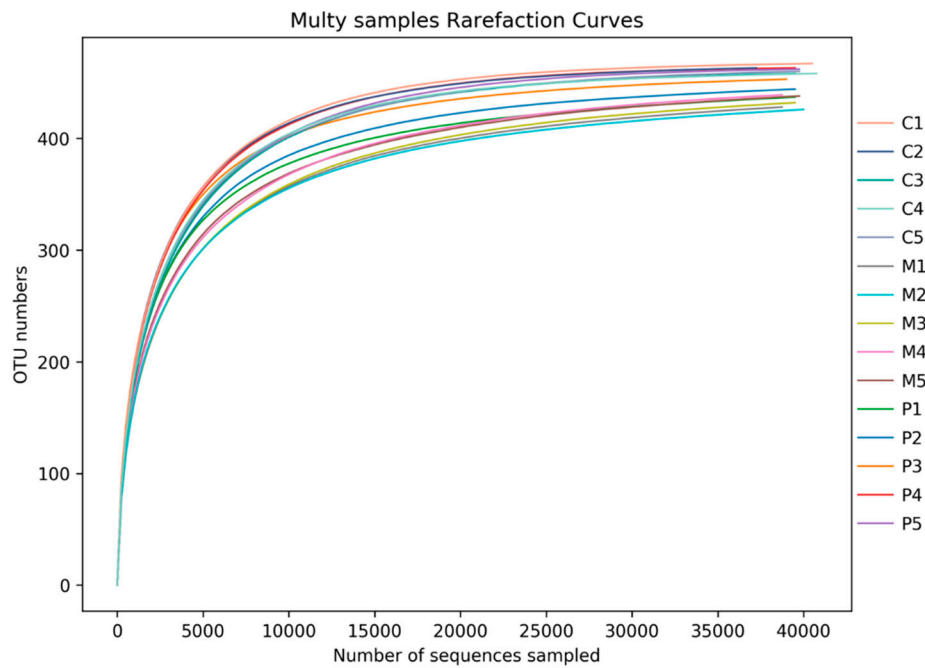
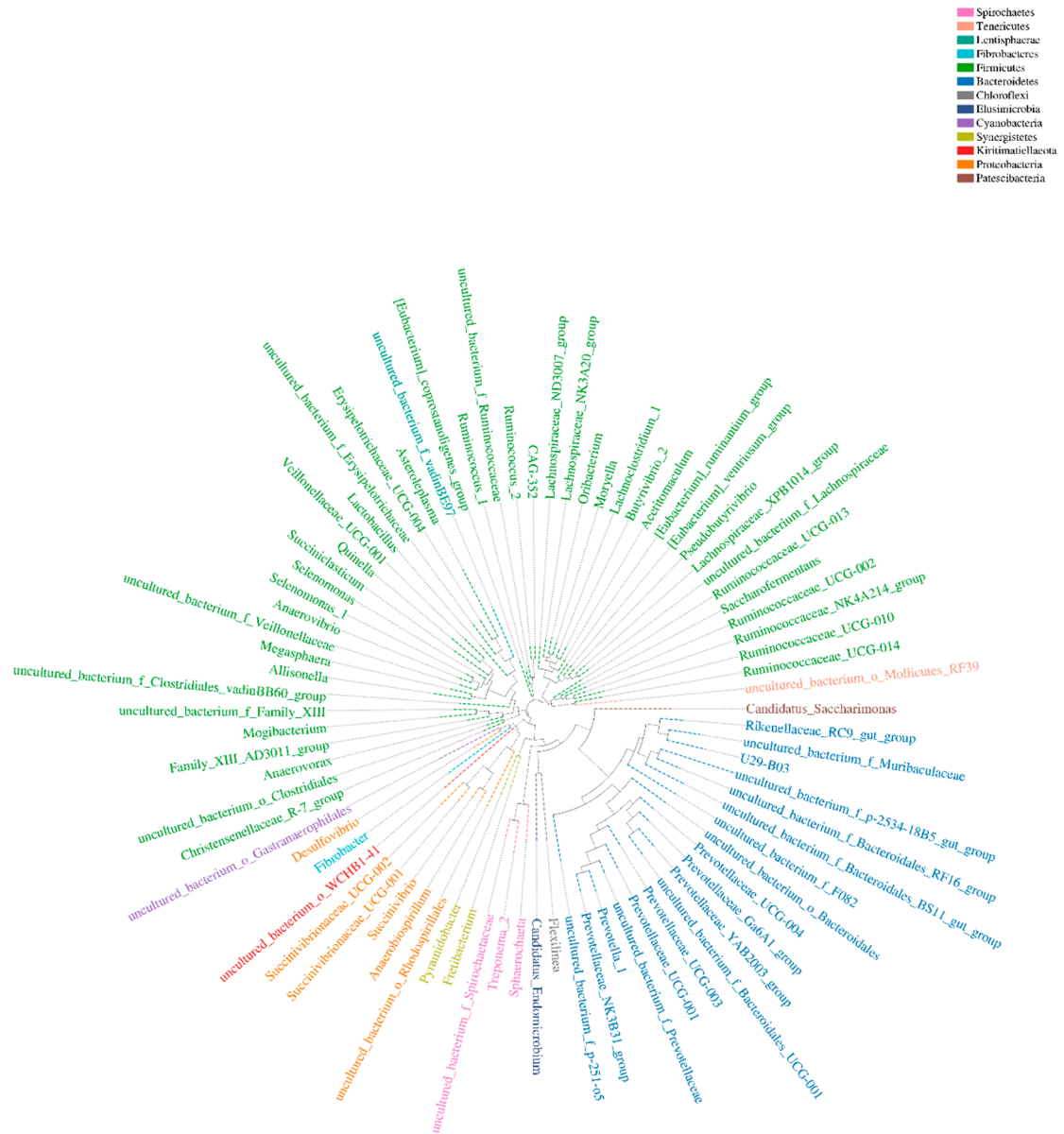


Supplementary Table S1. Statistics of sample sequencing data processing results

Sample ID	Raw Reads	Clean Reads	Effective Reads	AvgLen(bp)	GC(%)	Q20(%)	Q30(%)	Effective(%)
C1	68059	64703	63047	420	52.71	99.67	99.25	92.64
C2	68427	64565	62491	420	52.78	99.63	99.13	91.33
C3	68520	64519	62946	420	52.64	99.62	99.12	91.87
C4	68609	64815	63280	420	52.64	99.64	99.17	92.23
C5	68827	64843	63088	420	52.69	99.54	98.95	91.66
M1	68840	65311	62650	419	52.8	99.65	99.19	91.01
M2	68994	64866	62825	419	52.77	99.62	99.13	91.06
M3	68160	64450	62289	419	52.88	99.64	99.17	91.39
M4	68233	64736	62192	420	52.93	99.66	99.22	91.15
M5	68609	64543	62102	419	52.98	99.61	99.1	90.52
P1	68669	64568	61999	420	53.68	99.61	99.07	90.29
P2	68769	64731	62418	420	53.4	99.63	99.12	90.76
P3	68908	65072	63478	419	53.48	99.61	99.07	92.12
P4	69038	65262	63511	420	52.86	99.58	99	91.99
P5	69142	64866	63103	420	52.83	99.6	99.09	91.27



Supplementary Figure S1. All sample dilution curve



Supplementary Figure S2. The phylogenetic tree of genus-level species