

Supplemental Table 3. Bacterial lineages used to sort IBD from healthy pediatric controls. Results from Random Forests classifier of 97% ID OTUs (species-level phylotypes) that discriminate the fecal microbiota according to health (healthy pediatrics v. IBD).

OTU-ID	Taxonomic assignment	Importance Score		Relative abundance of 97% ID OTU in each group (mean ± SD)			
		Average	Standard Error	Pediatric Healthy		IBD	
681	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.004464	0.001474	11.786	± 11.696	0.063	± 0.246
213	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.003035	0.001149	61.143	± 67.995	0.188	± 0.535
548	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.002674	0.001536	6.571	± 9.549	0.000	± 0.000
714	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.002575	0.001012	4.214	± 4.173	0.156	± 0.448
9	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.002233	0.001691	3.714	± 3.872	0.031	± 0.177
649	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.002184	0.001041	12.000	± 22.668	0.000	± 0.000
1374	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.002033	0.000991	5.500	± 5.229	0.063	± 0.246
492	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001951	0.001021	3.714	± 3.730	0.125	± 0.336
16716	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.001932	0.000794	5.214	± 5.087	0.063	± 0.354
18	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus; s__eutactus	0.001900	0.000875	4.500	± 6.619	0.031	± 0.177
865	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001897	0.000912	3.000	± 3.508	0.063	± 0.246
1843	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Faecalibacterium; s__prausnitzii	0.001808	0.001139	2.786	± 4.098	0.000	± 0.000
778	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.001807	0.001123	8.571	± 13.608	0.125	± 0.421
1900	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001632	0.000995	3.857	± 4.016	0.000	± 0.000
765	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001569	0.000940	3.000	± 2.828	0.125	± 0.554
1991	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.001466	0.001165	5.000	± 9.519	0.000	± 0.000

456	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001463	0.000862	1.286	±	1.437	0.000	±	0.000
508	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.001440	0.000481	15.214	±	18.031	0.344	±	0.827
3485	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001388	0.000777	24.000	±	21.289	1.031	±	2.117
454	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001353	0.000751	4.357	±	6.990	0.000	±	0.000
514	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.001340	0.001076	11.000	±	15.522	0.094	±	0.390
1281	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001309	0.000785	2.429	±	2.593	0.156	±	0.448
1455	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001268	0.000952	1.143	±	1.292	0.000	±	0.000
11710	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001221	0.000674	1.429	±	1.505	0.031	±	0.177
2404	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001204	0.000497	2.857	±	4.055	0.000	±	0.000
2119	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001171	0.001011	2.143	±	2.538	0.000	±	0.000
21101	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001163	0.000796	0.714	±	0.825	0.000	±	0.000
17912	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__[Odoribacteraceae]; g__Odoribacter	0.001151	0.000875	3.000	±	3.508	0.000	±	0.000
1021	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.001150	0.000726	1.643	±	1.823	0.000	±	0.000
332	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001112	0.000702	3.500	±	3.322	0.188	±	0.644
168	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001096	0.001114	2.643	±	2.818	0.063	±	0.246
20573	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001059	0.000871	3.071	±	3.075	0.281	±	0.634
601	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.001050	0.000765	1.429	±	1.651	0.000	±	0.000