Supplementary information

Text S1 Information on uranium tailings depot

The uranium tailing depot was established in 1976, designed for the containment of residues generated through leaching processes. It comprises tailings dams and underlying facilities for water recovery, with a total capacity of approximately 300000 m^3. Since 2016, the mine has been completely shut down, and the tailing repository is currently in a state of maintenance.

Text S2 DNA extraction, PCR amplification, and illumine Miseq sequencing

All the above-mentioned samples' DNA was extracted and purified using an E.Z.N.A.® soil DNA kit following the manufacturer's instructions (Omega Bio-tek, Norcross, GA, USA). The DNA quality and concentrations were checked by agarose gel electrophoresis with the Quantus™ Fluorometer (Promega, Madison, WI, USA).

PCR amplification of the 16S rRNA gene was performed based on the literature, which selected the primers 338F (50-ACTCCTACGGGAGGCAG CAG-30) and 806R (50-GGACTACHVGGGTW TCTAAT-30) to amplify the V3–V4 regions. The PCR amplification system contained 15 µL 2×Taq master mix with 10 ng genomic DNA, 4 µL PCR reaction buffer, 0.4 mmol/L of each primer, 2.5 mmol/L of dNTPs, and ultrapure water was added to a final volume of 50 µL. The PCR conditions were as follows: 94 °C for 3 min, 27 cycles of 94 °C for 30 s, 45 °C for 20 s, 72 °C for 30 s, and a final extension of 72 °C for 5 min. All PCR products were visualized on agarose gels (2% in TAE buffer) containing ethidium bromide and purified with an AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA). Amplification products complete high-throughput gene sequencing was performed in the Illumina Miseq platform (Majorbio BioPharm Technology Co., Ltd., Shanghai, China).

Text S3 Co-occurrence network analysis

After filtration, OTU-level microbial taxa were selected for species coexistence analysis. Only these OTUs with Spearman $|R|>0.6$ and statistical significance $p<0.001$ were considered robust and then incorporated into the network analysis. An adjacency network was generated by the "igraph" package and visualized using Gephi v0.9.2. The network's topological properties, such as node degree, betweenness, closeness, clustering coefficient, and graph density, were considered keystone taxa.

Table S1 ANOVA correlation analysis between pH and uranium concentration

p-value	r^2
0.386	0.113

Table S2 Correlations between phylum taxa and uranium concentration

Phylum	Uranium concentration
Proteobacteria	0.590**
Actinobacteria	−0.177
Firmicutes	−0.21

Note: ** indicates $p<0.01$

Table S3 Distributions of degree and betweenness of nodes (Putative keystone taxa based on the criteria of nodes degree >10 and betweenness <100)

Group	Phylm	Genus	Id	Degree	Betweenness
CK	Proteobacteria	*Burkholderia-Caballeronia-Paraburkholderia*	OTU1587	13	9.378922
	Firmicutes	*unclassified_f__Lachnospiraceae*	OTU1341	13	9.378922
	Firmicutes	*Caproiciproducens*	OTU1187	16	11.251337
	Firmicutes	*unclassified_f__Ruminococcaceae*	OTU1234	16	11.251337
	Firmicutes	*Desulfitobacterium*	OTU873	17	14.662751
	Firmicutes	*Ruminiclostridium*	OTU2097	17	14.662751
	Firmicutes	*Caproiciproducens*	OTU2159	17	14.662751
	Firmicutes	*unclassified_f__Ruminococcaceae*	OTU2478	17	14.662751
	Firmicutes	*Desulfitobacterium*	OTU1372	17	14.662751
	Firmicutes	*Ruminiclostridium*	OTU2154	17	14.662751
	Actinobacteria	*Rhodococcus*	OTU2233	16	11.251337
	Firmicutes	*Oxobacter*	OTU812	13	8.670588
	Firmicutes	*norank_f__Veillonellaceae*	OTU3112	13	8.670588
	Firmicutes	*Ruminiclostridium*_1	OTU1193	13	8.670588
	Firmicutes	*Ruminiclostridium*_1	OTU2354	17	65.133333
	Firmicutes	*Ruminiclostridium*_1	OTU1517	17	65.133333
	Firmicutes	*Fonticella*	OTU2393	17	65.133333
HS	Firmicutes	*Ruminiclostridium*	OTU2154	14	92.452993
	Firmicutes	*Anaerocolumna*	OTU1373	14	92.452993
	Firmicutes	*Clostridium_sensu_stricto*_10	OTU1187	14	92.452993
	Firmicutes	*Anaerocolumna*	OTU3112	14	92.452993
	Firmicutes	*Clostridium_sensu_stricto*_12	OTU1234	14	29.141157
	Firmicutes	*Clostridium_sensu_stricto*_1	OTU2496	14	29.141157
	Firmicutes	*Clostridium_sensu_stricto*_10	OTU1192	14	29.141157
	Proteobacteria	*Azotobacter*	OTU2241	14	29.141157
	Firmicutes	*Oxobacter*	OTU812	14	29.141157
	Firmicutes	*Ruminiclostridium*_1	OTU1517	13	21.741157
	Firmicutes	*unclassified_f_Lachnospiraceae*	OTU2097	11	35.511418
	Firmicutes	*Lachnoclostridium*_5	OTU2251	11	35.511418
	Firmicutes	*unclassified_f_Ruminococcaceae*	OTU2736	11	35.511418
GP	Firmicutes	*Desulfitobacterium*	OTU2495	11	61.909524
	Firmicutes	*Ruminiclostridium*_1	OTU1517	11	91.843728

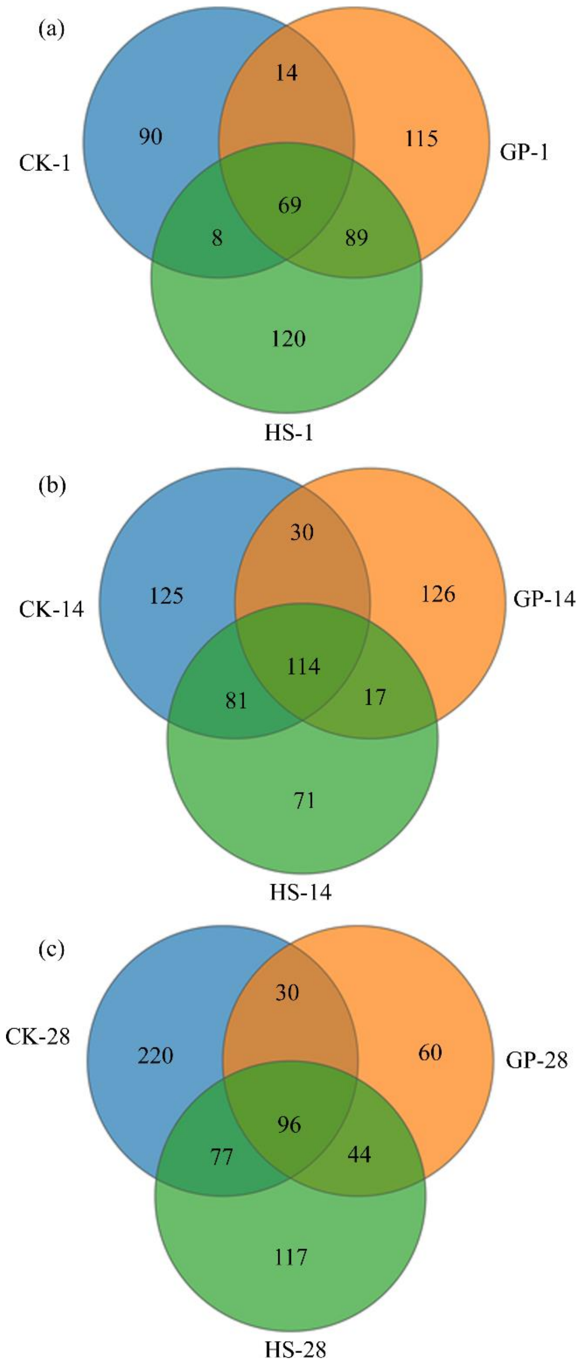

Figure S1 Venn diagrams with numbers of common or unique OUT: (a) 1 d; (b) 14 d; (c) 28 d

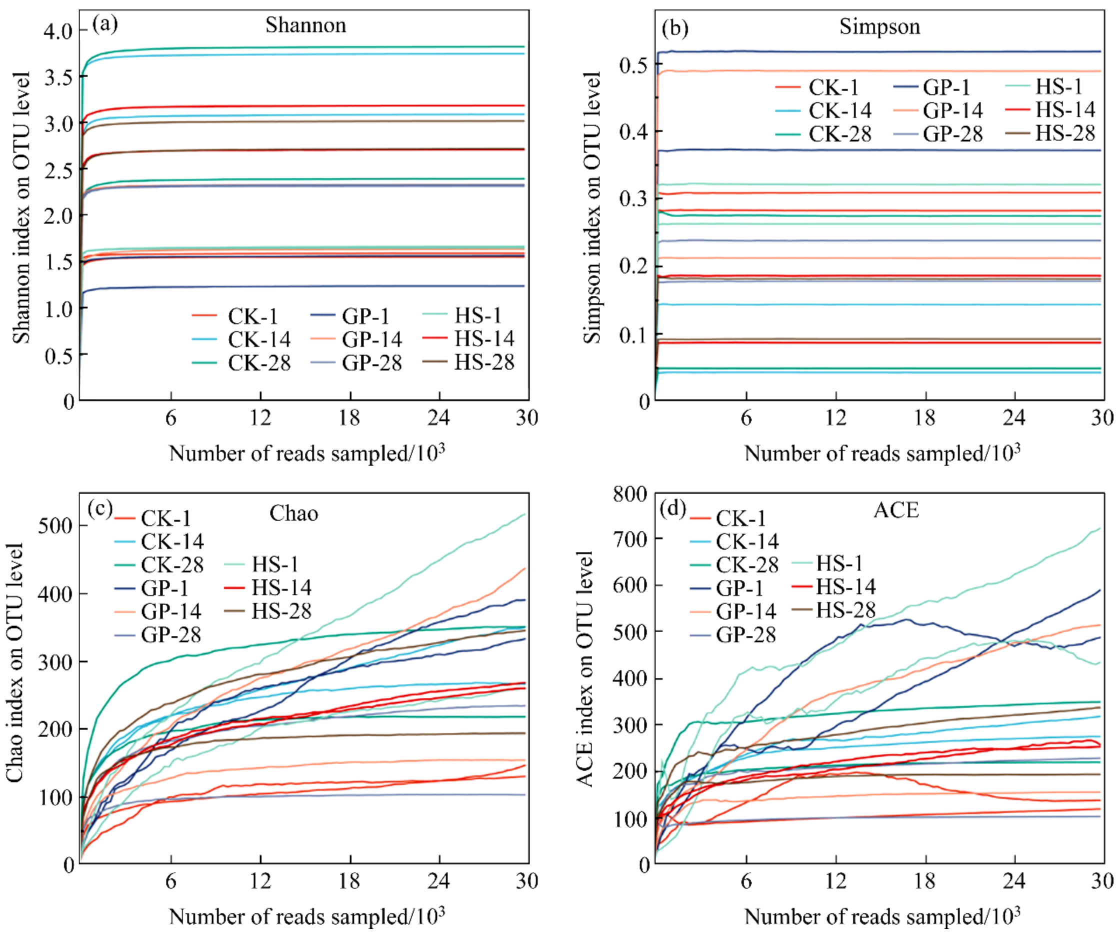

Figure S2 Rarefaction curves (a–d) in treatment and control during different times: (a) Shannon; (b) Simpson; (c) Chao; (d) ACE

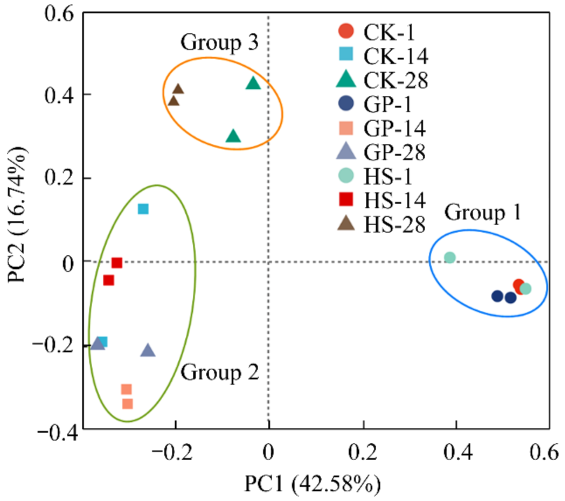

Figure S3 Principal coordinate analysis of different bioremediation treatments and analysis time

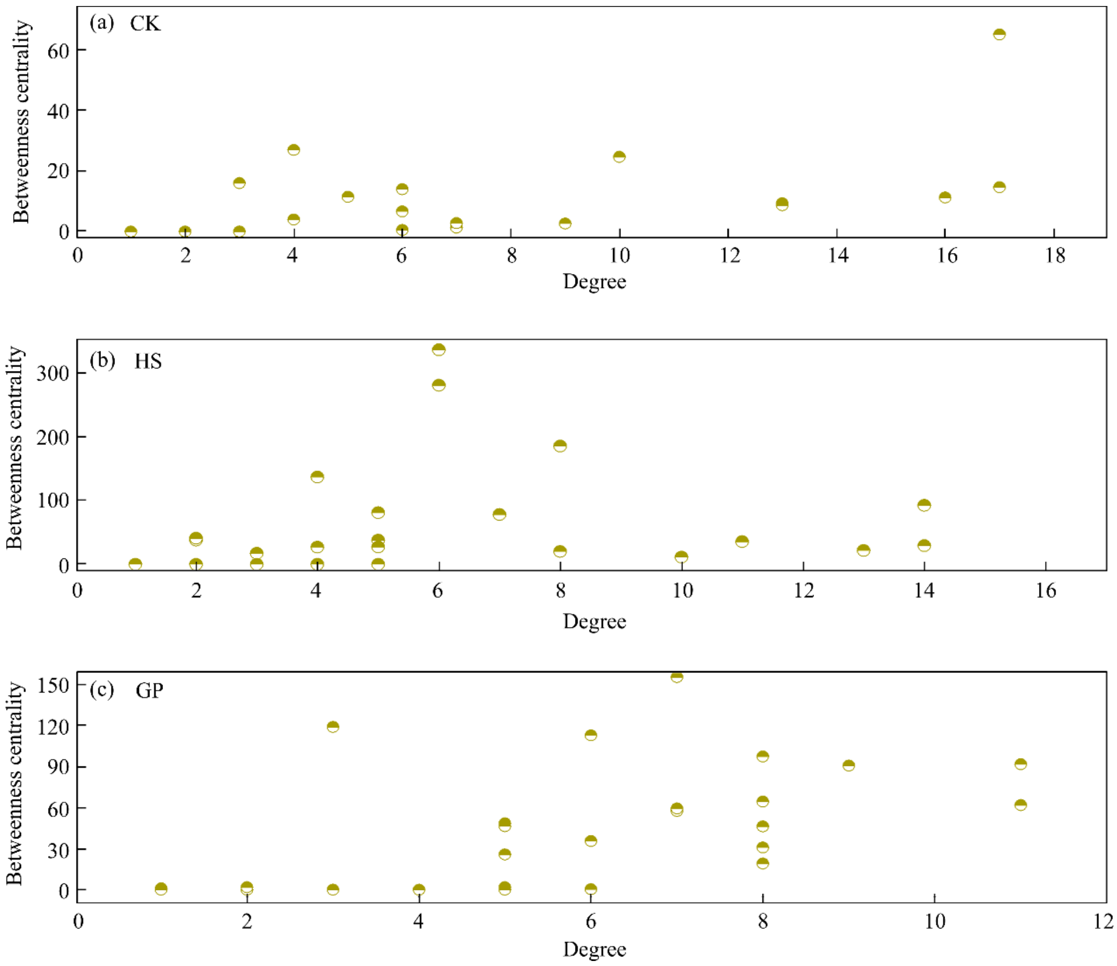

Figure S4 Distributions of degree and betweenness of nodes: (a) CK; (b) HS; (c) GP (Putative keystone taxa based on the criteria of nodes degree > 10 and betweenness < 100)

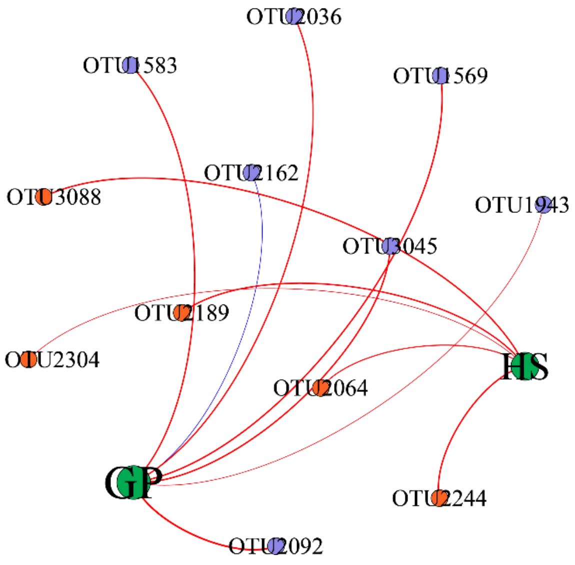

Figure S5 Co-occurrence network analysis of additives-microbial interactions among the most 500 abundant OTUs in samples

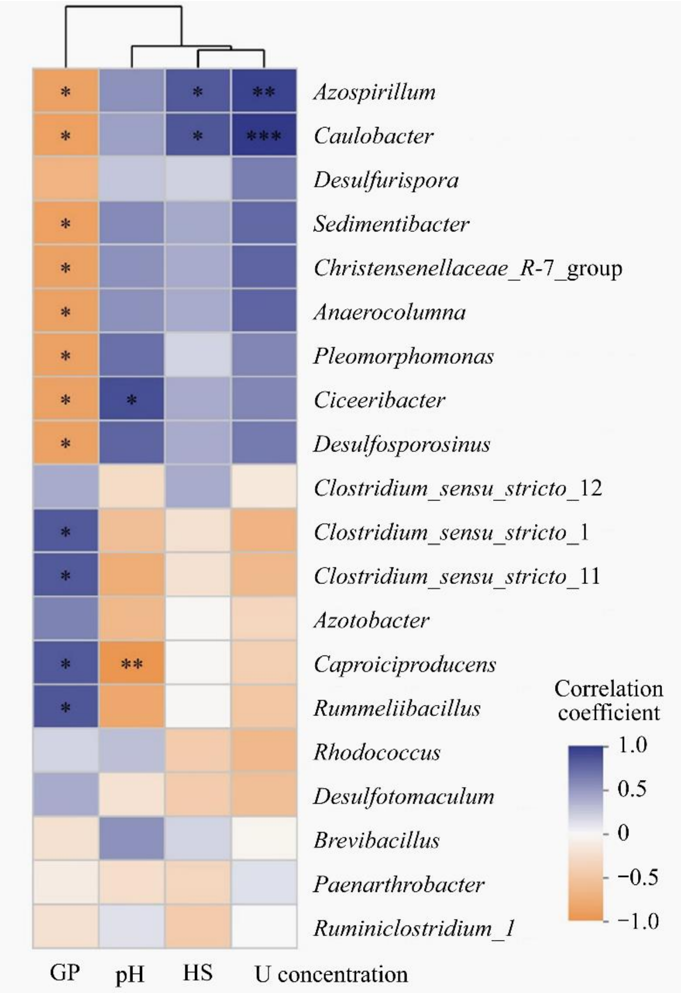

Figure S6 Spearman's rank correlation heatmap ($p<0.05$ *, $p<0.01$**) used to study the correlation between microbial communities at Day 28