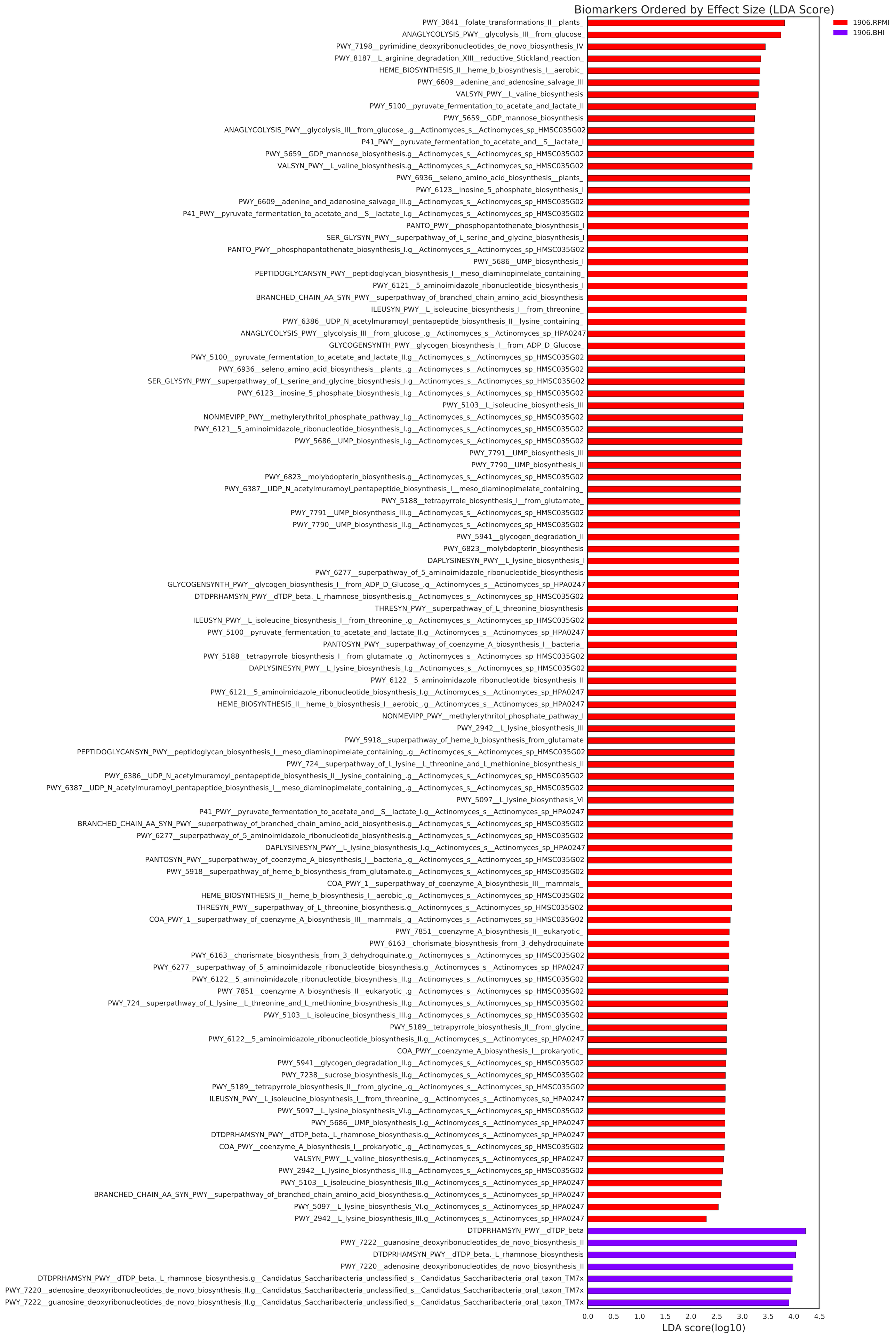

Biomarkers Ordered by Effect Size (LDA Score)
1906.RPMI
1906.BHI
PWY_3841__folate_transformations_II__plants_
ANAGLYCOLYSIS_PWY__glycolysis_III__from_glucose_
PWY_7198__pyrimidine_deoxyribonucleotides_de_novo_biosynthesis_IV
PWY_8187__L_arginine_degradation_XIII__reductive_Stickland_reaction_
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_
PWY_6609__adenine_and_adenosine_salvage_III
VALSYN_PWY__L_valine_biosynthesis
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II
PWY_5659__GDP_mannose_biosynthesis
ANAGLYCOLYSIS_PWY__glycolysis_III__from_glucose_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I
PWY_5659__GDP_mannose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
VALSYN_PWY__L_valine_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6936__seleno_amino_acid_biosynthesis__plants_
PWY_6123__inosine_5_phosphate_biosynthesis_I
PWY_6609__adenine_and_adenosine_salvage_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PANTO_PWY__phosphopantothenate_biosynthesis_I
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I
PANTO_PWY__phosphopantothenate_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5686__UMP_biosynthesis_I
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_chain_amino_acid_biosynthesis
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_
ANAGLYCOLYSIS_PWY__glycolysis_III__from_glucose_.g__Actinomyces_s__Actinomyces_sp_HPA0247
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6936__seleno_amino_acid_biosynthesis__plants_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6123__inosine_5_phosphate_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5103__L_isoleucine_biosynthesis_III
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5686__UMP_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7791__UMP_biosynthesis_III
PWY_7790__UMP_biosynthesis_II
PWY_6823__molybdopterin_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_
PWY_7791__UMP_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7790__UMP_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5941__glycogen_degradation_II
PWY_6823__molybdopterin_biosynthesis
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Actinomyces_s__Actinomyces_sp_HPA0247
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
PANTOSYN_PWY__superpathway_of_coenzyme_A_biosynthesis_I__bacteria_
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_.g__Actinomyces_s__Actinomyces_sp_HPA0247
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I
PWY_2942__L_lysine_biosynthesis_III
PWY_5918__superpathway_of_heme_b_biosynthesis_from_glutamate
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5097__L_lysine_biosynthesis_VI
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_chain_amino_acid_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
PANTOSYN_PWY__superpathway_of_coenzyme_A_biosynthesis_I__bacteria_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5918__superpathway_of_heme_b_biosynthesis_from_glutamate.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
COA_PWY_1__superpathway_of_coenzyme_A_biosynthesis_III__mammals_
HEME_BIOSYNTHESIS_II__heme_b_biosynthesis_I__aerobic_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
COA_PWY_1__superpathway_of_coenzyme_A_biosynthesis_III__mammals_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7851__coenzyme_A_biosynthesis_II__eukaryotic_
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7851__coenzyme_A_biosynthesis_II__eukaryotic_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5103__L_isoleucine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5189__tetrapyrrole_biosynthesis_II__from_glycine_
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HPA0247
COA_PWY__coenzyme_A_biosynthesis_I__prokaryotic_
PWY_5941__glycogen_degradation_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_7238__sucrose_biosynthesis_II.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5189__tetrapyrrole_biosynthesis_II__from_glycine_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_5097__L_lysine_biosynthesis_VI.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5686__UMP_biosynthesis_I.g__Actinomyces_s__Actinomyces_sp_HPA0247
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
COA_PWY__coenzyme_A_biosynthesis_I__prokaryotic_.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
VALSYN_PWY__L_valine_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_2942__L_lysine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HMSC035G02
PWY_5103__L_isoleucine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HPA0247
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_chain_amino_acid_biosynthesis.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_5097__L_lysine_biosynthesis_VI.g__Actinomyces_s__Actinomyces_sp_HPA0247
PWY_2942__L_lysine_biosynthesis_III.g__Actinomyces_s__Actinomyces_sp_HPA0247
DTDPRHAMSYN_PWY__dTDP_beta
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Candidatus_Saccharibacteria_unclassified_s__Candidatus_Saccharibacteria_oral_taxon_TM7x
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II.g__Candidatus_Saccharibacteria_unclassified_s__Candidatus_Saccharibacteria_oral_taxon_TM7x
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II.g__Candidatus_Saccharibacteria_unclassified_s__Candidatus_Saccharibacteria_oral_taxon_TM7x
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
LDA score(log10)