

Supplemental Table 4. Bacterial lineages used to sort IBD from healthy controls (pooled pediatric and adult). Results from Random Forests classifier of 97% bacterial OTUs (species-level phylotypes) that discriminate the fecal microbiota according to health (healthy adults and healthy pediatrics v. IBD).

OTU-ID	Taxonomic assignment	Importance Score		Relative abundance of 97% ID OTU in each group (mean ± SD)	
		Average	Standard Error	Healthy	IBD
28387	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae	0.001044	0.000693	0.125 ± 0.519	3.156 ± 8.101
213	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.005851	0.001082	40.078 ± 56.221	0.188 ± 0.535
681	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.005512	0.001542	8.531 ± 11.222	0.063 ± 0.246
548	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.004246	0.001644	4.578 ± 6.034	0.000 ± 0.000
508	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.003942	0.001240	15.609 ± 18.041	0.344 ± 0.827
778	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.003832	0.001153	8.516 ± 12.638	0.125 ± 0.421
1021	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.003256	0.001524	2.359 ± 3.083	0.000 ± 0.000
2426	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.003119	0.000728	5.172 ± 7.313	0.094 ± 0.390
601	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.002847	0.000961	2.953 ± 6.661	0.000 ± 0.000
18	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus; s__eutactus	0.002760	0.000930	8.469 ± 20.604	0.031 ± 0.177
16716	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.002568	0.001305	4.344 ± 5.680	0.063 ± 0.354
10542	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia	0.002491	0.001303	3.281 ± 3.794	0.594 ± 1.434
236	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.002386	0.000928	16.156 ± 20.266	0.813 ± 2.546
1144	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.002285	0.000766	4.969 ± 6.466	0.094 ± 0.296
1374	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.002272	0.000494	4.828 ± 6.199	0.063 ± 0.246
1652	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Lachnospira	0.002193	0.000866	1.406 ± 2.121	0.000 ± 0.000
280	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Lachnospira	0.002067	0.000838	2.766 ± 4.356	0.031 ± 0.177
1843	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Faecalibacterium; s__prausnitzii	0.002061	0.001113	3.047 ± 4.878	0.000 ± 0.000

649	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.002006	0.000570	7.797 ± 13.143	0.000 ± 0.000
3485	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001944	0.000765	20.859 ± 29.770	1.031 ± 2.117
865	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001925	0.000531	2.172 ± 2.640	0.063 ± 0.246
2934	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.001871	0.000578	3.844 ± 4.748	0.219 ± 0.659
492	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001834	0.000586	4.422 ± 5.354	0.125 ± 0.336
1900	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001794	0.000953	2.750 ± 4.239	0.000 ± 0.000
514	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.001754	0.000494	7.953 ± 11.070	0.094 ± 0.390
1833	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001611	0.000485	1.656 ± 2.169	0.000 ± 0.000
17912	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__[Odoribacteraceae]; g__Odoribacter	0.001574	0.000369	2.813 ± 3.389	0.000 ± 0.000
866	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__uniformis	0.001573	0.000668	13.031 ± 23.126	0.438 ± 0.840
5467	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Faecalibacterium; s__prausnitzii	0.001539	0.000805	7.578 ± 11.499	0.469 ± 0.950
2404	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001538	0.000557	1.469 ± 2.417	0.000 ± 0.000
2003	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.001478	0.001008	2.922 ± 3.248	0.125 ± 0.421
4387	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__uniformis	0.001473	0.000682	4.859 ± 8.207	0.000 ± 0.000
1991	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides	0.001458	0.000676	3.531 ± 6.404	0.000 ± 0.000
1123	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Ruminococcus; s__gnavus	0.001456	0.001046	14.172 ± 25.142	2.281 ± 5.413
4799	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.001419	0.000622	1.500 ± 2.175	0.000 ± 0.000
858	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001382	0.000701	1.188 ± 1.943	0.000 ± 0.000
765	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001375	0.000581	3.313 ± 4.279	0.125 ± 0.554
8632	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.001240	0.000789	1.719 ± 3.150	0.094 ± 0.530
304	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001229	0.000756	3.078 ± 5.168	0.188 ± 0.644
1535	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__uniformis	0.001223	0.000720	5.766 ± 9.343	0.125 ± 0.421
6958	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.001176	0.000554	0.750 ± 1.024	0.000 ± 0.000

714	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001129	0.000577	2.438 ± 3.075	0.156 ± 0.448
1455	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	0.001114	0.000505	1.016 ± 1.496	0.000 ± 0.000
1100	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus	0.001109	0.000695	0.969 ± 1.877	0.000 ± 0.000
146	p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	0.001097	0.000576	84.453 ± 92.216	13.906 ± 18.671
1262	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	0.001096	0.000588	1.547 ± 2.160	0.094 ± 0.390
4057	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.001037	0.000558	0.875 ± 1.496	0.031 ± 0.177
3278	p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Parabacteroides; s__distasonis	0.001036	0.000415	0.672 ± 1.113	0.000 ± 0.000