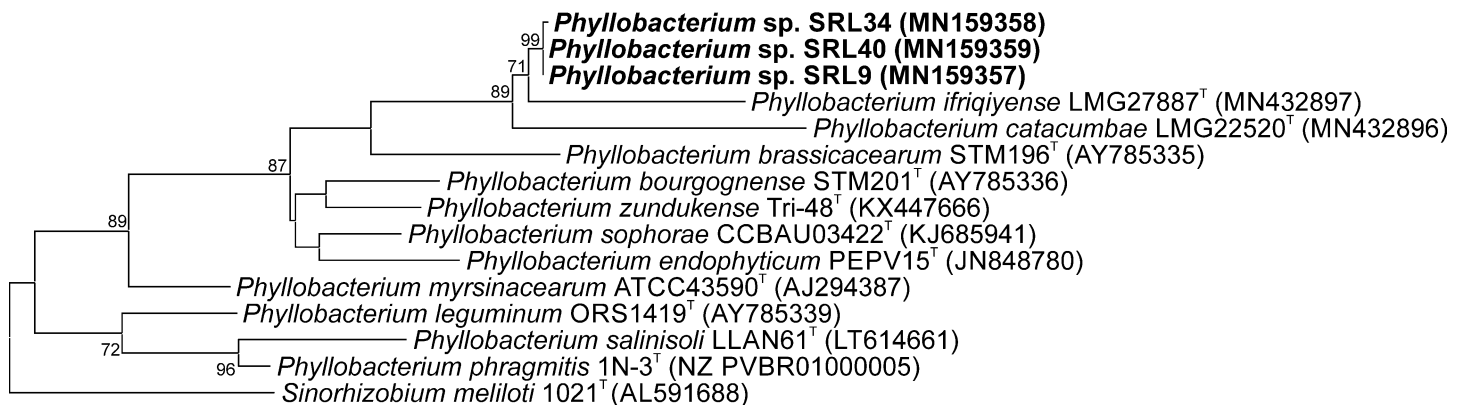Supplementary Figure S1. The phylogenetic trees of *atpD* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium* (top) and *Phyllobacterium* (bottom). The phylogenies were inferred by using the Maximum Likelihood method based on GTR+I+ Γ (top) and TrN+I+Γ (bottom) evolutionary models. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.
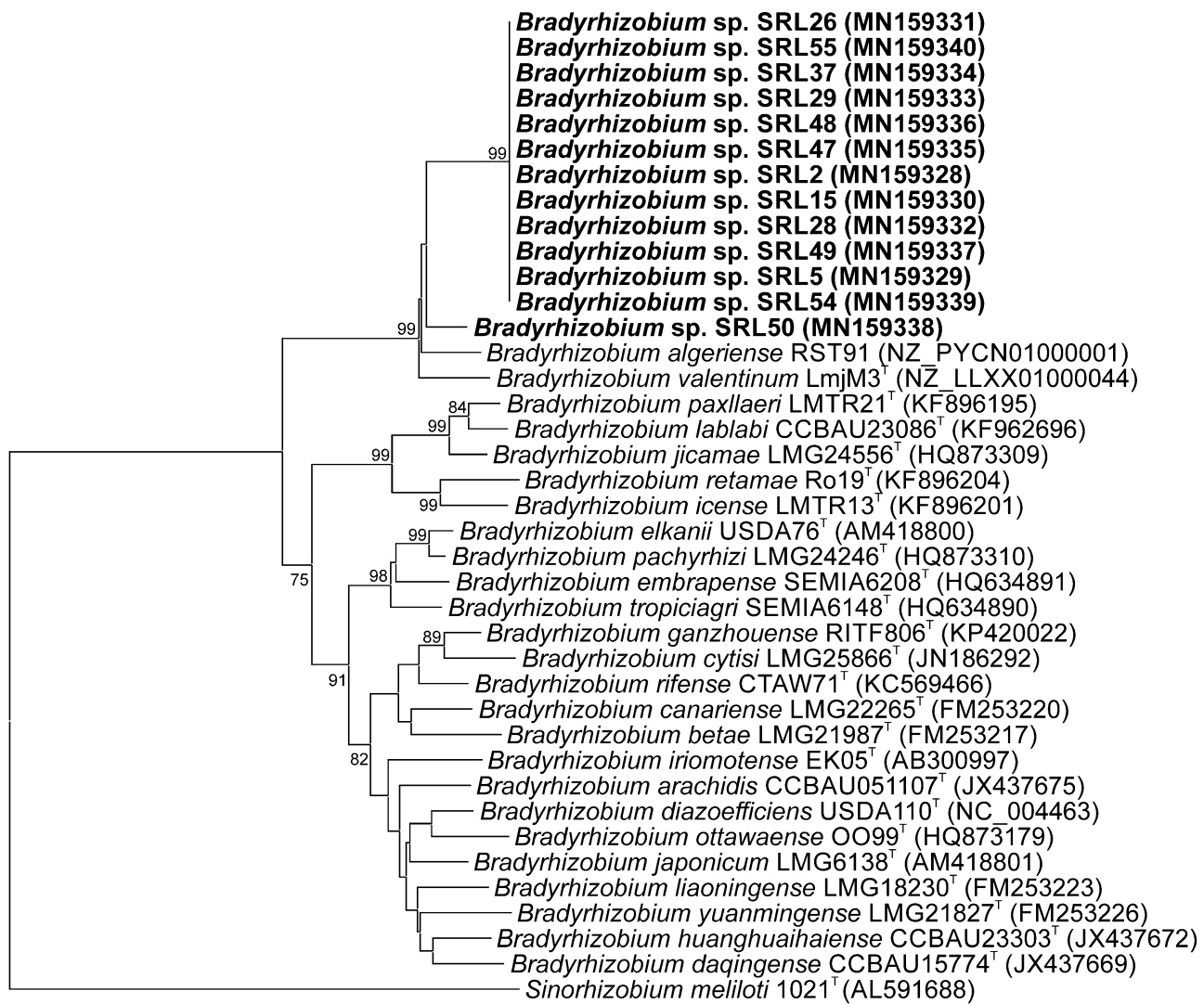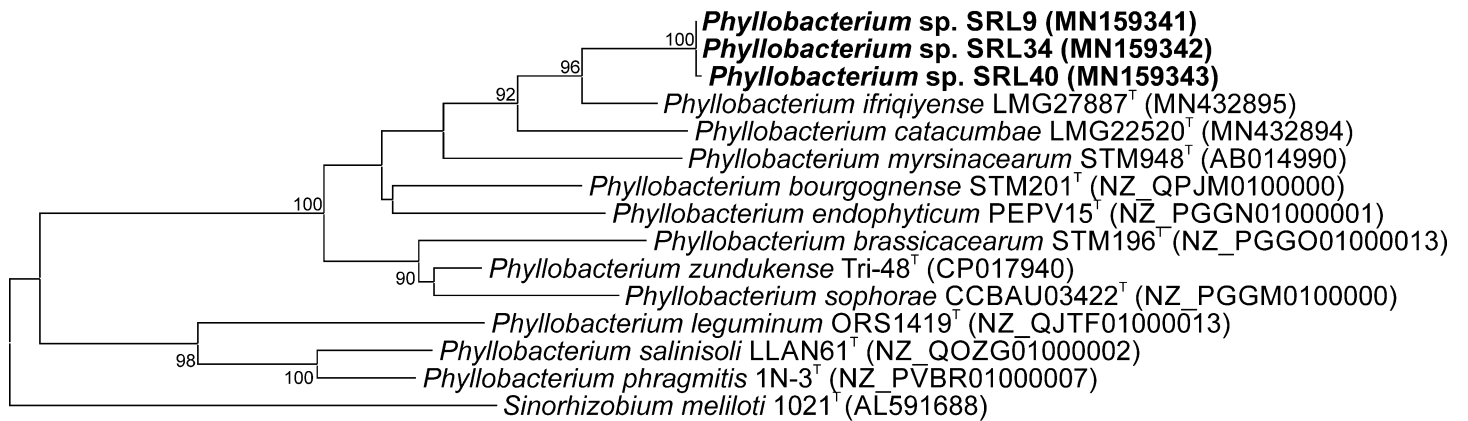
Supplementary Figure S2. The phylogenetic trees of *gyrB* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium* (top) and *Phyllobacterium* (bottom). The phylogenies were inferred by using the Maximum Likelihood method based on GTR+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.
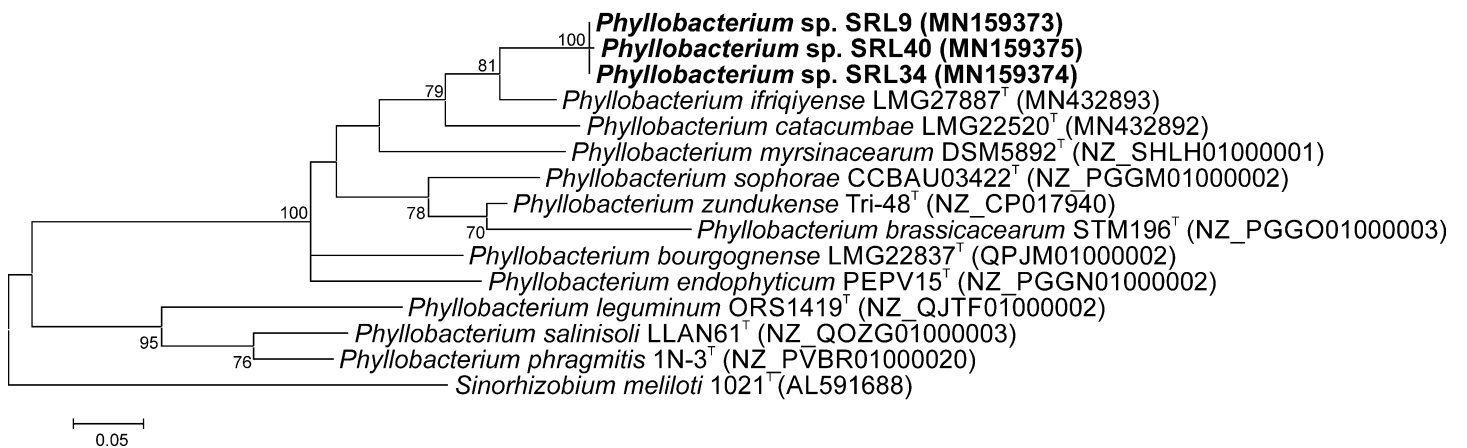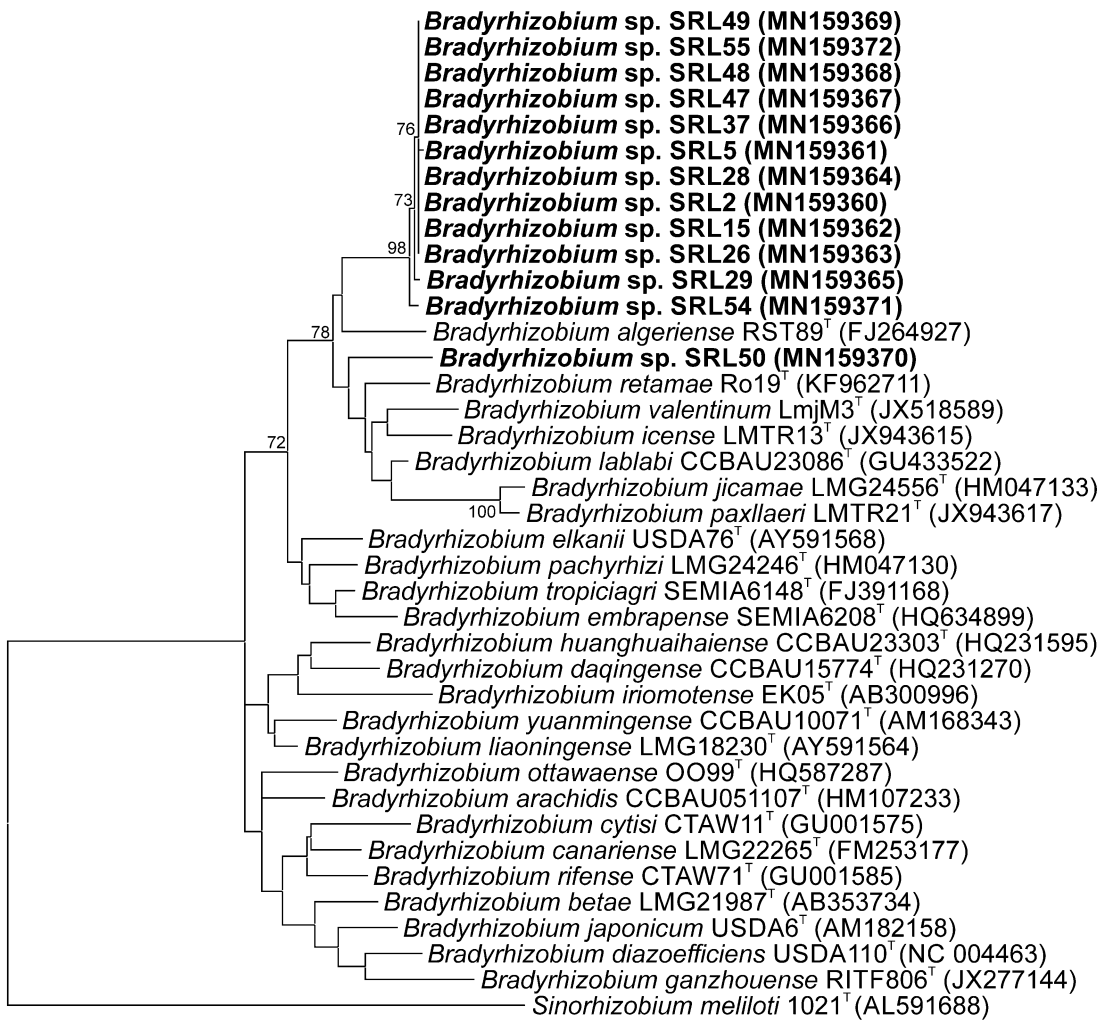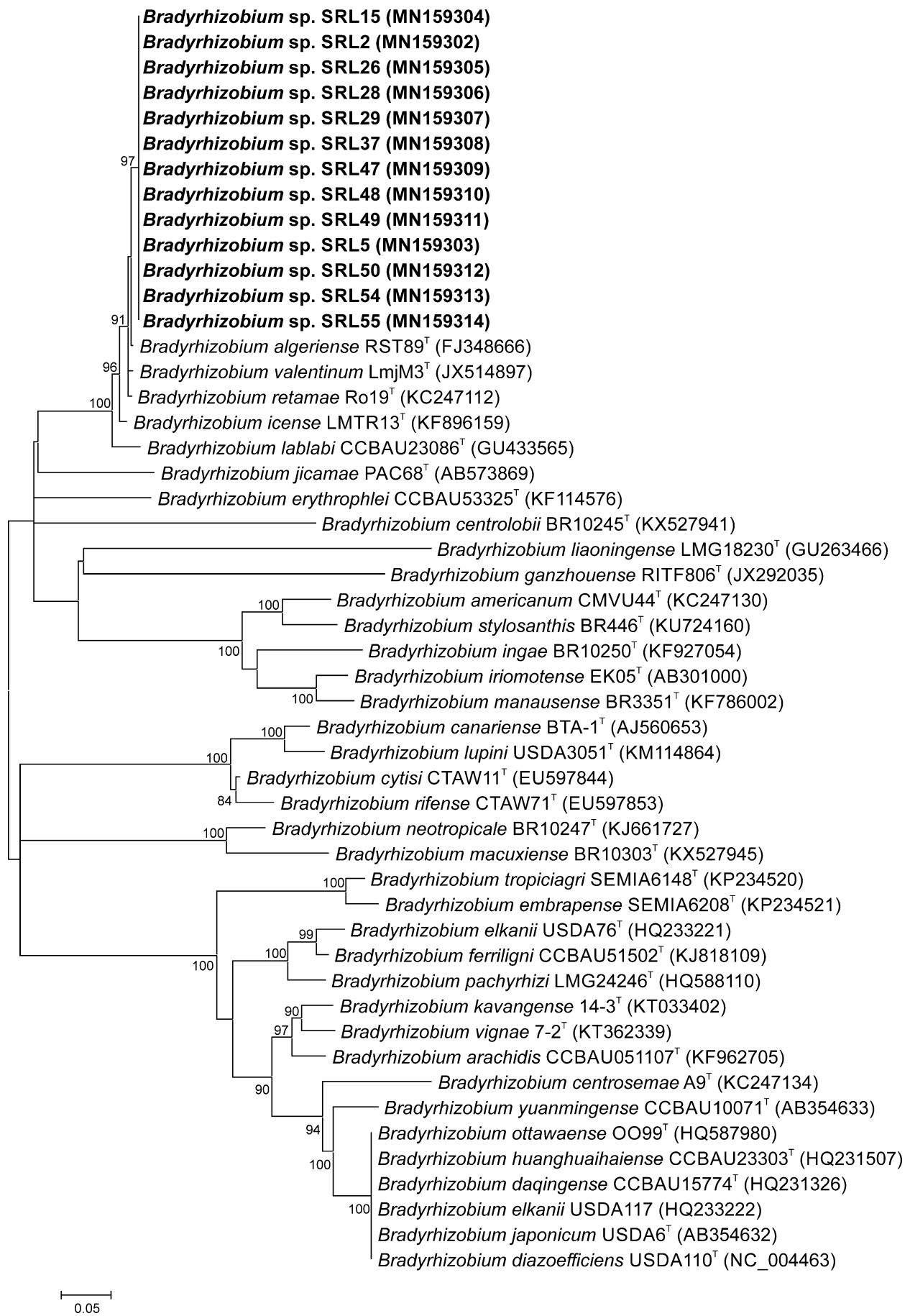
Bradyrhizobium sp. SRL49 (MN159369)
Bradyrhizobium sp. SRL55 (MN159372)
Bradyrhizobium sp. SRL48 (MN159368)
Bradyrhizobium sp. SRL47 (MN159367)
76 **Bradyrhizobium sp. SRL37 (MN159366)**
Bradyrhizobium sp. SRL5 (MN159361)
Bradyrhizobium sp. SRL28 (MN159364)
73 **Bradyrhizobium sp. SRL2 (MN159360)**
Bradyrhizobium sp. SRL15 (MN159362)
98 **Bradyrhizobium sp. SRL26 (MN159363)**
Bradyrhizobium sp. SRL29 (MN159365)
Bradyrhizobium sp. SRL54 (MN159371)
78 *Bradyrhizobium algeriense* RST89^T (FJ264927)
Bradyrhizobium sp. SRL50 (MN159370)
Bradyrhizobium retamae Ro19^T (KF962711)
72 *Bradyrhizobium valentinum* LmjM3^T (JX518589)
Bradyrhizobium icense LMTR13^T (JX943615)
Bradyrhizobium lablabi CCBAU23086^T (GU433522)
Bradyrhizobium jicamae LMG24556^T (HM047133)
100 *Bradyrhizobium paxllaeri* LMTR21^T (JX943617)
Bradyrhizobium elkanii USDA76^T (AY591568)
Bradyrhizobium pachyrhizi LMG24246^T (HM047130)
Bradyrhizobium tropiciagri SEMIA6148^T (FJ391168)
Bradyrhizobium embrapense SEMIA6208^T (HQ634899)
Bradyrhizobium huanghuaihaiense CCBAU23303^T (HQ231595)
Bradyrhizobium daqingense CCBAU15774^T (HQ231270)
Bradyrhizobium iriomotense EK05^T (AB300996)
Bradyrhizobium yuanmingense CCBAU10071^T (AM168343)
Bradyrhizobium liaoningense LMG18230^T (AY591564)
Bradyrhizobium ottawaense OO99^T (HQ587287)
Bradyrhizobium arachidis CCBAU051107^T (HM107233)
Bradyrhizobium cytisi CTAW11^T (GU001575)
Bradyrhizobium canariense LMG22265^T (FM253177)
Bradyrhizobium rifense CTAW71^T (GU001585)
Bradyrhizobium betae LMG21987^T (AB353734)
Bradyrhizobium japonicum USDA6^T (AM182158)
Bradyrhizobium diazoefficiens USDA110^T (NC 004463)
Bradyrhizobium ganzhouense RITF806^T (JX277144)
Sinorhizobium meliloti 1021^T (AL591688)

0.05

Phyllobacterium sp. SRL9 (MN159373)
100 **Phyllobacterium sp. SRL40 (MN159375)**
81 **Phyllobacterium sp. SRL34 (MN159374)**
79 *Phyllobacterium ifriqiyense* LMG27887^T (MN432893)
Phyllobacterium catacumbae LMG22520^T (MN432892)
Phyllobacterium myrsinacearum DSM5892^T (NZ_SHLH01000001)
100 *Phyllobacterium sophorae* CCBAU03422^T (NZ_PGGM01000002)
78 *Phyllobacterium zundukense* Tri-48^T (NZ_CP017940)
70 *Phyllobacterium brassicacearum* STM196^T (NZ_PGGO01000003)
Phyllobacterium bourgognense LMG22837^T (QPJM01000002)
Phyllobacterium endophyticum PEPV15^T (NZ_PGGN01000002)
Phyllobacterium leguminum ORS1419^T (NZ_QJTF01000002)
95 *Phyllobacterium salinisoli* LLAN61^T (NZ_QOZG01000003)
76 *Phyllobacterium phragmitis* 1N-3^T (NZ_PVBR01000020)
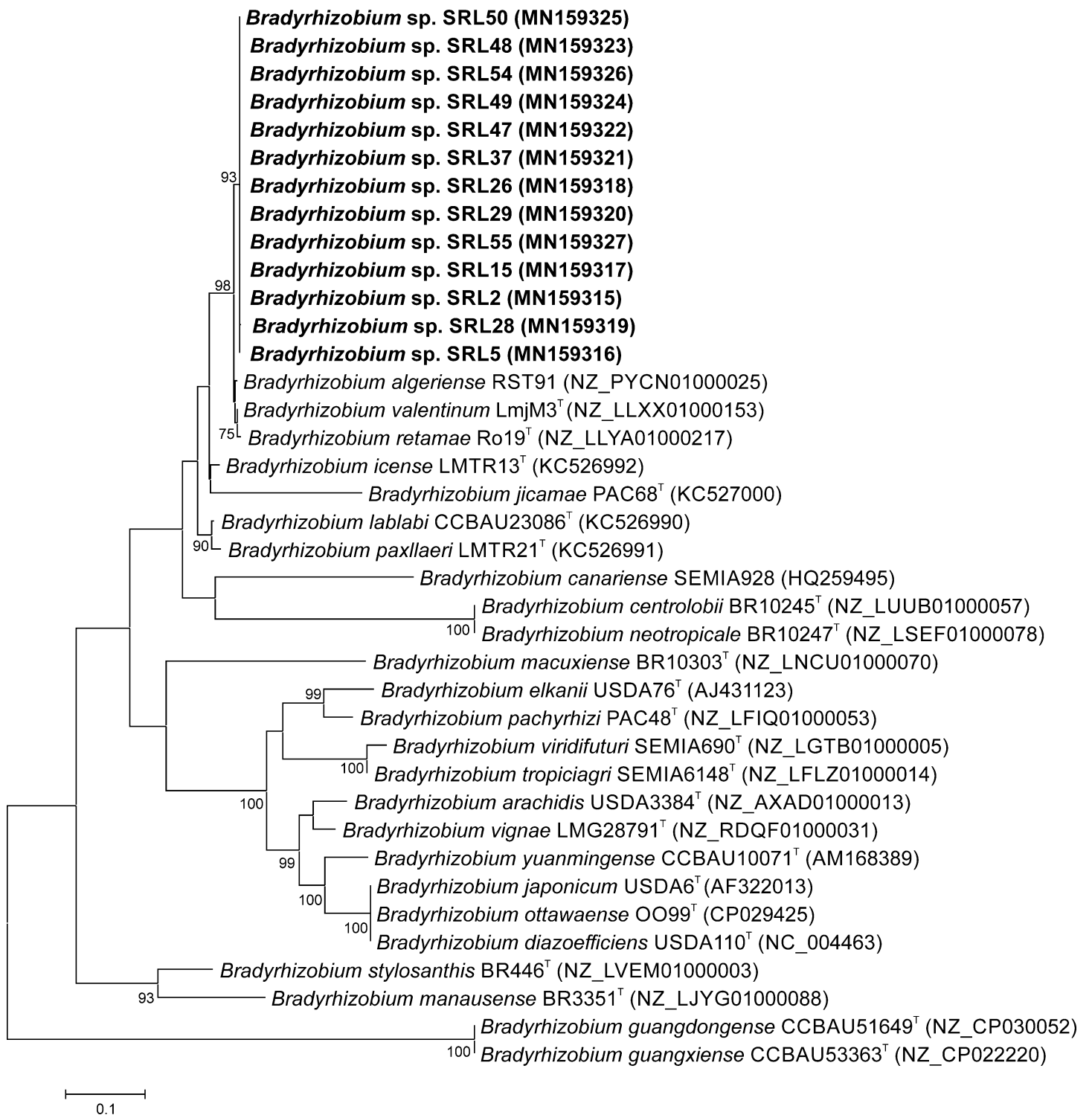*Sinorhizobium meliloti* 1021^T (AL591688)

0.05

Supplementary Figure S3. The phylogenetic trees of *recA* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium* (top) and *Phyllobacterium* (bottom). The phylogenies were inferred by using the Maximum Likelihood method based on GTR+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.

Bradyrhizobium sp. SRL15 (MN159304)
Bradyrhizobium sp. SRL2 (MN159302)
Bradyrhizobium sp. SRL26 (MN159305)
Bradyrhizobium sp. SRL28 (MN159306)
Bradyrhizobium sp. SRL29 (MN159307)
Bradyrhizobium sp. SRL37 (MN159308)
Bradyrhizobium sp. SRL47 (MN159309)
Bradyrhizobium sp. SRL48 (MN159310)
Bradyrhizobium sp. SRL49 (MN159311)
Bradyrhizobium sp. SRL5 (MN159303)
Bradyrhizobium sp. SRL50 (MN159312)
Bradyrhizobium sp. SRL54 (MN159313)
Bradyrhizobium sp. SRL55 (MN159314)
Bradyrhizobium algeriense RST89^T (FJ348666)
Bradyrhizobium valentinum LmjM3^T (JX514897)
Bradyrhizobium retamae Ro19^T (KC247112)
Bradyrhizobium icense LMTR13^T (KF896159)
Bradyrhizobium lablabi CCBAU23086^T (GU433565)
Bradyrhizobium jicamae PAC68^T (AB573869)
Bradyrhizobium erythrophlei CCBAU53325^T (KF114576)
Bradyrhizobium centrolobii BR10245^T (KX527941)
Bradyrhizobium liaoningense LMG18230^T (GU263466)
Bradyrhizobium ganzhouense RITF806^T (JX292035)
Bradyrhizobium americanum CMVU44^T (KC247130)
Bradyrhizobium stylosanthis BR446^T (KU724160)
Bradyrhizobium ingae BR10250^T (KF927054)
Bradyrhizobium iriomotense EK05^T (AB301000)
Bradyrhizobium manausense BR3351^T (KF786002)
Bradyrhizobium canariense BTA-1^T (AJ560653)
Bradyrhizobium lupini USDA3051^T (KM114864)
Bradyrhizobium cytisi CTAW11^T (EU597844)
Bradyrhizobium rifense CTAW71^T (EU597853)
Bradyrhizobium neotropicale BR10247^T (KJ661727)
Bradyrhizobium macuxiense BR10303^T (KX527945)
Bradyrhizobium tropiciagri SEMIA6148^T (KP234520)
Bradyrhizobium embrapense SEMIA6208^T (KP234521)
Bradyrhizobium elkanii USDA76^T (HQ233221)
Bradyrhizobium ferriligni CCBAU51502^T (KJ818109)
Bradyrhizobium pachyrhizi LMG24246^T (HQ588110)
Bradyrhizobium kavangense 14-3^T (KT033402)
Bradyrhizobium vignae 7-2^T (KT362339)
Bradyrhizobium arachidis CCBAU051107^T (KF962705)
Bradyrhizobium centrosemae A9^T (KC247134)
Bradyrhizobium yuanmingense CCBAU10071^T (AB354633)
Bradyrhizobium ottawaense OO99^T (HQ587980)
Bradyrhizobium huanghuaihaiense CCBAU23303^T (HQ231507)
Bradyrhizobium daqingense CCBAU15774^T (HQ231326)
Bradyrhizobium elkanii USDA117 (HQ233222)
Bradyrhizobium japonicum USDA6^T (AB354632)
Bradyrhizobium diazoefficiens USDA110^T (NC_004463)

0.05

Supplementary Figure S4. The phylogenetic tree of *nodC* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium*. The phylogeny was inferred by using the Maximum Likelihood method based on TrN+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.

Supplementary Figure S5. The phylogenetic tree of *nodZ* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium*. The phylogeny was inferred by using the Maximum Likelihood method based on TrN+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.
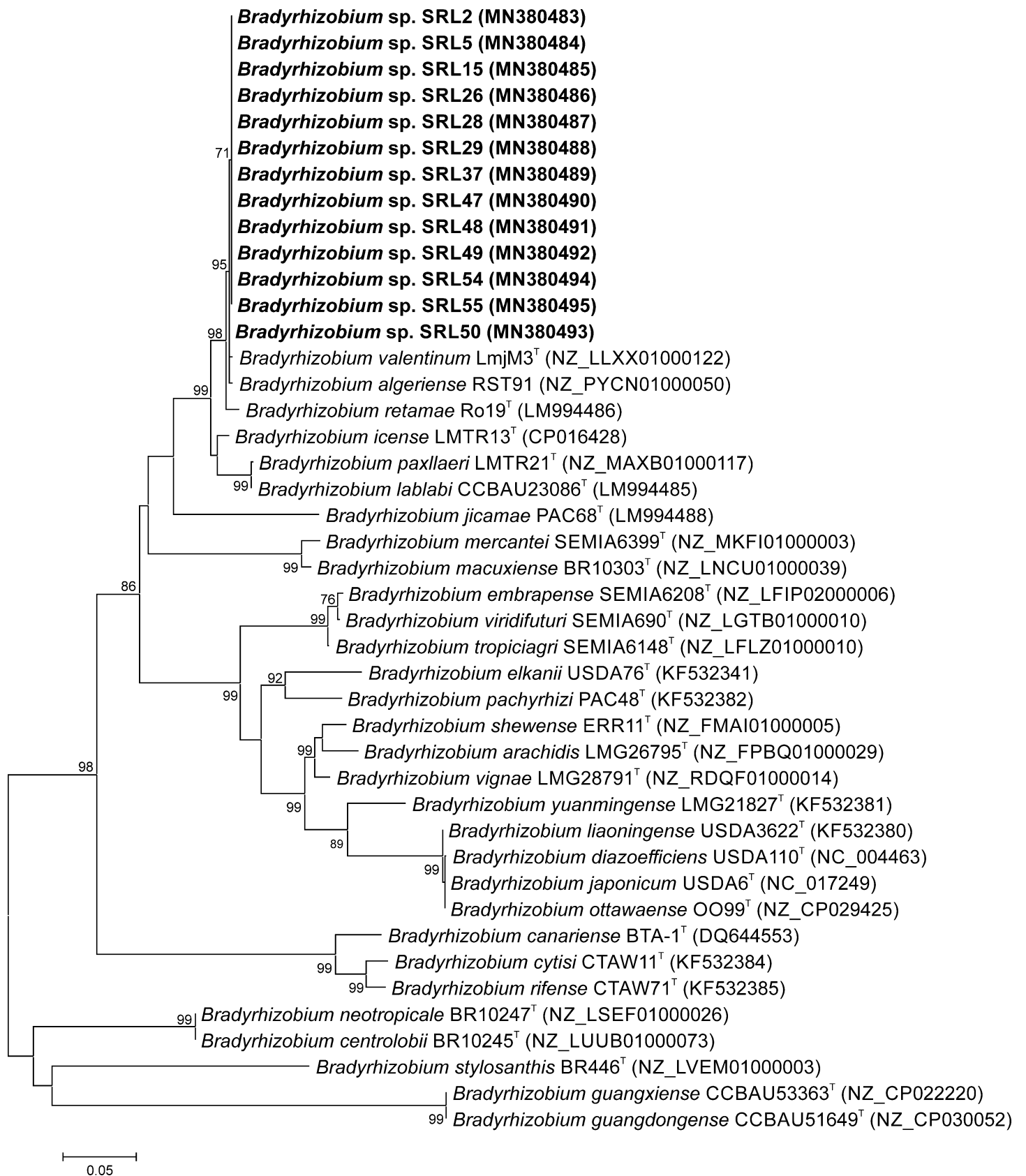
Supplementary Figure S6. The phylogenetic tree of *nifD* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium*. The phylogeny was inferred by using the Maximum Likelihood method based on GTR+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.
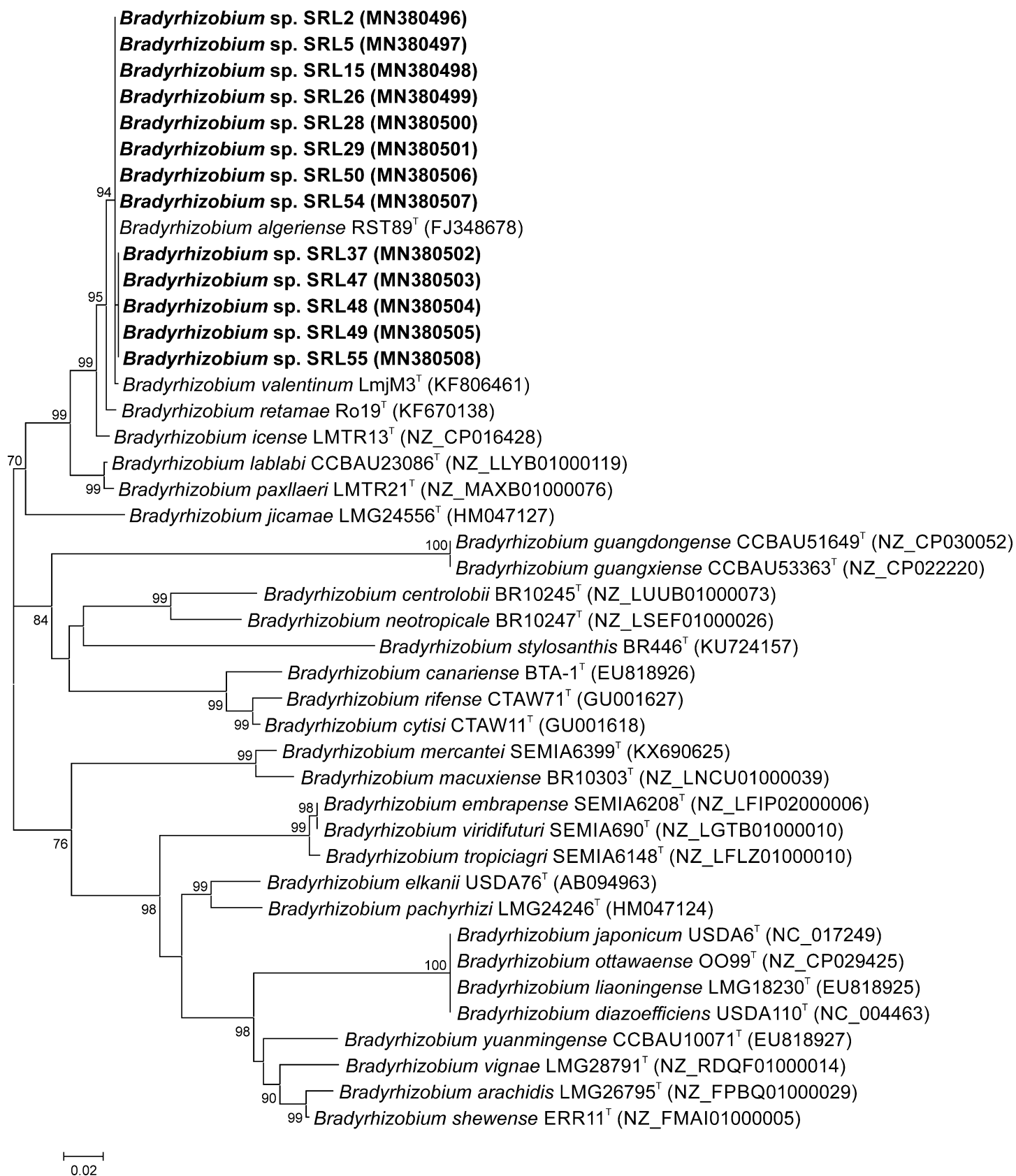
Supplementary Figure S7. The phylogenetic tree of *nifH* gene sequences of the *Chamaecytisus ruthenicus* root nodule isolates (shown in bold) and reference *Bradyrhizobium*. The phylogeny was inferred by using the Maximum Likelihood method based on GTR+I+Γ evolutionary model. Bootstrap values ≥70% are given at the branching points. The scale bar indicates the number of substitutions per site. GenBank accession numbers are given in parentheses.