

Field



Monoculture	1 st	2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th
Rotation potato	1 st	2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th
Rotation Soybean	1 st	2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th

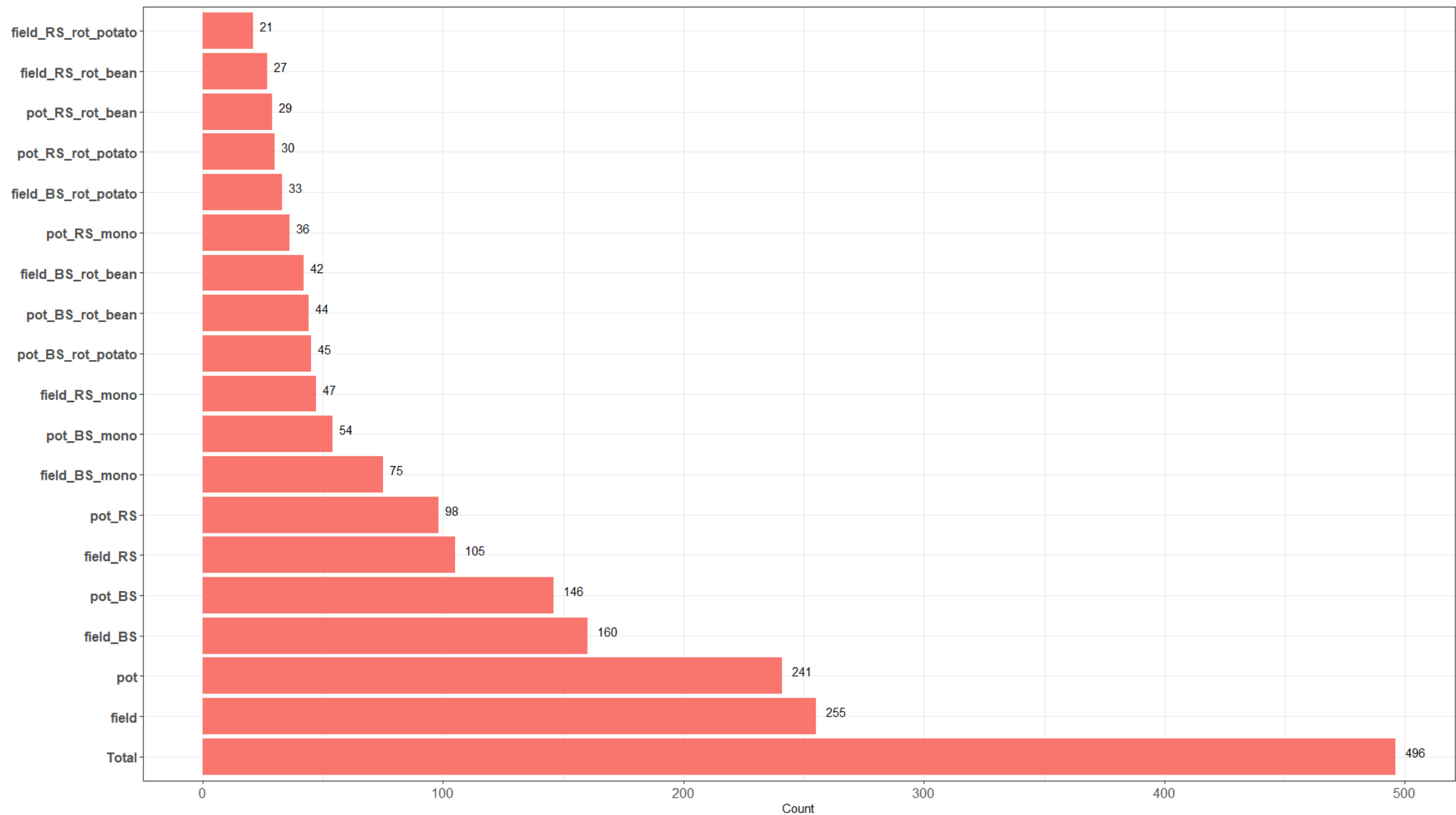
	Initial (One time)	Before planting(BP)	Planting after 30 days(30P)	Planting after 60 days(60P, harvest)
Rhizosphere soil			√	√
Bulk soil	√	√	√	√

Pot

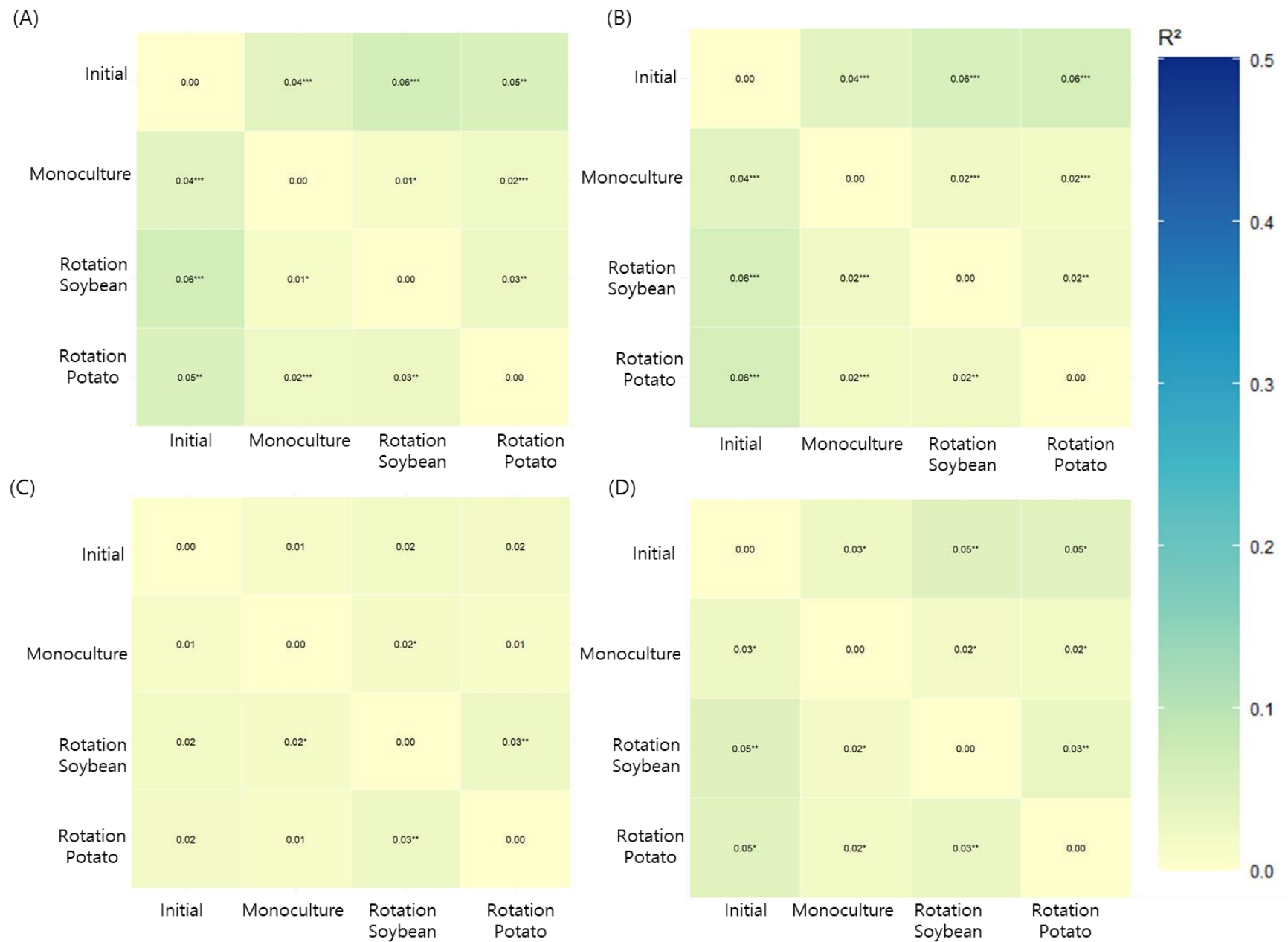


Monoculture	1 st	2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th	10 th
Rotation potato	1 st	2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th	10 th
Rotation Soybean	1 st		2 nd	3 rd	4 th	5 th	6 th	7 th	8 th	9 th

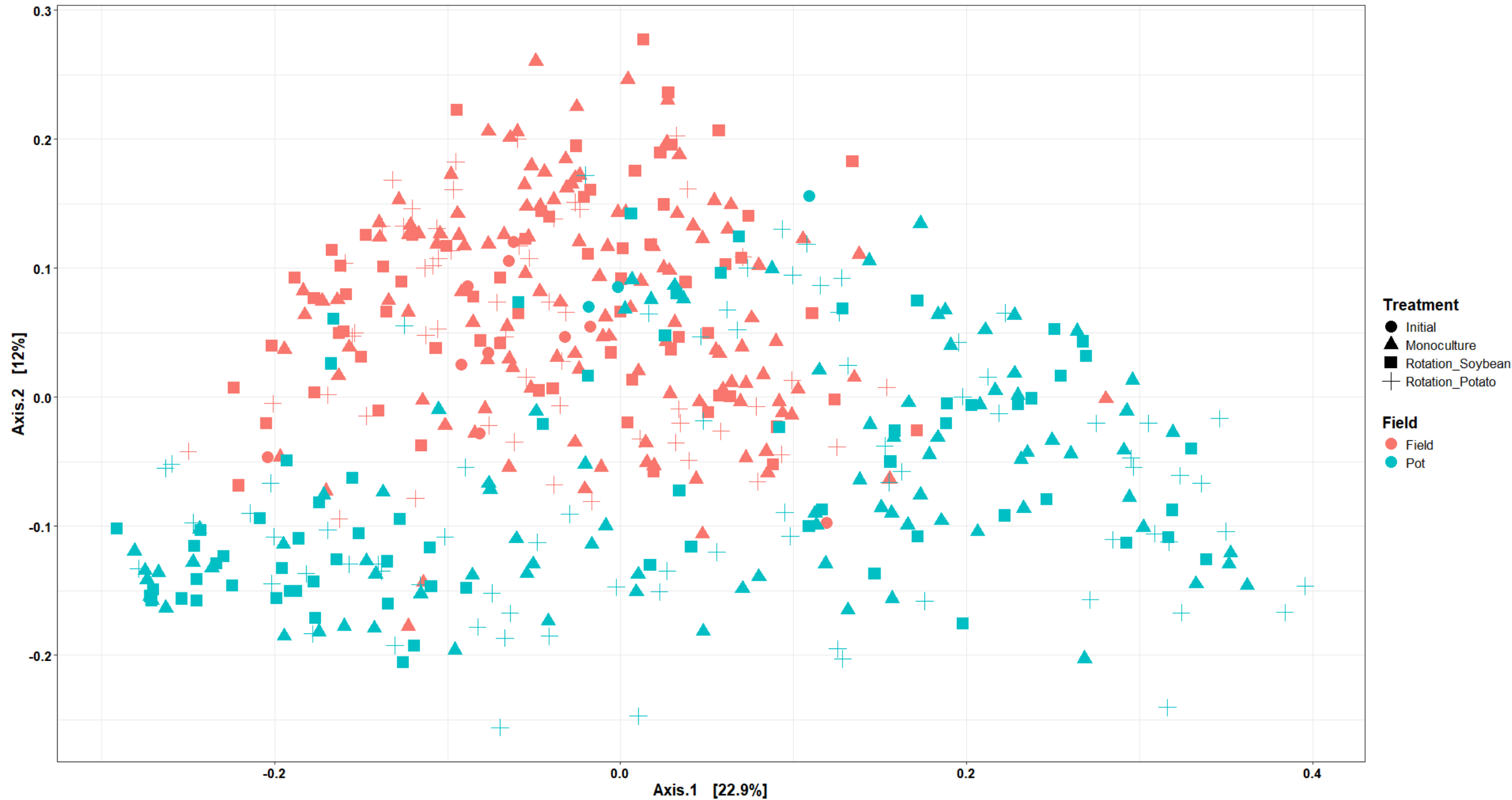
Supplementary Figure S1. Description of overall experimental design



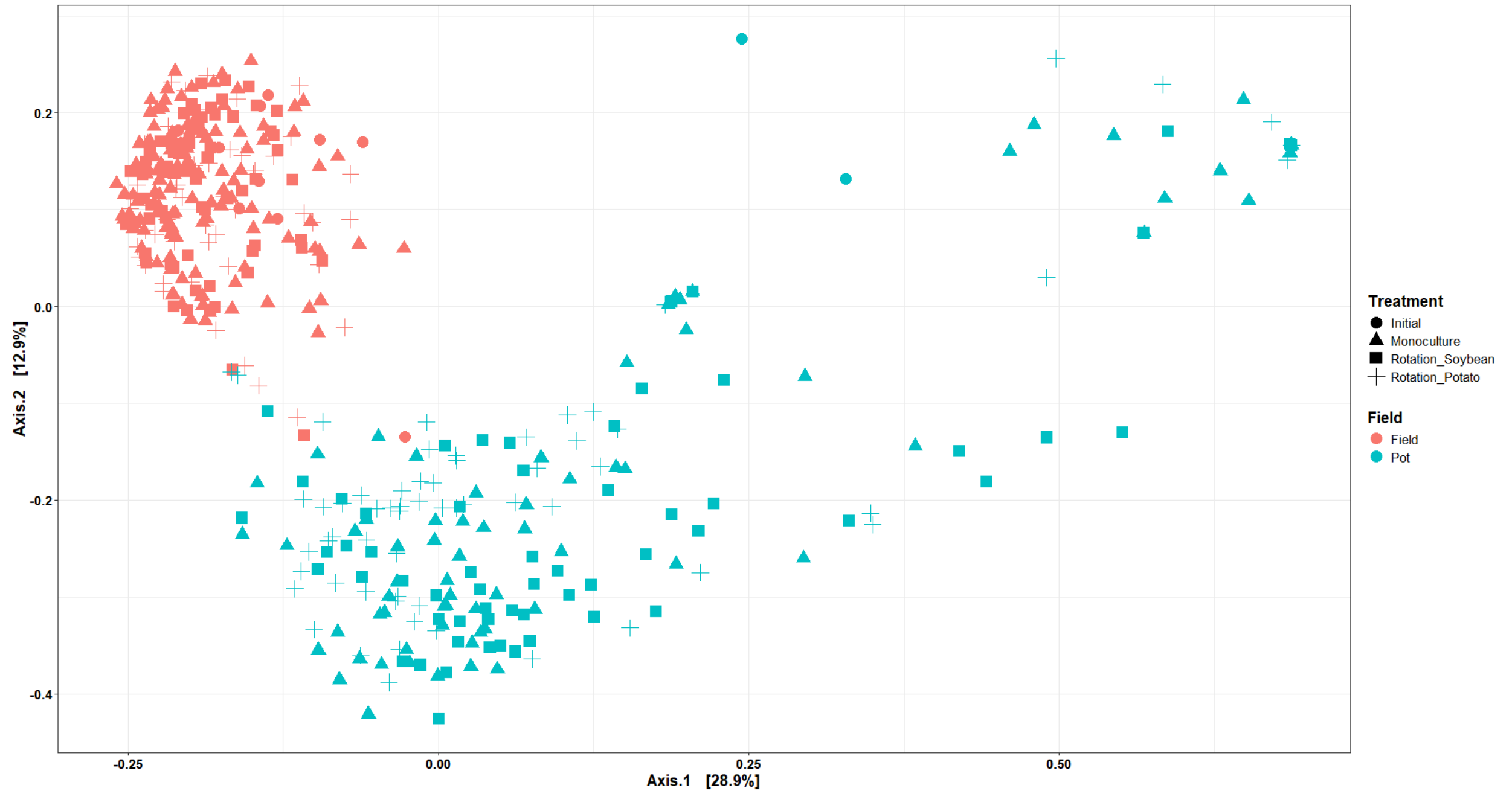
Supplementary Figure S2. The number of samples per subset. BS: bulk soil; RS: Rhizosphere soil; mono: monoculture; rot: rotation



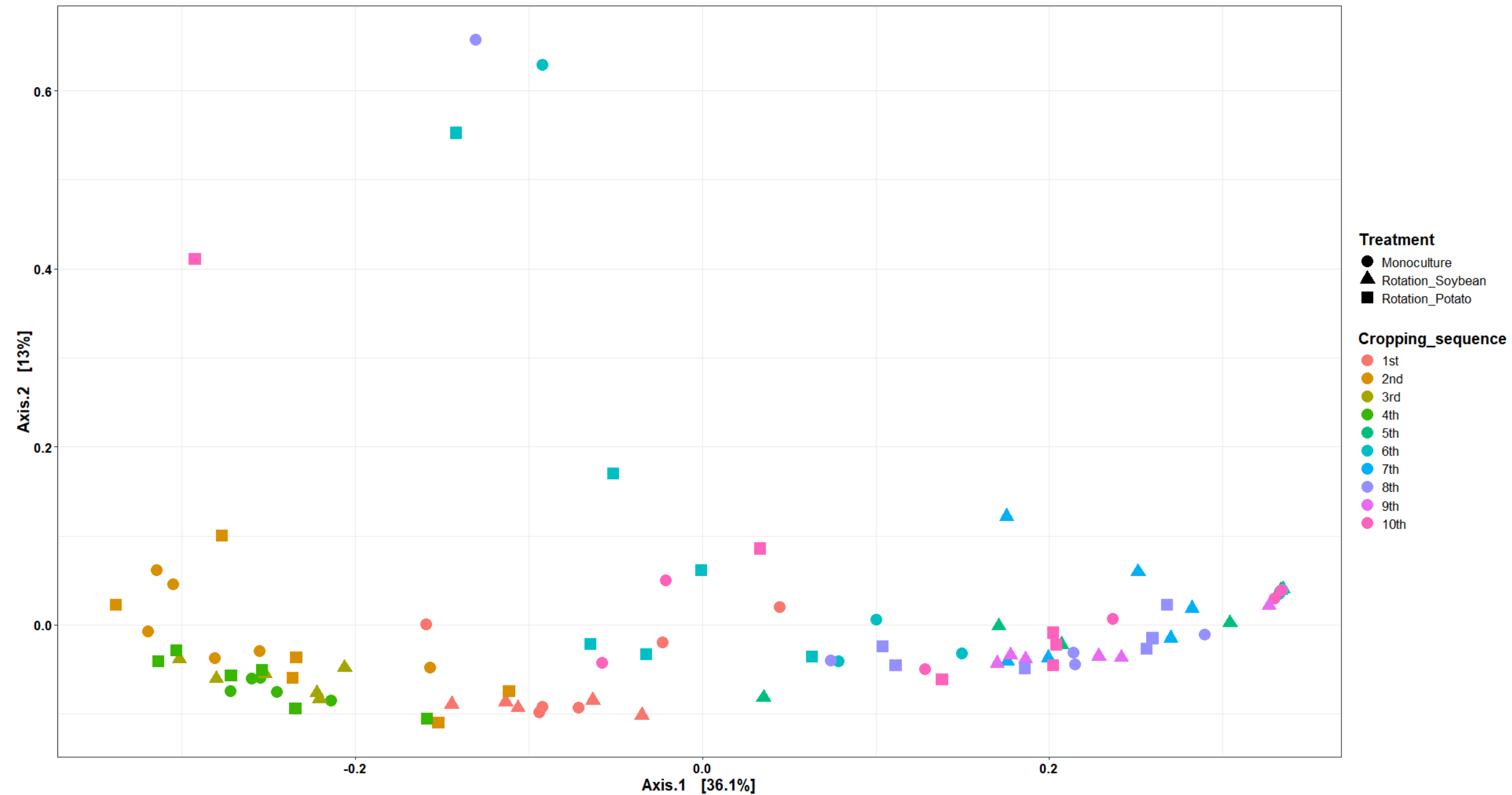
Supplementary Figure S3. Heatmap of bacterial (left) and fungal (right) microbiota dissimilarity according to cropping system on field (top) and pot (bottom) depending on R^2 of PERMANOVA result using Weighted UniFrac distance, Explained variance (R^2) was described in plot and significance was described using *p.adjust* value resulting from Bonfferonni pairwise analysis. (* < 0.05, ** < 0.01, *** < 0.001)



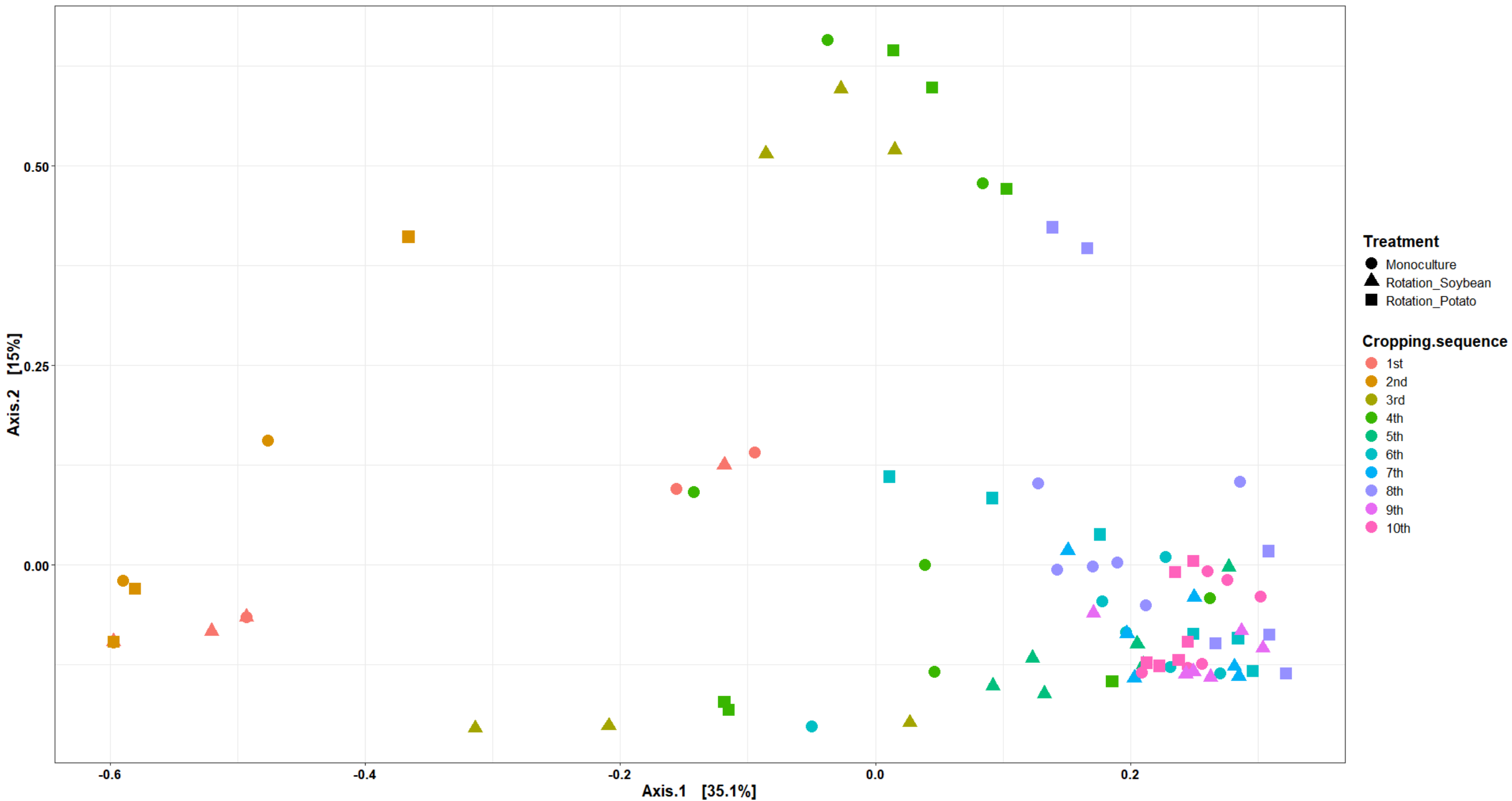
Supplementary Figure S4. PCoA plot of bacterial microbiota depending on field and cropping system using Weighted UniFrac distance described in treatment and environmental factor



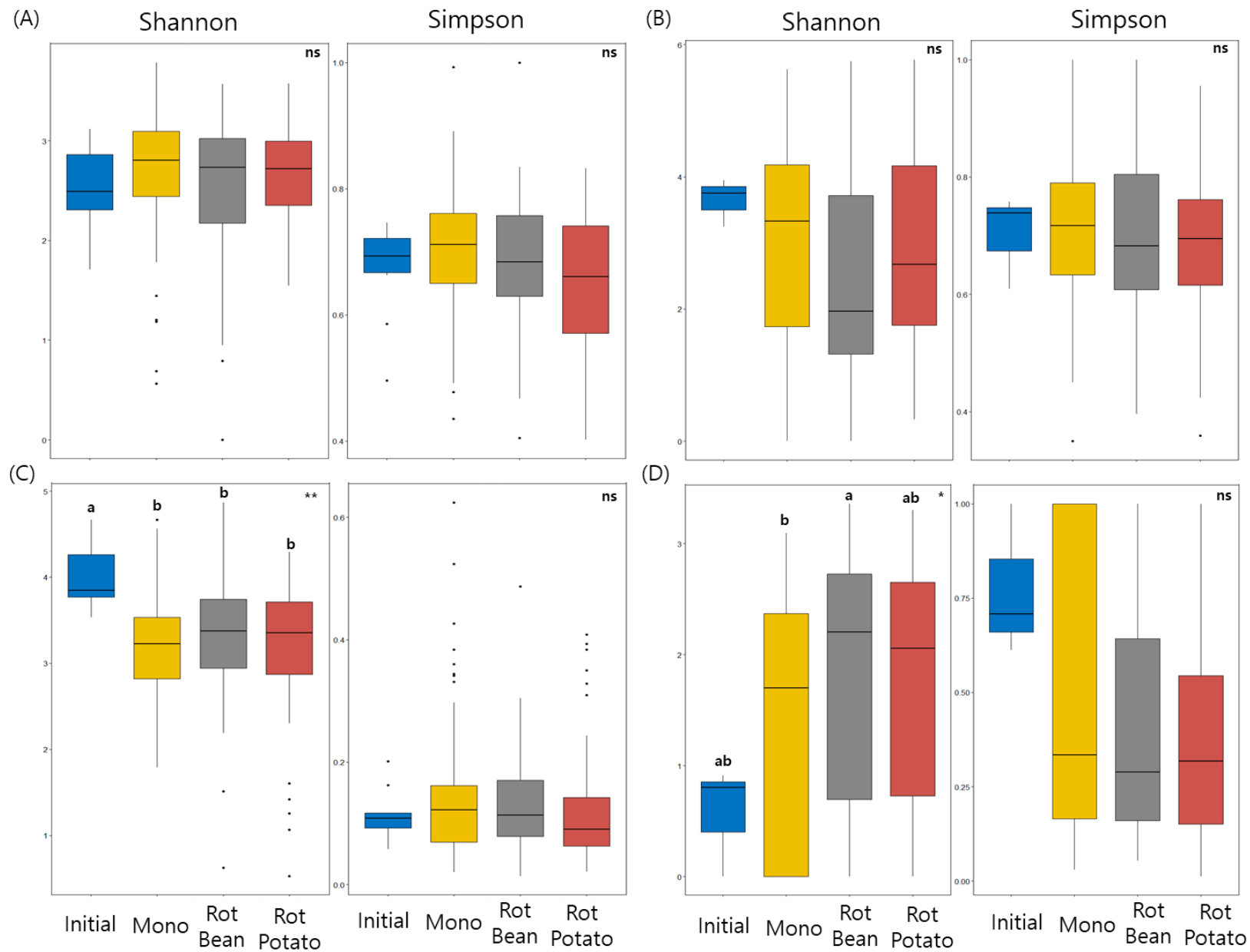
Supplementary Figure S5. PCoA plot of fungal microbiota depending on field and cropping system using Weighted UniFrac distance described in treatment and environmental factor



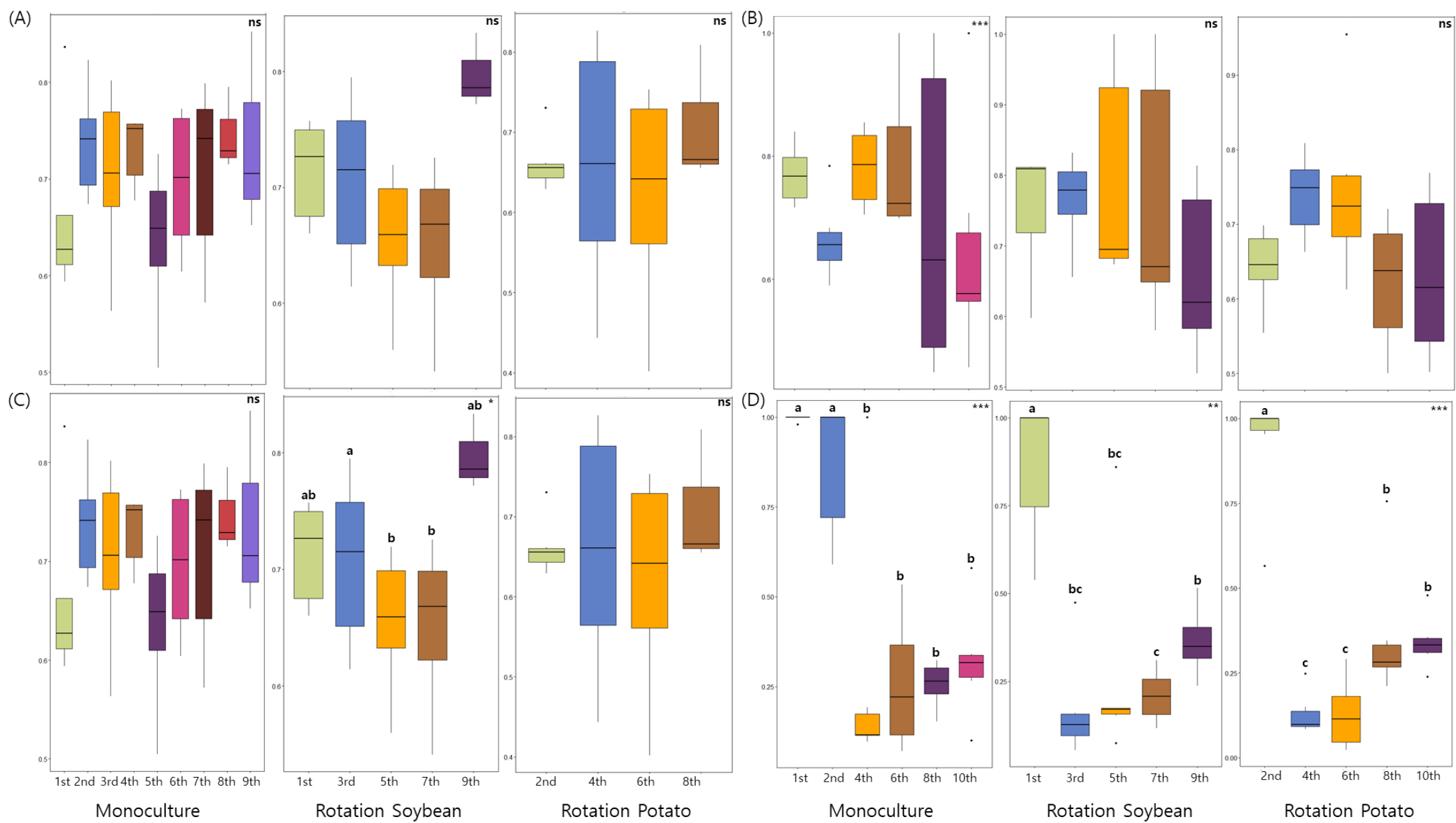
Supplementary Figure S6. PCoA plot of rhizosphere bacterial microbiota on pot according to cropping system and cropping sequence using Weighted UniFrac distance described in treatment and cropping sequence



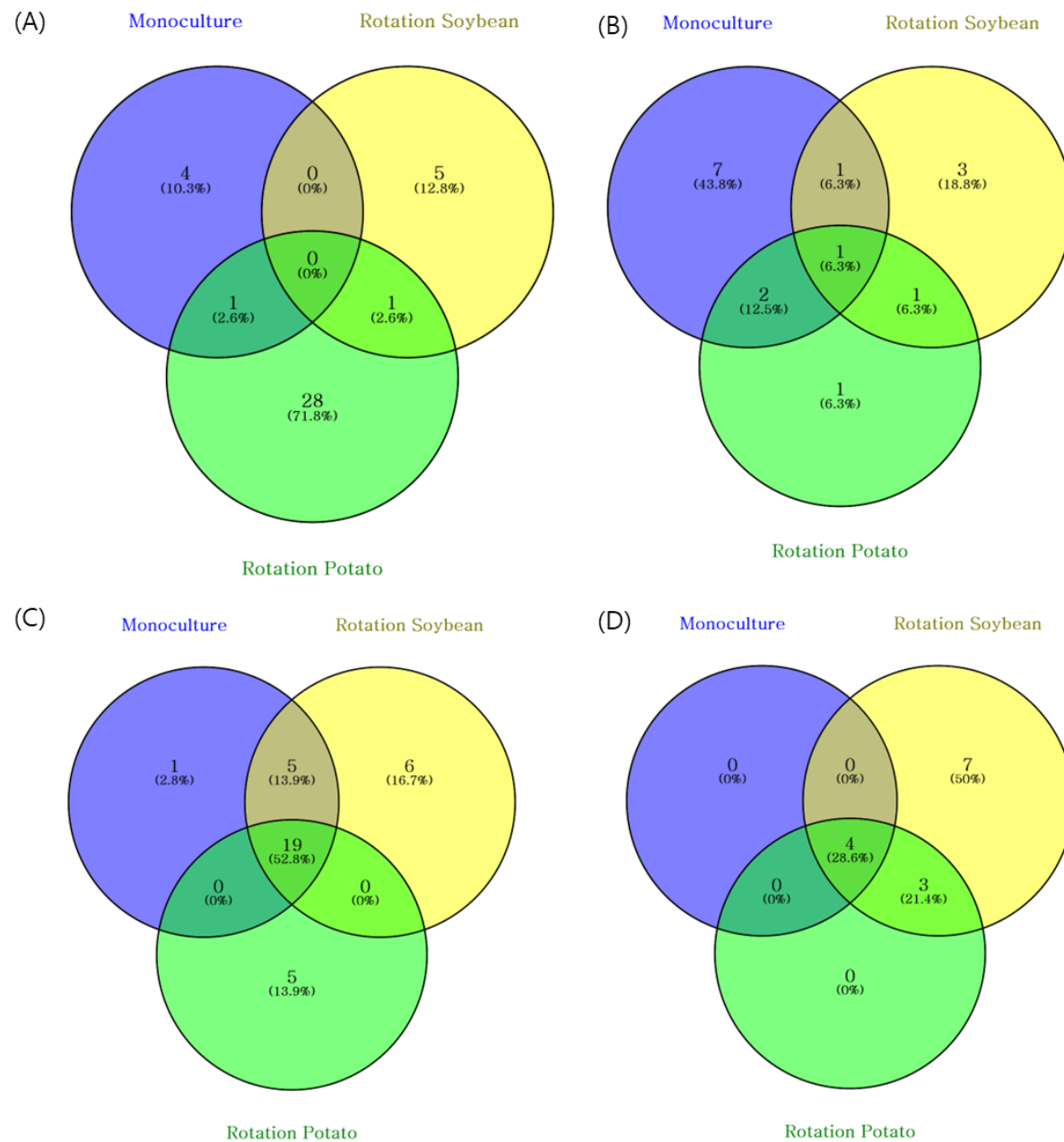
Supplementary Figure S7. PCoA plot of rhizosphere fungal microbiota on pot according to cropping system and cropping sequence using Weighted UniFrac distance described in treatment and cropping sequence



Supplementary Figure S8. Bacterial (top) and fungal (bottom) diversity depending on cropping system on field (left) and pot (right). Bonferroni pair-wise post-hoc test was conducted after Kruskal-Wallis test, ns: no significance, * p -value < 0.05, ** p -value < 0.01, *** p -value < 0.001. Mono: monoculture, Rot Bean: rotation with soybean, Rot Potato: rotation with potato

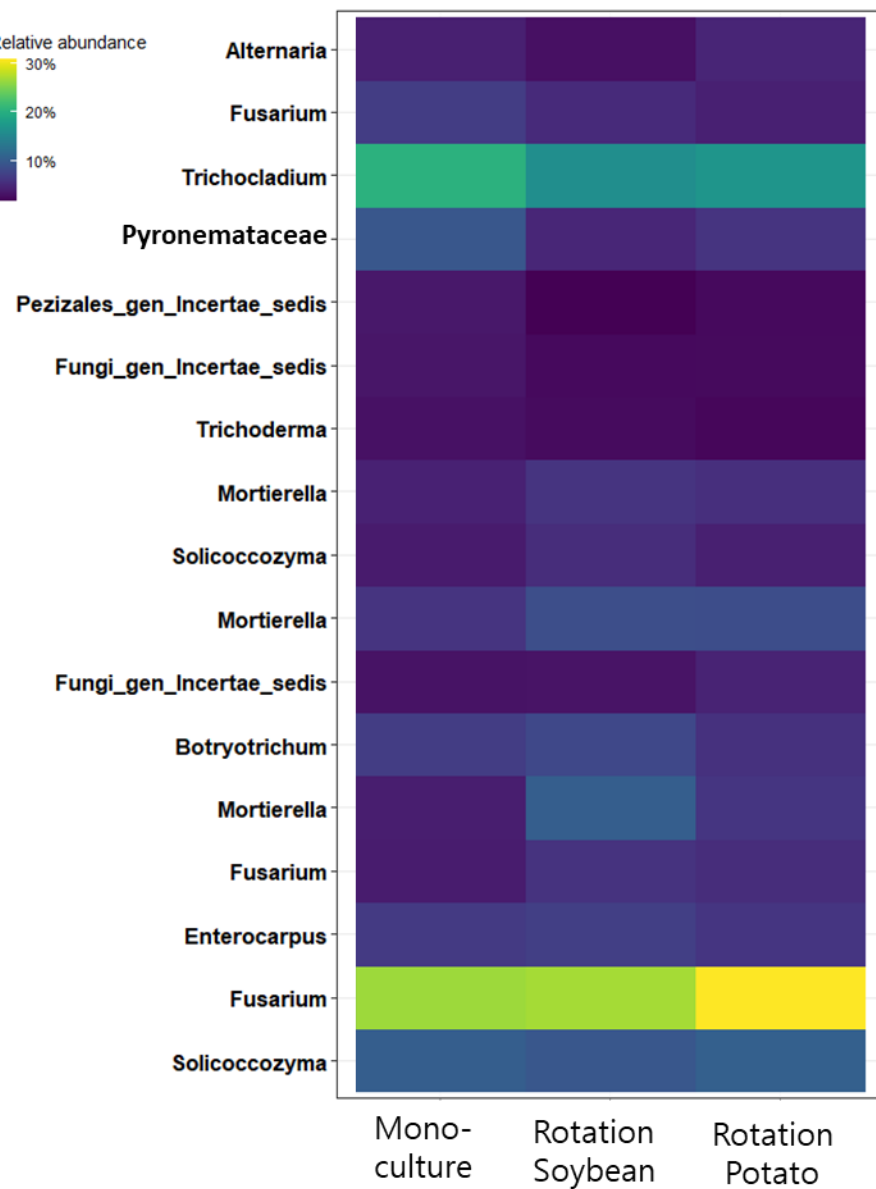


Supplementary Figure S9. Rhizosphere bacterial (top) and fungal (bottom) diversity depending on cropping sequence on field (left) and pot (right) using Simpson evenness. Benjamini-Hochberg(FDR) pair-wise post-hoc test was conducted after Kruskal-Wallis test, ns: no significance, * p -value < 0.05, ** p -value < 0.01, *** p -value < 0.001. Monoculture of (B) showed significant differences as results of Kruskal-Wallis test, but subsequent pairwise Wilcox tests with FDR adjustment did not identify significant differences between cropping sequences.

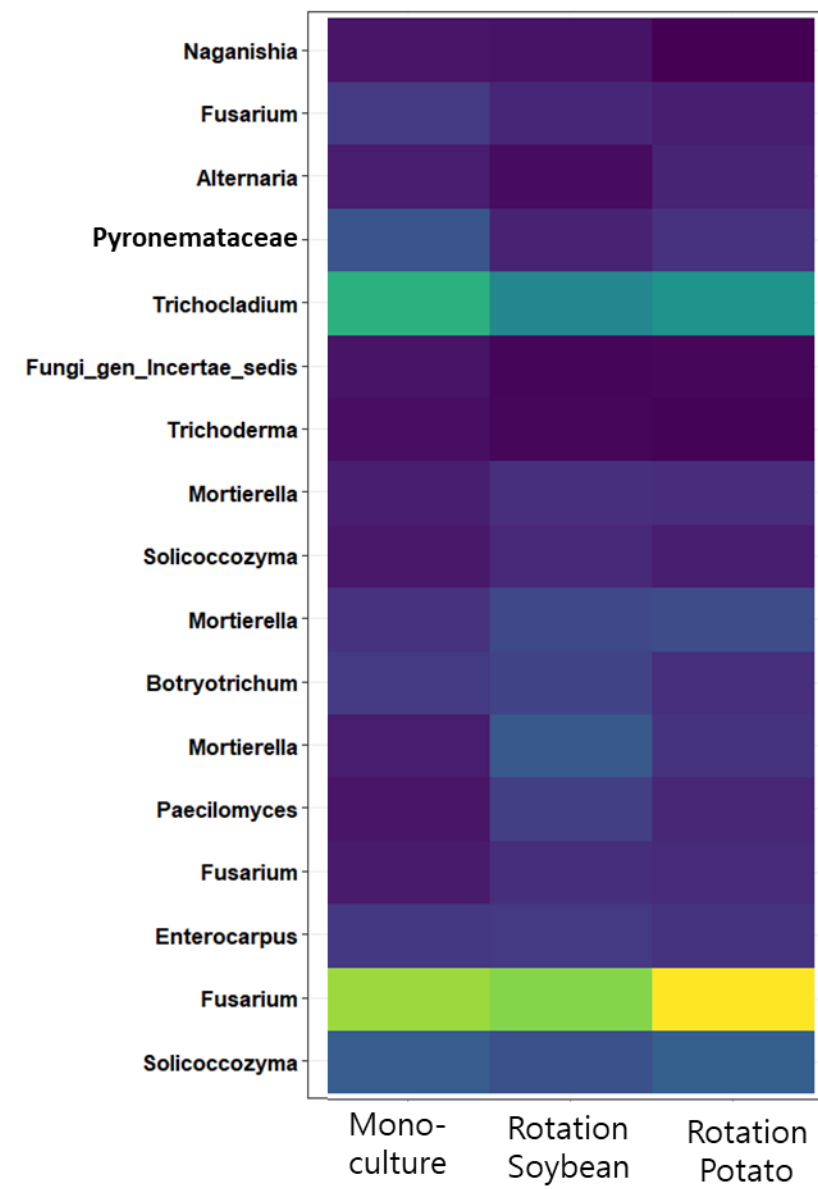


Supplementary Figure S10. Venn-diagram regarding core bacterial (top) and fungal (bottom) ASV. (A) bacterial rhizosphere soil on field (B) bacterial rhizosphere soil on pot (c) fungal rhizosphere soil on field (D) fungal rhizosphere soil on pot

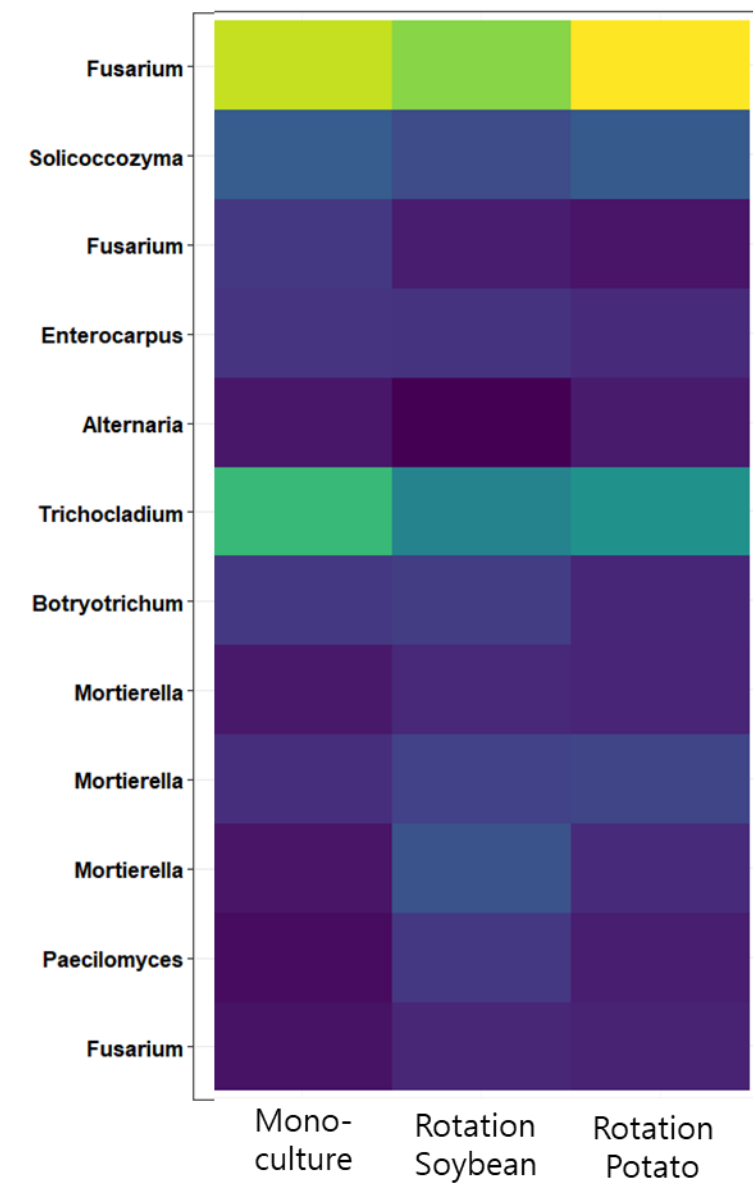
(A)



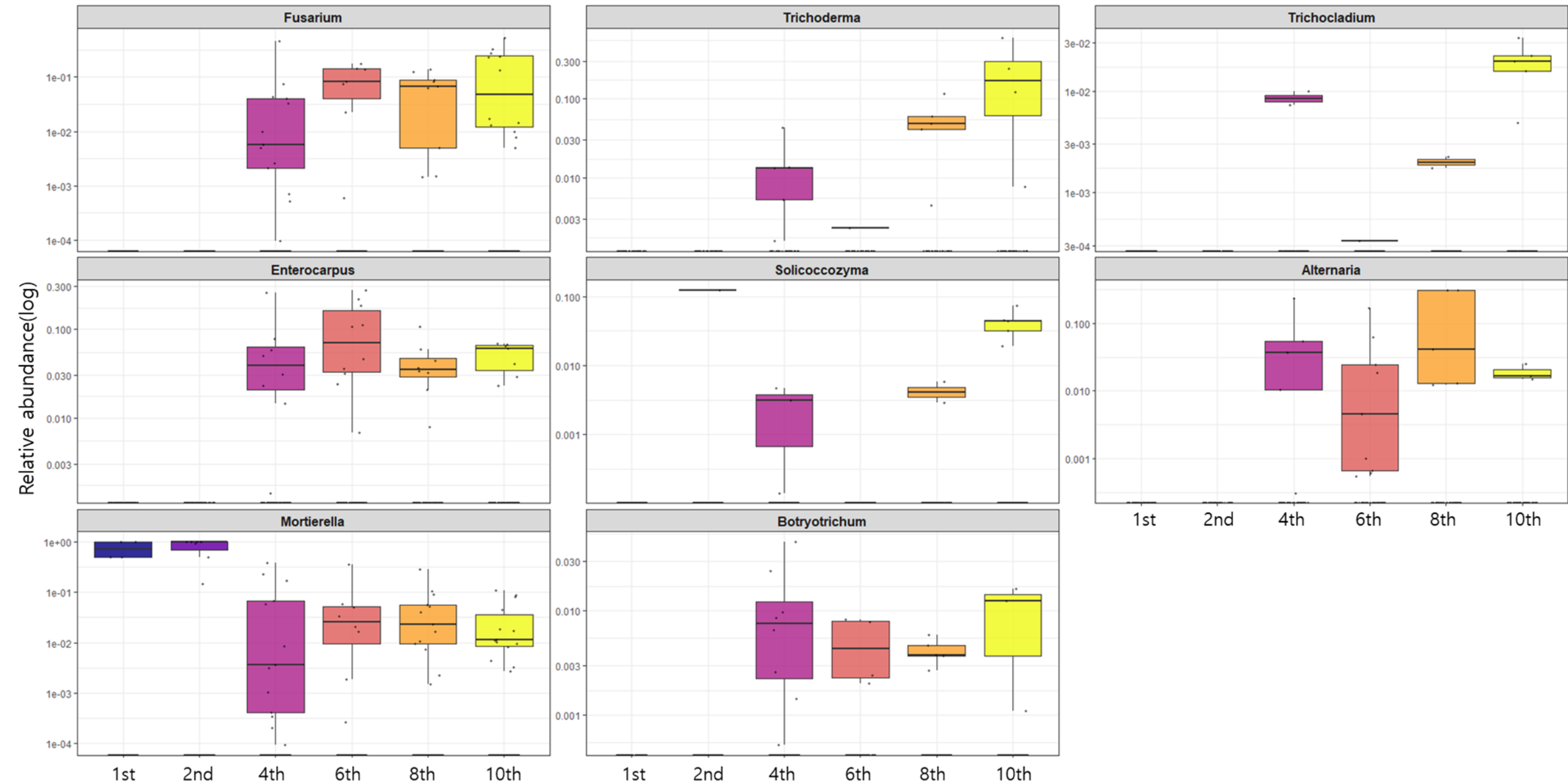
(B)



(C)



Supplementary Figure S11. Relative abundance plot regarding core fungal ASVs according to the cropping systems using total data set. (A) monoculture: 17 ASVs, (B) rotation with soybean: 17 ASVs, (C) rotation with potato: 12 ASVs



Supplementary Figure S12. Relative abundances of selected fungal (B) groups depending on cropping sequence under monoculture in the pot rhizosphere soil

Supplementary Table S1. The results of PERMANOVA analysis on bacterial and fungal microbiota

Sample set	Kingdom	Variable	<i>d.f.</i>	<i>SS</i>	R ²	F	Pr (>F)
Total	Bacteria	Treatment	3	0.977	0.01968	3.2926	***
		Niche	2	0.984	0.01982	4.9855	***
		Growth stage	3	1.041	0.02097	3.512	***
		Field/Pot	1	3.665	0.07385	39.39	***
		Cropping sequence	10	7.3	0.14708	8.3636	***
	Fungi	Treatment	3	2.719	0.02008	3.2997	***
		Niche	2	1.502	0.0111	2.7151	**
		Growth stage	3	2.821	0.02084	3.4271	***
		Field/Pot	1	26.044	0.1924	115.54	***
		Cropping sequence	10	18.937	0.13989	7.7419	***
Field	Bacteria	Treatment	3	0.7937	0.04499	3.9415	***
		Cropping sequence	9	3.0704	0.17405	5.7366	***
	Fungi	Treatment	3	1.845	0.04602	4.0364	***
		Cropping sequence	9	9.006646	0.22464	7.886914	***
Pot	Bacteria	Treatment	3	0.805	0.02842	2.3106	**
		Cropping sequence	10	9.2916	0.32799	11.226	***
	Fungi	Treatment	3	2.874489	0.041523	3.29243	***
		Cropping sequence	10	27.8994	0.403013	14.91923	***

SS: sum of squares, significance value based on 999 permutations, ns: no significance, **p-value* < 0.05, ***p-value* < 0.01, ****p-value* < 0.001

Supplementary Table S2. The number of indicator ASVs depending on cropping system considering subset

Kingdom	Data set	Monoculture	Rotation with soybean	Rotation with potato
Bacteria	Overall	3	15	7
	Field	1	8	50
	Pot	32	18	47
	Field Rhizosphere soil	0	2	10
	Pot Rhizosphere soil	2	3	4
Fungi	Overall	12	19	9
	Field	33	103	114
	Pot	17	45	37
	Field Rhizosphere soil	13	41	63
	Pot Rhizosphere soil	3	21	18

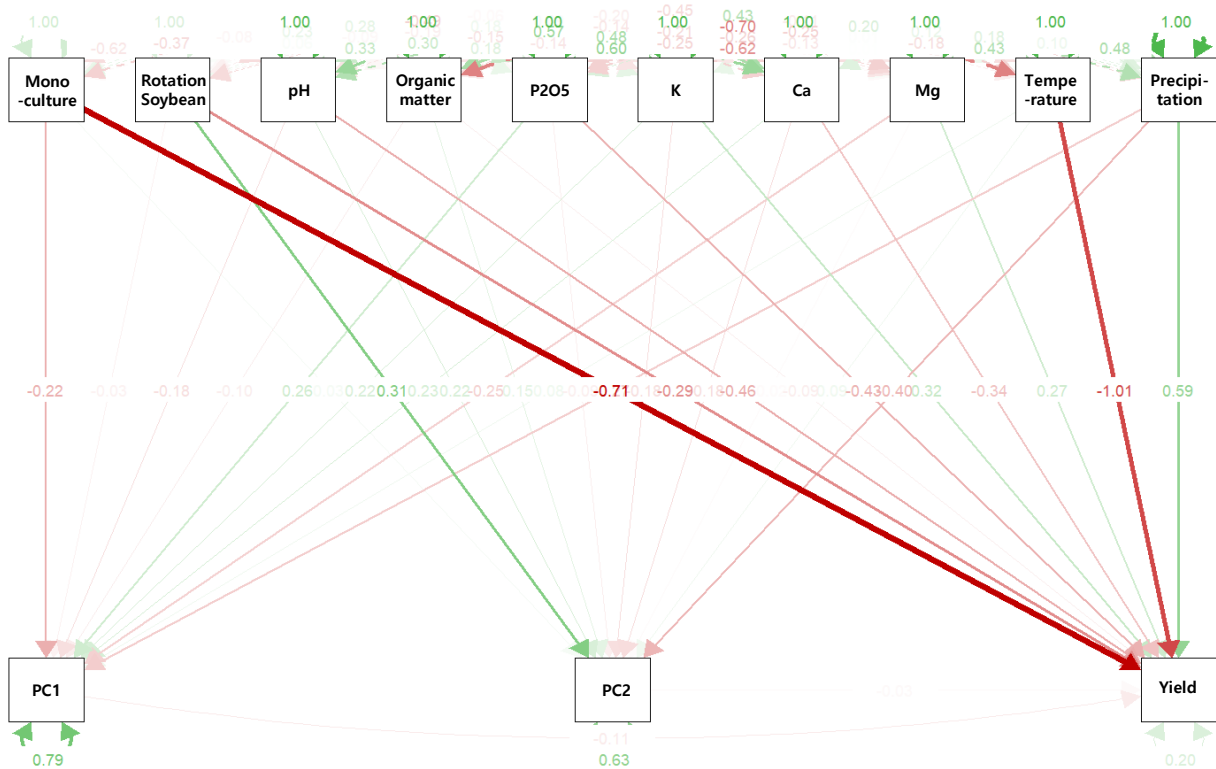
Supplementary Table S3. Bacterial core ASVs depending on cropping system on field rhizosphere soil

Group	ASV	Kingdom	Phylum	Class	Order	Family	Genus
Monoculture	b8b30e2a5f2d609c48c8591fd62a1cf3	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	8acacc127fb47989ec146ace0ea02e20	Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Uncultured
	3ea6277e9ff1f04fd6baf2f7f7da8ed	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Terrabacter
	5224d6e687ef7b3bdd9cb1266b361247	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
	827f93ff1da378b511620571a340b170	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
Rotation with soybean	f33fb6360c460bc73ad78352e0481ec5	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
	ae7cdfd994d6ba673705266efc16392d	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	43be2a8a568d26340faa19b1f7fb5206	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	870c030f249dded1d264a7943b623eda	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
	d664a0953fad3b106b2f18c70aa59f8f	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia-Caballeronia-Paraburkholderia
	3b99c2efa656747d40bff74769ff5096	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia-Caballeronia-Paraburkholderia
Rotation with potato	5593a9d301617a92f001ff2235a43381	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Uncultured	NA
	76a2d612da5cbda6175186492dc26035	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Uncultured	NA
	35751d6b26ba554c58e77246d889545f	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae	NA
	2d4e015b511c22b103810eea5c754773	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
	8a0b0a8f630bfcd06bb8cc54ed275616	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	NA
	4c44fc21b704185212f83ad9f9df979a	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
	9d25d5fcd939576cf825a239ca7e3c82	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	9f6b4470122e6f27dd554132957997c3	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	65b7aac8adc311a4933c444f38ab69a5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	d6c200219f2b028ee7064474781b0d66	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	bcecd775bc95d47dae63c9577725cf91	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Uncultured
	884bf7916619e05e64ff19da2b33dbb0	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	65ad44935b58e0057f3ce1225d787554	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus Udaeobacter
	d1cc70dd538a55c48ed6272be2eade92	Bacteria	Chloroflexi	Gitt-GS-136	NA	NA	NA
	898feb9c00aa34883d9e61ab25330386	Bacteria	Methyloirabilota	Methyloirabilia	Rokubacteriales	NA	NA
	466839b4b77ac05182ff0ac2bfccd2ac	Bacteria	Methyloirabilota	Methyloirabilia	Rokubacteriales	NA	NA
	ea74763a33a0b51822733fc86212ed52	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	NA
	3ea6277e9ff1f04fd6baf2f7f7da8ed	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Terrabacter
	6aefe9bc4c5ec272c8e03ca369be4315	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Terrabacter
	4693376916bc7bbcbfe0fcc18f09df3c	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Terrabacter
	651f53acf3dc636b4291cec4c92da62c	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	NA
	870c030f249dded1d264a7943b623eda	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
	fcced7e56ded40b0a6ec4f96ef11d50	Bacteria	Actinobacteriota	Actinobacteria	NA	NA	NA
	43acfb7009b6500647886efd3e303bef	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales	Uncultured	NA
	dcaea291b0ff4c229b9d003215283633	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriales	Uncultured	NA
	df88ede995ef7140439f75d2e4b9710	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosospira
	6b9b0e3cfff2e765d6b2c89b80758cd8	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax
	513b0bf7022d28e14a4248bdb64a719a	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia-Caballeronia-Paraburkholderia
	a0fd23286d9abad1db939cde7be716da	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Mizugakiibacter
	3331ba25dc37ac1d6d3857a05fd645f0	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Mizugakiibacter

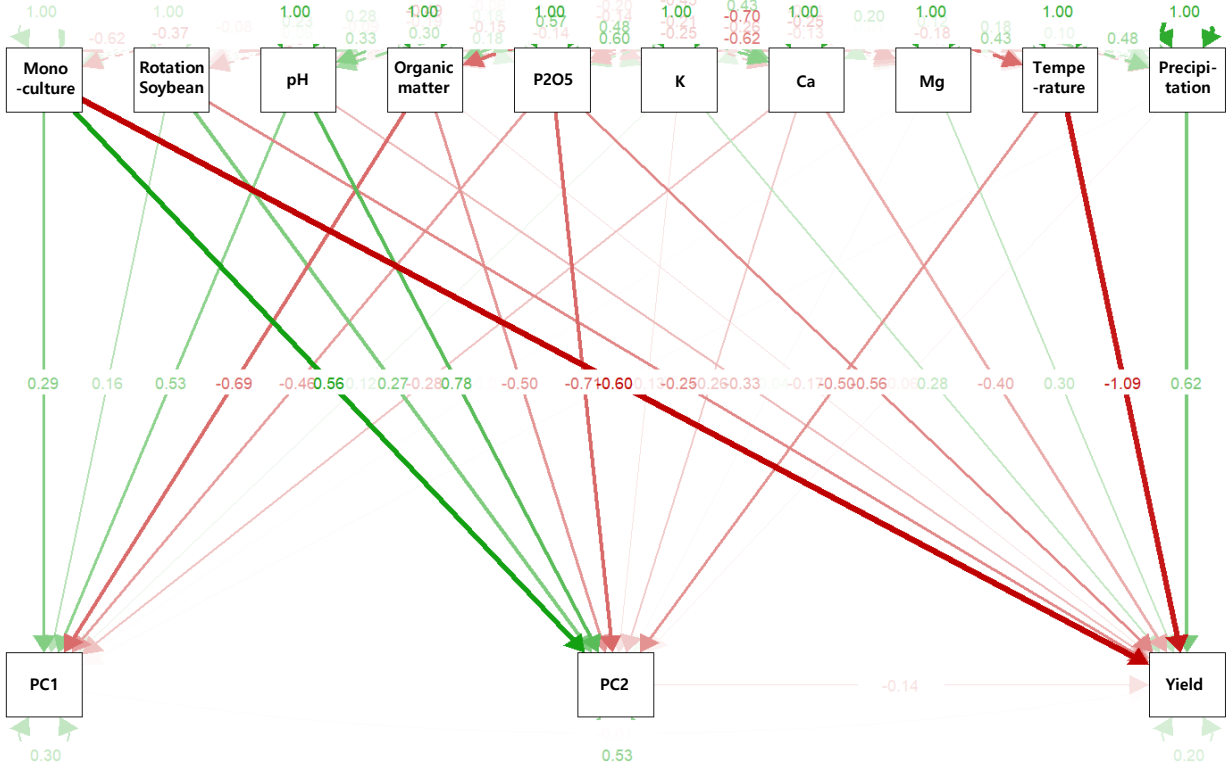
Supplementary Table S4. Bacterial core ASVs depending on cropping system on pot rhizosphere soil

Group	ASV	Kingdom	Phylum	Class	Order	Family	Genus
Monoculture	a4389ce2ab4d155462ca50c05f51310d	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9fce82762888c8cfe80a1afacfd004e7	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	09e05d6a1e9770ea0ded4e5faaaef8c2	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	7bb0064623e8855dd95f9f7a7ec3ca4d	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	6e129baa01e54866785850fd23d62ed3	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9b028e65f34ea22f5d17b15678805d58	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	42fe0719e7005583f11198477038a589	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	ea58f7a1cd9be6074fb251876ff1d0b6	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	84a78697b2524bead7c420d56fc5dddc	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	ebe50e6d6ab42eece6131bc5c4b54f6e	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
Rotation with soybean	fdc44695f2f529025b220177f943421b	Bacteria	Unidentified	Unidentified	Unidentified	Unidentified	Unidentified
	9cf2142758c4951d76dcc6bda90542fb	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	01f63f7be88c9431e665ee6904958b77	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9b028e65f34ea22f5d17b15678805d58	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	42fe0719e7005583f11198477038a589	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9c88de25549f6136dbb086f4798021bf	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
Rotation with potato	54466259de7ac6e2629bd4a96fa50ff3	Bacteria	Unidentified	Unidentified	Unidentified	Unidentified	Unidentified
	09e05d6a1e9770ea0ded4e5faaaef8c2	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	7bb0064623e8855dd95f9f7a7ec3ca4d	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9b028e65f34ea22f5d17b15678805d58	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9c88de25549f6136dbb086f4798021bf	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
	9fab7d809f548a17ce7727032f201d64	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Rhodanobacter

(A)



(B)



Supplementary Figure S13. Structure Equation Model (SEM) illustrating factors influencing Kimchi cabbage yield under monoculture and soybean rotation systems; (A) bacterial microbiota PC1 and PC2, (B) fungal microbiota PC1 and PC2