blautia_s__Ruminococcus_torques
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I_g__Dorea_s__Dorea_formicigenerans
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Collinsella_s__Collinsella_aerofaciens
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Dorea_s__Dorea_formicigenerans
PWY0_1586__peptidoglycan_maturation__meso_diaminopimelate_containing_,_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7357__thiamin_formation_from_pyrithiamine_and_oxythiamine__yeast_,_g__Blautia_s__Ruminococcus_torques
PWY_5659__GDP_mannose_biosynthesis_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Blautia_s__Ruminococcus_torques
PWY_6305__putrescine_biosynthesis_IV_g__Blautia_s__Ruminococcus_obeum
PWY_2942__L_lysine_biosynthesis_III_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
GLUTORN_PWY__L_ornithine_biosynthesis_g__Blautia_s__Ruminococcus_torques
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Dorea_s__Dorea_formicigenerans
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Dorea_s__Dorea_formicigenerans
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Blautia_s__Ruminococcus_obeum
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Eubacterium_s__Eubacterium_rectale
PWY_7198__pyrimidine_deoxyribonucleotides_de_novo_biosynthesis_IV
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I_g__Blautia_s__Ruminococcus_torques
PWY_5367__petroselinate_biosynthesis_g__Eubacterium_s__Eubacterium_rectale
PWY_2942__L_lysine_biosynthesis_III_g__Blautia_s__Ruminococcus_torques
VALSYN_PWY__L_valine_biosynthesis_g__Blautia_s__Ruminococcus_torques
PWY_6737__starch_degradation_V_g__Eubacterium_s__Eubacterium_rectale
PWY_6737__starch_degradation_V_g__Blautia_s__Ruminococcus_torques
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_,_g__Eubacterium_s__Eubacterium_rectale
PWY_6305__putrescine_biosynthesis_IV_g__Blautia_s__Ruminococcus_torques
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II_g__Blautia_s__Ruminococcus_torques
PWY_6936__seleno_amino_acid_biosynthesis_g__Dorea_s__Dorea_longicatena
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I_g__Collinsella_s__Collinsella_aerofaciens
PWY_6737__starch_degradation_V_g__Coprococcus_s__Coprococcus_comes
PWY_6737__starch_degradation_V_g__Collinsella_s__Collinsella_aerofaciens
ARGSYN_PWY__L_arginine_biosynthesis_I__via_L_ornithine_,_g__Blautia_s__Ruminococcus_torques
PWY_5367__petroselinate_biosynthesis_g__Blautia_s__Ruminococcus_torques
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis_g__Blautia_s__Ruminococcus_torques
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Collinsella_s__Collinsella_aerofaciens
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Collinsella_s__Collinsella_aerofaciens
PWY_4981__L_proline_biosynthesis_II__from_arginine_,_g__Collinsella_s__Collinsella_aerofaciens
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis_g__Dorea_s__Dorea_longicatena
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II_g__Dorea_s__Dorea_longicatena
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Coprococcus_s__Coprococcus_comes
VALSYN_PWY__L_valine_biosynthesis_g__Eubacterium_s__Eubacterium_rectale
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Eubacterium_s__Eubacterium_rectale
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I_g__Dorea_s__Dorea_longicatena
PWY_5686__UMP_biosynthesis_g__Dorea_s__Dorea_longicatena
PANTO_PWY__phosphopantothenate_biosynthesis_I_g__Dorea_s__Dorea_longicatena
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I_g__Eubacterium_s__Eubacterium_rectale
PWY_6737__starch_degradation_V_g__Dorea_s__Dorea_longicatena
PWY0_1296__purine_ribonucleosides_degradation_g__Eubacterium_s__Eubacterium_rectale
PWY_5304__superpathway_of_sulfur_oxidation__Acidianus_ambivalens_
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_,_g__Eubacterium_s__Eubacterium_rectale
PWY_6151__S_adenosyl_L_methionine_cycle_I_g__Collinsella_s__Collinsella_aerofaciens
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_,_g__Eubacterium_s__Eubacterium_rectale
PWY66_422__D_galactose_degradation_V__Leloir_pathway_,_g__Eubacterium_s__Eubacterium_rectale
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_,_g__Collinsella_s__Collinsella_aerofaciens
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_,_g__Dorea_s__Dorea_longicatena
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis_g__Eubacterium_s__Eubacterium_rectale
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_,_g__Collinsella_s__Collinsella_aerofaciens
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_,_g__Collinsella_s__Collinsella_aerofaciens
VALSYN_PWY__L_valine_biosynthesis_g__Dorea_s__Dorea_longicatena
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis_g__Dorea_s__Dorea_longicatena
PWY0_1296__purine_ribonucleosides_degradation_g__Dorea_s__Dorea_longicatena
RHAMCAT_PWY__L_rhamnose_degradation_I_g__Faecalibacterium_s__Faecalibacterium_prausnitzii
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
LDA score(log10)