**Table S1.** Bacterial diversity indices of different C/N ratio treatments as determined by Illumina MiSeq sequencing analysis.

Groups	OTUs	Chao1	ACE	Shannon	Simpson	Coverage (%)
P0	489±12	570±6	557±6	4.14±0.11	0.049±0.005	99.76±0.04
G1	580±8	666±19	653±9	4.46±0.02	0.030±0.001	99.74±0.01
G2	599±23	695±34	689±39	4.44±0.03	0.030±0.002	99.73±0.04
G3	564±23	655±22	652±24	4.34±0.09	0.034±0.002	99.70±0.06
G4	578±19	670±33	664±27	4.55±0.1	0.030±0.003	99.73±0.05
T1	545±27	644±30	640±5	3.36±0.3	0.113±0.025	99.76±0.04
T2	654±12	751±20	736±19	4.39±0.12	0.041±0.007	99.77±0.02
T3	602±10	702±24	685±17	4.77±0.06	0.017±0.002	99.73±0.00
T4	578±24	665±21	667±19	4.44±0.08	0.034±0.005	99.73±0.04
F1	513±6	635±65	614±41	3.73±0.05	0.070±0.006	99.73±0.07
F2	535±25	656±50	646±37	3.64±0.16	0.084±0.010	99.73±0.03
F3	613±19	726±44	702±35	4.4±0.04	0.041±0.003	99.73±0.04
F4	577±9	669±27	665±13	4.53±0.05	0.031±0.003	99.74±0.03
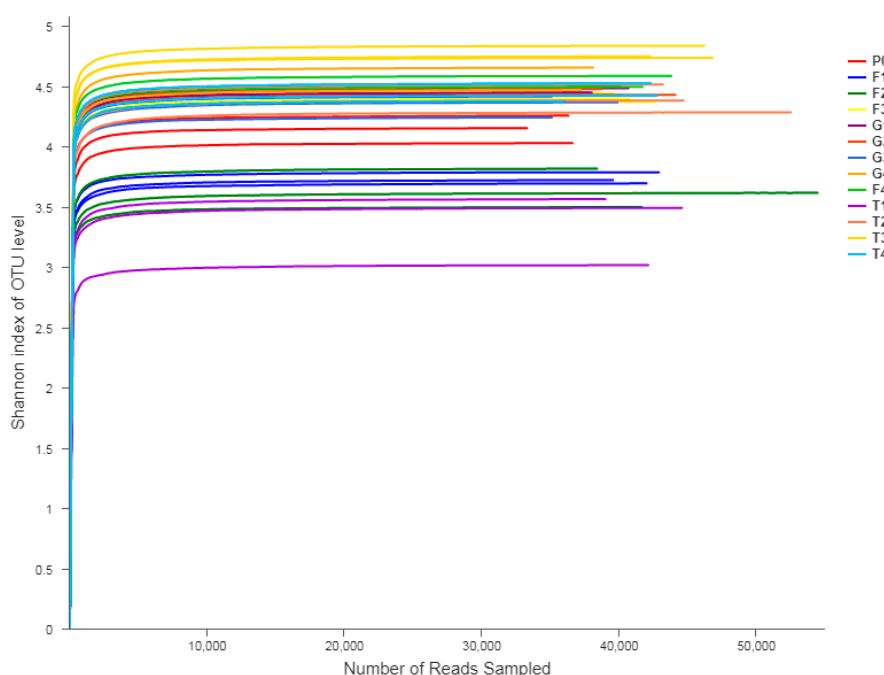
Figure S1 α-Diversity comparison. Rarefaction curves for Shannon index was calculated using Mothur (v1.27.0) for each sample using 0.03 distance OTUs. P0 was the DNA sample on day 1. The entire experimental cycle was divided into three periods, grow period (GP): day 1 to day 9; treatment period (TP): day 10 to day 19; finish period (FP): day 20 to day 29. DNA samples were extracted at the end of each period, and named G1-G4, T1-T4, F1-F4, the

sequence of ordinal numbers represents treatments C/N 10, C/N 15, C/N 20 and C/N 25,

respectively.