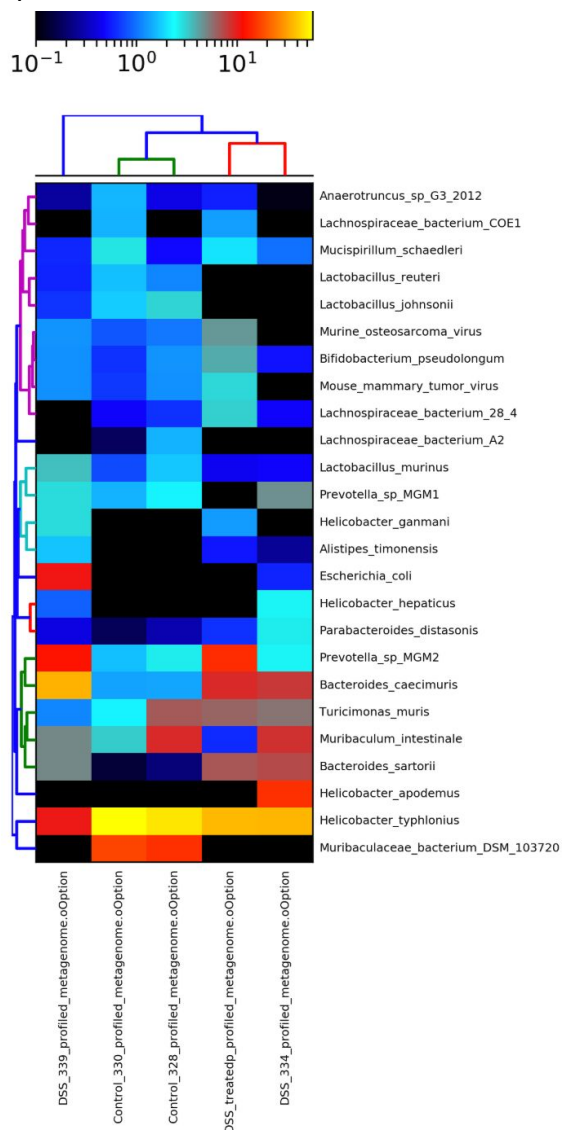


Taxonomy classification:

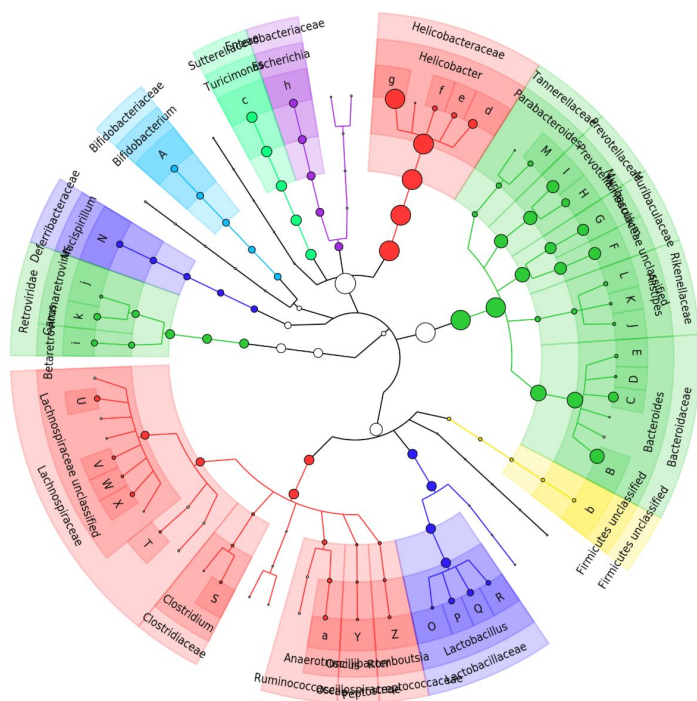
clade_name	sample1	sample2	sample3	sample4	sample5
k_Bacteria	92.00353	97.37691	100.0	98.26648	97.54932
k_Bacteria p_Actinobacteria	4.035019999999999			1.296179999999999	0.58616 0.672999999999999
k_Bacteria p_Actinobacteria c_Actinobacteria	3.99091 1.19846 0.52567 0.64456 1.23179				
k_Bacteria p_Actinobacteria c_Actinobacteria o_Bifidobacteriales	3.99091 1.19846 0.52567 0.64456 1.23179				
k_Bacteria p_Actinobacteria c_Actinobacteria o_Bifidobacteriales f_Bifidobacteriaceae	3.99091 1.19846 0.52567 0.64456 1.23179				
k_Bacteria p_Actinobacteria c_Actinobacteria o_Bifidobacteriales f_Bifidobacteriaceae g_Bifidobacterium	3.99091 1.19846 0.52567 0.64456 1.23179				
k_Bacteria p_Actinobacteria c_Actinobacteria o_Bifidobacteriales f_Bifidobacteriaceae g_Bifidobacterium s_Bifidobacterium_pseudolongum	3.99091 1.19846 0.52567 0.64456 1.23179				
k_Bacteria p_Actinobacteria c_Coriobacteriia	0.04412 0.09772 0.06048999999999995			0.02843999999999997	0.03889
k_Bacteria p_Actinobacteria c_Coriobacteriia o_Eggerthellales	0.04412 0.09772 0.06048999999999995			0.02843999999999997	0.03889

Taxonomy Level Wise heatmap:

Species:



Cladogram:



Functional Analysis:
GeneFamilies

#	Gene Family	demo_Abundance-RPKs
UNMAPPED	3897.0000000000	
UniRef90_unknown	1633.3754216411	
UniRef90_unknown g__Bacteroides.s__Bacteroides_dorei		894.7763053061
UniRef90_unknown g__Bacteroides.s__Bacteroides_vulgatus		738.5991163350
UniRef90_R6HHA8	333.3333333333	
UniRef90_R6HHA8 g__Bacteroides.s__Bacteroides_dorei		333.3333333333
UniRef90_R7NYS9	166.6666666667	
UniRef90_R7NYS9 g__Bacteroides.s__Bacteroides_vulgatus		166.6666666667
UniRef90_D1K9F5	66.6666666667	

Pathway

#	Pathway	demo_Abundance
	UNMAPPED	1225.9730368639
	UNINTEGRATED	5908.3755167593
	UNINTEGRATED g__Bacteroides.s__Bacteroides_dorei	3123.1902040899
	UNINTEGRATED g__Bacteroides.s__Bacteroides_vulgatus	2753.6043067990
	UNINTEGRATED unclassified	72.8101423152
	PWY-6305: putrescine biosynthesis IV	30.3913024756
	PWY-6305: putrescine biosynthesis IV unclassified	30.3913024756
	PWY-4203: volatile benzenoid biosynthesis I (ester formation)	22.5319052245
	PWY-4203: volatile benzenoid biosynthesis I (ester formation) unclassified	22.5319052245
	PWY490-3: nitrate reduction VI (assimilatory)	21.3761301200
	PWY490-3: nitrate reduction VI (assimilatory) unclassified	21.3761301200
	PWY-1269: CMP-3-deoxy-D-manno-octulosonate biosynthesis I	19.6850995143
	PWY-1269: CMP-3-deoxy-D-manno-octulosonate biosynthesis I unclassified	18.6035804538
	PWY-5173: superpathway of acetyl-CoA biosynthesis	17.0384635071
	PWY-5173: superpathway of acetyl-CoA biosynthesis unclassified	15.1040744758
	PWY-3781: aerobic respiration I (cytochrome c)	15.9398653899
	PWY-3781: aerobic respiration I (cytochrome c) unclassified	15.9398653899
	PWY-7279: aerobic respiration II (cytochrome c) (yeast)	15.9398653899
	PWY-7279: aerobic respiration II (cytochrome c) (yeast) unclassified	15.9398653899