

Figure S1 The relative abundance of *phoD*-harboring bacteria at the phylum level in different age of citrus orchards in the karst and non-karst regions. NF, natural forest soil; AL, abandoned land soil; Y5, 5-year citrus soil; Y10, 10-year citrus soil; Y15, 15-year citrus soil.

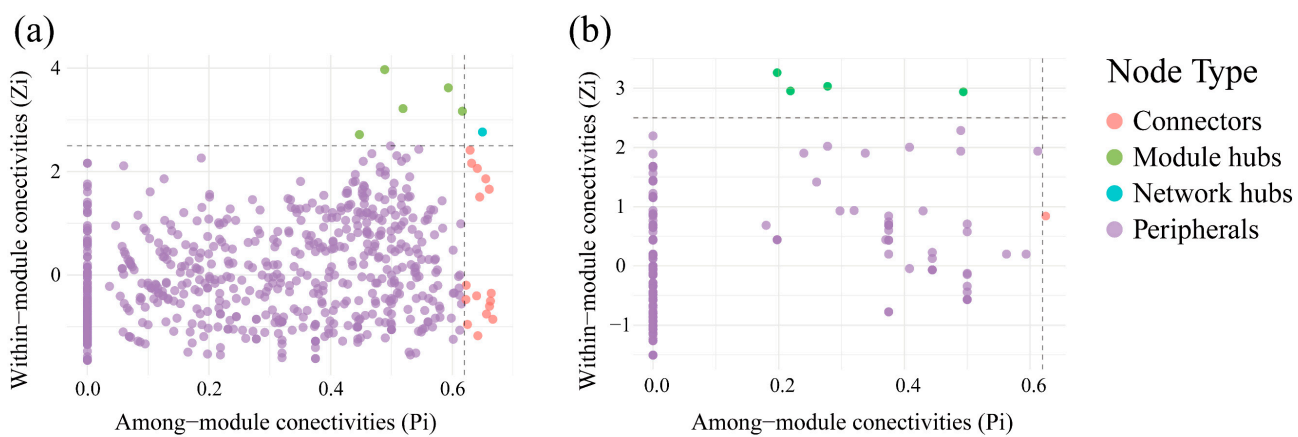


Figure S2 The within-modules connectivity ( $Z_i$ ) and between-modules connectivity ( $P_i$ ) ( $Z_i$ - $P_i$ ) plot display keystone species of *phoD* community in the treatments of the karst (a) and non-karst (b). Module hubs were identified as  $Z_i > 2.5$ ,  $P_i < 0.62$ ; connectors were identified as  $Z_i < 2.5$ ,  $P_i > 0.62$ ; network hubs were identified as  $Z_i \geq 2.5$ ,  $P_i > 0.62$ .

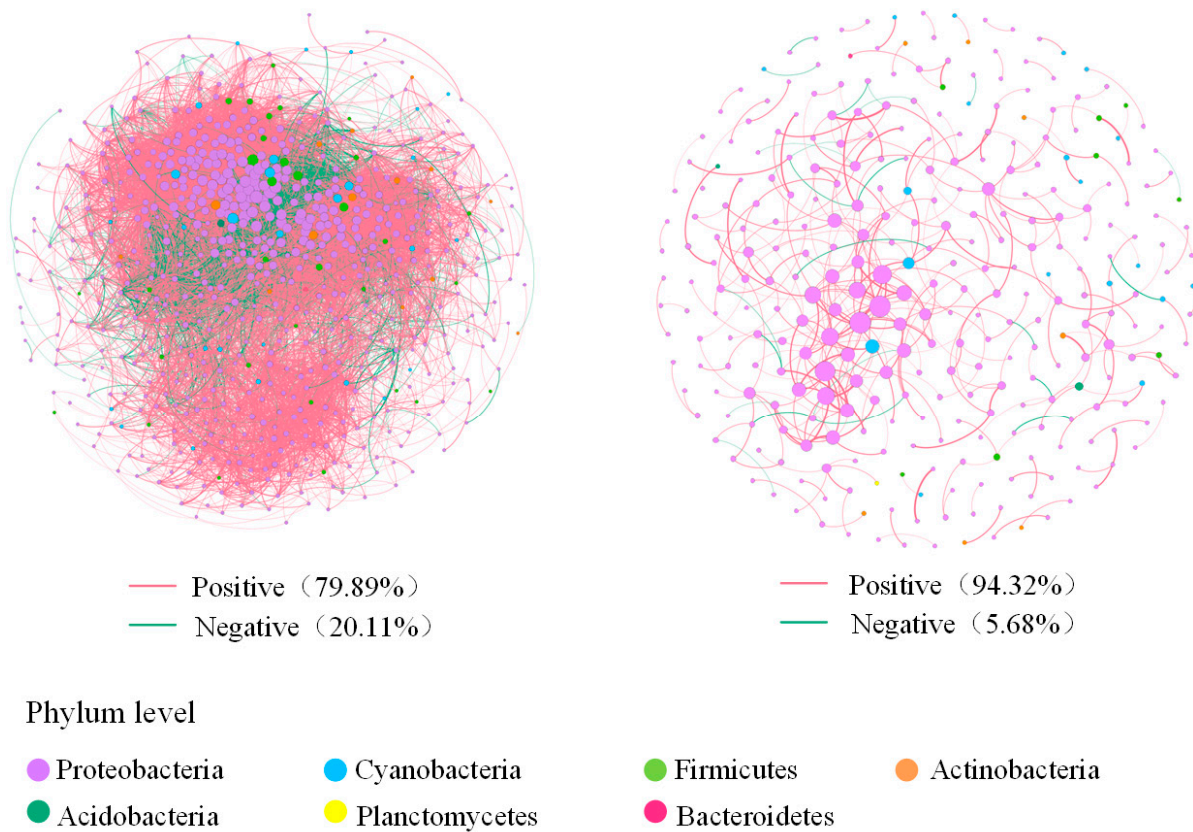


Figure S3 Co-occurrence networks of the soil *phoD*-harboring bacterial community at the phylum level in the karst (a) and non-karst (b) regions. A red line indicates a positive relation, and a green line indicates a negative relation.

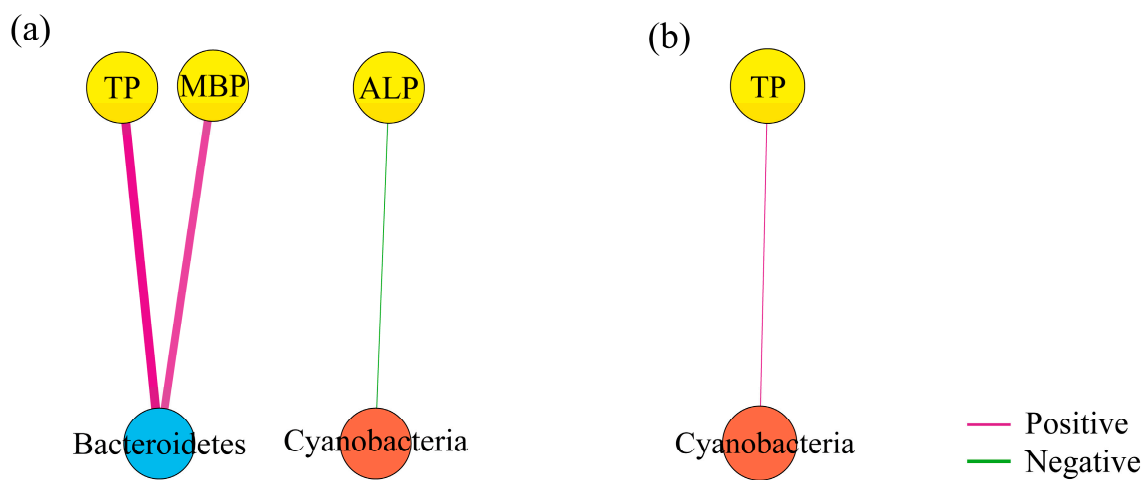


Figure S4 Correlation network between the *phoD*-harboring bacteria at the phylum level and the soil P fractions and phosphatase activities. A green edge represents a negative interaction between two nodes, and a red edge represents a positive interaction between two nodes. (a) Karst; (b) non-karst.

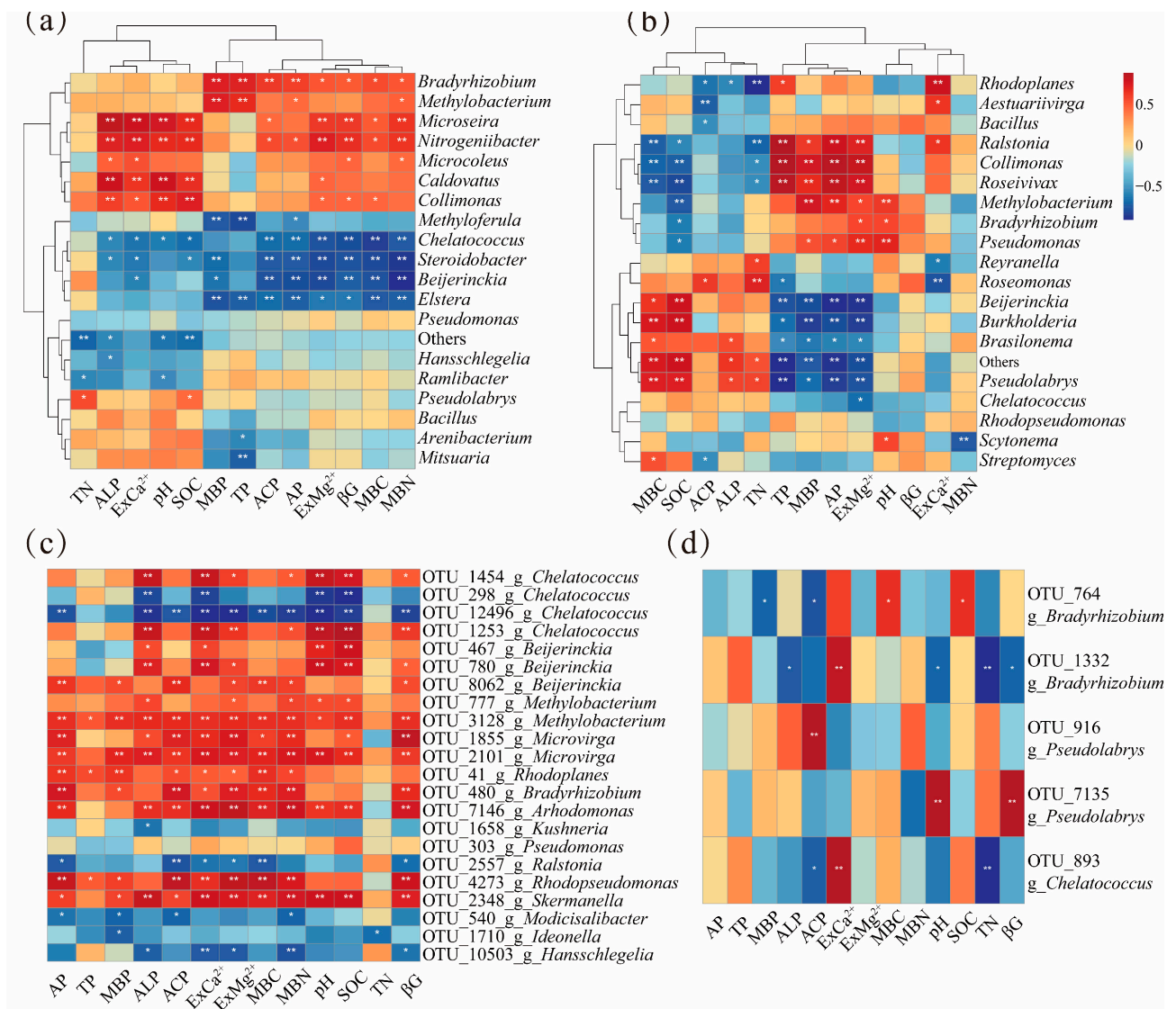


Figure S5 Relationship between the relative abundance of *phoD*-harboring bacteria at the genus level (top 19) and physicochemical parameters in the karst (a) and non-karst (b), as well as relationships between the microbial keystone taxa and physicochemical parameters in the karst (c) and non-karst (d). \*\* $p < 0.01$ ; \* $p < 0.05$ .