## Figure Legends:

**Figure 1** Alpha-diversity of the bacterial and fungal communities for five groups of microbial samples.

a & b, representing Shannon diversity and Chao1 of the bacterial community; b & d, representing Shannon diversity and Chao1 of the fungal community. Significances between different groups were compared using Wilcoxon's test, with the results indicated on the top (*p*-value ≤ 0.05 = *, *p*-value ≤ 0.01 = **).

**Figure 2** Beta diversity of the microbial community using PCoA analysis with the weighted_Unifrac metric.

a, bacterial community; b, fungal community.

**Figure 3** Taxonomic differences of the bacterial community among four groups of samples. a, the top 10 phyla;

b, the top 10 families; c, relative abundances of the top 20 genera were compared between different groups.

**Figure 4** Taxonomic differences of the fungal community among four groups of samples.a, the top 10 phyla;

b, the top 10 families; c, relative abundances of the top 20 genera were compared between different groups.

**Figure 5** Functional prediction of microbial community between five groups. a, bacterial community; b, annotation of fungal community using mode; c, annotation of fungal community using Guild.

**Figure 6** Abundance of some representative soil beneficial bacteria (*p*-value ≤ 0.05 = *, *p*-value ≤ 0.01 = **).

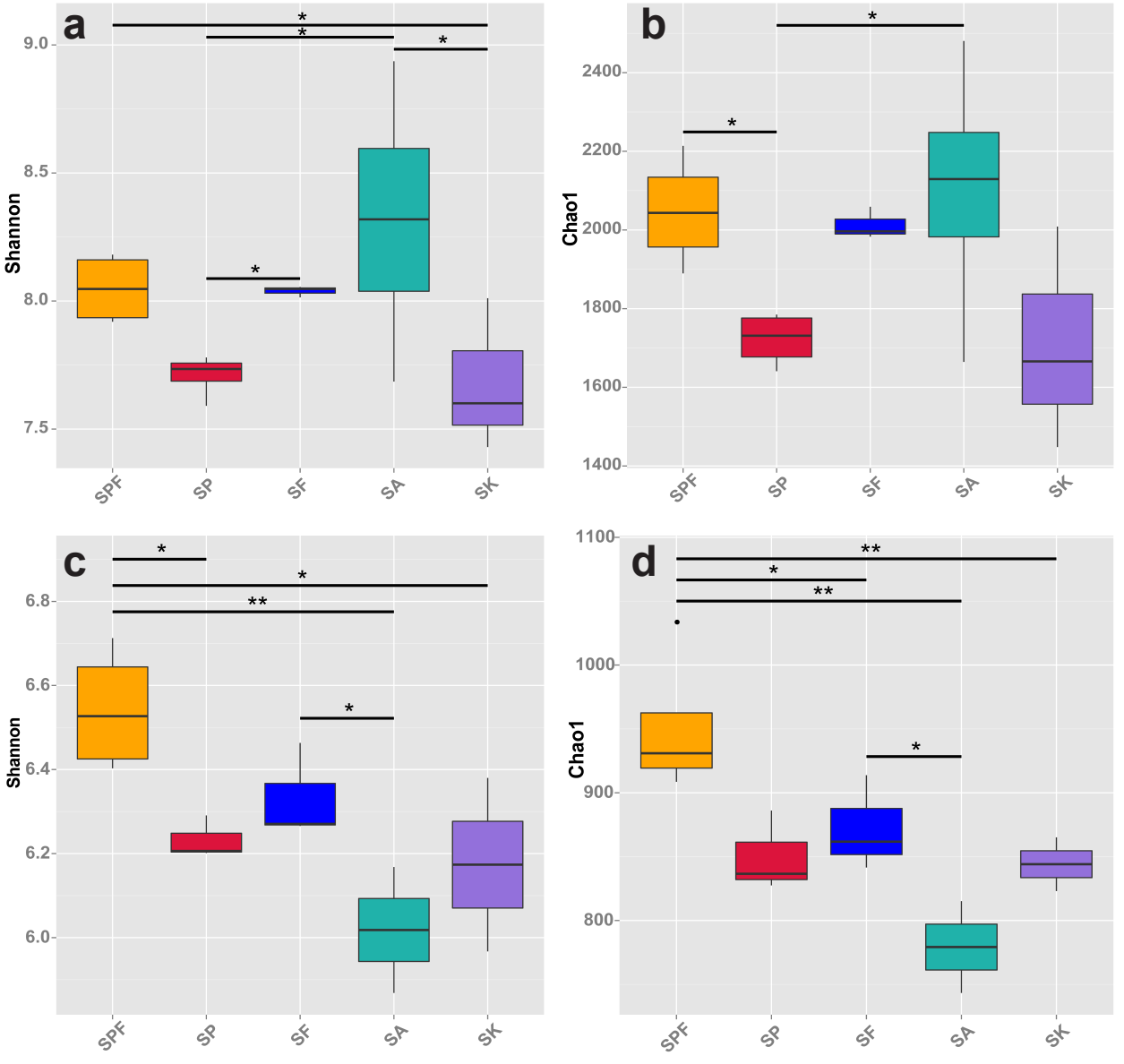



**Figure 1** Alpha-diversity of the bacterial and fungal communities for five groups of microbial samples. a & b, representing Shannon diversity and Chao1 of the bacterial community; b & d, representing Shannon diversity and Chao1 of the fungal community. Significances between different groups were compared using Wilcoxon's test, with the results indicated on the top (p-value ≤ 0.05 = *, p-value ≤ 0.01 = **).

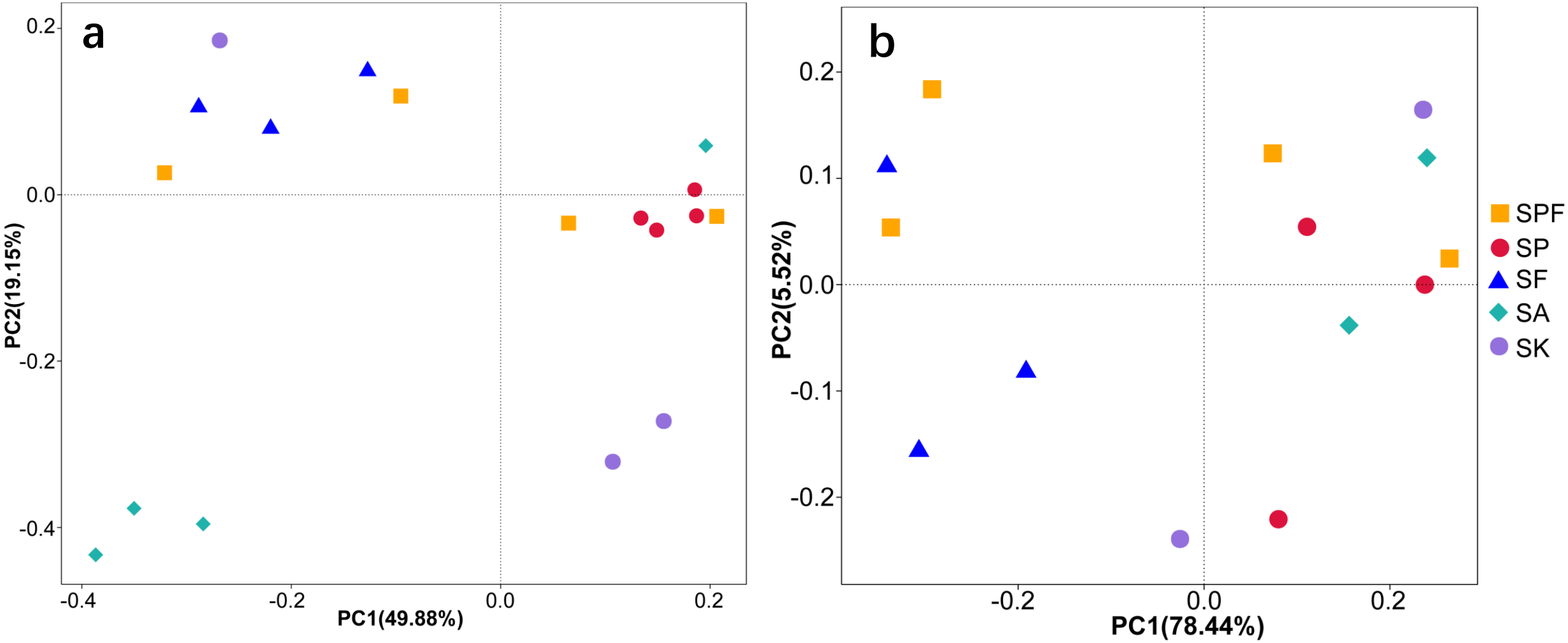



**Figure 2** Beta diversity of the microbial community using PCoA analysis with the weighted_Unifrac metric. **a**, bacterial community; **b**, fungal community.

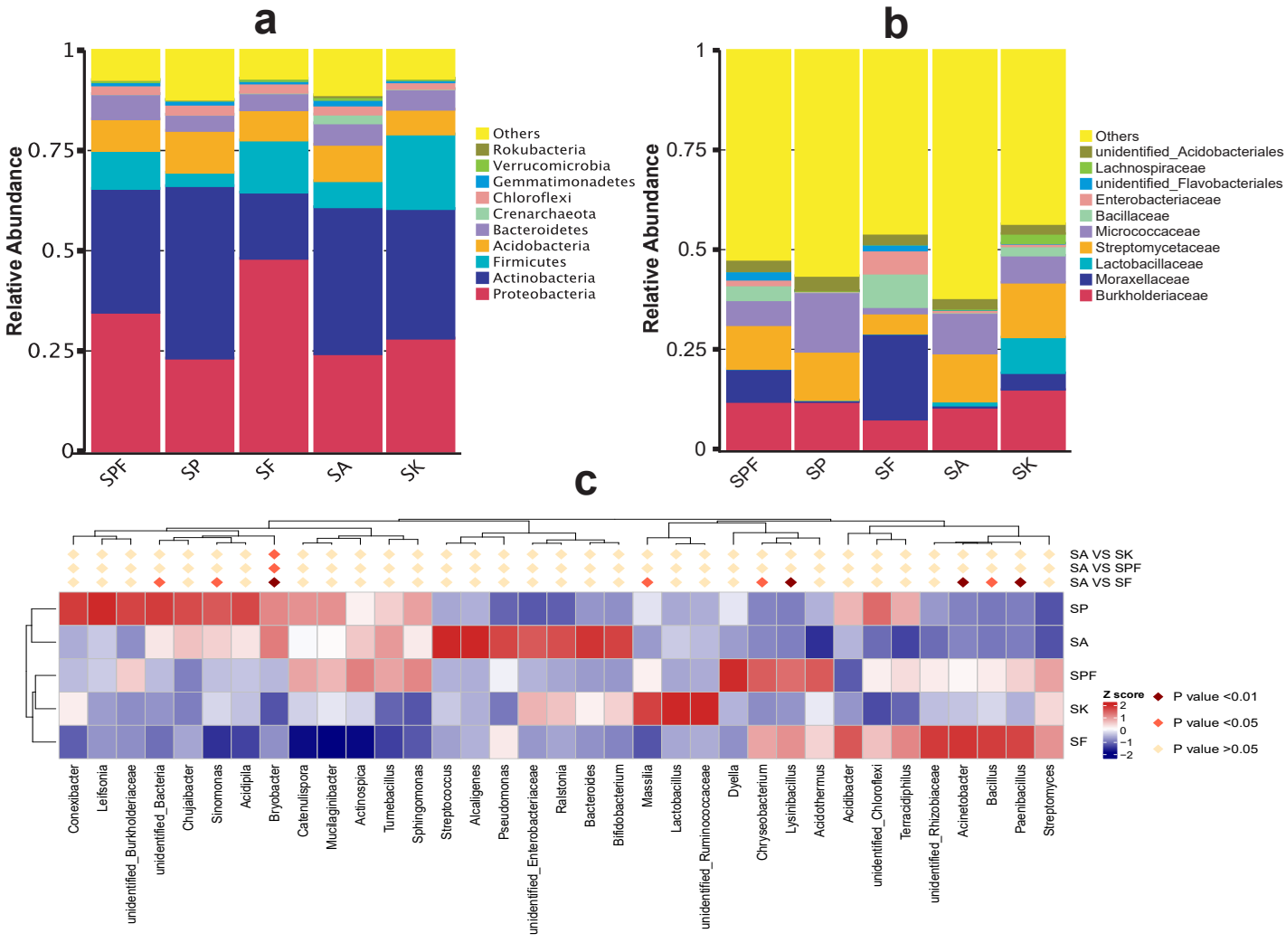



**Figure 3** Taxonomic differences of the bacterial community among five groups of samples. a, the top 10 phyla; b, the top 10 families; c, relative abundances of the top 20 genera were compared between different groups.

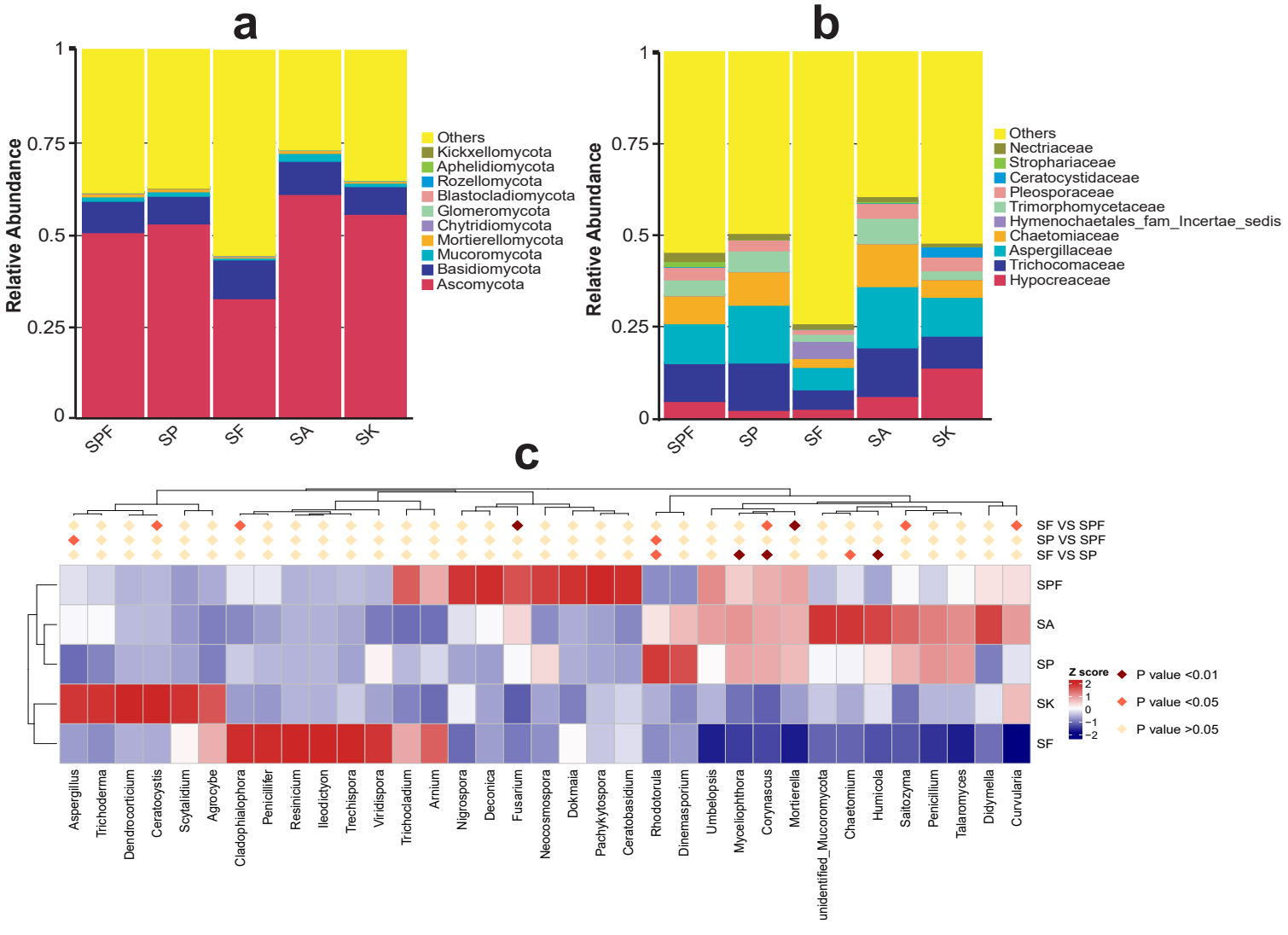



**Figure 4** Taxonomic differences of the fungal community among five groups of samples. a, the top 10 phyla; b, the top 10 families; c, relative abundances of the top 20 genera were compared between different groups.

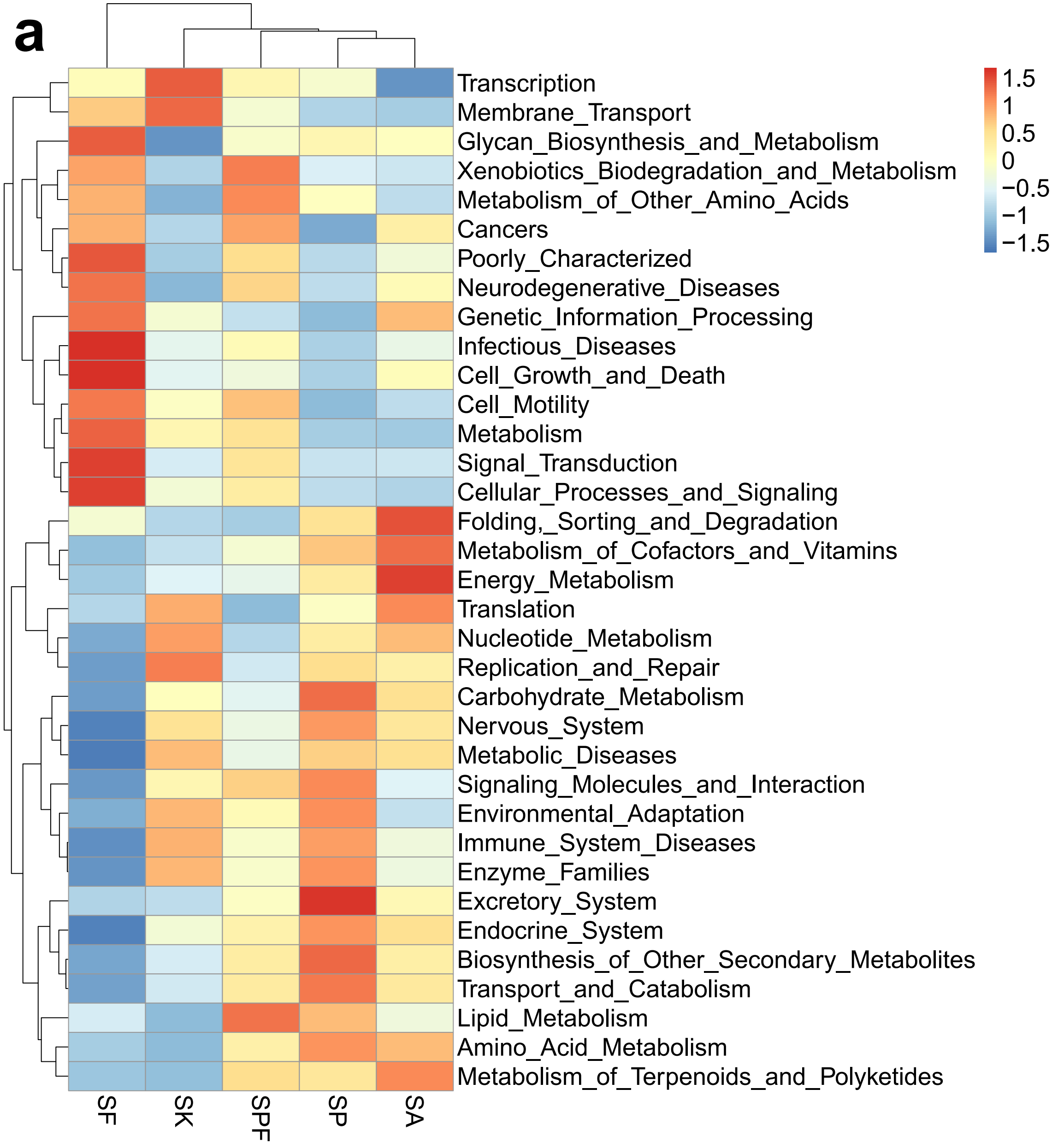
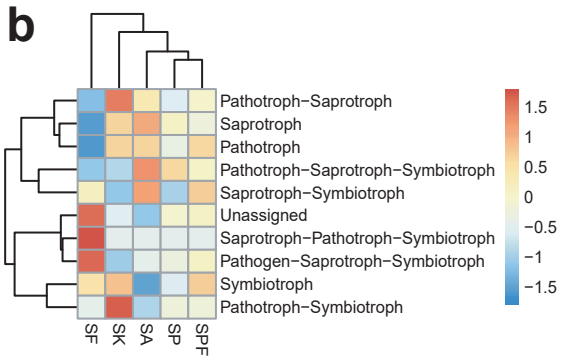



**Figure 5** Functional prediction of microbial community between five groups. a, bacterial community;



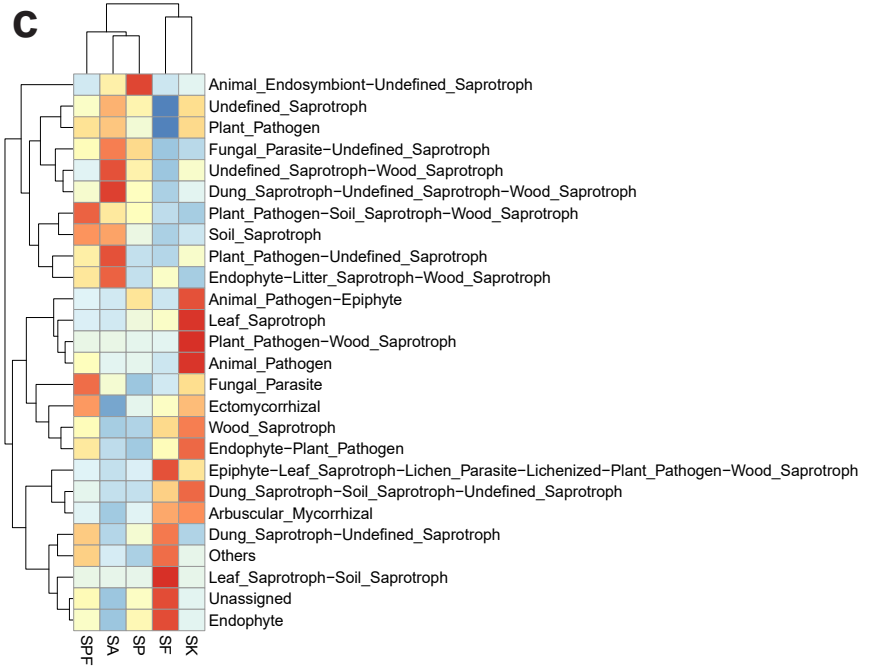




**Figure 5 (continued)** b, annotation of fungal community using mode; c, annotation of fungal community using Guild.

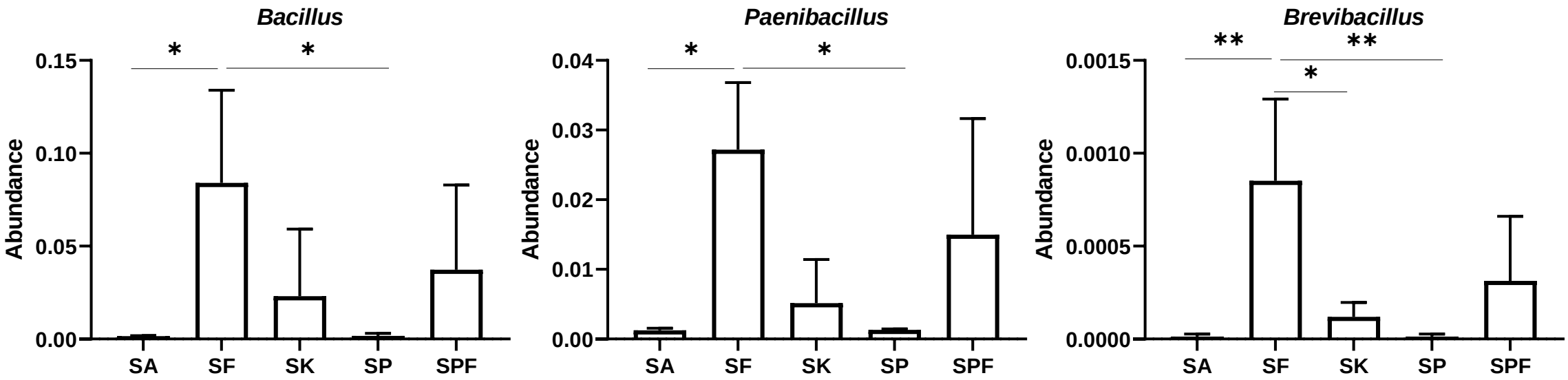



**Figure 6** Abundance of some representative soil beneficial bacteria (*p*-value ≤ 0.05 = *, *p*-value ≤ 0.01 = **).