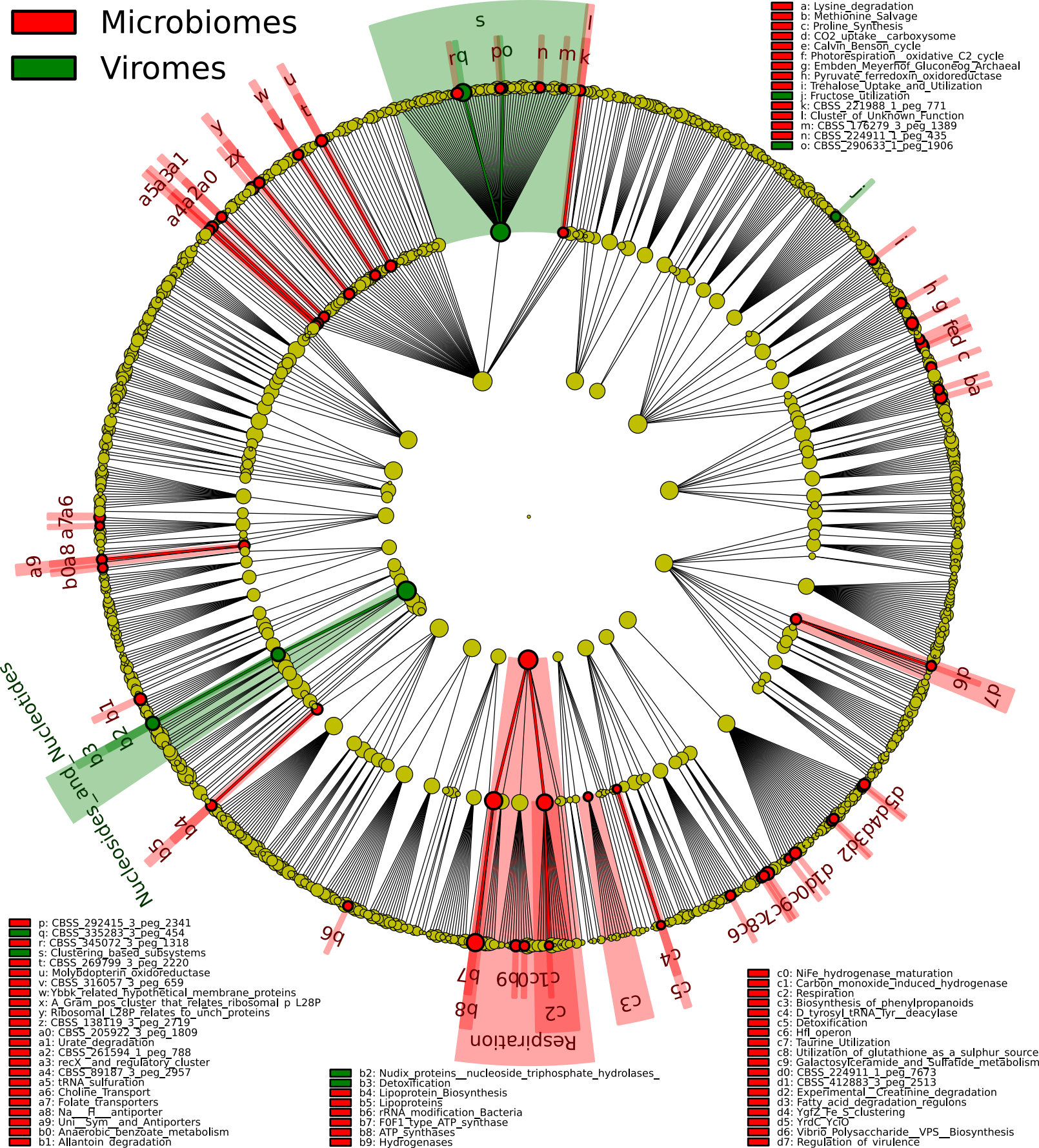
Microbiomes
Viromes
a: Lysine_degradation
b: Methionine_Salvage
c: Proline_Synthesis
d: CO2_uptake__carboxysome
e: Calvin_Benson_cycle
f: Photorespiration__oxidative_C2_cycle
g: Embden_Meyerhof_Gluconeog_Archaeal
h: Pyruvate_ferredoxin_oxidoreductase
i: Trehalose_Uptake_and_Utilization
j: Fructose_utilization
k: CBSS_221988_1_peg_771
l: Cluster_of_Unknown_Function
m: CBSS_176279_3_peg_1389
n: CBSS_224911_1_peg_435
o: CBSS_290633_1_peg_1906
Nucleosides_and_Nucleotides
Respiration
p: CBSS_292415_3_peg_2341
q: CBSS_335283_3_peg_454
r: CBSS_345072_3_peg_1318
s: Clustering_based_subsystems
t: CBSS_269799_3_peg_2220
u: Molybdopterin_oxidoreductase
v: CBSS_316057_3_peg_659
w: Ybbk_related_hypothetical_membrane_proteins
x: A_Gram_pos_cluster_that_relates_ribosomal_p_L28P
y: Ribosomal_L28P_relates_to_unch_proteins
z: CBSS_138119_3_peg_2719
a0: CBSS_205922_3_peg_1809
a1: Urate_degradation
a2: CBSS_261594_1_peg_788
a3: recX__and_regulatory_cluster
a4: CBSS_89187_3_peg_2957
a5: tRNA_sulfuration
a6: Choline_Transport
a7: Folate_transporters
a8: Na___H__antiporter
a9: Uni__Sym__and_Antiporters
b0: Anaerobic_benzoate_metabolism
b1: Allantoin_degradation
b2: Nudix_proteins__nucleoside_triphosphate_hydrolases_
b3: Detoxification
b4: Lipoprotein_Biosynthesis
b5: Lipoproteins
b6: rRNA_modification_Bacteria
b7: F0F1_type_ATP_synthase
b8: ATP_synthases
b9: Hydrogenases
c0: NiFe_hydrogenase_maturation
c1: Carbon_monoxide_induced_hydrogenase
c2: Respiration
c3: Biosynthesis_of_phenylpropanoids
c4: D_tyrosyl_tRNA_Tyr__deacylase
c5: Detoxification
c6: Hfl_operon
c7: Taurine_Utilization
c8: Utilization_of_glutathione_as_a_sulphur_source
c9: Galactosylceramide_and_Sulfatide_metabolism
d0: CBSS_224911_1_peg_7673
d1: CBSS_412883_3_peg_2513
d2: Experimental__Creatinine_degradation
d3: Fatty_acid_degradation_regulons
d4: YgfZ_Fe_S_clustering
d5: YrdC_YciO
d6: Vibrio_Polysaccharide__VPS__Biosynthesis
d7: Regulation_of_virulence