

**Supplementary Table 5** List of 34 OTUs that varied in abundance between Crohn's patients and healthy matched controls

#OTU ID	S_ab score	sequence name	phylum	class	order	family	genus	P value	direction of change
0	0.671	Prevotella oralis (T); ATCC 33269; AY323522	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	P<0.05	CD<HC
114	1.000	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.1	CD>HC
154	0.980	Bacteroides vulgatus; DJF_B081; EU728705	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.1	CD>HC
197	0.992	Bacteroides vulgatus; DJF_B081; EU728705	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
198	0.977	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
215	0.981	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.1	CD>HC
304	0.988	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
311	0.968	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
312	1.000	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
438	0.926	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
599	0.993	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.05	CD>HC
621	0.977	Ruminococcus sp. Eg2; FJ611794	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.1	CD<HC
680	0.682	Ruminococcaceae bacterium HZ254R; JN656278	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium III	P<0.05	CD>HC
760	0.971	butyrate-producing bacterium L2-21; AJ270477	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.1	CD<HC
783	0.734	Clostridiales bacterium CIEAF 021; AB702937	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter	P<0.1	CD<HC
784	0.672	unidentified eubacterium clone BSV28; AJ229190	unclassified_Bacteria					P<0.05	CD<HC
787	1.000	butyrate-producing bacterium L2-21; AJ270477	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.1	CD<HC
937	1.000	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.05	CD>HC
1013	0.924	Roseburia faecis (T); M72/1; AY305310	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	P<0.05	CD<HC
1039	1.000	butyrate-producing bacterium L2-21; AJ270477	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.1	CD<HC
1102	0.886	bacterium NLAE-zl-H75; JX006319	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium XIVa	P<0.05	CD<HC
1114	1.000	Bacteroides merdae; 1-18; AY169416	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides	P<0.05	CD<HC
1248	0.714	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.1	CD<HC
1282	0.948	Roseburia faecis (T); M72/1; AY305310	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	P<0.1	CD<HC
1534	0.991	Bacteroides vulgatus; DJF_B081; EU728705	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.1	CD>HC
1623	0.879	Faecalibacterium prausnitzii; A2-165; AJ270469	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	P<0.1	CD<HC
1821	0.977	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.05	CD>HC
1869	0.991	butyrate-producing bacterium L2-21; AJ270477	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.1	CD<HC
1927	0.985	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.1	CD>HC
2006	0.995	Ruminococcus gnavus (T); ATCC 29149; X94967	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_incertae_sedis	P<0.05	CD>HC
2345	0.984	Ruminococcus obeum; 1-33; AY169419	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.1	CD>HC

2670	0.987	Bacteroides vulgatus ATCC 8482; CP000139	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	P<0.05	CD>HC
2997	1.000	butyrate-producing bacterium SR1/1; AY305321	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	P<0.1	CD>HC
3928	0.947	Gemmiger formicilis (T); ATCC 27749; X2-56; GU562446	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Gemmiger	P<0.05	CD<HC