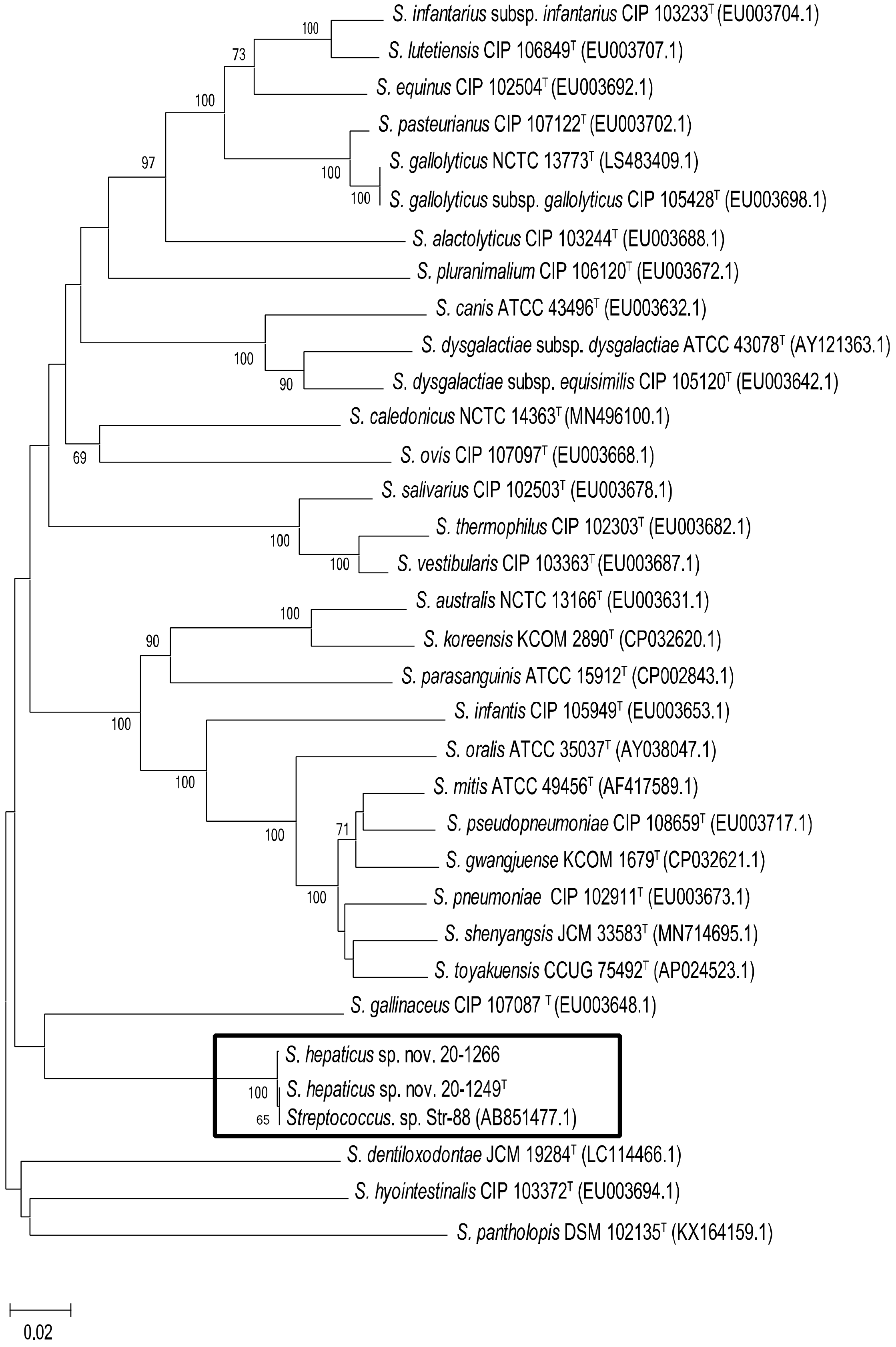
Figure 2.

Phylogenetic analysis of *groEL* carried out with MEGA X using the neighbour-joining approach with evolutionary distances computed using the Jukes-Cantor with a contig of 752bp. Analysis of the *S. hepaticus* sp. nov. *groEL* contig using BLASTn identified closely related sequences which were used to generate this tree. Sequences from type strains that had >80% sequence identity were included along with Str-88 (AB851477.1) and both *S. hepaticus* sp. nov. isolates (20-1249^T and 20-1266). Value at nodes correspond to proportions of 100 re-samplings that support the topology shown with only values >60% indicated. Bar, 0.02 substitutions per nucleotide position. Sequence accession numbers are shown in brackets.

Figure 2.



S. infantarius subsp. infantarius CIP 103233^{T} (EU003704.1)
100
S. lutetiensis CIP 106849^{T} (EU003707.1)
73
S. equinus CIP 102504^{T} (EU003692.1)
100
S. pasteurianus CIP 107122^{T} (EU003702.1)
S. gallolyticus NCTC 13773^{T} (LS483409.1)
97
100
100
S. gallolyticus subsp. gallolyticus CIP 105428^{T} (EU003698.1)
S. alactolyticus CIP 103244^{T} (EU003688.1)
S. pluranimalium CIP 106120^{T} (EU003672.1)
S. canis ATCC 43496^{T} (EU003632.1)
S. dysgalactiae subsp. dysgalactiae ATCC 43078^{T} (AY121363.1)
100
90
S. dysgalactiae subsp. equisimilis CIP 105120^{T} (EU003642.1)
S. caledonicus NCTC 14363^{T} (MN496100.1)
69
S. ovis CIP 107097^{T} (EU003668.1)
S. salivarius CIP 102503^{T} (EU003678.1)
S. thermophilus CIP 102303^{T} (EU003682.1)
100
100
S. vestibularis CIP 103363^{T} (EU003687.1)
S. australis NCTC 13166^{T} (EU003631.1)
100
90
S. koreensis KCOM 2890^{T} (CP032620.1)
S. parasanguinis ATCC 15912^{T} (CP002843.1)
S. infantis CIP 105949^{T} (EU003653.1)
100
S. oralis ATCC 35037^{T} (AY038047.1)
100
S. mitis ATCC 49456^{T} (AF417589.1)
S. pseudopneumoniae CIP 108659^{T} (EU003717.1)
100
71
S. gwangjuense KCOM 1679^{T} (CP032621.1)
S. pneumoniae CIP 102911^{T} (EU003673.1)
100
S. shenyangsis JCM 33583^{T} (MN714695.1)
S. toyakuensis CCUG 75492^{T} (AP024523.1)
S. gallinaceus CIP 107087 ^{T} (EU003648.1)
S. hepaticus sp. nov. 20-1266
100
S. hepaticus sp. nov. 20-1249^{T}
65
Streptococcus. sp. Str-88 (AB851477.1)
S. dentiloxodontae JCM 19284^{T} (LC114466.1)
S. hyointestinalis CIP 103372^{T} (EU003694.1)
S. pantholopis DSM 102135^{T} (KX164159.1)
0.02

Figure 3.

Phylogenetic analysis of *sodA* carried out with MEGA X using the neighbour-joining approach with evolutionary distances computed using the Jukes-Cantor with a contig of 380bp. Analysis of the *S. hepaticus* sp. nov. *sodA* contig using BLASTn identified closely related sequences which were used to generate this tree. Sequences from type strains that had >75% sequence identity were included. The tree includes the *sodA* sequence of isolate Str88 (AB827271.1) and both *S. hepaticus* sp. nov. strains (20-1249^T and 20-1266). Value at nodes correspond to proportions of 100 re-samplings that support the topology shown with only values >60% indicated. Bar, 0.05 substitutions per nucleotide position.

Figure 3.

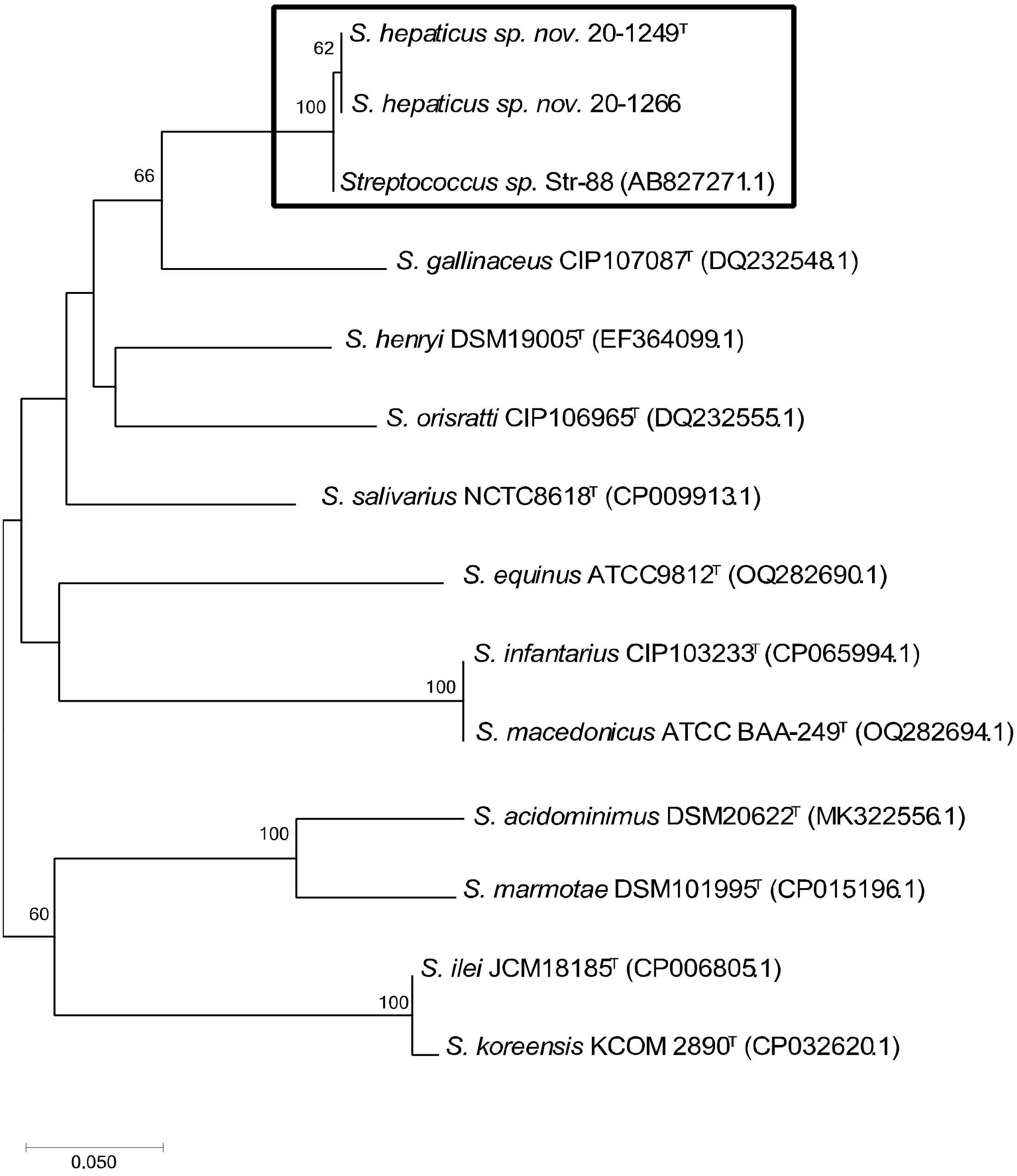
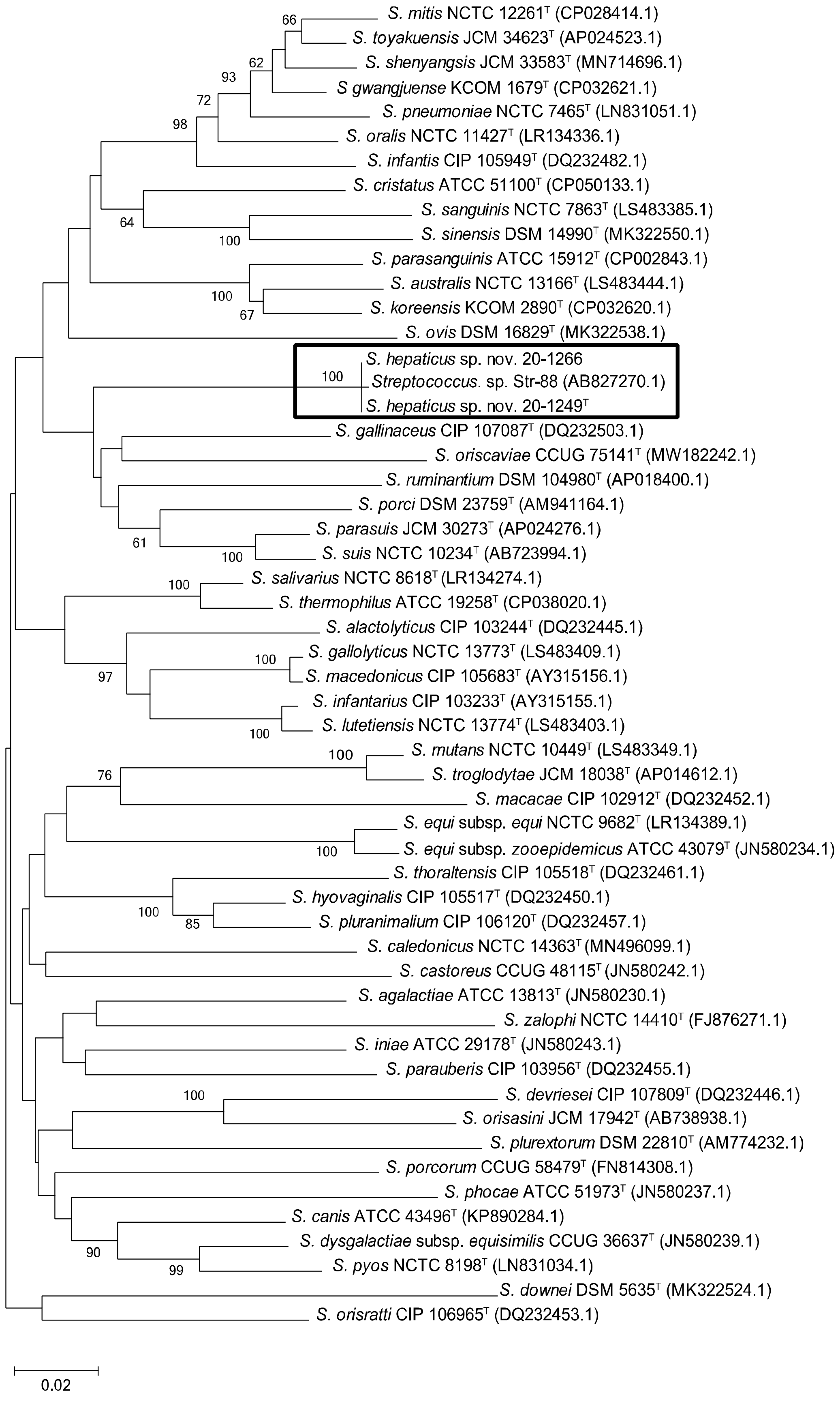

S. hepaticus sp. nov. 20-1249T
62
100
S. hepaticus sp. nov. 20-1266
66
Streptococcus sp. Str-88 (AB827271.1)
S. gallinaceus CIP107087T (DQ232548.1)
S. henryi DSM19005T (EF364099.1)
S. orisratti CIP106965T (DQ232555.1)
S. salivarius NCTC8618T (CP009913.1)
S. equinus ATCC9812T (OQ282690.1)
S. infantarius CIP103233T (CP065994.1)
100
S. macedonicus ATCC BAA-249T (OQ282694.1)
S. acidominimus DSM20622T (MK322556.1)
100
S. marmotae DSM101995T (CP015196.1)
60
S. ilei JCM18185T (CP006805.1)
100
S. koreensis KCOM 2890T (CP032620.1)
0.050

Figure 4.

Phylogenetic analysis of *rpoB* carried out with MEGA x using the neighbour-joining approach with evolutionary distances computed using the Jukes-Cantor with a contig of 638bp. Analysis of the *S. hepaticus* sp. nov. *rpoB* contig using BLASTn identified closely related sequences which were used to generate this tree. Sequences from type strains that have >80% sequence identity were included along with the contig from Str-88 (AB827270.1) and both *S. hepaticus sp. nov.* strains (20-1249^{T} and 20-1266). Value at nodes correspond to proportions of 100 re-samplings that support the topology shown with only values >60% indicated. Bar, 0.02 substitutions per nucleotide position.

Figure 4.


S. mitis NCTC 12261^{T} (CP028414.1)
S. toyakuensis JCM 34623^{T} (AP024523.1)
S. shenyangsis JCM 33583^{T} (MN714696.1)
S gwangjuense KCOM 1679^{T} (CP032621.1)
S. pneumoniae NCTC 7465^{T} (LN831051.1)
S. oralis NCTC 11427^{T} (LR134336.1)
S. infantis CIP 105949^{T} (DQ232482.1)
S. cristatus ATCC 51100^{T} (CP050133.1)
S. sanguinis NCTC 7863^{T} (LS483385.1)
S. sinensis DSM 14990^{T} (MK322550.1)
S. parasanguinis ATCC 15912^{T} (CP002843.1)
S. australis NCTC 13166^{T} (LS483444.1)
S. koreensis KCOM 2890^{T} (CP032620.1)
S. ovis DSM 16829^{T} (MK322538.1)
S. hepaticus sp. nov. 20-1266
Streptococcus. sp. Str-88 (AB827270.1)
S. hepaticus sp. nov. 20-1249^{T}
S. gallinaceus CIP 107087^{T} (DQ232503.1)
S. oriscaviae CCUG 75141^{T} (MW182242.1)
S. ruminantium DSM 104980^{T} (AP018400.1)
S. porci DSM 23759^{T} (AM941164.1)
S. parasuis JCM 30273^{T} (AP024276.1)
S. suis NCTC 10234^{T} (AB723994.1)
S. salivarius NCTC 8618^{T} (LR134274.1)
S. thermophilus ATCC 19258^{T} (CP038020.1)
S. alactolyticus CIP 103244^{T} (DQ232445.1)
S. gallolyticus NCTC 13773^{T} (LS483409.1)
S. macedonicus CIP 105683^{T} (AY315156.1)
S. infantarius CIP 103233^{T} (AY315155.1)
S. lutetiensis NCTC 13774^{T} (LS483403.1)
S. mutans NCTC 10449^{T} (LS483349.1)
S. troglodytae JCM 18038^{T} (AP014612.1)
S. macacae CIP 102912^{T} (DQ232452.1)
S. equi subsp. equi NCTC 9682^{T} (LR134389.1)
S. equi subsp. zooepidemicus ATCC 43079^{T} (JN580234.1)
S. thoraltensis CIP 105518^{T} (DQ232461.1)
S. hyovaginalis CIP 105517^{T} (DQ232450.1)
S. pluranimalium CIP 106120^{T} (DQ232457.1)
S. caledonicus NCTC 14363^{T} (MN496099.1)
S. castoreus CCUG 48115^{T} (JN580242.1)
S. agalactiae ATCC 13813^{T} (JN580230.1)
S. zalophi NCTC 14410^{T} (FJ876271.1)
S. iniae ATCC 29178^{T} (JN580243.1)
S. parauberis CIP 103956^{T} (DQ232455.1)
S. devriesei CIP 107809^{T} (DQ232446.1)
S. orisasini JCM 17942^{T} (AB738938.1)
S. plurextorum DSM 22810^{T} (AM774232.1)
S. porcorum CCUG 58479^{T} (FN814308.1)
S. phocae ATCC 51973^{T} (JN580237.1)
S. canis ATCC 43496^{T} (KP890284.1)
S. dysgalactiae subsp. equisimilis CCUG 36637^{T} (JN580239.1)
S. pyos NCTC 8198^{T} (LN831034.1)
S. downei DSM 5635^{T} (MK322524.1)
S. orisratti CIP 106965^{T} (DQ232453.1)
66
62
93
72
98
64
100
100
67
100
61
100
100
100
97
100
100
76
100
100
85
100
90
99
0.02