

Table S1. Summary of primers and PCR conditions for DNA amplification

Analyses	Target gene	Primers	Reaction mixture	PCR conditions
DGGE AOA	Ammonia oxidizing archaea amoA	arch-amoAF (5'- CGC CCG CCG CGC GCG GCG GGC GGG GCG GGG GC STA ATG GTC TGG CTT AGA CG-3') and arch-amoAR (5'- GCG GCC ATC CAT CTG TAT GT-3') [1]	4 ng of DNA template, 0.5 µM primers, RedTaq® ReadyMix™ PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO,USA) (in 30 µl)	95°C-3min//35x(95°C-1min/53°C-1min/72°C-1min)//72°C-7min
tRFLP AOA	Ammonia oxidizing archaea amoA	amoA19F (5'-ATGGTCTGGCTWAGACG-3') and amo643R (5'-TCCCACCTTGACCARGCGGCCATCCA-3') [2,3]	4 ng of DNA template, 0.5 µM primers, RedTaq® ReadyMix™ PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO,USA) (in 30 µl)	95°C-5min//35x(92°C-45s/59°C-30s/72°C-60s)//72°C-7min
	Fungal ITS 1	ITS1F 6-FAM (5'-CTTGGTCATTTAGAGGAAGTAA-3') [4] and ITS4R (5'-TCCTCCGCTTATTGATATGC-3') [5]	4 ng of DNA template, 1 µM primers, RedTaq® ReadyMix™ PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO,USA) (in 30 µl)	
Multiplex tRFLP	Bacterial 16S rDNA	63F (5'-AGGCCTAACACATGCAAGTC-3') (Marchesi et al., 1998), and 1087R HEX (5'-CTCGTTGCGGGACTTACCCC-3') [6,7]	4 ng of DNA template, 0,5 µM primers, RedTaq® ReadyMix™ PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO,USA) (in 30 µl)	95°C-5min//30x(95°C-30s/55°C-30s/72°C-60s)//72°C-15min
	Archaeal 16S rDNA	Ar3F (5'-TTCCGGTTGATCCTGCCGGA-3') [8] and AR927R ROX (5'-CCCGCCAATTCCTTTAAGTTTC-3') [6,9]	4 ng of DNA template, 1 µM primers, RedTaq® ReadyMix™ PCR Reaction Mix (Sigma-Aldrich, St. Louis, MO,USA) (in 30 µl)	
NGS	Bacterial and archaeal 16S rDNA	341F (5'-CCTACGGGNGGCWGCAG-3') and 785R (5'-GACTACHVGGGTATCTAATCC-3') [10]	10 ng of DNA template, 10 µM primers, Q5 Hot Start High-Fidelity 2X Master Mix (NEW ENGLAND BioLabs) (in 25 µl)	98°C-30s//25-35x(98°C-5-10s/50-72°C-10-30s/72°C-20-30s) //72°C-2min

Fungal ITS1	ITS1FI2 (5'-GAACCGCGGARGGATCA-3') 5.8S (5'-CGCTGCGTTCTTCATCG-3') [11,12]	10 ng of DNA template, 10 µM primers, Q5 Hot Start High-Fidelity 2X Master Mix (NEW ENGLAND BioLabs) (in 25 µl)	98°C-30s//25-35x(98°C-5- 10s/50-72°C-10-30s/72°C- 20-30s) //72°C-2min
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Table S2. Shannon – Weaver diversity index and number of fragments estimated by t-RFLP peaks profile for total archaea, bacteria and fungi. T2 and T3 denote: stem elongation and senescence stage of subsequent wheat crop, respectively. Different small letters for forecrop treatments within terms and big letters for sampling term within forecrop treatments indicate significant differences ( $p<0.05$ ).

Term	Treatment	Shannon – Weaver Index			Number of t-RFs		
		Archaea	Bacteria	Fungi	Archaea	Bacteria	Fungi
T2	Faba bean	3.29 aA	2.04 abA	2.17 aA	30	11	9
	Wheat	3.34 aA	2.01 bA	2.04 bB	31	12	8
	Reference soil	3.27 aA	2.08 aA	1.93 cB	29	11	7
T3	Faba bean	3.28 aA	1.68 cB	2.05 bB	29	10	8
	Wheat	3.19 aB	1.97 aA	2.17 aA	31	10	9
	Reference soil	3.32 aA	1.88 bB	2.20 aA	32	9	10

Table S3. Archaeal, bacterial and fungal genus in soil. Prediction was performed as *in silico* analysis using TRIFLe package.

Archaea	T-RFLP fragments	Bacteria	T-RFLP fragments	Fungi	T-RFLP fragments
<i>Haloprofundus</i>	60	<i>Aeromonas</i>	113	<i>Erysiphe</i>	113
<i>Haladaptatus</i>	100	<i>Klebsiella</i>	169	<i>Sarcodon</i>	113
<i>Haloarchaeobius</i>	100	<i>Serratia</i>	175	<i>Trochila</i>	113
<i>Halobium</i>	100	<i>Halobacillus</i>	209	<i>Yurkovia</i>	113
<i>Haloferacaceae</i>	100	<i>Saccharosporillum</i>	209	<i>Boletus</i>	113
<i>Halomarina</i>	100	<i>Anabaenopsis</i>	257	<i>Pannaria</i>	113
<i>Halonotius</i>	100			<i>Kluyveromyces</i>	113
<i>Halopiger</i>	100			<i>Venturia</i>	113
<i>Halostagnicola</i>	100			<i>Leptosphaeria</i>	170
<i>Halovarius</i>	100			<i>Cyberlindnera</i>	170
<i>Natrialba</i>	100			<i>Lobulomyces</i>	170
<i>Natribaculum</i>	100			<i>Ceratobasidium</i>	170
<i>Natrinema</i>	100			<i>Aleuria</i>	170
<i>Natronobacterium</i>	100			<i>Saccharomyces</i>	170
<i>Natronolimnobius</i>	100			<i>Corticium</i>	174
<i>Natronorubrum</i>	100			<i>Scopulariopsis</i>	180
<i>Salarchaeum</i>	100			<i>Yamadazyma</i>	180
<i>Salinirubrum</i>	100			<i>Arthrinium</i>	180
<i>Saliphagus</i>	180			<i>Talaromyces</i>	260
<i>Acidianus</i>	200			<i>Calloria</i>	260
<i>Methanoculleus</i>	215			<i>Conocybe</i>	300
<i>Methanosaeta</i>	215			<i>Periconia</i>	340
<i>Thaumarchaeote</i>	215			<i>Nodulisporium</i>	400
<i>Haloferax</i>	219			<i>Mollisia</i>	400
<i>Archaeon</i>	219			<i>Sarocladium</i>	400
<i>Halococcus</i>	219			<i>Gaeumannomyces</i>	400
<i>Methanobrevibacter</i>	219			<i>Aspergillus</i>	439
<i>Methanocalculus</i>	240			<i>Kodamaea</i>	439
<i>Methanomethylovorans</i>	319			<i>Metarhizium</i>	458
<i>Metallosphaera</i>	400			<i>Lachnellula</i>	458
				<i>Peltigera</i>	458
				<i>Candida</i>	478
				<i>Schizophyllum</i>	478
				<i>Hannaella</i>	515
				<i>Umbelopsis</i>	515

Table S5. Biodiversity indices for bacterial (16S rDNA) and fungal (ITS1) population depending on forecrop. T1, T2 and T3 denote: 2 months after residue incorporation into the soil, stem elongation and senescence stage of subsequent wheat crop, respectively.

Term	Treatment	16S rDNA			ITS1		
		Shannon	Simpson	Chao1	Shannon	Simpson	Chao1
T1	Faba bean	4.972	0.986	594	2.575	0.664	399
	Wheat	5.031	0.988	607	2.262	0.568	388
	Reference	5.072	0.989	612	2.287	0.569	438
T2	Faba bean	4.985	0.987	594	2.290	0.591	347
	Wheat	5.013	0.988	603	2.408	0.603	383
	Reference	5.079	0.989	592	2.116	0.529	419
T3	Faba bean	4.966	0.986	587	2.405	0.613	343
	Wheat	4.955	0.986	580	2.355	0.596	324
	Reference	4.990	0.988	574	1.968	0.506	387

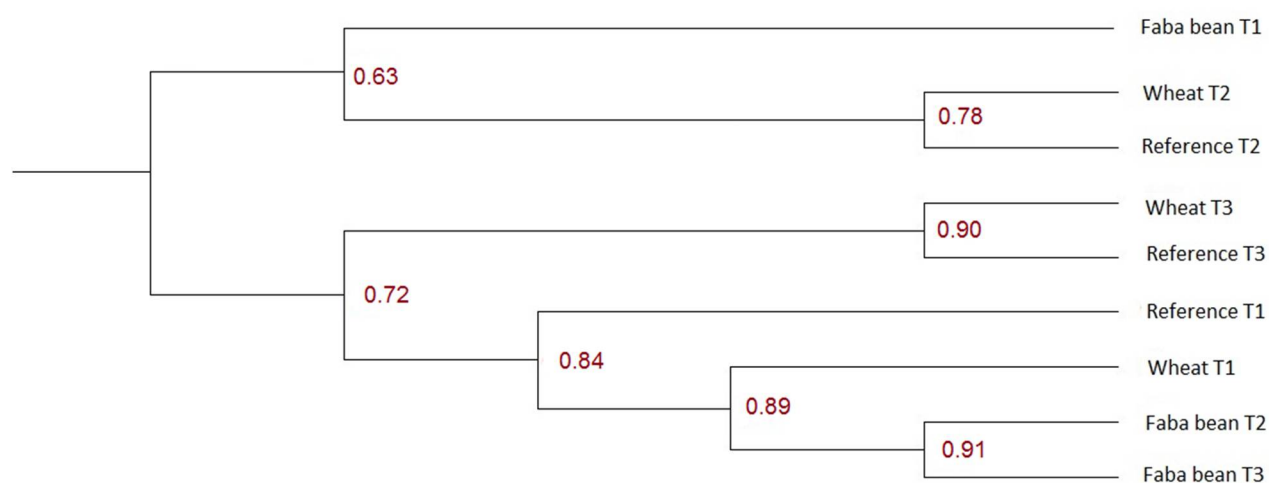
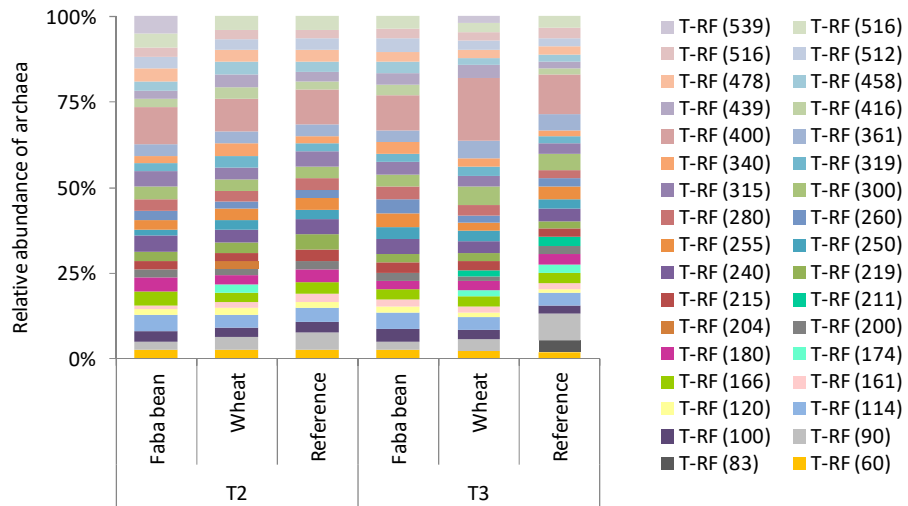
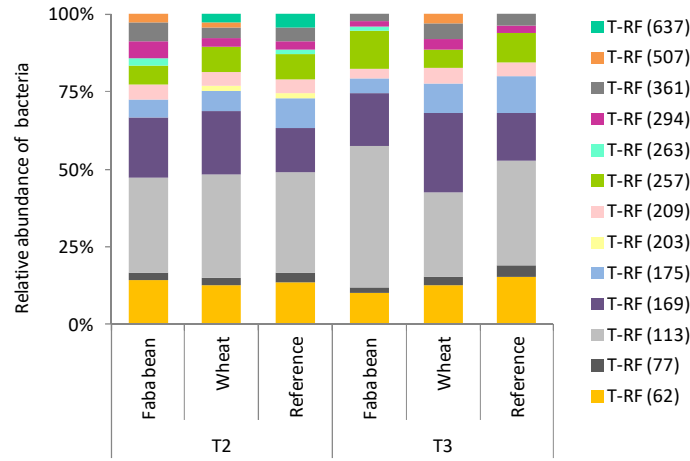


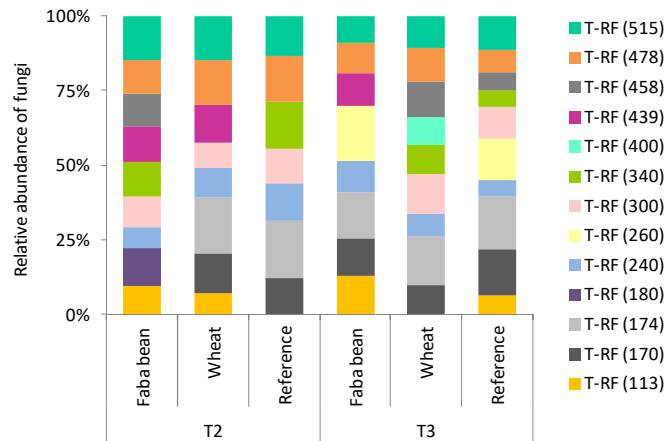
Figure S1. Dendrogram obtained by unweighted pair group mean average (UPGMA; Dice coefficient of similarity) for soil under subsequent crop (wheat) depending on forecrop type (faba bean and wheat) and referenced soil. T1, T2 and T3 denote: 2 months after residue incorporation into the soil, stem elongation and senescence stage of subsequent wheat crop.



(a)



(b)



(c)

Figure S2. Abundance of T-RFLP fragments of total archaea (a), bacteria (b) and fungi (c) in soil. T2 and T3 denote: stem elongation and senescence stage of subsequent wheat crop, respectively.



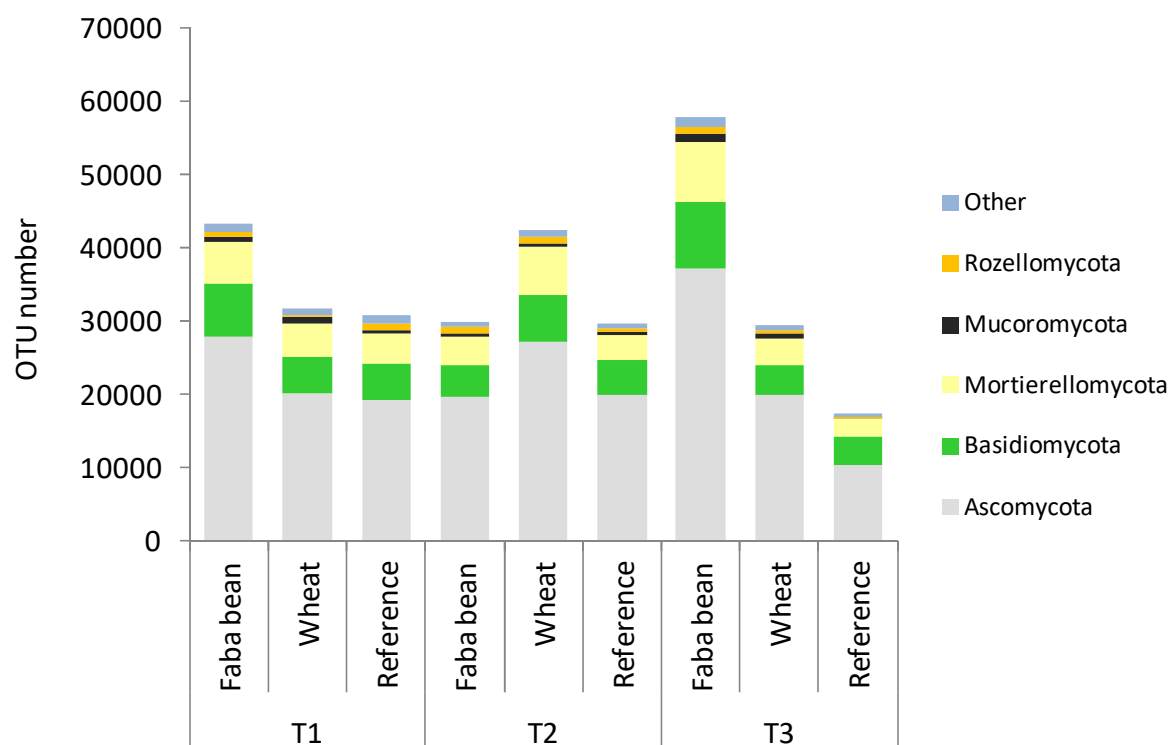


Figure S3. Distribution of the dominant fungal phyla detected in soils after faba bean, wheat cultivation and in reference soil. OTU less than 1% were grouped in other. T1, T2 and T3 denote: 2 months after residue incorporation into the soil, stem elongation and senescence stage of subsequent wheat crop, respectively.

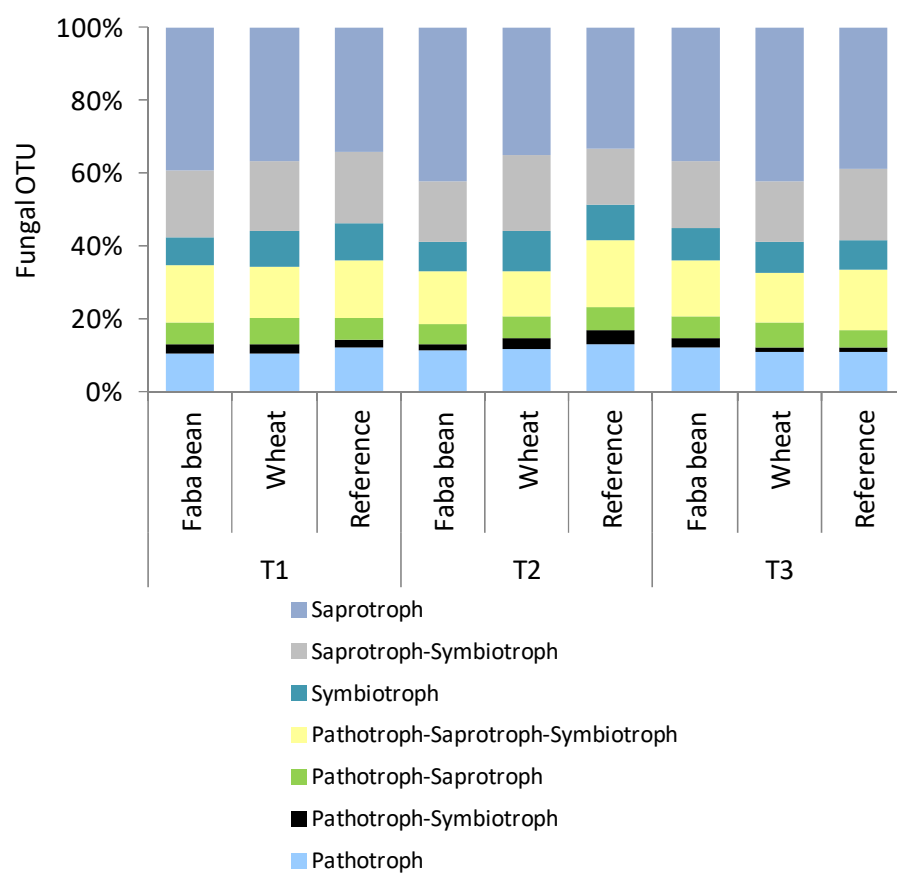


Figure S4. Fungal OTUs of trophic modes as affected by forecrop. T1, T2 and T3 denote: 2 months after residue incorporation into the soil, stem elongation and senescence stage of subsequent wheat crop, respectively.

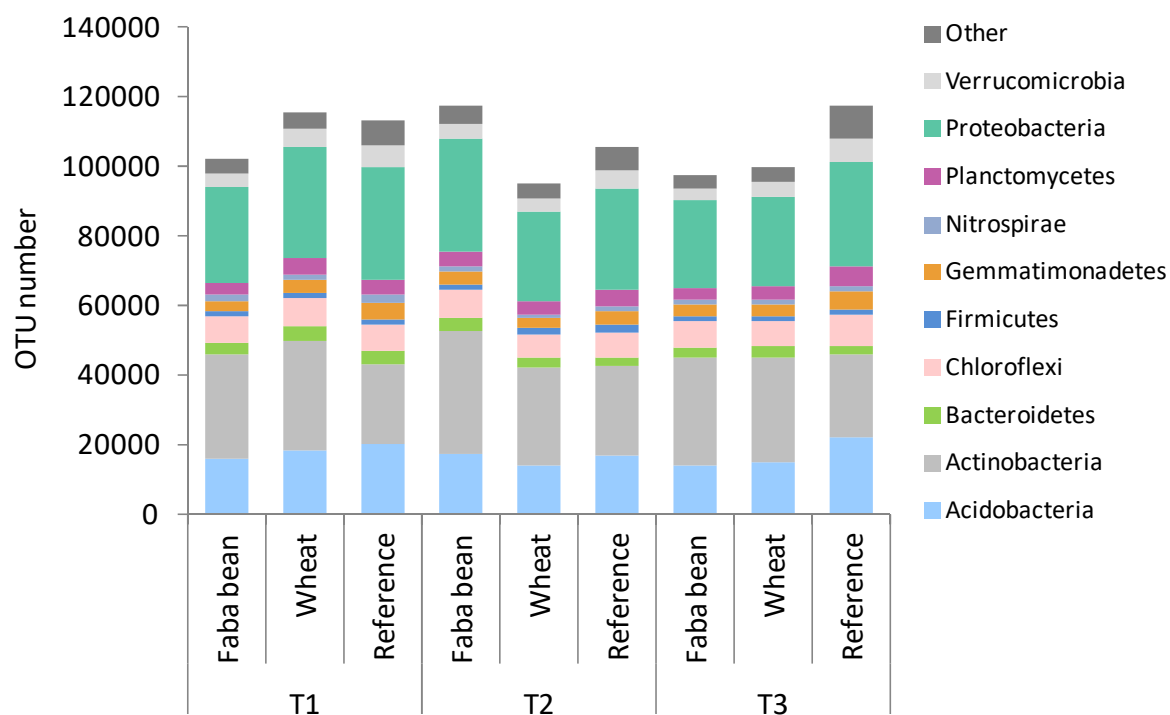


Figure S5. OTU number of the dominant bacterial phyla as affected by forecrop, OTU less than 1% were grouped in other. T1, T2 and T3 denote: 2 months after residue incorporation into the soil, stem elongation and senescence stage of subsequent wheat crop, respectively.