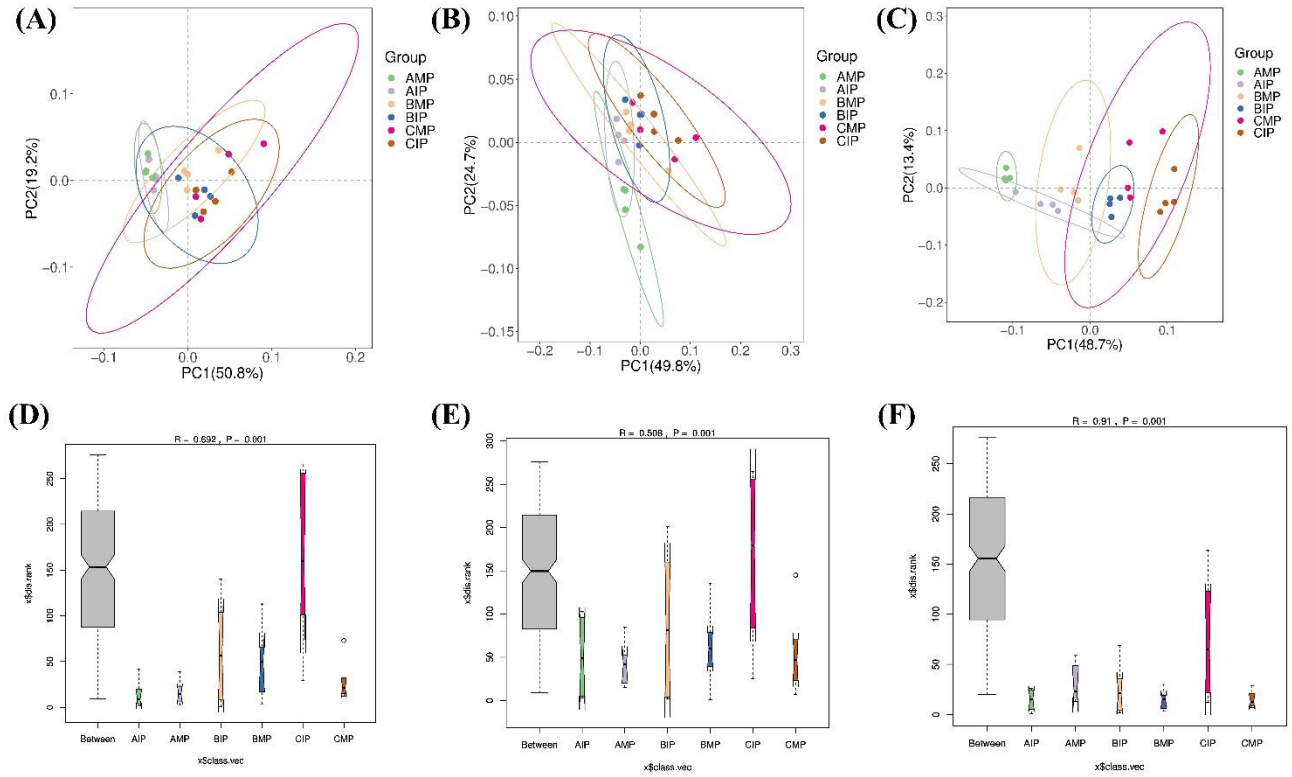
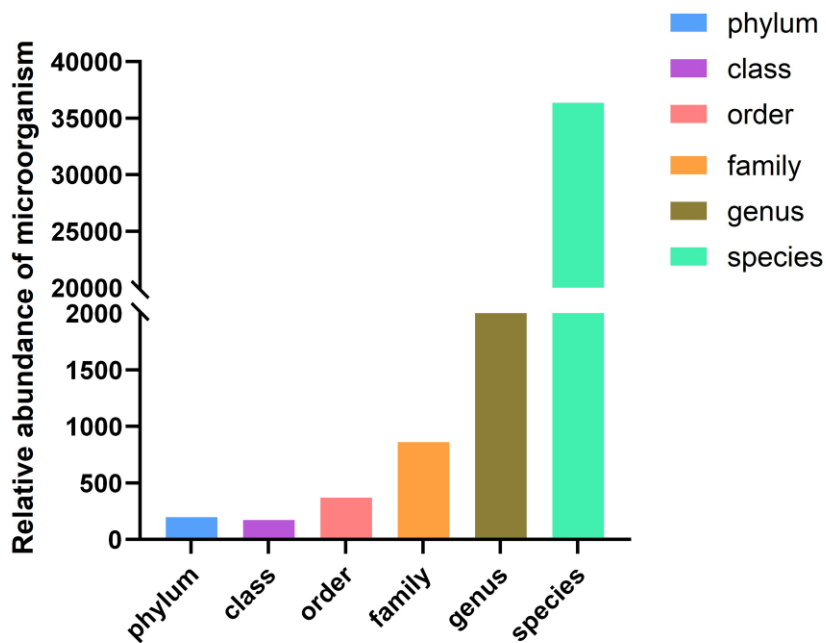


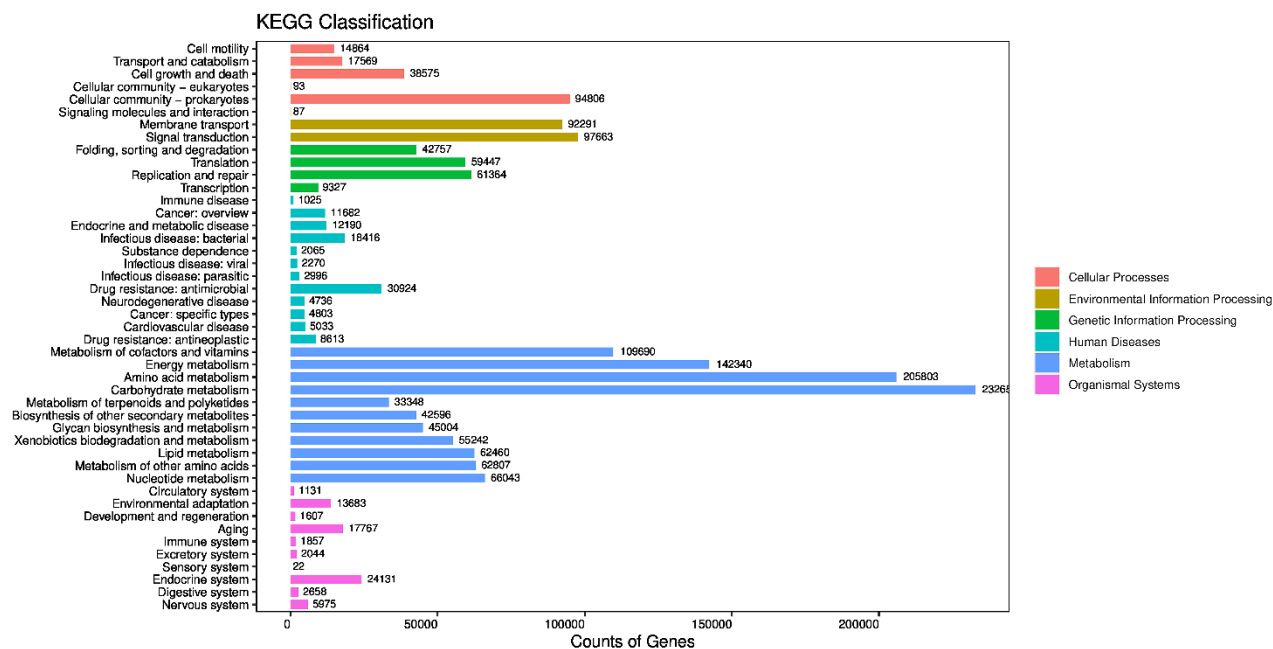
**Figure S1.** Analyses of microbial community alpha diversity in rhizosphere soil of peanuts. AMP, monocropping peanuts with low nitrogen levels; BMP, monocropping peanuts with intermediate nitrogen levels; CMP, monocropping peanuts with high nitrogen levels; AIP, intercropping peanuts with low nitrogen levels; BIP, intercropping peanuts with intermediate nitrogen levels; CIP, intercropping peanuts with high nitrogen levels.



**Figure S2.** Analyses of beta diversity for microbial communities at the phylum, genus, and species levels. AMP, monocropping peanuts with low nitrogen levels; BMP, monocropping peanuts with intermediate nitrogen levels; CMP, monocropping peanuts with high nitrogen levels; AIP, intercropping peanuts with low nitrogen levels; BIP, intercropping peanuts with intermediate nitrogen levels; CIP, intercropping peanuts with high nitrogen levels.



**Figure S3.** Relative abundance of microorganisms in rhizosphere soil under different classification levels.



**Figure S4.** Statistics on the number of annotated genes in the KEGG database.