Table S1. Bacterial taxa involved in dysbiosis

	Taxa	Healthy controls, proportion of sequences*	Patients, proportion of sequences*	P-value (Mann-Whitney U test)
higher abundance in healthy controls than in patients at baseline	unknown Oscillospira	0.016860	0.007793	P<0.03
	unknown Oscillospira	0.001047	0.000411	P<0.03
	Bacteroidespectinophilus	0.000819	0	P<0.02
	unknown Bacteroidales	0.000659	0.000266	P<0.02
	unknown Clostridiales	0.000343	0.000014	P<0.02
	unknown Ruminococcaceae	0.000117	0	P<0.02
	unknown Oscillospira	0.000077	0.000006	P<0.02
higher abundance in patients than in healthy controls at baseline	unknown Coprococcus	0.00688	0.01554	P<0.005
	Bacteroides ovatus	0.00382	0.01371	P<0.02
	unknown Bifidobacteriales	0.00950	0.01230	P<0.02
	unknown Blautia	0.00190	0.00348	P<0.02
	unknown Clostridium	0.00059	0.00237	P<0.004
	unknown Clostridium	0.00091	0.00215	P<0.02
	unknown Clostridium	0.00015	0.00036	P<0.02
	unknown Clostridium	0.00001	0.00026	P<0.03
	unknown Phascolarctobacterium	0	0.00013	P<0.009

* Data are mean values