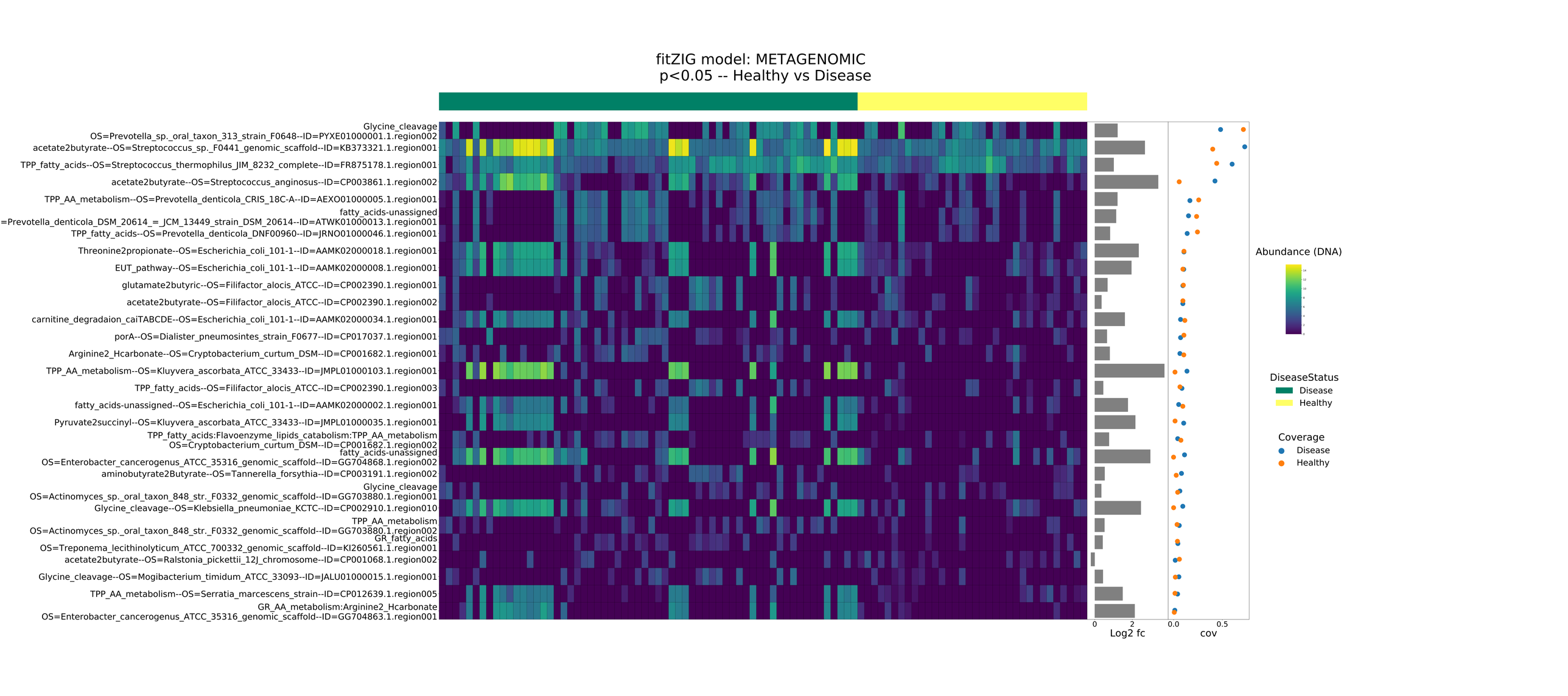
fitZIG model: METAGENOMIC
p<0.05 -- Healthy vs Disease
Glycine_cleavage
OS=Prevotella_sp._oral_taxon_313_strain_F0648--ID=PYXE01000001.1.region002
acetate2butyrate--OS=Streptococcus_sp._F0441_genomic_scaffold--ID=KB373321.1.region001
TPP_fatty_acids--OS=Streptococcus_thermophilus_JIM_8232_complete--ID=FR875178.1.region001
acetate2butyrate--OS=Streptococcus_anginosus--ID=CP003861.1.region002
TPP_AA_metabolism--OS=Prevotella_denticola_CRIS_18C-A--ID=AEXO01000005.1.region001
fatty_acids-unassigned
=Prevotella_denticola_DSM_20614_=_JCM_13449_strain_DSM_20614--ID=ATWK01000013.1.region001
TPP_fatty_acids--OS=Prevotella_denticola_DNF00960--ID=JRNO01000046.1.region001
Threonine2propionate--OS=Escherichia_coli_101-1--ID=AAMK02000018.1.region001
EUT_pathway--OS=Escherichia_coli_101-1--ID=AAMK02000008.1.region001
glutamate2butyric--OS=Filifactor_alocis_ATCC--ID=CP002390.1.region001
acetate2butyrate--OS=Filifactor_alocis_ATCC--ID=CP002390.1.region002
carnitine_degradaion_caiTABCDE--OS=Escherichia_coli_101-1--ID=AAMK02000034.1.region001
porA--OS=Dialister_pneumosintes_strain_F0677--ID=CP017037.1.region001
Arginine2_Hcarbonate--OS=Cryptobacterium_curtum_DSM--ID=CP001682.1.region001
TPP_AA_metabolism--OS=Kluyvera_ascorbata_ATCC_33433--ID=JMPL01000103.1.region001
TPP_fatty_acids--OS=Filifactor_alocis_ATCC--ID=CP002390.1.region003
fatty_acids-unassigned--OS=Escherichia_coli_101-1--ID=AAMK02000002.1.region001
Pyruvate2succinyl--OS=Kluyvera_ascorbata_ATCC_33433--ID=JMPL01000035.1.region001
TPP_fatty_acids:Flavoenzyme_lipids_catabolism:TPP_AA_metabolism
OS=Cryptobacterium_curtum_DSM--ID=CP001682.1.region002
fatty_acids-unassigned
OS=Enterobacter_cancerogenus_ATCC_35316_genomic_scaffold--ID=GG704868.1.region002
aminobutyrate2Butyrate--OS=Tannerella_forsythia--ID=CP003191.1.region002
Glycine_cleavage
OS=Actinomyces_sp._oral_taxon_848_str._F0332_genomic_scaffold--ID=GG703880.1.region001
Glycine_cleavage--OS=Klebsiella_pneumoniae_KCTC--ID=CP002910.1.region010
TPP_AA_metabolism
OS=Actinomyces_sp._oral_taxon_848_str._F0332_genomic_scaffold--ID=GG703880.1.region002
GR_fatty_acids
OS=Treponema_lecithinolyticum_ATCC_700332_genomic_scaffold--ID=KI260561.1.region001
acetate2butyrate--OS=Ralstonia_pickettii_12J_chromosome--ID=CP001068.1.region002
Glycine_cleavage--OS=Mogibacterium_timidum_ATCC_33093--ID=JALU01000015.1.region001
TPP_AA_metabolism--OS=Serratia_marcescens_strain--ID=CP012639.1.region005
GR_AA_metabolism:Arginine2_Hcarbonate
OS=Enterobacter_cancerogenus_ATCC_35316_genomic_scaffold--ID=GG704863.1.region001
0
2
Log2 fc
0.0
0.5
cov
Abundance (DNA)
DiseaseStatus
Disease
Healthy
Coverage
Disease
Healthy