Supplementary data for:

Microbiotas from UC patients have an altered metabolism and a reduced ability of lactic acid bacteria to colonize mucus

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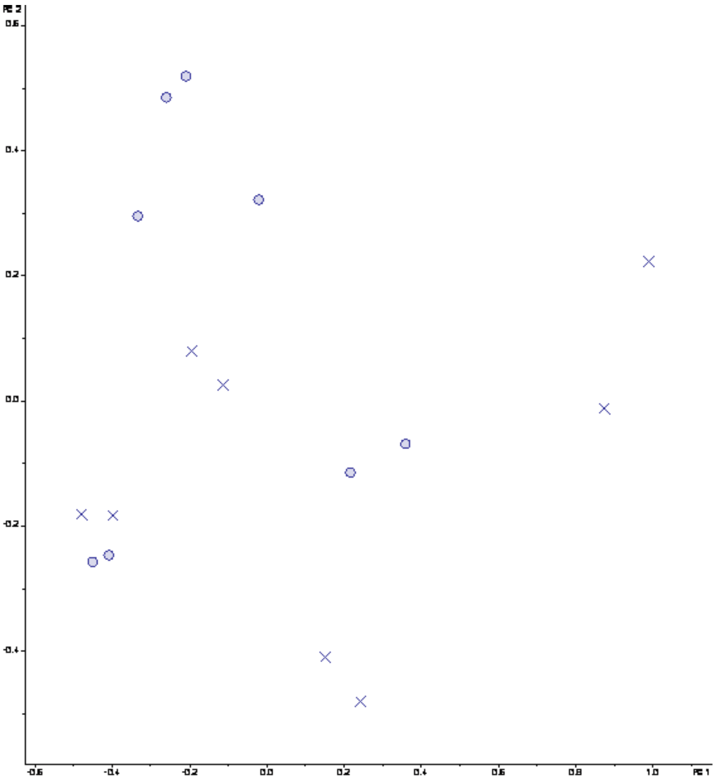
Supplementary figure legends

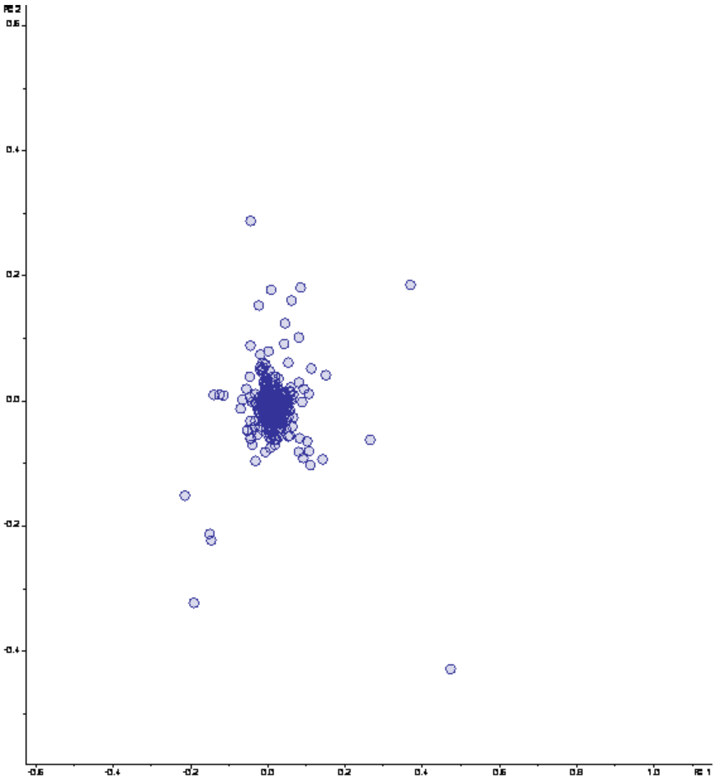
Figure S1 - PCA of LCMS data from mucosal samples of M-SHIME colonized with microbiota from healthy subjects (o) and UC patients in remission (x).. Score (left) and loading (right) plots are shown. Presented PC1 (36.3%) vs. PC2 (16.4%).

Figure S2 - PCA of LCMS data from luminal samples of M-SHIME colonized with microbiota from healthy subjects (o) and UC patients in remission (x). Score (left) and loading (right) plots are shown. Presented PC1 (30.3%) vs. PC2 (17.5%).

Figure S3 - PCA of LCMS data from mucosal samples of M-SHIME colonized with microbiota from UC patients in relapse (Δ) and in remission (x) . Score (left) and loading (right) plots are shown. Presented PC1 (33.7%) vs. PC2 (17.5%). Numbers in the loading plot, bucket mass from the PCA /retention time bucket, correspond to the metabolite candidates described in Table 4.

Figure S4 - PCA of LCMS data from luminal samples of M-SHIME colonized with microbiota from UC patients in relapse (Δ) and in remission (x). Score (left) and loading (right) plots are shown. Presented PC1 (26.9%) vs. PC2 (17.4%). Numbers in the loading plot, bucket mass from the PCA /retention time bucket, correspond to the metabolite candidates described in Table 5.


PC 2
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1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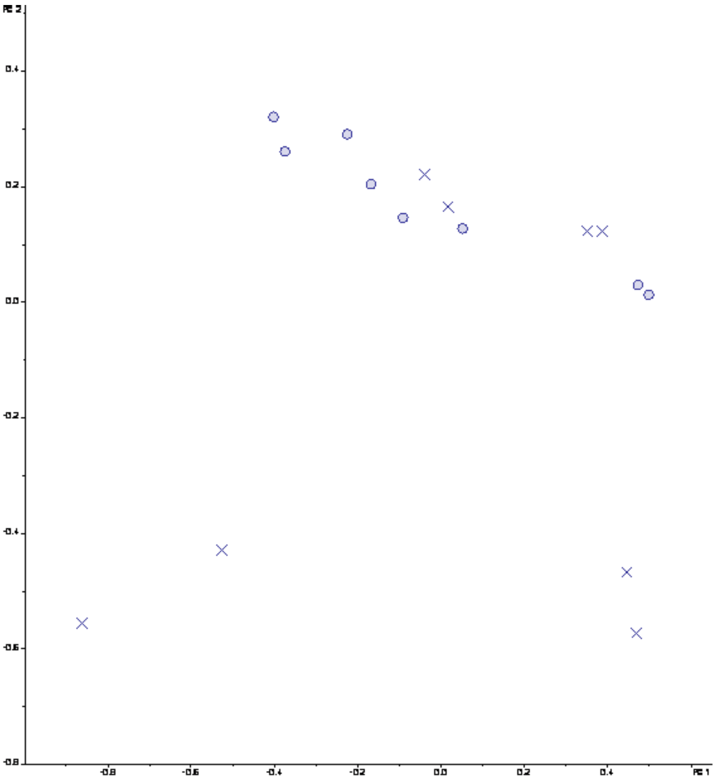
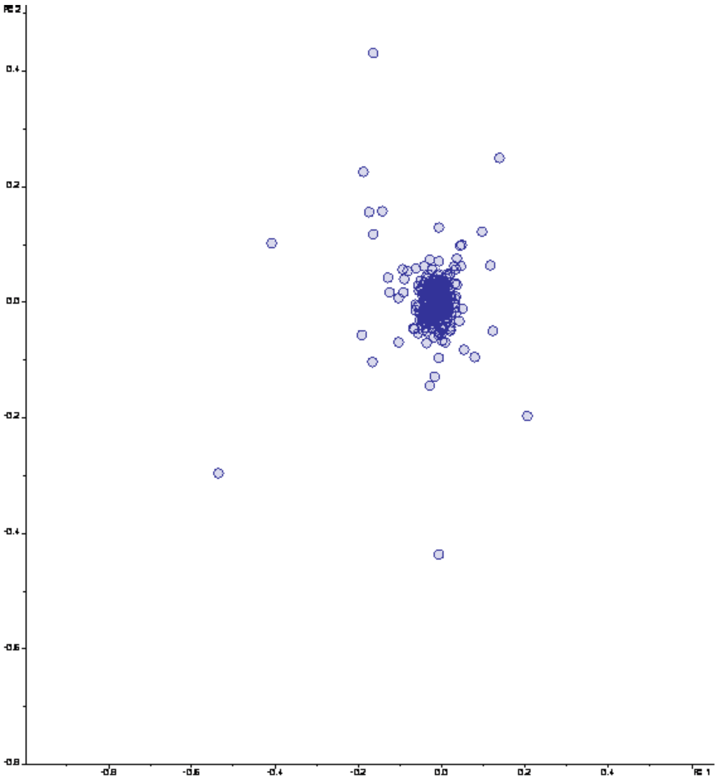
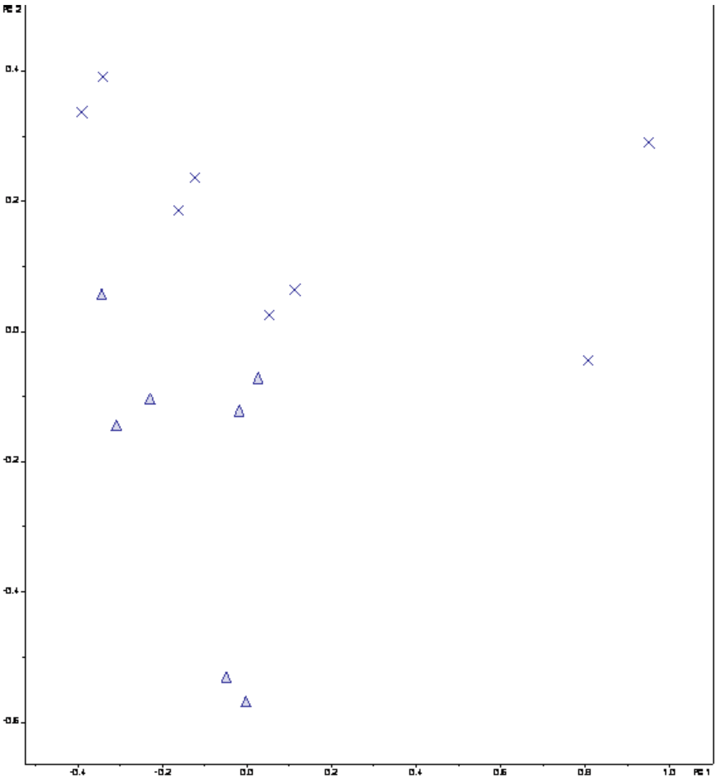
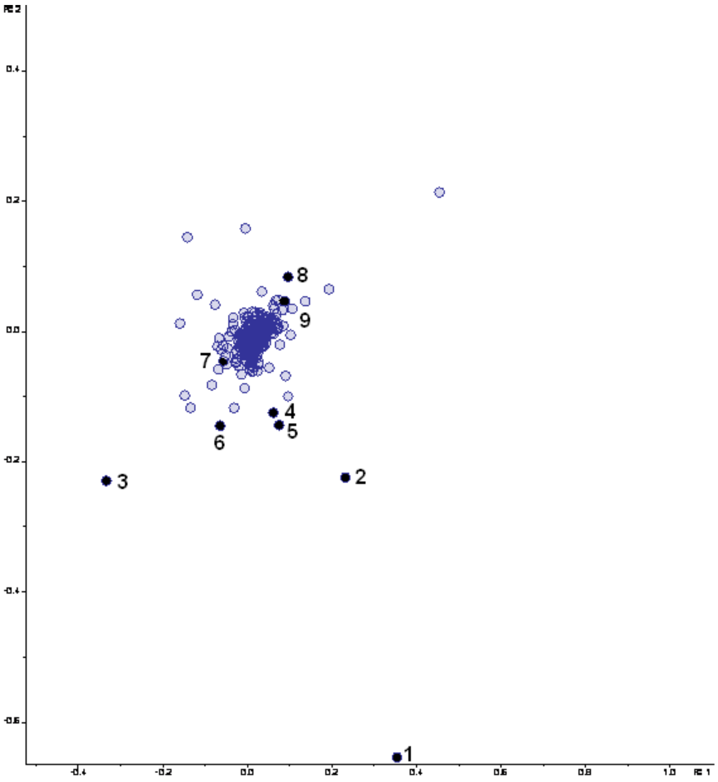
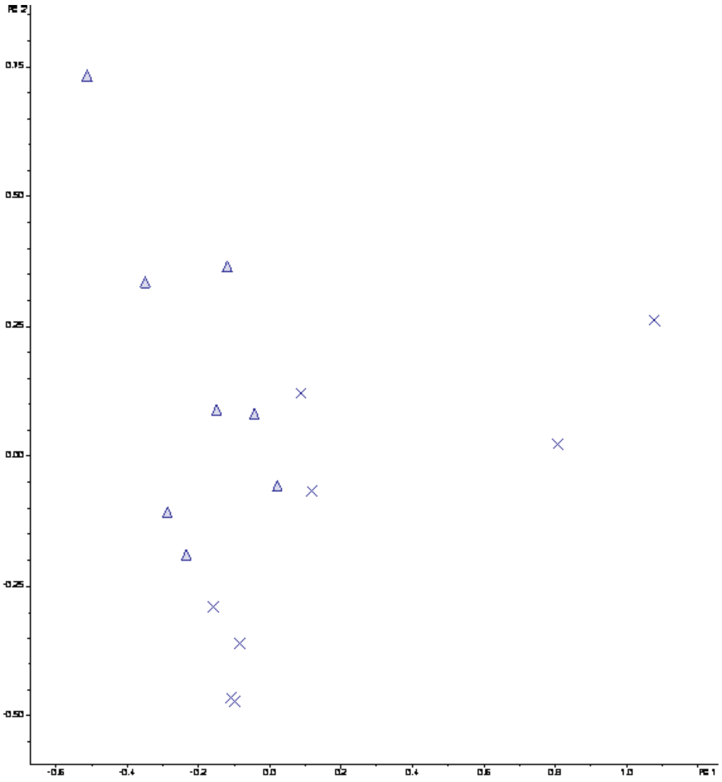
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1


PC 2
0.4
0.2
0.0
-0.2
-0.4
-0.6
-0.8
-0.8
-0.6
-0.4
-0.2
0.0
0.2
0.4
PC 1


PC 2
0.4
0.2
0.0
-0.2
-0.4
-0.6
-0.8
-0.8
-0.6
-0.4
-0.2
0.0
0.2
0.4
PC 1


PC 2
0.4
0.2
0.0
-0.2
-0.4
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1


PC 2
0.4
0.2
0.0
-0.2
-0.4
-0.6
8
9
7
4
5
6
3
2
1
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1


PC 2
0.75
0.50
0.25
0.00
-0.25
-0.50
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1

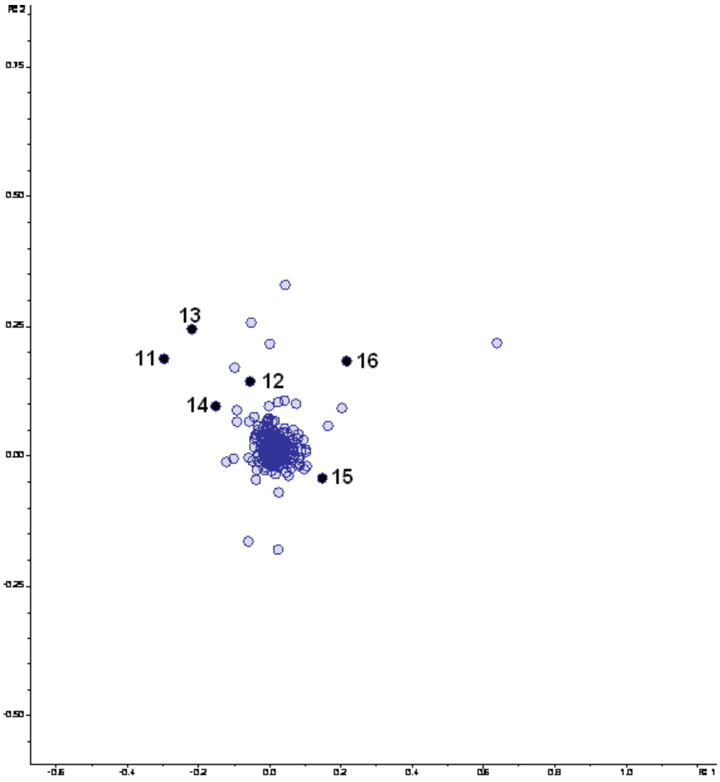

PC 2
0.75
0.50
0.25
0.00
-0.25
-0.50
13
11
16
12
14
15
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
PC 1

Table S1 - 16S rRNA gene sequences of phylum, group and species specific primers

Target taxon	Primer	Sequence (5'-3')	Fragment size (bp)	Reference
Firmicutes phylum*	Firm934F Firm1060R	gga gya tgt ggt tta att cga agc a agc tga cga caa cca tgc ac	126	(Guo et al, 2008)
Clostridiaceae/ Eubacterium	W18-F W109-R	gag ttt gat cmt ggc tca g ccc ttt aca ccc agt aa	552	(Cook et al, 2010)
Clostridium coccoides group	g-Ccoc-F g-Ccoc-R	aaa tga cgg tac ctg act aa ctt tga gtt tca ttc ttg cga a	440	(Matsuki et al, 2004)
Roseburia spp.	RosF RosR	tac tgc att gga aac tgt cg cgg cac cga aga gca at	230	(Larsen et al, 2010)
Clostridium leptum subgroup	sg-Clept-F sg-Clept-R	gca caa gca gtg gag t ctt cct ccg ttt tgt caa	239	(Matsuki et al, 2004;Shen et al, 2006)
Faecalibacterium prausnitzii	Fprau 07 Fprau 02	cca tga att gcc ttc aaa act gtt gag cct cag cgt cag ttg gt	140	(Sokol et al, 2009)
Lactobacillus spp.	Lacto-F Lacto-R	agc agt agg gaa tct tcc a cac cgc tac aca tgg ag	341	(Heilig et al, 2002;Walter et al, 2000)
Bacteroidetes phylum	Bact934F Bact1060R	gga rca tgt ggt tta att cga tga t agc tga cga caa cca tgc ag	126	(Guo et al, 2008)
Bacteroides spp.	BacAll_2F BacAll_2R	gtc agt tgt gaa agt ttg c caa tcg gag ttc ttc gtg	127	(Ahmed et al, 2007)
Bac. fragilis group	BfrF BfrR	ctg aac cag cca agt agc g ccg caa act ttc aca act gac tta	230	(Liu et al, 2003)
Alistipes spp.	Alis F1-124 Alis R1-423	tta gag atg ggc atg cgt tgt tga atc ctc cgt att acc gcg	320	(Vigsnaes et al, 2012a)
Akkermansia muciniphila	AM1 AM2	cag cac gtg aag gtg ggg ac cct tgc ggt tgg ctt cag at	327	(Collado et al, 2007a)
Desulfovibrio spp.	DSV691-F DSV826-R	ccg tag ata tct gga gga aca tca g aca tct agc atc cat cgt tta cag c	136	(Fite et al, 2004)
Actinobacteria	Act920F3 Act1200R	tac ggc cgc aag gct a tcr tcc cca cct tcc tcc g	281	(De Gregoris et al, 2011)
Bifidobacterium spp.	F-bifido R-bifido	cgc gtc ygg tgt gaa ag ccc cac atc cag cat cca	244	(Delroisse et al, 2008)
Bifidobacterium bifidum	BiBIF-1 BiBIF-2	cca cat gat cgc atg tga ttg ccg aag gct tgc tcc caa a	278	(Matsuki et al, 1998)

Bifidobacterium adolescentis	BiADO-1	ctc cag ttg gat gca tgt c	279	(Matsuki et al, 1998)
	BiADO-2	cga agg ctt gct ccc agt		
Bifidobacterium pseudocatenulatum/ Bifidobacterium catenulatum	BiCATg-1	cgg atg ctc cga ctc ct	289	(Matsuki et al, 1998)
	BiCATg-2	cga agg ctt gct ccc gat		
V2-V3 16S rRNA region#	HDA1	act cct acg gga ggc agc agt	200	(Walter et al, 2000)
	HDA2	gta tta ccg cgg ctg ctg gca c		
16S rRNA region#	TBA-F	cgg caa cga gcg caa ccc	130	(Denman &.McSweeney, 2006)
	TBA-R	cca ttg tag cac gtg tgt agc c		

HDA and TBA primers were used to target total bacterial DNA for normalization, hence correcting for differences in total DNA concentration between individual samples.

*Primer set targets the Firmicutes phylum and *Bifidobacterium* group (Table S2)

Table S2 – Primer sensitivity and selectivity

Bacterial Taxa		Firm934F	W18-F	g-Ccoc-F	RosF	C.lepF	Fprau 07	Lacto-F	Bact934F	BacF	Bfr-F	Alis F1	Act920F3	F-bifido	BiBIF-1	BiADO-1	BiCAT-1	AM1	DSV691-F	HDA1	TBA-F
	Strain	Firm1060R	W109-R	g-Ccoc-R	RosR	C.lepR	Fprau 02	Lacto-R	Bact1060R	BacR	Bfr-F	Alis R2	Act1200R	R-bifido	BiBIF-2	BiADO-2	BiCAT-2	AM2	DSV826-R	HDA2	TBA-R
Alistipes putredinis	DSM17216	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	+	+
Alistipes shahii	DSM19121	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	+	+
Prevotella copri	DSM18205	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+	+
Bacteroides vulgatus	DSM1447	-	-	-	-	-	-	-	+	+	+	-	-	-	-	-	-	-	-	+	+
Bacteroides fragilis	DSM2151	-	-	-	-	-	-	-	+	+	+	-	-	-	-	-	-	-	-	+	+
Bifidobacterium bifidum	DSM20215	+	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-	-	-	+	+
Bifidobacterium adolescentis	DSM 20083	+	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	-	+	+
Bifidobacterium pseudocatenulatum	DSM 20438	+	-	-	-	-	-	-	-	-	-	-	+	+	-	-	+	-	-	+	+
Lactobacillus acidophilus	DSM20079	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	+
Lactobacillus gasseri	DSM20604	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+	+
Clostridium butyricum	DSM10702	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Faecalibacterium prausnitzii	DSM17677	+	+	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Ruminococcus albus	DSM20455	+	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Blautia coccoides	DSM935	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Roseburia faecis	DSM16840	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Desulfovibrio intestinalis	DSM11275	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+
Escherichia coli	DSM20926	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
Akkermansia muciniphila	DSM959	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+

Table S3 – Growth rates (h^{-1}) for the measured bacterial taxa during the 42 h incubation

	Growth rate (h^{-1})		
	Healthy subjects	**UC remission**	**UC relapse**
Firmicutes	0.0063 (±0.003)	0.0011 (±0.009)	0.0026 (±0.003)
• *Clostridium leptum* subgroup	0.0346 (±0.024)	0.0411 (±0.028)	0.0548 (±0.003)
o *Faecalibacterium prausnitzii*	0.0600 (±0.015)	0.0350 (±0.019)	0.0444 (±0.010)
• *Clotridium coccoides* group	0.0315 (±0.024)	0.0269 (±0.040)	0.0431 (±0.021)
• *Lactobacillus* spp.	0.0160 (±0.018)	0.0256 (±0.013)	0.0237 (±0.026)
Bacteroidetes	0.0022 (±0.012)	0.0141 (±0.059)	0.0887 (±0.018)
• *Bacteroides* spp.	0.0043 (±0.013)	0.0199 (±0.058)	0.0707 (±0.007)
• *Alistipes* spp.	0.0022 (±0.019)	-0.0052 (±0.032)	0.0046 (±0.013)
Actinobacteria			
• *Bifidobacterium* spp.	0.0279 (±0.014)	0.0072 (±0.012)	0.0248 (±0.016)
Proteobacteria			
• *Desulfovibrio* spp.	0.0073 (±0.014)	0.0303 (±0.019)	0.0379 (±0.009)
Verrucomicrobia			
• *Akkermansia muciniphila*	0.0149 (±0.017)	0.0211 (±0.011)	0.0175 (±0.007)