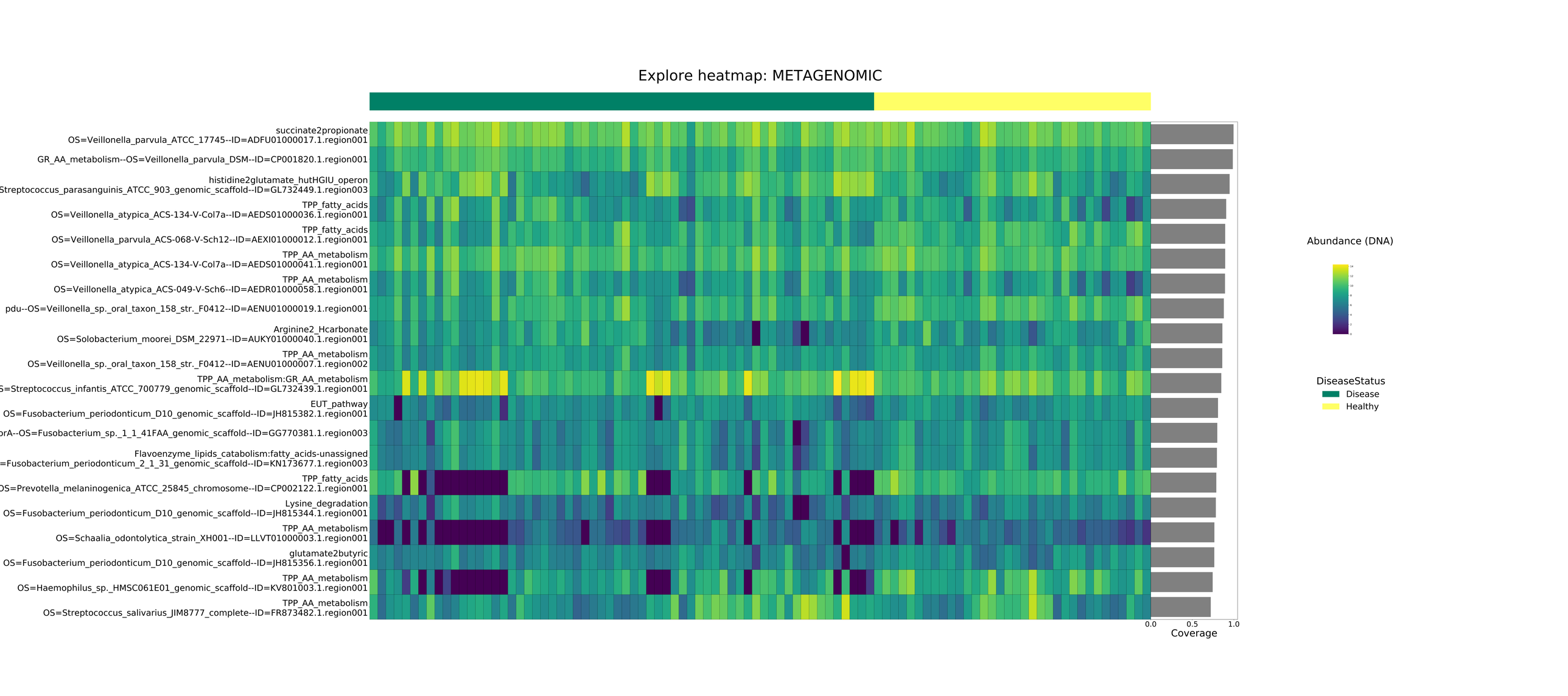
Explore heatmap: METAGENOMIC
succinate2propionate
OS=Veillonella_parvula_ATCC_17745--ID=ADFU01000017.1.region001
GR_AA_metabolism--OS=Veillonella_parvula_DSM--ID=CP001820.1.region001
histidine2glutamate_hutHGIU_operon
Streptococcus_parasanguinis_ATCC_903_genomic_scaffold--ID=GL732449.1.region003
TPP_fatty_acids
OS=Veillonella_atypica_ACS-134-V-Col7a--ID=AEDS01000036.1.region001
TPP_fatty_acids
OS=Veillonella_parvula_ACS-068-V-Sch12--ID=AEXI01000012.1.region001
TPP_AA_metabolism
OS=Veillonella_atypica_ACS-134-V-Col7a--ID=AEDS01000041.1.region001
TPP_AA_metabolism
OS=Veillonella_atypica_ACS-049-V-Sch6--ID=AEDR01000058.1.region001
pdu--OS=Veillonella_sp._oral_taxon_158_str._F0412--ID=AENU01000019.1.region001
Arginine2_Hcarbonate
OS=Solobacterium_moorei_DSM_22971--ID=AUKY01000040.1.region001
TPP_AA_metabolism
OS=Veillonella_sp._oral_taxon_158_str._F0412--ID=AENU01000007.1.region002
TPP_AA_metabolism:GR_AA_metabolism
S=Streptococcus_infantis_ATCC_700779_genomic_scaffold--ID=GL732439.1.region001
EUT_pathway
OS=Fusobacterium_periodonticum_D10_genomic_scaffold--ID=JH815382.1.region001
orA--OS=Fusobacterium_sp._1_1_41FAA_genomic_scaffold--ID=GG770381.1.region003
Flavoenzyme_lipids_catabolism:fatty_acids-unassigned
=Fusobacterium_periodonticum_2_1_31_genomic_scaffold--ID=KN173677.1.region003
TPP_fatty_acids
OS=Prevotella_melaninogenica_ATCC_25845_chromosome--ID=CP002122.1.region001
Lysine_degradation
OS=Fusobacterium_periodonticum_D10_genomic_scaffold--ID=JH815344.1.region001
TPP_AA_metabolism
OS=Schaalia_odontolytica_strain_XH001--ID=LLVT01000003.1.region001
glutamate2butyric
OS=Fusobacterium_periodonticum_D10_genomic_scaffold--ID=JH815356.1.region001
TPP_AA_metabolism
OS=Haemophilus_sp._HMSC061E01_genomic_scaffold--ID=KV801003.1.region001
TPP_AA_metabolism
OS=Streptococcus_salivarius_JIM8777_complete--ID=FR873482.1.region001
0.0
0.5
1.0
Coverage
Abundance (DNA)
14
12
10
8
6
4
2
0
DiseaseStatus
Disease
Healthy