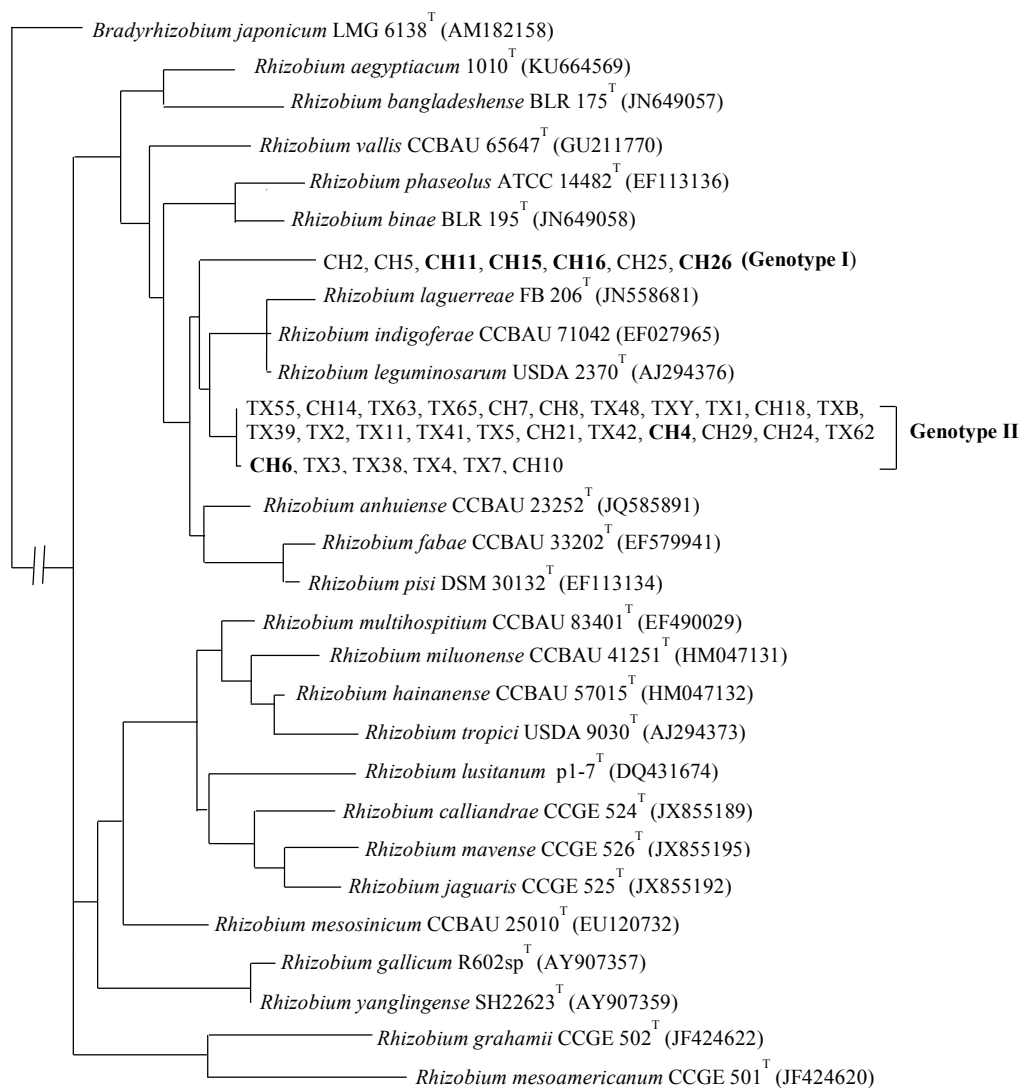
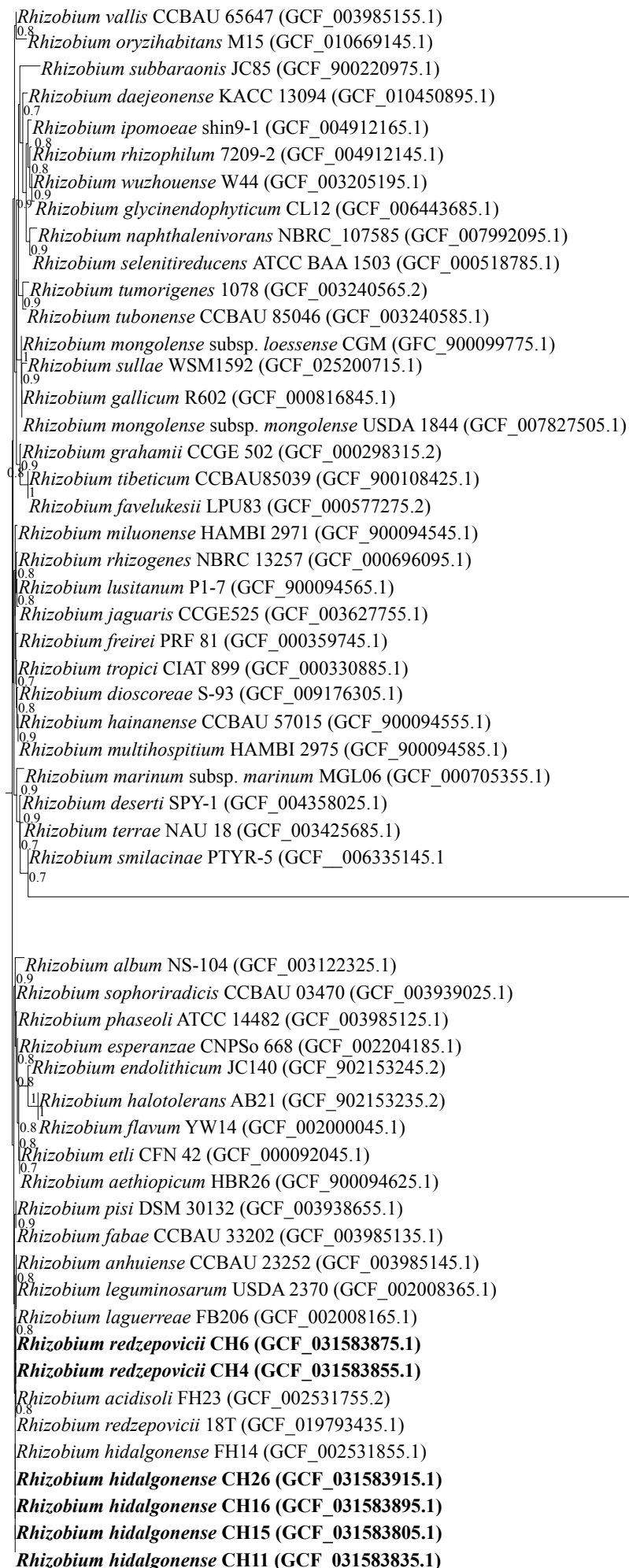




**Fig. S1A**

0.05



**Fig. S1**

Maximum likelihood phylogenetic tree of the *recA* gene. A. Phylogeny based on gene sequence amplified by PCR for all the isolates, in which *Bradyrhizobium japonicum* MLG 6138 was used as outgroup. B. Phylogeny based on aminoacidic sequences of *RecA* extracted from the genome sequences for the reference strains and type strains of *Rhizobium* species, in which *Klebsiella michiganensis* THO-011, *K. grimontii* 4928STDY7071328 and *K. variicola* LEMB11 were used as outgroups. The tree reconstruction was done using the LG + R model of amino acid substitution with a Lk value of -3243 under the Akaike Information Criteria (AIC). The bold names show the strains of this study. The numbers indicate the aLTR SH-like statistic support value of the branch, and the bar represents substitutions per nucleotide or amino acid position.

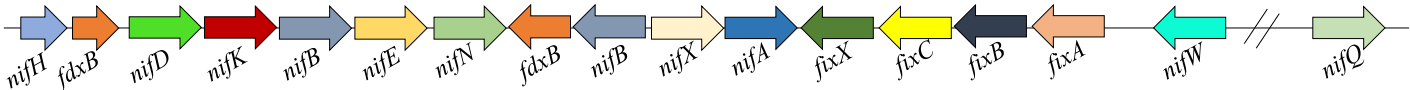
*Klebsiella grimontii* 4928STDY7071328 (GCF\_902164675.1)

*Klebsiella michiganensis* THO-011 (GCF\_015139575.1)

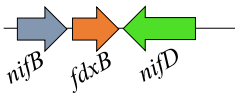
*Klebsiella variicola* LEMB11 (GCF\_009648975.1)

a) *nif* and *fix* genes of *Rhizobium hidalgonense* strains

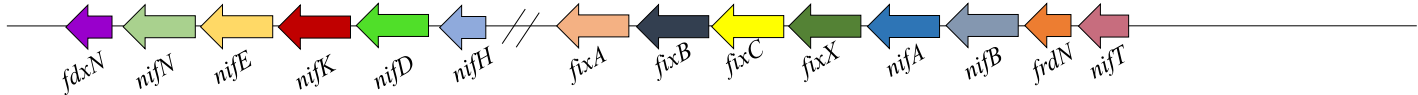
*Rhizobium hidalgonense* FH14



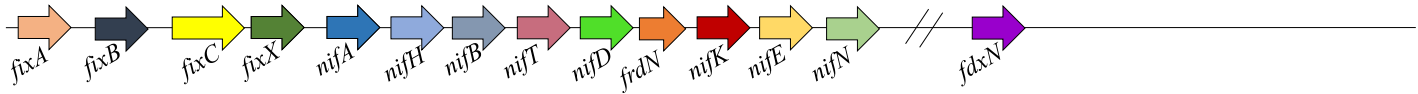
*Rhizobium hidalgonense* CH11



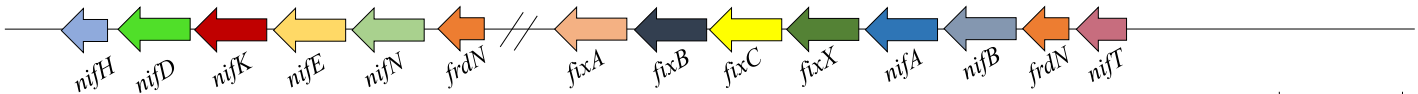
*Rhizobium hidalgonense* CH15



*Rhizobium hidalgonense* CH16

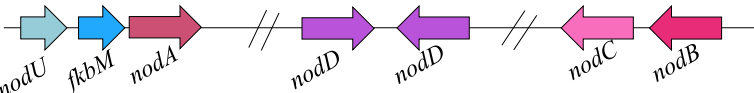


*Rhizobium hidalgonense* CH26

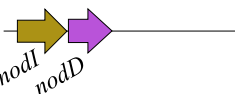


b) *nod* genes of *Rhizobium hidalgonense* strains

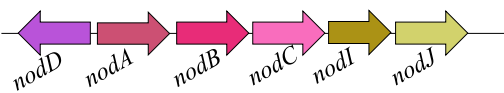
*Rhizobium hidalgonense* FH14



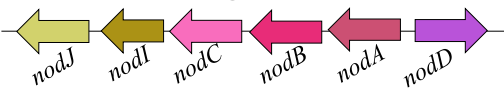
*Rhizobium hidalgonense* CH11



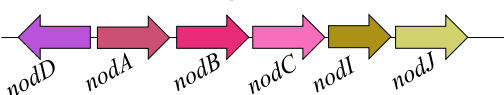
*Rhizobium hidalgonense* CH15



*Rhizobium hidalgonense* CH16

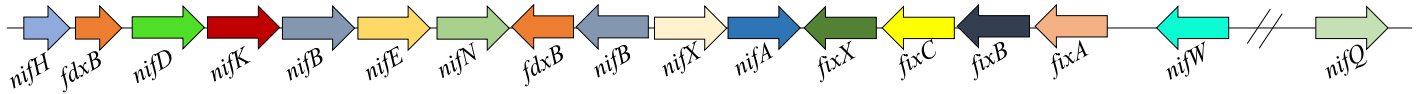


*Rhizobium hidalgonense* CH26

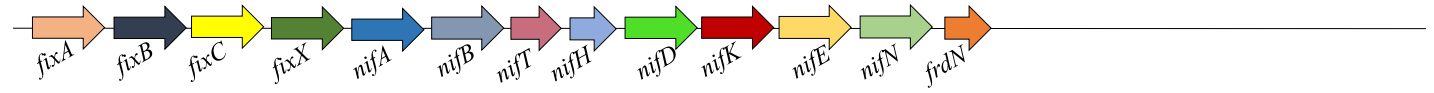


c) *nif* and *fix* genes of *Rhizobium redzepovicii* species

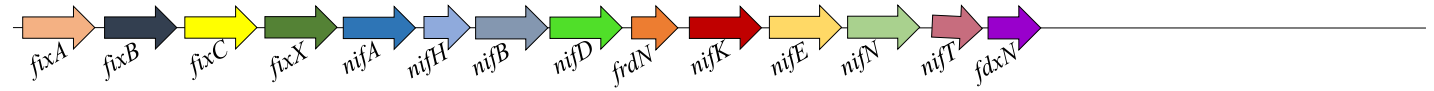
*Rhizobium redzepovicii* 18T



*Rhizobium redzepovicii* CH4



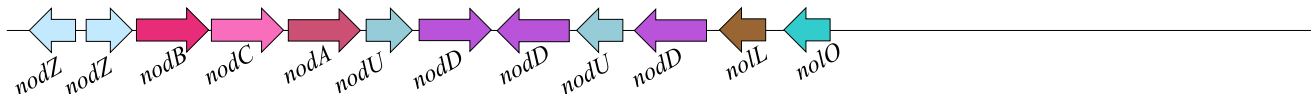
*Rhizobium redzepovicii* CH6



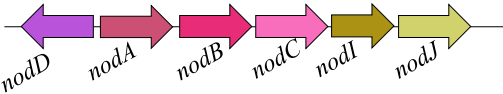
1 Kb

d) *nod* genes of *Rhizobium redzepovicii* strains

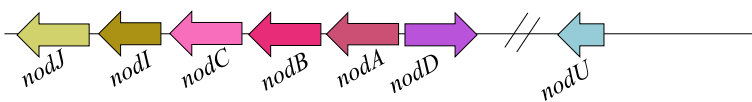
*Rhizobium redzepovicii* 18T



*Rhizobium redzepovicii* CH4



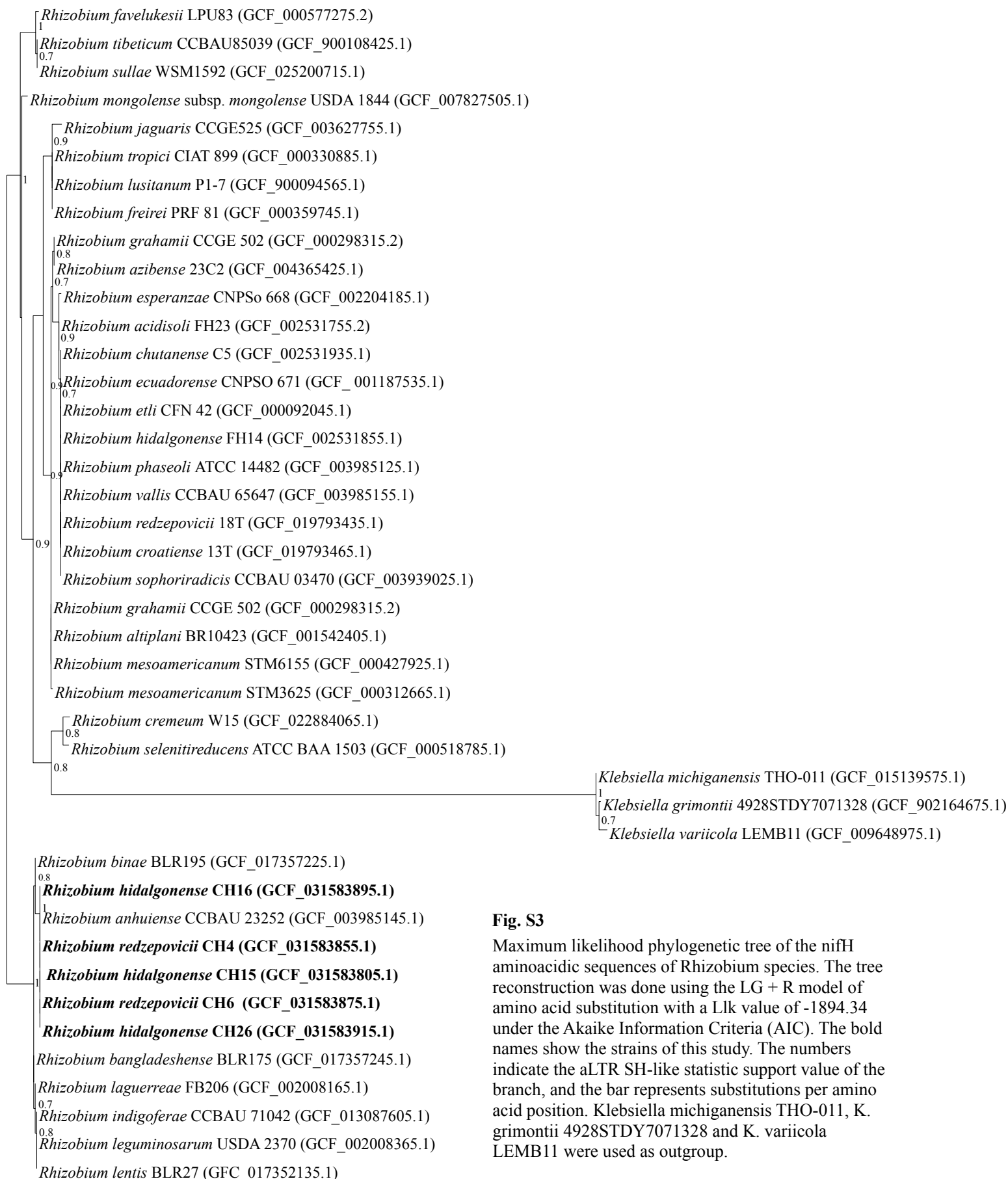
*Rhizobium redzepovicii* CH6



1 Kb

**Fig. S2**

Genetic organization of the nitrogen fixation and nodulation related genes in the genome of the analyzed *Rhizobium* species. a) nitrogen fixation and b) nodulation related genes of the *Rhizobium hidalgense* CH11, CH15, CH16 and CH26 strains compared to the *R. hidalgense* FH14 type strain. c) nitrogen fixation and d) nodulation related genes of the *Rhizobium redzepovicii* CH4 and CH6 strains compared to *R. redzepovicii* 18T type strain.



**Fig. S3**

Maximum likelihood phylogenetic tree of the *nifH* aminoacidic sequences of *Rhizobium* species. The tree reconstruction was done using the LG + R model of amino acid substitution with a Lk value of -1894.34 under the Akaike Information Criteria (AIC). The bold names show the strains of this study. The numbers indicate the aLTR SH-like statistic support value of the branch, and the bar represents substitutions per amino acid position. *Klebsiella michiganensis* THO-011, *K. grimontii* 4928STDY7071328 and *K. variicola* LEMB11 were used as outgroup.