Supporting Information

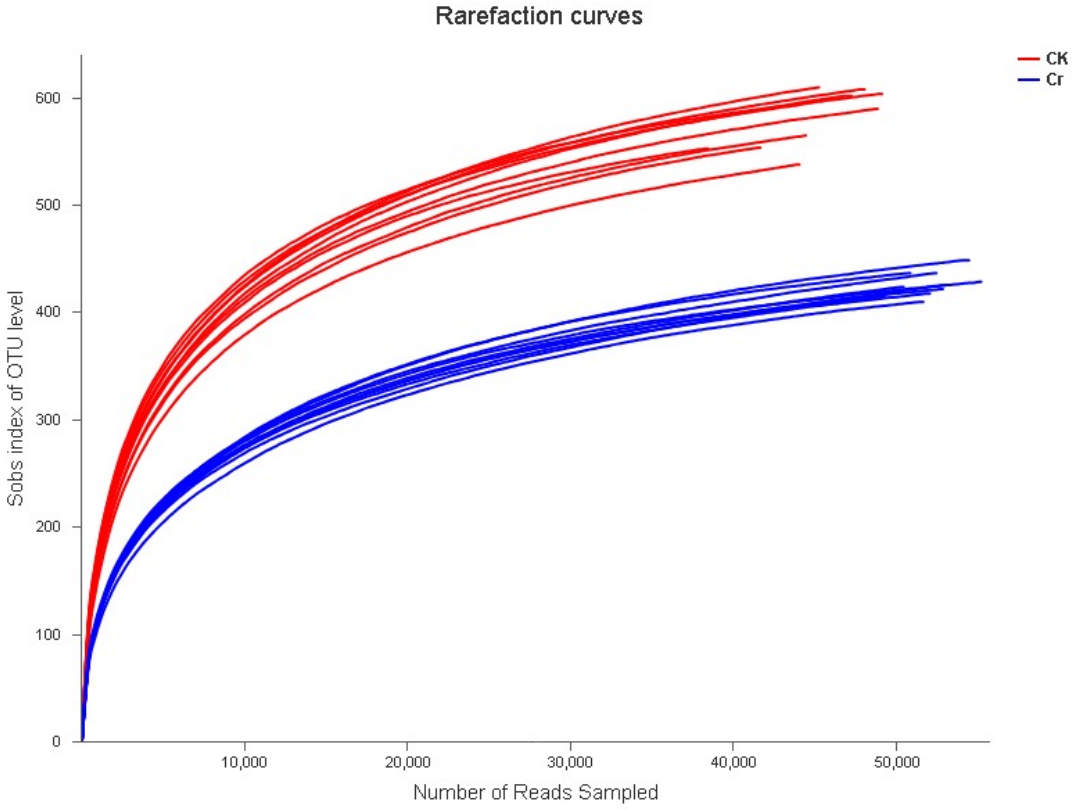

Fig. S1 Rarefaction curve of 20 samples**.**

Table S1. Microbial richness and diversity indices in the SBR system.

Sample [a]	OTU [b]	Shannon [c]	Simpson [d]	Chao [e]	Coverage [f]
CK1	579	4.41	0.03	639.68	0.998
CK2	578	4.35	0.03	644.45	0.997
CK3	552	4.14	0.05	617.63	0.998
CK4	554	4.14	0.04	615.32	0.997
CK5	586	4.17	0.05	678.50	0.997
CK6	576	4.17	0.05	647.96	0.997
CK7	593	4.13	0.06	693.83	0.997
CK8	528	3.81	0.09	618.37	0.997
CK9	546	3.82	0.09	607.88	0.997
CK10	565	4.11	0.06	664.49	0.997
Cr1	416	3.54	0.07	477.19	0.998
Cr2	414	3.53	0.07	479.27	0.998
Cr3	401	3.68	0.06	477.78	0.998
Cr4	402	3.66	0.06	503.33	0.998
Cr5	393	3.60	0.06	472.75	0.998
Cr6	400	3.65	0.07	463.53	0.998
Cr7	405	3.61	0.06	516.58	0.997
Cr8	389	3.63	0.06	470.73	0.998
Cr9	397	3.64	0.05	515.15	0.997
Cr10	384	3.43	0.08	473.20	0.998

[a] The characters CK and Cr represent the samples from control check and Cr NPs reactors, respectively; the arabic number after the characters represents number of the parallel samples.

[b] Detected OTU number.

[c] Shannon index; higher numbers represent higher levels of diversity.

[d] Simpson index; lower numbers represent higher levels of diversity.

[e] Chao index; higher numbers represent more species.

[f] Coverage index; higher numbers near 1 represent more coverage.

Table S2. Significance tests of the effects of Cr NPs on the overall bacterial community structure with two statistical approaches.

	Adonis		ANOSIM		
	R^2	P	Permutation number	R^2	P
16S rRNA gene 97% cutoff	0.81791	0.001	999	1	0.001

Table S3. Topological properties of the empirical MENs in the Cr NPs sample and control check, and their associated random networks. The characters CK and Cr represent the samples from control check and Cr NPs reactors, respectively.

Community	Empirical networks									Random networks[c]		
	No. of original OTUs[a]	Similarity threshold (s_t)	Network size (Total nodes)[b]	Total links	R^2 of power law	Average connectivity (avgK)	Average path distance (GD)	Average clustering coefficient (avgCC)	Modularity (No. of modules)	Average path distance (GD)	Average clustering coefficient (avgCC)	Modularity
CK	719	0.89	306	785	0.985	5.131	5.527[d]	0.227[d]	0.552 (37)[d]	3.389 ± 0.050	0.066 ± 0.008	0.390 ± 0.006
Cr	587	0.84	274	369	0.888	2.693	7.015[d]	0.215[d]	0.818 (40)[d]	5.148 ± 0.116	0.011 ± 0.006	0.663 ± 0.008

a The number of OTUs originally used for network construction using the RMT-based approach.

b The number of nodes in a network.

c The random networks were generated by rewiring all of the links of a network with the identical numbers of nodes and links to the corresponding empirical network.

d Significant difference ($P < 0.001$) between the networks of Cr and CK systems.