Figure.1 PCoA plot of fungal (A), bacterial (B) and archaeal (C) community composition among biotopes. Ternary plot depicting compartment relative abundance of fungal (D), bacterial (E) and archaeal (F) OTUs among biotopes of soil, phyllosphere and faeces. Each point corresponds to a class. Its position represents its relative abundance with respect to each biotope, and its size represents average relative abundance across biotopes. All the classes in the same phylum are exhibited in the same colour. GS, GP and GF represent the soil, phyllosphere and faeces samples in grazed grassland soil respectively.

Figure. 2 (A) Network like Venn plot of microbial communities across biotopes of soil, phyllosphere and faeces. OTUs in soil, phyllosphere and faeces and their mutual overlaps are presented with network topography. Venn plot of fungal (B), bacterial (C) and archaeal (D) OTUs among biotopes of soil, phyllosphere and faeces.

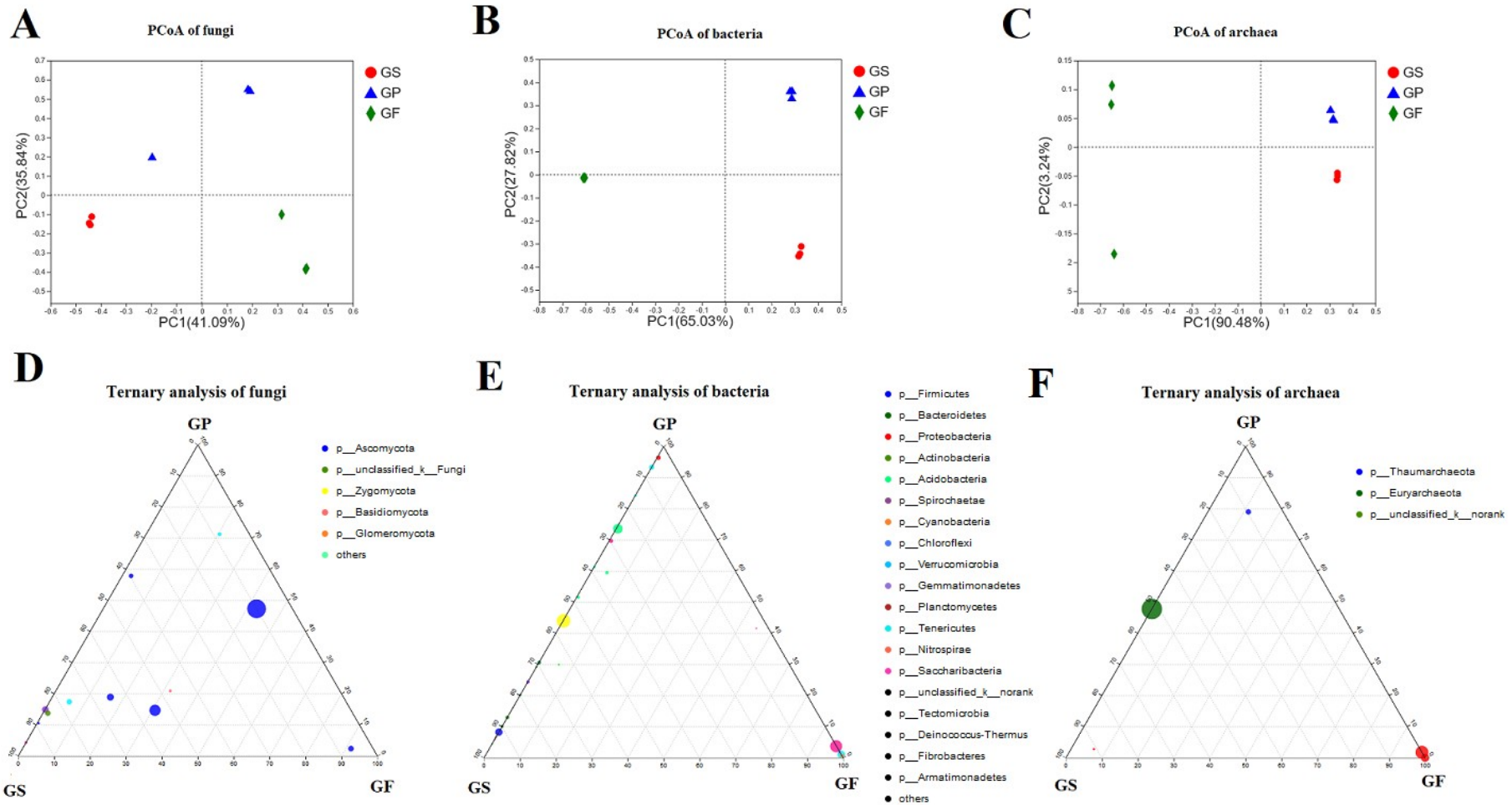
Figure. 3 Relative abundance analysis of fungal (A), bacterial (B) and archaeal (C) communities in biotopes of soil, phyllosphere and faeces on phylum level visualized by barplot; Relative abundance analysis of fungal (D) and bacterial (E) communities in biotopes of soil, phyllosphere and faeces on phylum level visualized by coxcomb analysis; The fungal genuses with top 15 relative abundance by random forest classification (F).

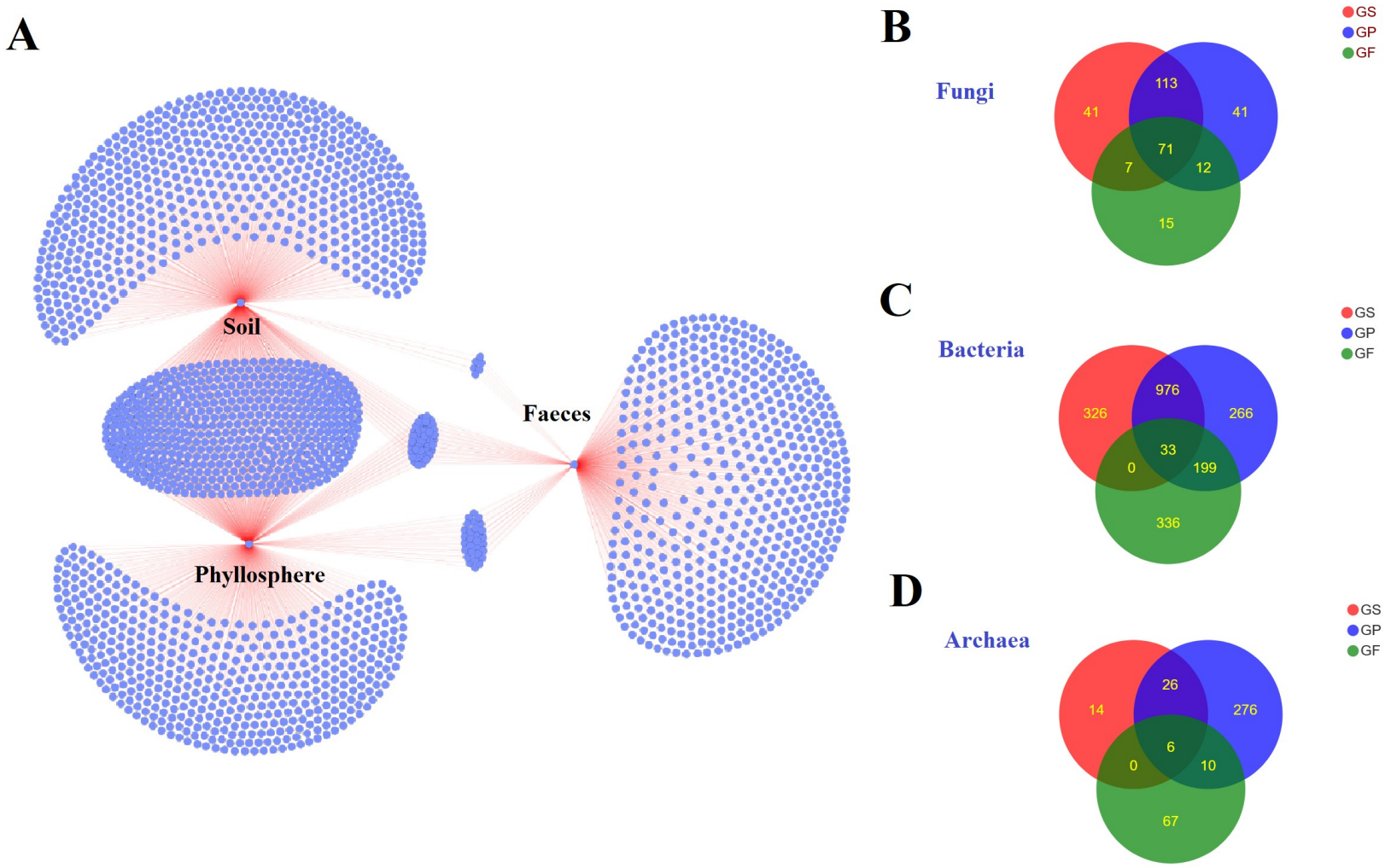
Figure. 4 Fungal (A), bacterial (B) and archaeal (C) co-occurrence networks of soil and phyllosphere biotopes in grazed and ungrazed grassland. Nodes represents individual species; edges represent significant spearman correlations ($|\rho| > 0.9$, $P < 0.001$). All the species classified in the same phylum are visualized in the same colour.

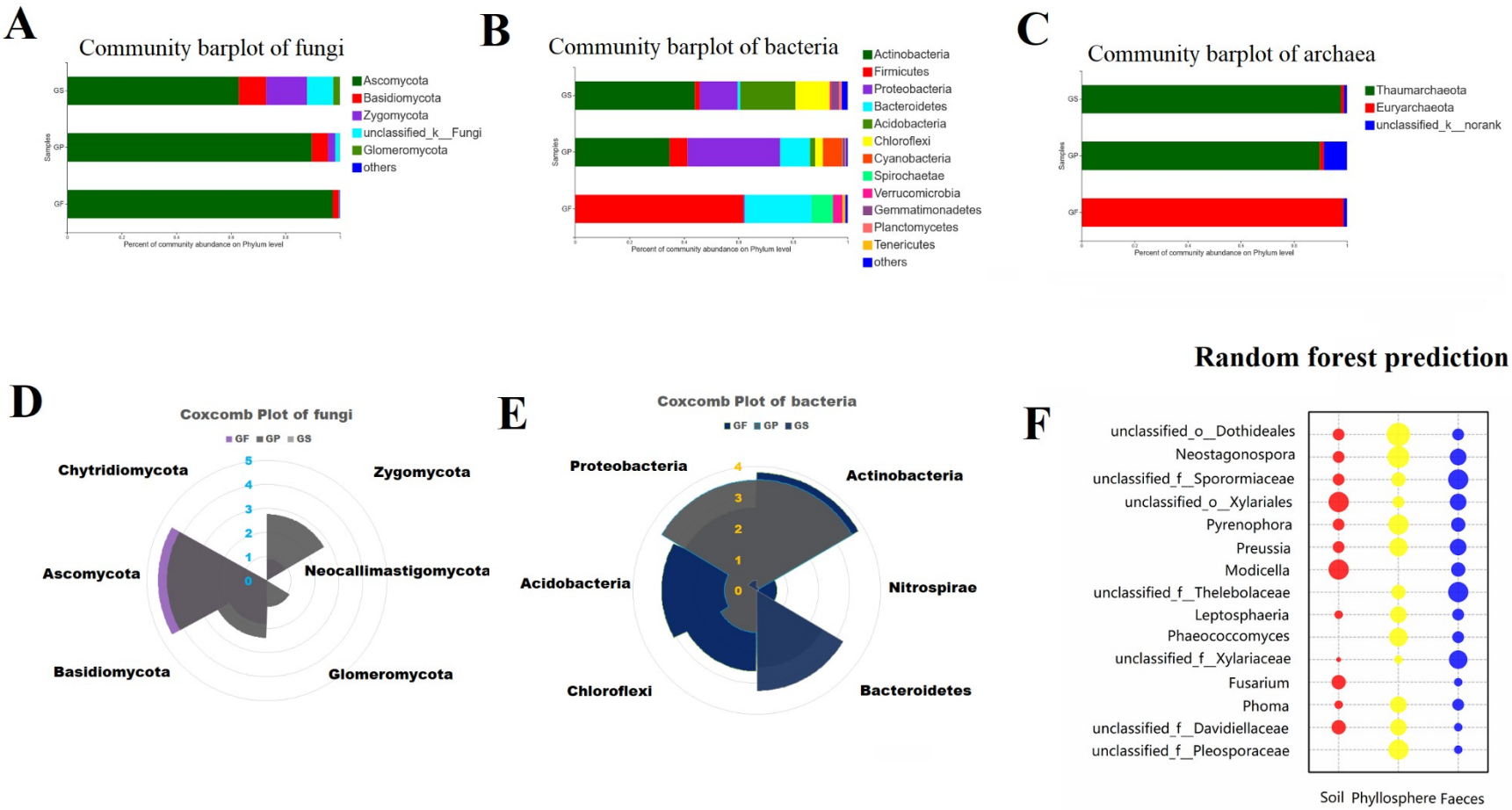
Figure. 5 Canonical correspondence analysis (CCA) of the environmental factor impacts on fungal, bacterial and archaeal community composition. GS, GP and GF

represent the soil, phyllosphere and faeces samples in grazed grassland soil respectively.

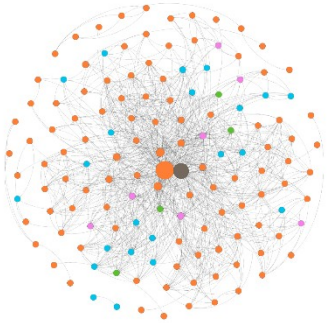
Figure. 6 Structural equation model (SEM) of relationship between physical factors, nutrient properties and microbiota. For each significant relationship, standardised coefficient and p = values are given alongside arrow, and arrow weights are proportional to standardised coefficients.


A
PCoA of fungi
PC2(35.84%)
PC1(41.09%)
GS
GP
GF
B
PCoA of bacteria
PC2(27.82%)
PC1(65.03%)
GS
GP
GF
C
PCoA of archaea
PC2(3.24%)
PC1(90.48%)
GS
GP
GF
D
Ternary analysis of fungi
GP
GS
GF
p__Ascomycota
p__unclassified_k__Fungi
p__Zygomycota
p__Basidiomycota
p__Glomeromycota
others
E
Ternary analysis of bacteria
GP
GS
GF
p__Firmicutes
p__Bacteroidetes
p__Proteobacteria
p__Actinobacteria
p__Acidobacteria
p__Spirochaetae
p__Cyanobacteria
p__Chloroflexi
p__Verrucomicrobia
p__Gemmatimonadetes
p__Planctomycetes
p__Tenericutes
p__Nitrospirae
p__Saccharibacteria
p__unclassified_k__norank
p__Tectomicrobia
p__Deinococcus-Thermus
p__Fibrobacteres
p__Armatimonadetes
others
F
Ternary analysis of archaea
GP
GS
GF
p__Thaumarchaeota
p__Euryarchaeota
p__unclassified_k__norank

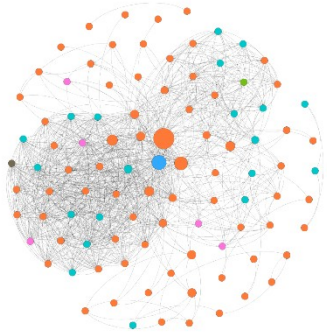

A
Soil
Faeces
Phyllosphere
B
Fungi
GS
GP
GF
41
113
41
71
7
12
15
C
Bacteria
GS
GP
GF
326
976
266
33
0
199
336
D
Archaea
GS
GP
GF
14
26
276
6
0
10
67


A
Community barplot of fungi
Ascomycota
Basidiomycota
Zygomycota
unclassified_k__Fungi
Glomeromycota
others
GS
GP
GF
Samples
Percent of community abundance on Phylum level
B
Community barplot of bacteria
Actinobacteria
Firmicutes
Proteobacteria
Bacteroidetes
Acidobacteria
Chloroflexi
Cyanobacteria
Spirochaetae
Verrucomicrobia
Gemmatimonadetes
Planctomycetes
Tenericutes
others
C
Community barplot of archaea
Thaumarchaeota
Euryarchaeota
unclassified_k__norank
D
Coxcomb Plot of fungi
GF GP GS
Chytridiomycota
Zygomycota
Ascomycota
Neocallimastigomycota
Basidiomycota
Glomeromycota
E
Coxcomb Plot of bacteria
Proteobacteria
Actinobacteria
Acidobacteria
Nitrospirae
Chloroflexi
Bacteroidetes
F
Random forest prediction
unclassified_o__Dothideales
Neostagonospora
unclassified_f__Sporormiaceae
unclassified_o__Xylariales
Pyrenophora
Preussia
Modicella
unclassified_f__Thelebolaceae
Leptosphaeria
Phaeococcomyces
unclassified_f__Xylariaceae
Fusarium
Phoma
unclassified_f__Davidiellaceae
unclassified_f__Pleosporaceae
Soil Phyllosphere Faeces

A

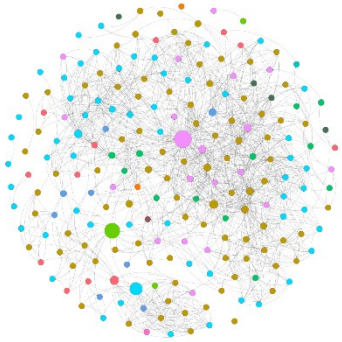


Fungi in grazed grassland

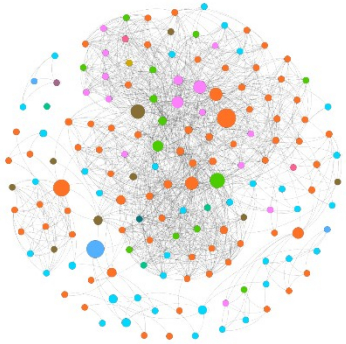


Fungi in ungrazed grassland

B

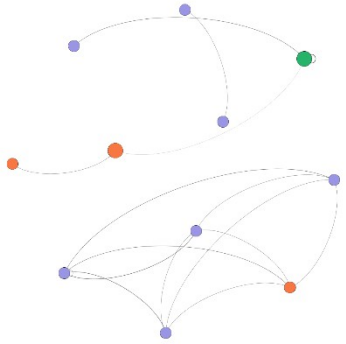


Bacteria in grazed grassland

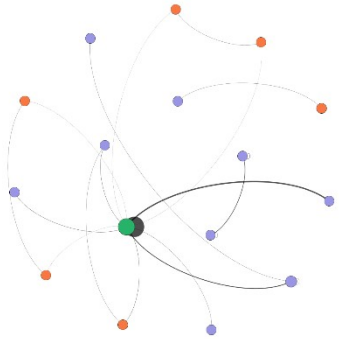


Bacteria in ungrazed grassland

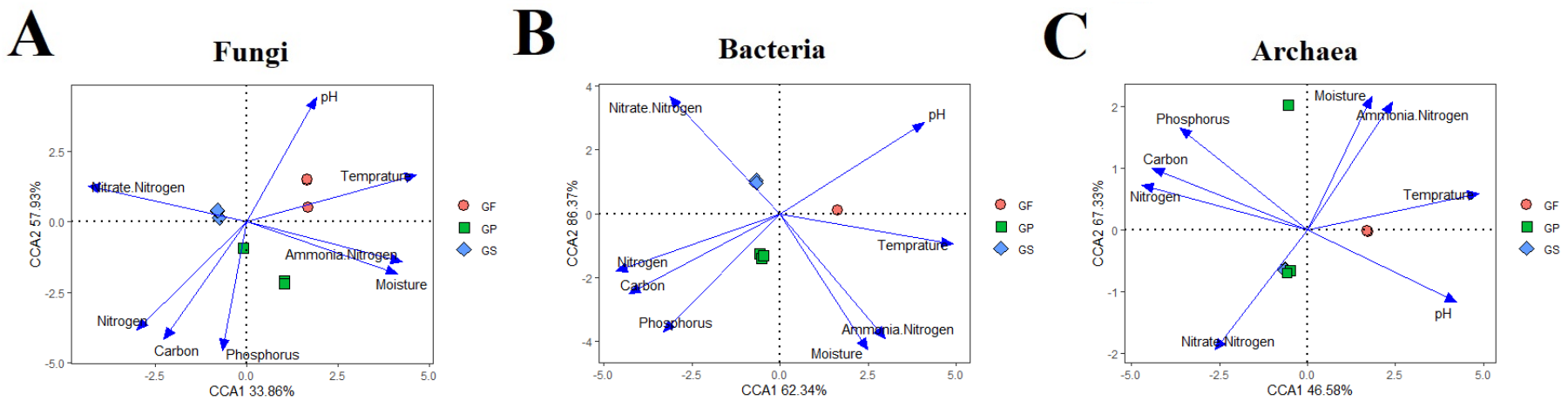
C

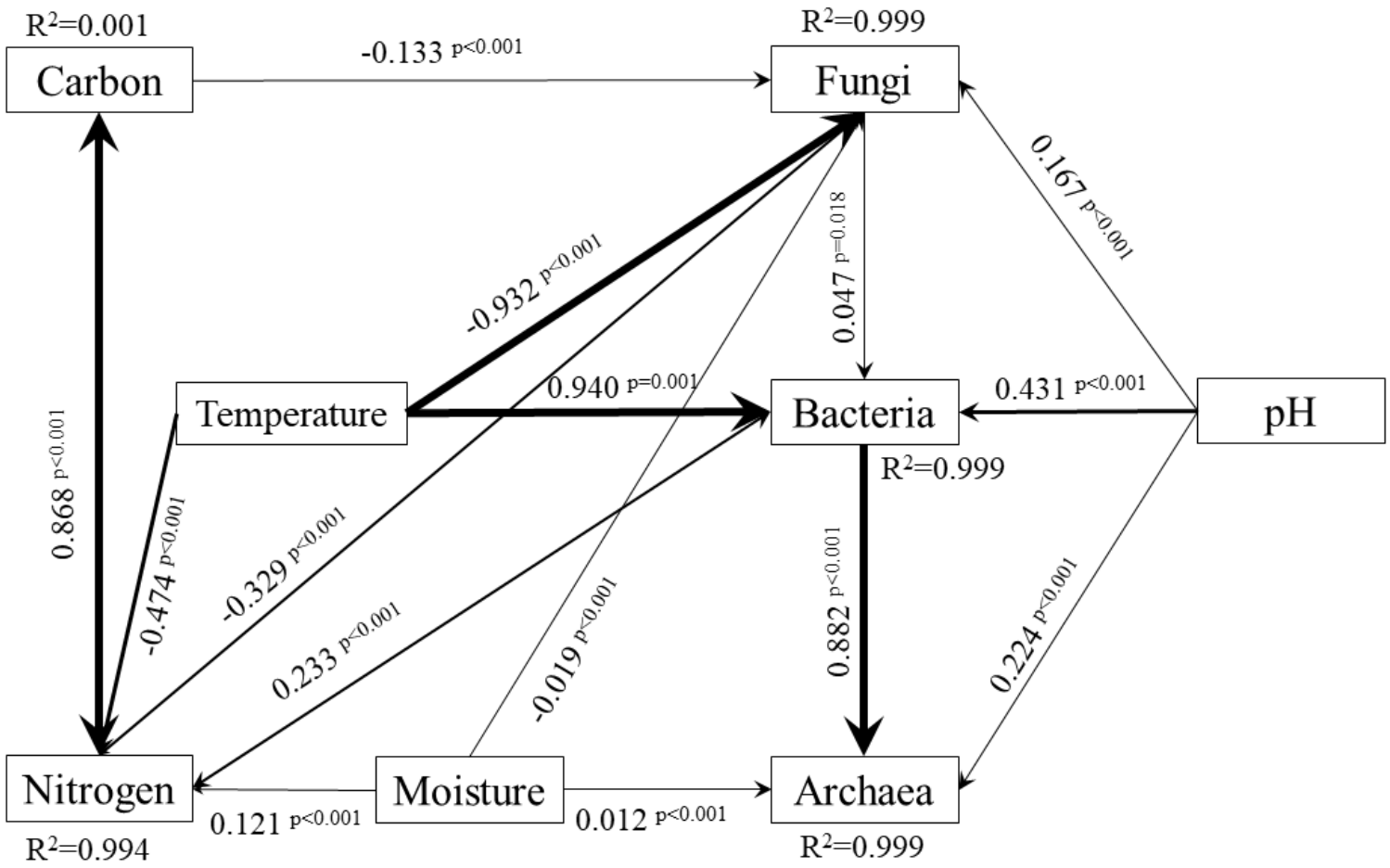


Archeae in grazed grassland



Archeae in ungrazed grassland


A
Fungi
pH
Temprature
Nitrate.Nitrogen
Ammonia.Nitrogen
Moisture
Nitrogen
Carbon
Phosphorus
CCA2 57.93%
CCA1 33.86%
GF
GP
GS
B
Bacteria
Nitrate.Nitrogen
pH
Temprature
Nitrogen
Carbon
Phosphorus
Ammonia.Nitrogen
Moisture
CCA2 86.37%
CCA1 62.34%
GF
GP
GS
C
Archaea
Moisture
Phosphorus
Ammonia.Nitrogen
Carbon
Nitrogen
Temprature
pH
Nitrate.Nitrogen
CCA2 67.33%
CCA1 46.58%
GF
GP
GS


R²=0.001
Carbon
-0.133 p<0.001
R²=0.999
Fungi
0.167 p<0.001
-0.932 p<0.001
0.047 p=0.018
0.940 p=0.001
Temperature
Bacteria
0.431 p<0.001
pH
R²=0.999
0.868 p<0.001
-0.474 p<0.001
-0.329 p<0.001
0.233 p<0.001
-0.019 p<0.001
0.882 p<0.001
0.224 p<0.001
Nitrogen
Moisture
Archaea
0.121 p<0.001
0.012 p<0.001
R²=0.994
R²=0.999