Dynamic microbe and molecule networks in a mouse model of colitis-associated colorectal cancer

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Supplementary information

Table S1 Barcodes and sequences number of samples

Sample ID	Barcode	Number of raw reads pairs	Number of sequences represented OTUs
C11	ACCTCA	1395623	1043035
C12	GCCTAA	886917	698154
C21	ACGGTA	1131961	885619
C22	GATCTG	778751	651044
C31	GTAGCC	1313896	1091203
C32	AGTTGG	1178678	909007
C33	CTCTCT	1013499	784671
C41	GCTCAA	1154459	960622
C42	CAAGTG	916887	708493
C43	CCTTGA	786794	614247
M11	TGGTCA	1117988	904088
M12	ACCACT	1077346	853359
M21	TCAAGT	805475	672753
M22	AGTGTC	1254538	956386
M31	TACAAG	1657483	984927
M32	AGAAGG	1193755	892718
M33	TTATCC	1048323	801159
M41	TCGCTT	992498	811872
M42	TTAAGG	1287952	984538
M43	TTCTTG	1388517	1037459
M44	TTCAAC	1117493	823291

Table S2 Differential OTUs between control and DSS treated groups

OTU	logFC	P-Value	FDR	Taxonomy
OTU00354	8.95	1.36E-04	1.86E-03	*uncl. S24-7*
OTU00491	8.53	3.44E-08	2.30E-06	*uncl. Erysipelotrichaceae*
OTU00199	7.75	1.22E-05	2.59E-04	*Prevotella*
OTU00047	7.61	1.32E-07	7.72E-06	*uncl. S24-7*
OTU00345	7.58	5.04E-05	8.40E-04	*Lachnobacterium*
OTU00063	7.46	5.13E-06	1.20E-04	*uncl. S24-7*
OTU00728	7.01	3.86E-09	6.00E-07	*Wandonia*
OTU00240	5.70	8.94E-05	1.39E-03	*AF12*
OTU00276	5.23	5.97E-04	6.06E-03	*Anaerostipes*
OTU00973	5.04	2.46E-04	2.73E-03	*uncl. Rikenellaceae*
OTU01356	4.77	1.23E-03	1.17E-02	*Faecalibacterium prausnitzii*
OTU00024	4.49	1.75E-04	2.25E-03	*Bacteroides*
OTU00549	4.38	2.95E-03	2.46E-02	*Moryella indoligenes*
OTU00218	4.31	4.07E-03	3.12E-02	*Ruminococcus*
OTU00111	4.30	1.34E-04	1.86E-03	*Ruminococcus*
OTU00260	3.98	5.76E-04	5.97E-03	*uncl. S24-7*
OTU00082	3.91	2.52E-06	6.91E-05	*Bacteroides uniformis*
OTU00363	3.82	3.61E-03	2.86E-02	*Bacteroides ovatus*
OTU00302	3.67	2.00E-03	1.77E-02	*Coprococcus*
OTU00495	3.60	3.07E-03	2.51E-02	*uncl. S24-7*
OTU00174	3.51	4.29E-04	4.66E-03	*Moryella indoligenes*
OTU00200	3.46	1.12E-03	1.09E-02	*Moryella indoligenes*
OTU01779	3.34	1.72E-03	1.54E-02	*Streptococcus luteciae*
OTU00358	3.22	4.85E-03	3.54E-02	*Odoribacter*
OTU00907	3.20	4.83E-03	3.54E-02	*Lactobacillus hamsteri*
OTU00101	3.19	5.56E-03	3.87E-02	*uncl. S24-7*
OTU00059	2.81	3.93E-03	3.06E-02	*Coprococcus*
OTU00408	2.70	6.40E-03	4.30E-02	*Roseburia faecis*
OTU00161	2.70	3.42E-03	2.76E-02	*Candidatus_Phytoplasma solani*
OTU00107	2.24	4.96E-03	3.56E-02	*uncl. S24-7*
OTU00084	1.95	6.37E-03	4.30E-02	*Oscillospira*
OTU00010	-2.12	5.55E-03	3.87E-02	*uncl. Rikenellaceae*
OTU00198	-2.26	6.45E-03	4.30E-02	*uncl. Rikenellaceae*
OTU00190	-3.07	8.58E-04	8.53E-03	*Faecalibacterium prausnitzii*
OTU00048	-3.26	2.53E-03	2.19E-02	*Rikenella*
OTU00135	-3.34	1.38E-05	2.80E-04	*uncl. Lachnospiraceae*
OTU01528	-3.47	4.78E-03	3.54E-02	*uncl. RF39*
OTU00441	-3.48	1.36E-03	1.27E-02	*Oribacterium*
OTU00108	-3.61	2.69E-03	2.29E-02	*uncl. S24-7*
OTU00191	-3.65	5.59E-04	5.94E-03	*cc_115*
OTU00393	-3.73	1.49E-04	1.99E-03	*Moryella indoligenes*

OTU00100	-3.84	1.94E-04	2.30E-03	*Ruminococcus gnavus*
OTU00068	-4.15	1.43E-03	1.31E-02	*uncl. Bacteroidales*
OTU00478	-4.72	2.41E-04	2.73E-03	*Moryella indoligenes*
OTU00124	-4.73	1.78E-04	2.25E-03	*Moryella indoligenes*
OTU00370	-4.74	4.36E-05	7.55E-04	*Moryella indoligenes*
OTU00062	-4.80	1.94E-04	2.30E-03	*Oribacterium*
OTU00157	-5.04	8.18E-05	1.32E-03	*Oribacterium*
OTU00090	-5.23	1.53E-06	4.56E-05	*Moryella indoligenes*
OTU00622	-5.35	1.10E-04	1.66E-03	*Candidatus_Phytoplasma witches-broom*
OTU06246	-5.52	1.97E-04	2.30E-03	*Ruminococcus*
OTU00514	-5.54	1.06E-06	3.53E-05	*Dorea*
OTU00106	-5.85	1.26E-08	1.17E-06	*uncl. Rikenellaceae*
OTU00329	-5.99	1.48E-05	2.87E-04	*Ruminococcus gnavus*
OTU00428	-6.13	1.26E-04	1.84E-03	*uncl. HDB_SIOH1004*
OTU00071	-6.58	1.02E-05	2.28E-04	*uncl. S24-7*
OTU00149	-6.61	7.15E-07	2.64E-05	*Moryella indoligenes*
OTU00303	-6.93	3.68E-07	1.72E-05	*Moryella indoligenes*
OTU00556	-7.21	1.56E-06	4.56E-05	*uncl. S24-7*
OTU05059	-7.21	3.17E-08	2.30E-06	*uncl. Mogibacteriaceae*
OTU00506	-7.25	8.92E-09	1.04E-06	*Moryella indoligenes*
OTU03118	-7.27	4.01E-05	7.20E-04	*Moryella indoligenes*
OTU00857	-7.34	7.35E-07	2.64E-05	*Candidatus_Phytoplasma solani*
OTU00534	-7.40	5.13E-06	1.20E-04	*Odoribacter*
OTU00178	-7.67	3.74E-06	9.70E-05	*uncl. S24-7*
OTU00586	-7.80	1.30E-15	3.03E-13	*Roseburia*
OTU00269	-8.01	2.18E-05	4.08E-04	*Ruminococcus gnavus*
OTU00377	-8.17	2.28E-07	1.18E-05	*Candidatus_Phytoplasma witches-broom*
OTU01385	-8.23	8.30E-17	3.88E-14	*Ruminococcus gnavus*
OTU00298	-8.30	6.15E-07	2.61E-05	*uncl. S24-7*

Table S3 Differential OTUs between mice with Inflammation and cancer

OTU	logFC	P-Value	FDR	Taxonomy
OTU00023	8.52	1.71E-05	3.19E-03	*uncl. S24-7*
OTU00024	-4.46	2.11E-04	2.35E-02	*Bacteroides*
OTU00491	-5.43	3.68E-05	5.13E-03	*uncl. Erysipelotrichaceae*
OTU02210	-6.00	4.52E-04	2.99E-02	*uncl. Christensenellaceae*
OTU00207	-7.54	4.83E-04	2.99E-02	*uncl. YS2*
OTU03781	-8.10	3.15E-04	2.51E-02	*uncl. Rikenellaceae*
OTU07075	-8.20	7.59E-04	4.24E-02	*Faecalibacterium prausnitzii*
OTU00199	-8.45	5.29E-07	2.95E-04	*Prevotella*
OTU01726	-9.67	2.85E-04	2.51E-02	*Flavobacterium succinicans*
OTU00354	-10.84	1.59E-06	4.43E-04	*uncl. S24-7*

Table S4 Differential OTUs after treatment of different AOM/DSS cycles

OTU	log FC	PValue	FDR	AOM/DSS_cycle	Taxonomy
OTU00354	10.61	1.12E-10	3.21E-08	AOM/DSS cycle1	*uncl. S24-7*
OTU00199	9.60	3.11E-13	1.78E-10	AOM/DSS cycle1	*Prevotella*
OTU03295	9.57	1.63E-07	1.86E-05	AOM/DSS cycle1	*Allobaculum*
OTU03781	8.77	2.82E-07	2.69E-05	AOM/DSS cycle1	*uncl. Rikenellaceae*
OTU00240	8.31	1.47E-08	2.10E-06	AOM/DSS cycle1	*AF12*
OTU07075	8.09	9.57E-06	6.85E-04	AOM/DSS cycle1	*Faecalibacterium prausnitzii*
OTU01228	6.96	3.33E-05	1.73E-03	AOM/DSS cycle1	*Allobaculum*
OTU26030	6.92	1.91E-05	1.09E-03	AOM/DSS cycle1	*02d06*
OTU00491	6.91	3.80E-09	7.25E-07	AOM/DSS cycle1	*uncl. Erysipelotrichaceae*
OTU00728	6.83	2.26E-06	1.85E-04	AOM/DSS cycle1	*Wandonia*
OTU01187	6.02	1.81E-04	7.96E-03	AOM/DSS cycle1	*uncl. S24-7*
OTU00276	5.66	2.79E-04	1.11E-02	AOM/DSS cycle1	*Anaerostipes*
OTU00358	5.65	5.00E-05	2.39E-03	AOM/DSS cycle1	*Odoribacter*
OTU00406	4.40	1.74E-05	1.09E-03	AOM/DSS cycle1	*Oscillospira*
OTU00161	4.15	1.10E-03	3.61E-02	AOM/DSS cycle1	*Candidatus_Phytoplasma solani*
OTU00266	4.14	1.13E-03	3.61E-02	AOM/DSS cycle1	*Butyrivibrio*
OTU00586	-7.67	3.88E-04	1.39E-02	AOM/DSS cycle1	*Roseburia*
OTU00019	-7.87	1.36E-03	4.11E-02	AOM/DSS cycle1	*Prevotella*
OTU01385	-8.02	2.91E-04	1.11E-02	AOM/DSS cycle1	*Ruminococcus gnavus*
OTU00679	13.98	1.89E-08	5.43E-06	AOM/DSS cycle2	*Parabacteroides distasonis*
OTU00117	13.40	8.25E-06	5.25E-04	AOM/DSS cycle2	*Bacteroides uniformis*
OTU00147	13.25	3.50E-06	2.80E-04	AOM/DSS cycle2	*Parabacteroides distasonis*
OTU00491	9.96	3.69E-15	2.11E-12	AOM/DSS cycle2	*uncl. Erysipelotrichaceae*
OTU00515	8.90	3.90E-06	2.80E-04	AOM/DSS cycle2	*uncl. S24-7*
OTU07948	8.44	2.71E-06	2.59E-04	AOM/DSS cycle2	*Salinispora tropica*
OTU00063	7.80	1.47E-05	8.40E-04	AOM/DSS cycle2	*uncl. S24-7*
OTU00047	7.57	5.89E-07	1.12E-04	AOM/DSS cycle2	*uncl. S24-7*
OTU02685	7.56	5.90E-05	2.82E-03	AOM/DSS cycle2	*uncl. S24-7*
OTU00728	6.90	1.79E-06	2.05E-04	AOM/DSS cycle2	*Wandonia*
OTU01105	6.76	3.71E-04	1.42E-02	AOM/DSS cycle2	*uncl. S24-7*
OTU01726	6.65	5.09E-04	1.72E-02	AOM/DSS cycle2	*Flavobacterium succinicans*
OTU03598	6.18	4.84E-04	1.72E-02	AOM/DSS cycle2	*uncl. Ruminococcaceae*
OTU01207	6.16	1.45E-04	6.41E-03	AOM/DSS cycle2	*Ruminococcus callidus*
OTU00024	5.79	1.22E-06	1.75E-04	AOM/DSS cycle2	*Bacteroides*
OTU00218	5.30	1.04E-03	2.84E-02	AOM/DSS cycle2	*Ruminococcus*
OTU00363	5.09	9.41E-04	2.74E-02	AOM/DSS cycle2	*Bacteroides ovatus*
OTU00111	4.47	1.38E-03	3.43E-02	AOM/DSS cycle2	*Ruminococcus*
OTU00168	4.27	1.28E-03	3.34E-02	AOM/DSS cycle2	*Lachnospira*
OTU00260	4.17	2.15E-03	4.53E-02	AOM/DSS cycle2	*uncl. S24-7*
OTU00174	3.93	2.47E-03	4.72E-02	AOM/DSS cycle2	*Moryella indoligenes*

OTU00266	3.89	2.29E-03	4.53E-02	AOM/DSS cycle2	*Butyrivibrio*
OTU00838	-5.02	2.24E-03	4.53E-02	AOM/DSS cycle2	*uncl. Ruminococcaceae*
OTU00048	-7.32	2.20E-03	4.53E-02	AOM/DSS cycle2	*Rikenella*
OTU00190	-7.42	2.13E-03	4.53E-02	AOM/DSS cycle2	*Faecalibacterium prausnitzii*
OTU01385	-8.02	2.99E-04	1.23E-02	AOM/DSS cycle2	*Ruminococcus gnavus*
OTU00296	-8.79	5.58E-04	1.78E-02	AOM/DSS cycle2	*Shuttleworthia*
OTU01528	-10.26	2.00E-03	4.53E-02	AOM/DSS cycle2	*uncl. RF39*
OTU00926	-10.55	9.55E-04	2.74E-02	AOM/DSS cycle2	*uncl. Rikenellaceae*
OTU00586	-10.81	3.42E-05	1.78E-03	AOM/DSS cycle2	*Roseburia*
OTU26030	8.52	1.87E-07	4.83E-05	AOM/DSS cycle3	*02d06*
OTU00603	8.12	3.03E-05	1.34E-03	AOM/DSS cycle3	*Sutterella*
OTU00345	8.06	1.95E-05	1.09E-03	AOM/DSS cycle3	*Lachnobacterium*
OTU01105	7.97	2.66E-05	1.27E-03	AOM/DSS cycle3	*uncl. S24-7*
OTU00047	7.91	8.65E-08	4.83E-05	AOM/DSS cycle3	*uncl. S24-7*
OTU02381	7.80	7.26E-05	2.73E-03	AOM/DSS cycle3	*Lactococcus garvieae*
OTU33993	7.60	8.24E-05	2.73E-03	AOM/DSS cycle3	*uncl. Ruminococcaceae*
OTU00063	7.59	1.09E-05	6.96E-04	AOM/DSS cycle3	*uncl. S24-7*
OTU00515	7.28	3.64E-05	1.49E-03	AOM/DSS cycle3	*uncl. S24-7*
OTU00728	7.21	2.53E-07	4.83E-05	AOM/DSS cycle3	*Wandonia*
OTU05397	7.15	1.36E-03	2.60E-02	AOM/DSS cycle3	*Proteus*
OTU03063	7.12	2.61E-03	3.74E-02	AOM/DSS cycle3	*Faecalibacterium prausnitzii*
OTU02685	7.05	7.80E-05	2.73E-03	AOM/DSS cycle3	*uncl. S24-7*
OTU00616	6.68	1.46E-04	4.40E-03	AOM/DSS cycle3	*Anaerostipes*
OTU00240	6.41	1.72E-06	1.97E-04	AOM/DSS cycle3	*AF12*
OTU00276	6.40	2.10E-05	1.09E-03	AOM/DSS cycle3	*Anaerostipes*
OTU00218	5.48	3.46E-04	8.45E-03	AOM/DSS cycle3	*Ruminococcus*
OTU25014	5.46	1.70E-03	2.78E-02	AOM/DSS cycle3	*uncl. RF39*
OTU01207	5.45	3.43E-04	8.45E-03	AOM/DSS cycle3	*Ruminococcus callidus*
OTU01356	5.37	1.52E-03	2.71E-02	AOM/DSS cycle3	*Faecalibacterium prausnitzii*
OTU00973	5.17	1.62E-03	2.78E-02	AOM/DSS cycle3	*uncl. Rikenellaceae*
OTU00260	5.01	8.56E-05	2.73E-03	AOM/DSS cycle3	*uncl. S24-7*
OTU00082	4.91	9.22E-07	1.32E-04	AOM/DSS cycle3	*Bacteroides uniformis*
OTU00491	4.77	8.31E-06	5.95E-04	AOM/DSS cycle3	*uncl. Erysipelotrichaceae*
OTU00130	4.46	8.40E-04	1.87E-02	AOM/DSS cycle3	*Rickettsia* *Rickettsia_endosymbiont_of_Deronectes_platynotus*
OTU00101	4.36	1.08E-03	2.15E-02	AOM/DSS cycle3	*uncl. S24-7*
OTU00111	4.33	8.47E-04	1.87E-02	AOM/DSS cycle3	*Ruminococcus*
OTU00234	3.65	3.81E-03	4.75E-02	AOM/DSS cycle3	*uncl. S24-7*
OTU00083	3.24	3.65E-03	4.75E-02	AOM/DSS cycle3	*Ruminococcus gnavus*
OTU00107	3.19	1.92E-03	2.97E-02	AOM/DSS cycle3	*uncl. S24-7*

OTU00135	-4.27	3.95E-03	4.82E-02	AOM/DSS cycle3	*uncl. Lachnospiraceae*
OTU00010	-4.34	1.65E-03	2.78E-02	AOM/DSS cycle3	*uncl. Rikenellaceae*
OTU00296	-5.84	9.67E-04	2.05E-02	AOM/DSS cycle3	*Shuttleworthia*
OTU00926	-6.33	2.61E-03	3.74E-02	AOM/DSS cycle3	*uncl. Rikenellaceae*
OTU00106	-6.68	3.11E-04	8.45E-03	AOM/DSS cycle3	*uncl. Rikenellaceae*
OTU00019	-6.85	3.54E-04	8.45E-03	AOM/DSS cycle3	*Prevotella*
OTU00090	-6.91	1.09E-03	2.15E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU02210	-6.99	2.48E-03	3.74E-02	AOM/DSS cycle3	*uncl. Christensenellaceae*
OTU00149	-7.34	4.19E-03	5.00E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU00124	-7.38	3.81E-03	4.75E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU01140	-7.38	3.65E-03	4.75E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU02602	-7.40	1.41E-03	2.61E-02	AOM/DSS cycle3	*Coprococcus catus*
OTU01904	-7.70	3.78E-03	4.75E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU00952	-8.35	2.69E-03	3.75E-02	AOM/DSS cycle3	*Moryella indoligenes*
OTU01385	-8.54	5.07E-06	4.15E-04	AOM/DSS cycle3	*Ruminococcus gnavus*
OTU00506	-8.76	2.13E-04	6.11E-03	AOM/DSS cycle3	*Moryella indoligenes*
OTU00586	-8.93	3.00E-06	2.86E-04	AOM/DSS cycle3	*Roseburia*
OTU00282	-9.73	1.88E-03	2.97E-02	AOM/DSS cycle3	*cc_115*
OTU26030	8.83	5.26E-08	1.51E-05	AOM/DSS cycle4	*02d06*
OTU00345	8.51	5.97E-06	4.88E-04	AOM/DSS cycle4	*Lachnobacterium*
OTU00047	8.05	3.16E-08	1.51E-05	AOM/DSS cycle4	*uncl. S24-7*
OTU00063	7.96	3.27E-06	3.12E-04	AOM/DSS cycle4	*uncl. S24-7*
OTU00957	7.20	3.18E-04	7.01E-03	AOM/DSS cycle4	*Moryella indoligenes*
OTU00728	7.20	1.37E-07	2.62E-05	AOM/DSS cycle4	*Wandonia*
OTU01105	6.85	1.24E-04	5.08E-03	AOM/DSS cycle4	*uncl. S24-7*
OTU00515	6.72	6.67E-05	3.19E-03	AOM/DSS cycle4	*uncl. S24-7*
OTU03598	6.53	8.58E-05	3.78E-03	AOM/DSS cycle4	*uncl. Ruminococcaceae*
OTU02685	6.20	2.23E-04	5.89E-03	AOM/DSS cycle4	*uncl. S24-7*
OTU01207	6.18	3.83E-05	2.00E-03	AOM/DSS cycle4	*Ruminococcus callidus*
OTU00675	6.14	2.33E-04	5.89E-03	AOM/DSS cycle4	*Moryella indoligenes*
OTU02381	5.90	1.06E-03	1.41E-02	AOM/DSS cycle4	*Lactococcus garvieae*
OTU33993	5.79	1.04E-03	1.41E-02	AOM/DSS cycle4	*uncl. Ruminococcaceae*
OTU00549	5.75	6.96E-04	1.14E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU01356	5.75	5.11E-04	9.16E-03	AOM/DSS cycle4	*Faecalibacterium prausnitzii*
OTU00471	5.50	4.22E-04	8.57E-03	AOM/DSS cycle4	*Ruminococcus gnavus*
OTU00973	5.30	8.45E-04	1.25E-02	AOM/DSS cycle4	*uncl. Rikenellaceae*
OTU01029	5.07	1.75E-03	2.01E-02	AOM/DSS cycle4	*uncl. Rikenellaceae*
OTU00302	4.75	2.58E-04	6.15E-03	AOM/DSS cycle4	*Coprococcus*
OTU00111	4.71	1.74E-04	5.89E-03	AOM/DSS cycle4	*Ruminococcus*
OTU00200	4.44	2.15E-04	5.89E-03	AOM/DSS cycle4	*Moryella indoligenes*
OTU00174	4.23	2.22E-04	5.89E-03	AOM/DSS cycle4	*Moryella indoligenes*
OTU00082	4.06	1.69E-05	1.07E-03	AOM/DSS cycle4	*Bacteroides uniformis*
OTU00058	3.86	6.86E-04	1.14E-02	AOM/DSS cycle4	*Moryella indoligenes*

OTU00260	3.70	1.93E-03	2.17E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU00059	3.67	2.89E-04	6.63E-03	AOM/DSS cycle4	*Coprococcus*
OTU00135	-3.89	2.03E-03	2.24E-02	AOM/DSS cycle4	*uncl. Lachnospiraceae*
OTU00090	-4.59	4.68E-03	4.00E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU01193	-5.95	1.55E-03	1.89E-02	AOM/DSS cycle4	*Shuttleworthia*
OTU00052	-6.04	4.35E-03	3.83E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU00610	-6.05	4.83E-03	4.01E-02	AOM/DSS cycle4	*uncl. Erysipelotrichaceae*
OTU00514	-6.12	1.22E-03	1.56E-02	AOM/DSS cycle4	*Dorea*
OTU00420	-6.30	5.25E-03	4.19E-02	AOM/DSS cycle4	*Desulfovibrio D168*
OTU03780	-6.48	9.14E-04	1.31E-02	AOM/DSS cycle4	*Ethanoligenens*
OTU00478	-6.51	2.75E-03	2.67E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU00106	-6.68	3.33E-05	1.91E-03	AOM/DSS cycle4	*uncl. Rikenellaceae*
OTU00329	-6.71	3.23E-03	3.03E-02	AOM/DSS cycle4	*Ruminococcus gnavus*
OTU05059	-6.71	6.95E-04	1.14E-02	AOM/DSS cycle4	*uncl. Mogibacteriaceae*
OTU00157	-6.71	2.27E-03	2.41E-02	AOM/DSS cycle4	*Oribacterium*
OTU00025	-6.84	4.34E-04	8.57E-03	AOM/DSS cycle4	*uncl. S24-7*
OTU00051	-6.97	1.93E-04	5.89E-03	AOM/DSS cycle4	*uncl. S24-7*
OTU02210	-6.99	4.95E-04	9.14E-03	AOM/DSS cycle4	*uncl. Christensenellaceae*
OTU00149	-7.00	1.41E-03	1.76E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU00303	-7.05	2.34E-03	2.44E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU02545	-7.06	5.22E-03	4.19E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU00926	-7.09	2.07E-04	5.89E-03	AOM/DSS cycle4	*uncl. Rikenellaceae*
OTU00506	-7.18	1.59E-04	5.89E-03	AOM/DSS cycle4	*Moryella indoligenes*
OTU01528	-7.19	4.09E-04	8.57E-03	AOM/DSS cycle4	*uncl. RF39*
OTU00586	-7.21	1.57E-06	1.80E-04	AOM/DSS cycle4	*Roseburia*
OTU00062	-7.25	1.12E-03	1.45E-02	AOM/DSS cycle4	*Oribacterium*
OTU01140	-7.38	8.14E-04	1.25E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU02602	-7.40	2.36E-04	5.89E-03	AOM/DSS cycle4	*Coprococcus catus*
OTU00068	-7.45	7.49E-04	1.19E-02	AOM/DSS cycle4	*uncl. Bacteroidales*
OTU00978	-7.47	2.40E-03	2.46E-02	AOM/DSS cycle4	*Roseburia faecis*
OTU02315	-7.51	4.76E-03	4.01E-02	AOM/DSS cycle4	*uncl. RF39*
OTU00556	-7.53	3.34E-03	3.09E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU20801	-7.55	4.14E-03	3.71E-02	AOM/DSS cycle4	*uncl. RF39*
OTU01761	-7.58	2.82E-03	2.69E-02	AOM/DSS cycle4	*uncl. RF39*
OTU00048	-7.59	1.14E-05	8.17E-04	AOM/DSS cycle4	*Rikenella*
OTU00036	-7.62	2.52E-03	2.53E-02	AOM/DSS cycle4	*uncl. Bacteroidales*
OTU00389	-7.65	2.23E-03	2.41E-02	AOM/DSS cycle4	*uncl. Bacteroidales*
OTU01904	-7.70	8.49E-04	1.25E-02	AOM/DSS cycle4	*Moryella indoligenes*
OTU00178	-7.87	6.17E-03	4.85E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU00428	-7.92	5.27E-03	4.19E-02	AOM/DSS cycle4	*uncl. HDB_SIOH1004*
OTU00298	-7.94	3.46E-03	3.15E-02	AOM/DSS cycle4	*uncl. S24-7*
OTU03160	-7.95	1.72E-03	2.01E-02	AOM/DSS cycle4	*uncl. RF39*
OTU01385	-8.13	2.98E-07	4.26E-05	AOM/DSS cycle4	*Ruminococcus gnavus*

OTU01559	-8.20	4.57E-03	3.97E-02	AOM/DSS cycle4	*cc_115*
OTU00534	-8.32	1.58E-03	1.89E-02	AOM/DSS cycle4	*Odoribacter*
OTU00857	-8.36	9.53E-04	1.33E-02	AOM/DSS cycle4	*Candidatus_Phytoplasma solani*
OTU00377	-9.63	4.91E-04	9.14E-03	AOM/DSS cycle4	*Candidatus_Phytoplasma witches-broom*
OTU01192	-10.57	2.66E-03	2.63E-02	AOM/DSS cycle4	*uncl. S24-7*

Table S5 OTU profiles

OTU	Profile ID	Log normalize OTU relative abundance*					Taxonomy
		Control	AOM/DDS cycle 1	AOM/DDS cycle 2	AOMDDS cycle 3	AOM/DDS cycle 4	
OTU00556	0	0	-0.47	-1.89	-1.63	-0.54	*uncl. S24-7*
OTU00219	0	0	-2.29	-5.72	-4.74	-4.78	*Moryella indoligenes*
OTU02192	0	0	-0.43	-0.71	-1.17	0.11	*uncl. Ruminococcaceae*
OTU00057	0	0	-0.71	-0.77	-1.14	-0.14	*Ruminococcus gnavus*
OTU03337	0	0	-0.59	-1.79	-1.94	-1.14	*Ruminococcus*
OTU00124	0	0	-4.14	-4.13	-5.33	-3.96	*Moryella indoligenes*
OTU00010	0	0	-2.18	-3.36	-4.05	-2.79	*uncl. Rikenellaceae*
OTU00119	0	0	-1.29	-1.76	-1.42	-1.02	*Coprococcus*
OTU00077	0	0	-1	-0.94	-1.88	-1.16	*Coprococcus*
OTU00100	0	0	-3.45	-5.25	-5.97	-3.06	*Ruminococcus gnavus*
OTU00035	0	0	-2.06	-1.48	-5.85	-0.76	*uncl. S24-7*
OTU00048	1	0	-7.09	-6.98	-6.35	-7.06	*Rikenella*
OTU00825	1	0	-1.37	-2.52	-0.26	-2.26	*Ethanoligenens*
OTU00090	1	0	-6.84	-5.92	-5.79	-5.92	*Moryella indoligenes*
OTU00178	1	0	-1.49	-1.23	-1.18	-0.81	*uncl. S24-7*
OTU00377	1	0	-4.48	-5.67	-4.22	-6.29	*Candidatus_Phytoplasma witches-broom*
OTU00393	1	0	-3.48	-4.61	-3.35	-4.65	*Moryella indoligenes*
OTU00143	1	0	-0.77	-1.39	-0.78	-1.06	*Ruminococcus gnavus*
OTU00062	2	0	-3.07	-1.69	-1.96	-2.26	*Oribacterium*
OTU00068	2	0	-5.95	-5.33	-5.39	-5.98	*uncl. Bacteroidales*
OTU00157	2	0	-1.62	-0.71	-0.93	-1.46	*Oribacterium*
OTU00071	2	0	-1.01	-0.5	-0.83	-1.21	*uncl. S24-7*
OTU00191	2	0	-7.04	-4.73	-6.39	-5.89	*cc_115*
OTU00036	2	0	-8.43	-4.55	-6.56	-6.81	*uncl. Bacteroidales*
OTU00042	3	0	-1.86	-1.11	-0.67	-0.28	*uncl. S24-7*
OTU03324	3	0	-0.16	-0.71	0.39	0.72	*uncl. Christensenellaceae*
OTU00136	3	0	-3.14	-1.33	-0.96	-0.32	*uncl. S24-7*
OTU00002	3	0	-1.09	-0.49	0.32	0.85	*uncl. S24-7*
OTU00065	3	0	0.01	-1.14	0.42	1.92	*Ruminococcus gnavus*
OTU02149	3	0	-1.15	-0.27	-0.36	0.1	*Adlercreutzia*
OTU00023	3	0	-5.62	-5.41	1.28	3.02	*uncl. S24-7*
OTU00851	3	0	-0.11	-0.59	0.5	1.06	*Moryella indoligenes*
OTU01282	3	0	-0.86	-0.01	-0.24	0.56	*Ethanoligenens*
OTU00140	3	0	-2.29	-0.35	1.42	1.85	*uncl. S24-7*
OTU00441	4	0	-2.08	-0.66	-0.14	-1.02	*Oribacterium*
OTU00182	4	0	-3.58	-0.01	0.22	-1.78	*Candidatus_Phytoplasma witches-broom*
OTU25185	4	0	-2.74	0.45	0.4	-0.06	*uncl. Peptococcaceae*
OTU00413	4	0	-2.68	-0.34	-0.4	-0.16	*Oscillospira*
OTU00026	4	0	-2.33	-0.84	-0.36	-0.27	*uncl. S24-7*
OTU00237	4	0	-7.35	-1.19	0.55	-2.7	*Ruminococcus*
OTU00270	4	0	-2.44	0.12	-0.71	-0.59	*uncl. S24-7*
OTU00263	4	0	-2.87	0.56	0.55	-0.28	*uncl. OPB3*
OTU00714	4	0	-1.73	0.15	1.01	-1.17	*Ruminococcus*
OTU00329	4	0	-1.45	0.5	0.22	-0.37	*Ruminococcus gnavus*
OTU00817	4	0	-4.47	0.7	-1.27	-1.81	*Persicobacter diffluens*
OTU00044	5	0	-0.55	-0.4	-1.54	-1.52	*Candidatus_Phytoplasma witches-broom*
OTU00135	5	0	-2.12	-2.07	-3.93	-3.84	*uncl. Lachnospiraceae*

OTU00514	5	0	-0.74	-3.93	-3.45	-3.5	*Dorea*
OTU00428	5	0	-0.8	-1.54	-3.79	-4.83	*uncl. HDB_SIOH1004*
OTU00052	5	0	-0.41	0.19	-4.29	-5.84	*uncl. S24-7*
OTU00460	5	0	-0.17	-0.96	-1.41	-2.04	*Ruminococcus gnavus*
OTU00069	5	0	3.02	-2.33	-6.17	-5.52	*uncl. S24-7*
OTU00029	5	0	0.14	-7.06	-6.33	-7.22	*uncl. S24-7*
OTU00153	5	0	0.37	-2.01	-1.68	-2.56	*Moryella indoligenes*
OTU00076	5	0	-0.14	-0.79	-1.46	-1.32	*Lactobacillus*
OTU00215	6	0	0.27	-2.2	-0.56	0.48	*Moryella indoligenes*
OTU00455	6	0	0.16	-1.75	-0.8	0.37	*uncl. SJA-15*
OTU00126	6	0	-2.03	-3.74	-0.3	-0.47	*Coprococcus*
OTU00765	6	0	-0.2	-6.73	-4.43	0.11	*Moryella indoligenes*
OTU00235	6	0	-1.56	-2	-2.67	1.58	*Mucispirillum schaedleri*
OTU00296	6	0	-6.39	-9.1	-5.42	-2.84	*Shuttleworthia*
OTU00190	6	0	-2.48	-6.78	-3.57	-2.86	*Faecalibacterium prausnitzii*
OTU00198	6	0	-3.37	-4.79	-3.61	-1.68	*uncl. Rikenellaceae*
OTU00812	6	0	-0.6	-2.69	-2.51	-0.06	*Coprococcus*
OTU00418	7	0	-5.22	-5.02	2.94	-4.27	*Candidatus_Phytoplasma solani*
OTU00223	7	0	-0.93	-2.55	0.74	-0.37	*uncl. TM7-1*
OTU00127	7	0	-1.74	-0.35	1.25	0.26	*uncl. OPB3*
OTU00163	7	0	-0.2	-0.46	0.93	0.09	*Oscillospira*
OTU00275	7	0	-1.93	-1.4	0.82	0.67	*Faecalibacterium prausnitzii*
OTU00196	7	0	-3.47	-4.86	0.22	-1.31	*Oscillospira*
OTU06927	7	0	-1.53	-1.83	0.46	0.45	*Adlercreutzia*
OTU00141	7	0	-1.45	0.08	2.14	0.06	*Anaerotruncus*
OTU00362	8	0	-1.48	0.35	-1.83	-0.47	*uncl. envOPS12*
OTU00255	8	0	-3.4	-1.31	-4.14	0.8	*Coprococcus*
OTU00250	8	0	-7.58	-1.27	-7.04	-2.86	*Moryella indoligenes*
OTU01157	8	0	-2.69	1.96	-0.77	0.95	*uncl. envOPS12*
OTU00122	8	0	-3.22	2.17	-4.27	1.66	*uncl. S24-7*
OTU00019	8	0	-8.07	-1.44	-7.02	-1.82	*Prevotella*
OTU00236	8	0	-5.16	1.35	-5.14	0.87	*uncl. S24-7*
OTU00278	8	0	-0.98	0.45	-2.05	0	*Ruminococcus gnavus*
OTU01764	9	0	-0.62	0.08	0.49	-0.78	*Faecalibacterium prausnitzii*
OTU00130	9	0	-2.31	-1.1	-1.35	-4.52	*Rickettsia Rickettsia_endosymbiont_of_Deronectes_platynotus*
OTU00305	9	0	-0.21	0.53	0.46	-0.72	*Moryella*
OTU00360	10	0	-0.04	2.26	-0.24	-0.98	*Oscillospira*
OTU00045	10	0	-1.03	1.42	-1.81	-1.03	*Moryella indoligenes*
OTU00388	10	0	-4.51	1.76	-4.92	-4.02	*uncl. S24-7*
OTU00709	10	0	-6.22	4.5	-0.63	-3.17	*Anaeroplasma*
OTU00099	10	0	-0.98	1.38	-2.85	-1.27	*uncl. Lachnospiraceae*
OTU00093	10	0	0.34	1.91	-0.91	-0.49	*Ruminococcus gnavus*
OTU01779	10	0	-0.94	3.98	0.7	-0.64	*Streptococcus luteciae*
OTU00056	10	0	-1.53	0.82	-1.86	-1.28	*Oribacterium*
OTU00125	10	0	-0.46	2.57	-0.31	-2.82	*Moryella indoligenes*
OTU00160	10	0	-0.25	1.68	-1.96	-0.23	*Ruminococcus gnavus*
OTU00112	10	0	-2.05	1.07	-1.85	-1.82	*Ruminococcus*
OTU02959	10	0	-4.74	1.8	-2.13	-3.11	*uncl. Enterobacteriaceae*
OTU00074	10	0	-2.15	3.49	-2.6	-1.53	*uncl. Desulfovibrionaceae*

OTU00105	10	0	-0.42	1.48	-0.39	-0.44	*Oscillospira*
OTU00319	11	0	-1.24	0.62	1.55	1.39	*Bilophila*
OTU00176	11	0	-3.23	0.6	1.07	1.55	*uncl. S24-7*
OTU00459	11	0	-1.24	0.65	0.57	0.17	*Dehalobacterium*
OTU00128	11	0	-1.43	0.35	0.14	0.02	*Ruminococcus*
OTU00011	11	0	-0.37	0.73	2.28	1.48	*uncl. S24-7*
OTU00260	11	0	-4.25	4.12	5.44	3.66	*uncl. S24-7*
OTU00060	11	0	-5.31	1.66	3.4	2.99	*uncl. S24-7*
OTU00281	11	0	-1.47	2.62	1.71	1.13	*uncl. Lachnospiraceae*
OTU00284	11	0	-2	1.68	1.76	1.53	*Ruminococcus gnavus*
OTU00165	11	0	-1.3	2.09	1.12	0.57	*Oscillospira*
OTU01343	11	0	-0.27	1.09	1.49	0.75	*Moryella indoligenes*
OTU00113	11	0	-0.77	0.27	0.79	1.19	*uncl. S24-7*
OTU00027	11	0	-4.01	0.12	0.56	0.76	*uncl. S24-7*
OTU00239	11	0	-6.73	1.47	0.78	1.89	*Coprococcus*
OTU01093	11	0	-0.43	0.84	1.25	1.12	*Oscillospira*
OTU01891	11	0	-1.74	-0.02	0.13	0.59	*Oscillospira*
OTU00299	11	0	-2.4	-0.4	0.91	0.52	*uncl. OPB3*
OTU00209	11	0	-0.76	0.75	1.57	0.51	*Coprococcus*
OTU00101	11	0	-2.7	4.42	5.51	3.76	*uncl. S24-7*
OTU00038	11	0	-4.15	0.15	0.63	1.58	*uncl. S24-7*
OTU01130	11	0	-1.45	1.64	2.73	2.31	*uncl. Rikenellaceae*
OTU00212	12	0	0.32	-3.94	-0.99	-1.81	*Candidatus_Phytoplasma solani*
OTU00822	12	0	1.51	-3.88	2.03	-0.4	*uncl. RF39*
OTU00005	12	0	0.09	-1.46	-0.4	-0.25	*uncl. S24-7*
OTU00386	12	0	2.88	-3.63	2.81	-2.03	*Candidatus_Phytoplasma*
OTU00314	12	0	0.86	-1.02	0.91	0.06	*Moryella indoligenes*
OTU00095	12	0	0.62	-0.8	0.41	0.2	*Coprococcus*
OTU00673	12	0	-0.32	-4.17	-0.37	-1.32	*uncl. Erysipelotrichaceae*
OTU03654	12	0	1.68	-1.71	0.83	-0.99	*Coprobacillus*
OTU00517	12	0	2.93	-5.95	2.75	-2.71	*Faecalibacterium prausnitzii*
OTU00058	12	0	0.75	-2.91	0.24	-0.82	*Moryella indoligenes*
OTU00225	12	0	-0.26	-3.11	-0.95	-1.01	*Moryella indoligenes*
OTU00032	12	0	1.23	-1.16	0.19	-1.07	*uncl. S24-7*
OTU00838	12	0	-0.93	-4.56	0.94	0.38	*uncl. Ruminococcaceae*
OTU06498	12	0	0.31	-2.14	1.93	-1.01	*uncl. TM7-1*
OTU00017	12	0	0.58	-2.06	0.47	0.75	*Moryella indoligenes*
OTU00262	12	0	-2.32	-6.38	-0.73	-2.75	*Clostridium*
OTU00061	12	0	-0.1	-2.13	1.02	-1.89	*Lactobacillus*
OTU00066	12	0	0	-2.8	0.13	-1.89	*Roseburia*
OTU00164	12	0	1.86	-5.04	0.29	-0.81	*Faecalibacterium prausnitzii*
OTU00379	12	0	-0.1	-2.22	0.81	0.31	*uncl. Mogibacteriaceae*
OTU00343	12	0	0.11	-5.12	1.4	-4.4	*Candidatus_Phytoplasma solani*
OTU00025	12	0	-0.64	-7.38	-1.1	-7.31	*uncl. S24-7*
OTU02321	12	0	-2.16	-5.7	-0.89	-2.76	*Ruminococcus*
OTU00433	12	0	-0.58	-7.23	1.36	-4.37	*uncl. RF39*
OTU00804	12	0	1.58	-5.67	-2.71	-5.51	*Paenibacillus illinoisensis*
OTU00681	12	0	-0.06	-1.95	-0.6	-1.92	*cc_115*
OTU00297	12	0	0.08	-1.94	-0.35	-1.01	*Oscillospira*
OTU00039	12	0	3.17	-5.65	0.74	-2.73	*uncl. S24-7*

OTU00394	12	0	0.53	-4.96	2.97	0.45	*uncl. RF39*
OTU00088	12	0	0.09	-1.74	-0.53	-0.37	*Oscillospira*
OTU00085	12	0	-0.59	-6.11	0.89	-5.9	*uncl. S24-7*
OTU00664	12	0	-0.32	-1.69	-0.32	-0.69	*Anaerofilum*
OTU00149	12	0	0.11	-2.35	-1.38	-1.44	*Moryella indoligenes*
OTU00173	13	0	1.1	-3.54	1.37	-3.63	*Candidatus_Phytoplasma solani*
OTU00300	13	0	-0.56	-1.1	-0.5	-1.85	*Moryella indoligenes*
OTU00238	13	0	-0.6	-2.7	-1.22	-2.95	*Moryella indoligenes*
OTU01176	13	0	-0.24	-0.97	-0.45	-1.66	*rc4-4*
OTU00478	13	0	2.52	-1.63	-1.49	-4.07	*Moryella indoligenes*
OTU00857	13	0	-0.4	-1.03	0.72	-2.32	*Candidatus_Phytoplasma solani*
OTU06707	13	0	-0.01	-1.6	-0.2	-1.94	*rc4-4*
OTU00051	13	0	1.56	-6.67	-3.1	-6.95	*uncl. S24-7*
OTU00188	14	0	-1.1	-1.3	-3.78	-3.08	*uncl. S24-7*
OTU00525	14	0	0.32	-0.07	-1.34	-1.09	*uncl. Rikenellaceae*
OTU00773	14	0	-0.24	-0.31	-1.65	-0.04	*Anaerotruncus*
OTU00733	14	0	0.26	0.8	-1.77	-0.92	*Nitratireductor*
OTU00013	14	0	0.4	0.74	-0.5	-0.45	*Ruminococcus gnavus*
OTU00844	14	0	0.09	-0.74	-1.5	-0.83	*Tsukamurella*
OTU00020	14	0	-0.96	-0.18	-6.16	-0.78	*uncl. S24-7*
OTU00333	14	0	-0.54	1.39	-4.48	-0.67	*cc_115*
OTU00193	14	0	0.51	0.76	-0.4	-0.18	*Moryella*
OTU00047	15	0	-0.07	8.14	1.15	8.24	*uncl. S24-7*
OTU00115	15	0	-0.34	1.74	-0.14	1.47	*Ruminococcus gnavus*
OTU00014	15	0	-0.44	0.63	-1.58	2.07	*uncl. S24-7*
OTU00079	15	0	-1.88	7.09	0.95	7.75	*Odoribacter*
OTU00109	15	0	-0.28	1.29	0.47	2.2	*uncl. Ruminococcaceae*
OTU00081	15	0	0	1.09	-0.36	1.15	*Moryella indoligenes*
OTU00561	16	0	1.07	0.55	6	-0.08	*Ruminococcus*
OTU00211	16	0	0.41	1.61	2.42	0.64	*uncl. S24-7*
OTU00216	16	0	1.11	1.56	2.6	-0.26	*uncl. S24-7*
OTU00218	16	0	-1.36	7.68	8.08	0	*Ruminococcus*
OTU00286	16	0	-0.54	-0.37	1	-0.65	*uncl. S24-7*
OTU00080	16	0	0.74	0.97	2.59	0.93	*Desulfovibrio C21_c20*
OTU00345	16	0	0.7	0.56	2.46	0.1	*Lachnobacterium*
OTU00103	16	0	0.55	0.56	2.75	1.37	*Desulfovibrio C21_c20*
OTU01451	16	0	0.75	1.38	2.07	0.31	*Adlercreutzia*
OTU00034	16	0	-0.29	0.23	0.81	0.1	*Oscillospira*
OTU00813	16	0	0.02	0.83	1.26	-0.22	*uncl. Mogibacteriaceae*
OTU25227	16	0	0.13	-0.14	2.25	-0.43	*Ethanoligenens*
OTU00449	17	0	3.9	-1.02	0.49	2.03	*Ruminococcus gnavus*
OTU00366	17	0	0.34	-5.59	-3.78	0.45	*Moryella indoligenes*
OTU00213	17	0	1.98	-2.62	-3.87	-3.09	*Oscillospira*
OTU00001	17	0	0.83	-0.45	-0.55	-0.44	*uncl. Rikenellaceae*
OTU00031	17	0	-0.07	-1.06	-0.63	-0.31	*Oscillospira*
OTU04198	17	0	-0.12	-3.44	-2.34	-1.23	*Moryella indoligenes*
OTU01165	17	0	2.14	-4.84	-3.09	-2.84	*Blautia*
OTU00118	17	0	3.5	0.12	-2.51	1.76	*Ruminococcus gnavus*
OTU01128	17	0	4.44	-1.09	-0.5	-0.05	*Ruminococcus*
OTU00330	17	0	3.53	-4.24	-2.63	1.54	*Ruminococcus gnavus*

OTU00159	17	0	3.73	-1.77	0.01	-0.57	*Coprococcus*
OTU00277	17	0	2.3	-1.58	-2.33	-2.06	*Oscillospira*
OTU00279	17	0	-0.55	-5.46	-4.21	-2.29	*uncl. S24-7*
OTU00199	17	0	10.13	-1.54	1.41	0.09	*Prevotella*
OTU00104	17	0	1.72	-0.49	0.32	0.35	*Coprococcus*
OTU00033	17	0	0.7	-1.8	-1.55	-0.52	*uncl. Lachnospiraceae*
OTU00030	17	0	1.47	-0.27	0.16	0.42	*uncl. S24-7*
OTU00269	17	0	2.04	-2.43	-0.95	-0.88	*Ruminococcus gnavus*
OTU01089	17	0	2.43	-4.84	-0.36	1.72	*Butyrivibrio*
OTU00040	18	0	2.39	0.76	-0.34	4.08	*uncl. S24-7*
OTU00004	18	0	0.24	-0.56	-0.75	0.73	*uncl. S24-7*
OTU00098	18	0	1.46	0.52	0.29	1.36	*Ruminococcus gnavus*
OTU00097	18	0	0.3	-0.52	-0.28	0.59	*Ruminococcus gnavus*
OTU01605	18	0	1.33	-0.32	-1.73	1.74	*Moryella indoligenes*
OTU01171	18	0	1.63	0.26	0.24	1.29	*uncl. Mogibacteriaceae*
OTU00302	18	0	2.39	0.85	2.1	5.24	*Coprococcus*
OTU00430	18	0	2.01	0.4	0.57	1.58	*Ruminococcus gnavus*
OTU00342	18	0	0.85	-0.12	-0.02	1.58	*Ruminococcus gnavus*
OTU00437	18	0	2.69	-3.36	0.32	4.57	*Moryella indoligenes*
OTU00205	18	0	0.45	-0.24	0.78	2.97	*uncl. RF32*
OTU00249	18	0	2.79	-1.8	0.3	4.49	*Moryella indoligenes*
OTU00046	19	0	1.04	-0.54	0.31	-0.27	*uncl. S24-7*
OTU00041	19	0	4.66	1.09	2.01	0.21	*Turicibacter*
OTU00183	19	0	3.39	-1.73	0.83	-2.21	*uncl. S24-7*
OTU00184	19	0	1.79	1.46	1.92	0.47	*Lactobacillus reuteri*
OTU00006	19	0	2.08	1.18	1.49	0.24	*Bacteroides acidifaciens*
OTU00355	19	0	1.1	0.55	1.81	0.59	*uncl. S24-7*
OTU00463	19	0	3.46	-3.26	4.58	-3.04	*Faecalibacterium prausnitzii*
OTU00504	19	0	1	0.42	2.12	0.55	*Oscillospira*
OTU00083	19	0	0.81	-0.21	3.31	0.4	*Ruminococcus gnavus*
OTU00272	19	0	3.13	0.97	1.51	0.69	*Moryella indoligenes*
OTU00998	19	0	8.27	1.03	5.69	-0.4	*Ruminococcus gnavus*
OTU00247	19	0	1.55	0.1	1.69	0.59	*uncl. Bacteriovoraceae*
OTU00498	19	0	4.24	-0.95	2.12	0.82	*Moryella indoligenes*
OTU00861	19	0	0.53	-0.09	0.49	-0.5	*Tepidibacter*
OTU00624	20	0	0.87	0.24	1.6	1.59	*uncl. Ruminococcaceae*
OTU00210	20	0	0.44	-1.65	1.59	0.97	*Coprococcus*
OTU00009	20	0	1.89	0.21	1.86	1.41	*uncl. Rikenellaceae*
OTU00312	20	0	3.63	-0.74	2.11	1.74	*Shuttleworthia*
OTU01988	20	0	4.02	1.53	3.19	2.33	*Adlercreutzia*
OTU00055	20	0	1.43	0.62	2.54	2.29	*uncl. S24-7*
OTU00540	20	0	2	-3.07	1.81	1.35	*Dehalobacterium*
OTU00012	20	0	0.53	-0.61	0.72	0.42	*uncl. S24-7*
OTU00064	20	0	2.47	1.56	3.07	3.27	*uncl. S24-7*
OTU00028	20	0	0.5	-0.53	0.29	0.56	*uncl. S24-7*
OTU00234	20	0	2.81	-0.76	5.3	4.02	*uncl. S24-7*
OTU00481	20	0	1.02	-1.61	1.08	1.27	*Moryella indoligenes*
OTU01177	20	0	1.98	0.56	1.72	2.19	*Ruminococcus*
OTU00155	20	0	1.82	-1.13	2.08	1.18	*Coprococcus*
OTU00273	20	0	3.09	-2.21	0.48	2.95	*Ruminococcus gnavus*

OTU00294	20	0	2.21	-0.32	3.71	2.45	*uncl. Rikenellaceae*
OTU00195	20	0	1.23	-2.89	2.73	4.39	*Ruminococcus gnavus*
OTU00107	20	0	2.03	1.32	3.59	2.41	*uncl. S24-7*
OTU00530	20	0	1.38	-0.44	2.91	1.26	*uncl. S24-7*
OTU00406	20	0	4.99	-0.56	1.84	2	*Oscillospira*
OTU02669	20	0	0.37	-0.43	0.92	0.68	*uncl. Christensenellaceae*
OTU00145	20	0	1.36	0.26	1.02	1.14	*Ruminococcus*
OTU00144	20	0	0.8	0.55	1.47	0.89	*uncl. S24-7*
OTU03291	20	0	5.83	-0.29	1.97	3.85	*uncl. RF39*
OTU01640	20	0	0.77	-1.23	2.5	0.77	*Candidatus_Phytoplasma solani*
OTU01718	20	0	1.68	-1.59	1.69	1.21	*uncl. Christensenellaceae*
OTU00365	21	0	0.98	0.47	-0.64	0.66	*uncl. S24-7*
OTU00137	21	0	4.94	3.1	-2.25	3.22	*Moryella indoligenes*
OTU00559	21	0	0.73	4.27	-2.62	1.12	*Candidatus_Phytoplasma witches-broom*
OTU00257	21	0	2.91	0.63	-2.52	2.04	*Ruminococcus gnavus*
OTU00252	21	0	0.52	0.98	-0.09	0.56	*Coprococcus*
OTU00772	21	0	0.73	2.14	-3.39	0.23	*Candidatus_Arthromitus*
OTU00871	21	0	2.2	1.3	-0.19	1.19	*Coprococcus*
OTU00054	21	0	0.72	1.89	-0.63	0.92	*Oscillospira*
OTU00229	21	0	2.29	3.34	-0.62	1.64	*Moryella indoligenes*
OTU00072	21	0	0.72	1.14	-6.93	0.44	*uncl. S24-7*
OTU00037	21	0	0.51	1.23	-0.59	0.95	*Blautia producta*
OTU00391	21	0	1.67	1.29	-0.17	0.79	*uncl. YS2*
OTU00148	21	0	0.68	1	-0.96	1.69	*Coprococcus*
OTU00003	22	0	-0.32	0.61	-0.44	-3.58	*Bacteroides*
OTU00175	22	0	0.02	0.54	-0.68	-0.95	*uncl. Christensenellaceae*
OTU00114	22	0	1.31	0.58	0.01	-1.01	*uncl. S24-7*
OTU00022	22	0	0.29	2.17	0.14	-2.21	*Bacteroides*
OTU00233	22	0	1.46	1.44	-3.47	-4.72	*Moryella indoligenes*
OTU00078	22	0	2.83	0.57	0.65	-1.92	*Ruminococcus gnavus*
OTU00241	22	0	-0.14	0.04	-1.13	-2.25	*Flexithrix dorotheae*
OTU01061	23	0	5.7	2.86	3.54	4.11	*Moryella indoligenes*
OTU00007	23	0	3.81	2.43	3.41	2.87	*uncl. S24-7*
OTU00008	23	0	3.81	2.42	3.42	2.86	*uncl. S24-7*
OTU00907	23	0	5.04	5	3.03	4.97	*Lactobacillus hamsteri*
OTU02444	23	0	2.02	1.2	1.75	2.48	*Adlercreutzia*
OTU03300	23	0	1.24	2.02	1.66	1.81	*Arthrobacter crystallopoietes*
OTU00121	23	0	1.04	1.48	1.6	1.51	*uncl. S24-7*
OTU01784	23	0	2.09	1.42	0.93	1.51	*uncl. YS2*
OTU00261	23	0	5.08	3.07	2.67	4.01	*Coprococcus*
OTU00110	23	0	2.92	4.17	3.72	2.85	*uncl. S24-7*
OTU00021	23	0	1.51	0.95	1.55	1.48	*uncl. S24-7*
OTU02328	23	0	3.44	3.83	3.17	3.06	*uncl. S24-7*
OTU00152	23	0	1.94	1.48	1.79	1.98	*Coprococcus*
OTU00070	23	0	3.76	3.03	3.81	3.39	*uncl. S24-7*
OTU00202	23	0	1.59	2.06	1.11	1.14	*Ruminococcus*
OTU00757	23	0	4.78	4.27	2.64	2.96	*Faecalibacterium prausnitzii*
OTU02724	23	0	3.15	2.3	1.97	2.06	*uncl. Rikenellaceae*
OTU00082	23	0	4.1	4	4.31	4.82	*Bacteroides uniformis*
OTU00084	23	0	1.46	1.05	1.71	1.19	*Oscillospira*

OTU00929	23	0	4.47	4.78	6.05	1.92	*uncl. envOPS12*
OTU00444	24	0	4.03	4.53	1.46	1.31	*Ruminococcus*
OTU00318	24	0	1.1	1.45	0.67	0.41	*Moryella*
OTU00875	24	0	1	4.22	0.81	-0.82	*cc_115*
OTU00639	24	0	0.88	2.07	0.57	-0.13	*Candidatus_Phytoplasma witches-broom*
OTU00120	24	0	1.21	2.34	0.13	-0.42	*Helicobacter hepaticus*
OTU01837	24	0	3.42	3.45	1.87	0.77	*uncl. HDB_SIOH1004*
OTU00280	24	0	1.95	3.47	0.67	0.37	*Oribacterium*
OTU00024	24	0	3.51	6.48	1.15	0.43	*Bacteroides*
OTU00156	24	0	1.28	2.22	1.48	0.28	*Moryella indoligenes*
OTU00206	24	0	2.07	2.43	0.49	-0.03	*Moryella indoligenes*
OTU00102	24	0	1.95	4.86	2.2	-0.31	*Moryella indoligenes*
OTU00491	24	0	7.04	10.08	4.2	1.15	*uncl. Erysipelotrichaceae*
OTU00089	24	0	0.44	1.18	0.8	0.13	*Ruminococcus gnavus*
OTU05301	25	0	1.21	0.82	2.54	2.18	*uncl. S24-7*
OTU00258	25	0	1.34	0.89	1.99	3.44	*Moryella indoligenes*
OTU00059	25	0	-0.14	1.76	4.16	6.01	*Coprococcus*
OTU00228	25	0	-0.3	0.09	1.05	1.04	*Moryella indoligenes*
OTU00018	25	0	0.92	0.81	2.12	2.44	*uncl. Rikenellaceae*
OTU00849	25	0	-0.31	0.39	0.74	1.3	*uncl. Mogibacteriaceae*
OTU00200	25	0	2.67	3.86	4.64	5.59	*Moryella indoligenes*
OTU00246	25	0	-0.82	0.32	2.11	2.54	*Moryella indoligenes*
OTU25661	25	0	1.1	1.43	1.66	2.03	*Dehalobacterium*
OTU00363	26	0	3.23	7.29	3.72	4.32	*Bacteroides ovatus*
OTU00599	26	0	2	2.9	0.94	1.91	*Staphylococcus epidermidis*
OTU00217	26	0	0.39	1.04	-0.23	0.59	*Moryella indoligenes*
OTU01446	26	0	2.6	6.9	0.97	6	*Christensenella*
OTU01336	26	0	2.22	4.82	0.14	1.3	*Oscillospira*
OTU00174	26	0	1.04	4.35	1.99	4.05	*Moryella indoligenes*
OTU00091	26	0	-0.87	4.86	0.46	1.59	*Ruminococcus gnavus*
OTU00220	26	0	0	2.05	0.41	0.57	*Ruminococcus gnavus*
OTU00542	26	0	0.31	2.46	0.39	1.88	*Adlercreutzia*
OTU00067	26	0	1.47	3.34	1.62	1.34	*Coprococcus*
OTU00154	26	0	-0.97	2.39	0.28	0.53	*uncl. envOPS12*
OTU00158	26	0	1.28	2.33	1.42	1.7	*Ruminococcus gnavus*
OTU01178	26	0	0.64	1.07	0.23	1	*Prevotella*
OTU00203	26	0	1.14	4.33	1.45	2.88	*uncl. Clostridiales*
OTU00538	26	0	0.23	3.35	0.59	1.49	*Ruminococcus gnavus*
OTU00408	26	0	-0.1	4.46	1.25	1.47	*Roseburia faecis*
OTU00245	26	0	-0.29	2.22	-0.09	1.04	*Moryella indoligenes*
OTU00457	27	0	0.25	1.38	1.51	1.04	*Dehalobacterium*
OTU01776	27	0	-0.39	1.56	1.84	0.74	*uncl. Ruminococcaceae*
OTU02184	27	0	1.31	3.88	2.82	2.12	*Odoribacter*
OTU00111	27	0	0.77	5.66	5.32	5.71	*Ruminococcus*
OTU00231	27	0	-0.28	0.9	0.5	-0.01	*Dehalobacterium*
OTU00809	27	0	0.85	6.55	5.49	3.12	*Moryella indoligenes*
OTU00993	27	0	1.55	2.18	2.14	1.04	*uncl. S24-7*
OTU00569	28	0	2.53	0.91	-0.13	-0.34	*Oribacterium*
OTU00180	28	0	1.99	0.44	0.33	0.12	*uncl. S24-7*
OTU00185	28	0	3.84	2.56	-2.33	-0.16	*Moryella indoligenes*

OTU00189	28	0	3.01	1.99	-0.32	-1.29	*Oribacterium*
OTU00134	28	0	4.3	2.84	1.55	0.32	*uncl. Lachnospiraceae*
OTU00417	28	0	4.44	4.23	0.09	0.38	*Moryella indoligenes*
OTU01020	28	0	8.46	2.42	0.95	2.21	*SMB53*
OTU00259	28	0	5.47	6.08	-0.4	1.09	*Coprococcus*
OTU00256	28	0	5.36	3.42	0.35	-0.36	*Lachnobacterium*
OTU00316	28	0	2.5	0.45	-0.91	0.22	*Ruminococcus gnavus*
OTU00317	28	0	2.24	0.9	0.77	0.99	*Parabacteroides*
OTU00170	28	0	2.39	-0.16	0.14	-0.9	*uncl. Rikenellaceae*
OTU00899	28	0	1.06	0.84	0.43	0.59	*Oscillospira*
OTU01345	28	0	3.13	3.31	-0.38	-1.01	*uncl. Ruminococcaceae*
OTU00313	28	0	2.66	2.14	-0.76	-0.27	*Ruminococcus gnavus*
OTU00356	28	0	1.99	2.1	-0.62	-0.06	*Ruminococcus gnavus*
OTU00357	28	0	2.29	2.24	0.23	0.45	*Oxobacter*
OTU00588	28	0	2.63	2.6	-0.21	-1.11	*uncl. Ruminococcaceae*
OTU00464	28	0	1.57	2.15	-0.25	0.41	*Adlercreutzia*
OTU00308	28	0	3.16	2.08	-2.07	-1.63	*uncl. Lachnospiraceae*
OTU00266	28	0	4.49	4.23	1.05	0.86	*Butyrivibrio*
OTU00168	28	0	4.05	4.65	-0.6	1.13	*Lachnospira*
OTU00166	28	0	1.06	-0.23	-0.55	-0.75	*uncl. Ruminococcaceae*
OTU00161	28	0	4.13	1.92	1.69	1.26	*Candidatus_Phytoplasma solani*
OTU00116	28	0	3.15	2.92	-1.72	-0.21	*Lachnospira*
OTU00500	28	0	5.29	2.83	0.38	0.66	*uncl. Christensenellaceae*
OTU00434	28	0	6.17	6.97	-0.93	0.17	*uncl. Desulfovibrionaceae*
OTU00276	28	0	7.58	-0.59	1.24	-0.66	*Anaerostipes*
OTU00073	28	0	3.16	1.99	-0.2	0	*Oribacterium*
OTU00075	28	0	5.18	2.23	2.14	2.89	*Sutterella*
OTU00192	28	0	0.96	0.26	-0.34	0.09	*Faecalibacterium prausnitzii*
OTU00204	28	0	3.55	1.55	1.87	1.28	*uncl. S24-7*
OTU00207	28	0	10.13	-0.78	1.54	-0.12	*uncl. YS2*
OTU00614	28	0	2	0.37	0.68	0.24	*Adlercreutzia*
OTU00240	28	0	9.49	-0.15	0.26	-0.5	*AF12*
OTU00327	28	0	1.48	0.01	0.19	-0.9	*Coprococcus*
OTU00086	28	0	4.26	3.78	-0.33	0.68	*Moryella indoligenes*
OTU00142	28	0	1.38	0.49	-0.37	-0.28	*Oscillospira*
OTU00096	29	0	0.81	0.85	0.35	1.9	*uncl. S24-7*
OTU00053	29	0	5.58	6.55	1.01	6.54	*uncl. Bacteroidales*
OTU02317	29	0	2.8	4.08	0.87	3.98	*uncl. envOPS12*
OTU00712	29	0	7.97	7.78	1.45	7.96	*uncl. Ruminococcaceae*
OTU00087	29	0	5.99	4.67	1.67	4.58	*uncl. S24-7*

* The data was transformed as $\log_2$ (median of relative abundance of AOM/DSS cycle i /median of relative abundance of control)

Table S6 OTUs correlated with tumor counts

OTU	Green gene classification	Correlation coefficient	P-value
OTU00002	*uncl. S24-7*	0.88	0.05
OTU00014	*uncl. S24-7*	0.94	0.02
OTU00016	*Odoribacter*	0.94	0.02
OTU00023	*uncl. S24-7*	0.97	0.01
OTU00052	*uncl. S24-7*	-0.93	0.02
OTU00058	*Moryella indoligenes*	1.00	0.00
OTU00059	*Coprococcus*	1.00	0.00
OTU00065	*Ruminococcus gnavus*	0.93	0.02
OTU00131	*Bacteroides*	-0.91	0.03
OTU00152	*Coprococcus*	0.98	0.00
OTU00195	*Ruminococcus gnavus*	0.94	0.02
OTU00200	*Moryella indoligenes*	0.97	0.01
OTU00205	*uncl. RF32*	0.93	0.02
OTU00206	*Moryella indoligenes*	-0.89	0.05
OTU00210	*Coprococcus*	0.89	0.04
OTU00246	*Moryella indoligenes*	1.00	0.00
OTU00258	*Moryella indoligenes*	0.92	0.03
OTU00302	*Coprococcus*	0.99	0.00
OTU00338	*Moryella indoligenes*	0.96	0.01
OTU00345	*Lachnobacterium*	0.90	0.04
OTU00471	*Ruminococcus gnavus*	0.95	0.01
OTU00531	*uncl. S24-7*	0.98	0.00
OTU00549	*Moryella indoligenes*	0.94	0.02
OTU00561	*Ruminococcus*	1.00	0.00
OTU00588	*uncl. Ruminococcaceae*	-0.92	0.03
OTU00597	*uncl. S24-7*	0.97	0.01
OTU00634	*Faecalibacterium prausnitzii*	0.91	0.03
OTU00675	*Moryella indoligenes*	0.97	0.01
OTU00850	*Moryella indoligenes*	0.94	0.02
OTU00957	*Moryella indoligenes*	1.00	0.00
OTU01029	*uncl. Rikenellaceae*	0.90	0.04
OTU01136	*uncl. S24-7*	0.96	0.01
OTU01356	*Faecalibacterium prausnitzii*	0.89	0.04
OTU01692	*Adlercreutzia*	0.93	0.02
OTU02929	*Moryella indoligenes*	0.98	0.00
OTU03214	*uncl. Rikenellaceae*	0.88	0.05

Table S7 OTUs correlated with molecule expressions

Molecule	OTU	Correlation coefficient	P-value	Taxonomy
β-catenin	OTU00038	0.93	0.02	*uncl. S24-7*
β-catenin	OTU00047	0.93	0.02	*uncl. S24-7*
β-catenin	OTU00059	0.88	0.05	*Coprococcus*
β-catenin	OTU00063	0.89	0.04	*uncl. S24-7*
β-catenin	OTU00084	0.89	0.04	*Oscillospira*
β-catenin	OTU00110	0.99	0.00	*uncl. S24-7*
β-catenin	OTU00111	0.91	0.03	*Ruminococcus*
β-catenin	OTU00134	-0.91	0.03	*uncl. Lachnospiraceae*
β-catenin	OTU00185	-0.89	0.04	*Moryella indoligenes*
β-catenin	OTU00195	0.89	0.05	*Ruminococcus gnavus*
β-catenin	OTU00200	0.97	0.01	*Moryella indoligenes*
β-catenin	OTU00205	0.89	0.04	*uncl. RF32*
β-catenin	OTU00246	0.90	0.04	*Moryella indoligenes*
β-catenin	OTU00302	0.89	0.04	*Coprococcus*
β-catenin	OTU00313	-0.91	0.03	*Ruminococcus gnavus*
β-catenin	OTU00327	-0.89	0.04	*Coprococcus*
β-catenin	OTU00345	0.92	0.03	*Lachnobacterium*
β-catenin	OTU00357	-0.92	0.03	*Oxobacter*
β-catenin	OTU00525	-0.90	0.04	*uncl. Rikenellaceae*
β-catenin	OTU00757	-0.93	0.02	*Faecalibacterium prausnitzii*
β-catenin	OTU00849	0.97	0.01	*uncl. Mogibacteriaceae*
β-catenin	OTU00957	0.89	0.05	*Moryella indoligenes*
β-catenin	OTU00973	0.96	0.01	*uncl. Rikenellaceae*
β-catenin	OTU01070	-0.90	0.04	*Coprococcus*
β-catenin	OTU01356	0.91	0.03	*Faecalibacterium prausnitzii*
β-catenin	OTU02507	0.91	0.03	*uncl. S24-7*
β-catenin	OTU02576	0.92	0.03	*uncl. S24-7*
β-catenin	OTU25661	0.88	0.05	*Dehalobacterium*
β-catenin	OTU26030	0.88	0.05	*02d06*
CCR2	OTU00044	-0.94	0.02	*Candidatus_Phytoplasma witches-broom*
CCR2	OTU00064	0.93	0.02	*uncl. S24-7*
CCR2	OTU00069	-0.90	0.04	*uncl. S24-7*
CCR2	OTU00084	0.94	0.02	*Oscillospira*
CCR2	OTU00110	0.91	0.03	*uncl. S24-7*
CCR2	OTU00134	-0.93	0.02	*uncl. Lachnospiraceae*
CCR2	OTU00241	-0.95	0.01	*Flexithrix dorotheae*
CCR2	OTU00313	-0.89	0.04	*Ruminococcus gnavus*
CCR2	OTU00318	-0.90	0.04	*Moryella*
CCR2	OTU00357	-1.00	0.00	*Oxobacter*
CCR2	OTU00460	-0.95	0.01	*Ruminococcus gnavus*
CCR2	OTU00525	-0.94	0.02	*uncl. Rikenellaceae*
CCR2	OTU00728	0.93	0.02	*Wandonia*
CCR2	OTU00907	0.91	0.03	*Lactobacillus hamsteri*
CCR2	OTU00926	-0.89	0.04	*uncl. Rikenellaceae*
CCR2	OTU00973	0.98	0.00	*uncl. Rikenellaceae*
CCR2	OTU01029	0.88	0.05	*uncl. Rikenellaceae*

CCR2	OTU02724	-0.93	0.02	*uncl. Rikenellaceae*
CCR2	OTU25661	0.95	0.01	*Dehalobacterium*
CCR2	OTU26030	0.90	0.04	*02d06*
COX2	OTU00029	-0.89	0.04	*uncl. S24-7*
COX2	OTU00047	1.00	0.00	*uncl. S24-7*
COX2	OTU00063	0.97	0.01	*uncl. S24-7*
COX2	OTU00069	-0.91	0.03	*uncl. S24-7*
COX2	OTU00104	-0.88	0.05	*Coprococcus*
COX2	OTU00110	0.95	0.01	*uncl. S24-7*
COX2	OTU00111	0.97	0.01	*Ruminococcus*
COX2	OTU00134	-0.99	0.00	*uncl. Lachnospiraceae*
COX2	OTU00153	-0.91	0.03	*Moryella indoligenes*
COX2	OTU00176	0.88	0.05	*uncl. S24-7*
COX2	OTU00185	-0.95	0.01	*Moryella indoligenes*
COX2	OTU00192	-0.92	0.03	*Faecalibacterium prausnitzii*
COX2	OTU00313	-0.94	0.02	*Ruminococcus gnavus*
COX2	OTU00327	-0.96	0.01	*Coprococcus*
COX2	OTU00357	-0.88	0.05	*Oxobacter*
COX2	OTU00378	0.97	0.01	*Christensenella*
COX2	OTU00460	-0.90	0.04	*Ruminococcus gnavus*
COX2	OTU00525	-0.94	0.02	*uncl. Rikenellaceae*
COX2	OTU00757	-0.91	0.03	*Faecalibacterium prausnitzii*
COX2	OTU00849	0.90	0.04	*uncl. Mogibacteriaceae*
COX2	OTU00871	-0.91	0.03	*Coprococcus*
COX2	OTU00973	0.96	0.01	*uncl. Rikenellaceae*
COX2	OTU00978	-0.98	0.00	*Roseburia faecis*
COX2	OTU01070	-0.97	0.01	*Coprococcus*
COX2	OTU01165	-0.95	0.02	*Blautia*
COX2	OTU01207	0.90	0.04	*Ruminococcus callidus*
COX2	OTU02210	-0.98	0.00	*uncl. Christensenellaceae*
COX2	OTU02507	0.91	0.03	*uncl. S24-7*
COX2	OTU02576	0.89	0.04	*uncl. S24-7*
COX2	OTU02724	-0.98	0.00	*uncl. Rikenellaceae*
COX2	OTU03405	-0.96	0.01	*uncl. Ruminococcaceae*
COX2	OTU25221	-0.94	0.02	*Moryella indoligenes*
COX2	OTU25661	0.93	0.02	*Dehalobacterium*
p53	OTU00044	-0.89	0.04	*Candidatus_Phytoplasma witches-broom*
p53	OTU00047	0.93	0.02	*uncl. S24-7*
p53	OTU00060	0.88	0.05	*uncl. S24-7*
p53	OTU00069	-0.93	0.02	*uncl. S24-7*
p53	OTU00082	0.90	0.04	*Bacteroides uniformis*
p53	OTU00101	0.90	0.04	*uncl. S24-7*
p53	OTU00134	-0.97	0.00	*uncl. Lachnospiraceae*
p53	OTU00166	-0.88	0.05	*uncl. Ruminococcaceae*
p53	OTU00254	-0.89	0.04	*Ruminococcus gnavus*
p53	OTU00260	0.90	0.04	*uncl. S24-7*
p53	OTU00272	-0.88	0.05	*Moryella indoligenes*
p53	OTU00288	0.92	0.03	*Oscillospira*
p53	OTU00313	-0.93	0.02	*Ruminococcus gnavus*
p53	OTU00357	-0.91	0.03	*Oxobacter*

p53	OTU00378	0.98	0.00	*Christensenella*
p53	OTU00460	-0.92	0.03	*Ruminococcus gnavus*
p53	OTU00525	-0.97	0.01	*uncl. Rikenellaceae*
p53	OTU00728	0.88	0.05	*Wandonia*
p53	OTU00871	-0.98	0.00	*Coprococcus*
p53	OTU00925	-0.90	0.04	*Coprococcus catus*
p53	OTU00926	-0.90	0.04	*uncl. Rikenellaceae*
p53	OTU00973	0.95	0.01	*uncl. Rikenellaceae*
p53	OTU00978	-0.90	0.04	*Roseburia faecis*
p53	OTU01105	0.93	0.02	*uncl. S24-7*
p53	OTU01165	-0.95	0.01	*Blautia*
p53	OTU02210	-0.91	0.03	*uncl. Christensenellaceae*
p53	OTU02724	-0.99	0.00	*uncl. Rikenellaceae*
p53	OTU25661	0.98	0.00	*Dehalobacterium*
p65	OTU00021	1.00	0.00	*uncl. S24-7*
p65	OTU00064	0.89	0.05	*uncl. S24-7*
p65	OTU00070	0.93	0.02	*uncl. S24-7*
p65	OTU00084	0.90	0.04	*Oscillospira*
p65	OTU00131	-0.92	0.03	*Bacteroides*
p65	OTU00145	0.96	0.01	*Ruminococcus*
p65	OTU00184	0.91	0.03	*Lactobacillus reuteri*
p65	OTU00204	0.89	0.04	*uncl. S24-7*
p65	OTU00244	-0.88	0.05	*Coprococcus*
p65	OTU00250	-0.89	0.04	*Moryella indoligenes*
p65	OTU00318	-0.88	0.05	*Moryella*
p65	OTU00585	-0.93	0.02	*Moryella indoligenes*
p65	OTU00648	-0.93	0.02	*uncl. Holosporaceae*
p65	OTU00907	0.92	0.03	*Lactobacillus hamsteri*
p65	OTU01171	0.93	0.02	*uncl. Mogibacteriaceae*
p65	OTU01270	-0.92	0.03	*Moryella indoligenes*
p65	OTU01413	-0.95	0.01	*uncl. Ruminococcaceae*
p65	OTU02444	0.94	0.02	*Adlercreutzia*
p65	OTU05670	-0.97	0.00	*Ruminococcus*
PPARG	OTU00002	0.93	0.02	*uncl. S24-7*
PPARG	OTU00003	-0.88	0.05	*Bacteroides*
PPARG	OTU00013	-0.91	0.03	*Ruminococcus gnavus*
PPARγ	OTU00023	0.92	0.03	*uncl. S24-7*
PPARγ	OTU00040	0.91	0.03	*uncl. S24-7*
PPARγ	OTU00052	-0.97	0.01	*uncl. S24-7*
PPARγ	OTU00058	0.93	0.02	*Moryella indoligenes*
PPARγ	OTU00059	0.93	0.02	*Coprococcus*
PPARγ	OTU00064	0.91	0.03	*uncl. S24-7*
PPARγ	OTU00065	0.95	0.01	*Ruminococcus gnavus*
PPARγ	OTU00084	0.93	0.02	*Oscillospira*
PPARγ	OTU00131	-0.92	0.02	*Bacteroides*
PPARγ	OTU00152	0.89	0.05	*Coprococcus*
PPARγ	OTU00195	1.00	0.00	*Ruminococcus gnavus*
PPARγ	OTU00200	0.94	0.02	*Moryella indoligenes*
PPARγ	OTU00205	0.99	0.00	*uncl. RF32*
PPARγ	OTU00206	-0.95	0.01	*Moryella indoligenes*

PPARγ	OTU00210	0.97	0.01	*Coprococcus*
PPARγ	OTU00241	-0.91	0.03	*Flexithrix dorotheae*
PPARγ	OTU00246	0.94	0.02	*Moryella indoligenes*
PPARγ	OTU00302	0.96	0.01	*Coprococcus*
PPARγ	OTU00345	0.99	0.00	*Lachnobacterium*
PPARγ	OTU00356	-0.96	0.01	*Ruminococcus gnavus*
PPARγ	OTU00561	0.91	0.03	*Ruminococcus*
PPARγ	OTU00624	0.95	0.01	*uncl. Ruminococcaceae*
PPARγ	OTU00849	0.93	0.02	*uncl. Mogibacteriaceae*
PPARγ	OTU00850	0.96	0.01	*Moryella indoligenes*
PPARγ	OTU00929	0.89	0.04	*uncl. envOPS12*
PPARγ	OTU00957	0.94	0.02	*Moryella indoligenes*
PPARγ	OTU01029	0.97	0.01	*uncl. Rikenellaceae*
PPARγ	OTU01356	0.99	0.00	*Faecalibacterium prausnitzii*
PPARγ	OTU25580	0.95	0.01	*Adlercreutzia*
PPARγ	OTU26030	0.98	0.00	*02d06*

Table S8 Comparisons of sequence divergence distributions between OTUs in dynamic profiles and randomly selected sequences of 97% OTUs.

Profile ID	P-value
28	7.47E-55
12	4.04E-23
20	6.62E-07
11	2.56E-06
23	2.20E-04
17	3.55E-10
26	3.22E-14
10	2.87E-11
19	5.94E-04
21	2.39E-08
24	3.66E-07
16	4.75E-07
18	7.72E-05
0	2.83E-02
4	2.76E-03
3	1.28E-02
5	3.28E-04
6	3.26E-04
14	4.32E-03
25	3.47E-02
7	2.39E-03
8	2.81E-02
13	8.67E-01
1	6.51E-01
22	9.70E-02
27	8.27E-01
2	7.66E-01
15	3.44E-01
29	8.21E-02
9	4.98E-02

Table S9 mothur commands

```
pcr.seqs(fasta=gg_13_5_99.fasta,oligos=pcrV3.oligos,keepdots=F, processors=4)
make.contigs(file=dds_sample.files, processors=4)
summary.seqs(fasta=dds_sample.trim.contigs.fasta,processors=4)
screen.seqs(fasta=dds_sample.trim.contigs.fasta, group=dds_sample.contigs.groups,
summary=dds_sample.trim.contigs.summary, maxambig=0, maxlength=210)
summary.seqs(fasta=dds_sample.trim.contigs.good.fasta)
unique.seqs(fasta=dds_sample.trim.contigs.good.fasta)
count.seqs(name=dds_sample.trim.contigs.good.names, group=dds_sample.contigs.good.groups)
summary.seqs(count=dds_sample.trim.contigs.good.count_table,processors=4)
align.seqs(fasta=dds_sample.trim.contigs.good.unique.fasta, reference=v3.fasta,processors=4)
summary.seqs(fasta=dds_sample.trim.contigs.good.unique.align,
count=dds_sample.trim.contigs.good.count_table)
screen.seqs(fasta=dds_sample.trim.contigs.good.unique.align,
count=dds_sample.trim.contigs.good.count_table,
summary=dds_sample.trim.contigs.good.unique.summary, start=2, end=6699,
maxhomop=8,processors=4)
summary.seqs(fasta=current, count=current)
filter.seqs(fasta=dds_sample.trim.contigs.good.unique.good.align, vertical=T, trump=.)
unique.seqs(fasta=dds_sample.trim.contigs.good.unique.good.filter.fasta,
count=dds_sample.trim.contigs.good.good.count_table)
pre.cluster(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.fasta,
count=dds_sample.trim.contigs.good.unique.good.filter.count_table, diffs=2)
chimera.uchime(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.fasta,
count=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.count_table, dereplicate=t)
remove.seqs(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.fasta,
accnos=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.uchime.accnos)
summary.seqs(fasta=current, count=current)
classify.seqs(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta,
count=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.uchime.pick.count_table,
reference=trainset.fasta, taxonomy=trainset.pds.tax)
remove.lineage(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta,
count=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.uchime.pick.count_table,
taxonomy=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pds.wang.taxonomy, taxon=Chloroplast-Mitochondria-unknown-Archaea-Eukaryota)
dist.seqs(fasta=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.fasta,
cutoff=0.2)
cluster(column=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.dist,
count=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.uchime.pick.pick.count_table)
make.shared(list=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.list,
count=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.uchime.pick.pick.count_table)
```

```
sub.sample(shared=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.shared,size=614247)
rarefaction.single(shared=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.shared,calc=sobs, freq=1000,processors=4)
summary.single(shared=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.shared,calc=sobs-chao-ace-invsimpson-shannon-simpsoneven-shannoneven)
tree.shared(shared=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.shared,calc=jest-thetayc-braycurtis)
dist.shared(shared=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.shared, calc=jest-thetayc-braycurtis)
nmds(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.jest.0.03.lt.dist,mindim=3,maxdim=3)
nmds(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.thetayc.0.03.lt.dist,mindim=3,maxdim=3)
nmds(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.braycurtis.0.03.lt.dist,mindim=3,maxdim=3)
amova(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.jest.0.03.lt.dist, design=dds_design)
amova(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.thetayc.0.03.lt.dist, design=dds_design)
amova(phylip=dds_sample.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.an.unique_list.0.03.subsample.braycurtis.0.03.lt.dist, design=dds_design)
```

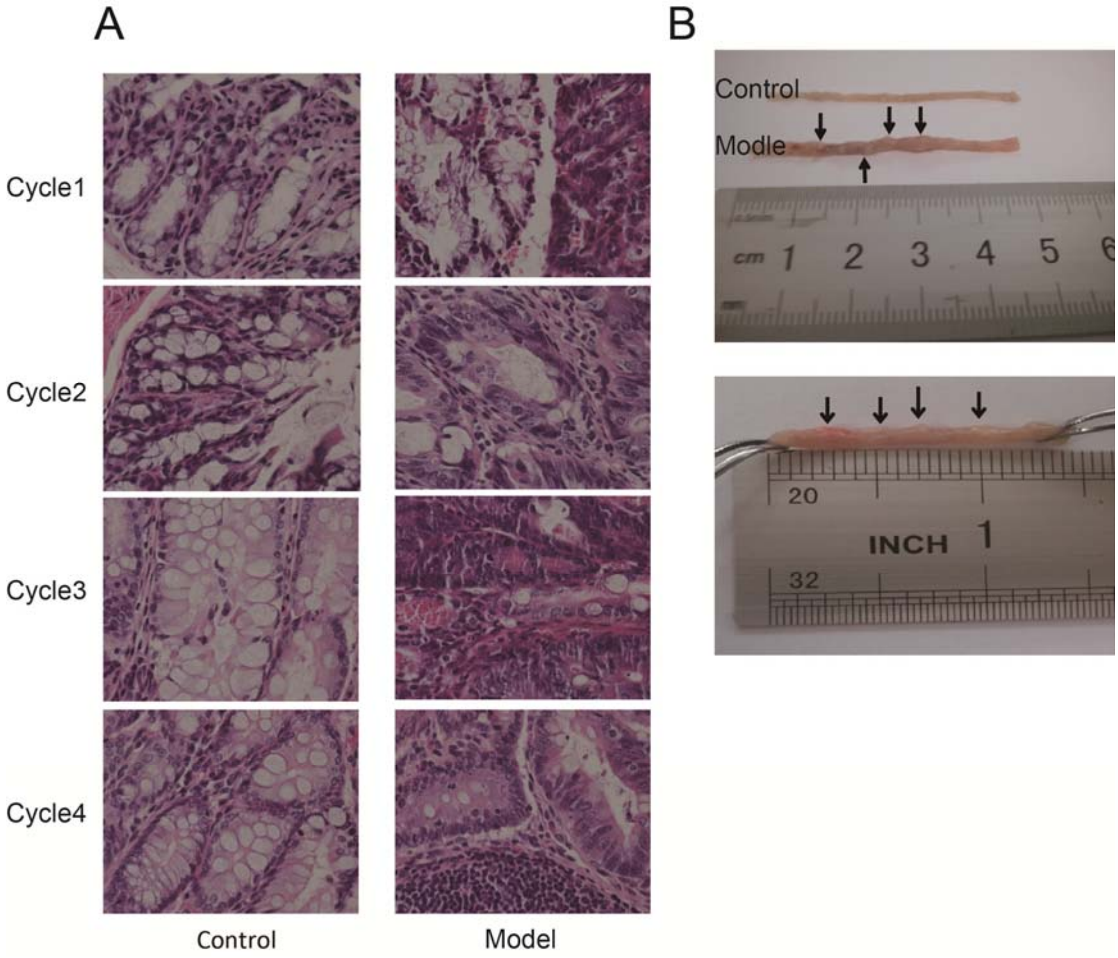

Fig. S1 Pathological development of colitis-associated colorectal cancer murine model. (A) H&E stains of sections of mouse colon tissues, model group mice treated with AOM+1~4 DSS cycles. (B) Macroscopic view shows tumors in the distal colons of mice with AOM+3 DSS cycles.

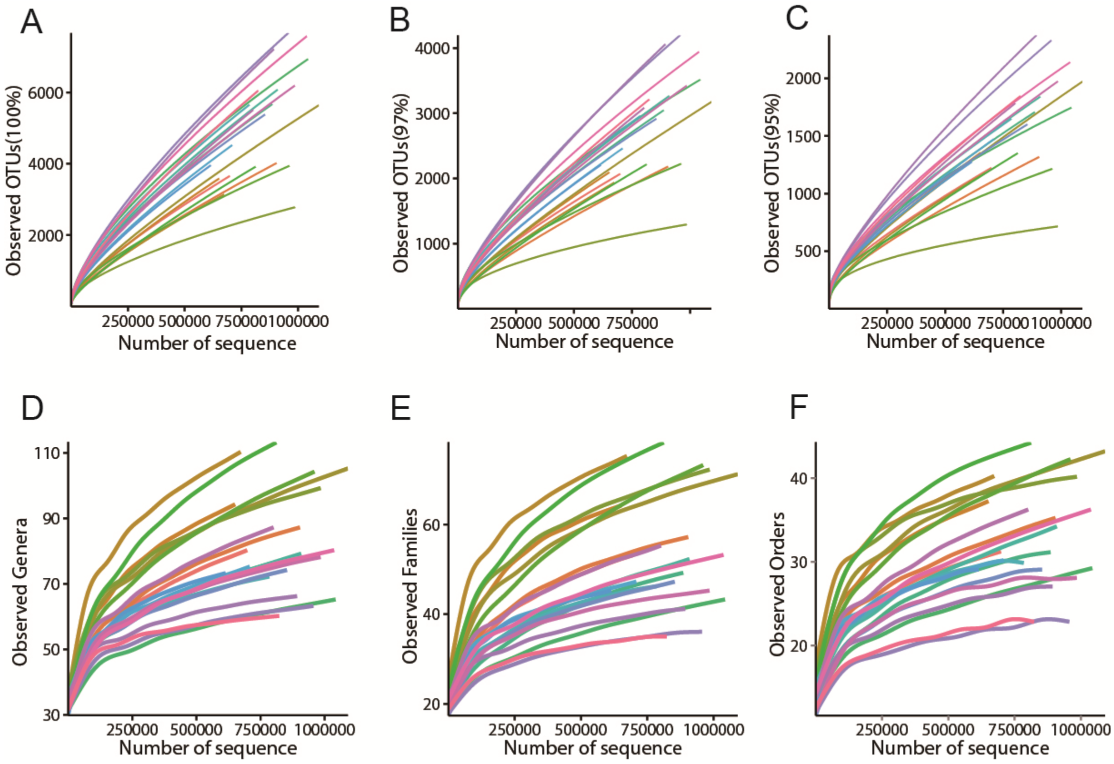

Fig. S2 Rarefaction curves of samples. Rarefaction curves were based on (A) unique sequences, (B) 97% OTUs, (C) 95% OTUs, (D) observed genera, (E) observed families and (F) observed orders.

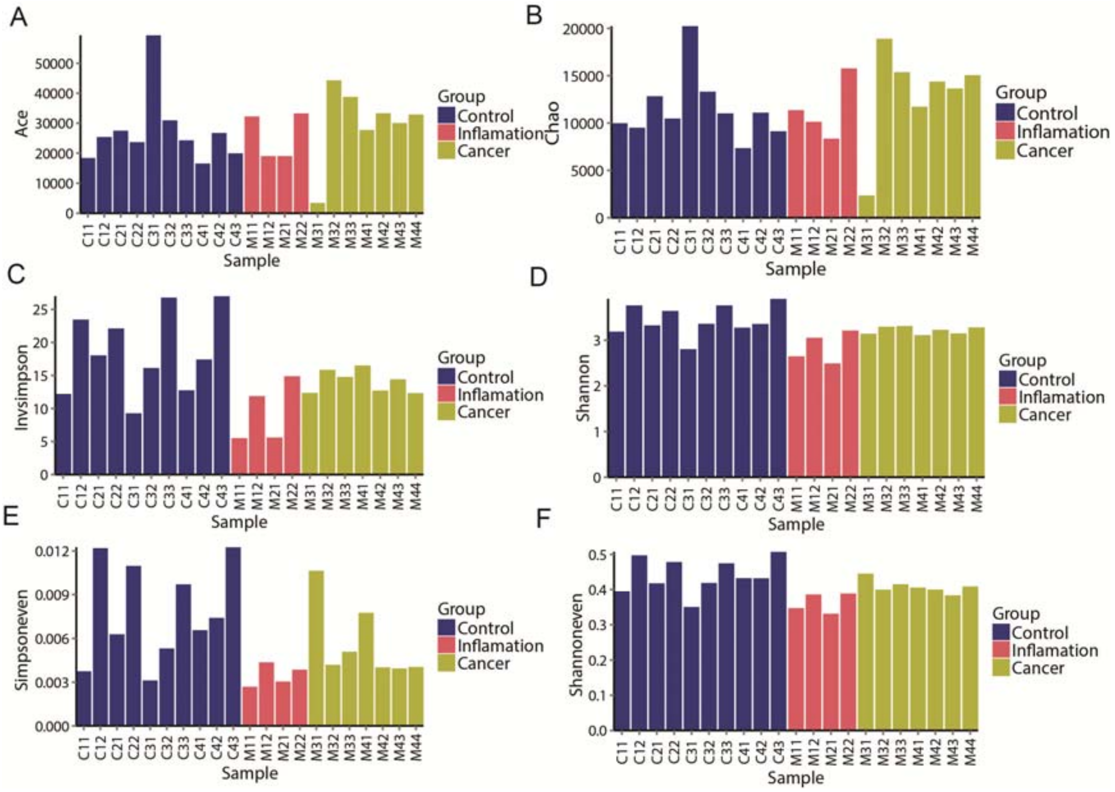

Fig. S3 Bar plots of estimators of alpha diversity. (A) Chao, (B) ACE, (C) Inverse Simpson index, (D) Shannon index, (E) Simpson index-based measure of evenness, (F) Shannon index-based measure of evenness. Sample was denominated as following rules: the beginning C/M represents control or model group; the middle number represents the number of AOM/DSS cycles for model group or batch of euthanization for control group; the last number represents different mice for repeats. Blue: control group, red: Inflammation group (treated with 1-2 AOM/DSS cycles), yellow: cancer group (treated with 3-4 AOM/DSS cycles),

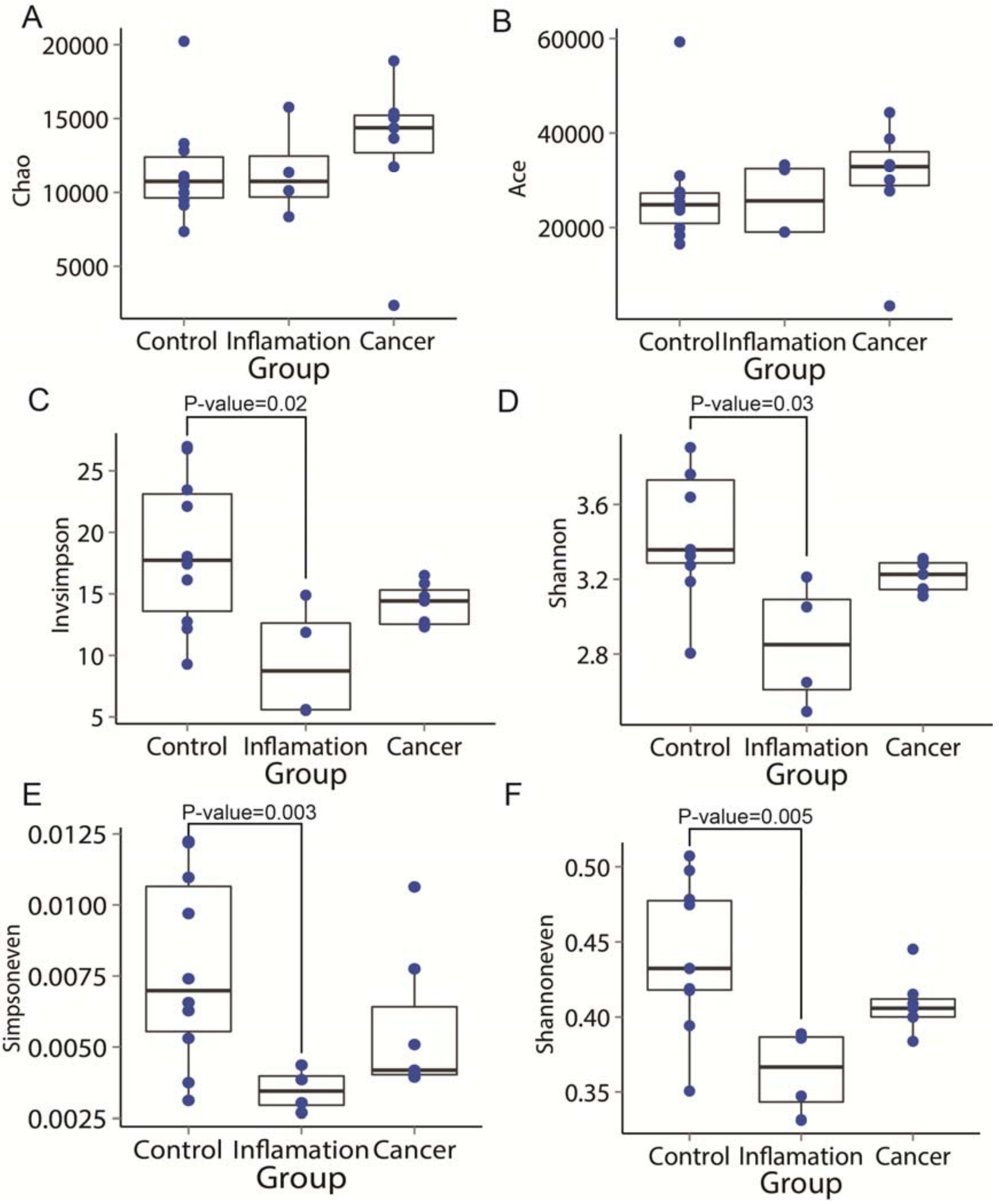

Fig. S4 Box plots of estimators of alpha diversity. (A) Chao, (B) ACE, (C) Inverse Simpson index, (D) Shannon index, (E) Simpson index-based measure of evenness, (F) Shannon index-based measure of evenness. Two-tailed Student's t tests were performed.

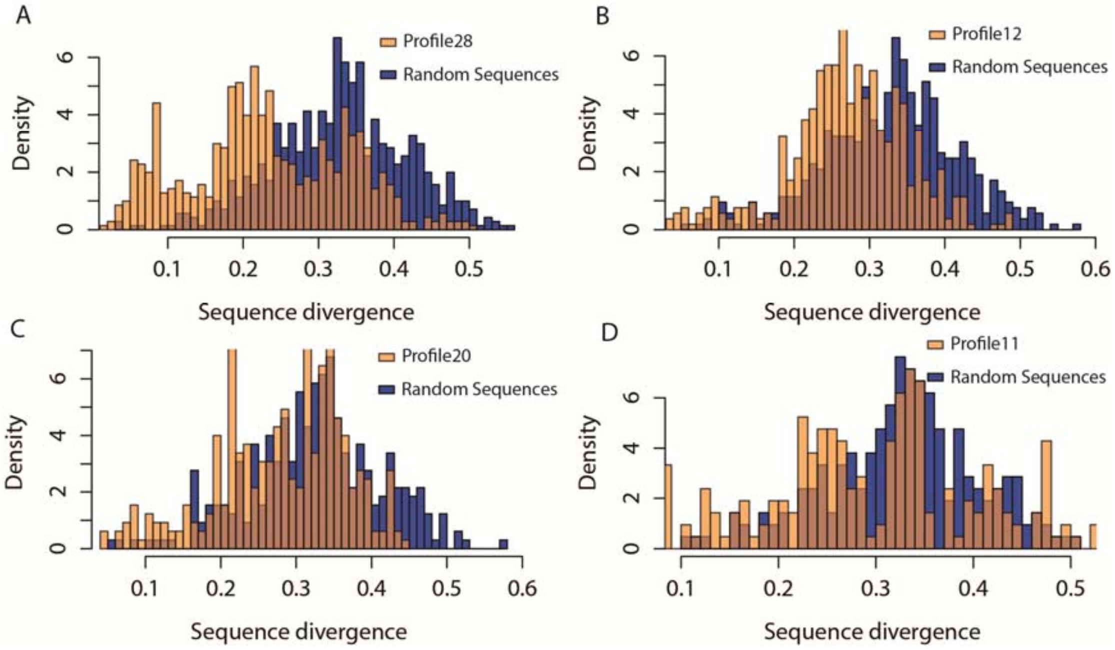

Fig. S5 OTUs in the four largest profiles showed significant similarity than random sequences. (A) Profile 28, P-value= 7.47E-55, (B) profile 12, P-value= 4.04E-23, (C) profile 20, P-value= 6.62E-07, (D) profile 11, P-value= 2.56E-06. Distributions were compared to random background by one tail non-parametric Kolmogorov-Smirnov test. Random background were calculated from randomly selected sequences of 97% OTUs in our study.

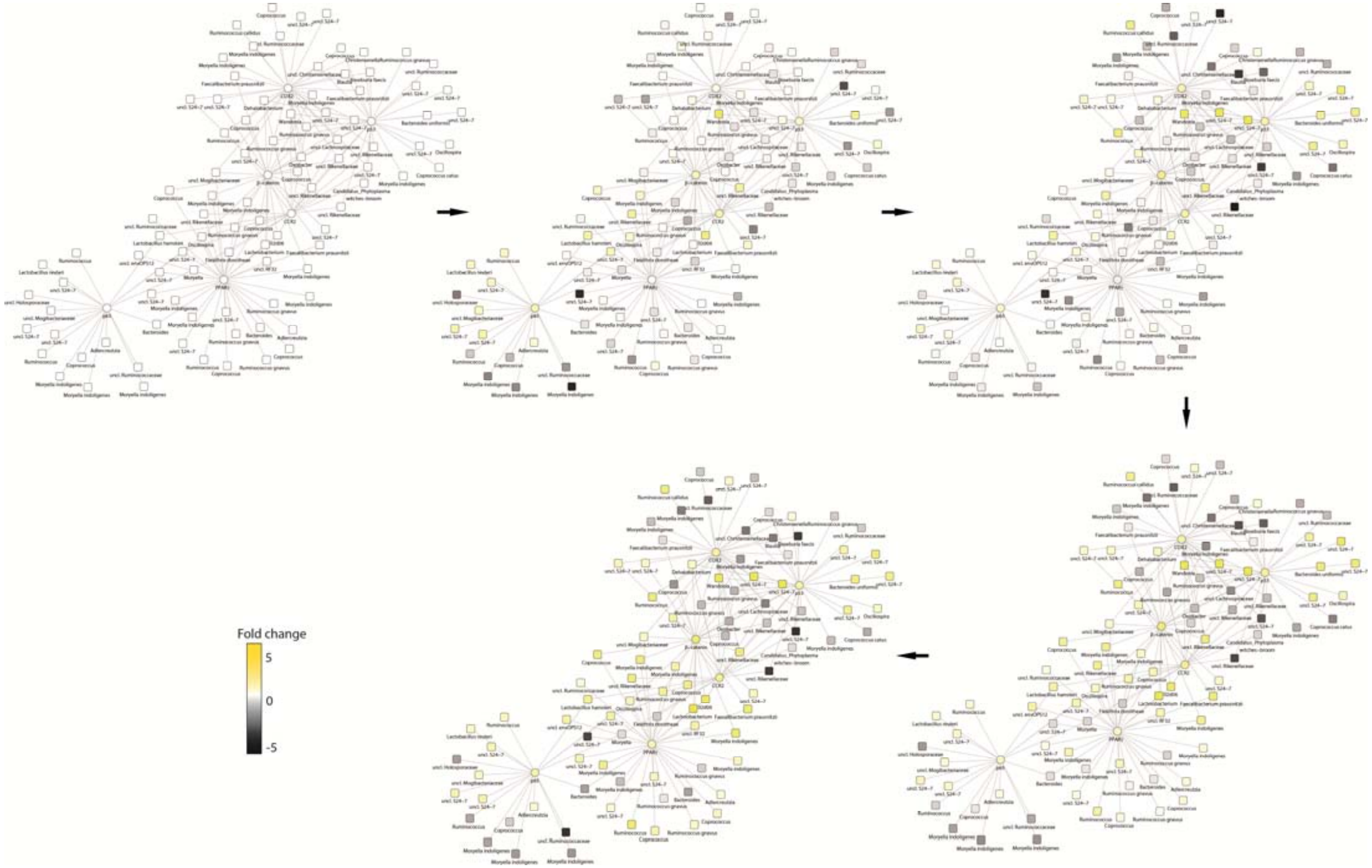

Fig. S6 A dynamic network shows the coordinated changes of molecules and OTUs. Six molecules (eclipse nodes) were connected to OTUs (square nodes) whose changes were significantly correlated with these molecules (P-value<0.05). The dynamic changes in the expression levels (trans-nuclear rate for p65) of the molecular markers and relative abundances of OTUs were log normalized and represented by color scale.