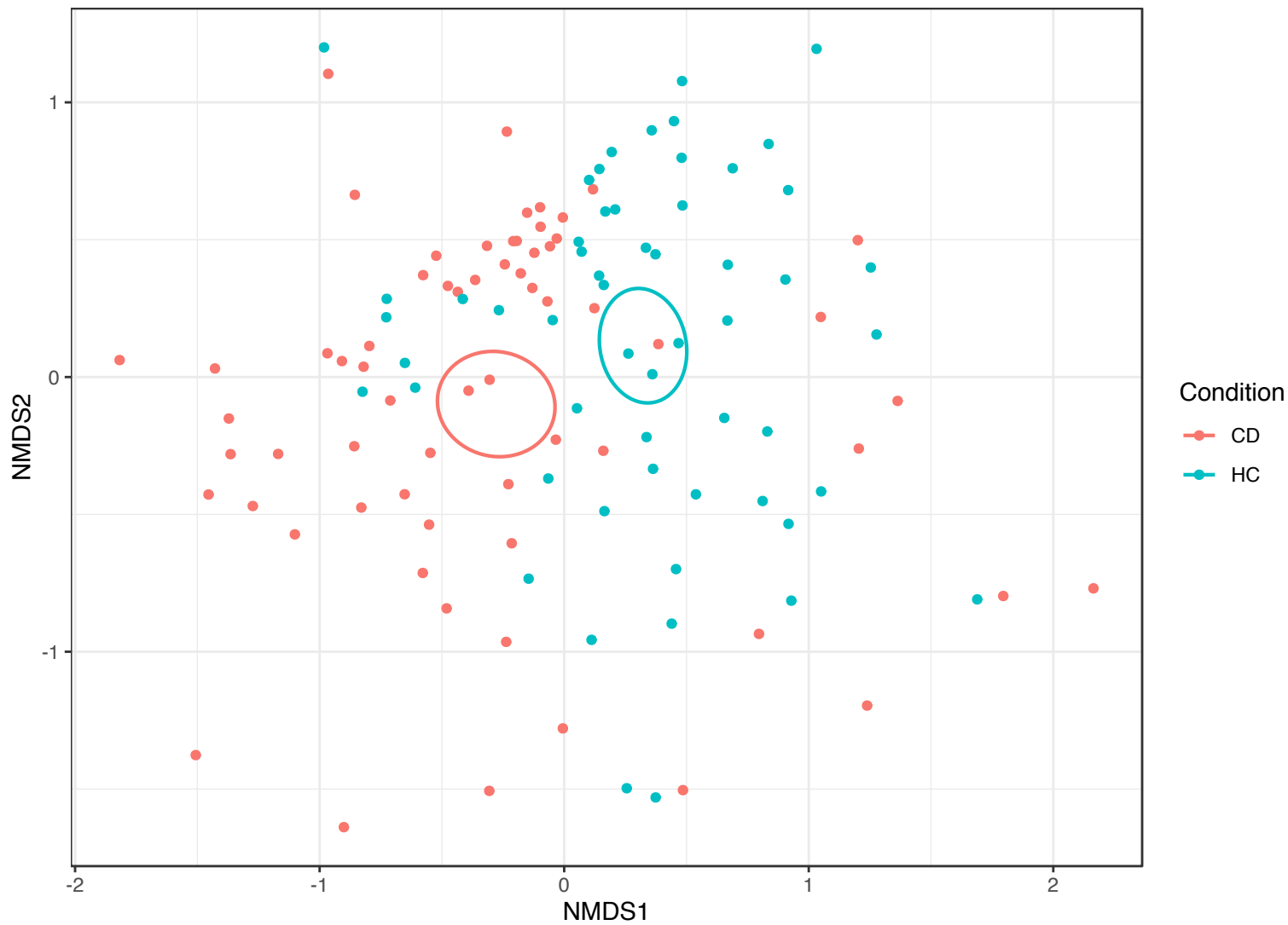
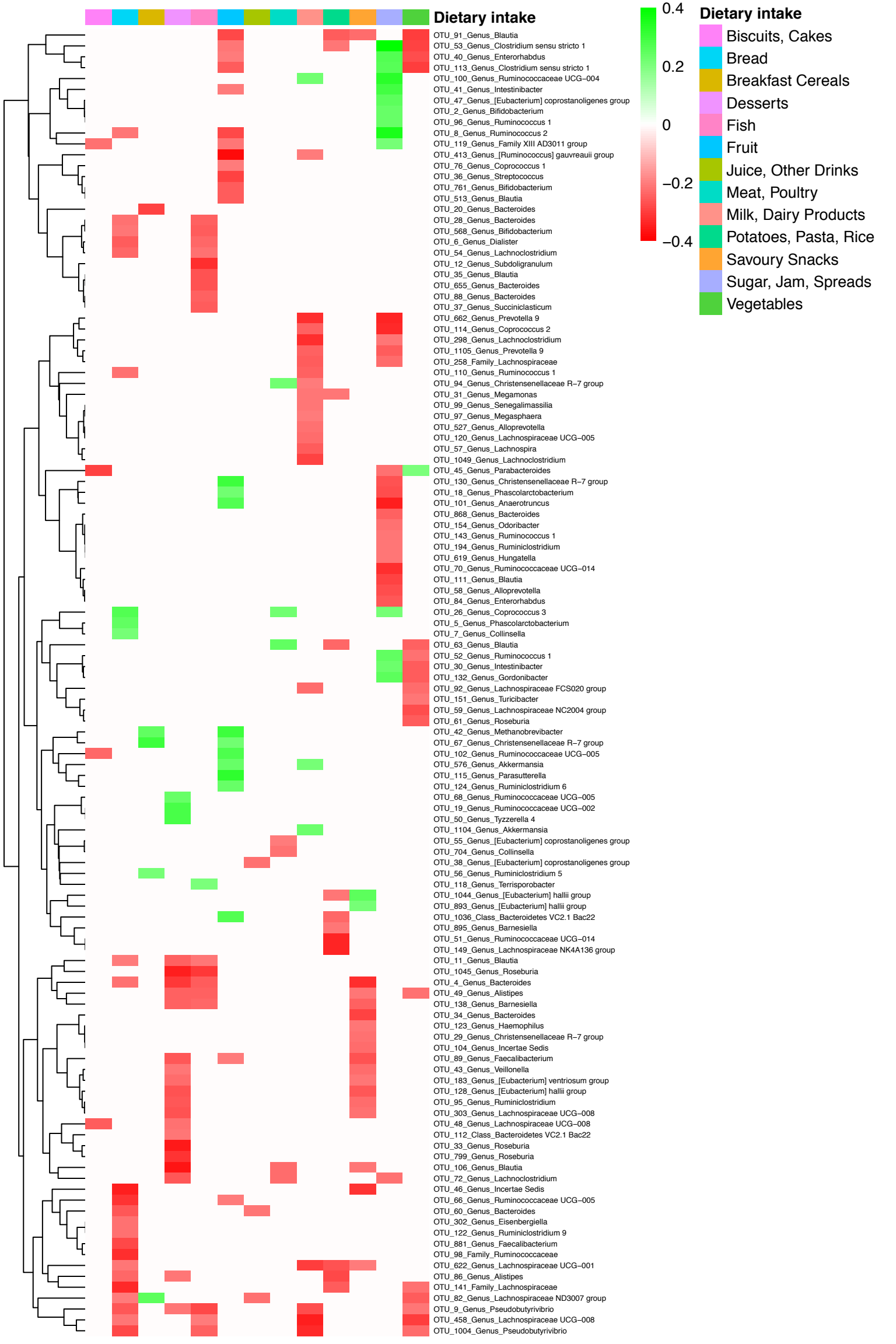


# Bray-Curtis NMDS - Disease Specific OTUs







Log2 fold change

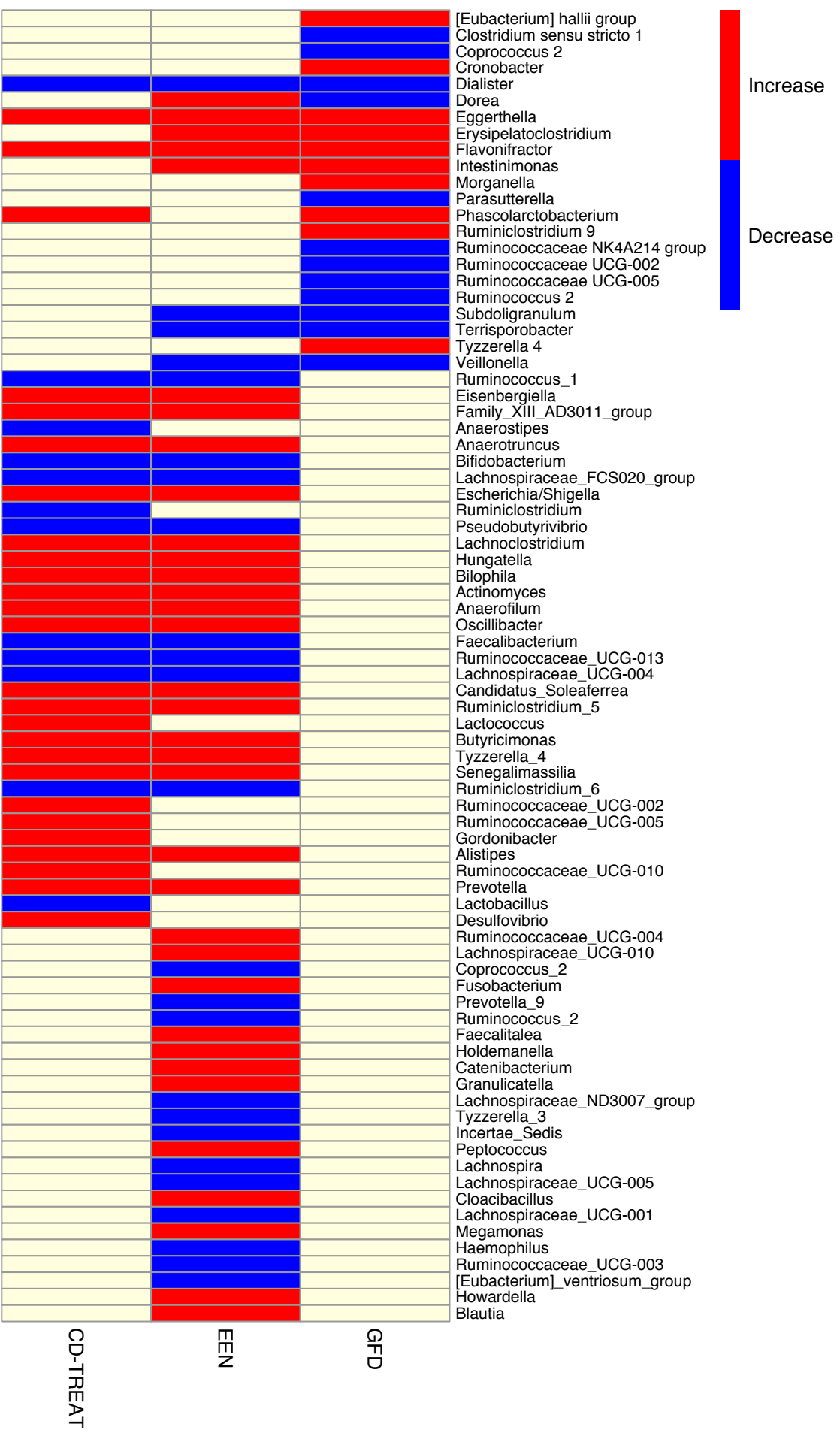
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0.0  
-2.5  
-5.0

OTU\_99 Senegalimassilia  
OTU\_239 Clostridiales vadinBB60 group  
OTU\_192 Defluvitaleaceae UCG-011  
OTU\_218 Collinsella  
OTU\_2 Bifidobacterium  
OTU\_257 Oscillibacter  
OTU\_253 [Eubacterium] ventriosum group  
OTU\_142 Ruminococcus 1  
OTU\_355 Lachnospostridium  
OTU\_33 Roseburia  
OTU\_106 Blautia  
OTU\_361 Prevotella  
OTU\_326 [Eubacterium] ventriosum group  
OTU\_57 Lachnospira  
OTU\_100 Ruminococcaceae UCG-004  
OTU\_39 Dorea formicigenens ATCC 27755  
OTU\_761 Bifidobacterium pseudocalenulatum  
OTU\_65 Bacteroides  
OTU\_78 Ruminiclostridium 5  
OTU\_9 Ruminococcaceae  
OTU\_167 Lachnospiraceae  
OTU\_274 Ruminiclostridium 5  
OTU\_249 Blautia  
OTU\_34 Bacteroides  
OTU\_199 Ruminococcaceae UCG-010  
OTU\_303 Lachnospiraceae UCG-008  
OTU\_38 [Eubacterium] coprostanoligenes group  
OTU\_826 Lachnospostridium  
OTU\_910 [Eubacterium] hallii group  
OTU\_98 Lachnospiraceae  
OTU\_752 Subdoligranulum  
OTU\_210 Family XIII AD3011 group  
OTU\_194 Ruminiclostridium  
OTU\_116 Ruminococcaceae UCG-014  
OTU\_108 Coriobacteriaceae  
OTU\_872 Lachnospostridium  
OTU\_26 Coprococcus 3  
OTU\_622 Lachnospiraceae UCG-001  
OTU\_172 Ruminococcaceae UCG-003  
OTU\_92 Lachnospiraceae FCS020 group  
OTU\_21 Coprococcus 2  
OTU\_8 Ruminococcus 2  
OTU\_704 Collinsella  
OTU\_4 Bacteroides  
OTU\_1036 Bacteroidetes  
OTU\_267 Ruminiclostridium 9  
OTU\_302 Eisenbergiella  
OTU\_130 Christensenellaceae R-7 group  
OTU\_86 Alisipes  
OTU\_458 Lachnospiraceae UCG-008  
OTU\_102 Ruminococcaceae UCG-005  
OTU\_13 Araeosipites  
OTU\_655 Bacteroides  
OTU\_54 Odoribacter  
OTU\_50 Tyzzerella 4  
OTU\_163 Ruminiclostridium 5  
OTU\_185 Dorea  
OTU\_45 Parabacteroides  
OTU\_128 [Eubacterium] hallii group  
OTU\_89 Faecalibacterium  
OTU\_149 Lachnospiraceae NK4A136 group  
OTU\_1054 Alisipes  
OTU\_48 Lachnospiraceae UCG-008  
OTU\_227 Anaerotruncus  
OTU\_90 Ruminococcaceae UCG-002  
OTU\_828 Coriobacteriaceae  
OTU\_60 Bacteroides  
OTU\_988 Lachnospostridium  
OTU\_123 Haemophilus  
OTU\_1059 [Eubacterium] coprostanoligenes group  
OTU\_136 [Eubacterium] coprostanoligenes group  
OTU\_122 Ruminiclostridium 9  
OTU\_37 Veillonellaceae bacterium canine oral taxon 211  
OTU\_138 Bacteroides  
OTU\_188 Bacteroides  
OTU\_88 Bacteroides  
OTU\_120 Lachnospiraceae UCG-005  
OTU\_64 Alisipes  
OTU\_576 Akkermansia  
OTU\_148 Ruminococcaceae UCG-013  
OTU\_49 Alisipes  
OTU\_115 Parasutterella  
OTU\_125 Parabacteroides  
OTU\_135 Holdemanella  
OTU\_18 Phascolarctobacterium  
OTU\_47 [Eubacterium] coprostanoligenes group  
OTU\_183 [Eubacterium] ventriosum group  
OTU\_28 Bacteroides  
OTU\_1002 Lachnospira  
OTU\_868 Bacteroides

OTU

Significant

- No
- TCD < HC
- TCD > UCD
- TCD > UCD and HC



**Supplementary Table 1:** PERMANOVA analysis using Bray-Curtis and unweighted UniFrac distance metrics at OTU and genus level

		Bray-Curtis	Unweighted UniFrac
<b>OTU level</b>			
Overall		p=0.025, R <sup>2</sup> =2.76%	p=0.027, R <sup>2</sup> =2.49%
<i>Within group comparison</i>			
UCD (20)	HC (57)	p=0.506, R <sup>2</sup> =1.21%	p=0.125, R <sup>2</sup> =1.77%
TCD (45)	HC (57)	p=0.017, R <sup>2</sup> =2.32%	p=0.045, R <sup>2</sup> =1.57%
	UCD (20)	p=0.106, R <sup>2</sup> =2.35%	p=0.056, R <sup>2</sup> =2.46%
UCD (13)	6mos GFD (13)	p=0.951, R <sup>2</sup> =1.53%	p=0.377, R <sup>2</sup> =2.54%
	12mos GFD (13)	p=0.762, R <sup>2</sup> =2.42%	p=0.691, R <sup>2</sup> =2.44%
Siblings (19)	TCD (18)	p=0.384, R <sup>2</sup> =2.89%	p=0.336, R <sup>2</sup> =2.96%
	HC (57)	p=0.745, R <sup>2</sup> =0.97%	p=0.183, R <sup>2</sup> =1.67%
<b>Genus level</b>			
Overall		p=0.026, R <sup>2</sup> = 3.0%	n/a
<i>Within group comparison</i>			
UCD (20)	HC (57)	p=0.515, R <sup>2</sup> = 1.15%	n/a
TCD (45)	HC (57)	p=0.013, R <sup>2</sup> = 2.56%	n/a
	UCD (20)	p=0.069, R <sup>2</sup> = 2.77%	n/a
UCD (13)	6mos GFD (13)	p=0.998, R <sup>2</sup> =1.28%	n/a
	12mos GFD (13)	p=0.904, R <sup>2</sup> =2.21%	n/a
Siblings (19)	TCD (18)	p=0.296, R <sup>2</sup> =3.21%	n/a
	HC (57)	p=0.696, R <sup>2</sup> =0.94%	n/a

OTU: operational taxonomic unit; n/a: not applicable

**Supplementary Table 2:** Bioenv selected OTU that explain part [(a) 92.3% in UCD, TCD and HC, (b) 92% in UCD and TCD, (c) 91.4% in HC and TCD children] of the variance in microbiota structure described by the full OTU dataset:

a)

"OTU_6: Bacteria; Firmicutes; Negativicutes; Selenomonadales; Veillonellaceae; Dialister;"
"OTU_4: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_2: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium;"
"OTU_881: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium;"
"OTU_14: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Subdoligranulum;"
"OTU_33: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia;"
"OTU_129: Bacteria; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella;"
"OTU_568: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium bifidum NCIMB 41171"
"OTU_72: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium;"
"OTU_655: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_35: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia;"
"OTU_20: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_458: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospiraceae UCG-008;"

b)

"OTU_6*: Bacteria; Firmicutes; Negativicutes; Selenomonadales; Veillonellaceae; Dialister;"
"OTU_4*: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_2*: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium;"
"OTU_881: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium;"
"OTU_60*: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_14*: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Subdoligranulum;"
"OTU_33*: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia;"
"OTU_129*: Bacteria; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella;"
"OTU_568*: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium bifidum NCIMB 41171"
"OTU_72*: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium;"
"OTU_35: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia;"
"OTU_20: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
"OTU_10: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium;"

"OTU_57: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira;"
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c)

"OTU_6*: Bacteria; Firmicutes; Negativicutes; Selenomonadales; Veillonellaceae; Dialister;"
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"OTU_4*: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
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"OTU_2*: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium;"
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"OTU_60*: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
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"OTU_14*: Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Subdoligranulum;"
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"OTU_33*: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia;"
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"OTU_129*: Bacteria; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella;"
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"OTU_568*: Bacteria; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium bifidum NCIMB 41171"
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"OTU_72*: Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium;"
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"OTU_655: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides;"
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"OTU_86: Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae; Alistipes;"
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"OTU_41: Bacteria; Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae; Intestinibacter;"
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\*Asterisk indicates Bioenv-selected OTUs that partially explain the variance in community structure of UCD vs TCD as well as HC vs TCD; OTU: operational taxonomic unit



**Supplementary Table 3:** OTUs with significantly different relative abundance in faecal samples of UCD, TCD and HC

	Group comparison	BaseMean	log2Fold Change	<i>p</i> -value	<i>p</i> -value (adjusted)
OTU_60 <i>Bacteroides</i>	HC Vs UCD	7.06	-0.23	6.3E-01	7.83E-01
	HC Vs TCD	122.96	5.17	3.03E-23	2.17E-20
	UCD Vs TCD	80.26	4.15	1.43E-08	8.46E-07
OTU_143 <i>Ruminococcus 1</i>	HC Vs UCD	25.1	-2.08	8.85E-04	1.16E-02
	HC Vs TCD	18.11	-4.37	8.31E-23	2.98E-20
	UCD Vs TCD	3.30	-2.28	5.05E-08	2.44E-06
OTU_31 <i>Megamonas</i>	HC Vs UCD	39.6	-2.09	4.56E-03	3.55E-02
	HC Vs TCD	28.46	-4.72	3.43E-21	8.21E-19
	UCD Vs TCD	4.94	-2.64	3.99E-08	2.12E-06
OTU_244 <i>Ruminococcus 1</i>	HC Vs UCD	24.72	-1.37	3.2E-02	1.06E-01
	HC Vs TCD	17.06	-4.26	5.95E-21	1.07E-18
	UCD Vs TCD	2.15	-1.19	1.28E-03	9.45E-03
OTU_78 <i>Ruminiclostridium 5</i>	HC Vs UCD	2.71	-0.69	9.89E-02	2.34E-01
	HC Vs TCD	30.16	4.40	1.54E-20	2.21E-18
	UCD Vs TCD	44.97	5.09	1.97E-12	5.22E-10
OTU_42 <i>Methanobrevibacter</i>	HC Vs UCD	38.78	-3.84	1.33E-07	1.47E-05
	HC Vs TCD	29.62	-4.36	1.88E-17	2.24E-15
	UCD Vs TCD	2.84	-0.51	2.78E-01	4.25E-01
OTU_114 <i>Caprococcus 2</i>	HC Vs UCD	32.92	-0.25	7.13E-01	8.41E-01
	HC Vs TCD	38.73	-4.27	2.92E-17	2.99E-15
	UCD Vs TCD	4.24	-0.79	1.22E-01	2.32E-01
OTU_70 <i>Ruminococcaceae</i> <i>UCG-014</i>	HC Vs UCD	11.29	-3.43	1.28E-07	1.47E-05
	HC Vs TCD	8.89	-3.36	5.94E-14	5.32E-12
	UCD Vs TCD	1.42	0.07	8.52E-01	n/a
OTU_120 <i>Lachnospiraceae</i> <i>UCG-005</i>	HC Vs UCD	4.48	0.63	1.34E-01	2.97E-01
	HC Vs TCD	69.03	3.59	7.21E-13	5.74E-11

	UCD Vs TCD	99.05	4.43	3.74E-11	3.43E-09
OTU_135 <i>Holdemanella</i>	HC Vs UCD	21.19	-1.04	1.10E-01	2.55E-01
	HC Vs TCD	14.82	-3.20	4.31E-12	3.09E-10
	UCD Vs TCD	5.52	-2.20	3.0E-06	7.23E-05
OTU_197 <i>Ruminococcaceae</i>	HC Vs UCD	8.55	1.18	1.27E-02	5.63E-02
<i>UCG – 005</i>	HC Vs TCD	22.96	2.76	1.12E-11	7.29E-10
	UCD Vs TCD	23.17	0.85	1.42E-01	2.56E-01
OTU_908 <i>Anaerostipes</i>	HC Vs UCD	12.70	-0.83	1.60E-01	3.32E-01
	HC Vs TCD	8.98	-2.66	4.46E-10	2.66E-08
	UCD Vs TCD	4.04	-1.83	2.57E-04	2.73E-03
OTU_979 <i>Bifidobacterium</i>	HC Vs UCD	45.70	-0.18	7.36E-01	8.59E-01
<i>Pseudocatenulatum</i>	HC Vs TCD	31.04	-2.13	5.39E-09	2.74E-07
	UCD Vs TCD	19.91	-1.97	3.0E-05	5.69E-04
OTU_53 <i>Clostridium</i>	HC Vs UCD	200.98	-2.58	1.1E-05	4.04E-04
<i>sensu stricto 1</i>	HC Vs TCD	239.45	-2.77	5.72E-09	2.74E-07
	UCD Vs TCD	52.52	0.39	5.09E-01	6.45E-01
OTU_186	HC Vs UCD	1.35	-0.11	7.66E-01	n/a
<i>Gastranaerophilales</i>	HC Vs TCD	3.42	2.11	5.74E-09	2.74E-07
	UCD Vs TCD	4.53	2.22	7.91E-05	1.14E-03
OTU_84 <i>Enterorhabdus</i>	HC Vs UCD	7.93	-2.34	1.20E-04	2.54E-03
	HC Vs TCD	6.52	-2.32	3.29E-08	1.48E-06
	UCD Vs TCD	1.99	0.02	9.53E-01	9.71E-01
OTU_174 <i>Catenibacterium</i>	HC Vs UCD	1.56	0.70	2.74E-02	n/a
	HC Vs TCD	3.19	2.04	3.64E-08	1.54E-06
	UCD Vs TCD	4.47	1.32	1.81E-02	7.2E-02
OTU_336 <i>Holdemanella</i>	HC Vs UCD	7.99	-2.38	6.68E-05	1.76E-03
	HC Vs TCD	6.59	-2.30	6.27E-08	2.5E-06
	UCD Vs TCD	2.02	0.06	8.75E-01	9.27E-01
OTU_776 <i>Bifidobacterium</i>	HC Vs UCD	21.81	-2.25	5.29E-04	8.59E-03
<i>Animalis</i>	HC Vs TCD	17.47	-2.50	9.08E-08	3.26E-06
	UCD Vs TCD	4.47	1.32	1.81E-02	7.2E-02

OTU_88 <i>Bacteroides</i>	HC Vs UCD	281.31	0.02	9.79E-01	9.82E-01
	HC Vs TCD	863.13	2.49	1.02E-07	3.48E-06
	UCD Vs TCD	1,187.7	2.48	2.66E-04	2.77E-03
OTU_1002 <i>Lachnospira</i>	HC Vs UCD	8.97	-1.75	8.59E-04	1.16E-02
	HC Vs TCD	33.92	2.49	1.08E-07	3.51E-06
	UCD Vs TCD	45.22	3.23	1.54E-06	3.89E-05
OTU_28 <i>Bacteroides</i>	HC Vs UCD	151.07	-1.06	6.32E-02	1.7E-01
	HC Vs TCD	728.21	2.57	2.80E-07	8.72E-06
	UCD Vs TCD	552.60	3.13	1.08E-06	2.85E-05
OTU_1049 <i>Lachnoclostridium</i>	HC Vs UCD	53.35	0.60	3.14E-01	5.04E-01
	HC Vs TCD	128.17	2.28	8.26E-07	2.28E-05
	UCD Vs TCD	180.41	1.68	1.09E-02	5.23E-02
OTU_125 <i>Parabacteroides</i>	HC Vs UCD	34.72	-1.85	9.65E-04	1.22E-02
	HC Vs TCD	116.40	2.28	9.30E-07	2.47E-05
	UCD Vs TCD	148.10	4.02	3.88E-11	3.43E-09
OTU_278 <i>Akkermansia</i>	HC Vs UCD	4.46	0.34	4.50E-01	6.47E-01
	HC Vs TCD	15.59	2.17	1.13E-06	2.88E-05
	UCD Vs TCD	20.63	2.37	1.87E-04	2.2E-03
OTU_537 <i>Dialister</i>	HC Vs UCD	18.0	-2.46	1.10E-04	2.43E-03
	HC Vs TCD	15.10	-2.20	1.37E-06	3.40E-05
	UCD Vs TCD	4.68	0.23	6.11E-01	7.29E-01
OTU_62 <i>Ruminococcaceae</i> <i>UCG-014</i>	HC Vs UCD	23.89	-3.94	1.84E-08	1.01E-05
	HC Vs TCD	11.97	-2.27	1.69E-06	3.90E-05
	UCD Vs TCD	3.30	0.88	7.0E-02	1.79E-01
OTU_752 <i>Subdoligranulum</i>	HC Vs UCD	43.81	-1.87	1.49E-03	1.68E-02
	HC Vs TCD	164.0	2.47	2.72E-06	5.57E-05
	UCD Vs TCD	122.66	3.48	5.24E-07	1.74E-05
OTU_99 <i>Senegalimassilia</i>	HC Vs UCD	73.24	-3.88	1.05E-07	1.47E-05
	HC Vs TCD	61.70	-2.47	9.10E-06	1.52E-04
	UCD Vs TCD	14.06	1.48	2.37E-02	8.5E-02
OTU_112 <i>Bacteroidetes</i>	HC Vs UCD	22.60	-3.07	1.16E-07	1.47E-05

	HC Vs TCD	31.79	-1.19	1.0E-02	4.2E-02
	UCD Vs TCD	13.92	2.42	1.43E-05	3.15E-04
OTU_1054 <i>Alistipes</i>	HC Vs UCD	17.29	-2.95	7.37E-07	6.78E-05
	HC Vs TCD	30.12	0.81	8.83E-02	2.18E-01
	UCD Vs TCD	28.41	3.74	1.82E-09	1.38E-07
OTU_146 <i>Slackia</i>	HC Vs UCD	7.95	-3.09	1.02E-06	8.05E-05
	HC Vs TCD	7.16	-1.73	1.27E-04	1.26E-03
	UCD Vs TCD	2.57	1.36	9.44E-03	4.91E-02
OTU_226 [ <i>Eubacterium</i> ] <i>oxidroducens</i> group	HC Vs UCD	5.92	-2.79	2.55E-06	1.76E-04
	HC Vs TCD	6.68	-0.48	2.6E-01	4.48E-01
	UCD Vs TCD	4.11	2.37	4.87E-05	8.33E-04
OTU_45 <i>Parabacteroides</i>	HC Vs UCD	56.41	-3.08	3.60E-06	2.21E-04
	HC Vs TCD	73.21	0.84	1.04E-01	2.47E-01
	UCD Vs TCD	69.9	3.44	3.06E-07	1.25E-05
OTU_895 <i>Barnesiella</i>	HC Vs UCD	58.0	-3.11	5.04E-06	2.77E-04
	HC Vs TCD	54.13	-1.48	5.16E-03	2.4E-02
	UCD Vs TCD	21.56	1.65	1.02E-02	5.03E-02
OTU_101 <i>Anaerotruncus</i>	HC Vs UCD	15.61	-3.11	5.53E-06	2.77E-04
	HC Vs TCD	17.95	-0.46	3.83E-01	5.67E-01
	UCD Vs TCD	11.03	2.64	4.55E-05	8.05E-04
OTU_572 Family XVIII <i>AD3011</i> group	HC Vs UCD	9.54	-2.43	7.14E-06	3.16E-04
	HC Vs TCD	11.51	-0.19	6.55E-01	7.82E-01
	UCD Vs TCD	7.94	2.20	6.21E-05	9.70E-04
OTU_230 <i>Bacteroides</i>	HC Vs UCD	6.20	-2.79	7.43E-06	3.16E-04
	HC Vs TCD	6.79	-0.60	1.79E-01	3.62E-01
	UCD Vs TCD	4.02	2.18	1.13E-04	1.58E-03
OTU_65 <i>Bacteroides</i>	HC Vs UCD	9.79	-2.44	8.18E-06	3.23E-04
	HC Vs TCD	25.82	1.73	7.37E-05	1.28E-03
	UCD Vs TCD	29.9	4.19	1.17E-12	5.22E-10
OTU_49 <i>Alistipes</i>	HC Vs UCD	56.57	-2.40	1.86E-05	6.42E-04
	HC Vs TCD	174.05	1.50	3.31E-03	1.72E-02

	UCD Vs TCD	192.53	4.41	5.95E-12	1.05E-09
OTU_109 <i>Ruminococcus 2</i>	HC Vs UCD	6.0	-2.54	2.39E-05	7.75E-04
	HC Vs TCD	5.40	-1.57	2.12E-04	1.88E-03
	UCD Vs TCD	2.22	0.96	3.83E-02	1.17E-01
OTU_51 <i>Ruminococcaceae</i>	HC Vs UCD	13.48	-2.49	4.88E-05	1.50E-03
<i>UCG-014</i>	HC Vs TCD	16.15	-0.22	6.38E-01	7.66E-01
	UCD Vs TCD	11.22	2.25	1.20E-04	1.60E-03
OTU_111 <i>Blautia</i>	HC Vs UCD	23.54	-2.33	6.14E-05	1.7E-03
	HC Vs TCD	28.78	-0.13	7.87E-01	8.72E-01
	UCD Vs TCD	20.82	2.19	4.69E-04	4.61E-03
OTU_868 <i>Bacteroides</i>	HC Vs UCD	136.18	-2.64	7.33E-05	1.76E-03
	HC Vs TCD	293.71	1.33	1.42E-02	5.4E-02
	UCD Vs TCD	310.64	4.83	8.47E-12	1.12E-09
OTU_923 <i>Mavinbryantia</i>	HC Vs UCD	10.23	-2.00	7.03E-05	1.76E-03
	HC Vs TCD	13.06	0.07	8.63E-01	9.2E-01
	UCD Vs TCD	10.29	2.06	2.49E-04	2.7E-03
OTU_190 <i>Alistipes</i>	HC Vs UCD	6.26	-2.16	1.09E-04	2.43E-03
	HC Vs TCD	11.02	0.07	8.74E-01	9.26E-01
	UCD Vs TCD	13.20	3.35	5.57E-08	2.46E-06
OTU_168 <i>Alistipes</i>	HC Vs UCD	4.43	-2.01	4.11E-04	7.31E-03
	HC Vs TCD	3.92	-1.54	8.38E-05	9.40E-04
	UCD Vs TCD	1.75	0.45	2.5E-02	3.9E-01
OTU_3 <i>Akkermansia</i>	HC Vs UCD	2,041.4	-2.17	1.41E-03	1.63E-02
	HC Vs TCD	2,863.9	0.33	5.55E-01	7.09E-01
	UCD Vs TCD	2,466.0	1.45	5.12E-02	1.43E-01
OTU_1 <i>Prevotella 9</i>	HC Vs UCD	6,760.4	-2.68	3.77E-03	3.15E-02
	HC Vs TCD	5,953.8	-1.79	1.22E-02	4.84E-03
	UCD Vs TCD	193.2	0.85	2.36E-01	3.75E-01
OTU_302 <i>Eisenbergiella</i>	HC Vs UCD	26.32	-1.38	1.01E-02	4.74E-02
	HC Vs TCD	55.97	1.44	7.21E-04	5.23E-03
	UCD Vs TCD	97.89	3.49	2.47E-09	1.64E-07

OTU_259 <i>Erysipelatoclostridium</i>	HC Vs UCD	4.86	-1.71	6.88E-04	1.07E-02
	HC Vs TCD	8.45	0.95	1.27E-02	5.0E-02
	UCD Vs TCD	8.6	2.61	4.31E-07	1.64E-05
OTU_448 <i>Ruminiclostridium 5</i>	HC Vs UCD	9.97	-1.66	5.36E-05	1.56E-03
	HC Vs TCD	15.06	0.61	5.6E-02	1.57E-01
	UCD Vs TCD	13.72	2.20	4.8E-07	1.7E-05
OTU_270 <i>Butyricimonas</i>	HC Vs UCD	5.25	-1.88	4.56E-04	7.63E-03
	HC Vs TCD	10.0	1.13	8.16E-03	3.52E-02
	UCD Vs TCD	10.47	3.00	7.49E-07	2.34E-05
OTU_248 <i>Clostridium sensu stricto 1</i>	HC Vs UCD	2.07	-0.77	7.32E-02	1.87E-01
	HC Vs TCD	4.37	1.57	2.49E-05	3.5E-04
	UCD Vs TCD	7.89	2.96	9.12E-07	2.69E-05
OTU_317 <i>Lachnospiraceae NK4A136 group</i>	HC Vs UCD	3.81	-1.83	1.52E-04	2.89E-03
	HC Vs TCD	7.29	1.56	4.05E-03	1.99E-02
	UCD Vs TCD	7.67	2.97	9.99E-07	2.79E-05
OTU_34 <i>Bacteroides</i>	HC Vs UCD	243.37	-1.75	4.11E-03	3.29E-02
	HC Vs TCD	425.59	0.96	3.8E-02	1.19E-01
	UCD Vs TCD	431.67	2.72	6.24E-06	1.44E-04
OTU_235 <i>Lachnospiraceae</i>	HC Vs UCD	6.69	-1.52	1.35E-03	1.60E-02
	HC Vs TCD	10.74	0.79	3.9E-02	1.21E-01
	UCD Vs TCD	10.62	2.31	1.95E-05	4.15E-04
OTU_1036 <i>Bacteroidetes</i>	HC Vs UCD	59.31	-1.43	3.60E-02	1.14E-01
	HC Vs TCD	76.45	0.23	6.5E-01	7.8E-01
	UCD Vs TCD	61.94	2.57	2.07E-05	4.22E-04
OTU_73 <i>Bacteroides</i>	HC Vs UCD	6.31	-1.26	8.05E-03	4.38E-02
	HC Vs TCD	11.31	1.08	7.24E-03	3.24E-02
	UCD Vs TCD	12.07	2.32	3.22E-05	5.89E-04
OTU_154 <i>Odoribacter</i>	HC Vs UCD	30.05	-0.95	1.06E-01	2.48E-01
	HC Vs TCD	61.85	1.48	1.13E-03	7.18E-03
	UCD Vs TCD	72.08	2.43	5.23E-05	8.68E-04
OTU_139 <i>Bilophila</i>	HC Vs UCD	22.05	-0.67	2.20E-01	3.99E-01

	HC Vs TCD	49.71	0.44	9.57E-05	1.01E-03
	UCD Vs TCD	59.99	2.37	5.65E-05	9.09E-04
OTU_77 <i>Lachnospirillum</i>	HC Vs UCD	47.57	-0.75	1.61E-01	3.32E-01
	HC Vs TCD	120.45	1.11	1.82E-02	6.59E-02
	UCD Vs TCD	128.1	2.40	7.94E-05	1.14E-03
OTU_343 <i>Christensenellaceae</i>	HC Vs UCD	1.84	-0.42	2.68E-01	4.55E-01
	HC Vs TCD	4.18	1.82	4.55E-07	1.36E-05
	UCD Vs TCD	4.98	2.14	7.97E-05	1.14E-03
OTU_355 <i>Lachnospirillum</i>	HC Vs UCD	24.25	-0.88	9.18E-02	2.20E-01
	HC Vs TCD	43.33	1.19	3.82E-03	1.9E-02
	UCD Vs TCD	46.44	2.01	1.19E-04	1.60E-03
OTU_98 <i>Ruminococcaceae</i>	HC Vs UCD	58.58	-0.55	3.0E-01	4.9E-01
	HC Vs TCD	118.5	1.54	1.46E-04	1.36E-03
	UCD Vs TCD	139.21	2.06	1.39E-04	1.80E-03
OTU_282 <i>Christensenellaceae</i>	HC Vs UCD	4.57	-0.49	3.34E-01	5.24E-01
	HC Vs TCD	11.23	1.37	1.8E-03	1.1E-02
	UCD Vs TCD	12.46	2.21	1.59E-04	1.92E-03
OTU_1104 <i>Akkermansia</i>	HC Vs UCD	8.04	-0.82	9.76E-02	2.32E-01
	HC Vs TCD	17.76	1.65	2.25E-04	1.97E-03
	UCD Vs TCD	21.41	2.46	1.56E-04	1.92E-03
OTU_46 <i>Incertae Sedis</i>	HC Vs UCD	192.02	-0.67	1.88E-01	3.69E-01
	HC Vs TCD	480.32	1.09	1.38E-02	6.17E-02
	UCD Vs TCD	512.68	2.34	1.94E-04	2.24E-03
OTU_63 <i>Blautia</i>	HC Vs UCD	154.0	-0.70	2.24E-01	4.02E-01
	HC Vs TCD	341.42	1.69	4.03E-04	3.14E-03
	UCD Vs TCD	415.46	2.33	2.2E-04	2.43E-03
OTU_176 <i>Lachnospirillum</i>	HC Vs UCD	10.20	-0.71	1.39E-01	3.04E-01
	HC Vs TCD	19.53	1.37	8.38E-04	5.89E-03
	UCD Vs TCD	21.77	2.03	2.17E-04	2.43E-03
OTU_134 <i>Ruminiclostridium</i>	HC Vs UCD	30.41	-1.31	9.4E-03	4.59E-02
	HC Vs TCD	46.6	0.72	7.65E-02	1.94E-01

	UCD Vs TCD	45.40	2.02	2.77E-04	2.83E-03
OTU_136 [ <i>Eubacterium</i> ]	HC Vs UCD	117.66	-1.32	5.59E-02	1.57E-01
<i>coprostanoligenes</i> group	HC Vs TCD	158.56	0.38	4.9E-01	6.54E-01
	UCD Vs TCD	218.81	2.38	1.57E-03	1.13E-02
OTU_245 <i>Christensenellaceae</i>	HC Vs UCD	11.55	-0.64	2.71E-01	4.57E-01
<i>R-7</i> group	HC Vs TCD	23.45	1.52	1.55E-03	9.45E-03
	UCD Vs TCD	25.55	2.00	2.23E-03	1.54E-02

n/a: not applicable; log2Fold change is negative when the second group in the pairwise comparison has lower relative abundance than the first one; OTU: operational taxonomic unit



**Supplementary Table 4:** OTUs with significantly different relative abundance in faecal samples of (a) paired data from 13 CD children at diagnosis and at six and 12 months after the initiation of GFD, and (b) from cross-sectional data from UCD patients (n=20) and TCD patients (n=45)

	Group comparison	BaseMean	log2Fold Change	<i>p</i> -value	<i>p</i> -value (adjusted)
OTU_576 <i>Akkermansia</i>	UCD Vs GFD 6 mos	212.2	-8.53	1.79E-05	1.27E-03
	UCD Vs GFD 12 mos	109.1	-7.00	3.20E-06	1.31E-03
	UCD Vs TCD	124.9	1.19	1.27E-01	2.38E-01
OTU_6 <i>Dialister</i>	UCD Vs GFD 6 mos	1,428.3	6.82	1.99E-06	2.83E-04
	UCD Vs GFD 12 mos	1,283.0	6.88	1.48E-05	1.52E-03
	UCD Vs TCD	1,540.8	-0.21	7.67E-01	8.48E-01
OTU_5 <i>Phascolarctobacterium</i>	UCD Vs GFD 6 mos	1,522.3	-9.80	5.98E-11	1.70E-08
	UCD Vs GFD 12 mos	1,256.2	-7.66	8.71E-06	1.52E-03
	UCD Vs TCD	2,385.3	0.83	3.26E-01	4.69E-01
OTU_537 <i>Dialister</i>	UCD Vs GFD 6 mos	25.8	6.82	2.51E-05	1.42E-03
	UCD Vs GFD 12 mos	25.9	7.69	1.15E-05	1.52E-03
	UCD Vs TCD	4.68	0.23	3.11E-01	7.29E-01
OTU_8 <i>Ruminococcus 2</i>	UCD Vs GFD 6 mos	2,208.9	4.79	6.18E-03	4.46E-02
	UCD Vs GFD 12 mos	3,458.3	6.24	1.71E-04	1.40E-02
	UCD Vs TCD	2,692.5	0.21	7.48E-01	8.33E-01
OTU_43 <i>Veillonella</i>	UCD Vs GFD 6 mos	343.6	4.80	6.14E-04	1.43E-02
	UCD Vs GFD 12 mos	1,222.8	5.26	3.85E-04	2.26E-02
	UCD Vs TCD	367.3	-0.42	4.66E-01	6.00E-01
OTU_55 [ <i>Eubacterium</i> ] <i>coprostanoligenes group</i>	UCD Vs GFD 6 mos	119.2	6.46	1.39E-03	2.28E-02
	UCD Vs GFD 12 mos	129.2	6.76	3.69E-04	2.26E-02
	UCD Vs TCD	86.6	-0.38	5.89E-01	7.09E-01
OTU_1045 <i>Roseburia</i>	UCD Vs GFD 6 mos	98.6	0.85	5.22E-01	8.06E-01
	UCD Vs GFD 12 mos	140.7	5.49	5.53E-04	2.52E-02
	UCD Vs TCD	276.2	-0.27	6.85E-01	7.87E-01
OTU_50 <i>Tyzzereella 4</i>	UCD Vs GFD 6 mos	59.9	-6.20	1.22E-04	3.84E-03
	UCD Vs GFD 12 mos	62.6	-5.39	5.08E-04	2.52E-02

	UCD Vs TCD	55.6	1.74	5.06E-03	3.02E-02
OTU_191 <i>Christensenellaceae</i>	UCD Vs GFD 6 mos	16.9	6.09	1.01E-04	3.57E-03
<i>R-7 group</i>	UCD Vs GFD 12 mos	17.4	6.00	6.65E-04	2.73E-02
	UCD Vs TCD	14.4	-0.74	2.07E-01	3.39E-01
OTU_22 <i>Ruminococcaceae</i>	UCD Vs GFD 6 mos	748.0	3.92	1.29E-03	2.28E-02
<i>UCG-002</i>	UCD Vs GFD 12 mos	772.1	6.01	8.30E-04	2.84E-02
	UCD Vs TCD	785.6	-0.22	7.35E-01	8.24E-01
OTU_18 <i>Phascolarctobacterium</i>	UCD Vs GFD 6 mos	732.0	-0.48	7.88E-01	9.85E-01
	UCD Vs GFD 12 mos	109.8	-5.38	7.91E-04	2.84E-02
	UCD Vs TCD	9.4	0.96	1.36E-01	2.46E-01
OTU_166 <i>Cronobacter</i>	UCD Vs GFD 6 mos	25.3	-7.90	5.84E-06	5.53E-04
	UCD Vs GFD 12 mos	3.57	-0.02	9.91E-01	9.98E-01
	UCD Vs TCD	3.4	0.65	1.54E-01	2.73E-01
OTU_113 <i>Clostridium sensu stricto 1</i>	UCD Vs GFD 6 mos	268.6	5.73	7.91E-05	3.21E-03
	UCD Vs GFD 12 mos	297.8	4.92	2.03E-03	6.43E-02
	UCD Vs TCD	148.6	0.67	2.78E-01	4.25E-01
OTU_259 <i>Erysipelatoclostridium</i>	UCD Vs GFD 6 mos	26.8	-6.95	7.37E-05	3.21E-03
	UCD Vs GFD 12 mos	10.5	-1.98	2.78E-01	9.98E-01
	UCD Vs TCD	8.6	2.61	4.31E-07	1.64E-05
OTU_24 <i>Lachnoclostridium</i>	UCD Vs GFD 6 mos	1,315.9	5.22	2.79E-04	7.91E-03
	UCD Vs GFD 12 mos	1,471.1	2.51	9.34E-02	6.32E-01
	UCD Vs TCD	939.0	-0.70	2.28E-01	2.83E-02
OTU_14 <i>Subdoligranulum</i>	UCD Vs GFD 6 mos	1,006.0	4.16	6.55E-04	1.43E-02
	UCD Vs GFD 12 mos	1,258.2	2.21	1.30E-01	7.30E-01
	UCD Vs TCD	1,446.3	1.24	2.59E-02	9.09E-02
OTU_83 <i>Alistipes</i>	UCD Vs GFD 6 mos	93.9	5.52	6.50E-04	1.43E-02
	UCD Vs GFD 12 mos	113.2	5.40	9.00E-03	1.83E-01
	UCD Vs TCD	132.2	0.65	3.06E-01	4.49E-01
OTU_66 <i>Ruminococcaceae</i> <i>UCG-005</i>	UCD Vs GFD 6 mos	558.9	4.49	7.20E-04	1.46E-02
	UCD Vs GFD 12 mos	505.6	2.38	1.64E-01	7.98E-01
	UCD Vs TCD	304.6	0.77	1.55E-01	2.73E-01

OTU_98 <i>Ruminococcaceae</i>	UCD Vs GFD 6 mos	57.0	-3.66	8.64E-04	1.63E-02
	UCD Vs GFD 12 mos	53.1	-1.81	2.57E-01	9.98E-01
	UCD Vs TCD	139.2	2.06	1.39E-04	1.80E-03
OTU_3 <i>Akkermansia</i>	UCD Vs GFD 6 mos	1,033.2	5.40	1.45E-03	2.28E-02
	UCD Vs GFD 12 mos	1,582.8	2.19	2.35E-01	9.95E-01
	UCD Vs TCD	2,466.0	1.45	5.12E-02	1.43E-01
OTU_129 <i>Eggerthella</i>	UCD Vs GFD 6 mos	73.1	-3.76	2.99E-03	3.14E-02
	UCD Vs GFD 12 mos	72.6	-1.69	2.12E-01	9.49E-01
	UCD Vs TCD	70.16	0.53	2.89E-01	4.36E-01
OTU_893 [ <i>Eubacterium</i> ] <i>hallii</i> group	UCD Vs GFD 6 mos	82.7	-2.95	2.60E-03	3.14E-02
	UCD Vs GFD 12 mos	85.3	-1.93	8.97E-02	6.32E-01
	UCD Vs TCD	50.2	0.48	3.50E-01	4.91E-01
OTU_303 <i>Lachnospiraceae</i> <i>UCG-008</i>	UCD Vs GFD 6 mos	46.0	-3.69	2.90E-03	3.14E-02
	UCD Vs GFD 12 mos	62.5	-0.42	7.67E-01	9.98E-01
	UCD Vs TCD	114.8	1.47	3.77E-03	2.47E-02
OTU_115 <i>Parasutterella</i>	UCD Vs GFD 6 mos	56.8	4.42	2.33E-03	3.14E-02
	UCD Vs GFD 12 mos	73.4	3.26	4.43E-02	4.54E-01
	UCD Vs TCD	36.5	1.62	5.14E-03	3.03E-02
OTU_1005 <i>Fusicatenibacteri</i>	UCD Vs GFD 6 mos	9.71	-4.70	2.31E-03	3.14E-02
	UCD Vs GFD 12 mos	8.7	-2.47	1.28E-01	7.30E-01
	UCD Vs TCD	4.25	0.11	8.07E-01	8.76E-01
OTU_133 <i>Flavonifractor</i>	UCD Vs GFD 6 mos	57.0	-3.64	4.45E-03	4.36E-02
	UCD Vs GFD 12 mos	59.1	-2.48	1.07E-01	6.58E-01
	UCD Vs TCD	99.5	1.02	5.73E-02	1.55E-01
OTU_1044 [ <i>Eubacterium</i> ] <i>hallii</i> group	UCD Vs GFD 6 mos	150.3	-3.14	5.18E-03	4.37E-02
	UCD Vs GFD 12 mos	149.9	-2.11	1.40E-01	7.58E-01
	UCD Vs TCD	152.3	0.04	9.38E-01	9.61E-01
OTU_185 <i>Dorea</i>	UCD Vs GFD 6 mos	19.4	4.18	5.41E-03	4.37E-02
	UCD Vs GFD 12 mos	20.0	3.10	7.03E-02	5.77E-01
	UCD Vs TCD	6.5	-0.05	9.29E-01	9.56E-01
OTU_90 <i>Ruminococcaceae</i>	UCD Vs GFD 6 mos	103.6	4.71	5.05E-03	4.37E-02

<i>UCG-002</i>	UCD Vs GFD 12 mos	92.9	3.83	4.53E-02	4.54E-01
	UCD Vs TCD	83.8	1.83	1.89E-03	1.34E-02
OTU_122 <i>Ruminiclostridium 9</i>	UCD Vs GFD 6 mos	25.3	-4.32	5.09E-03	4.37E-02
	UCD Vs GFD 12 mos	83.1	-4.10	1.70E-02	2.79E-01
	UCD Vs TCD	16.9	0.20	7.33E-01	8.23E-01
OTU_15 <i>Dorea</i>	UCD Vs GFD 6 mos	275.7	3.58	6.28E-03	4.46E-02
	UCD Vs GFD 12 mos	446.8	2.15	1.67E-01	7.98E-01
	UCD Vs TCD	538.8	0.82	1.62E-01	2.81E-01
OTU_68 <i>Ruminococcaceae</i>	UCD Vs GFD 6 mos	152.6	5.45	6.19E-03	4.46E-02
<i>UCG-005</i>	UCD Vs GFD 12 mos	77.5	3.89	4.99E-02	4.88E-01
	UCD Vs TCD	150.1	1.36	4.10E-02	1.24E-01

n/a: not applicable; log2Fold change is negative when the second group in the pairwise comparison has lower relative abundance than the first one; OTU: operational taxonomic unit

**Supplementary Table 5:** OTUs with significantly different relative abundance in faecal samples of 18 TCD children and their unaffected 19 siblings

	BaseMean	log2Fold Change	<i>p</i> -value	<i>p</i> -value (adjusted)	Higher in
OTU_38 [Eubacterium] <i>coprostanoligenes</i> group	75.9	5.27	3.09E-12	1.88E-09	SIBLINGS
OTU_107 <i>Prevotella</i> 7	42.2	5.05	7.62E-10	2.32E-07	SIBLINGS
OTU_111 <i>Blautia</i>	34.0	4.17	4.98E-09	1.01E-06	SIBLINGS
OTU_62 <i>Ruminococcaceae</i> UCG-014	19.1	4.01	3.05E-08	4.65E-06	SIBLINGS
OTU_114 <i>Coprococcus</i> 2	12.9	3.85	9.00E-08	1.10E-05	SIBLINGS
OTU_568 <i>Bifidobacterium bifidum</i> NCIMB 41171	232.0	4.26	2.10E-07	1.72E-05	SIBLINGS
OTU_135 <i>Holdemanella</i>	10.6	3.39	2.26E-07	1.72E-05	SIBLINGS
OTU_143 <i>Ruminococcus</i> 1	9.9	3.51	2.18E-07	1.72E-05	SIBLINGS
OTU_295 <i>Christensenellaceae</i> R-7 group	6.8	3.43	4.18E-07	2.83E-05	SIBLINGS
OTU_1059 [Eubacterium] <i>coprostanoligenes</i> group	8.5	3.61	2.93E-06	1.79E-04	SIBLINGS
OTU_228 <i>Faecalibacterium</i>	6.5	3.36	3.61E-06	2.00E-04	SIBLINGS
OTU_212 <i>Ruminiclostridium</i> 9	7.5	2.73	6.28E-06	3.06E-04	SIBLINGS
OTU_74 [Eubacterium] <i>ruminantium</i> group	5.7	3.18	6.53E-06	3.06E-04	SIBLINGS
OTU_78 <i>Ruminiclostridium</i> 5	11.2	-3.08	1.11E-05	4.60E-04	TCD
OTU_140 <i>Collinsella</i>	6.9	3.13	1.13E-05	4.60E-04	SIBLINGS
OTU_230 <i>Bacteroides</i>	6.8	-2.84	1.21E-05	4.62E-04	TCD
OTU_299 [ <i>Ruminococcus</i> ] <i>gauvreauii</i> group	9.2	-2.72	1.71E-05	6.07E-04	TCD
OTU_324 <i>Peptococcaceae</i>	4.7	2.60	1.79E-05	6.07E-04	SIBLINGS
OTU_88 <i>Bacteroides</i>	954.3	-2.89	1.95E-05	6.23E-04	TCD

OTU_665 <i>Ruminococcaceae</i> UCG-014	9.1	3.26	2.20E-05	6.68E-04	SIBLINGS
OTU_130 <i>Christensenellaceae</i> R-7 group	10.1	2.72	2.67E-05	7.39E-04	SIBLINGS
OTU_576 <i>Akkermansia</i>	28.4	-3.03	3.18E-05	8.43E-04	TCD
OTU_80 <i>Ruminococcaceae</i> UCG-014	5.7	2.77	3.39E-05	8.60E-04	SIBLINGS
OTU_70 <i>Ruminococcaceae</i> UCG-014	5.2	2.75	4.15E-05	1.01E-03	SIBLINGS
OTU_178 <i>Ruminococcaceae</i>	8.4	2.42	4.96E-05	1.16E-03	SIBLINGS
OTU_42 <i>Methanobrevibacter</i>	17.2	3.21	5.55E-05	1.25E-03	SIBLINGS
OTU_908 <i>Anaerostipes</i>	4.3	2.50	7.12E-05	1.46E-03	SIBLINGS
OTU_85 <i>Bacteroidales</i> S24-7 group	6.5	-2.68	7.21E-05	1.46E-03	TCD
OTU_272 [ <i>Eubacterium</i> ] <i>oxidoreducens</i> group	3.4	2.35	7.14E-05	1.46E-03	SIBLINGS
OTU_180 <i>Ruminiclostridium</i> 5	6.2	2.71	8.01E-05	1.57E-03	SIBLINGS
OTU_442 <i>Christensenellaceae</i>	3.7	2.44	9.44E-05	1.80E-03	SIBLINGS
OTU_163 <i>Ruminiclostridium</i> 5	26.9	-2.34	1.12E-04	2.07E-03	TCD
OTU_33 <i>Roseburia</i>	427.7	-2.68	1.17E-04	2.09E-03	TCD
OTU_622 <i>Lachnospiraceae</i> UCG-001	52.9	-2.73	1.26E-04	2.20E-03	TCD
OTU_783 <i>Bacteroides</i>	4.4	-2.05	2.31E-04	3.71E-03	TCD
OTU_315 <i>Christensenellaceae</i> R-7 group	8.9	2.40	2.25E-04	3.71E-03	SIBLINGS
OTU_337 <i>Coriobacteriaceae</i>	7.0	2.45	2.31E-04	3.71E-03	SIBLINGS
OTU_67 <i>Christensenellaceae</i> R-7 group	53.2	2.71	2.56E-04	4.00E-03	SIBLINGS
OTU_434 <i>Christensenellaceae</i>	3.7	2.19	3.06E-04	4.55E-03	SIBLINGS
OTU_155 <i>Lachnoclostridium</i>	23.8	-2.56	3.25E-04	4.71E-03	TCD
OTU_179 <i>Howardella</i>	3.6	2.28	4.45E-04	6.30E-03	SIBLINGS

OTU_441 <i>Thalassospira</i>	3.8	2.13	4.58E-04	6.34E-03	SIBLINGS
OTU_895 <i>Barnesiella</i>	21.4	-2.62	5.37E-04	7.26E-03	TCD
OTU_868 <i>Bacteroides</i>	112.1	-2.68	6.00E-04	7.77E-03	TCD
OTU_704 <i>Collinsella</i>	91.7	-2.16	6.34E-04	7.88E-03	TCD
OTU_133 <i>Flavonifractor</i>	82.0	-2.07	9.31E-04	1.09E-02	TCD
OTU_225 <i>Butyrivibrio</i>	3.1	2.03	1.16E-03	1.26E-02	SIBLINGS
OTU_149 <i>Lachnospiraceae</i> NK4A136 group	25.9	-2.37	1.55E-03	1.58E-02	TCD
OTU_195 <i>Bacteroides plebeius</i> DSM 17135	12.2	-2.48	1.84E-03	1.81E-02	TCD
OTU_116 <i>Ruminococcaceae</i> UCG-014	9.2	2.07	2.64E-03	2.40E-02	SIBLINGS
OTU_1105 <i>Prevotella</i> 9	192.5	3.03	3.33E-03	2.98E-02	SIBLINGS
OTU_137 <i>Ruminococcaceae</i> UCG-014	6.6	2.08	3.48E-03	3.05E-02	SIBLINGS
OTU_1049 <i>Lachnoclostridium</i>	181.3	-2.06	4.73E-03	3.60E-02	TCD
OTU_63 <i>Blautia</i>	388.5	-2.06	4.87E-03	3.66E-02	TCD
OTU_156 <i>Christensenellaceae</i> R-7 group	58.7	2.25	4.94E-03	3.67E-02	SIBLINGS
OTU_1054 <i>Alistipes</i>	45.1	-2.01	5.82E-03	4.07E-02	TCD

OTU: operational taxonomic unit

**Supplementary Table 6:** Faecal metabolites in coeliac disease children with or without recent ingestion of gluten, based on GIP results

	GIP negative (59)	GIP positive (12)	<i>p</i> *
Ammonia (*10 <sup>-4</sup> mg/g)	11.2 (1.8)	7.7 (6.1)	0.043
Free sulphide (μmol/g)	0.11 (0.03)	0.08 (0.01)	0.228
Total sulphide (μmol/g)	1.2 (0.25)	0.8 (0.08)	0.121
L-lactic acid (μg/g)	106.4 (30.6)	86.4 (6.5)	0.750
D-lactic acid (μg/g)	80.5 (8.4)	87.1 (7.5)	0.925
Total lactic acid (μg/g)	186.9 (33.9)	173.5 (9.1)	0.414
Acetic acid (μmol/g)	110.2 (9.5)	125.7 (6.1)	0.338
Propionic acid (μmol/g)	22.8 (3.1)	23.0 (1.7)	0.956
Butyric acid (μmol/g)	19.3 (3.1)	21.0 (2.2)	0.675
Valeric acid (μmol/g)	2.5 (0.51)	2.5 (0.19)	0.856
Isobutyric acid (μmol/g)	3.1 (0.42)	3.0 (0.20)	0.794
Isovaleric acid (μmol/g)	3.2 (0.49)	2.95 (0.22)	0.640
Total SCFA (μmol/g)	161.0 (13.3)	178.0 (9.9)	0.722

Values expressed as mean (SEM); \* Mann-Whitney non-parametric test; gluten ingestion indicated by a faecal GIP concentration  $\geq 0.156\mu\text{g/g}$