

**Additional file 7 Microbial taxa fold-changes (V2/V1 and V3/V1) in the total cohort.**

Taxa		Total cohort (n=79)							
		Placebo (n=40)				EpiCor (n=39)			
		V2/V1	p-val.	FC	p-val.	V2/V1	p-val.	FC	p-val.
<b>Phylum Actinobacteria</b>									
Bifidobacteriaceae	-	0.88	0.536	0.97	0.952	0.95	0.885	1.02	0.979
Coriobacteriaceae	<i>Bifidobacterium</i>	0.88	0.296	0.97	0.906	0.95	0.776	1.02	0.957
	-	1.13	0.753	1.20	0.507	1.07	0.908	1.07	0.896
	<i>Asaccharobacter</i>	1.35	0.990	2.46	0.842	1.40	0.928	1.67	0.815
	<i>Collinsella</i>	1.35	0.306	1.34	0.330	0.80	0.699	0.65	0.352
	Coriobacteriaceae_uncl.	0.70	0.771	0.99	0.999	1.53	0.456	1.98	<b>0.085</b>
	<i>Eggerthella</i>	2.60	1.000	1.87	1.000	0.53	0.997	0.52	0.997
	<i>Enterorhabdus</i>	1.34	0.985	0.52	0.972	0.50	0.949	0.63	0.972
	<i>Slackia</i>	1.09	0.999	0.55	0.983	1.23	0.974	0.32	0.805
Propionibacteriaceae	-	0.05	0.994	0.01	1.000	2.65	0.993	1.48	0.999
	<i>Propionibacterium</i>	0.05	0.988	0.01	1.000	2.65	0.985	1.48	0.999
<b>Phylum Bacteroidetes</b>									
Bacteroidaceae	-	0.99	0.973	1.07	0.463	1.06	0.480	1.08	0.293
	<i>Bacteroides</i>	0.99	0.946	1.07	0.224	1.06	0.231	1.08	<b>0.088</b>
Bacteroidetes_uncl.	-	1.29	0.944	1.07	0.996	0.99	1.000	0.76	0.888
Bacteroidales_uncl.	-	1.43	0.968	0.86	0.997	1.20	0.997	1.94	0.936
Porphyromonadaceae	-	0.71	<b>0.004</b>	0.79	<b>0.050</b>	1.09	0.666	0.99	0.998
	<i>Barnesiella</i>	0.64	0.199	0.65	0.227	1.39	0.201	1.36	0.262
	<i>Butyrimonas</i>	1.56	0.987	1.54	0.988	0.72	0.950	0.88	0.991
	<i>Odoribacter</i>	0.72	0.977	1.16	0.993	1.30	0.989	1.26	0.992
	Porphyromonadaceae_uncl.	0.90	0.852	0.97	0.983	1.08	0.907	0.89	0.846
Prevotellaceae	<i>Parabacteroides</i>	0.62	<b>0.099</b>	0.67	0.170	0.78	0.718	0.67	0.491
	-	0.80	0.464	0.98	0.988	1.33	0.186	1.11	0.796
	<i>Alloprevotella</i>	1.07	0.999	1.44	0.951	0.74	0.994	0.81	0.997
	<i>Hallella</i>	1.00	1.000	0.00	1.000	0.00	0.937	0.00	0.937
	<i>Paraprevotella</i>	0.02	0.723	0.01	0.718	1.71	0.729	0.14	0.633
	<i>Prevotella</i>	0.82	0.495	1.04	0.955	1.48	<b>0.075</b>	1.43	0.121
	Prevotellaceae_uncl.	1.16	0.986	0.99	1.000	1.02	0.999	1.12	0.982
Rikenellaceae	-	1.10	0.721	0.86	0.563	0.70	<b>0.093</b>	0.80	0.320
	<i>Alistipes</i>	1.10	0.523	0.86	0.326	0.70	<b>0.009</b>	0.80	0.105
<b>Phylum Firmicutes</b>									
Acidaminococcaceae	-	1.40	0.177	1.63	<b>0.017</b>	0.93	0.911	1.04	0.977
	<i>Acidaminococcus</i>	14.74	0.296	18.26	0.157	0.40	0.963	1.96	0.910
	Acidaminococcaceae_uncl.	1.25	0.994	2.01	0.904	0.98	1.000	1.06	0.999
	<i>Succinilasticum</i>	1.53	0.688	1.60	0.622	1.70	0.755	0.97	0.999
	<i>Phascolarctobacterium</i>	1.04	0.980	1.21	0.606	0.82	0.564	0.98	0.991
Clostridiales_uncl.	-	0.99	0.997	0.98	0.990	1.09	0.776	1.19	0.342
Clostridiaceae	-	0.79	0.970	0.63	0.914	0.93	0.999	1.23	0.991
	<i>Clostridium_sensu_stricto</i>	0.79	0.940	0.63	0.833	0.93	0.998	1.23	0.981
Enterococcaceae	-	1.20	1.000	1.79	0.995	0.72	1.000	0.38	0.999
	<i>Enterococcus</i>	1.20	0.999	1.79	0.990	0.72	1.000	0.38	0.998
Erysipelotrichaceae	-	1.17	0.965	0.92	0.992	1.57	0.666	1.54	0.688
	<i>Catenibacterium</i>	1.20	0.999	1.39	0.997	1.56	0.908	0.23	0.833
	<i>Clostridium_XVIII</i>	2.72	0.900	1.09	1.000	2.80	0.702	3.19	0.595
	<i>Coprobacillus</i>	1.08	1.000	1.07	1.000	0.71	1.000	0.67	1.000
	Erysipelotrichaceae_uncl.	0.93	0.992	0.75	0.918	0.96	0.999	1.47	0.925
	<i>Turicibacter</i>	0.71	1.000	4.19	0.993	1.68	0.995	4.19	0.895
Firmicutes_uncl.	-	0.96	0.932	1.07	0.757	0.80	<b>0.085</b>	0.71	<b>0.006</b>
Lachnospiraceae	-	1.08	<b>0.000</b>	1.02	0.561	1.00	1.000	1.04	<b>0.057</b>
	<i>Anaerostipes</i>	0.86	0.840	1.02	0.998	2.31	<b>0.006</b>	2.25	<b>0.010</b>
	<i>Blautia</i>	1.52	<b>0.000</b>	1.21	<b>0.003</b>	0.95	0.484	0.97	0.704

	<i>Clostridium_XIVa_uncl.</i>	1.08	0.987	1.00	1.000	1.03	0.992	1.05	0.976
	<i>Clostridium_XIVb_uncl.</i>	1.15	0.998	0.76	0.995	0.96	1.000	0.61	0.983
	<i>Coprococcus</i>	0.97	0.970	0.96	0.942	0.80	0.168	0.70	<b>0.019</b>
	<i>Dorea</i>	0.96	0.942	0.83	0.338	1.13	0.730	0.79	0.476
	<i>Lachnospira</i>	0.96	0.998	1.83	0.569	0.45	0.711	1.13	0.981
	<i>Lachnospiraceae_uncl.</i>	0.88	<b>0.038</b>	0.92	0.271	1.01	0.963	1.13	<b>0.039</b>
	<i>Howardella</i>	0.98	1.000	1.68	0.984	0.40	0.998	0.52	0.999
	<i>Roseburia</i>	1.11	0.134	0.94	0.504	1.00	1.000	1.08	0.414
	<i>Ruminococcus</i>	0.95	0.979	1.33	0.354	0.90	0.871	1.26	0.438
Lactobacillaceae	-	1.30	0.996	0.17	0.966	0.77	1.000	1.42	0.999
Peptostreptococcaceae	<i>Lactobacillus</i>	1.30	0.991	0.17	0.932	0.77	0.999	1.42	0.997
Ruminococcaceae	-	1.04	0.994	1.21	0.874	0.91	0.963	0.77	0.777
	<i>Clostridium_XI</i>	1.04	0.988	1.21	0.763	0.91	0.925	0.77	0.597
	-	0.90	<b>0.000</b>	0.91	<b>0.000</b>	0.99	0.954	0.91	<b>0.000</b>
	<i>Butyricicoccus</i>	1.04	0.997	0.89	0.976	1.10	0.994	0.90	0.994
	<i>Faecalibacterium</i>	0.67	<b>0.000</b>	0.75	<b>0.001</b>	0.91	0.224	0.82	<b>0.004</b>
Streptococcaceae	<i>Flavonifractor</i>	1.41	0.950	1.28	0.978	1.07	0.999	0.90	0.996
	<i>Gemmiger</i>	0.96	0.977	0.75	0.458	0.89	0.885	1.09	0.916
	<i>Clostridium_IV_uncl.</i>	0.49	0.861	0.89	0.993	0.68	0.983	0.45	0.953
	<i>Oscillibacter</i>	0.61	0.878	1.28	0.935	2.12	0.467	2.16	0.443
	<i>Ruminococcaceae_uncl.</i>	0.96	0.263	0.96	0.241	0.97	0.616	0.91	<b>0.009</b>
	<i>Ruminococcus</i>	1.08	0.758	1.02	0.977	1.10	0.725	0.90	0.763
	-	0.78	0.958	0.94	0.997	0.74	0.923	0.91	0.990
	<i>Lactococcus</i>	0.82	0.998	1.15	0.999	0.59	0.999	1.29	0.999
Veillonellaceae	<i>Streptococcus</i>	0.77	0.937	0.89	0.986	0.75	0.869	0.89	0.972
	-	1.76	<b>0.026</b>	1.41	0.303	0.89	0.860	1.24	0.537
	<i>Dialister</i>	1.92	<b>0.001</b>	1.42	0.172	0.93	0.926	1.33	0.211
	<i>Megamonas</i>	2.42	0.998	3.15	0.995	2.40	0.999	0.81	1.000
	<i>Megasphaera</i>	0.85	0.997	1.22	0.993	0.59	0.918	0.76	0.970
	<i>Mitsuokella</i>	0.65	0.999	0.80	1.000	1.13	1.000	1.78	0.998
	<i>Veillonella</i>	0.82	0.999	1.68	0.992	0.53	0.999	0.78	1.000

#### Phylum Proteobacteria

Alphaproteobacteria_uncl.	-	1.00	1.000	1.00	1.000	0.63	0.991	1.41	0.989
Desulfovibrionaceae	-	1.30	0.987	1.66	0.939	0.73	0.990	1.02	1.000
	<i>Desulfovibrio</i>	1.32	0.980	1.67	0.916	0.69	0.999	1.13	1.000
Enterobacteriaceae	Desulfovibrionaceae_uncl.	1.24	0.999	1.61	0.996	0.74	0.988	0.99	1.000
	-	0.69	0.953	1.17	0.985	0.58	0.676	0.90	0.976
Sutterellaceae	<i>Escherichia/Shigella</i>	0.67	0.925	1.27	0.950	0.59	0.715	1.01	1.000
	<i>Klebsiella</i>	0.81	0.999	0.72	0.997	0.56	0.895	0.70	0.947
Oxalobacteraceae	-	0.84	1.000	1.05	1.000	3.41	0.665	0.88	0.999
Pasteurellaceae	<i>Parasutterella</i>	1.09	1.000	0.65	1.000	1.04	1.000	0.59	0.997
	<i>Sutterella</i>	0.77	0.999	1.12	1.000	4.60	0.440	1.03	1.000
	-	1.00	1.000	1.00	1.000	1.28	0.999	1.32	0.999
	Oxalobacteraceae_uncl.	1.00	1.000	1.00	1.000	1.28	0.998	1.32	0.998
	-	0.70	1.000	0.22	1.000	1.79	0.998	1.22	1.000
	<i>Haemophilus</i>	0.70	1.000	0.22	1.000	1.79	0.996	1.22	1.000

#### Phylum Spirochaetae

Brachyspiraceae	-	1.02	1.000	1.08	1.000	0.95	1.000	0.76	0.998
	<i>Brachyspira</i>	1.02	1.000	1.08	0.999	0.95	1.000	0.76	0.996
Spirochaetaceae	-	1.98	1.000	1.67	1.000	0.99	1.000	0.36	0.999
	<i>Treponema</i>	1.98	0.999	1.67	1.000	0.99	1.000	0.36	0.999

#### Phylum Verrucomicrobia

Verrucomicrobiaceae	Akkermansia	1.11	0.855	1.07	0.931	1.35	0.425	1.20	0.737
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**Legend:** A two-way repeated measures ANOVA with Dunnett's multiple comparison's test against V1 was performed to test for significant changes over time within each group (*p*-values ≤ 0.05 and < 0.1 are depicted in bold text). FC, fold-change; V, visit.