Table 3. Bacterial taxa that differ between IBS, D-IBS, C-IBS, M-IBS and healthy controls

Rank	Taxon	Group	Mean Abundance*	Std Dev.	Std Err	N	P-ANOVA	Significant Groups	P-Tukey
species	Collinsella_OTU0	D-IBS	-2.785	1.276	0.285	20	0.037		
species	Collinsella_OTU0	C-IBS	-1.85	0.697	0.145	23	0.037	C-IBS	0.043
species	Collinsella_OTU0	M-IBS	-2.645	1.362	0.378	13	0.037		
species	Collinsella_OTU0	HC	-2.645	1.262	0.326	15	0.037		
species	OTU438	D-IBS	-2.492	1.095	0.245	20	0.058		
species	OTU438	C-IBS	-2.495	0.665	0.139	23	0.058		
species	OTU438	M-IBS	-2.995	1.048	0.291	13	0.058	M-IBS/HC	0.033
species	OTU438	HC	-2.065	0.639	0.165	15	0.058		
species	Streptococcus thermophilus	D-IBS	-2.425	0.695	0.155	20	0.042		
species	Streptococcus thermophilus	C-IBS	-2.171	0.592	0.123	23	0.042		
species	Streptococcus thermophilus	M-IBS	-2.469	0.861	0.239	13	0.042		
species	Streptococcus thermophilus	HC	-2.862	0.746	0.192	15	0.042	HC	0.023
species	OTU2063	D-IBS	-2.958	0.886	0.198	20	0.036		
species	OTU2063	C-IBS	-3.257	0.654	0.136	23	0.036		
species	OTU2063	M-IBS	-3.649	0.934	0.259	13	0.036		
species	OTU2063	HC	-2.843	0.719	0.186	15	0.036	HC	0.044
species	Anaerovorax_OTU14	D-IBS	-3.713	0.59	0.132	20	0.001	D-IBS	0.005
species	Anaerovorax_OTU14	C-IBS	-3.103	0.497	0.104	23	0.001	C-IBS/M-IBS	0.001
species	Anaerovorax_OTU14	M-IBS	-3.879	0.646	0.179	13	0.001		

species	Anaerovorax_OTU14	HC	-3.496	0.613	0.158	15	0.001		
species	Roseburia_OTU15	D-IBS	-3.492	0.479	0.107	20	0.016		
species	Roseburia_OTU15	C-IBS	-3.996	0.434	0.091	23	0.016	C-IBS	0.009
species	Roseburia_OTU15	M-IBS	-3.823	0.609	0.169	13	0.016		
species	Roseburia_OTU15	HC	-3.722	0.523	0.135	15	0.016		
genus	Collinsella	D-IBS	-2.774	1.278	0.286	20	0.039		
genus	Collinsella	C-IBS	-1.841	0.698	0.146	23	0.039	C-IBS	0.034
genus	Collinsella	M-IBS	-2.518	1.255	0.348	13	0.039		
genus	Collinsella	HC	-2.578	1.185	0.306	15	0.039		
genus	Streptococcus	D-IBS	-2.277	0.612	0.137	20	0.061		
genus	Streptococcus	C-IBS	-2.05	0.539	0.112	23	0.061		
genus	Streptococcus	M-IBS	-2.377	0.856	0.237	13	0.061		
genus	Streptococcus	HC	-2.639	0.648	0.167	15	0.061	HC	0.039
genus	Oscillibacter	D-IBS	-2.817	0.812	0.182	20	0.032		
genus	Oscillibacter	C-IBS	-2.118	0.746	0.156	23	0.032	C-IBS	0.028
genus	Oscillibacter	M-IBS	-2.587	0.968	0.269	13	0.032		
genus	Oscillibacter	HC	-2.275	0.68	0.176	15	0.032		
genus	Lactobacillus	D-IBS	-3.149	0.274	0.061	20	0		
genus	Lactobacillus	C-IBS	-3.037	0.699	0.146	23	0		
genus	Lactobacillus	M-IBS	-3.502	1.108	0.307	13	0	M-IBS/HC	0.022
genus	Lactobacillus	HC	-4.237	0.376	0.097	15	0	HC	0
genus	Eubacterium	D-IBS	-2.743	0.974	0.218	20	0.024		
genus	Eubacterium	C-IBS	-3.078	0.934	0.195	23	0.024		
genus	Eubacterium	M-IBS	-3.721	0.903	0.25	13	0.024	M-IBS/HC	0.03
genus	Eubacterium	HC	-2.709	1.062	0.274	15	0.024	M-IBS/HC	0.037

genus	Anaerovorax	D-IBS	-3.397	0.634	0.142	20	0.004	D-IBS/C-IBS	0.011
genus	Anaerovorax	C-IBS	-2.744	0.558	0.116	23	0.004	C-IBS/M-IBS	0.011
genus	Anaerovorax	M-IBS	-3.489	0.78	0.216	13	0.004		
genus	Anaerovorax	HC	-3.062	0.761	0.197	15	0.004		
genus	Actinomyces	D-IBS	-3.625	0.54	0.121	20	0.014		
genus	Actinomyces	C-IBS	-3.69	0.449	0.094	23	0.014	C-IBS/M-IBS	0.03
genus	Actinomyces	M-IBS	-3.806	0.376	0.104	13	0.014		
genus	Actinomyces	HC	-4.137	0.495	0.128	15	0.014	HC	0.013
family	Coriobacteriaceae	D-IBS	-2.291	0.863	0.193	20	0.025		
family	Coriobacteriaceae	C-IBS	-1.667	0.453	0.094	23	0.025	C-IBS	0.021
family	Coriobacteriaceae	M-IBS	-2.101	0.703	0.195	13	0.025		
family	Coriobacteriaceae	HC	-2.147	0.7	0.181	15	0.025		
family	Lactobacillaceae	D-IBS	-3.093	0.416	0.093	20	0		
family	Lactobacillaceae	C-IBS	-3.037	0.699	0.146	23	0	C-IBS/HC	0
family	Lactobacillaceae	M-IBS	-3.502	1.108	0.307	13	0	M-IBS/HC	0
family	Lactobacillaceae	HC	-4.237	0.376	0.097	15	0	HC	0.028
family	Eubacteriaceae	D-IBS	-2.703	0.929	0.208	20	0.031		
family	Eubacteriaceae	C-IBS	-3.048	0.924	0.193	23	0.031		
family	Eubacteriaceae	M-IBS	-3.645	0.889	0.247	13	0.031	M-IBS	0.035
family	Eubacteriaceae	HC	-2.703	1.061	0.274	15	0.031		
family	Incertae Sedis XIII	D-IBS	-3.317	0.627	0.14	20	0.016		
family	Incertae Sedis XIII	C-IBS	-2.729	0.574	0.12	23	0.016	C-IBS/D-IBS	0.026
family	Incertae Sedis XIII	M-IBS	-3.341	0.841	0.233	13	0.016	M-IBS/C-	0.047

								IBS	
family	Incertae Sedis XIII	HC	-3.008	0.676	0.174	15	0.016		
family	Actinomycetaceae	D-IBS	-3.625	0.54	0.121	20	0.011		
family	Actinomycetaceae	C-IBS	-3.662	0.455	0.095	23	0.011		
family	Actinomycetaceae	M-IBS	-3.806	0.376	0.104	13	0.011		
family	Actinomycetaceae	HC	-4.137	0.495	0.128	15	0.011		0.013
order	Lactobacillales	D-IBS	-2.11	0.515	0.115	20	0.03		
order	Lactobacillales	C-IBS	-1.887	0.508	0.106	23	0.03		
order	Lactobacillales	M-IBS	-2.129	1.006	0.279	13	0.03		
order	Lactobacillales	HC	-2.539	0.561	0.145	15	0.03		0.016
order	Coriobacteriales	D-IBS	-2.291	0.863	0.193	20	0.025		
order	Coriobacteriales	C-IBS	-1.667	0.453	0.094	23	0.025	C-IBS/D-IBS	0.021
order	Coriobacteriales	M-IBS	-2.101	0.703	0.195	13	0.025		
order	Coriobacteriales	HC	-2.147	0.7	0.181	15	0.025		
order	Actinomycetales	D-IBS	-3.568	0.56	0.125	20	0.001		
order	Actinomycetales	C-IBS	-3.492	0.385	0.08	23	0.001		
order	Actinomycetales	M-IBS	-3.778	0.395	0.109	13	0.001		
order	Actinomycetales	HC	-4.088	0.477	0.123	15	0.001		0.001
phylum	Actinobacteria	D-IBS	-2.225	0.801	0.179	20	0.019		
phylum	Actinobacteria	C-IBS	-1.63	0.406	0.085	23	0.019	C-IBS	0.019
phylum	Actinobacteria	M-IBS	-2.077	0.679	0.188	13	0.019		
phylum	Actinobacteria	HC	-2.125	0.687	0.177	15	0.019		

D-IBS=Diarrhea predominant IBS; C-IBS=Constipation predominant IBS; M-IBS= IBS with mixed bowel pattern;

HC=Healthy controls

*mean of log10-transformed relative abundances

** P-value by ANOVA analyses