

Description of Additional Supplementary Files

Supplementary Data Legends:

Supplementary Data 1: General statistics for the root-associated microbiome sequencing data of all genotypes

Supplementary Data 2: Filtered amplicon sequence variants (ASVs) table from all samples in present study

Supplementary Data 3: Marker sequences and taxonomic information of all isolates

Supplementary Data 4: Differentially expressed genes in plant roots after inoculation with different Rhizobiaceae strains. Differential analysis with a two-sided test was used for the statistical analysis (DeSeq2, adjusted $P < 0.05$).

Supplementary Data 5: Gene cluster analysis of DEGs on the basis of the similarity expression

Supplementary Data 6: Raw abundance values of root metabolites of different genotypes in negative ESI modes.

Supplementary Data 7: Raw abundance values of root metabolites of different genotypes in positive ESI modes.

Supplementary Data 8: Normalized abundance values of root metabolites detected in different genotypes.

Supplementary Data 9: Differential abundant metabolites between *gl2* mutant and Col-0

Supplementary Data 10: Differential abundant metabolites between *rs12 rs14* mutant and Col-0