Supplementary

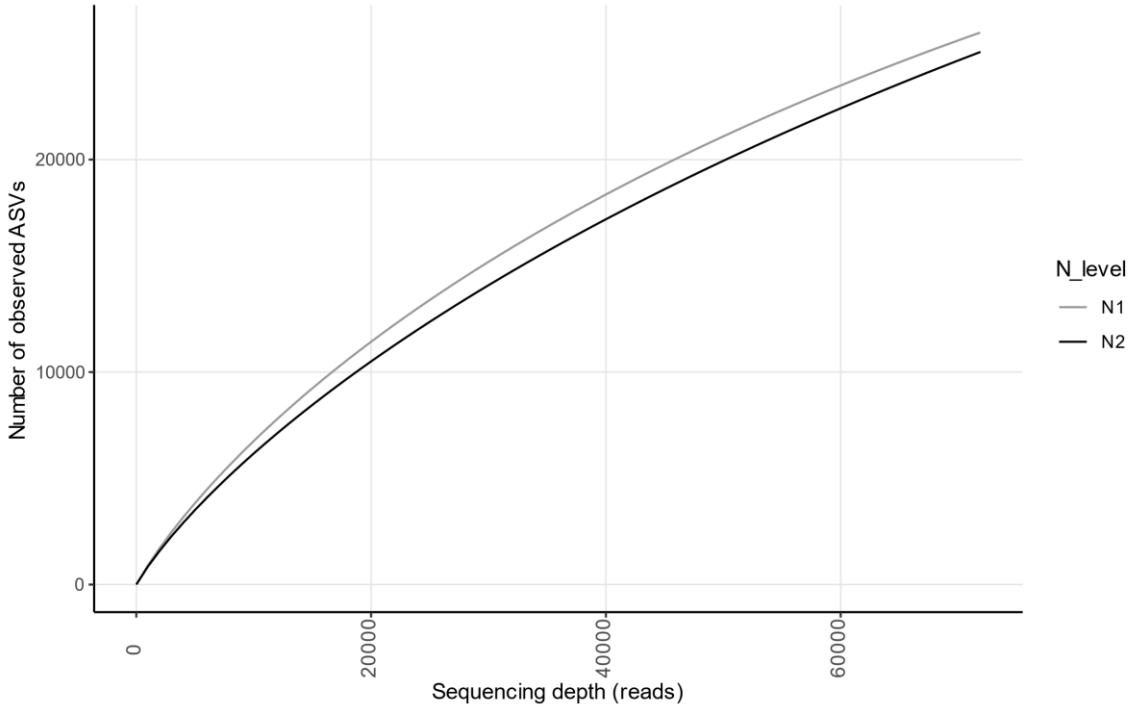

Figure S1: Rarefaction curve of the observed amplicons sequence variants (ASVs) of the soil inhabiting bacterial communities within the two different N-fertilizer treatments (N1 and N2). Samples of the same N treatment were aggregated and rarefied to the same number of raw reads (61206).

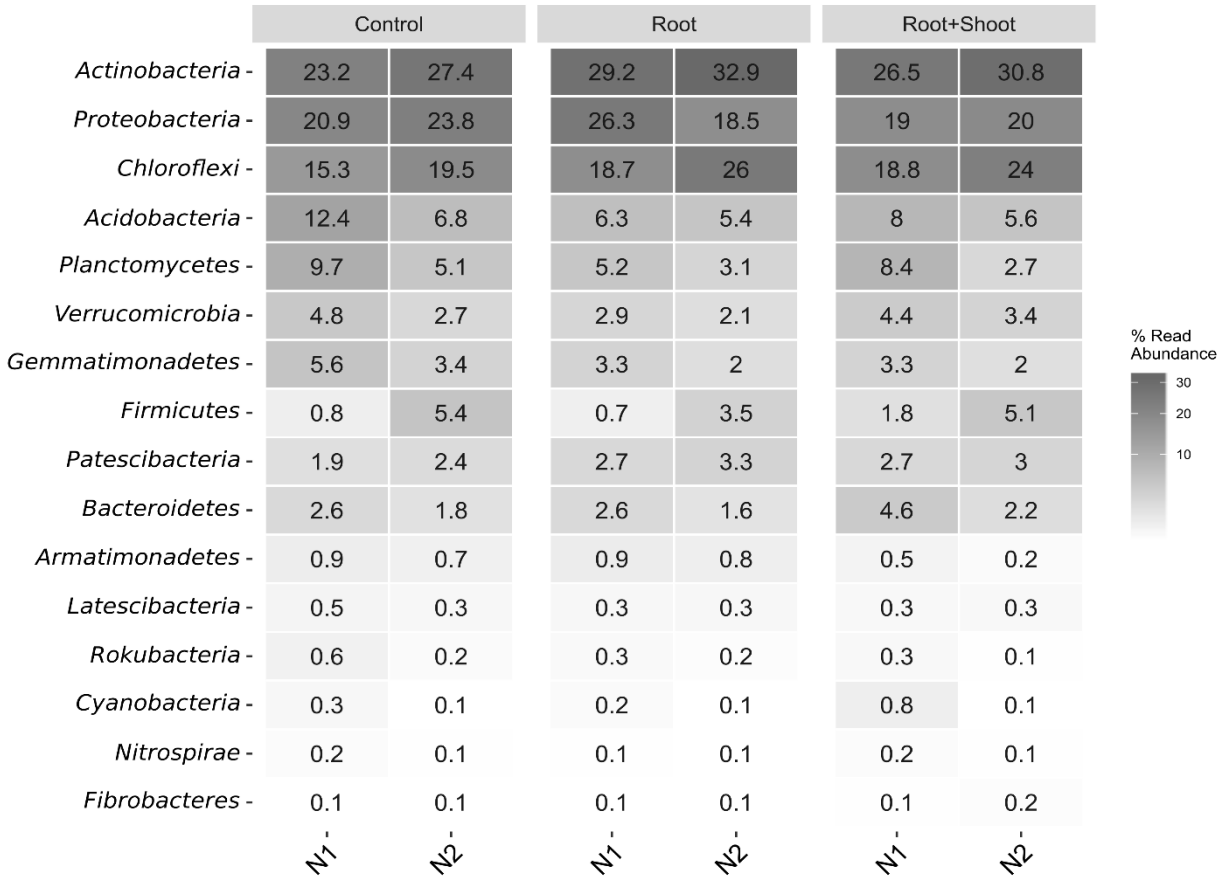

Figure S2: Heatmap of the 16 most abundant phyla (>0.1%) in the analyzed soil samples grouped by N levels and litter input treatments (n=4, except for N2 Root: n=3).

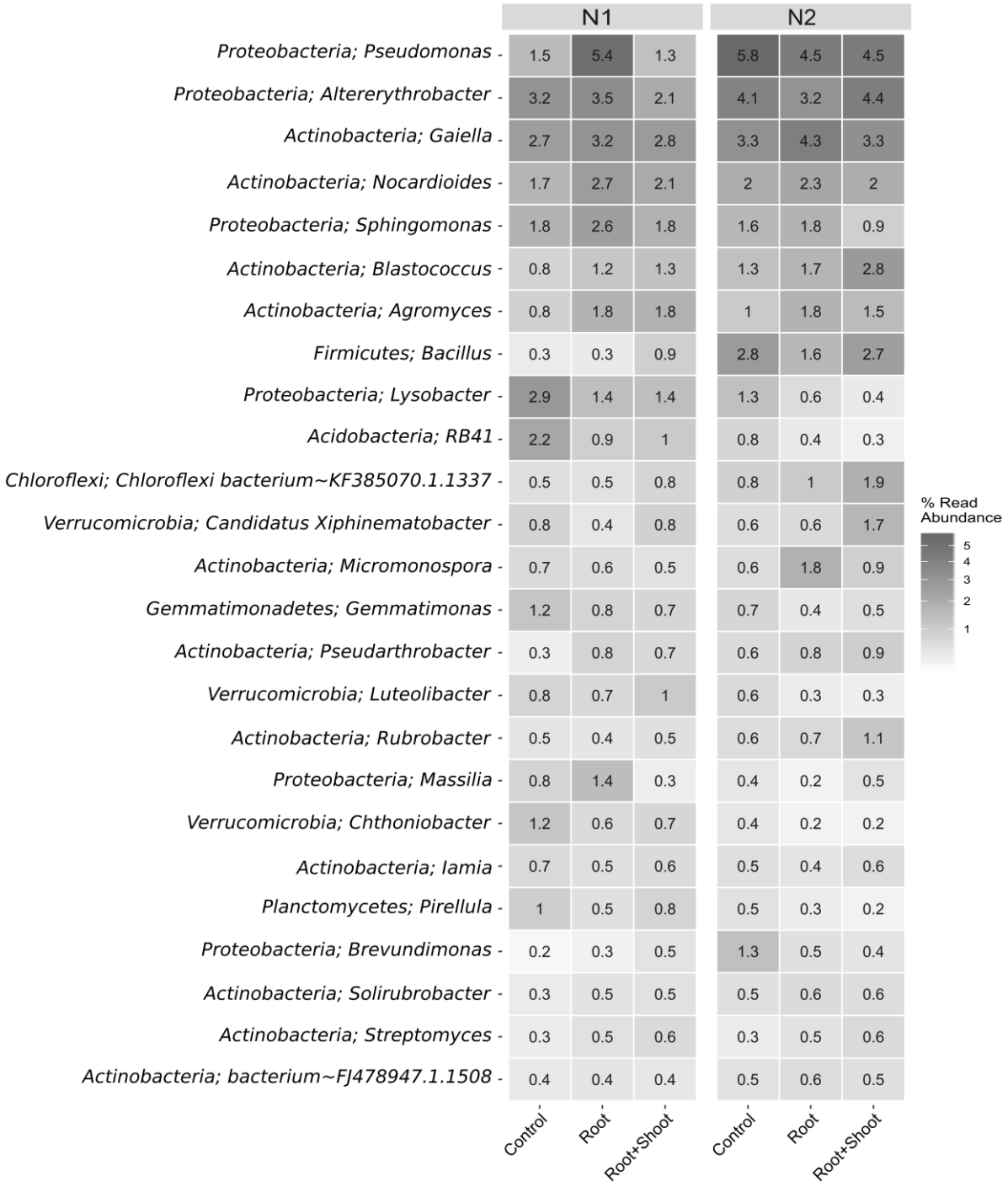

Figure S3: Heatmap of the 25 most abundant bacterial genera in the analyzed soil samples grouped by N levels and litter input treatments (n=4, except for N2 Root: n=3).

Table S4: Sequence summary, alpha diversity indices and PD (phylogenetic diversity) for each treatment. Shown are read sums and mean values of diversity indices.

Sample ID	Number of Replicates	Raw Reads	Reads after Pipeline	Reads after Taxonomy filter	Subsample size	Observed ASVs	Shannon	Simpson	PD
N1_C	4	537242	443228	442610	61206	21113	9.22	0.9997	423.2
N1_R	4	590494	492088	491280	61206	21447	9.10	0.9995	431.0
N1_RS	4	557072	439132	438456	61206	21789	9.29	0.9997	436.6
N2_C	4	531926	441286	440968	61206	19142	8.79	0.9992	420.4
N2_R	3	848974	735676	735366	61206	18891	8.78	0.9991	409.2
N2_RS	4	536532	463944	463504	61206	20301	8.89	0.9990	403.3