



Fig. S1 Animal experiment design.

Table S1 Statistical analysis of 16S rDNA sequencing pretreatment

Sample	Clean_paired_reads	GC(%)	Q30(%)	num_seqs	sum_len	min_len	avg_len	max_len
Control 1	63897	53%	96.31%	54871	21798743	402	415.3	437
Control 2	67581	52%	95.82%	58996	23757811	401	416.2	443
Control 3	59894	54%	96.72%	49793	19673948	402	415.1	433
Control 4	71075	53%	96.17%	60836	26984473	402	416.5	445
Control 5	65489	53%	96.36%	56891	22964728	402	416.4	445
Control 6	57931	54%	96.25%	48226	18318901	401	415.1	432
U-1CM-L 1	62974	53%	96.30%	53692	20978153	402	415.4	433
U-1CM-L 2	58413	53%	96.68%	48842	19436238	401	415.3	433
U-1CM-L 3	72961	53%	95.33%	63996	27136188	402	417.8	447
U-1CM-L 4	64908	54%	95.94%	55783	21978232	403	416.1	437
U-1CM-L 5	67354	52%	96.62%	68228	23634462	402	415.2	432
U-1CM-L 6	71984	53%	95.69%	60942	26567134	401	418.4	447
U-1CM-M 1	67495	53%	96.53%	57996	23781382	401	417.8	445
U-1CM-M 2	57932	53%	96.49%	48908	18320133	402	417.9	445
U-1CM-M 3	69773	53%	96.88%	59891	24689341	402	415.2	433
U-1CM-M 4	63892	53%	95.45%	54916	21479211	403	418.6	447
U-1CM-M 5	72806	53%	96.39%	63872	27063483	402	418.1	446
U-1CM-M 6	68849	53%	95.88%	57056	23671563	402	416.3	432
U-1CM-H 1	73721	52%	96.52%	64883	27893723	401	417.6	446
U-1CM-H 2	61743	53%	96.06%	50937	20778349	401	417.4	445
U-1CM-H 3	72992	54%	95.90%	63098	27134216	403	416.3	432
U-1CM-H 4	64197	53%	96.01%	54198	22793154	402	417.9	445
U-1CM-H 5	73229	53%	96.63%	64962	28544932	402	416.6	437
U-1CM-H 6	68482	53%	95.71%	57438	23974612	403	418.2	447