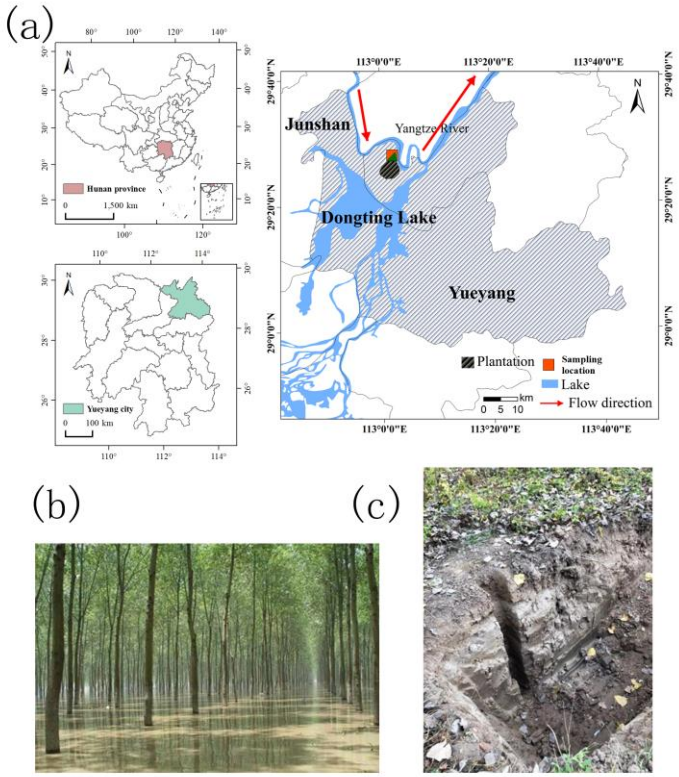


Figure S1. Sampling site (a)， sampling site suffering the seasonally flooding (b) and the soil profile (c).

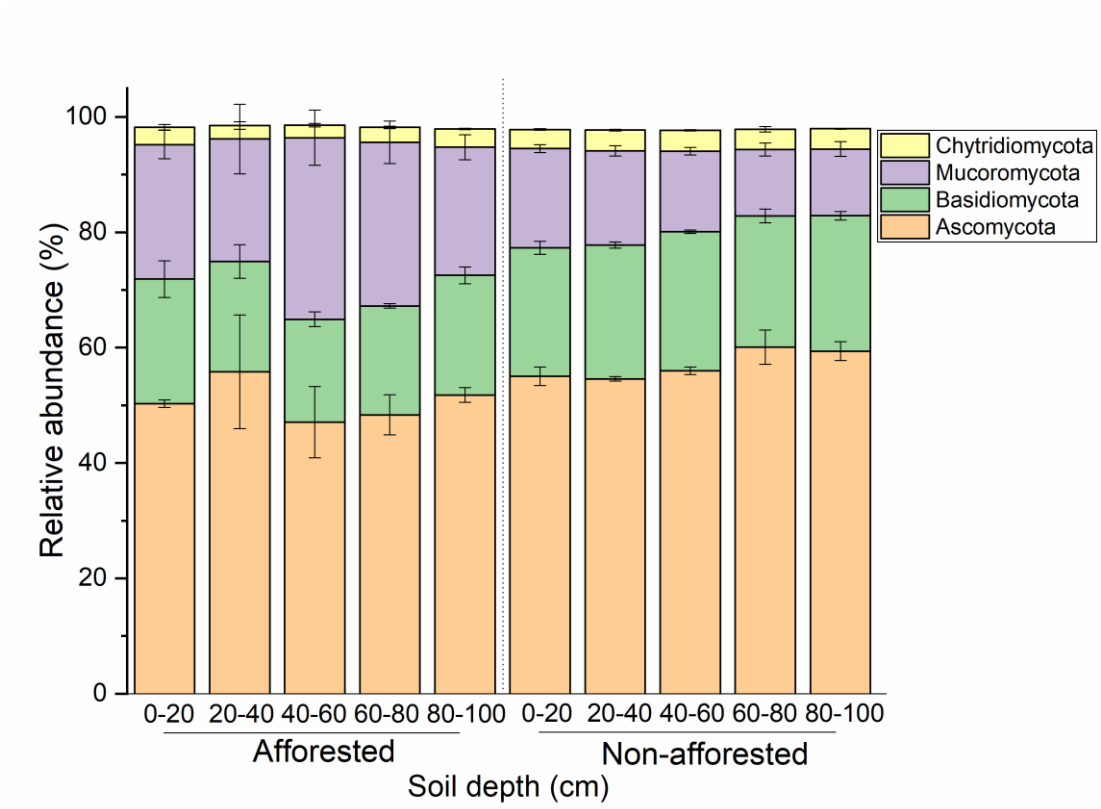


Figure S2. Relative abundance of the dominant fungal phylum with relative abundance >1% across all the samples. Bars represent S.E..

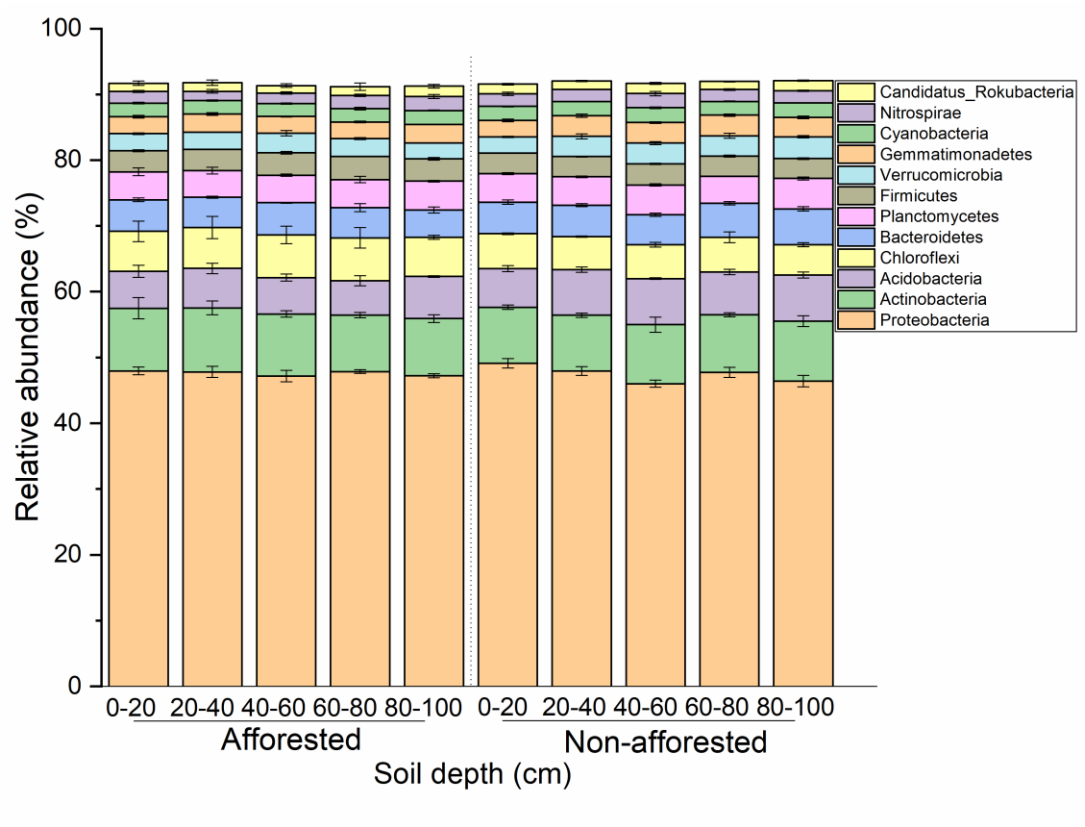


Figure S3. Relative abundance of the dominantbacterial phylum with relative abundance >1% across all the samples. Bars represent S.E..

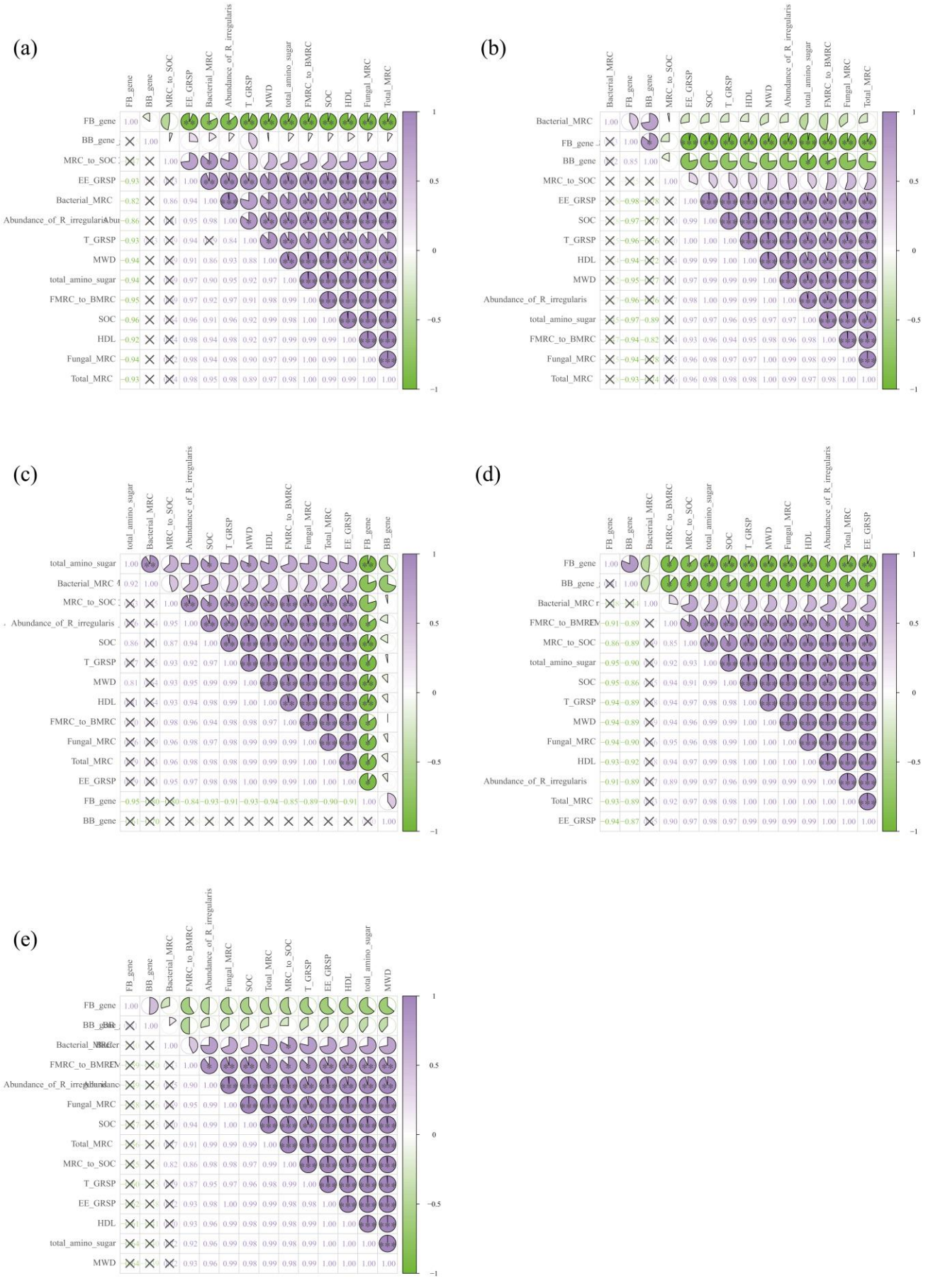

(a)
FB_gene
BB_gene
MRC_to_SOC
EE_GRSP
Bacterial_MRC
Abundance_of_R_irregularis
T_GRSP
MWD
total_amino_sugar
FMRC_to_BMRC
SOC
HDL
Fungal_MRC
Total_MRC
(b)
Bacterial_MRC
FB_gene
BB_gene
MRC_to_SOC
EE_GRSP
SOC
T_GRSP
HDL
MWD
Abundance_of_R_irregularis
total_amino_sugar
FMRC_to_BMRC
Fungal_MRC
Total_MRC
(c)
total_amino_sugar
Bacterial_MRC
MRC_to_SOC
Abundance_of_R_irregularis
SOC
T_GRSP
MWD
HDL
FMRC_to_BMRC
Fungal_MRC
Total_MRC
EE_GRSP
FB_gene
BB_gene
(d)
FB_gene
BB_gene
Bacterial_MRC
FMRC_to_BMRC
MRC_to_SOC
total_amino_sugar
SOC
T_GRSP
MWD
Fungal_MRC
HDL
Abundance_of_R_irregularis
Total_MRC
EE_GRSP
(e)
FB_gene
BB_gene
Bacterial_MRC
FMRC_to_BMRC
Abundance_of_R_irregularis
Fungal_MRC
SOC
Total_MRC
MRC_to_SOC
T_GRSP
EE_GRSP
HDL
total_amino_sugar
MWD

Figure S4. Pearson's correlations among microbial residues (amino sugars and MRCs), AMF-related physiochemical properties (abundance of *Rhizophagus irregularis*, HLD, t-GRSP, ee-GRSP) and soil organic carbon at each of the soil sampling depth.

*:$p<0.05$; **: $p<0.01$; ***: $p<0.001$.