Suppplementary Materials

Response of Bacterial Community Structure and Function in Rhizosphere Soil on the Photosynthesis of Selected Plant Types C$_3$ and C$_4$ under bis(2,4,6-tribromophenoxy) ethane Exposure

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Two tables (Table S1 and S2) and eight figures (Figure S1–S8), 15 pages.

Table S1. Sequencing results and the number of ASVs in rhizosphere soil of different treatments.

Sample	raw_tags	clean_tags	ASVs	Sample	raw_tags	clean_tags	ASVs
CK1	81800	63724	622	TA1	147175	118446	643
CK2	125861	99570	736	TA2	171338	138377	668
CK3	81343	62398	591	TA3	84439	67020	413
CK1_1	41134	34401	436	GM1	114900	90495	637
CK1_2	103836	89233	715	GM2	141511	112161	705
CK1_3	115455	90797	984	GM3	102583	81324	568
SI1	101450	79015	552	MS1	109000	86427	695
SI2	83762	66062	533	MS2	109879	86726	816
SI3	77789	62724	494	MS3	66994	53316	523
ZM1	92511	73762	696	LP1	95360	76391	775
ZM2	99838	80088	505	LP2	186419	147484	761
ZM3	90569	70590	657	LP3	72892	60632	542
AT1	133214	107091	822				
AT2	129155	99498	785				
AT3	164856	130017	620				

Note: 1. raw_tags are the results obtained by filtering low-quality fastq data splicing, and clean_tags are the results obtained by further removing chimeras and short sequences from the splicing results. 2. CK (no BTBPE-contaminated soil without plant), CK1 (BTBPE-contaminated soil without plant), SI (*Setaria italica* (L.) Beauv.), ZM (*Zea mays* L.), AT (*Amaranthus tricolor* L.), TA (*Triticum aestivum* L.), GM (*Glycine max* (L.) Merr.), MS (*Medicago sativa* L.), LP (*Lolium perenne* L.).

Table S2. Bacterial species richness and diversity indices in rhizosphere soil of different treatments.

Sample	ASVs	Chao1	PD whole	Shannon	Simpson
CK1	711.67±223.73a	719.58±229.01a	50.33±7.97a	7.31±0.35a	0.98±0.0047a
SI (C_4)	526.33±24.14ab	526.09±23.98a	41.05±2.43a	7.08±0.10b	0.97±0.0000a
ZM (C_4)	619.33±82.40ab	620.72±83.42a	44.04±4.97a	7.23±0.79a	0.94±0.0403a
AT (C_4)	742.33±87.81ab	752.62±88.63a	51.76±1.97a	7.84±0.26a	0.98±0.0047a
TA (C_3)	574.67±114.77ab	581.04±118.08a	38.73±6.75a	7.25±0.17a	0.98±0.0047a
GM (C_3)	636.67±55.93ab	641.52±59.08a	43.77±2.69a	7.78±0.15a	0.98±0.0000a
MS (C_3)	678.00±120.22ab	6684.83±125.50a	49.34±7.26a	7.59±0.20a	0.98±0.0047a
LP (C_3)	692.67±106.69a	698.25±111.01a	49.00±8.02a	7.62±0.08a	0.98±0.0000a

Note: 1. CK1, BTBPE-contaminated soil without plant; SI, *Setaria italica* (L.) Beauv.; ZM, *Zea mays* L.; AT, *Amaranthus tricolor* L.; TA, *Triticum aestivum* L.; GM, *Glycine max* (L.) Merr.; MS, *Medicago sativa* L.; LP, *Lolium perenne* L. 2. Values are the mean ± Standard Deviation (SD) (*n* = 3), and different letters in the same column indicate significant difference ($p < 0.05$).
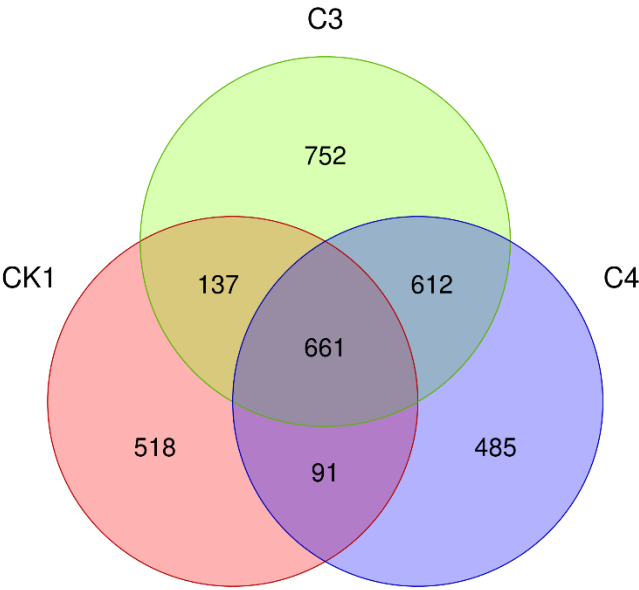

Figure S1. ASV distribution of bacteria in rhizosphere soil of C_3 and C_4 plants. (CK1, BTBPE-contaminated soil without plant.).
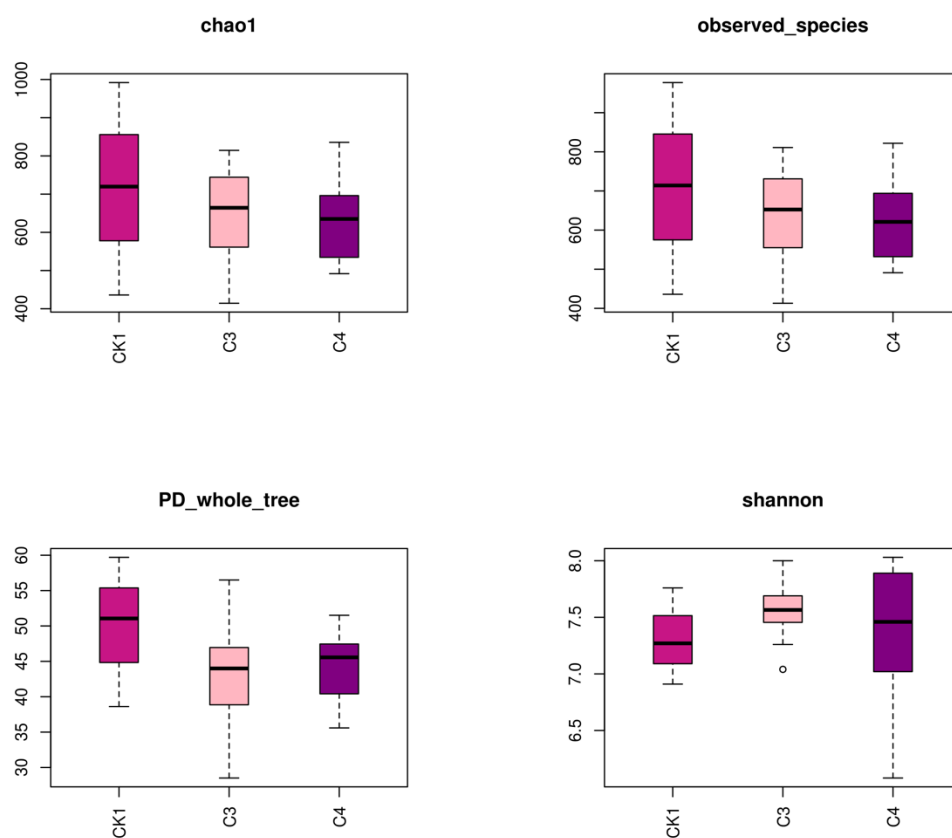
Figure S2. α-diversity of bacteria in rhizosphere soil of different treatments. (CK1, BTBPE-contaminated soil without plant.).
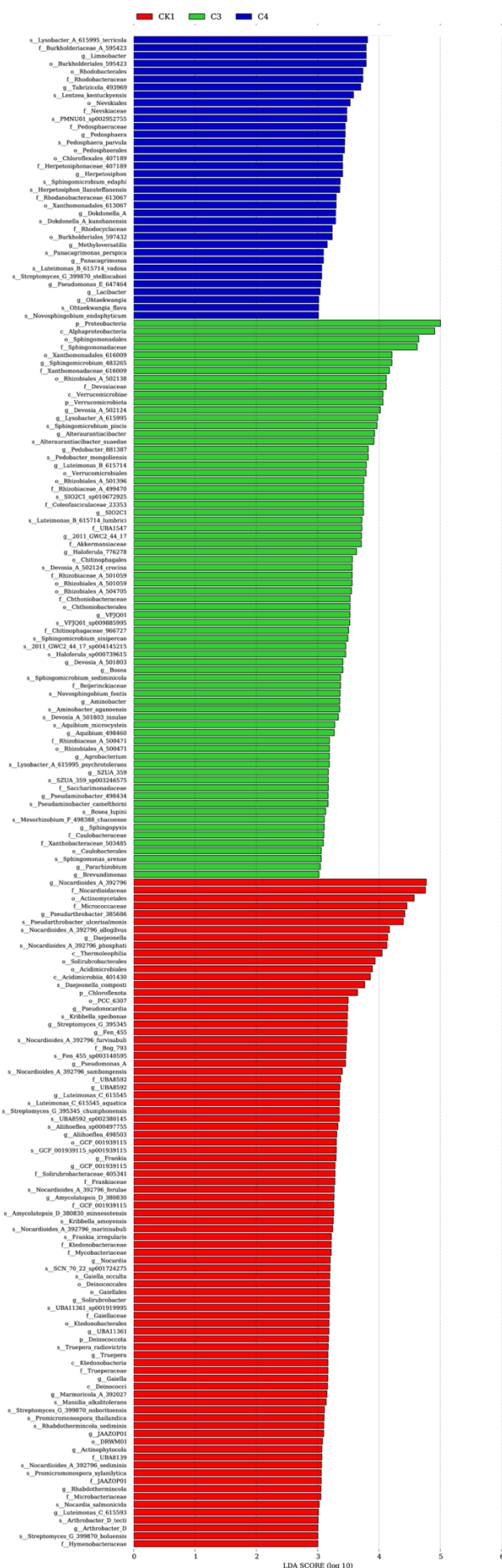
Figure S3. LDA distribution of C₃ and C₄ plant rhizosphere soil bacteria based on LEfSe analysis. (CK1 BTBPE-contaminated soil).
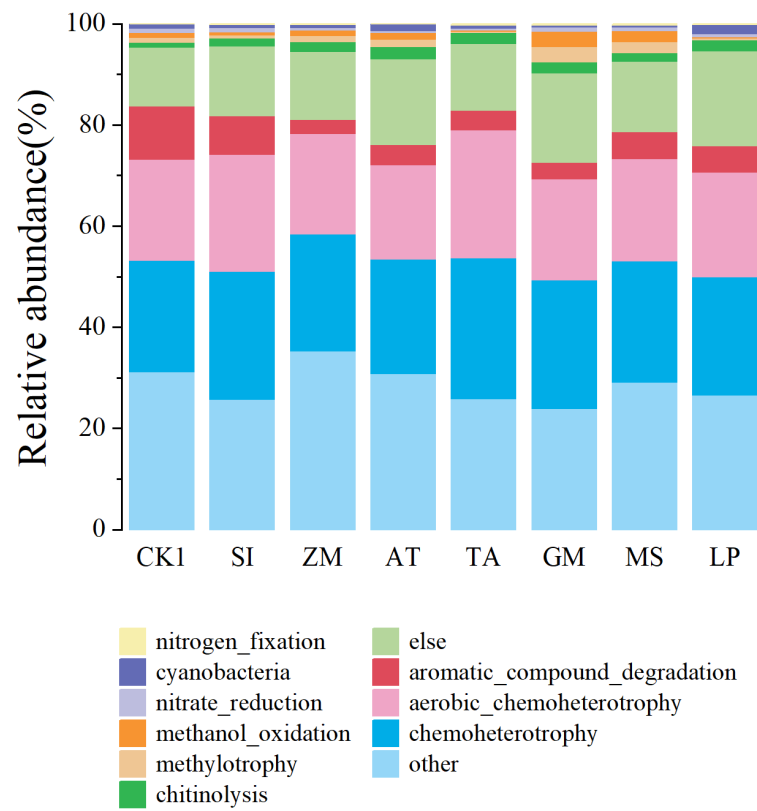

Figure S4. FAPROTAX function prediction of bacterial community in rhizosphere soil of different treatments. (CK1 BTBPE-contaminated soil, SI *Setaria italica* (L.) Beauv., ZM *Zea mays* L., AT *Amaranthus tricolor* L., TA *Triticum aestivum* L., GM *Glycine max* (L.) Merr., MS *Medicago sativa* L., LP *Lolium perenne* L.).
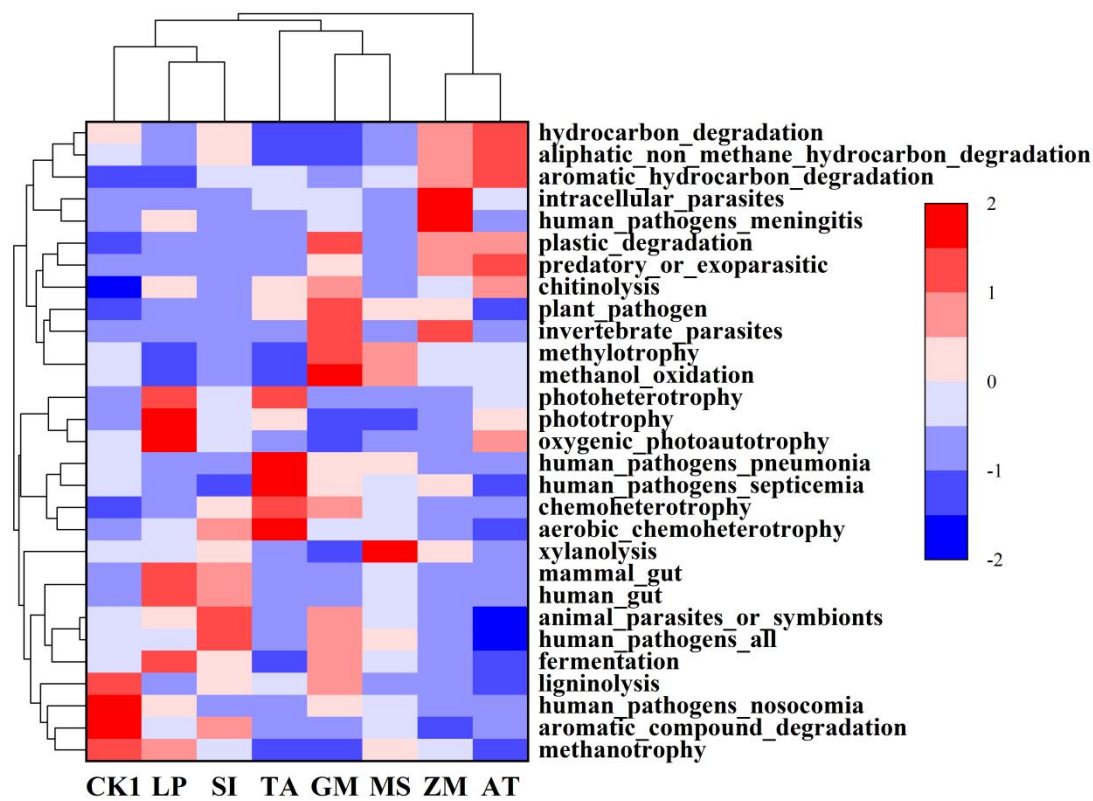
Figure S5. Distribution of related functions of carbon cycle in rhizosphere soil of different treatments. The numerical scale (-2 to 2) represents the relative strength of the functional group. The value of function relative greater than zero stands for the strongest functionality. (CK1 BTBPE-contaminated soil, SI *Setaria italica* (L.) Beauv., ZM *Zea mays* L., AT *Amaranthus tricolor* L., TA *Triticum aestivum* L., GM *Glycine max* (L.) Merr., MS *Medicago sativa* L., LP *Lolium perenne* L.).
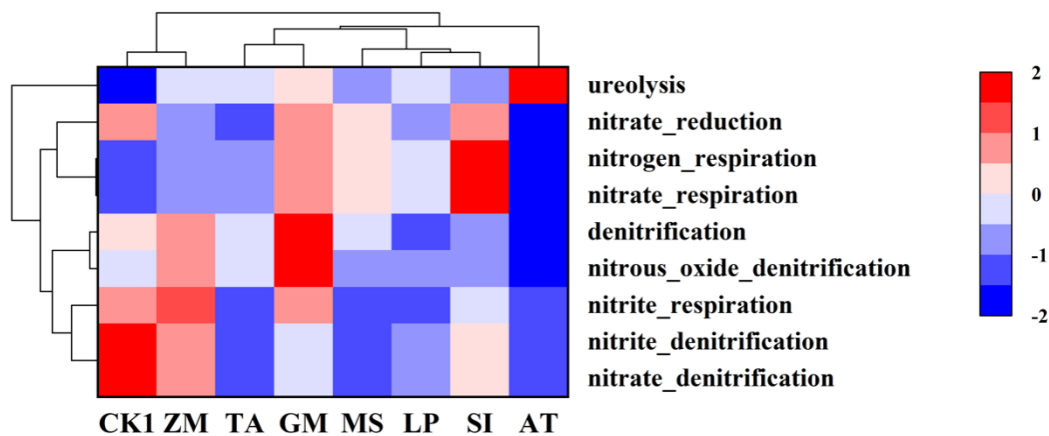

Figure S6. Distribution of related functions of nitrogen cycle in rhizosphere soil of different treatments. The numerical scale (-2 to 2) represents the relative strength of the functional group. The value of function relative greater than zero stands for the strongest functionality. (CK1 BTBPE-contaminated soil, SI *Setaria italica* (L.) Beauv., ZM *Zea mays* L., AT *Amaranthus tricolor* L., TA *Triticum aestivum* L., GM *Glycine max* (L.) Merr., MS *Medicago sativa* L., LP *Lolium perenne* L.).
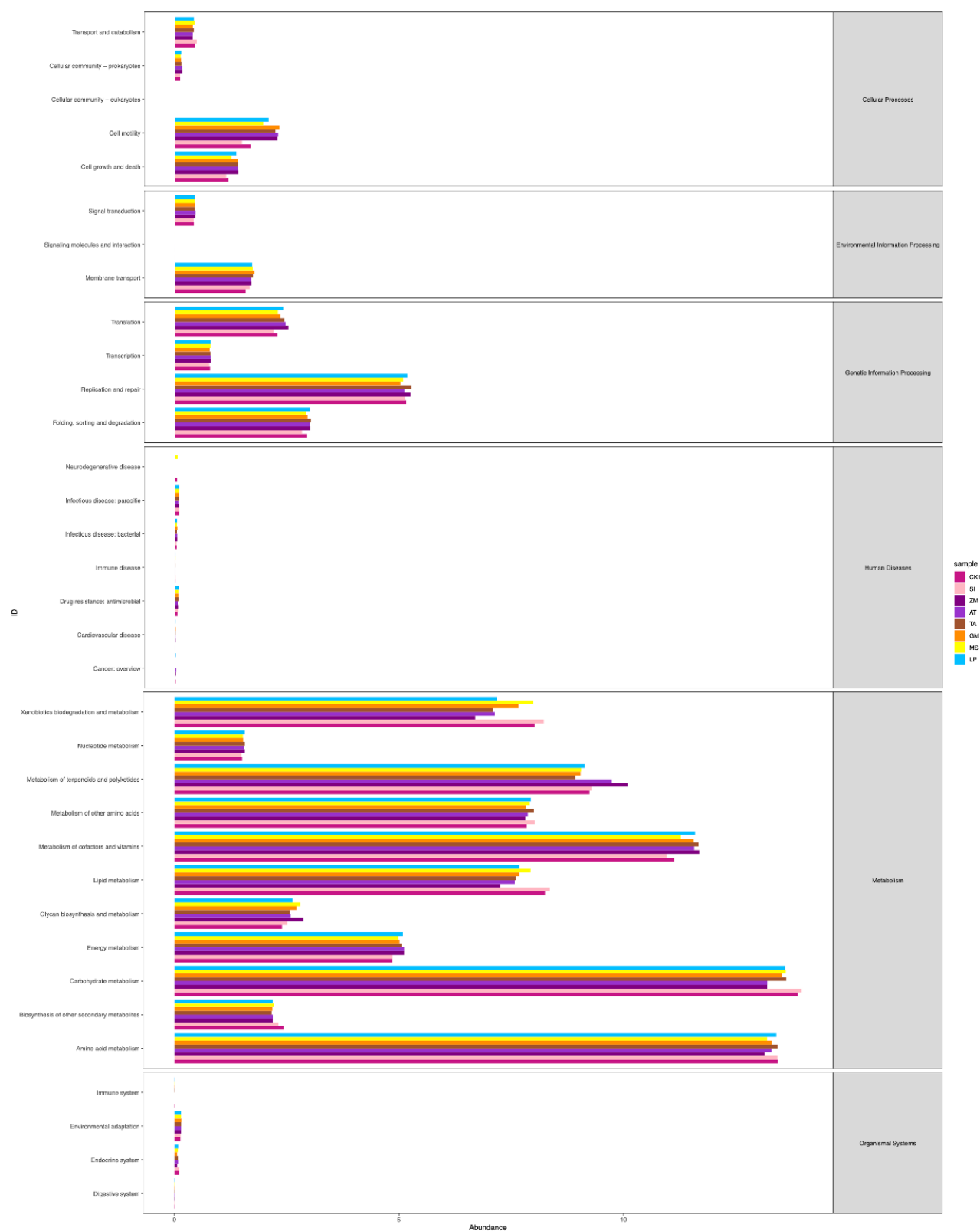
Figure S7. Functional prediction of PICRUSt 2 bacterial communities in rhizosphere soil of different treatments (KEGG level 2). (CK1 BTBPE-contaminated soil, SI *Setaria italica* (L.) Beauv., ZM *Zea mays* L., AT *Amaranthus tricolor* L., TA *Triticum aestivum* L., GM *Glycine max* (L.) Merr., MS *Medicago sativa* L., LP *Lolium perenne* L.).
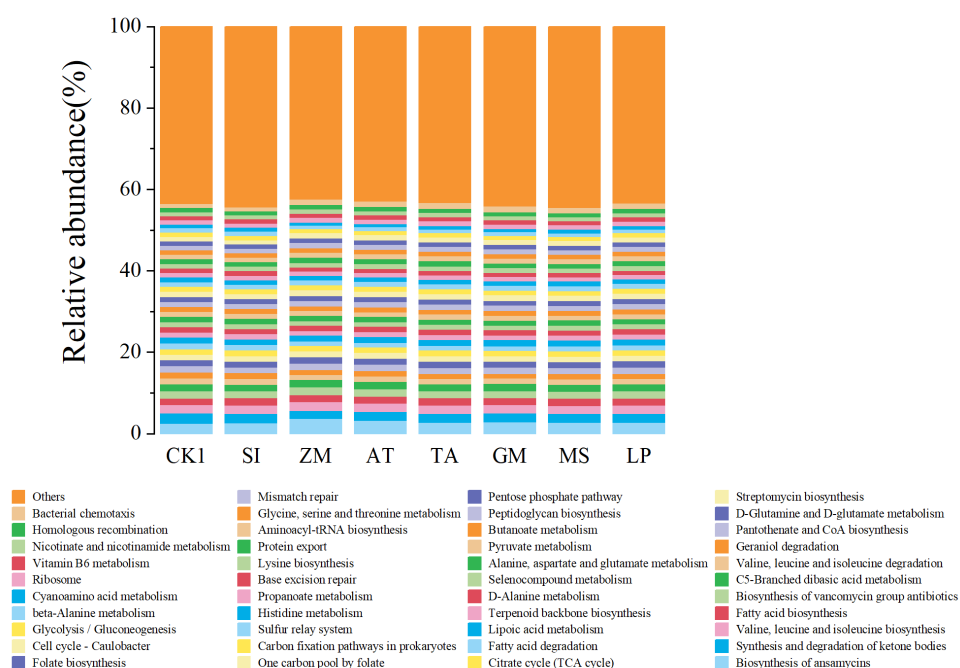
Figure S8. Functional prediction of PICRUSt 2 bacterial communities in rhizosphere soil of different treatments (KEGG level 3) (CK1 BTBPE-contaminated soil, SI *Setaria italica* (L.) Beauv., ZM *Zea mays* L., AT *Amaranthus tricolor* L., TA *Triticum aestivum* L., GM *Glycine max* (L.) Merr., MS *Medicago sativa* L., LP *Lolium perenne* L.).