Supporting information

Table S1 Physicochemical properties of bauxite residue and amendments

Sample	pH	EC/(MS·cm^{-1})	ESP/%	TOC/(g·kg^{-1})	TN/(g·kg^{-1})	TP/(g·kg^{-1})
Bauxite residue	10.92±0.02a	0.94±0.15a	68.24±8.67a	4.36±1.23b	0.28±0.07b	0.87±0.12b
Phosphogypsum	2.75±0.08c	0.16±0.023b	13.89±3.47b	3.68±0.42c	0.11±0.01c	4.76±0.49a
Straw	7.91±0.03b	0.067±0.003c	7.59±2.42c	459.1±7.11a	6.72±0.32a	0.42±0.04c

EC: electrical conductivity; ESP: exchangeable sodium percentage; TOC: total organic carbon; TN: total nitrogen; TP: total phosphorus; Different letters of each column represent the significant difference at $P<0.05$.

Table S2 Physicochemical properties in bauxite residue under different treatment

Treatment	pH	EC/(MS·cm^{-1})	ESP/%	TOC/(g·kg^{-1})	TN/(g·kg^{-1})	AP/(mg·kg^{-1})
CK	10.87±0.23a	0.82±0.05a	0.65±0.03a	4.28±0.37b	0.24±0.03b	6.33±0.81c
SF	9.41±0.18b	0.67±0.09b	0.49±0.05b	12.48±0.99a	0.73±0.05a	25.93±2.86b
PGSF	7.88±0.25d	0.29±0.03d	0.19±0.04d	11.22±0.21a	0.68±0.07a	50.73±9.03a

EC: electrical conductivity; ESP: exchangeable sodium percentage; TOC: total organic carbon; TN: total nitrogen; AP: available phosphorus; CK, no addition; SF, 5% straw; PGSF, 2% phosphogypsum+5% straw. Different letters of each column represent the significant difference at $P<0.05$.

Table S3 Multiple comparisons of relative abundance of the dominant microbial group in bauxite residue at the phylum level

Community	Phylum	CK	SF	PGSF
Bacterial community	*Firmicutes*	82.29±6.28a	46.97±6.3b	18.41±4.09c
	Proteobacteria	6.87±6.03c	22.95±5.39b	41.3±4.32a
	Actinobacteria	10.68±0.59b	18.18±6.82a	11.65±0.85b
	Bacteroidetes	0.01±0.01c	11.52±8.19b	24.68±1.41a
	Chloroflexi	0±0b	0.31±0.08b	1.7±0.33a
	Patescibacteria	0±0b	0.01±0.01b	0.63±0.4a
	Verrucomicrobia	0±0b	0±0b	0.47±0.16a
	Gemmatimonadetes	0±0b	0.02±0.01b	0.38±0.14a
	Deinococcus-Thermus	0±0b	0.02±0b	0.38±0.15a
	Planctomycetes	0±0b	0±0.01b	0.24±0.15a
Fungal community	*Ascomycota*	96.41±0.53b	98.14±0.52a	97.87±0.36a
	Basidiomycota	2.23±1.44a	1.71±0.52ab	0.35±0.13b
	Mucoromycota	1.15±1.97a	0±0a	0.05±0.03a
	Chytridiomycota	0.01±0.01a	0.03±0.05a	0.42±0.17a
	Mortierellomycota	0.06±0.02a	0.12±0.03a	0±0a

CK, no addition; SF, 5% straw; PGSF, 2% phosphogypsum+5% straw. Different letters of each column represent the significant difference at $P<0.05$.

Table S4 Multiple comparisons of relative abundance of the dominant microbial group in bauxite residue at the family level

Community	Family	CK	SF	PGSF
Bacterial community	*Bacillaceae*	65.52±10.95a	1.64±1.48b	5.53±1.35b
	Planococcaceae	8.87±3.31b	42.67±5.35a	12.4±5.18b
	Cyclobacteriaceae	0±0.01b	5.67±6.34ab	12.88±3.82a
	Micrococcaceae	9.86±0.29a	5.05±2.95b	0.54±0.2c
	Halomonadaceae	5.4±4.94a	5.01±1.42a	1.17±0.35a
	Devosiaceae	0.17±0.16c	2.36±0.72b	8.78±1.45a
	Rhizobiaceae	0.62±0.52c	2.09±0.86b	7.04±0.42a
	Xanthomonadaceae	0±0b	4.04±1.97a	5.71±1.18a
	Sporolactobacillaceae	7.9±1.76a	0.15±0.25b	0±0b
	Sphingobacteriaceae	0.01±0.01b	4.65±1.98a	2.71±1.08a
	Microbacteriaceae	0.05±0.06c	2.44±0.7b	4.25±0.66a
	Flavobacteriaceae	0±0b	1.11±0.89b	4.8±1.16a
	Caulobacteraceae	0±0b	1.49±1.6b	4.12±0.82a
	Rhodobacteraceae	0.63±0.42b	2.19±0.55a	1.63±0.37a
	Cellvibrionaceae	0±0b	0.16±0.06b	4±0.44a
	Dermabacteraceae	0±0b	3.92±1.54a	0.22±0.11b
	Nocardiopsaceae	0.07±0.1b	3.12±2.24a	0.51±0.28b
	Pseudomonadaceae	0.01±0.01b	1.7±0.77a	1.59±0.71a
	Sphingomonadaceae	0.01±0b	0.6±0.16b	2.22±0.66a
	Saprospiraceae	0±0b	0±0b	2.36±0.38a
	Bogoriellaceae	0±0.01b	0.73±0.38a	0.9±0.11a
	Streptomycetaceae	0.01±0.01b	0.27±0.04b	1.3±0.68a
	Staphylococcaceae	0±0b	1.24±0.38a	0.07±0.03b
	Nocardioidaceae	0.36±0.38a	0.38±0.11a	0.56±0.17a
Fungal community	*Chaetomiaceae*	1.35±1.87c	15.06±2.98b	44.39±6.87a
	Aspergillaceae	8.05±0.04c	21.37±4.21a	14.51±2.33b
	Microascaceae	16.61±1.44a	1.41±0.08b	2.07±0.19b
	Nectriaceae	1.26±0.27b	6.46±5.49ab	10.04±4.22a
	Stachybotryaceae	1.06±0.67b	1.33±0.09b	11.4±1.24a
	Bionectriaceae	0.93±0.63b	9.47±1.08a	1.21±0.18b
	Lasiosphaeriaceae	2.27±1.61b	4.52±0.11a	2.21±0.87b
	Hypocreales	0.45±0.62b	3.47±0.19a	0.5±0.05b
	Wallemiaceae	1.09±0.45a	1.65±0.5a	0.28±0.08b
	Trichosphaeriaceae	1.27±2.18a	0±0a	0.01±0.02a
	Rhizopodaceae	1.15±1.97a	0±0a	0.05±0.03a
	Plectosphaerellaceae	0.61±0.22a	0.06±0b	0.47±0.11a
	Myrmecridiaceae	0.58±0.5a	0±0a	0±0a
	Trichosporonaceae	0.46±0.4a	0±0a	0±0a
	Spizellomycetaceae	0.01±0.01b	0.03±0.05b	0.42±0.17a
	Trichocomaceae	0.42±0.73a	0.02±0.01a	0.01±0a
	Phaeosphaeriaceae	0.45±0.39a	0±0a	0±0a
	Pleosporaceae	0.08±0.08b	0.29±0.11a	0.03±0.02b
	Diatrypaceae	0.35±0.16a	0±0b	0±0b
	Clavicipitaceae	0.01±0.01b	0.33±0.05a	0±0b

CK, no addition; SF, 5% straw; PGSF, 2% phosphogypsum+5% straw. Different letters of each column represent the significant difference at $P<0.05$.

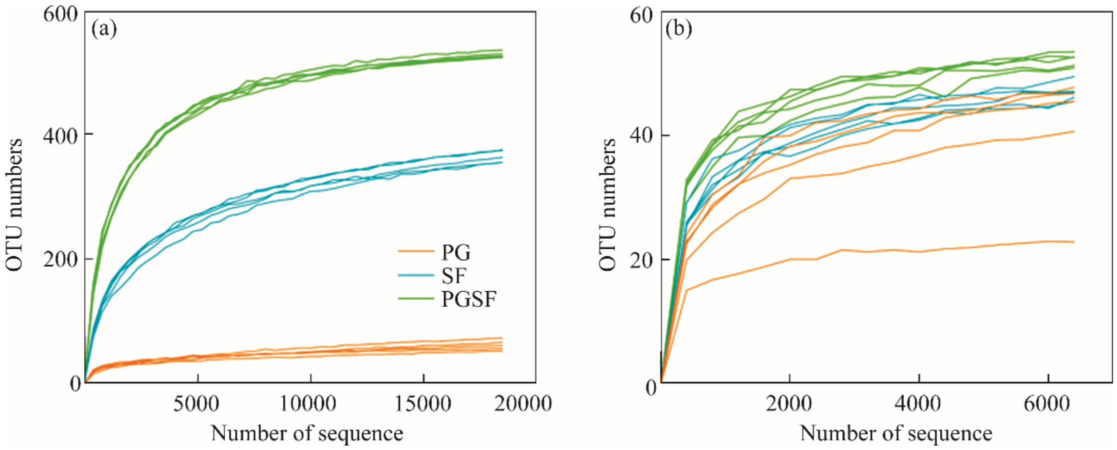

Figure S1 Rarefaction curve of bacterial community (a) and fungal community (b) in bauxite residue following biomass addition

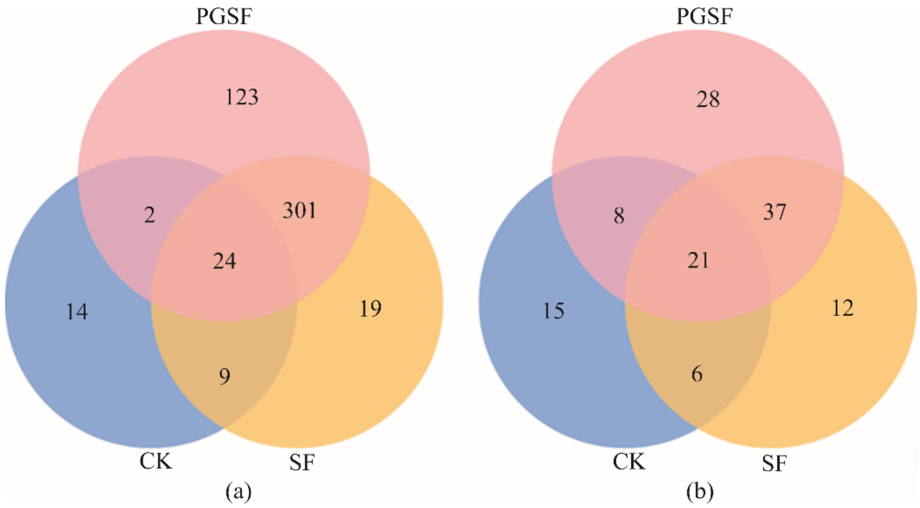

Figure S2 Venn diagram of the OTUs of the bacterial community (a) and fungal community (b) in bauxite residue by different treatments

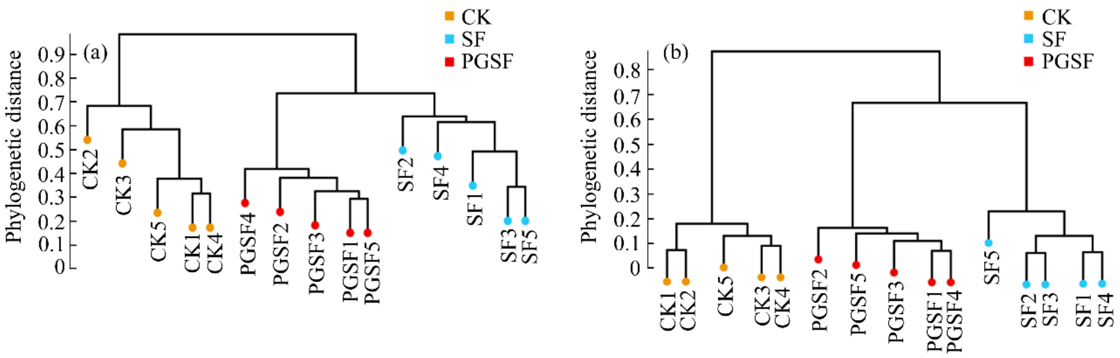

Figure S3 UPGMA cluster analysis diagrams of bacterial community (a) and fungal community (b) in bauxite residue under different treatments

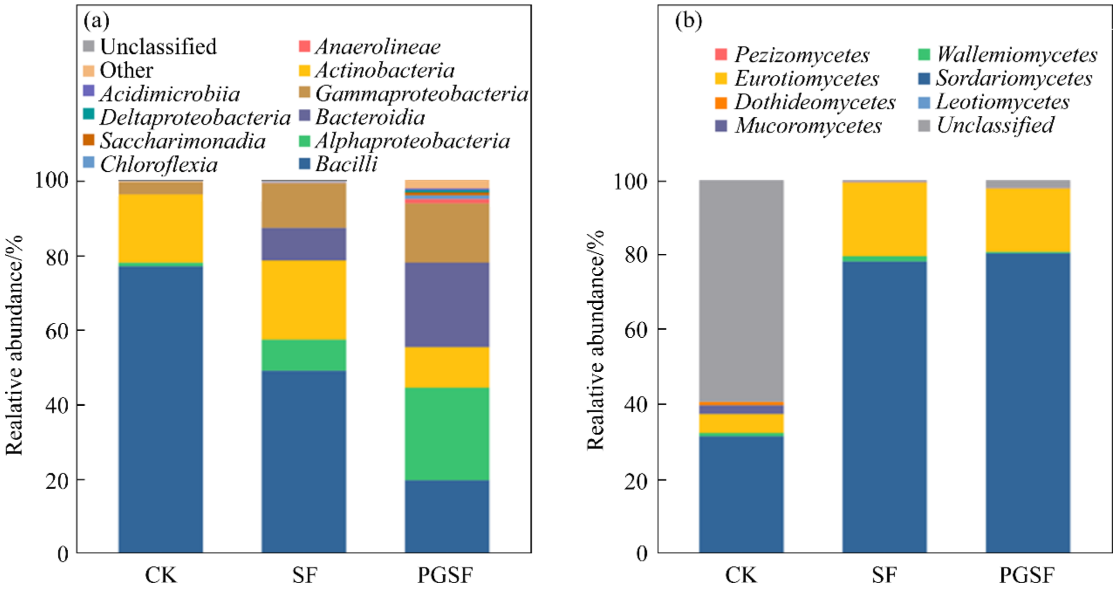

Figure S4 The relative abundances of bacterial community (a) and fungal community (b) at class level in bauxite residue by different treatments

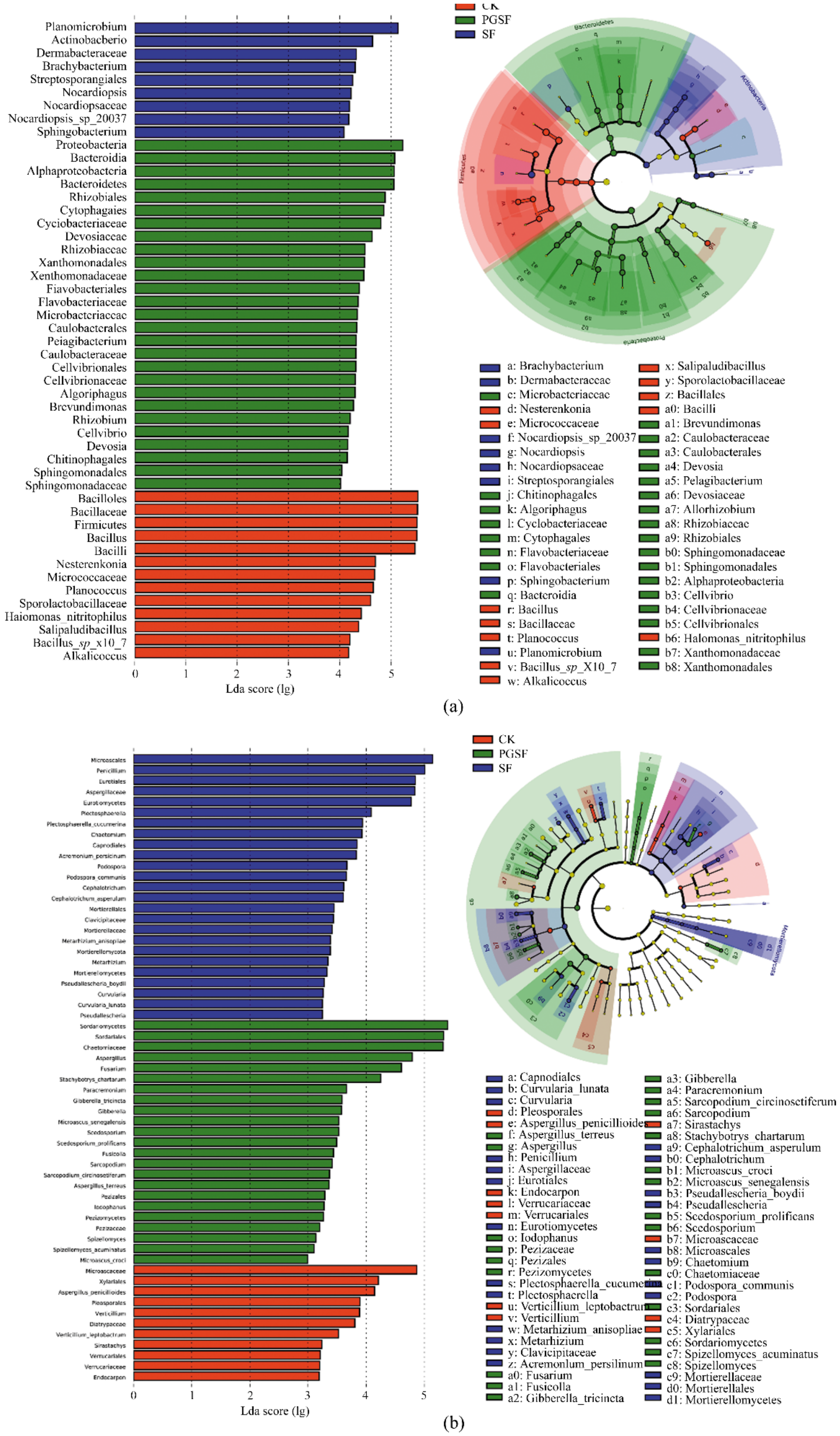

Figure S5 LEfSe analysis of bacterial community (a) and fungal community (b) in bauxite residue under different treatments