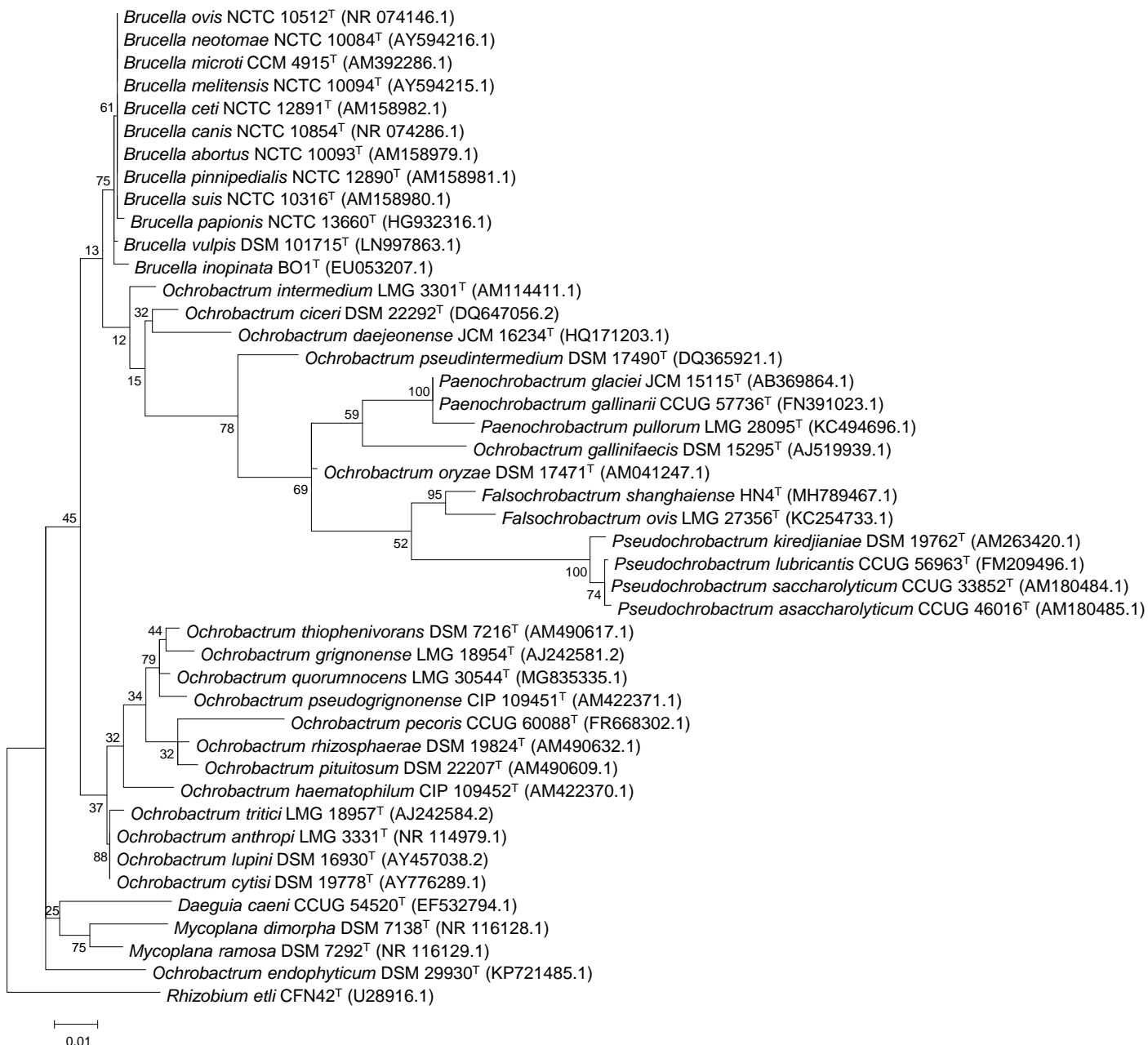
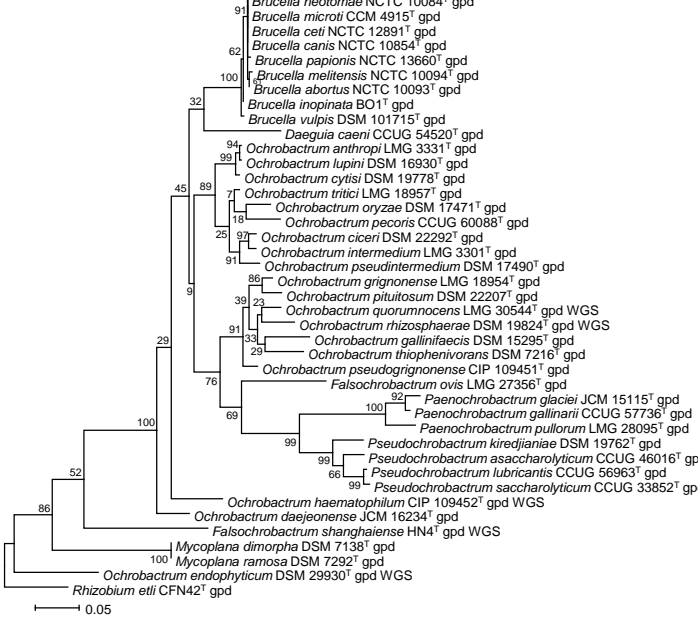


# Supplementary Figure S2

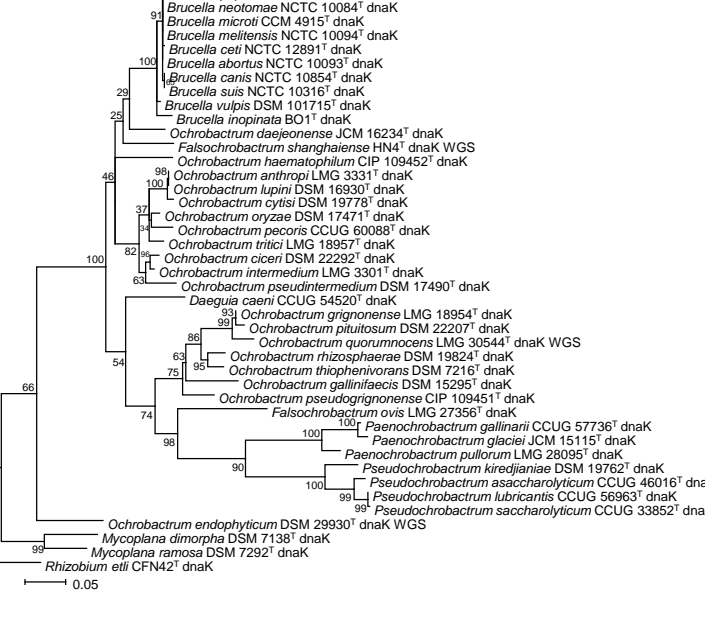


**Figure S2.1** Phylogenetic relationship between type strains of the family *Brucellaceae* (n=43), based on analysis of 16 rRNA sequence. The evolutionary history was inferred using the maximum likelihood method, based on the general time reversible model. Node labels give percentage bootstrap support. The scale bar shows the number of base substitutions per site. *Rhizobium etli* (CFN42<sup>T</sup>) was used to root the phylogenetic trees.

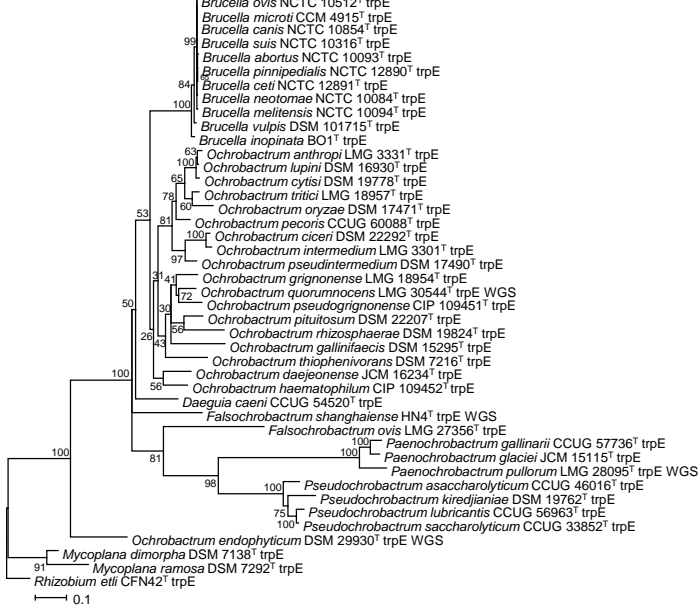
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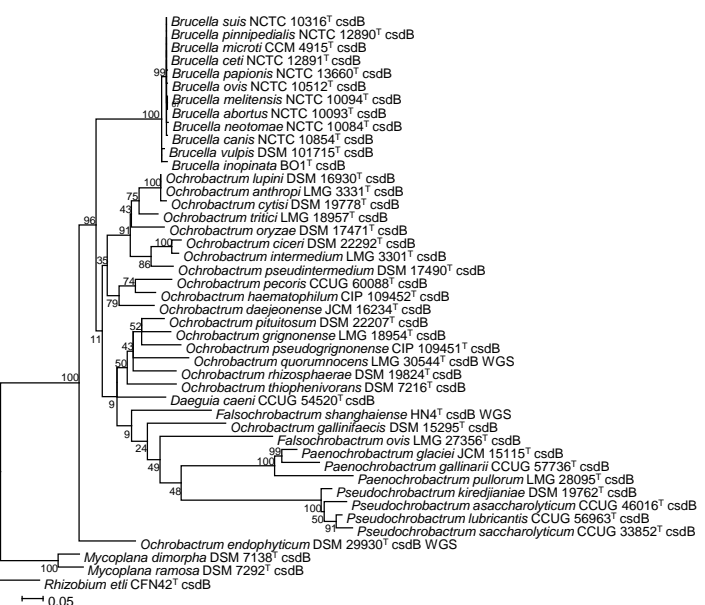
**dnaK**



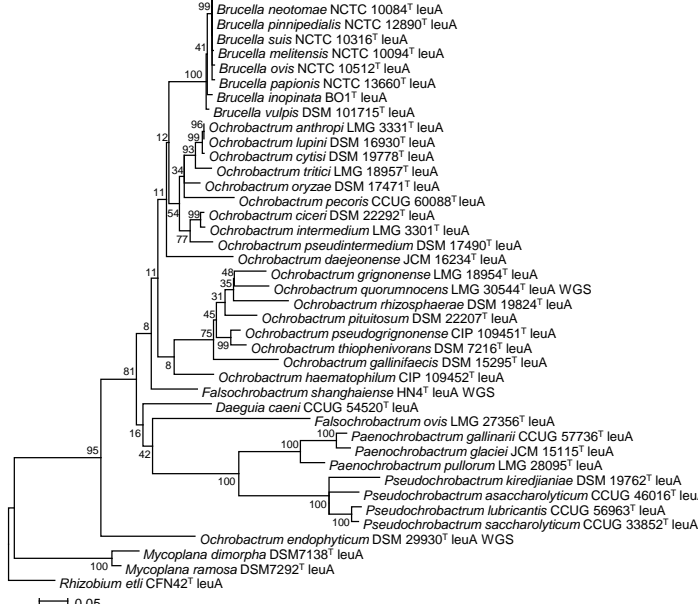
**trpE**



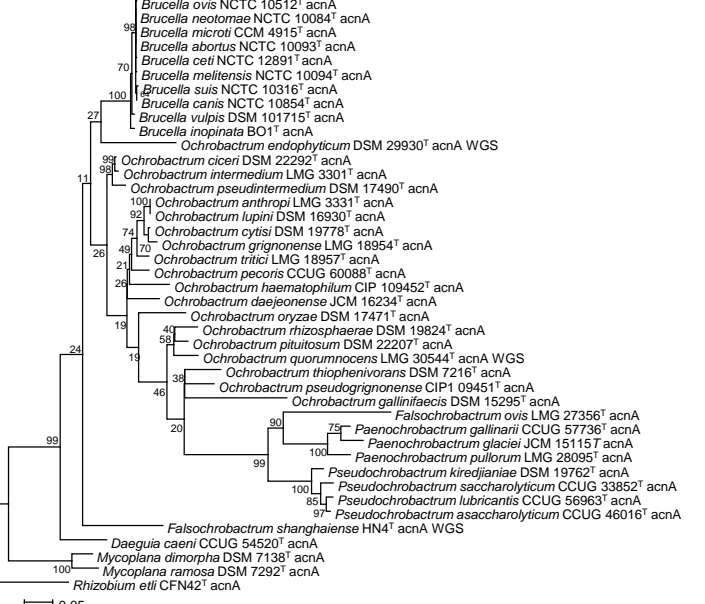
**csdB**



**leuA**



**acnA**



**Figure S2.2** Phylogenetic relationship between type strains of the family *Brucellaceae* (n=43), based on analysis of individual MLSA loci. The evolutionary history was inferred using the maximum likelihood method, based on the GTR model. Node labels give percentage bootstrap support. The scale bar shows the number of base substitutions per site. *Rhizobium etli* (CFN42<sup>T</sup>) was used as root the phylogenetic trees. Sequences retrieved from WGS data are annotated (WGS).