

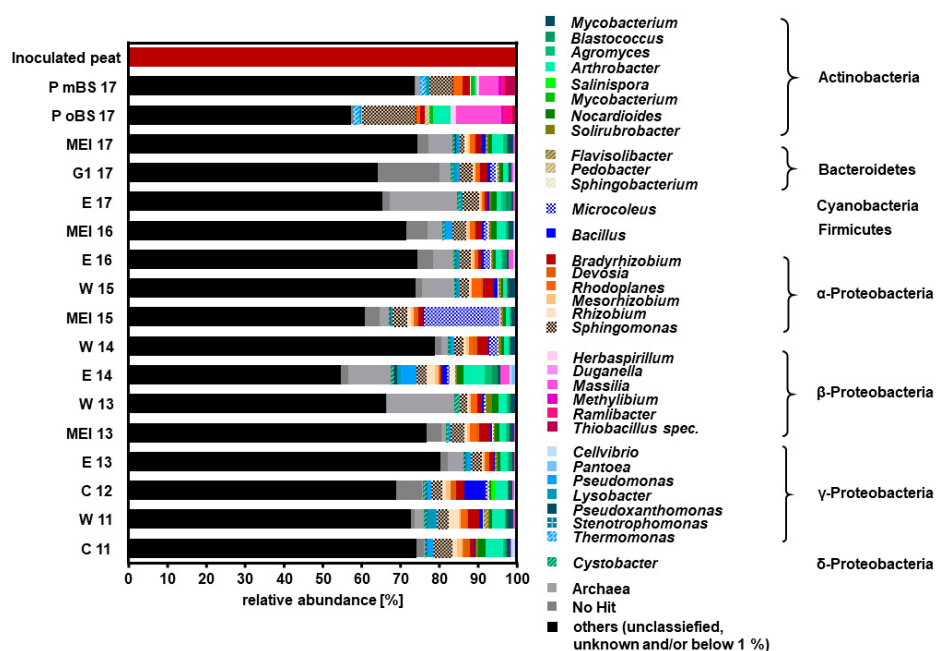


Figure S1. Microbial diversity of selected soil samples. Shown are the relative abundances of detected genera. The microbial community was analyzed by amplifying and sequencing the V4 region of the 16S rRNA gene via MiSeq Illumina. The respective sequence data are available under the bioproject accession number PRJNA663446.

Table S1. Detected *Bradyrhizobium* OTUs. Operational taxonomic units (OTUs) consist of defined and assembled taxa. The use of OTUs is widely accepted and applied to describe bacterial communities using amplicon sequencing of 16S rRNA gene". For more information, please visit the rtl-genomics webpage (www.rtlgenomics.com/docs/Data_Analysis_Methodology.pdf).

	Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium sp	Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Unknown
Inoculated turf	27.319	–
P mBS 17	232	–
P oBS 17	226	–
MEI 2017	110	2
G 2017	431	2
E 2017	114	1
MEI 2016	232	2
E 2016	234	0
W 2015	414	9
MEI 2015	80	0
W 2014	699	8
E 2014	28	0
W 2013	115	4
MEI 2013	233	2

E 2013	197	1
C 2012	342	3
W 2011	442	7
C 2011	834	16
Σ	32282	57