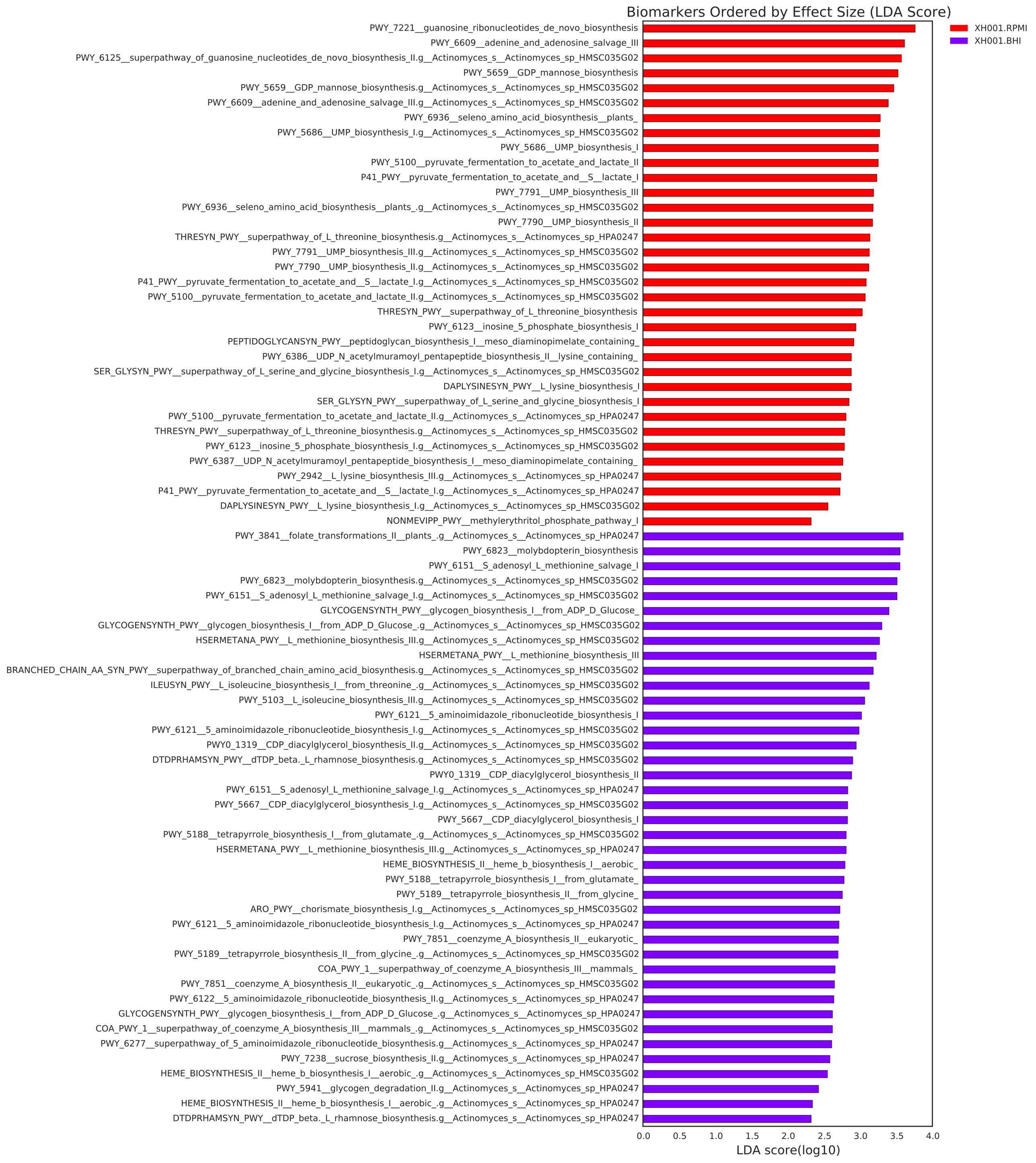

Biomarkers Ordered by Effect Size (LDA Score)
XH001.RPMI
XH001.BHI
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis
PWY_6609__adenine_and_adenosine_salvage_III
PWY_6125__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5659__GDP_mannose_biosynthesis
PWY_5659__GDP_mannose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6609__adenine_and_adenosine_salvage_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6936__seleno_amino_acid_biosynthesis__plants_
PWY_5686__UMP_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5686__UMP_biosynthesis_I
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I
PWY_7791__UMP_biosynthesis_III
PWY_6936__seleno_amino_acid_biosynthesis__plants_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7790__UMP_biosynthesis_II
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_7791__UMP_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7790__UMP_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis
PWY_6123__inosine_5_phosphate_biosynthesis_I
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6123__inosine_5_phosphate_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_
PWY_2942__L_lysine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HPA0247
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I
PWY_3841__folate_transformations_II__plants_.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_6823__molybdopterin_biosynthesis
PWY_6151__S_adenosyl_L_methionine_salvage_I
PWY_6823__molybdopterin_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6151__S_adenosyl_L_methionine_salvage_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
HSERMETANA_PWY__L_methionine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
HSERMETANA_PWY__L_methionine_biosynthesis_III
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_chain_amino_acid_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5103__L_isoleucine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY0_1319__CDP_diacylglycerol_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY0_1319__CDP_diacylglycerol_biosynthesis_II
PWY_6151__S_adenosyl_L_methionine_salvage_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_5667__CDP_diacylglycerol_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5667__CDP_diacylglycerol_biosynthesis_I
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
HSERMETANA_PWY__L_methionine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HPA0247
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_
PWY_5189__tetrapyrrole_biosynthesis_II__from_glycine_
ARO_PWY__chorismate_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_7851__coenzyme_A_biosynthesis_II__eukaryotic_
PWY_5189__tetrapyrrole_biosynthesis_II__from_glycine_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
COA_PWY_1__superpathway_of_coenzyme_A_biosynthesis_III__mammals_
PWY_7851__coenzyme_A_biosynthesis_II__eukaryotic_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Actinomyces_s__Actinomyces_sp_HPA0247
COA_PWY_1__superpathway_of_coenzyme_A_biosynthesis_III__mammals_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_7238__sucrose_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5941__glycogen_degradation_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_.g__Actinomyces_s__Actinomyces_sp_HPA0247
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
LDA score(log10)