

Additional file 4 - RDP library compare results for sequences and OTUs.

Significantly differing ($p < 0.01$) groups of sequences and OTUs in the IBS-D and HC libraries and their phylogenetic affiliation according to RDP library compare [34]. The more abundant group is indicated in boldface.

RDP classifier taxonomic rank for sequences	IBS-D	HC	p-value
phylum <i>Proteobacteria</i>	155	42	6.00E-14
class <i>Gammaproteobacteria</i>	130	8	6.00E-14
order <i>Enterobacteriales</i>	127	2	4.68E-35
family <i>Enterobacteriaceae</i>	127	2	4.68E-35
genus <i>Enterobacter</i>	116	0	4.09E-35
phylum <i>Actinobacteria</i>	712	850	1.08E-5
class <i>Actinobacteria</i>	712	850	1.08E-5
genus <i>Slackia</i>	3	18	7.20E-4
genus <i>Collinsella</i>	111	228	2.10E-11
genus <i>Eggerthella</i>	233	144	6.80E-6
subclass <i>Actinobacteridae</i>	342	422	7.00E-4
order <i>Actinomycetales</i>	8	24	3.74E-3
order <i>Bifidobacteriales</i>	334	398	4.96E-3
family <i>Bifidobacteriaceae</i>	334	398	4.96E-3
genus <i>Bifidobacterium</i>	334	398	4.96E-3
phylum <i>Bacteroidetes</i>	29	99	2.99E-10
class <i>Bacteroidetes</i>	28	95	5.67E-10
order <i>Bacteroidales</i>	28	95	5.67E-10
family <i>Bacteroidaceae</i>	20	56	2.67E-5
genus <i>Bacteroides</i>	20	56	2.67E-5
phylum <i>Firmicutes</i>	2338	2115	2.60E-6
class <i>Bacilli</i>	111	61	2.00E-4
order <i>Lactobacillales</i>	106	59	3.60E-4
family <i>Streptococcaceae</i>	106	21	6.00E-14
genus <i>Streptococcus</i>	106	20	6.00E-14
family <i>Lactobacillaceae</i>	0	33	8.13E-11
genus <i>Lactobacillus</i>	0	31	3.32E-10
class <i>Erysipelotrichi</i>	124	78	1.68E-3
order <i>Erysipelotrichales</i>	124	78	1.68E-3
family <i>Erysipelotrichaceae</i>	124	78	1.68E-3
genus <i>Coprobacillus</i>	61	29	9.60E-4
class <i>Clostridia</i>	2098	1937	2.36E-3
order <i>Clostridiales</i>	2095	1919	6.00E-4
family Incertae Sedis XIII	0	7	7.18E-3
genus <i>Megasphaera</i>	13	2	4.75E-3
family <i>Lachnospiraceae</i>	1467	1057	6.00E-14
genus <i>Coproccoccus</i>	4	54	9.88E-13
genus <i>Lachnosp. Incertae Sedis</i>	797	452	6.00E-14
family <i>Ruminococcaceae</i>	525	709	5.67E-10
genus <i>Ruminococcus</i>	70	135	2.60E-6
RDP classifier taxonomic rank for OTUs	IBS-D	HC	p-value
phylum <i>Firmicutes</i>	236	291	2.52E-3
class <i>Clostridia</i>	214	257	2.62E-3
order <i>Clostridiales</i>	213	252	1.28E-3
family <i>Lachnospiraceae</i>	130	124	8.00E-5
genus <i>Lachnosp. Incertae Sedis</i>	62	52	2.14E-3