Supplementary methods

Seed collection and sowing

Seeds of most of the plant species were collected from the natural grassland field site and a further 5% were obtained from nearby seed production fields (Planta Naturalis, Markvartice, Czech Republic). Seeds of all plant species were sown simultaneously. For this, seeds were placed on the soil surface and gently pressed into the soil to avoid seeds from blowing away (Münzbergová, 2012).

Soil chemical analyses

All soil was sieved on a 2 mm mesh an thoroughly mixed. Plant available nitrogen (N) (mg kg^{-1} dry soil) was determined by adding 50 mL of 0.5 M K_2SO_4 to 5 g of fresh soil, shaking for 30 min and filtering the soil out. NO_3^-, NH_4^+ and NO_2^- concentrations in the filtrate were determined by Flow Injection Analysis (QuickChem 8000 FIA; Lachat Instruments, Loveland, CO, USA). Plant available P was determined following Olsen et al (1954). In brief, 5 g air dried soil was extracted with 50 mL of 1 M $NaHCO_3$ adjusted to pH 8.5 with addition of activated carbon to eliminate discoloration resulting from humic acid release. The solution was shaken for 2 h and soil was filtered out. Available P in the filtrate was determined by the Olsen photometric method (ATI Unicam UV 400/VIS Spectrophotometer at 630 nm) (Olsen et al., 1954). K was determined in 5 g air dried soil by shaking with 50 mL Mehlich II soil extraction solution (Hach Lange GmbH, Düsseldorf, Germany) for 30 min. Soil was filtered out and and Mg, Ca, and K were measured in the filtrate using atomic absorption spectrometry (ContrAA 700 with C_2H_2-air flame for Mg and K, and C_2H_2-N_2O for Ca; Analytik Jena GmbH, Jena, Germany). Exchangeable pH was measured in a solution of 5 mL in 25 mL 0.1M KCl shaken for 30 min (WTW Multilab 540; Xylem Analytics, Weilheim, Germany). Total N, C and organic C were determined in dried soil ground to <0.1 mm particle size using combustion analyses (FLASH 2000 CHNS/O Analyzer; Thermo Fisher Scientific, Waltham, MA, USA).

Soil bacterial and fungal biomass

Soil bacterial and fungal biomass was determined using PLFA and NLFA analysis following García-Sánchez et al (2019). In short, 1 g of fresh soil taken from the mixed soil cores was freeze-dried in a chloroform-methanol-phosphate buffer (1:2:0.8, v/v/v)(Bligh, E.G. and Dyer, 1959). Lipids were fractioned into polar lipids (PLFAs), glycolipids and neutral lipids (NLFAs), using an extraction cartridge (LiChrolut Si-60; Merck KGaA, Darmstadt, Germany) and subjected to alkaline methanolysis (Šnajdr et al., 2008). Following Sampedro et al (2009), free methyl esters of PFLAs and NLFAs were analysed by gas chromatography-mass spectrometry (450-GC with 240-MS IT Mass Spectrometer; Varian Medical Systems Inc., Palo Alto, CA, USA). Total microbial biomass was estimated by the sum of all PLFA

contents. Bacterial biomass was based on the summed PLFA contents i14:0, i15:0, a15:0, 16:1w5, 16:1w7; 16:1w9, 10Me-16:0, i16:0, i17:0, a17:0, cy17:0, 17:0, 10Me-17:0, 18:1w7, 10Me-18:0 and cy19:0, and actinobacterial biomass based on the summed contents 10Me-16:0, 10Me-17:0 and 10-Me18:0. Gram-positive and gram-negative bacterial were quantified based on i14:0, i15:0, a15:0, i16:0, i17:0, a17:0 and 16:1w7, 16:1w9, 18:1w7, cy17:0, cy19:0, respectively. Fungal biomass was quantified based on PLFA content 18:2w6,9 (Šnajdr et al., 2008) and NLFA 16:1w5 was used as a marker for AM fungi (Olsson et al., 2003).

16S and ITS amplicon sequencing

All frozen soil samples (250 mg each, in duplicates for each sample) were homogenized and lysed in PowerBead Pro Tubes (Qiagen, Germany) on a Vortex adapter. Subsequently, DNA was extracted using the DNeasy PowerSoil Kit (Qiagen, Germany) according to the manufacturer's instructions and eluted in 50 µl of elution buffer. The fungal internal transcribed spacer of the rDNA (ITS2 rDNA) was amplified using primers gITS7ngs (Ihrmark et al., 2012) and ITS4 (White et al., 1990). The bacterial 16S rRNA gene (V4 region) was amplified from the same DNA extracts using primers 515f and 806r (Caporaso et al., 2011). All primers were tagged with sample-specific barcodes of 10-12 bases. PCR mix was performed in the total volume of 15 µl and contained 0.07 U Thermo Scientific™ *Taq* DNA Polymerase, 10x PCR Buffer, 2.5 mM $MgCl_2$, 20 µg BSA (all Thermo Fisher Scientific, Waltham, Massachusetts, USA), 0.3 mM each dNTP, 0.3 µM of each primer and 1 µl of the DNA extract. Thermocycling conditions were 94 °C for 4 min, 25 cycles of 94 °C for 45 s, 52 °C for 60 s and 72 °C for 35 s, followed by 10 min at 72 °C. Each DNA extract was amplified in duplicate. PCR products were visualized on a 1% agarose gel. The pooled duplicates were purified through columns with the QIAquick PCR Purification Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol and eluted into 20 µl of ddH_2O. DNA concentrations of the amplicon pools were quantified using a Qubit 2.0 Fluorometer (Thermo Fisher Scientific) with High Sensitivity Assay Kit. The purified amplicons were pooled in equimolar ratios. Both negative PCR controls (with ddH_2O instead of a template) were processed in the same way as the experimental samples and included into the sequencing library, together with sixty fungal and sixty bacterial amplicons. The library was sequenced on an Illumina MiSeq instrument (2 × 250 bp) (SEQme, Dobříš, Czech Republic).

16S and ITS bioinformatics

In total, Illumina paired end sequencing of 120 samples and 2 negative controls yielded 4 261 236 raw sequences. The data were processed using the pipeline SEED2 ver. 2.1.1b (Větrovský et al., 2018). First, low-quality sequences were discarded (mean quality score < 30). The reads were demultiplexed

(no mismatch allowed in the tag sequences) and tag switches (i.e. reads with non-matching tags) were discarded.

The ITS2 region was extracted from the fungal amplicons using ITSx ver. 1.0.11 (Bengtsson-Palme et al., 2013) and sequences shorter than 20 bp were excluded. This yielded 982 036 sequences which were clustered to OTUs using UPARSE implementation in USEARCH ver. 8.1.1861 (Edgar, 2013) with 97% similarity threshold (45 480 chimeric sequences were excluded during this step). The most abundant sequences were selected for each of the resulting 10 685 OTUs. These sequences were checked for their identity via BLASTn algorithm against the UNITE database ver. 8.3 (Nilsson et al., 2019) and non-fungal, no-hit sequences as well as global singletons, doubletons and tripletons were excluded from further analyses leaving 2638 OTUs represented by 840 206 reads. Two OTUs represented by six reads detected in the negative control were subtracted from the corresponding OTUs across the dataset. The ecological guilds of the fungal OTUs were parsed using the database FungalTraits (Põlme et al., 2020) at genus and sequence levels.

Primers were cut from prokaryote reads (1 319 594 reads after demultiplexing) and sequences shorter than 20 bp were excluded. The reads were clustered to OTUs using UPARSE implementation in USEARCH ver. 8.1.1861 (Edgar, 2013) with 97% similarity threshold (442 826 chimeric sequences were excluded during this step). OTUs with $n < 5$ were discarded. The most abundant sequences were selected for each of the resulting 6532 OTUs. These sequences were checked for their identity via BLASTn algorithm against the RDP trainset 16 (Cole et al., 2014). 179 reads detected in the negative control were subtracted from the corresponding OTUs across the dataset. OTUs with non-target and no BLASTn hits were excluded from further analyses leaving 6369 OTUs represented by 841 512 reads.

Structural equation models

To keep the number of potential pathways relative low and avoid spurious effects occurring due to correlating exogeneous variables, we first calculated three base models for each soil type following (Radujković et al., 2021). These three base models captured effects of the plant community onto soil chemical changes after the 13th growing season of (a) the plant community in the year of sampling (aboveground and belowground productivity, plant diversity and plant compositional NMDS axes 1-3), (b) overall effects of the plant community from the past (initial invasion effect on plant diversity, aboveground productivity and plant diversity trajectories in time), and (c) plant compositional effects from the past (invasion effect size on plant compositional NMDS axis 2, plant compositional NMDS axes 1-3 trajectories in time). All base models included the same soil chemical parameters: total soil N, C, organic C and pH, and plant available P, NO_3^-, NH_4^+, NO_2^-.

Since a few of the exogeneous plant community parameters significantly correlated in various cases between the three base models, we replaced each plant community parameter in each model with significantly correlating plant community parameters from the other two base models (Fig S11). In case this replacement improved the AIC of the model, the plant community parameter belonging to one of the other base models was considered to represent the effects best. Model selection was then re-run without inclusion of the correlating parameter as these effects were better represented in one of the other base models. The three base models were then merged for each soil origin and another round of stepwise selection was run to end up with the most parsimonious model.

Secondly, in each SEM, we ran through each bacterial, fungal and microbial biomass parameter (biomass pools based on PLFA/NLFA analyses and summed relative reads per 16S or ITS cluster from the calculated co-occurrence networks per soil type) as the final parameter to be estimated. Per run, one microbial parameter was considered, which could be affected either directly by the plant community parameters or indirectly via the soil chemical variables. Each run, a backward stepwise elimination procedure to consecutively remove non-significant pathways was followed in the same way as performed for the base models (in 't Zandt et al., 2020). All microbial variables not following a normal distribution were ln- or sqrt-transformed.

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Supplementary figures

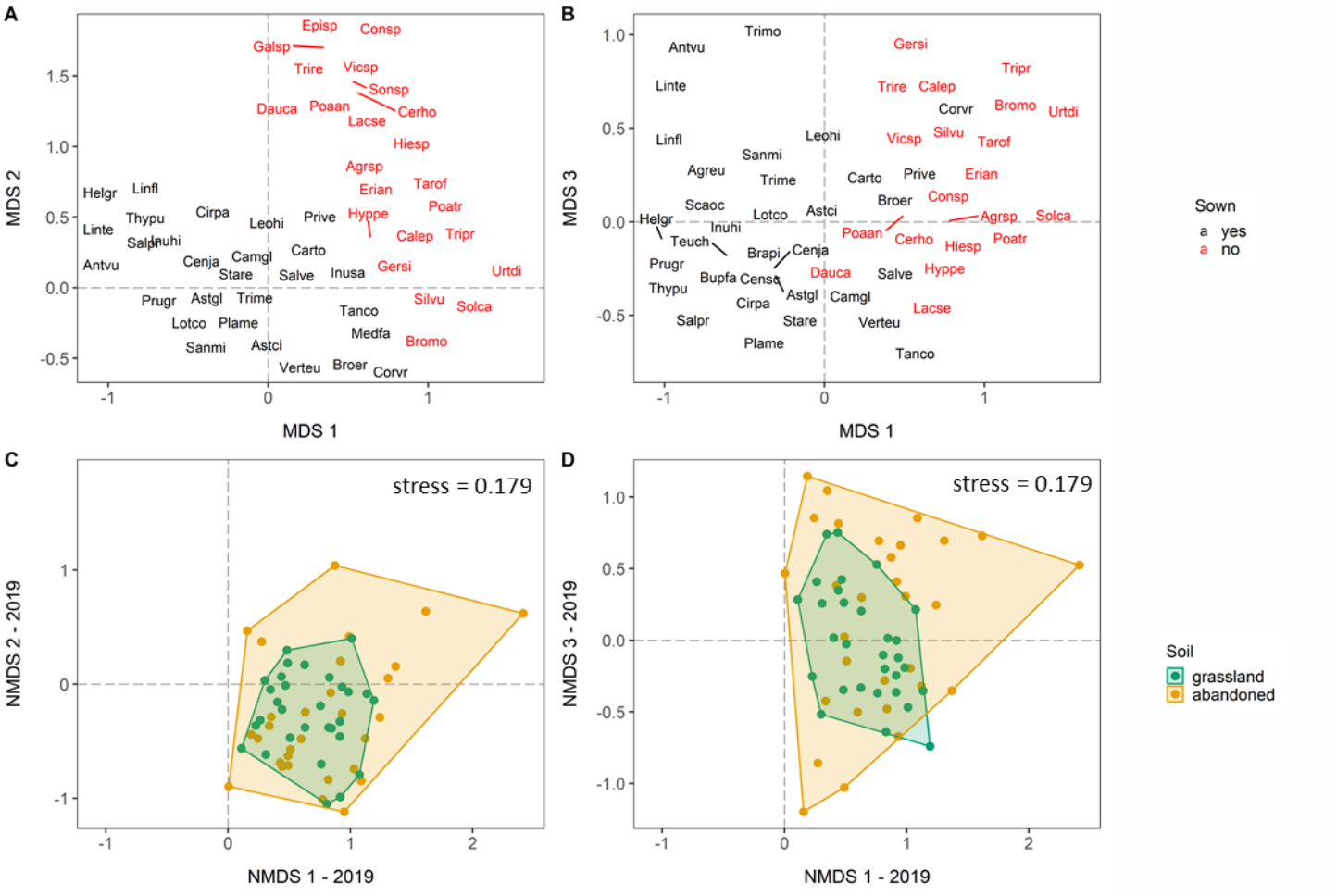

Figure S1 Plant species position on the non-metric multidimensional scaling (NMDS) axes (A) 1 and 2, and (B) 1 and 3 (n = 59 plant species). Plant community positions in 2019 on the NMDS axes (C) 1 and 2, and (D) 1 and 3 on natural grassland (green) and abandoned arable soil (yellow) (n = 30 communities on each soil). For NMDS patterns over time, see Fig 1. For plant species abbreviations, see Table S9.

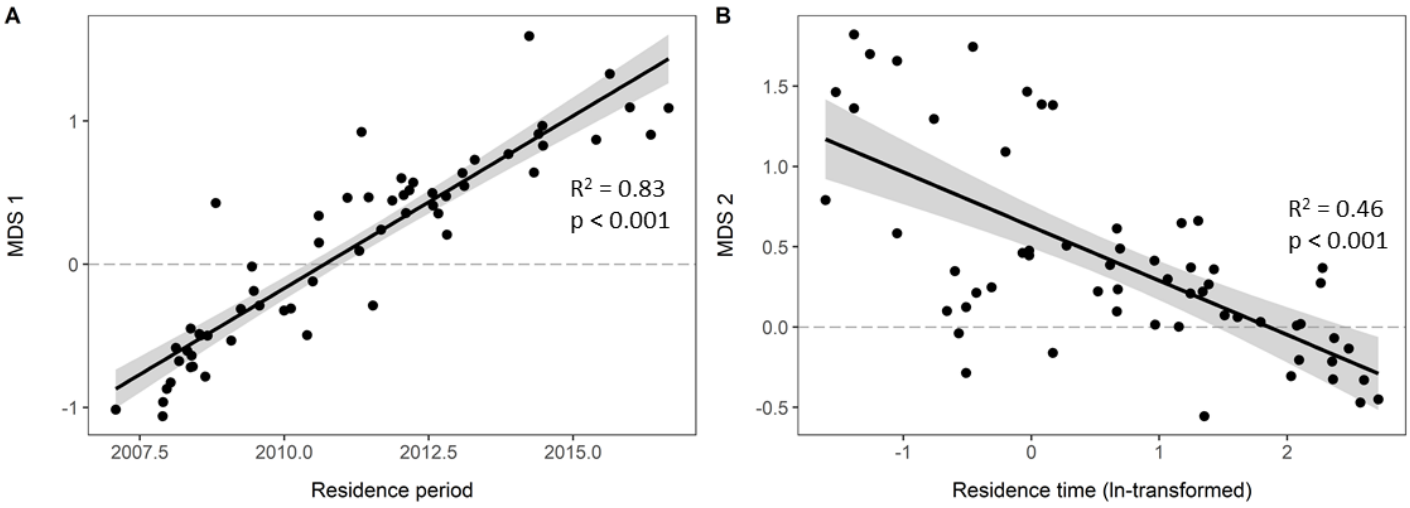

Figure S2 Scores of plant species resulting from non-metric multidimension scaling (NMDS). (A) MDS score 1 correlated to the average residence period (in calendar years) of the plant species (present in early or later years of the experiment; 2007 to 2019) and (B) MDS score 2 correlated to the average residence time (in years, ln-transformed) of the plant species (present for 1 to 13 years) (*n* = 59 species, rare species excluded).

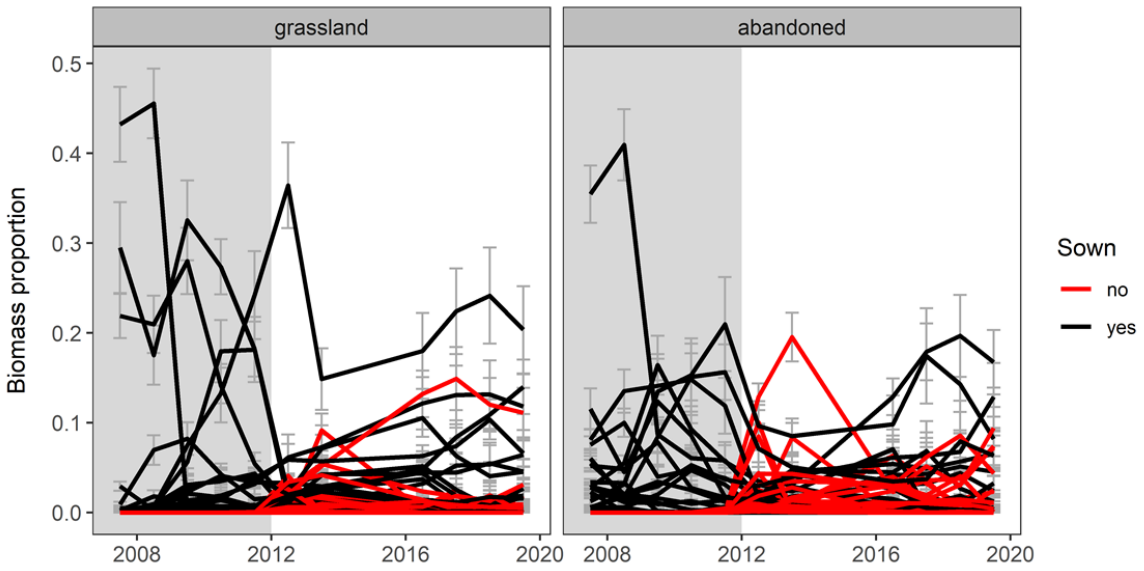

Figure S3 Biomass proportion of sown plant species (black) and invaded plant species (red) over time in plant communities established on natural grassland and abandoned arable soil. Grey shading indicates the period where no invasion was allowed to occur. Averages ± SE; *n* = 59 plant species per soil, rare species excluded.

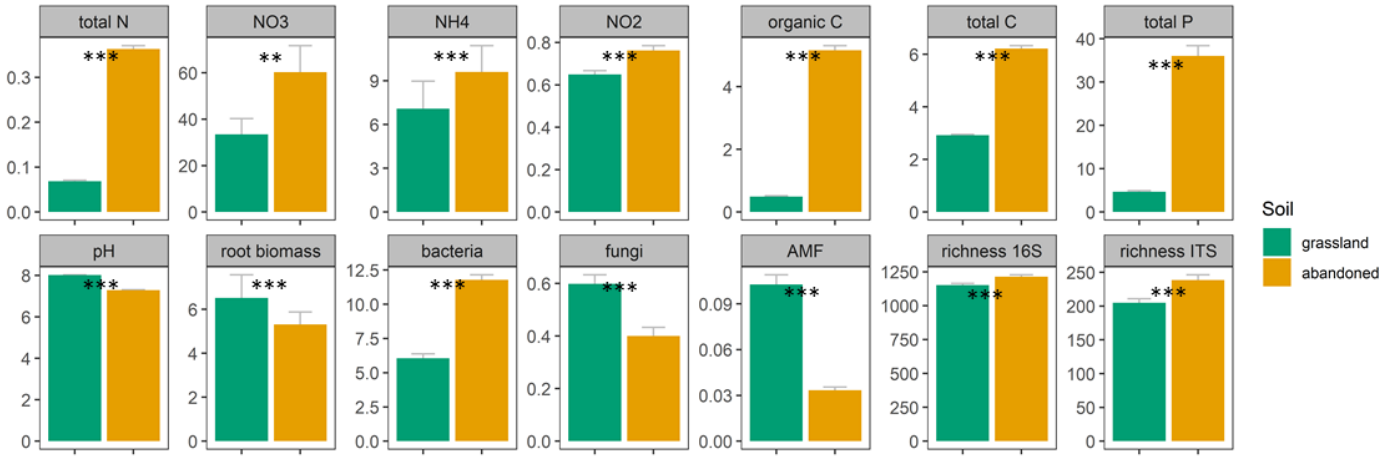

Figure S4 Soil chemical and microbial properties after the 13th growing season in communities grown on natural grassland (green) and abandoned arable (yellow). Total N, C and organic C are given in percentage; NO3, NH4, NO2, K and P, as well as bacterial, fungal and AMF biomass are given in mg · kg^{-1} dry soil. Root biomass is given in g. 16S and ITS richness represent the number of unique OTUs. Averages ± SE (*n* = 30), asterisks indicate significant differences between natural grassland and abandoned arable soil (tested in a linear mixed effects model with seed density as random effect). Significance codes: *** p < 0.001; ** p <0.01.

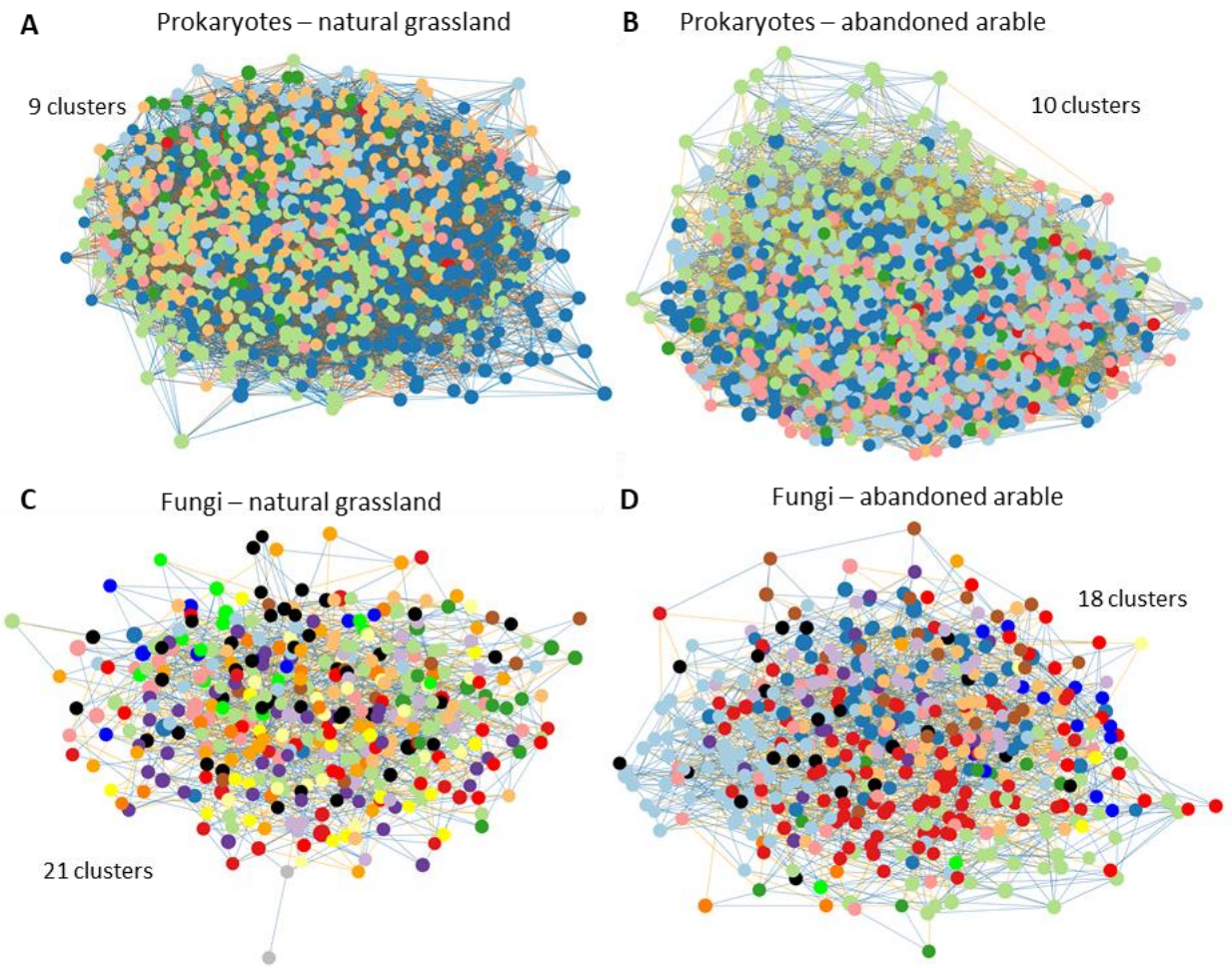

Figure S5 Soil microbial co-occurrence networks of prokaryotes in (A) natural grassland soil and (B) in abandoned arable soil, and of fungi in (C) natural grassland soil and (D) abandoned arable soil. Each dot represents one OTU. Different colours indicate that OTUs belonged to different co-occurrence clusters within the network (*n* =30 communities).

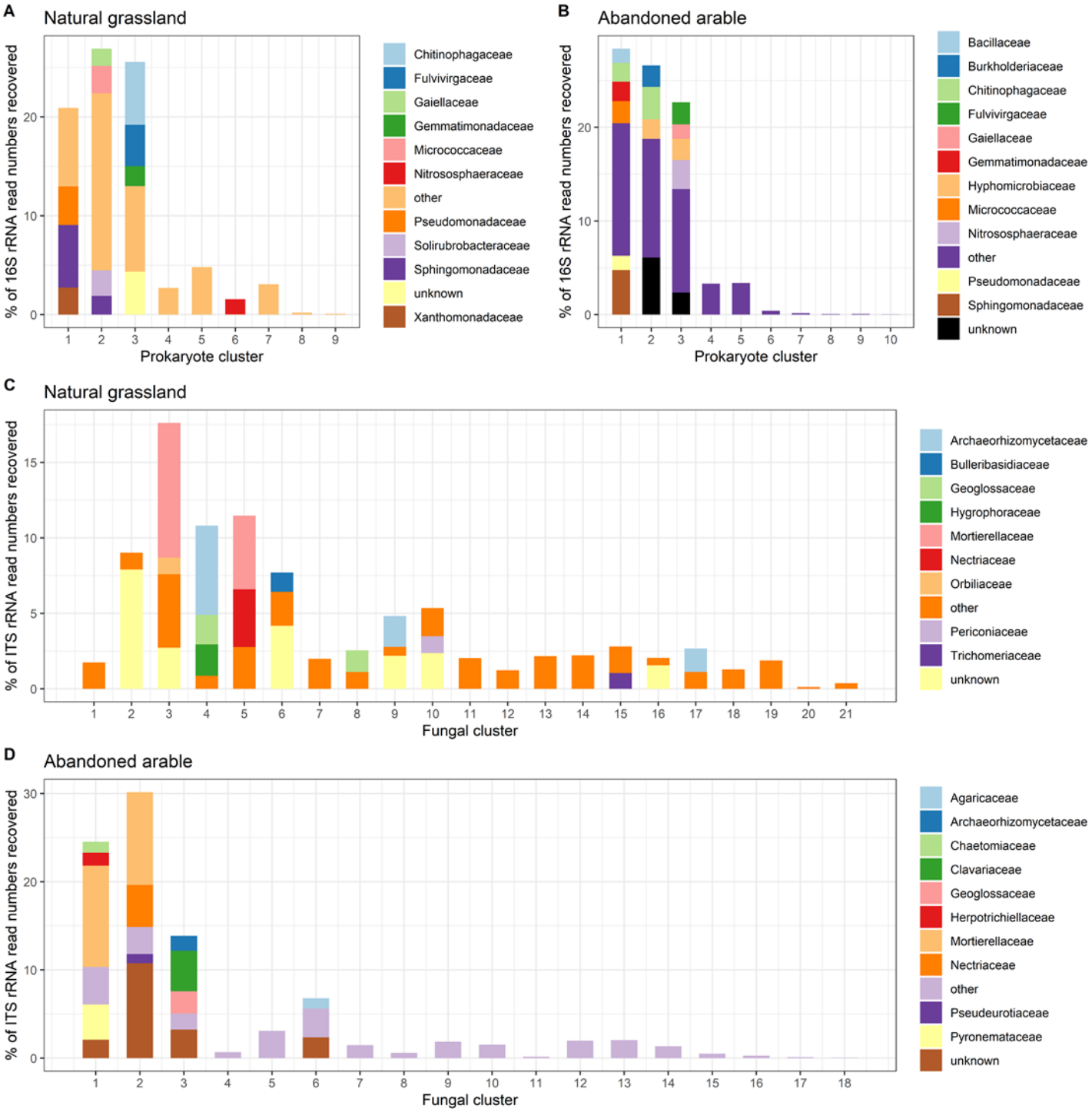

Figure S6 Average percentage of 16S and ITS rRNA read numbers recovered per family level over similarly responding prokaryote in (A) natural grassland and (B) abandoned arable soil, and fungal clusters in (C) natural grassland and (D) abandoned arable soil obtained from co-occurrence networks. For 16S, families < 1.5% relative abundances are grouped in 'other', for ITS, families <1% relative abundances are grouped in 'other'.

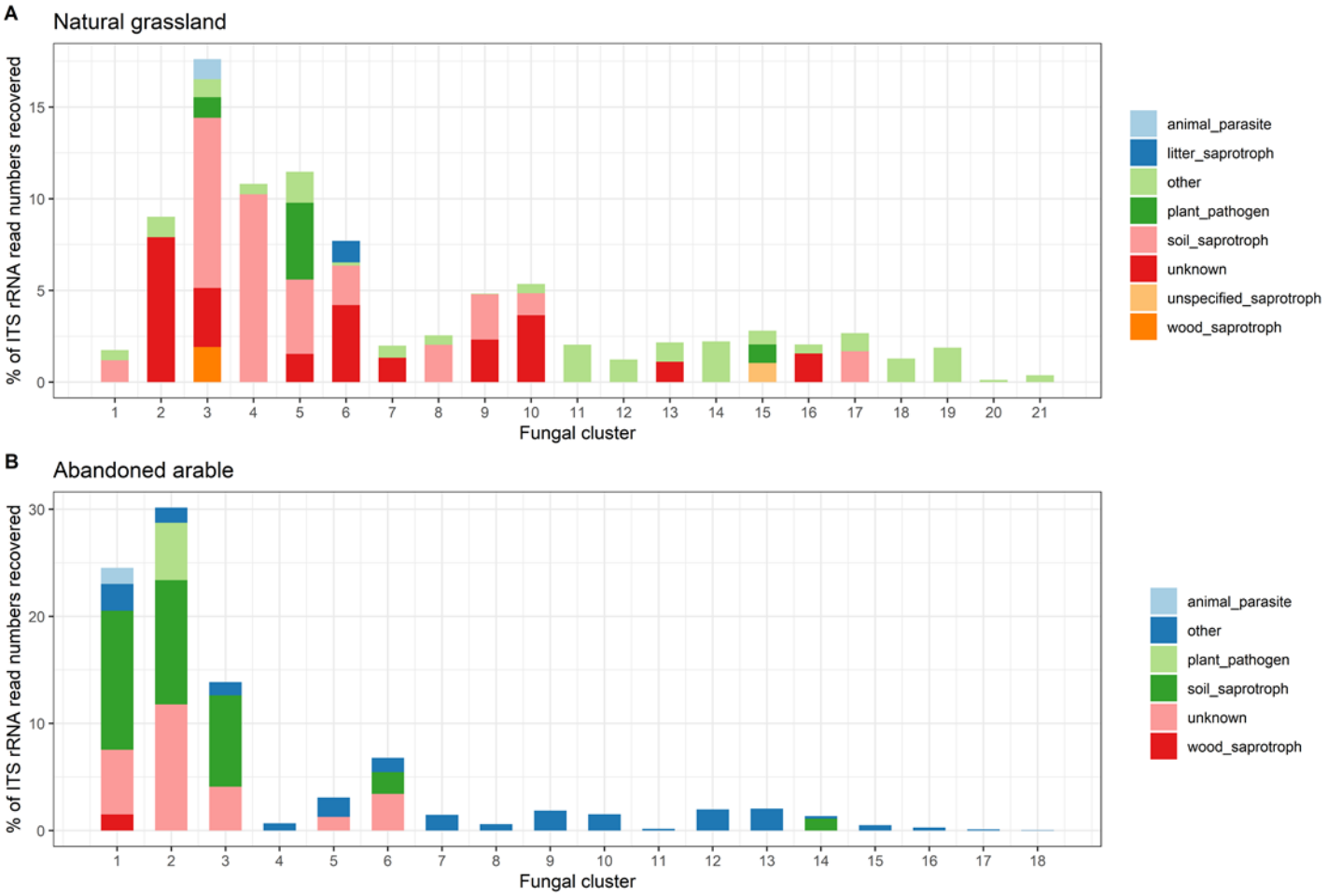

Figure S7 Average percentage of ITS rRNA read numbers recovered per putative fungal trait over similarly responding fungal clusters obtained from co-occurrence networks in (A) natural grassland and (B) abandoned arable soil. Putative fungal traits < 1% relative abundances are grouped in 'other'.

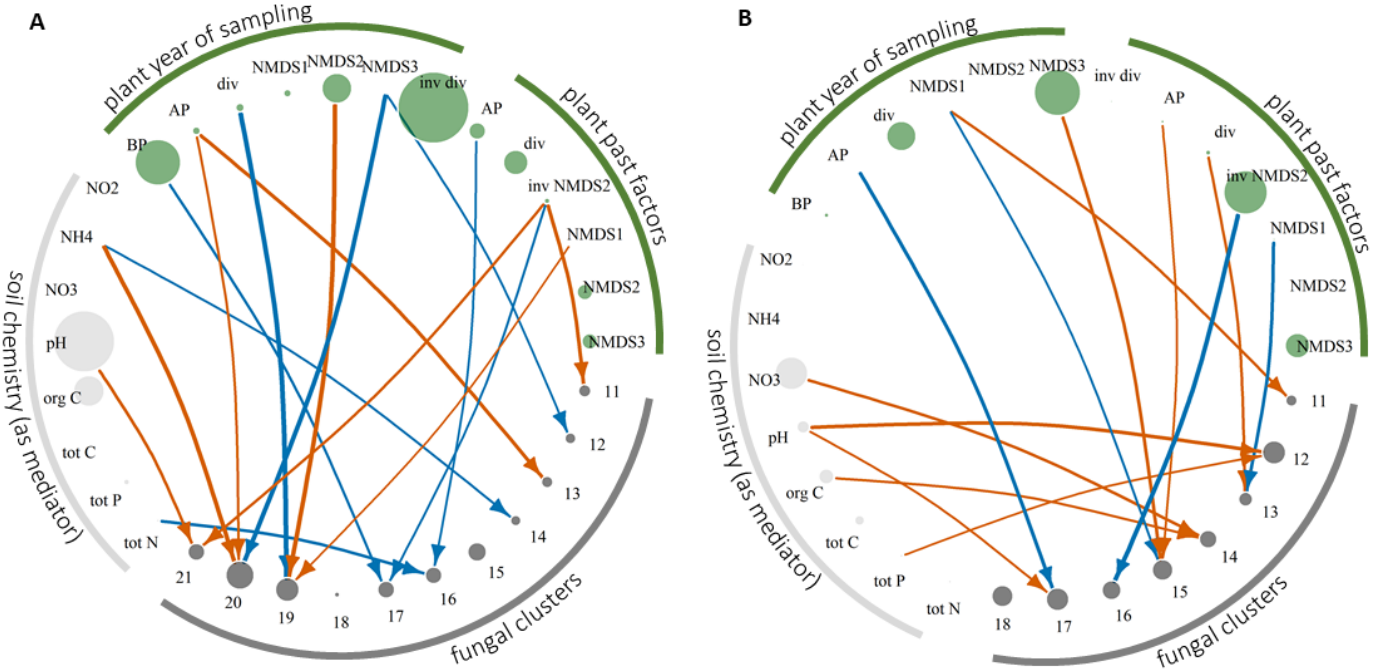

Figure S8 continued from Fig 5 representing fungal clusters 11 and beyond. Significant pathways obtained from structural equation models testing effects of plant community parameters in the year of sampling (2019) and the past (2007-2019) on soil fungal networks in (A) natural grassland soil and (B) abandoned arable soil. Direct effects were separated from *in*direct effects that occurred via changes in soil chemical properties. Plant vertices are indicated in green, soil chemical vertices in light grey and microbial vertices in dark grey. Plant vertice sizes *in*dicate the summed direct and indirect pathway effect sizes onto microbial parameters. Soil chemical vertices indicate only the summed *in*direct pathway effect sizes. Microbial vertices indicate the summed direct and *in*direct pathway effect sizes that these microbial parameters were affected by. All summed pathway effect sizes were scaled to the size of the microbial parameters involved. Negative pathways are represented in vermillion, positive in blue. Arrows indicate the direction of the pathways and the width of the arrows its effect size. Soil chemical pathways are only included when the plant community affected the soil chemical variable. For plant-soil chemical pathways, see Fig S9.
Plant year of sampling factors: BP – belowground productivity, AP – aboveground productivity, div – plant diversity, NMDS1 – plant composition related to species residence period, NMDS2 – plant composition related to species residence time, NMDS3 – plant composition related to species differential dominance. Plant past factors: inv div – initial invasion effect size on plant diversity (increase in diversity between 2011 and 2013), AP – aboveground productivity trajectory, div – plant diversity trajectory, inv NMDS2 – initial invasion effect size on plant composition NMDS2 (increase in new individuals between 2011 and 2012), NMDS1-3 – plant compositional trajectories (see Fig 4A, S1-S2 for more details). Only significant pathways are included ($p < 0.05$; $n = 30$).

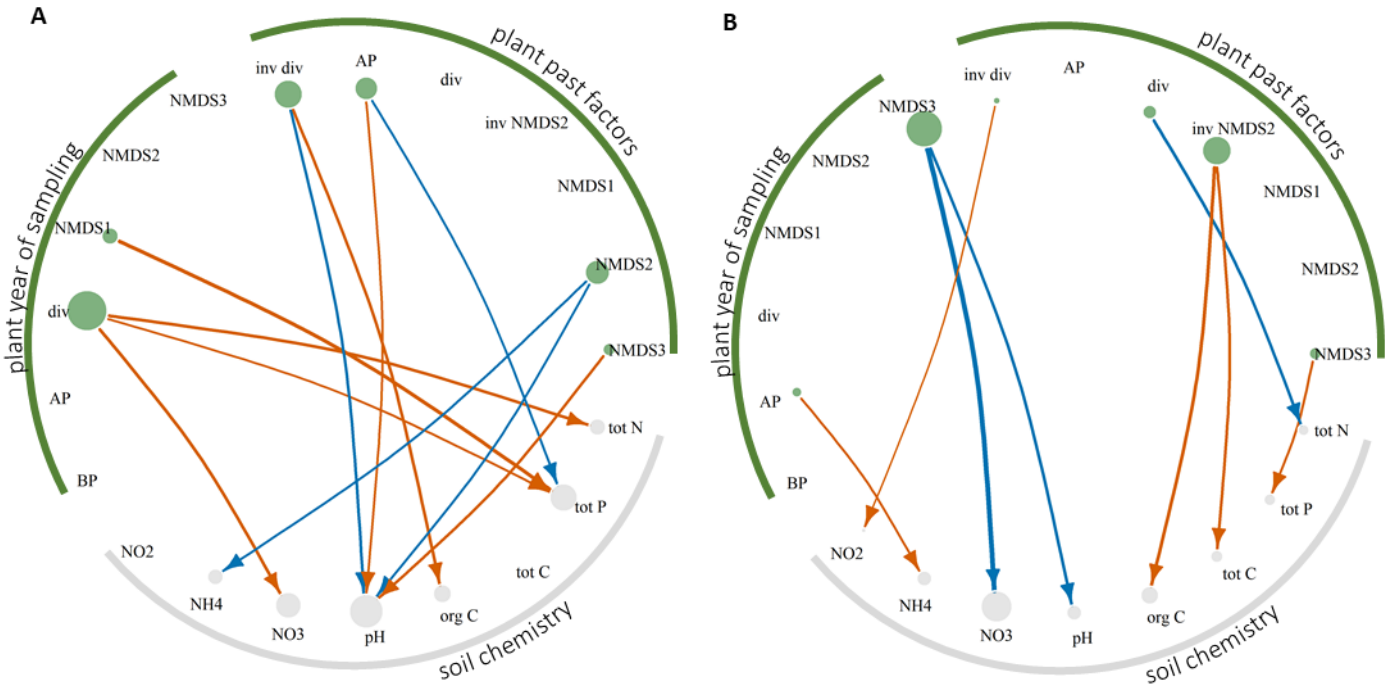

Figure S9 Significant pathways obtained from structural equation models showing effects of plant community parameters in the year of sampling (2019) and the past (2007-2019) on soil chemical properties in (A) natural grassland soil and (B) abandoned arable soil. Plant vertices are indicated in green and soil chemical vertices in grey. Plant vertice sizes indicate the summed pathway effect sizes of the parameter onto all soil chemical properties. Soil chemical vertice sizes indicate the summed pathway effect sizes of all plant community parameters the chemical parameter was affected by. Negative pathways are represented in vermillion, positive in blue. Arrows indicate the direction of the pathways and the width of the arrows its effect size.
Plant year of sampling factors: BP – belowground productivity, AP – aboveground productivity, div – plant diversity, NMDS1 – plant composition related to species residence period, NMDS2 – plant composition related to species residence time, NMDS3 – plant composition related to species differential dominance. Plant past factors: inv div – initial invasion effect size on plant diversity (increase in diversity between 2011 and 2013), AP – aboveground productivity trajectory, div – plant diversity trajectory, inv NMDS2 – initial invasion effect size on plant composition NMDS2 (increase in new individuals between 2011 and 2012), NMDS1-3 – plant compositional trajectories (see Fig 4A, S1-S2 for more details). Only significant pathways are included ($p < 0.05$; $n = 30$).

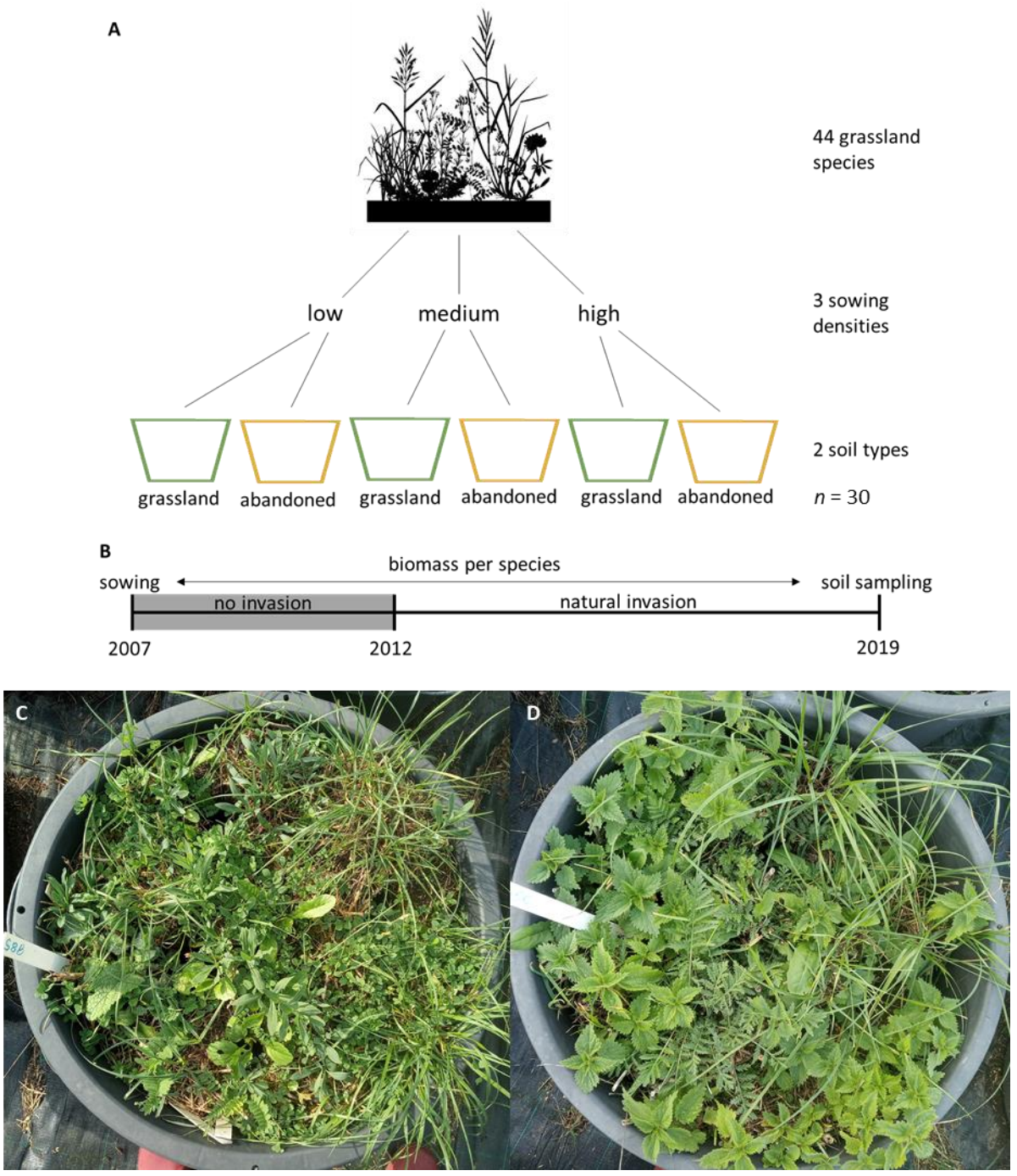

Figure S10 (A) Experimental design, (B) timeline of the experiment and two typical images of a (C) natural grassland and (D) abandoned arable plant communities (summer 2020). In A, sowing densities represent 25% (low), 100% (medium) and 400% (high) of the natural seed densities as determined in a natural grassland community were the 44 plant species naturally coexist. Grassland soil was taken from a natural grassland and abandoned soil from an arable field that was abandoned in the 1950s (see also Münzbergová, 2012). In B, plant communities were sown in 2007 followed by a 5 year period in which invasion of other plant species was avoided. From 2012 to 2019, natural invasion occurred. In 2019 after the growing season, soil cores for chemical and microbial analysis were taken. For sown and invaded plant species, see Table S9.

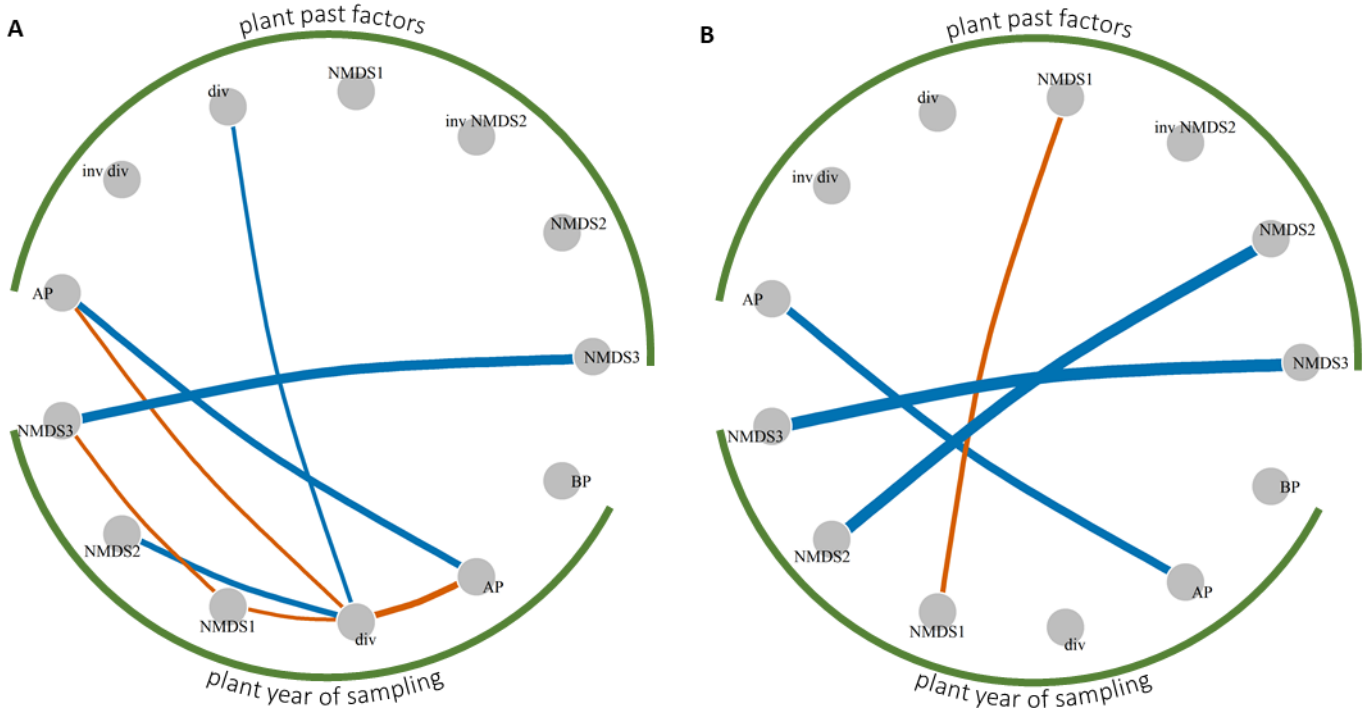

Figure S11 Correlations between aboveground plant community parameters in (A) natural grassland and (B) abandoned arable soil. Blue lines indicate significant ($p < 0.05$) positive correlations, vermillion significant negative correlations. The width of the line indicate the correlation strength ($n = 30$). Plant year of sampling factors: BP – belowground productivity, AP – aboveground productivity, div – plant diversity, NMDS1 – plant composition related to species residence period, NMDS2 – plant composition related to species residence time, NMDS3 – plant composition related to species differential dominance. Plant past factors: inv div – initial invasion effect size on plant diversity (increase in diversity between 2011 and 2013), AP – aboveground productivity trajectory, div – plant diversity trajectory, inv NMDS2 – initial invasion effect size on plant composition NMDS2 (increase in new individuals between 2011 and 2012), NMDS1-3 – plant compositional trajectories.

Supplementary tables

Table S1 Microbial co-occurrence network parameters typically associated with network stability for networks based on 16S and ITS amplicon sequencing

	Prokaryote network		**Fungal network**	
	Natural grassland	Abandoned arable	Natural grassland	Abandoned arable
Number of nodes	1008	1024	403	455
Number of edges	10209	10079	1470	1874
Average number of edges per node	20.3	19.7	7.3	8.2
Negative edges	46%	46%	36%	33%
Edge betweenness	132	139	467	510
Average edge weight	0.07	0.07	0.08	0.08
Number of clusters	9	10	21	18
Clustering coefficient	0.36	0.35	0.54	0.56

Table S2 Dominant phyla, orders and families in soil prokaryote clusters of plant communities grown on natural grassland soil

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Putative metabolic traits and functions
1 (large)	*Proteobacteria (77.6%)*	*Sphingomondales (30.4%)* *Pseudomonadales (18.6%)* *Xanthomonadales (13.1%)*	*Sphingomonadaceae (30.3%)* *Pseudomonadaceae (18.6%)* *Xanthomonadaceae (13.1%)*	Belowground productivity (+)	Generalist, fast growing metabolically diverse chemoheterotrophs
2 (large)	*Actinobacteria (57.7%)* *Proteobacteria (32.6%)*	*Micrococcales (16.2%)* *Solibrubacterales (12.2%)* *Rhizobiales (11.1%)*	*Micrococcaceae (10.0%)* *Solirubrobacteraceae (9.6%)*	Plant diversity trajectory (-), NMDS2 trajectory (-)	Specialist chemoheterotrophs. Partially likely involved in N-fixation. Many unknown.
3 (large)	*Bacteroidetes (44.6%)* *Proteobacteria (26.9%)*	*Chitinophagales (24.9%)* *Cytophagales (17.3%)*	*Chitinophagaceae (24.9%)* *Fulvivirgaceae (16.3%)*	Total N (+), plant diversity trajectory (+), NMDS2 trajectory (+)	Specialist, fast growing chemoheterotrophs
4 (small)	*Proteobacteria (80.6%)*	*Burkholderiales (38.0%)* *Nitrosomonadales (13.3%)*	*Burkholderiaceae (33.9%)* *Nitrosomonadaceae (13.3%)*	Belowground productivity (-)	Generalist, slow growing chemoheterotrophs. Partially likely involved in nitrification
5 (small)	*Proteobacteria (66.1%)*	*Rhizobiales (27.6%)* *Nevskiales (21.3%)*	*Steroidobacteraceae (21.3%)* *Hyphomicrobiaceae (14.7%)*	Organic C (+), belowground productivity (-), NMDS1 (+), invasion effect size diversity (+)	Specialist, slow growing chemolithoautotrophs and chemoheterotrophs
6 (small)	*Thaumarchaeota (98.7%)*	*Nitrososphaerales (98.7%)*	*Nitrososphaeraceae (98.7%)*	Organic C (+), NMDS1 (+), invasion effect size diversity (+)	Specialists. Ammonia oxidising archaea: chemolithoautotrophs, but likely also -heterotroph
7 (small)	*Proteobacteria (57.3%)*	*All below 9%*	*All below 9%*	Plant diversity (-)	Unclear generalists
8 (small)	*Actinobacteria (100%)*	*Acidimicrobiales (60.5%)* *Streptomycetales (39.5%)*	*Acidimicrobiaceae (60.5%)* *Streptomycetaceae (39.5%)*	NMDS2 (+)	Specialists heterothrophs and root endophytes (*Streptomyces*)
9 (small)	*Actinobacteria (52.3%)* *Proteobacteria (47.7%)*	*Thermoleophilales (52.3%)* *Rhodobacterales (47.7%)*	*Thermoleophilaceae (52.3%)* *Rhodobacteraceae (47.7%)*	Invasion effect size diversity (+)	Generalist chemolithoautothrophs

Percentages indicate the relative read abundance of the phylogenetic group within the cluster. Clusters are divided in large and small clusters based on their average relative read abundance (Fig 3). Putative generalist functions are based on relations to overall plant community parameters (productivity, diversity) or absence of a relation to the plant community. Putative specialist functions are based on relations with plant community composition, indicating that plant identity played a role. Putative fast growing characteristics were based on a high relative abundance of the cluster with high soil N, NO3 or NH4, as well as the likely presence of readily available C sources (high belowground productivity). Putative slow growing characteristics were based on a low relative abundance of the cluster in these same soil conditions.

Table S3 Dominant phyla, orders and families in soil prokaryote clusters of plant communities grown on abandoned arable soil

Cluster	Dominant phyla (>20%)	Dominant orders (>10%)	Dominant families (>9%)	Relates to	Putative metabolic traits and function
1 (large)	*Proteobacteria (50.4%)* *Actinobacteria (20.1%)*	*Spingomonadales (18.2%)*	*Sphingomonadaceae (16.8%)*	NMDS1 trajectory (-), invasion effect size composition (-)	Specialist metabolically diverse chemoheterotrophs. Many unknown
2 (large)	*Proteobacteria (54.2%)*	*Burkholderiales (14.0%)* *Chitinophagales (13.1%)*	*Chitinophagaceae (13.1%)*	pH (-), NO3 (-), plant diversity (+)	Generalist, slow growing chemoheterotrophs. Many unknown
3 (large)	*Proteobacteria (28.5%)* *Actinobacteria (21.4%)*	*Nitrososphaerales (13.6%)* *Rhizobiales (12.8%)* *Cytophagales (10.6%)*	*Nitrososphaeraceae (13.6%)* *Fulvivirgaceae (10.4%)* *Hyphomicrobiaceae (9.9%)*	Total N (-), pH (+), invasion effect size NMDS2 (+)	Specialist, slow growing. Ammonia oxidising archaea, chemolithoautotroph and likely also -heterotroph. Likely N-fixing taxa
4 (small)	*Actinobacteria (44.2%)* *Acidobacteria (25.7%)* *Proteobacteria (22.2%)*	*Solirubrobacterales (15.8%)* *Xanthomonadales (13.2%)* *Gaiellales (12.5%)*	*Solirubrobacteraceae (15.8%)* *Xanthomonadaceae (13.2%)* *Gaiellaceae (12.5%)*	NMDS2 (-)	Specialist chemoheterotrophs
5 (small)	*Proteobacteria (52.0%)* *Actinobacteria (22.2%)*	*Solirubrobacterales (12.4%)* *Sphingomonadales (12.4%)* *Rhizobiales (11.1%)*	*Solirubrobacteraceae (12.4%)* *Sphingomonadaceae (12.0%)* *Chitinophagaceae (9.0%)*	Total N (+), organic C (-), NO2 (+), aboveground productivity (+)	Generalist, fast growing chemoheterotrophs
6 (small)	*Proteobacteria (60.5%)*	*Gemmatimonadales (17.3%)* *Myxococcales (16.6%)* *Burkholderiales (14.0%)* *Micropepsales (12.8%)* *Desulfuromonadales (11.9%)* *Chthoniobacterales (11.0%)*	*Gemmatimonadaceae (17.3%)* *Comamonadaceae (14.0%)* *Micropepsaceae (12.8%)* *Chthoniobacteraceae (11.0%)*	-	Generalist chemoheterotrophs, various likely N-fixing taxa
7 (small)	*Proteobacteria (45.9%)* *Acidobacteria (27.4%)*	*Rhizobiales (45.9%)* *Verrucomicrobiales (18.4%)*	*Methylocystaceae (45.9%)* *Verrucomicrobia subdivision 3 (18.4%)*	Plant diversity (+)	Generalist chemolithotrophs, aerobic methane oxidisers (more likely surviving on organic material) and N-fixing taxa
8 (small)	*Bacteroidetes (63.6%)* *Acidobacteria (36.4%)*	*Chitinophagales (63.6%)*	*Chitinophagaceae (63.6%)*	Organic C (+), belowground productivity (-), plant diversity (-), NMDS3 trajectory (-)	Specialist, slow growing chemoheterotrophs
9 (small)	*Acidobacteria (76.8%)*	*Burkholderiales (14.8%)*	*Alcaligenaceae (14.8%)*	Plant diversity trajectory (+)	Unclear generalists, many unknown
10 (small)	*Actinobacteria (68.0%)* *Bacteroidetes (32.0%)*	*Acidimicrobiales (68.0%)* *Chitinophagales (32.0%)*	*Acidimicrobiaceae (68.0%)* *Chitinophagaceae (32.0%)*	NH4 (+), plant diversity (+), invasion effect size diversity (-)	Generalist, fast growing chemoheterotrophs

Percentages indicate the relative read abundance of the phylogenetic group within the cluster. Clusters are divided in large and small clusters based on their average relative read abundance (Fig 3). Putative generalist functions are based on relations to overall plant community parameters (productivity, diversity) or absence of a relation to the plant community. Putative specialist functions are based on relations with plant community composition, indicating that plant identity played a role. Putative fast growing characteristics were based on a high relative abundance of the cluster with high soil N, NO3 or NH4, as well as the likely presence of readily available C sources (high belowground productivity). Putative slow growing characteristics were based on a low relative abundance of the cluster in these same soil conditions.

Table S4 Dominant phyla, orders, families and putative traits in soil fungal clusters of plant communities grown on natural grassland soil

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits (>9%)	Putative metabolic traits and functions
1 (small)	*Ascomycota (41.0%) Mucoromycota (37.5%)*	*Mucorales (37.5%) Archaeorhizomycetales (15.7%) Mortierellales (15.0%)*	*Mucoraceae (37.5%) Archaeorhizomycetaceae (15.7%) Mortierellaceae (15.0%)*	Tot N (-), aboveground productivity (+)	Soil saprotroph (68.2%)	Generalist, slow growing soil saprotrophs
2 (large)	*Ascomycota (89.0%)*	*Filobasidiales (9.4%)*	*Piskurozymaceae (9.4%)*	Organic C (+), plant diversity trajectory (+)	Soil saprotroph (9.4%)	Largely unknown *Ascomycota*. Likely generalist soil saprotrophs
3 (large)	*Mortierellomycota (50.7%) Ascomycota (36.3%)*	*Mortierellales (50.7%)*	*Mortierellaceae (50.7%)*	Organic C (+), pH (+), belowground productivity (-)	Soil saprotroph (52.7%) Wood saprotroph (10.9%)	Generalist, slow growing saprotrophs
4 (large)	*Ascomycota (77.3%) Basidiomycota (22.7%)*	*Archaeorhizomycetales (54.7%) Agaricales (21.9%) Geoglossales (18.1%)*	*Archaeorhizomycetaceae (54.6%) Hygrophoraceae (19.2%) Geoglossaceae (18.1%)*	Organic C (-), NMDS2 (+), plant diversity trajectory (-), invasion effect size diversity (-)	Soil saprotroph (94.7%)	Specialist soil saprotrophs
5 (large)	*Ascomycota (52.5%) Mortierellomycota (42.5%)*	*Mortierellales (42.5%) Hypocreales (35.8%)*	*Mortierellaceae (42.5%) Nectriaceae (33.4%)*	Organic C (+), invasion effect size diversity (+)	Plant pathogen (36.5%) Soil saprotroph (35.4%)	Generalist soil saprotrophs and plant pathogens (*Fusarium, Ilyonectria, Verticillium, Leptosphaeria, Gibberella*)
6 (large)	*Ascomycota (82.2%)*	*Helotiales (57.5%) Tremellales (16.5%) Capnodiales (12.0%) Thelebolales (11.2%)*	*Bulleribasidiaceae (16.5%) Cladosporiaceae (12.0%) Pseudeurotiaceae (11.2%)*	Belowground productivity (+), NMDS2 (-)	Soil saprotroph (27.9%) Litter saprotroph (15.3%)	Specialist saprotrophs possibly profiting from rhizodeposits. Fast growing
7 (small)	*Ascomycota (86.4%)*	*Pezizales (50.1%) Mortierellales (11.4%)*	*Pyronemataceae (46.3%) Mortierellaceae (11.4%)*	pH (+)	Soil saprotroph (13.6%) Plant pathogen (9.2%)	Generalist, soil saprotrophs and plant pathogens (*Fusarium*, *Lectera*)
8 (small)	*Ascomycota (69.5%) Basidiomycota (23.7%)*	*Geoglossales (56.0%) Agaricales (23.7%)*	*Geoglossaceae (56.0%) Clavariaceae (23.7%)*	Tot N (+), aboveground productivity (-), NMDS2 (+)	Soil saprotroph (79.7%)	Specialist, fast growing soil saprotrophs

Table S4 continued

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits	Putative function
9 (small)	*Ascomycota (84.8%)*	*Archaeorhizomycetales (42.3%)*	*Archaeorhizomycetaceae (42.3%)*	NMDS1 (-), NMDS2 (+)	Soil saprotroph (51.2%)	Specialist soil saprotrophs
10 (small)	*Ascomycota (55.8%)*	*Pleosporales (38.0%) Agaricales (13.5%)*	*Periconiaceae (21.0%) Hygrophoraceae (13.0%)*	Tot P (-), pH (+), plant diversity trajectory (+)	Soil saprotroph (22.4%)	Generalist soil saprotrophs
11 (small)	*Ascomycota (64.1%)*	*Pleosporales (35.9%) Helotiales (14.3%)*	*Didymellaceae (21.2%) Sclerotiniaceae (13.8%) Pleosporaceae (11.2%)*	Invasion effect size NMDS2 (-)	Plant pathogen (46.5%)	Specialist plant pathogens (*Phoma, Botrytis, Stemphylium, Ophiosphaerella*)
12 (small)	*Mucoromycota (49.0%) Ascomycota (30.2%)*	*Mucorales (49.0%) Pleosporales (21.1%)*	*Mucoraceae (49.0%) Melanommataceae (21.1%)*	NMDS3 (+)	Soil saprotroph (50.4%) Plant pathogen (21.1%)	Specialist soil saprotrophs and plant pathogens (*Herpotrichia*)
13 (small)	*Ascomycota (81.0%)*	*Pleosporales (61.2%)*	*Phaeosphaeriaceae (32.2%) Pleosporales (24.5%)*	Aboveground productivity (-)	Plant pathogen (37.7%)	Generalist plant pathogens (*Paraphoma, Septoria, Plenodomus*)
14 (small)	*Ascomycota (82.3%)*	*Pleosporales (33.0%) Geoglossales (19.7%)*	*Didymellaceae (25.6%) Geoglossaceae (19.7%)*	NH4 (+)	Soil saprotroph (28.6%) Plant pathogen (26.7%)	Generalist soil saprotrophs and plant pathogens (*Stagonosporopsis, Plectosphaerella*)
15 (small)	*Ascomycota (79.9%)*	*Chaetothyriales (41.7%) Pleosporales (30.7%)*	*Trichomeriaceae (37.3%) Didymellaceae (25.8%)*	-	Unspecified saprotroph (37.3%) Plant pathogen (36.3%)	Generalist saprotrophs and plant pathogens (*Ascochyta, Gibberella, Coniosporium*)
16 (small)	*Ascomycota (69.4%)*	*Pleosporales (44.0%)*	*Unidentified (76.3%)*	Tot N (+), aboveground productivity trajectory (+)	Plant pathogen (11.1%)	Generalist fast growing fungi. Possibly plant pathogens as order contains many putative plant pathogens, but also many unknown.

Table S4 continued

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits	Putative function
17 (small)	*Ascomycota (72.1%)* *Basidiomycota (25.9%)*	*Archaeorhizomycetales (58.2%)* *Trechisporales (12.2%)*	*Archaeorhizomycetaceae (58.2%)*	Belowground productivity (+), invasion effect size NMDS2 (+)	Soil saprotroph (62.7%) Wood saprotroph (9.1%)	Specialist, fast growing saprotrophs possibly profiting from root exudates
18 (small)	*Ascomycota (32.3%)* *Basidiomycota (27.9%)*	*Sebacinales (18.5%)* *Mortierallales (14.1%)* *Rhizophlyctidales (9.9%)*	*Sebacinaceae (18.5%)* *Mortierellaceae (14.1%)* *Rhizophlyctidaceae (9.9%)*	-	Litter saprotroph (22.8%) Soil saprotroph (14.1%)	Generalist saprotrophs including litter
19 (small)	*Ascomycota (57.4%)* *Basidiomycota (38.0%)*	*Hypocreales (21.0%)* *Agaricales (15.1%)* *Chaetothyriales (13.7%)* *Cantharellales (9.8%)*	*Ceratobasidiaceae (9.8%)*	Plant diversity (+), NMDS2 (-), NMDS1 trajectory (-)	Litter saprotroph (17.1%) Animal parasite (11.0%) Soil saprotroph (10.9%)	Specialist saprotrophs including litter. Possible nematode parasites
20 (small)	*Kickxellomycota (100%)*	*Kickxellales (100%)*	*Kickxellaceae (100%)*	NH4 (-), aboveground productivity (-), NMDS3 (+)	Soil saprotroph (100%)	Specialist, slow growing soil saprotrophs
21 (small)	*Ascomycota (54.9%)*	*Pleosporales (26.5%)* *Verrucariales (16.7%)* *Orbiliales (11.4%)*	*Phaeosphaeriaceae (26.5%)* *Verrucariaceae (16.7%)* *Orbiliaceae (11.4%)*	pH (-), invasion effect size composition (-)	Plant pathogen (26.5%) Lichenized (16.7%) Animal parasite (11.4%)	Specialist lichens, nematode parasites (*Arthrobotrys*) and plant pathogens (*Chaetosphaeronema*)

Percentages indicate the relative read abundance of the phylogenetic group within the cluster. Clusters are divided in large and small clusters based on their average relative read abundance (Fig 3). Putative generalist functions are based on relations to overall plant community parameters (productivity, diversity) or absence of a relation to the plant community. Putative specialist functions are based on relations with plant community composition, indicating that plant identity played a role. Putative fast growing characteristics were based on a high relative abundance of the cluster with high soil N, NO3 or NH4, as well as the likely presence of readily available C sources (high belowground productivity). Putative slow growing characteristics were based on a low relative abundance of the cluster in these same soil conditions. Genera identified as putative plant pathogens presented in brackets.

Table S5 Dominant phyla, orders, families and putative traits in soil fungal clusters of plant communities grown on abandoned arable soil

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits	Putative function
1 (large)	*Mortierellomycota (46.8%)* *Ascomycota (43.8%)*	*Mortierellales (46.8%)* *Pezizales (18.4%)*	*Mortierellaceae (46.8%)* *Pyronemataceae (16.2%)*	Tot C (-), pH (+), plant diversity (-), NMDS3 trajectory (+)	Soil saprotroph (52.8%)	Specialist soil saprotrophs
2 (large)	*Ascomycota (61.3%)* *Mortierellomycota (34.8%)*	*Mortierellales (34.8%)* *Hypocreales (18.7%)*	*Mortierellaceae (34.8%)* *Nectriaceae (15.8%)*	Organic C (+), NO3 (+)	Soil saprotroph (38.5%) Plant pathogen (17.8%)	Generalist, fast growing soil saprotrophs and plant pathogens (*Fusarium, Ilyonectria, Nectria, Plenodomus, Thielaviopsis, Lectera, Paraphoma, Ascochyta, Plectosphaerella, Stagonosporopsis*)
3 (medium)	*Ascomycota (46.3%)* *Basidiomycota (42.3%)*	*Agaricales (35.7%)* *Geoglossales (18.2%)* *Archaeorhizomycetales (12.2%)* *Incertae (9.8%)*	*Clavariaceae (33.0%)* *Geoglossaceae (18.2%)* *Archaeorhizomycetaceae (12.2%)*	NO3 (-), NO2 (-), invasion effect size composition (+)	Soil saprotroph (61.4%)	Specialist, slow growing soil saprotrophs
4 (small)	*Ascomycota (62.4%)* *Basidiomycota (37.6%)*	*Agaricales (37.6%)* *Geoglossales (20.5%)* *Eurotiales (14.2%)* *Hypocreales (12.0%)* *Saccharomycetales (11.6%)*	*Tricholomataceae (37.6%)* *Geoglossaceae (20.5%)* *Aspergillaceae (14.2%)* *Nectriaceae (12.0%)* *Debaryomycetaceae (11.6%)*	NMDS2 trajectory (-), NMDS3 trajectory (+)	Litter saprotroph (37.6%) Soil saprotroph (20.5%) Plant pathogen (16.1%) Unspecified saprotroph (14.2%) Nectar/tap saprotroph (11.6%)	Specialist saprotrophs and plant pathogens (*Fusarium*, *Protomyces*)
5 (small)	*Ascomycota (48.9%)* *Mortierellomycota (23.0%)*	*Hypocreales (34.1%)* *Mortierellales (23.0%)* *Glomerales (9.4%)*	*Mortierellaceae (23.0%)* *Hypocreaceae (18.3%)* *Nectriaceae (15.8%)*	Belowground productivity (-), aboveground productivity trajectory (-)	Soil saprotroph (23.0%) Mycoparasite (18.3%)	Generalist, slow growing soil saprotrophs and mycoparasites

Table S5 Dominant phyla, orders, families and putative traits in soil fungal clusters of plant communities grown on abandoned arable soil

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits	Putative function
6 (small)	*Ascomycota (56.3%) Basidiomycota (21.3%)*	*Agaricales (17.4%) Sordariales (15.0%) Pleosporales (14.2%) Orbiliales (12.4%)*	*Agaricaceae (17.1%) Orbiliaceae (12.4%)*	Tot N (+), tot P (-), plant diversity (+)	Soil saprotroph (29.8%)	Generalist, fast growing soil saprotrophs. Small proportion, but high diversity of plant pathogens (*Herpotrichia, Chaetosphaeronema, Verticillium, Stemphylium, Periconia, Leptosphaeria, Fusarium, Alternaria, Gibellulopsis, Botrytis, Gibberella*).
7 (small)	*Ascomycota (48.3%) Basidiomycota (36.5%)*	*Sebacinales (21.9%) Pezizales (19.5%) Pleosporales (12.7%)*	*Sebacinaceae (21.9%) Pyronemataceae (14.3%)*	Tot C (-), pH (+)	Soil saprotroph (25.5%) Litter saprotroph (11.6%)	Generalist soil and litter saprotrophs
8 (small)	*Kickxellomycota (57.4%)*	*Kickxellales (57.4%) Mortierellales (11.9%)*	*Kickxellaceae (57.4%) Mortierellaceae (11.9%)*	Invasion effect size composition (-)	Soil saprotroph (69.3%)	Specialist soil saprotrophs
9 (small)	*Basidiomycota (42.1%) Ascomycota (36.2%)*	*Sebacinales (29.1%)*	*Serendipitaceae (29.1%)*	Belowground productivity (+)	Root endophyte (29.1%) Litter saprotroph (10.9%)	Generalist root endophytes (*Serendipita*) and litter saprotrophs
10 (small)	*Ascomycota (88.9%)*	*Pleosporales (39.8%) Geoglossales (18.6%) Pezizales (9.2%)*	*Didymellaceae (24.1%) Geoglossaceae (18.6%) Lentitheciaceae (9.2%) Pyronemataceae (9.2%)*	NMDS2 trajectory (-)	Soil saprotroph (28.1%) Plant pathogen (24.1%) Root endophyte (9.2%)	Specialist soil saprotrophs, plant pathogens (*Ascochyta*) and root endophytes (*Darksidea*).
11 (small)	*Chytridiomycota (100%)*	*Rhizophydiales (100%)*	*Rhizophydiaceae (100%)*	NMDS1 (-)	Algal parasite (100%)	Specialist algal parasites
12 (small)	*Ascomycota (51.2%) Olpidiomycota (36.3%)*	*Olpidiales (36.3%)*	*Olpidiaceae (36.3%)*	Tot P (-), pH (-)	Algal parasite (36.3%) Litter saprotroph (10.8%)	Generalist litter saprotrophs and algal parasites

Table S5 continued

Cluster	Dominant phyla (>20%)	Dominant orders (>9%)	Dominant families (>9%)	Relates to	Dominant fungal traits	Putative function
13 (small)	*Ascomycota (43.4%) Basidiomycota (35.3%)*	*Agaricales (18.9%) Mortierellales (15.3%) Cantharellales (15.3%) Pezizales (14.8%) Hypocreales (10.4%)*	*Mortierellaceae (15.3%) Cantharellales (15.3%) Pyronemataceae (14.8%) Marasmiaceae (12.8%)*	Plant diversity trajectory (-), NMDS1 trajectory (+)	Soil saprotroph (17.2%) Litter saprotroph (17.1%) Lichen parasite (15.3%) Wood saprotroph (14.3%)	Specialist soil, litter and wood saprotrophs as well as lichen parasites.
14 (small)	*Ascomycota (50.4%) Basidiomycota (37.7%)*	*Archaeorhizomycetales (44.6%) Agaricales (37.7%) Rhizophydiales (10.9%)*	*Archaeorhizomycetaceae (44.6%) Clavariaceae (30.5%)*	Organic C (-), NO3 (-)	Soil saprotroph (82.3%)	Generalist, slow growing soil saprotrophs
15 (small)	*Ascomycota (74.9%)*	*Chaetothyriales (19.9%) Pleosporales (16.5%) Helotiales (15.7%) Orbiliales (10.8%) Cystofilobasidiales (10.3%)*	*Sporormiaceae (16.5%) Orbiliaceae (10.8%)) Mrakiaceae (10.3%)*	NMDS1 (+), NMDS3 (-), aboveground productivity trajectory (-)	Dung saprotroph (16.5%) Plant pathogen (10.3%) Litter saprotroph (9.9%)	Specialist litter and dung saprotrophs and plant pathogens (*Itersonilia*).
16 (small)	*Basidiomycota (100%)*	*Unidentified (100%)*	*Unidentified (100%)*	Invasion effect size NMDS2 (+)	Unknown (100%)	Unknown specialists
17 (small)	*Ascomycota (100%)*	*Melanosporales (60.6%)*	*Melanosporaceae (60.6%)*	pH (-), aboveground productivity (+)	Mycoparasite (60.6%)	Generalist mycoparasites
18 (small)	*Basidiomycota (53.3%) Ascomycota (46.7%)*	*Sebacinales (53.3%) Helotiales (46.7%)*	*Serendipitaceae (53.3%)*	-	Root endophyte (53.3%)	Generalist root endophytes (*Serendipita*)

Percentages indicate the relative read abundance of the phylogenetic group within the cluster. Clusters are divided in large and small clusters based on their average relative read abundance (Fig 3). Putative generalist functions are based on relations to overall plant community parameters (productivity, diversity) or absence of a relation to the plant community. Putative specialist functions are based on relations with plant community composition, indicating that plant identity played a role. Putative fast growing characteristics were based on a high relative abundance of the cluster with high soil N, NO3 or NH4, as well as the likely presence of readily available C sources (high belowground productivity). Putative slow growing characteristics were based on a low relative abundance of the cluster in these same soil conditions. Genera identified as putative plant pathogens presented in brackets.

Table S6 Marginal R^2 of soil chemistry, microbial biomass pools and clusters from SEM models in natural grassland and abandoned arable plant communities

	Natural grassland	Abandoned arable		Natural grassland	Abandoned arable
Soil chemistry			**Fungal clusters**		
Total N	0.22	0.15	1	0.51	**0.56**
Total P	0.36	0.16	2	**0.49**	**0.55**
Total C	0.00	0.17	3	**0.53**	**0.59**
Organic C	0.24	0.24	4	**0.45**	0.34
NO3	0.34	0.41	5	**0.62**	0.39
NH4	0.21	0.20	6	**0.65**	0.46
NO2	0.00	0.07	7	0.34	0.38
pH	0.44	0.20	8	0.43	0.29
PLFA/NLFA			9	0.71	0.31
Bacterial biomass	0.65	0.55	10	0.38	0.42
Fungal biomass	0.42	0.69	11	0.26	0.24
AMF biomass	0.53	0.57	12	0.23	0.47
Prokaryote clusters			13	0.24	0.29
1	**0.29**	**0.33**	14	0.22	0.36
2	**0.51**	**0.51**	15	0.38	0.42
3	**0.46**	**0.58**	16	0.34	0.39
4	0.53	0.27	17	0.35	0.46
5	0.33	0.64	18	0.12	0.43
6	0.60	0.27	19	0.48	
7	0.15	0.29	20	0.57	
8	0.16	0.45	21	0.35	
9	0.17	0.17			
10		0.58			

R^2 in bold belong to large clusters (Fig 3). Note: sowing density was incorporated as a random effect, but in most cases explained no variation. Marginal R^2 indicates variation explained by fixed factors only.

Table S7 Summarised putative effects of the strongest pathways of the plant community in the year of sampling and past on microbial communities in natural grassland soil.

Time point	Plant parameter	Pathway	Microbial biomass	Prokaryote clusters	Fungal clusters	Putative metabolic traits and functions
Year of sampling	Plant diversity	direct		↓7	↑19	↑ nitrifying taxa; generalist slow growing soil saprotrophs; specialist fast growing soil saprotrophs; generalist litter saprotrophs ↓ bacterial biomass; dominant fast growing chemoheterotrophs; generalist fast growing fungi (in part plant pathogens)
		via ↓N		**↓3**	↑1 ↑8 ↓16	
		via ↓P	↓bacteria	↑4	↑10	
		via ↓NO3				
Year of sampling	Belowground productivity	direct	↑ bacteria	**↑1** ↓4 ↓5	**↓3 ↑6** ↑17	↑ bacterial biomass; dominant fast chemoheterotrophs; dominant and other fast specialist soil saprotrophs; litter and wood saprotrophs ↓ nitrifying taxa; slow chemolithoautotrophs and heterotrophs; dominant slow generalist soil and wood saprotrophs
Year of sampling	Composition (NMDS2) – residence time	direct		↑8	**↑4 ↓6** ↑8 ↑9 ↓19	↑ root endophytes; dominant specialist soil saprotrophs; specialist fast growing soil saprotrophs ↓ dominant fast and other specialist soil and litter saprotrophs
Year of sampling	Composition (NMDS3) – differential dominance	direct			↑12 ↑20	↑ specialist soil saprotrophs and plant pathogens
Past	AP trajectory	direct			↑16	↑ bacterial biomass; generalist fast growing fungi (in part plant pathogens); specialist lichens, nematode parasites and plant pathogens ↓ nitrifying taxa; dominant and other generalist soil and wood saprotrophs; generalist plant pathogens
		via ↑P	↑bacteria	↓4	↓10	
		via ↓pH			**↓3** ↓7 ↓10 ↑21	
Past	Plant diversity trajectory	direct	↓AMF	**↓2 ↑3**	**↑2 ↓4** ↑10	↑ dominant fast-growing chemoheterotrophs; dominant and other generalist soil saprotrophs ↓ AMF biomass; dominant chemoheterotrophs; N-fixing taxa; dominant specialist soil saprotrophs
Past	Invasion effect size diversity	direct		↑5 ↑6 ↑9	**↓4 ↑5**	↑ AMF biomass, chemolithoautotrophs; dominant generalist and other soil saprotrophs and plant pathogens ↓ dominant generalist soil saprotrophs; specialist lichens, nematode parasites and plant pathogens
		via ↓org C	↑AMF	↓5 ↓6	**↓2 ↓3 ↑4 ↑5**	
		via ↑pH			**↑3** ↑7 ↑10 ↓21	

In bold: dominant clusters. See Fig 5 for overview of pathways strengths.

Table S7 continued

Time point	Plant parameter	Pathway	Microbial biomass	Prokaryote clusters	Fungal clusters	Putative metabolic traits and functions
Past	NMDS2 trajectory	direct	↓fungi	**↓2 ↑3**	↑19	↑ dominant fast-growing chemoheterotrophs; dominant and other generalist soil and wood saprotrophs; specialist soil and litter saprotrophs; generalist plant pathogens ↓ fungal and AMF biomass; dominant chemoheterotrophs; N-fixing taxa; generalist soil saprotrophs and plant pathogens; specialist lichens, nematode parasite and plant pathogens
		via ↑pH			**↑3** ↑7 ↑10 ↓21	
		via ↓NH4	↓fungi ↓AMF		↓14 ↑20	
Past	NMDS3 trajectory	direct	↑bacteria ↑fungi			↑ bacterial and fungal biomass; specialist lichens, nematode parasites and plant pathogens ↓ dominant and other generalist soil and wood saprotrophs; generalist plant pathogens
		via ↓pH			**↓3** ↓7 ↓10 ↑21	
Past	Invasion effect size composition	direct			↓11 ↑17 ↓21	↑ specialist soil and wood saprotrophs ↓ specialist plant pathogens, lichens and nematode parasites

In bold: dominant clusters. See Fig 5 for overview of pathways strengths.

Table S8 Summarised putative effects of the strongest pathways of the plant community in the year of sampling and past on microbial communities in abandoned arable soil.

Time point	Plant parameter	Pathway	Microbial biomass	Prokaryote clusters	Fungal clusters	Putative metabolic traits and functions
Year of sampling	Plant diversity	direct	↓bacteria ↓fungi ↓AMF	**↑2** ↑7 ↓8 ↑10	**↓1** ↑6	↑ dominant slow growing chemoheterotrophs; aerobic methane oxidisers and N-fixing taxa; generalist fast growing soil saprotrophs and plant pathogens ↓ bacterial, fungal and AMF biomass; slow growing chemoheterotrophs; dominant specialist soil saprotrophs
Year of sampling	Belowground productivity	direct		↓8	↓5 ↑9	↑ root endophytes and litter saprotrophs ↓ chemoheterotrophs (dead material); generalist soil saprotrophs and mycoparasites
Year of sampling	Composition (NMDS2) – residence time	direct		↓4		↓ Specialist chemoheterotrophs
Year of sampling	Composition (NMDS3) – differential dominance	direct	↓AMF		↓15	↑ dominant slow AOA and N-fixing taxa; dominant specialist soil saprotrophs; dominant generalist fast-growing soil saprotrophs and plant pathogens; generalist mycoparasites ↓ fungal and AMF biomass; dominant slow growing chemoheterotrophs; generalist litter saprotrophs; generalist slow growing soil saprotrophs; specialist litter saprotrophs and plant pathogens
		via ↑NO3	↓fungi ↓AMF	**↓2**	**↑2 ↓3** ↓14	
		via ↑pH		**↓2 ↑3**	**↑1** ↑7 ↓12 ↑17	
Past	AP trajectory	direct			↓5 ↓15	↓ generalist soil saprotrophs and mycoparasites; specialist litter saprotrophs and plant pathogens
Past	Plant diversity trajectory	direct		↑9	↓13	↑ fast-growing chemoheterotrophs; generalist fast-growing soil saprotrophs and plant pathogens ↓ bacterial biomass; dominant AOA and N-fixing taxa; specialist soil, litter and wood saprotrophs
		via ↑N	↓bacteria	**↓3** ↑5	↑6	
Past	Invasion effect size plant diversity	direct		↓10		↑ fast-growing chemoheterotrophs; dominant specialist slow-growing soil saprotrophs ↓ bacterial biomass; chemoheterotrophs
		via ↓NO2	↓bacteria	↑5	**↑3**	

In bold: dominant clusters. See Fig 5 for overview of pathways strengths.

Table S8 Summarised putative effects of the most important plant community parameters in the year of sampling and past effects on microbial soil legacies in abandoned arable soil communities

Time point	Plant parameter	Pathway	Microbial biomass	Prokaryote clusters	Fungal clusters	Putative function
Past	NMDS1 trajectory	direct		**↓1**	↑13	↑ specialist soil, litter and wood saprotrophs ↓ dominant chemoheterotrophs
Past	NMDS2 trajectory	direct			↓4 ↓10	↓ specialist soil saprotrophs, plant pathogens and root endophytes
Past	NMDS3 trajectory	direct	↓fungi	↓8	**↑1** ↑4	↑ dominant and other specialist soil saprotrophs; specialist plant pathogens; generalist fast-growing soil saprotrophs and plant pathogens; generalist litter saprotrophs ↓ fungal biomass; chemoheterotrophs (dead material)
		via ↓P			↑6 ↑12	
Past	Invasion effect size composition (NMDS2)	direct		**↓1 ↑3**	**↑3** ↓8 ↑16	↑ dominant AOA and N-fixing taxa; fast-growing chemoheterotrophs; dominant specialist soil saprotrophs; dominant slow-growing soil saprotrophs; generalist soil and litter saprotrophs; generalist slow-growing soil saprotrophs; unknown specialists ↓ dominant chemoheterotrophs; chemoheterotrophs (dead material); dominant generalist fast-growing soil saprotrophs and plant pathogens; specialist soil saprotrophs
		via ↓C			**↑1** ↑7	
		via ↓orgC		↑5 ↓8	**↓2** ↑14	

In bold: dominant clusters. See Fig 5 for overview of pathways strengths.

Table S9 Sown and invaded plant species and their abbreviations

Plant species	Abbreviation	Sown/invaded
Acer spp	Acesp	Invaded
Agrimonia eupatorium	Agreu	Sown
Agrostis spp	Agrsp	Invaded
Anthericum ramosum	Antra	Sown, not established
Anthylis vulneraria	Antvu	Sown
Arabidopsis thaliana	Arath	Invaded
Arenaria serpyllifolia	Arese	Invaded
Arrhenatherum elatior	Arrel	Invaded
Artemisia vulgaris	Artvu	Invaded
Asperula spp	Aspsp	Sown
Aster amellus	Astam	Sown, not established
Astragalus cicer	Astci	Sown
Astragalus glycyphylos	Astgl	Sown
Atriplex spp	Atrsp	Invaded
Brachypodium pinnatum	Brapi	Sown
Bromus erectus	Broer	Sown
Bromus mollis	Bromo	Invaded
Bupleurum falcatum	Bupfa	Sown
Calamagrostis epigejos	Calep	Invaded
Campanula gentilis	Camge	Sown
Campanula glomerata	Camgl	Sown
Campanula patula	Campa	Invaded
Carex flacca	Carfl	Sown
Carex hirta	Carhi	Invaded
Cardamine spp	Carsp	Invaded
Carex tomentosa	Carto	Sown
Centaurea jacea	Cenja	Sown
Centaurea scabiosa	Censc	Sown
Cerastium holosteoides	Cerho	Invaded
Cirsium acaule	Cirac	Sown, not established
Cirsium pannonicum	Cirpa	Sown
Conyza spp	Consp	Invaded
Coronila varia	Corva	Sown, not established
Crepis biennis	Crebi	Invaded
Dactylis glomerata	Dacgl	Invaded
Daucus carota	Dauca	Invaded
Dianthus carthusianorum	Diaca	Sown, not established
Dipsacus sylvestris	Dipsy	Invaded
Elymus repens	Elyre	Invaded
Epilobium spp	Episp	Invaded
Erigeron annuus	Erian	Invaded
Euphorbia cyparissias	Eupcy	Invaded
Fallopia convolvulus	Falco	Invaded
Falcaria vulgaris	Falvu	Invaded
Galeopsis spp	Galsp	Invaded
Geranium sibiricum	Gersi	Invaded
Helianthemum grandiflorum	Helgr	Sown
Heracleum mantegazzianum	Herma	Invaded
Hieracium spp	Hiesp	Invaded
Holcus mollis	Holmo	Invaded
Hypericum perforatum	Hyppe	Invaded
Inula hirta	Inuhi	Sown
Inula salicina	Inusa	Sown

Table S9 Continued

Plant species	Abbreviation	Sown/invaded
Lactuca serriola	Lacse	Invaded
Lamium purpureum	Lampu	Invaded
Laserpitium latifolium	Lasla	Sown
Lathyrus pratensis	Latpr	Invaded
Leontodon autumnalis	Leoau	Invaded
Leontodon hispidus	Leohi	Sown
Linum catharticum	Linca	Invaded
Linum flavum	Linfl	Sown
Linum tenuifolium	Linte	Sown
Lolium perenne	Lolpe	Invaded
Lotus corniculatus	Lotco	Sown
Medicago falcata	Medfa	Sown
Medicago lupulina	Medlu	Invaded
Myos spp	Myosp	Invaded
Plantago lanceolata	Plala	Invaded
Plantago media	Plame	Sown
Poa annua	Poaan	Invaded
Poa trivialis	Poatr	Invaded
Polygonum spp	Polsp	Invaded
Primula veris	Prive	Sown, not established
Prunella grandiflora	Prugr	Sown
Ranunculus spp	Ransp	Invaded
Raphanus raphanistrum	Rapra	Invaded
Rumex spp	Rumsp	Invaded
Salvia pratensis	Salpr	Sown
Salix spp	Salsp	Invaded
Salvia verticilata	Salve	Sown
Sanquisorba minor	Sanmi	Sown
Scabiosa ochroleuca	Scaoc	Sown
Silene vulgaris	Silvu	Invaded
Solidago canadensis	Solca	Invaded
Sonchus spp	Sonsp	Invaded
Stachys recta	Stare	Sown
Stipa spp	Stisp	Invaded
Tanacetum corymbosum	Tanco	Sown
Tanacetum spp	Tansp	Invaded
Tanacetum vulgaris	Tanvu	Invaded
Taraxacum officinalis	Tarof	Invaded
Teucrium chamaedrys	Teuch	Sown
Thlaspi arvense	Thlar	Invaded
Thymus pulegioides	Thypu	Sown
Trifolium medium	Trime	Sown
Trifolium montanum	Trimo	Sown
Trifolium pratensis	Tripr	Invaded
Trifolium repens	Trire	Invaded
Tussilago farfara	Tusfa	Invaded
Urtica dioica	Urtdi	Invaded
Veronica teucrium	Verteu	Sown
Viccia spp	Vicsp	Invaded