

Supplementary Figures

Intraspecific Comparative Analysis Reveals Genomic Variation of *Didymella arachidicola* and Pathogenicity Factors Potentially Related to Lesion Phenotype

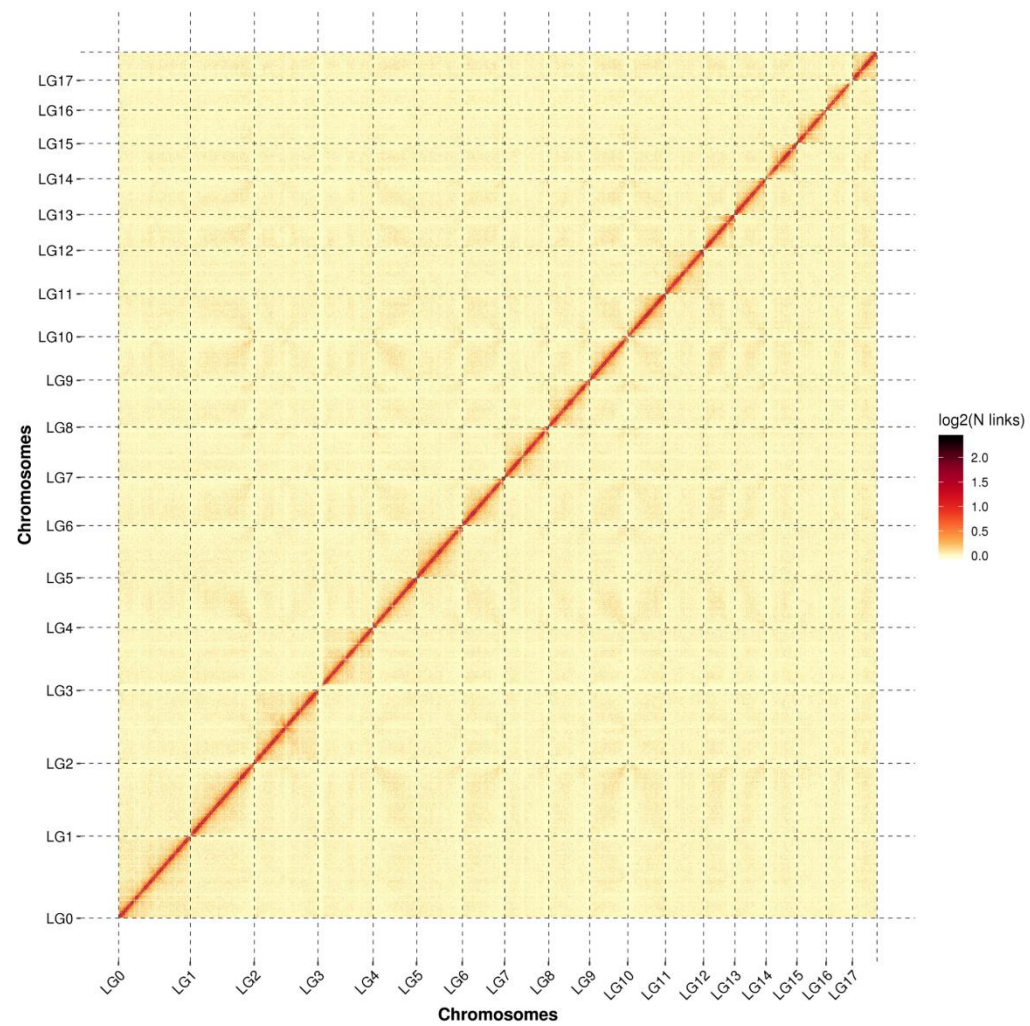
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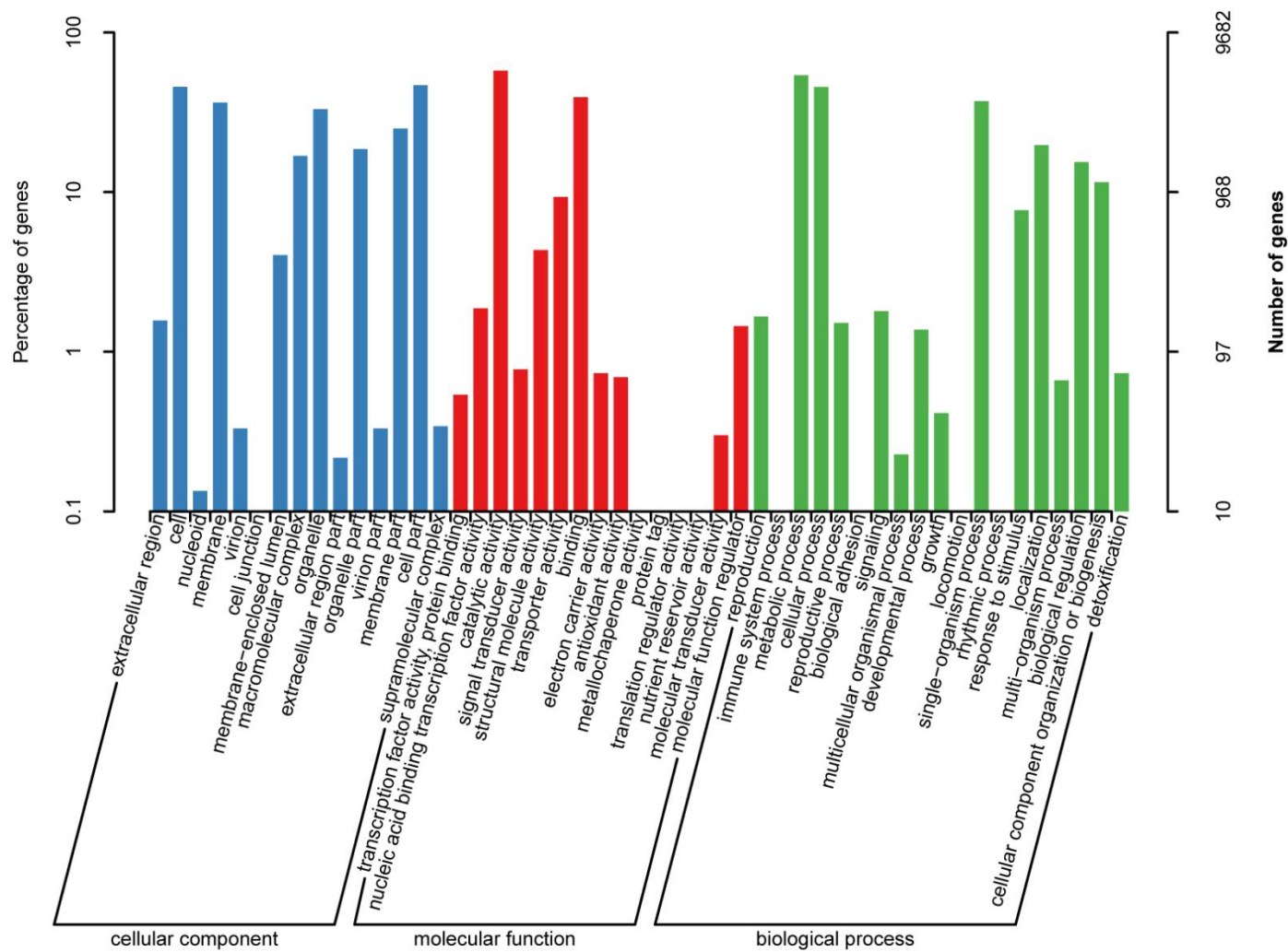
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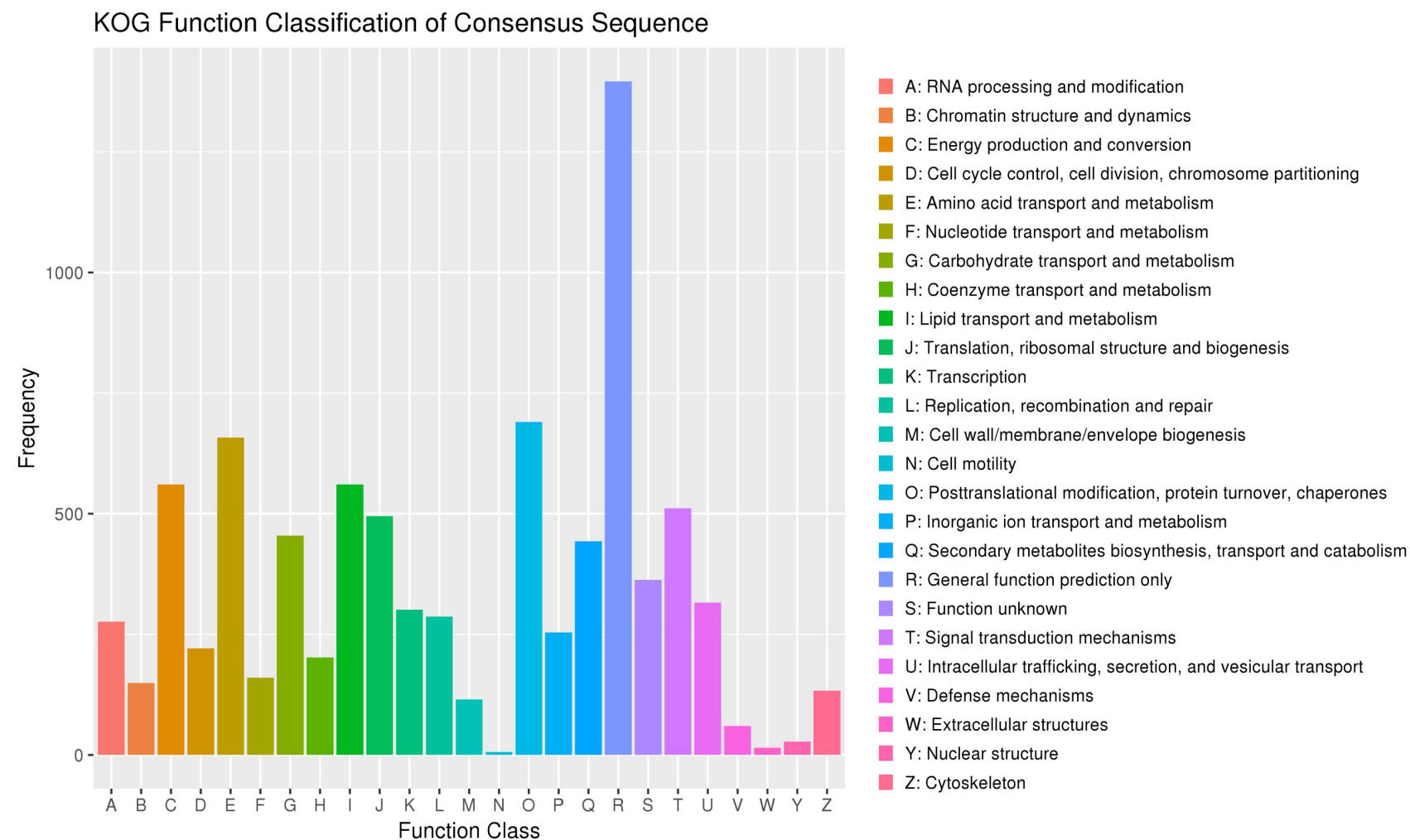
Supplementary Figure S1. Sampling sites of the 41 *D. arachidicola* isolates used in this study in China. The map was modified based on map GS(2019)1673.



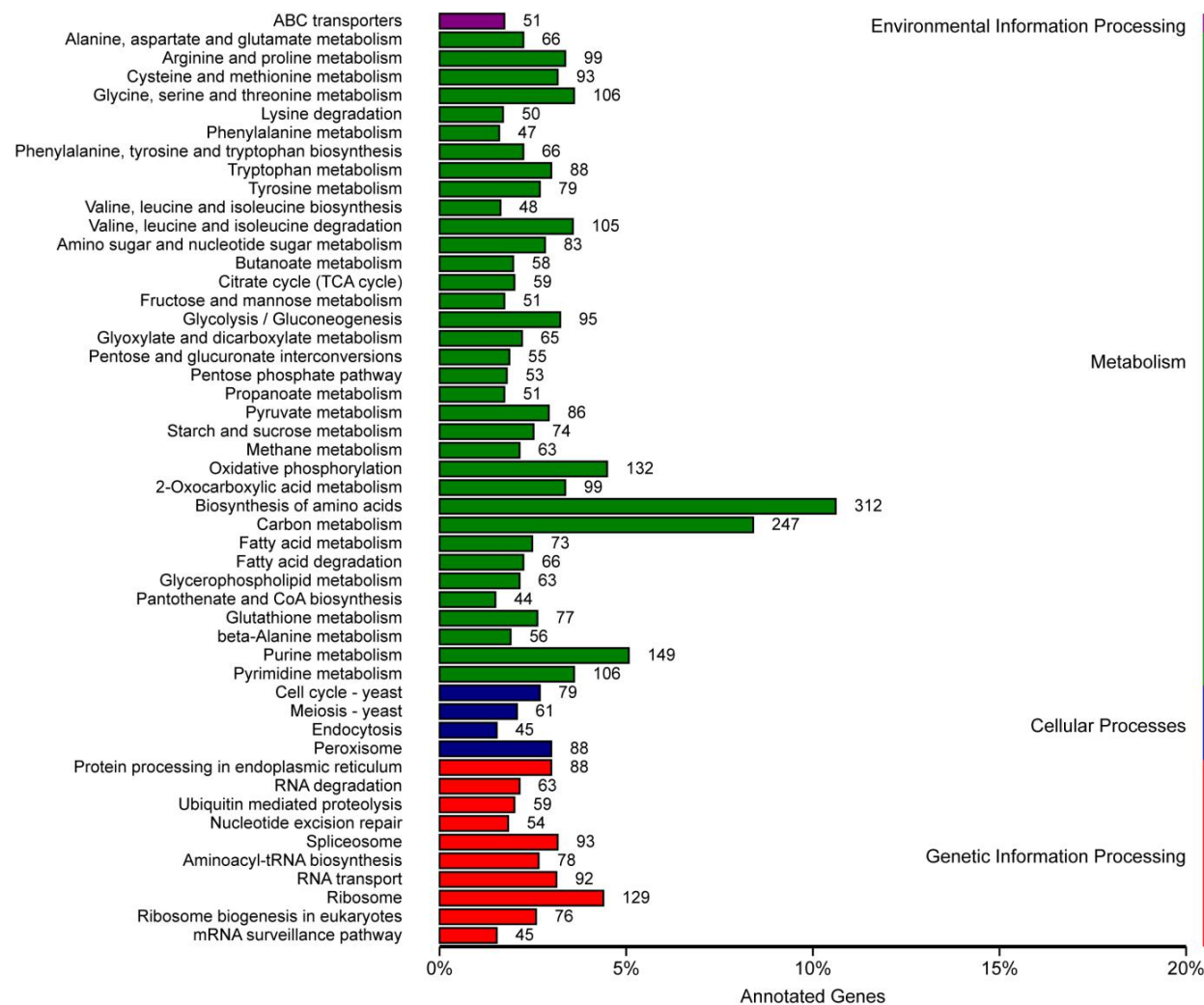
Supplementary Figure S2. Heat map of chromosomal interaction based on Hi-C assembly. “LG” means Lachesis group.



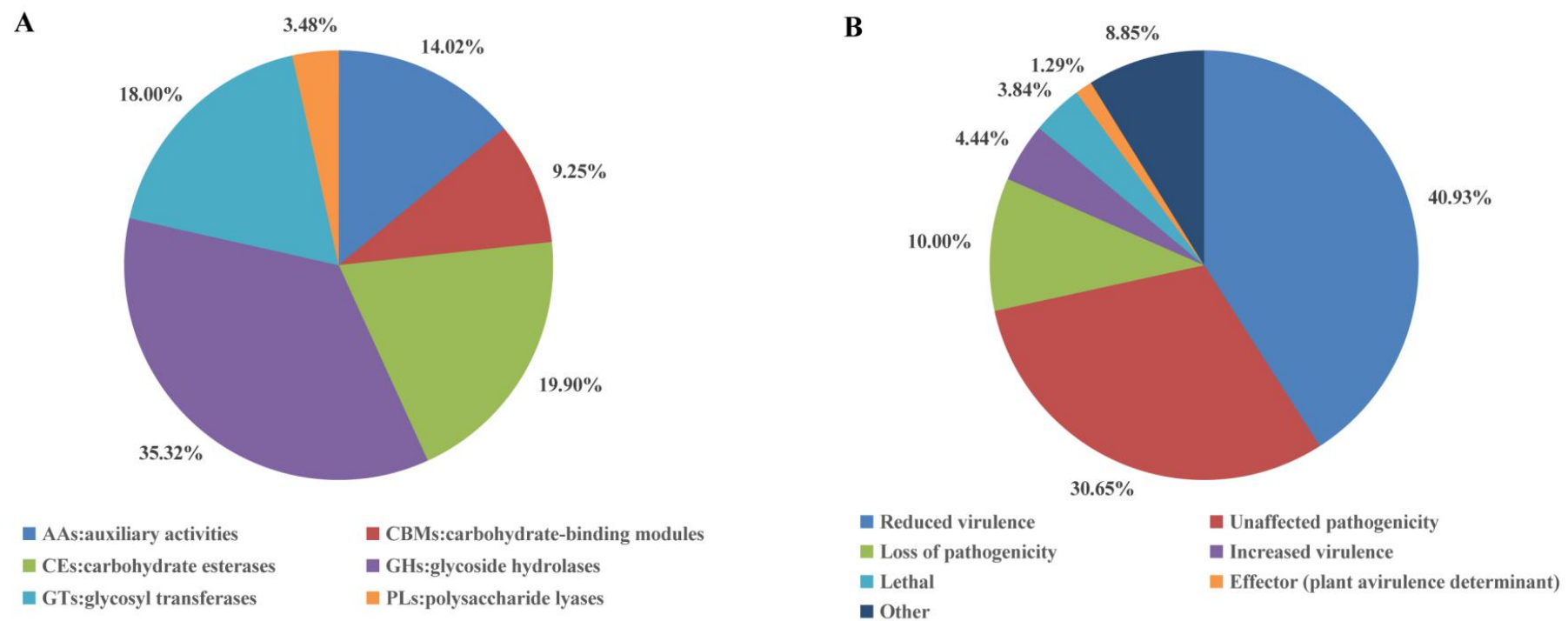
Supplementary Figure S3. Category statistics for GO annotation of *D. arachidicola* genes.



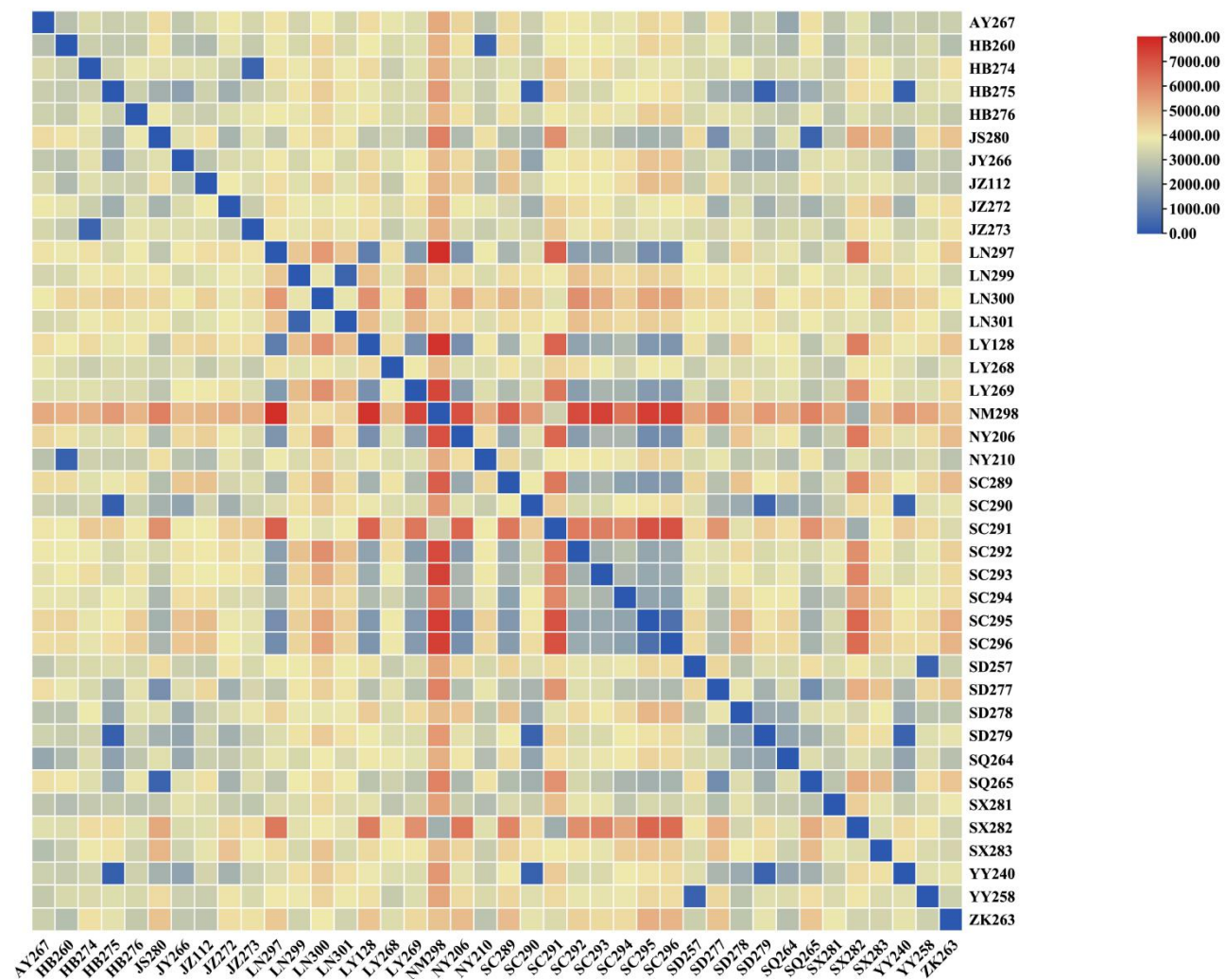
Supplementary Figure S4. Category statistics for KOG annotation of *D. arachidicola* genes.



Supplementary Figure S5. Category statistics for KEGG annotation of *D. arachidicola* genes.



Supplementary Figure S7. Percentage of genes belonged to different categories. (A) Percentage of genes that have hits in different families of CAZyme. (B) Percentage of genes with different PHI phenotypes.



Supplementary Figure S8. Intraspecific comparison of variations of *D. arachidicola* isolates. Results visualized by TBtools v1.098769.