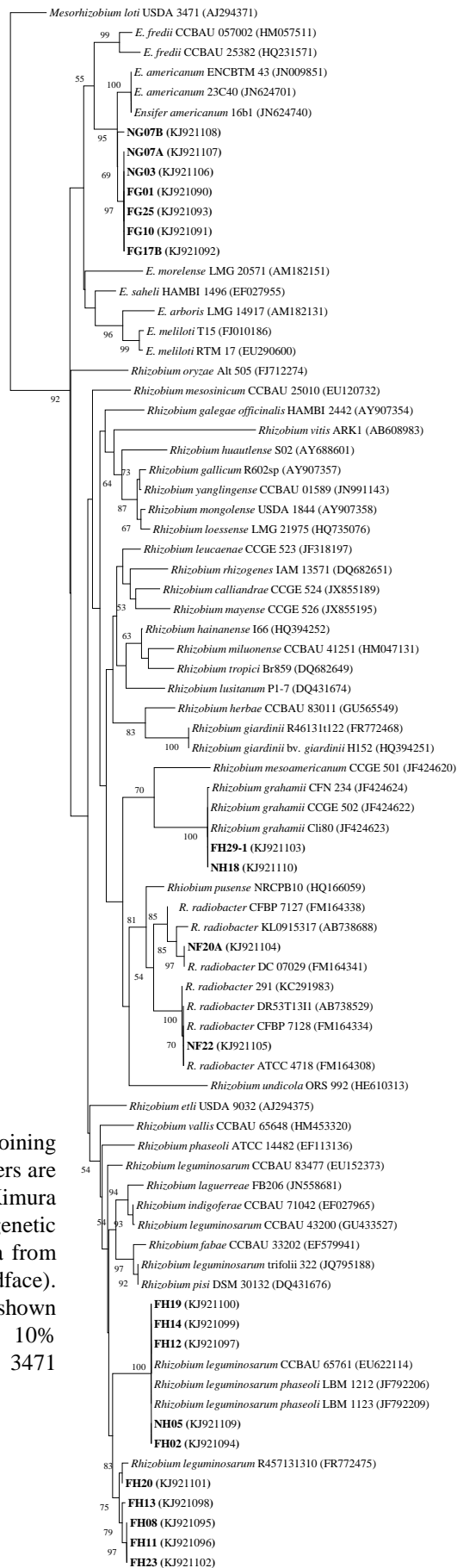


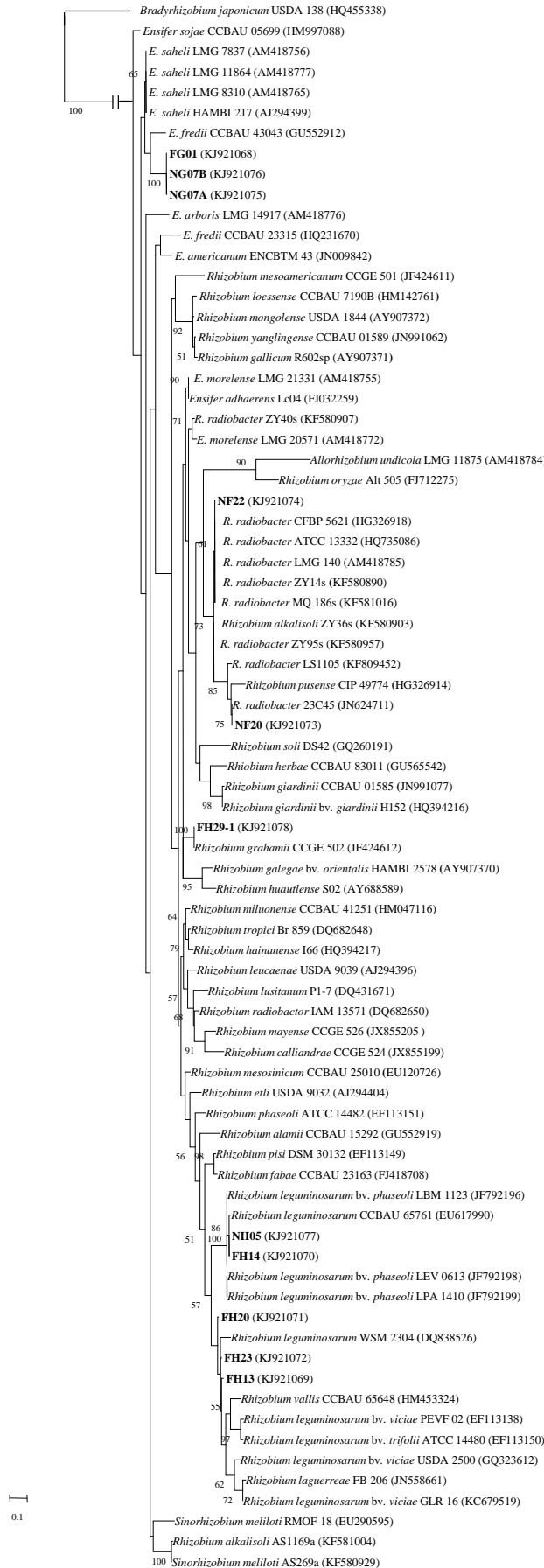
Supplementary Fig. S1. Neighbor-joining (NJ) tree of 16S rRNA genes (accession numbers are in brackets) reconstructed with the Jukes–Cantor distance, showing the genus positions of the bean nodule bacteria from acid and alkaline soils in Mexico (boldface). Bootstrap values greater than 50% are shown at the nodes. The scale bar indicates 5% nucleotide substitution. *Azorhizobium caulinodans* ORS 571 was used as an out group.

0.05

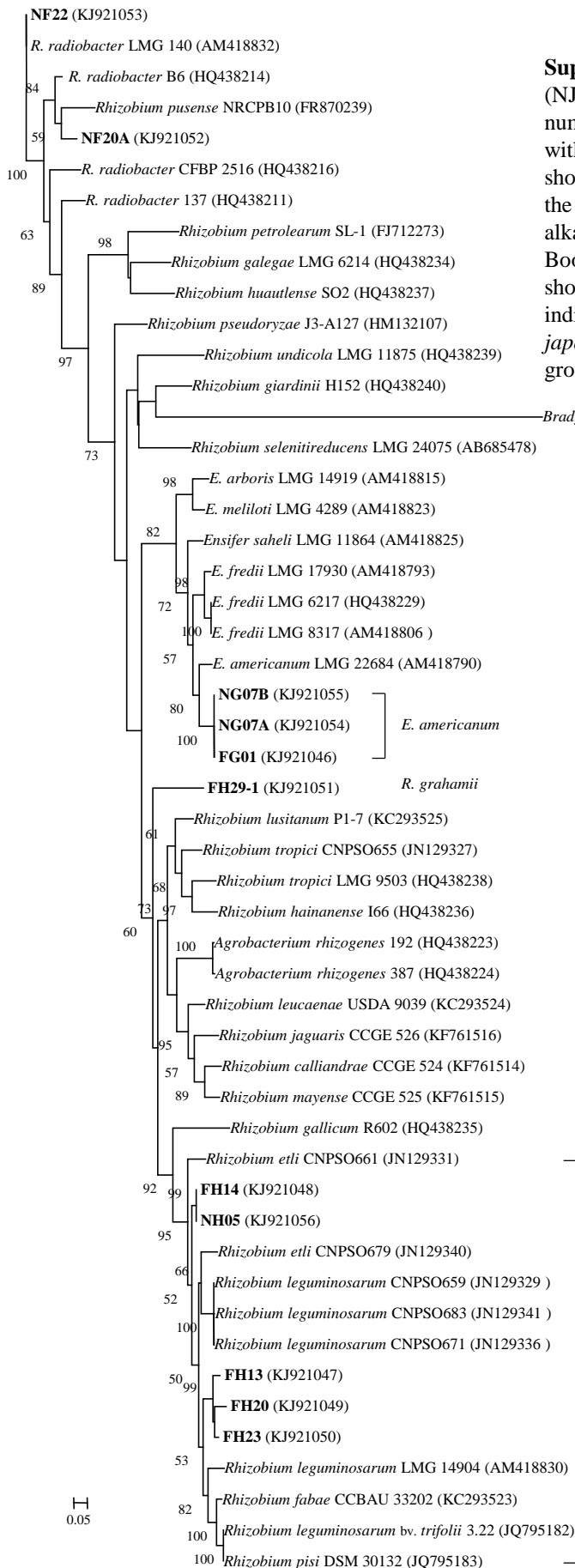


Supplementary Fig. S2. Neighbor-joining (NJ) tree of *recA* genes (accession numbers are in brackets) reconstructed with the Kimura two-parameter test, showing the phylogenetic relationships of the bean nodule bacteria from acid and alkaline soils in Mexico (boldface). Bootstrap values greater than 50% are shown at the nodes. The scale bar indicates 10% nucleotide substitution. *M. loti* USDA 3471 was used as an out group.

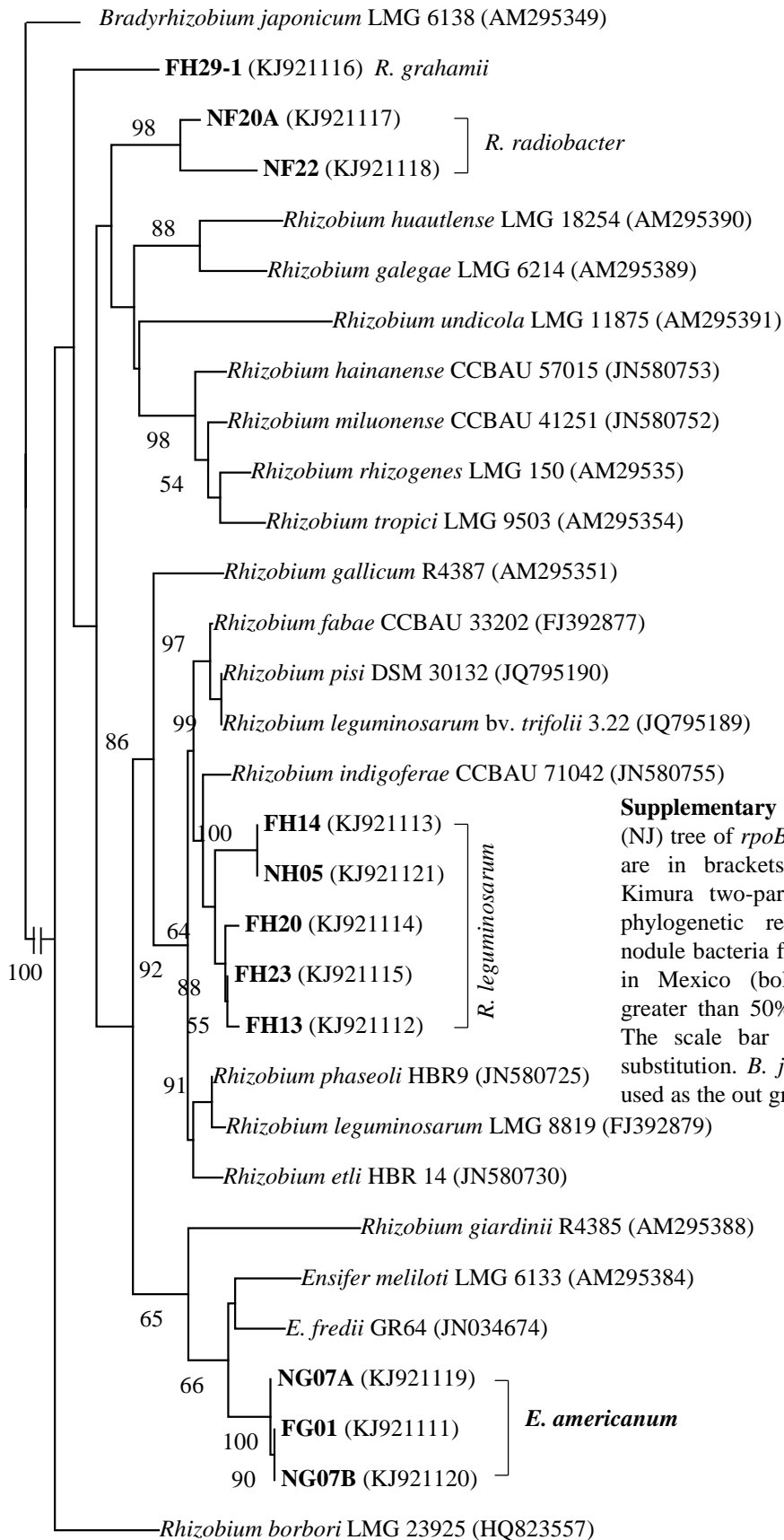
0.1



Supplementary Fig. S3. Neighbor-joining (NJ) tree of *atpD* genes (accession numbers are in brackets) reconstructed with the Kimura two-parameter test, showing the phylogenetic relationships of the bean nodule bacteria from acid and alkaline soils in Mexico (boldface). Bootstrap values greater than 50% are shown at the nodes. The scale bar indicates 10% nucleotide substitution. *B. japonicum* USDA 138 was used as an out group.



Supplementary Fig. S5. Neighbor-joining (NJ) tree of *gyrB* genes (accession numbers are in brackets) reconstructed with the Kimura two-parameter test, showing the phylogenetic relationships of the bean nodule bacteria from acid and alkaline soils in Mexico (boldface). Bootstrap values greater than 50% are shown at the nodes. The scale bar indicates 5% nucleotide substitution. *B. japonicum* USDA 122 was used as an out group.



Supplementary Fig. S6. Neighbor-joining (NJ) tree of *rpoB* genes (accession numbers are in brackets) reconstructed with the Kimura two-parameter test, showing the phylogenetic relationships of the bean nodule bacteria from acid and alkaline soils in Mexico (boldface). Bootstrap values greater than 50% are shown at the nodes. The scale bar indicates 10% nucleotide substitution. *B. japonicum* LMG 6138 was used as the out group.

0.1

