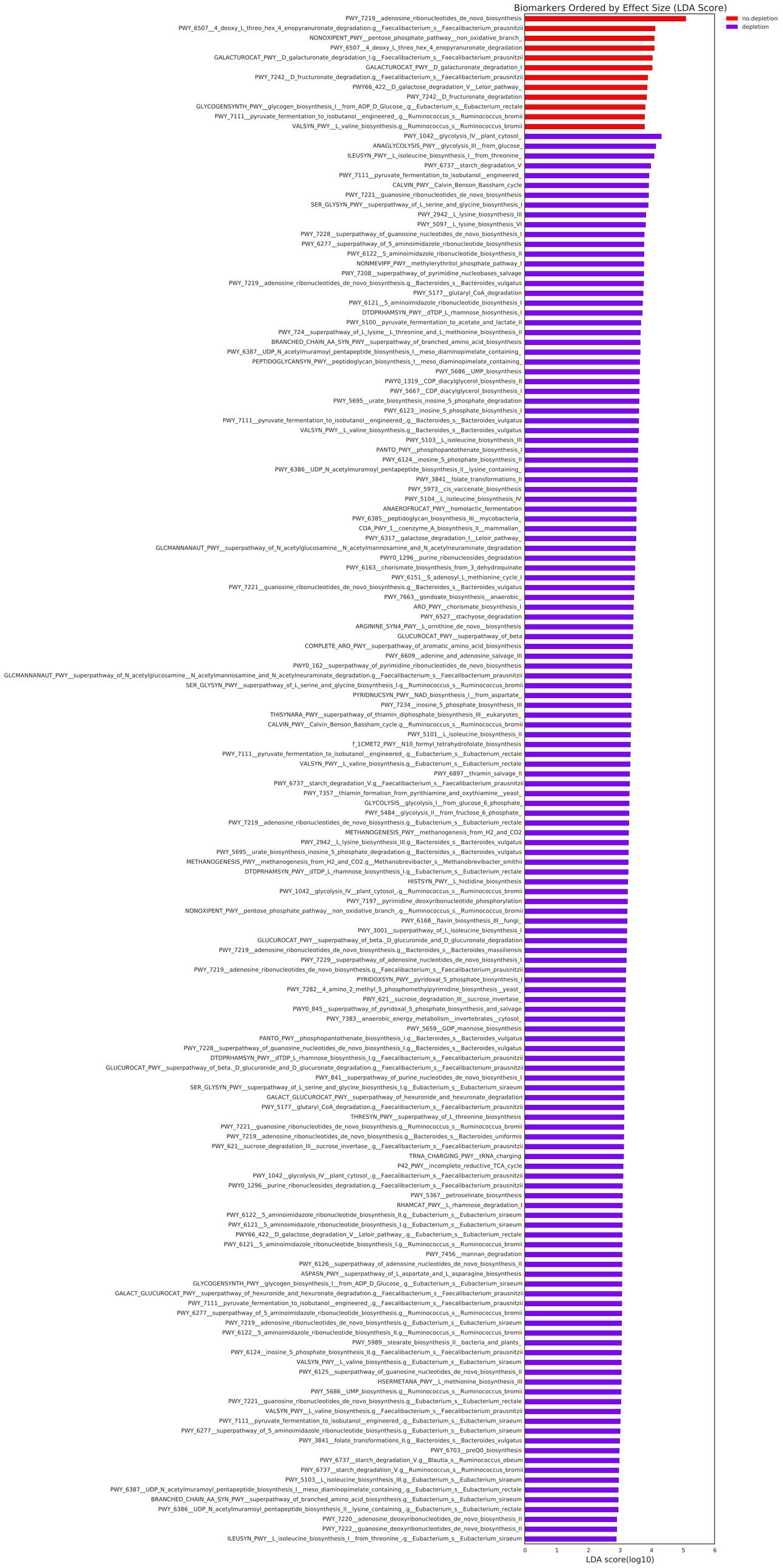
Biomarkers Ordered by Effect Size (LDA Score)
no.depletion
depletion
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis
PWY_6507__4_deoxy_L_threo_hex_4_enopyranuronate_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
NONOXIPENT_PWY__pentose_phosphate_pathway__non_oxidative_branch_
PWY_6507__4_deoxy_L_threo_hex_4_enopyranuronate_degradation
GALACTUROCAT_PWY__D_galacturonate_degradation_I.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
GALACTUROCAT_PWY__D_galacturonate_degradation_I
PWY_7242__D_fructuronate_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY66_422__D_galactose_degradation_V__Leloir_pathway_
PWY_7242__D_fructuronate_degradation
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Eubacterium_s__Eubacterium_rectale
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Ruminococcus_s__Ruminococcus_bromii
VALSYN_PWY__L_valine_biosynthesis.g__Ruminococcus_s__Ruminococcus_bromii
PWY_1042__glycolysis_IV__plant_cytosol_
ANAGLYCOLYSIS_PWY__glycolysis_III__from_glucose_
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_
PWY_6737__starch_degradation_V
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_
CALVIN_PWY__Calvin_Benson_Bassham_cycle
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I
PWY_2942__L_lysine_biosynthesis_III
PWY_5097__L_lysine_biosynthesis_VI
PWY_7228__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_I
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I
PWY_7208__superpathway_of_pyrimidine_nucleobases_salvage
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Bacteroides_s__Bacteroides_vulgatus
PWY_5177__glutaryl_CoA_degradation
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_amino_acid_biosynthesis
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_
PWY_5686__UMP_biosynthesis
PWY0_1319__CDP_diacylglycerol_biosynthesis_II
PWY_5667__CDP_diacylglycerol_biosynthesis_I
PWY_5695__urate_biosynthesis_inosine_5_phosphate_degradation
PWY_6123__inosine_5_phosphate_biosynthesis_I
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Bacteroides_s__Bacteroides_vulgatus
VALSYN_PWY__L_valine_biosynthesis.g__Bacteroides_s__Bacteroides_vulgatus
PWY_5103__L_isoleucine_biosynthesis_III
PANTO_PWY__phosphopantothenate_biosynthesis_I
PWY_6124__inosine_5_phosphate_biosynthesis_II
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_
PWY_3841__folate_transformations_II
PWY_5973__cis_vaccenate_biosynthesis
PWY_5104__L_isoleucine_biosynthesis_IV
ANAEROFRUCAT_PWY__homolactic_fermentation
PWY_6385__peptidoglycan_biosynthesis_III__mycobacteria_
COA_PWY_1__coenzyme_A_biosynthesis_II__mammalian_
PWY_6317__galactose_degradation_I__Leloir_pathway_
GLCMANNANAUT_PWY__superpathway_of_N_acetylglucosamine__N_acetylmannosamine_and_N_acetylneuraminate_degradation
PWY0_1296__purine_ribonucleosides_degradation
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate
PWY_6151__S_adenosyl_L_methionine_cycle_I
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis.g__Bacteroides_s__Bacteroides_vulgatus
PWY_7663__gondoate_biosynthesis__anaerobic_
ARO_PWY__chorismate_biosynthesis_I
PWY_6527__stachyose_degradation
ARGININE_SYN4_PWY__L_ornithine_de_novo__biosynthesis
GLUCUROCAT_PWY__superpathway_of_beta
COMPLETE_ARO_PWY__superpathway_of_aromatic_amino_acid_biosynthesis
PWY_6609__adenine_and_adenosine_salvage_III
PWY0_162__superpathway_of_pyrimidine_ribonucleotides_de_novo_biosynthesis
GLCMANNANAUT_PWY__superpathway_of_N_acetylglucosamine__N_acetylmannosamine_and_N_acetylneuraminate_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I.g__Ruminococcus_s__Ruminococcus_bromii
PYRIDNUCSYN_PWY__NAD_biosynthesis_I__from_aspartate_
PWY_7234__inosine_5_phosphate_biosynthesis_III
THISYNARA_PWY__superpathway_of_thiamin_diphosphate_biosynthesis_III__eukaryotes_
CALVIN_PWY__Calvin_Benson_Bassham_cycle.g__Ruminococcus_s__Ruminococcus_bromii
PWY_5101__L_isoleucine_biosynthesis_II
f_1CMET2_PWY__N10_formyl_tetrahydrofolate_biosynthesis
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Eubacterium_s__Eubacterium_rectale
VALSYN_PWY__L_valine_biosynthesis.g__Eubacterium_s__Eubacterium_rectale
PWY_6897__thiamin_salvage_II
PWY_6737__starch_degradation_V.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7357__thiamin_formation_from_pyrithiamine_and_oxythiamine__yeast_
GLYCOLYSIS__glycolysis_I__from_glucose_6_phosphate_
PWY_5484__glycolysis_II__from_fructose_6_phosphate_
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Eubacterium_s__Eubacterium_rectale
METHANOGENESIS_PWY__methanogenesis_from_H2_and_CO2
PWY_2942__L_lysine_biosynthesis_III.g__Bacteroides_s__Bacteroides_vulgatus
PWY_5695__urate_biosynthesis_inosine_5_phosphate_degradation.g__Bacteroides_s__Bacteroides_vulgatus
METHANOGENESIS_PWY__methanogenesis_from_H2_and_CO2.g__Methanobrevibacter_s__Methanobrevibacter_smithii
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I.g__Eubacterium_s__Eubacterium_rectale
HISTSYN_PWY__L_histidine_biosynthesis
PWY_1042__glycolysis_IV__plant_cytosol_.g__Ruminococcus_s__Ruminococcus_bromii
PWY_7197__pyrimidine_deoxyribonucleotide_phosphorylation
NONOXIPENT_PWY__pentose_phosphate_pathway__non_oxidative_branch_.g__Ruminococcus_s__Ruminococcus_bromii
PWY_6168__flavin_biosynthesis_III__fungi_
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I
GLUCUROCAT_PWY__superpathway_of_beta._D_glucuronide_and_D_glucuronate_degradation
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Bacteroides_s__Bacteroides_massiliensis
PWY_7229__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_I
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PYRIDOXSYN_PWY__pyridoxal_5_phosphate_biosynthesis_I
PWY_7282__4_amino_2_methyl_5_phosphomethylpyrimidine_biosynthesis__yeast_
PWY_621__sucrose_degradation_III__sucrose_invertase_
PWY0_845__superpathway_of_pyridoxal_5_phosphate_biosynthesis_and_salvage
PWY_7383__anaerobic_energy_metabolism__invertebrates__cytosol_
PWY_5659__GDP_mannose_biosynthesis
PANTO_PWY__phosphopantothenate_biosynthesis_I.g__Bacteroides_s__Bacteroides_vulgatus
PWY_7228__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_I.g__Bacteroides_s__Bacteroides_vulgatus
DTDPRHAMSYN_PWY__dTDP_L_rhamnose_biosynthesis_I.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
GLUCUROCAT_PWY__superpathway_of_beta._D_glucuronide_and_D_glucuronate_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_841__superpathway_of_purine_nucleotides_de_novo_biosynthesis_I
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I.g__Eubacterium_s__Eubacterium_siraeum
GALACT_GLUCUROCAT_PWY__superpathway_of_hexuronide_and_hexuronate_degradation
PWY_5177__glutaryl_CoA_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis.g__Ruminococcus_s__Ruminococcus_bromii
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Bacteroides_s__Bacteroides_uniformis
PWY_621__sucrose_degradation_III__sucrose_invertase_.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
TRNA_CHARGING_PWY__tRNA_charging
P42_PWY__incomplete_reductive_TCA_cycle
PWY_1042__glycolysis_IV__plant_cytosol_.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY0_1296__purine_ribonucleosides_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_5367__petroselinate_biosynthesis
RHAMCAT_PWY__L_rhamnose_degradation_I
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Eubacterium_s__Eubacterium_siraeum
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Eubacterium_s__Eubacterium_siraeum
PWY66_422__D_galactose_degradation_V__Leloir_pathway_.g__Eubacterium_s__Eubacterium_rectale
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Ruminococcus_s__Ruminococcus_bromii
PWY_7456__mannan_degradation
PWY_6126__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_II
ASPASN_PWY__superpathway_of_L_aspartate_and_L_asparagine_biosynthesis
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Eubacterium_s__Eubacterium_siraeum
GALACT_GLUCUROCAT_PWY__superpathway_of_hexuronide_and_hexuronate_degradation.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Ruminococcus_s__Ruminococcus_bromii
PWY_7219__adenosine_ribonucleotides_de_novo_biosynthesis.g__Eubacterium_s__Eubacterium_siraeum
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Ruminococcus_s__Ruminococcus_bromii
PWY_5989__stearate_biosynthesis_II__bacteria_and_plants_
PWY_6124__inosine_5_phosphate_biosynthesis_II.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
VALSYN_PWY__L_valine_biosynthesis.g__Eubacterium_s__Eubacterium_siraeum
PWY_6125__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_II
HSERMETANA_PWY__L_methionine_biosynthesis_III
PWY_5686__UMP_biosynthesis.g__Ruminococcus_s__Ruminococcus_bromii
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis.g__Eubacterium_s__Eubacterium_rectale
VALSYN_PWY__L_valine_biosynthesis.g__Faecalibacterium_s__Faecalibacterium_prausnitzii
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Eubacterium_s__Eubacterium_siraeum
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Eubacterium_s__Eubacterium_siraeum
PWY_3841__folate_transformations_II.g__Bacteroides_s__Bacteroides_vulgatus
PWY_6703__preQ0_biosynthesis
PWY_6737__starch_degradation_V.g__Blautia_s__Ruminococcus_obeum
PWY_6737__starch_degradation_V.g__Ruminococcus_s__Ruminococcus_bromii
PWY_5103__L_isoleucine_biosynthesis_III.g__Eubacterium_s__Eubacterium_siraeum
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_.g__Eubacterium_s__Eubacterium_rectale
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_amino_acid_biosynthesis.g__Eubacterium_s__Eubacterium_siraeum
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_.g__Eubacterium_s__Eubacterium_rectale
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_.g__Eubacterium_s__Eubacterium_siraeum
0
1
2
3
4
5
6
LDA score(log10)