

Supplementary:

Table S1. Mean biomass (grams) for individual plants from each brassica treatment. A random individual was chosen from each plot to get the mean weight of individuals grown in the field. Samples collected September 2020.

Brassica species	Mean biomass (g)	Standard Error	Mean total biomass per plot	Standard error
Tillage radish	54.89	10.40	585.45	85.03
Shepherd's purse	0.80	0.24	18.82	3.73
Rockcress	1.07	0.24	116.49	12.43
White mustard	19.48	6.90	355.83	39.94

Table S2. Planned comparison results for indices of diversity of the soil fungal community between all brassica cover crop treatments (tillage radish, white mustard, shepherd's purse, rockcress) and the undisturbed control (n = 3 for control, n = 5 for all other treatments). Diversity measurements as follows: Pielou's evenness Index, Shannon Diversity Index (SDI), Species richness, and Faith Phylogenetic Diversity (FPD).

Diversity measurement	P value	F
Evenness	0.007	9.169
SDI	0.032	5.431
Richness	0.980	0.001
FPD	0.857	0.033

Table S3. Planned comparison results for indices of diversity of the soil fungal community between native brassica cover crop treatments (shepherd's purse and rockcress) and non-native brassica cover crop treatments (tillage radish and white mustard) (n = 5 for each brassica species). Diversity measurements as follows: Pielou's evenness Index, Shannon Diversity Index (SDI), Species richness, and Faith's Phylogenetic Diversity (FPD).

Diversity measurement	P value	F
Evenness	0.943	0.005
SDI	0.265	1.325
Richness	0.324	1.030
FPD	0.215	1.651

Table S4. One-way ANOVA results for indices of diversity of the soil fungal community among different cover crop treatments (tillage radish, white mustard, shepherd's purse, rockcress) (n = 5). Block used as a random factor. Diversity measurements as follows: Pielou's evenness Index, Shannon Diversity Index (SDI), Species richness, and Faith Phylogenetic Diversity (FPD).

Diversity measurement	P value	F	df
Evenness	0.732	0.434	3, 12
SDI	0.682	0.511	3, 12
Richness	0.594	0.657	3, 12
FPD	0.654	0.556	3, 12

Table S5. Spearman correlation coefficients relating estimated brassica cover crop biomass to various diversity measurements (Pielou's evenness Index, Shannon Diversity Index (SDI), Species richness, and Faith Phylogenetic Diversity (FPD)) (n = 20). Includes all brassica treatments (tillage radish, white mustard, shepherd's purse, and rockcress).

Diversity measurement	<i>P</i> value	Correlation coefficient
Evenness	0.833	-0.050
SDI	0.554	-0.141
Richness	0.332	-0.229
FPD	0.282	-0.253

Table S6. PERMANOVA results for fungal community composition of different cover crop treatments (tillage radish, white mustard, shepherd's purse, rockcress, and control) at different taxonomic levels (n = 3 for control, n = 5 for all other treatments). Species level analysis includes all detected phylotypes (not all detected to species level). Permutations = 999.

Taxonomic level	<i>P</i> value	F	df	R ²
Phylum	0.207	1.471	4	0.246
Class	0.237	1.320	4	0.227
Species	0.217	1.167	4	0.206

Table S7. PERMANOVA results for beta diversity of detected fungal OTUs of different cover crop treatments (tillage radish, white mustard, shepherd's purse, rockcress, and control) (n = 3 for control, n = 5 for all other treatments). Permutations = 999.

Method	<i>P</i> value	F	df
Weighted UniFrac	0.295	1.127	4, 18
Unweighted UniFrac	0.327	1.028	4, 18
Bray-Curtis	0.363	1.029	4, 18

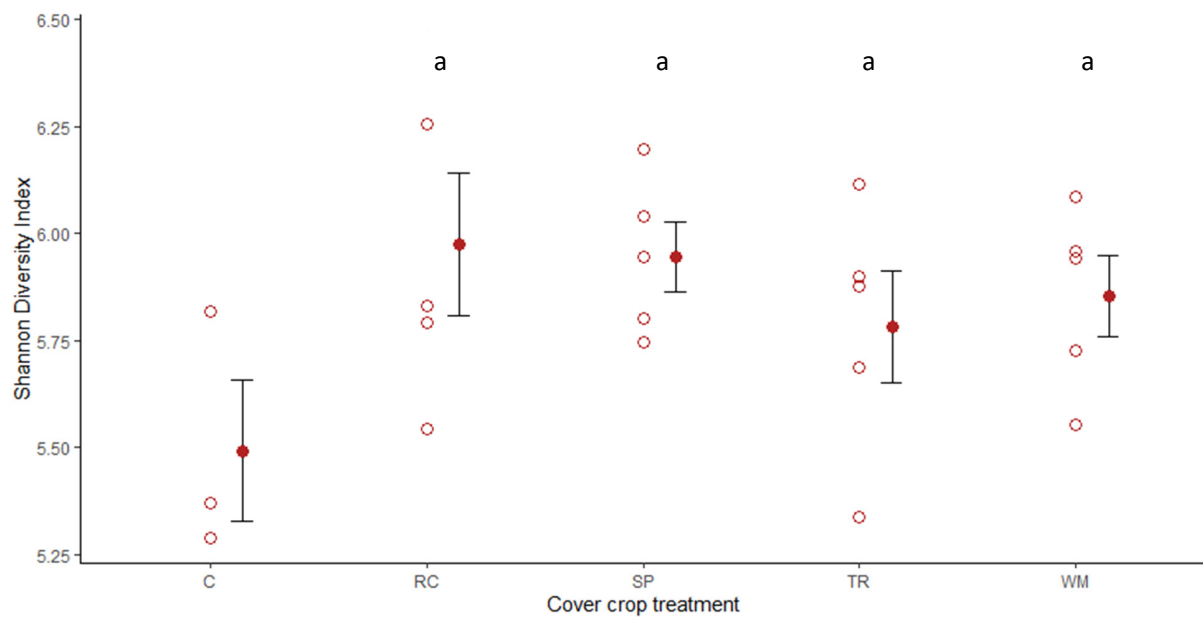


Figure S1. Shannon diversity index of fungal communities in soil samples from plots with different cover crop treatments. Treatments: C, undisturbed control; RC, Rockcress; SP, Shepherd's purse; TR, Tillage radish; WM, White mustard (n = 3 for control, n = 5 for all other treatments). Values were obtained in QIIME2. Hollow red circles represent individual replicates, solid red dots and black lines represent mean and standard error. Group means sharing the same letter are not significantly different.

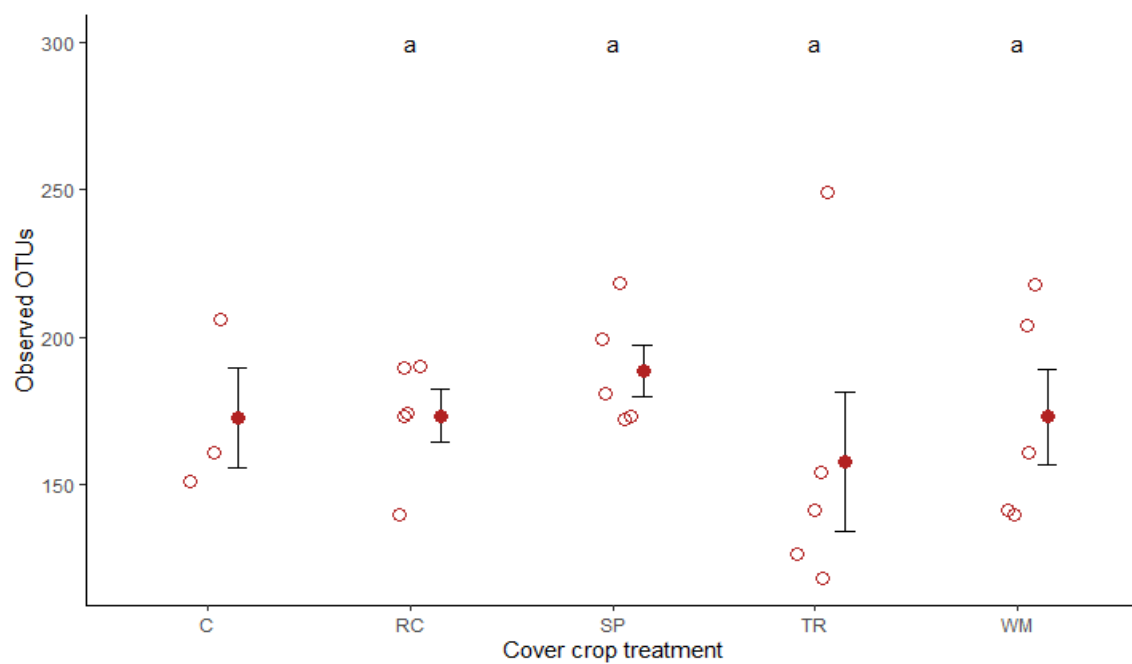


Figure S2. Species richness as measured by number of observed OTUs in fungal communities in soil samples from plots with different cover crop treatments. Treatments: C, undisturbed control; RC, Rockcress; SP, Shepherd's purse; TR, Tillage radish; WM, White mustard (n = 3 for control, n = 5 for all other treatments). Values were obtained in QIIME2. Hollow red circles represent individual replicates, solid red dots and black lines represent mean and standard error. ANOVA; $F = 0.50$; $df = 4, 18$; $P = 0.735$; $R^2 = 0.100$. Group means sharing the same letter are not significantly different.

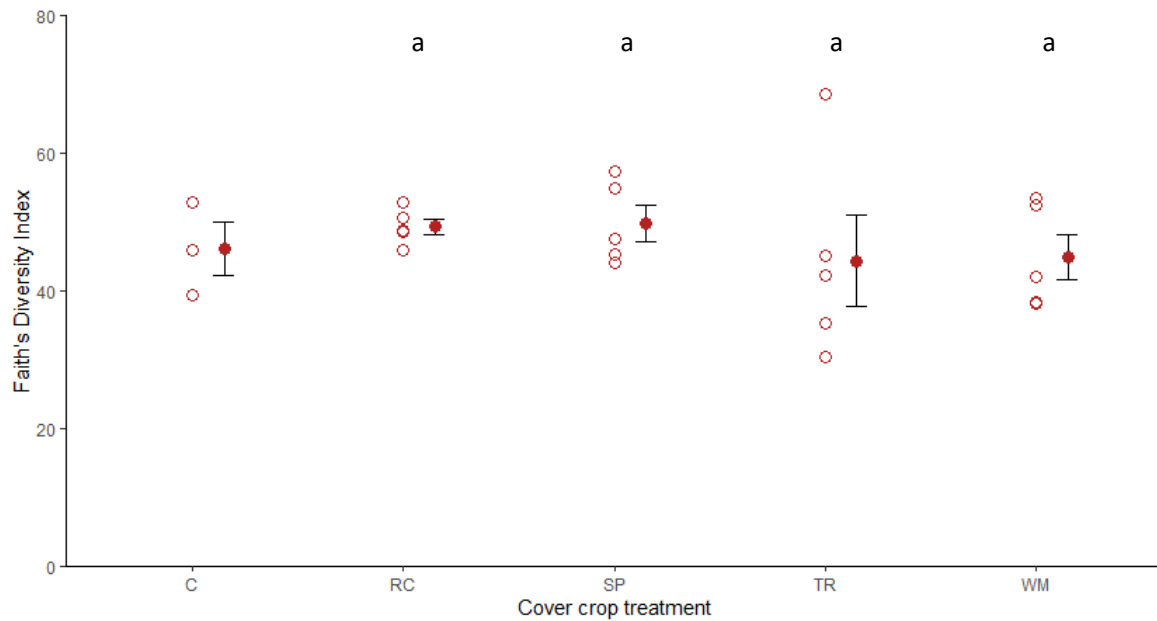


Figure S3. Faith's Phylogenetic Diversity index of fungal communities in soil samples from plots with different cover crop treatments. Treatments: C, undisturbed control; RC, Rockcress; SP, Shepherd's purse; TR, Tillage radish; WM, White mustard (n = 3 for control, n = 5 for all other treatments). Values were obtained in QIIME2. Hollow red circles represent individual replicates, solid red dots and black lines represent mean and standard error. Group means sharing the same letter are not significantly different.