

Table S1. Alpha diversity indexes among different treatments.

	Sobs Richness	Shannon–Weaver Diversity	Pielou Evenness	Goods Coverage
NC10	4038±382 ^{ab}	9.75±0.28 ^a	0.8145±0.01 ^a	0.9907±0.0003 ^{ab}
NC100	4067±160 ^{ab}	9.75±0.04 ^a	0.8136±0.003 ^a	0.9902±0.0006 ^{ab}
NC500	4098±158 ^{ab}	9.77±0.15 ^a	0.8140±0.01 ^a	0.9900±0.0004 ^{bc}
IC10	3932±138 ^{ab}	9.68±0.09 ^a	0.8106±0.01 ^a	0.9903±0.0007 ^{ab}
IC100	3837±96 ^b	9.63±0.07 ^a	0.8186±0.003 ^a	0.9903±0.0003 ^{ab}
IC500	4284±191 ^a	9.69±0.20 ^a	0.8035±0.02 ^a	0.9888±0.0016 ^c
CK	3766±65 ^b	9.64±0.03 ^a	0.8117±0.002 ^a	0.9915±0.0002 ^a

NC = nanoceria; IC = ionic cerium; the number means the concentration of cerium (mg/kg); CK = negative control.

Table S2. Summary of the taxonomic classification of all samples.

Sample ID	Number of Taxa					
	Phylum	Class	Order	Family	Genus	OTUs
NC10-1	30	92	167	247	392	4513
NC10-2	28	84	159	220	347	3742
NC10-3	30	90	169	232	352	3914
NC100-1	30	92	163	236	360	3859
NC100-2	29	93	176	241	392	4176
NC100-3	28	89	166	225	383	4141
NC500-1	30	91	162	226	344	3913
NC500-2	30	92	172	240	426	4181
NC500-3	28	90	172	229	358	4196
IC10-1	29	86	161	227	373	4096
IC10-2	29	85	159	221	346	3857
IC10-3	29	88	158	222	369	3886
IC100-1	25	83	151	208	329	3754
IC100-2	30	87	157	225	354	3854
IC100-3	25	77	153	225	365	3985
IC500-1	29	90	167	235	372	4094
IC500-2	31	93	183	254	446	4484
IC500-3	30	90	172	244	387	4244
CK-1	30	88	164	231	381	3826
CK-2	29	83	151	227	381	3702
CK-3	26	82	154	225	366	3771
All	35	108	222	334	661	8874

Table S3. Two-way ANOVA of cerium's effect on soil bacterial phyla abundance.

Carbon Sources	Ce Species	Ce Dose	Interaction
Planctomycetes	NS	NS	NS
Proteobacteria	*	NS	NS
Acidobacteria	**	*	NS
Actinobacteria	*	*	NS
Verrucomicrobia	*	*	NS
Chloroflexi	*	*	NS
Firmicutes	NS	NS	NS
Patescibacteria	NS	NS	NS
Gemmatimonadetes	*	*	NS
Bacteroidetes	*	NS	NS
BR1C	*	NS	.
Rokubacteria	*	NS	NS
Cyanobacteria	NS	*	NS
Armatimonadetes	*	**	NS
Nitrospirae	**	**	.
Deinococcus-Thermus	NS	NS	NS
Tenericutes	NS	NS	NS
Hydrogenedentes	NS	**	NS
Epsilonbacteraeota	NS	**	NS
Elusimicrobia	*	NS	NS
Chlamydiae	NS	NS	.
Spirochaetes	NS	NS	NS
Fibrobacteres	*	NS	**
Omnitrophicaeota	.	NS	NS
Kiritimatiellaeota	NS	NS	NS
WPS-2	.	NS	NS
Dependentiae	NS	NS	NS
Deferrabacteres	NS	.	NS
Dadabacteria	NS	NS	NS
Lentisphaerae	NS	NS	NS
Latescibacteria	NS	NS	NS

., $P < 0.1$; *, $P < 0.05$; **, $P < 0.01$.

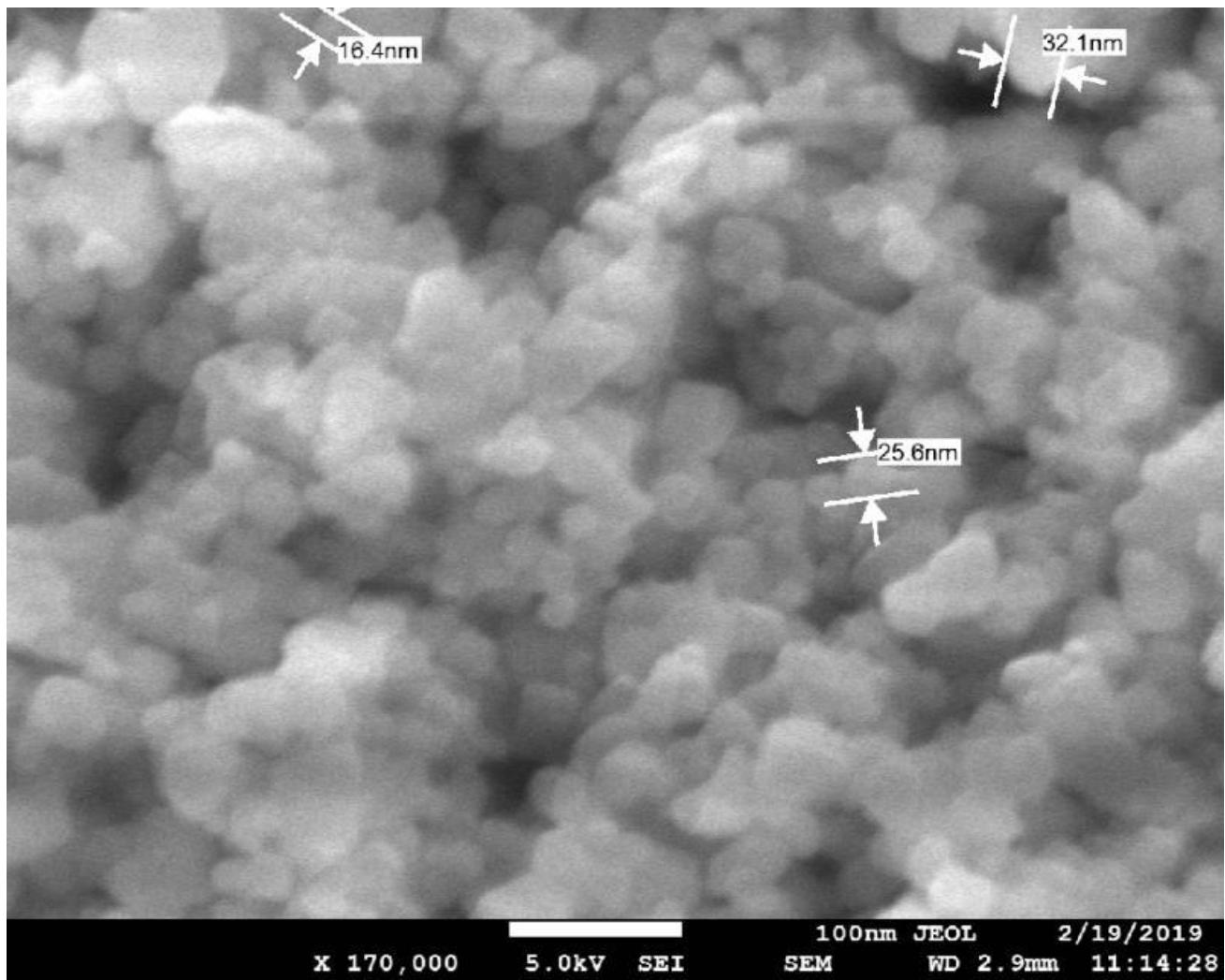


Figure S1. SEM micrograph of nanoceria particles used in this study (acceleration voltage of 5.0 kV, magnification of 170,000 \times).

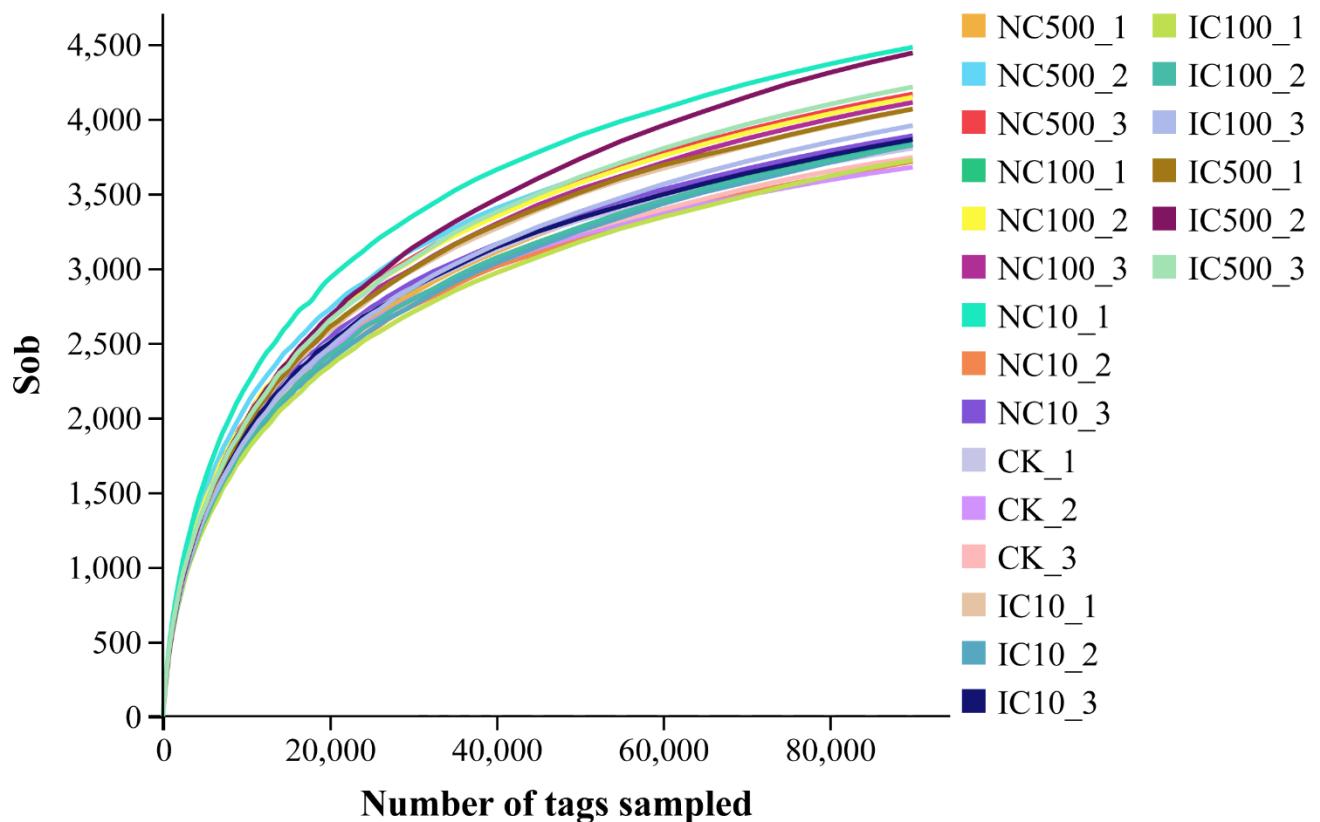


Figure S2. Rarefaction curves of bacterial 16S rRNA gene sequencing in different treatments.

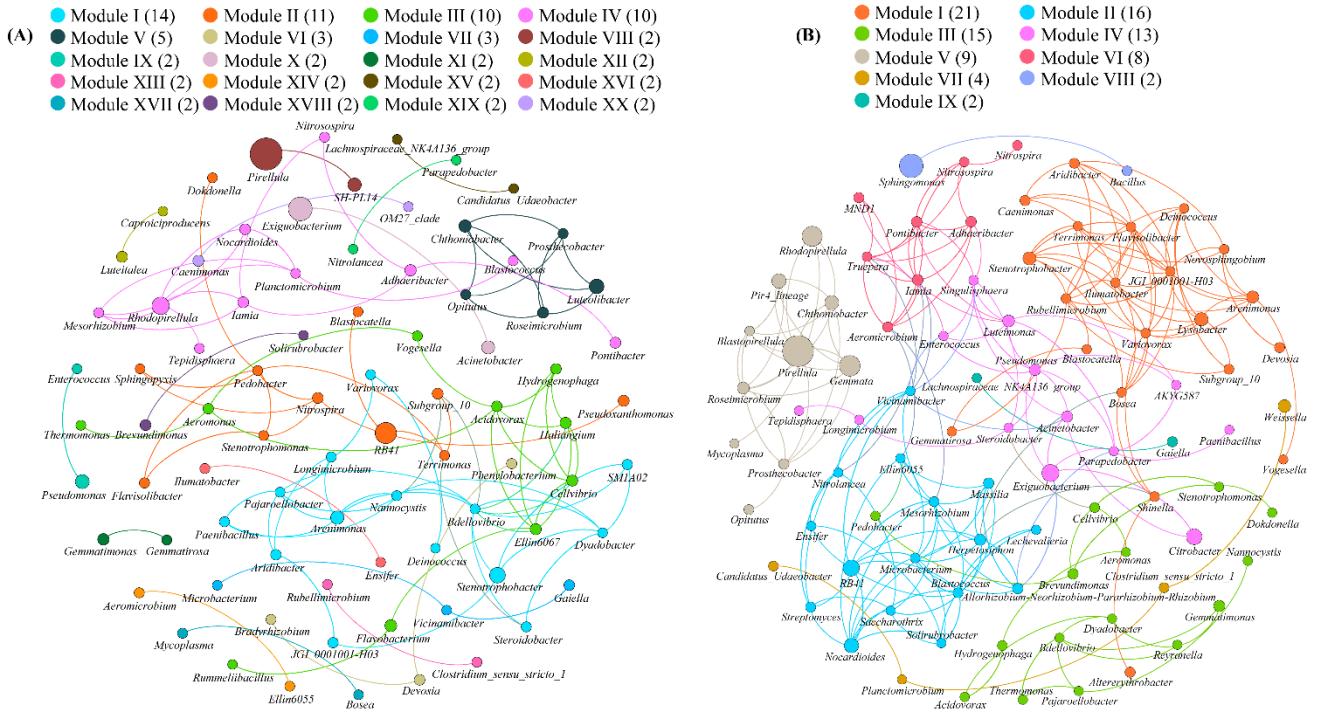


Figure S3. Network of co-occurring bacterial genera of nanoceria (A) and ionic cerium (B) treatments based on Spearman correlation analysis, sorted in color by modularity. A connection indicates a significant ($r>0.6$, $P<0.01$) correlation. The size of each node (genus) is proportional to its abundance; the thickness of each connection between two nodes (edge) is proportional to the corresponding correlation coefficient.