

Additional file 8 Microbial taxa fold-changes (V2/V1 and V3/V1) in the severe subgroup.

Taxa		Severe subgroup (n=54)							
		Placebo (n=27)				EpiCor (n=27)			
		V2/V1		V3/V1		V2/V1		V3/V1	
		FC	p-val.	FC	p-val.	FC	p-val.	FC	p-val.
Phylum Actinobacteria									
Bifidobacteriaceae	-	0.72	0.162	1.05	0.927	1.04	0.956	1.07	0.879
	<i>Bifidobacterium</i>	0.72	0.032	1.05	0.859	1.04	0.911	1.07	0.766
Coriobacteriaceae	-	1.06	0.928	1.07	0.904	1.21	0.637	0.96	0.981
	<i>Asaccharobacter</i>	1.41	0.982	1.42	0.982	1.40	0.967	1.34	0.976
	<i>Collinsella</i>	1.29	0.383	1.30	0.351	0.82	0.847	0.66	0.560
	Coriobacteriaceae_uncl.	0.61	0.620	0.73	0.789	1.84	0.383	1.43	0.769
	<i>Eggerthella</i>	2.60	1.000	1.87	1.000	1.00	1.000	0.00	1.000
	<i>Enterorhabdus</i>	1.33	0.993	0.64	0.991	0.51	0.953	0.63	0.973
	<i>Slackia</i>	0.95	1.000	0.38	0.964	3.20	0.854	0.80	0.999
Propionibacteriaceae	-	0.07	0.991	0.01	1.000	2.11	0.997	1.56	0.999
	<i>Propionibacterium</i>	0.07	0.983	0.01	0.999	2.11	0.993	1.56	0.998
Phylum Bacteroidetes									
Bacteroidaceae	-	0.84	0.054	0.89	0.216	1.15	0.118	1.14	0.161
	<i>Bacteroides</i>	0.84	0.004	0.89	0.054	1.15	0.015	1.14	0.027
Bacteroidetes_uncl.	-	1.31	0.949	0.86	0.989	0.96	0.999	0.89	0.989
Bacteroidales_uncl.	-	1.21	0.992	0.67	0.981	1.20	0.997	1.93	0.943
Porphyromonadaceae	-	0.86	0.549	1.03	0.979	1.13	0.513	0.96	0.926
	<i>Barnesiella</i>	0.83	0.883	0.84	0.892	1.39	0.227	1.31	0.371
	<i>Butyricimonas</i>	1.82	0.979	1.63	0.988	0.80	0.987	0.77	0.984
	<i>Odoribacter</i>	0.65	0.969	1.27	0.982	1.59	0.980	1.68	0.973
	Porphyromonadaceae_uncl.	0.93	0.973	1.17	0.836	1.07	0.944	0.85	0.779
	<i>Parabacteroides</i>	0.93	0.969	0.98	0.998	0.84	0.893	0.54	0.415
Prevotellaceae	-	0.77	0.539	1.03	0.987	1.43	0.138	1.01	0.999
	<i>Alloprevotella</i>	1.33	0.987	2.11	0.860	0.71	0.991	0.79	0.996
	<i>Hallella</i>	1.00	1.000	1.00	1.000	0.00	0.924	0.00	0.924
	<i>Paraprevotella</i>	0.02	0.624	0.01	0.619	1.71	0.681	0.14	0.575
	<i>Prevotella</i>	0.80	0.603	1.11	0.856	1.68	0.039	1.35	0.389
	Prevotellaceae_uncl.	1.41	0.971	1.21	0.992	0.94	0.998	1.19	0.982
Rikenellaceae	-	1.15	0.524	0.74	0.154	0.55	0.035	0.64	0.113
	<i>Alistipes</i>	1.15	0.288	0.74	0.029	0.55	0.001	0.64	0.013
Phylum Firmicutes									
Acidaminococcaceae	-	1.51	0.099	1.70	0.017	1.06	0.975	1.07	0.965
	<i>Acidaminococcus</i>	14.95	0.174	18.50	0.070	0.00	1.000	0.00	1.000
	Acidaminococcaceae_uncl.	1.15	0.999	1.85	0.953	1.53	0.977	1.45	0.984
	<i>Succinoclasticum</i>	1.62	0.614	1.46	0.760	3.09	0.646	0.90	0.999
	<i>Phascolarctobacterium</i>	1.06	0.972	1.21	0.669	0.83	0.712	1.05	0.969
Clostridiales_uncl.	-	0.82	0.564	1.04	0.969	1.16	0.594	1.19	0.488
Clostridiaceae	-	0.75	0.956	0.66	0.918	0.92	0.999	0.84	0.996
	<i>Clostridium_sensu_stricto</i>	0.75	0.914	0.66	0.843	0.92	0.998	0.84	0.992
Enterococcaceae	-	1.02	1.000	1.28	0.999	0.81	1.000	0.59	1.000
	<i>Enterococcus</i>	1.02	1.000	1.28	0.999	0.81	1.000	0.59	1.000
Erysipelotrichaceae	-	1.41	0.910	1.12	0.991	1.61	0.895	2.13	0.686
	<i>Catenibacterium</i>	1.16	0.999	1.17	0.999	0.27	0.999	0.27	0.999
	<i>Clostridium_XVIII</i>	4.08	0.932	1.79	0.995	3.16	0.660	2.95	0.712
	<i>Coprobacillus</i>	1.45	1.000	1.66	0.999	0.40	0.999	0.74	1.000
	Erysipelotrichaceae_uncl.	1.17	0.985	1.01	1.000	0.75	0.993	0.96	1.000
	<i>Turicibacter</i>	1.00	1.000	1.29	1.000	0.70	1.000	8.85	0.870
Firmicutes_uncl.	-	1.04	0.936	1.15	0.386	0.82	0.227	0.59	0.002
Lachnospiraceae	-	1.09	0.000	0.98	0.593	1.03	0.294	1.09	0.001
	<i>Anaerostipes</i>	0.89	0.901	0.63	0.318	2.81	0.001	2.69	0.003
	<i>Blautia</i>	1.86	0.000	1.36	0.000	1.00	0.999	1.05	0.585

	<i>Clostridium_XIVa_uncl.</i>	0.92	0.991	1.08	0.991	1.10	0.959	0.99	1.000
	<i>Clostridium_XIVb_uncl.</i>	0.98	1.000	0.83	0.998	1.06	1.000	0.62	0.988
	<i>Coprococcus</i>	0.86	0.505	0.78	0.195	0.78	0.257	0.71	0.104
	<i>Dorea</i>	1.03	0.979	0.95	0.952	1.08	0.935	0.75	0.510
	<i>Lachnospira</i>	0.62	0.968	2.29	0.691	0.29	0.653	1.10	0.990
	Lachnospiraceae_uncl.	0.91	0.296	0.89	0.189	0.86	0.152	1.07	0.581
	<i>Howardella</i>	1.04	1.000	1.98	0.986	0.40	0.998	0.52	0.999
	<i>Roseburia</i>	0.92	0.432	0.75	0.002	1.15	0.197	1.21	0.043
	<i>Ruminococcus</i>	1.13	0.942	1.97	0.070	1.21	0.802	1.41	0.439
Lactobacillaceae	-	1.29	0.994	0.17	0.950	0.84	1.000	1.04	1.000
	<i>Lactobacillus</i>	1.29	0.987	0.17	0.902	0.84	1.000	1.04	1.000
Peptostreptococcaceae	-	1.01	1.000	1.22	0.855	0.60	0.679	0.79	0.894
	<i>Clostridium_XI</i>	1.01	1.000	1.22	0.733	0.60	0.456	0.79	0.793
Ruminococcaceae	-	0.90	0.000	0.92	0.004	0.93	0.031	0.89	0.000
	<i>Butyricoccus</i>	0.66	0.819	0.67	0.820	1.12	0.994	0.78	0.980
	<i>Faecalibacterium</i>	0.64	0.000	0.70	0.001	0.87	0.086	0.77	0.001
	<i>Flavonifractor</i>	1.74	0.930	1.49	0.969	1.38	0.984	1.28	0.991
	<i>Gemmiger</i>	0.82	0.727	0.67	0.358	0.72	0.640	0.95	0.985
	<i>Clostridium_IV_uncl.</i>	0.40	0.809	0.89	0.993	0.35	0.958	0.36	0.959
	<i>Oscillibacter</i>	0.53	0.834	0.86	0.984	1.87	0.844	2.53	0.606
	Ruminococcaceae_uncl.	0.98	0.760	1.04	0.445	0.92	0.177	0.92	0.182
	<i>Ruminococcus</i>	1.13	0.618	0.95	0.935	1.15	0.626	0.89	0.782
Streptococcaceae	-	0.98	1.000	1.10	0.996	0.70	0.943	0.98	1.000
	<i>Lactococcus</i>	0.78	0.996	1.10	0.999	0.44	0.999	1.24	1.000
	<i>Streptococcus</i>	1.07	0.998	1.10	0.997	0.71	0.902	0.96	0.998
Veillonellaceae	-	1.82	0.014	1.48	0.202	0.95	0.980	1.34	0.371
	<i>Dialister</i>	1.98	0.000	1.50	0.085	1.00	1.000	1.43	0.103
	<i>Megamonas</i>	3.26	0.996	2.12	0.999	2.40	0.999	0.81	1.000
	<i>Megasphaera</i>	0.74	0.990	1.19	0.995	0.53	0.942	0.77	0.986
	<i>Mitsuokella</i>	0.40	0.999	1.03	1.000	1.49	1.000	1.34	1.000
	<i>Veillonella</i>	0.87	1.000	2.05	0.990	0.40	1.000	0.62	1.000
Phylum Proteobacteria									
Alphaproteobacteria_uncl.	-	1.00	1.000	1.00	1.000	0.71	0.997	1.93	0.967
Desulfovibrionaceae	-	1.88	0.993	4.18	0.915	0.80	0.996	1.01	1.000
	<i>Desulfovibrio</i>	2.88	0.989	7.83	0.860	1.28	1.000	2.02	0.999
	Desulfovibrionaceae_uncl.	1.12	1.000	1.41	0.999	0.77	0.990	0.94	0.999
Enterobacteriaceae	-	0.50	0.911	1.23	0.981	0.66	0.838	0.77	0.926
	<i>Escherichia/Shigella</i>	0.46	0.871	1.33	0.947	0.63	0.772	0.83	0.945
	<i>Klebsiella</i>	0.64	0.997	0.77	0.999	0.75	0.991	0.59	0.974
Sutterellaceae	-	0.94	1.000	1.44	0.999	1.26	0.998	0.95	1.000
	<i>Parasutterella</i>	1.07	1.000	0.65	1.000	1.10	1.000	0.62	0.998
	<i>Sutterella</i>	0.86	1.000	1.72	0.997	1.44	0.997	1.27	0.999
Oxalobacteraceae	-	1.00	1.000	1.00	1.000	0.00	0.997	0.00	0.997
	Oxalobacteraceae_uncl.	1.00	1.000	1.00	1.000	0.00	0.994	0.00	0.994
Pasteurellaceae	-	0.70	1.000	0.19	1.000	1.76	0.998	1.20	1.000
	<i>Haemophilus</i>	0.70	1.000	0.19	1.000	1.76	0.996	1.20	1.000
Phylum Spirochaetae									
Brachyspiraceae	-	1.00	1.000	1.56	0.997	1.01	1.000	0.76	0.999
	<i>Brachyspira</i>	1.00	1.000	1.56	0.994	1.01	1.000	0.76	0.999
Spirochaetaceae	-	1.83	1.000	1.48	1.000	1.78	1.000	0.78	1.000
	<i>Treponema</i>	1.83	0.999	1.48	1.000	1.78	1.000	0.78	1.000
Phylum Verrucomicrobia									
Verrucomicrobiaceae	<i>Akkermansia</i>	1.22	0.707	1.23	0.680	0.77	0.825	0.84	0.908

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.