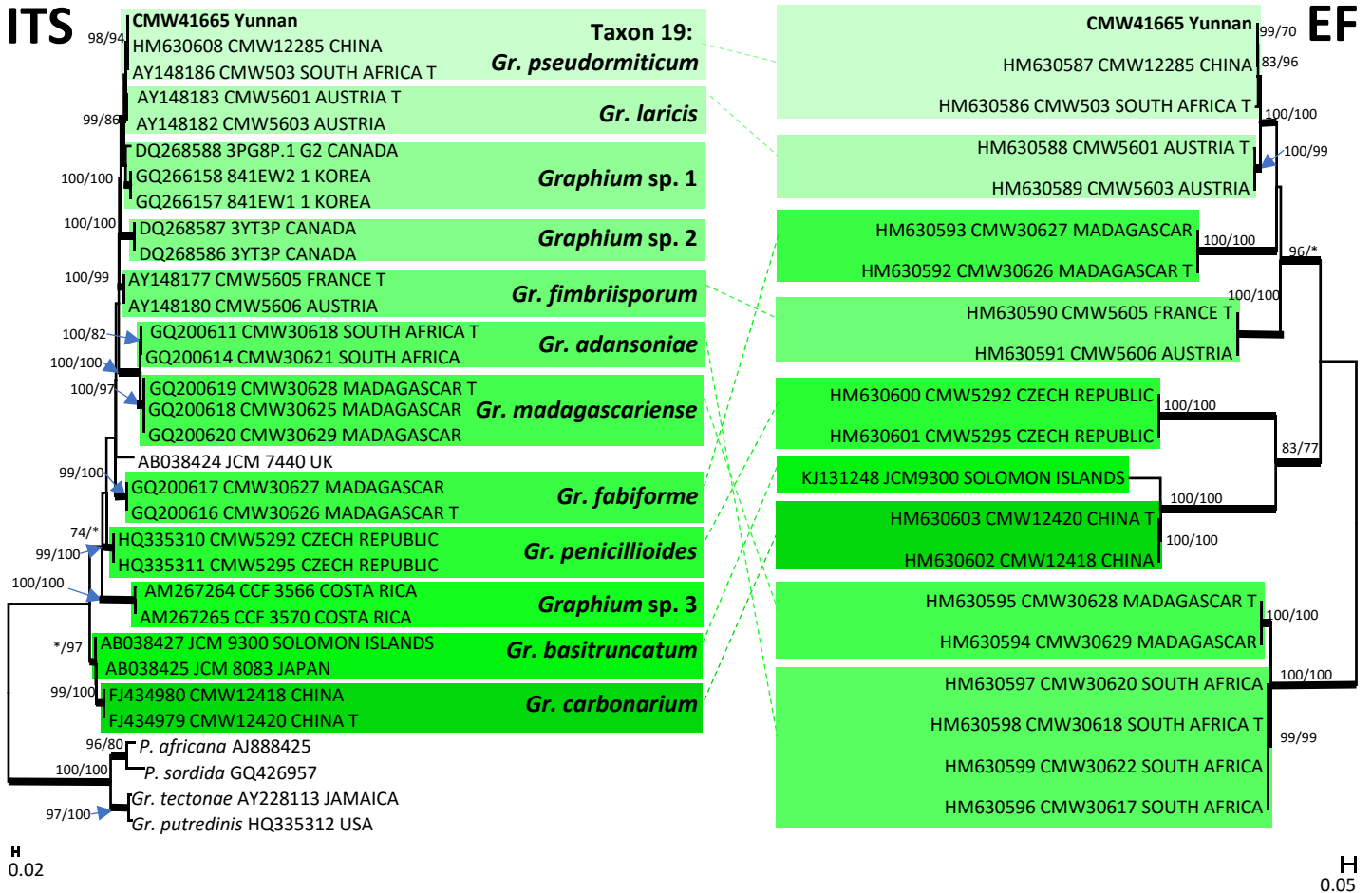
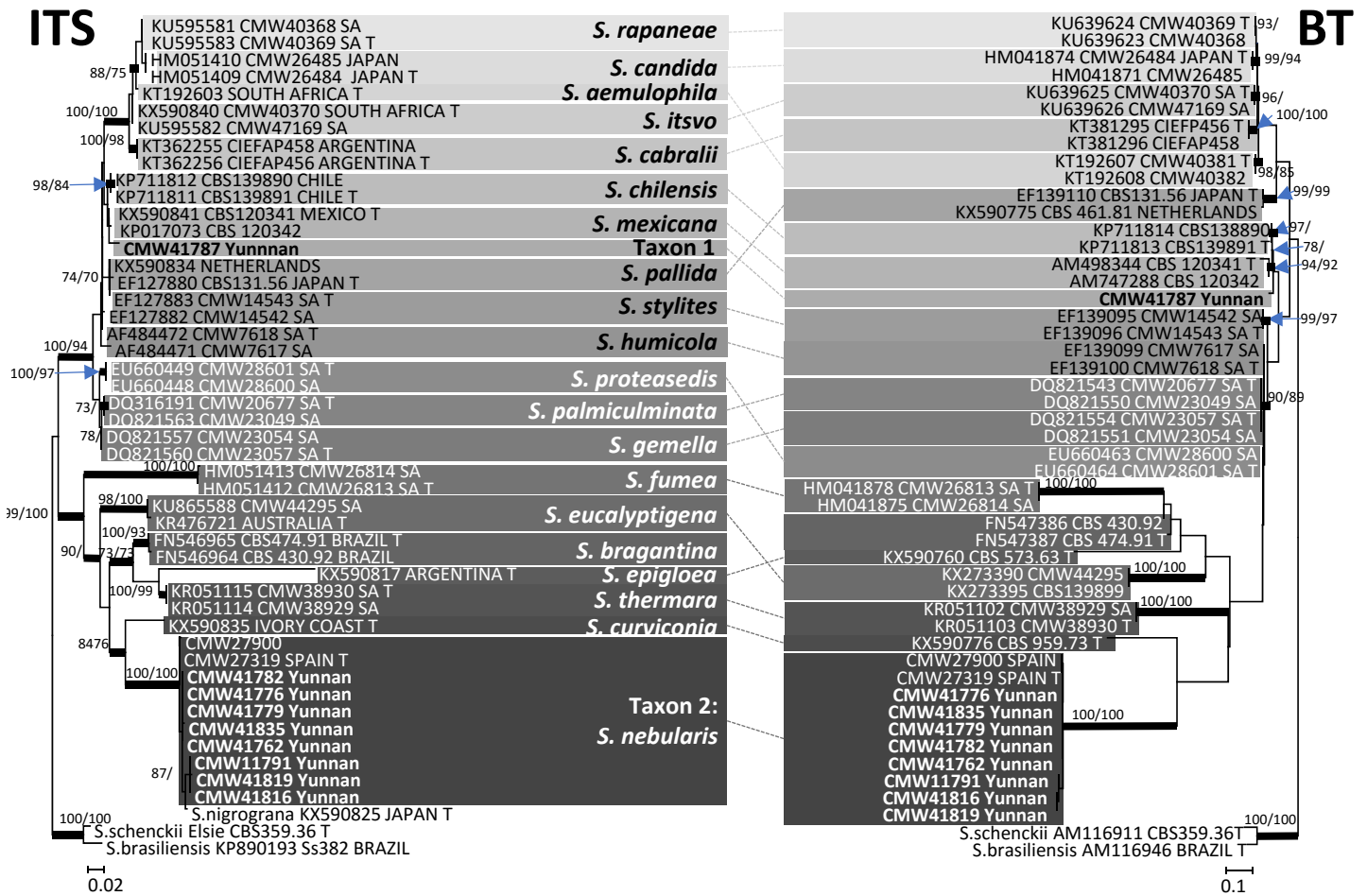


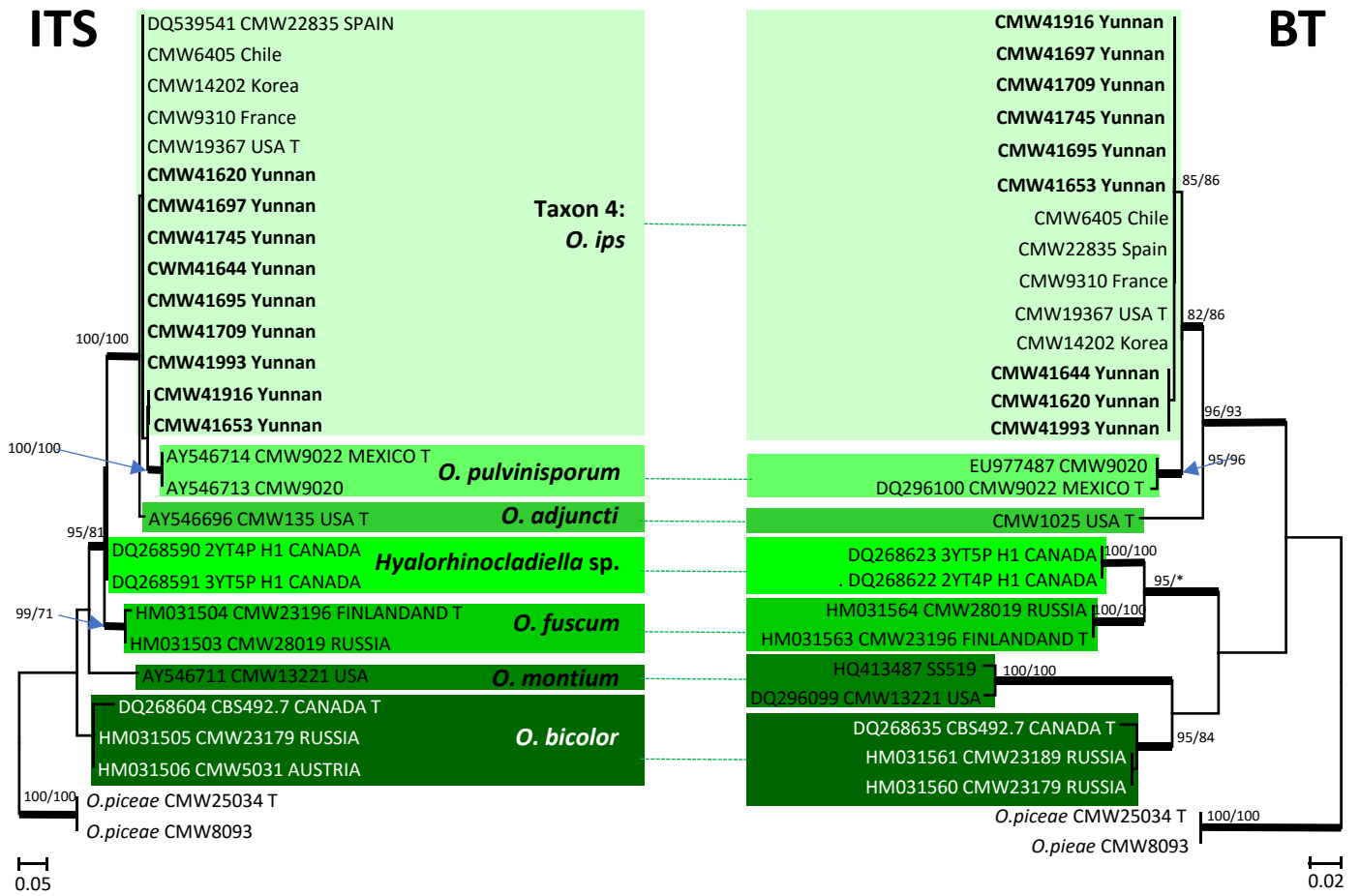
**Figure S1.** Map of Yunnan Province in China showing the sites and tree hosts from which samples were collected during the three surveys in 2001, 2002 and 2010.



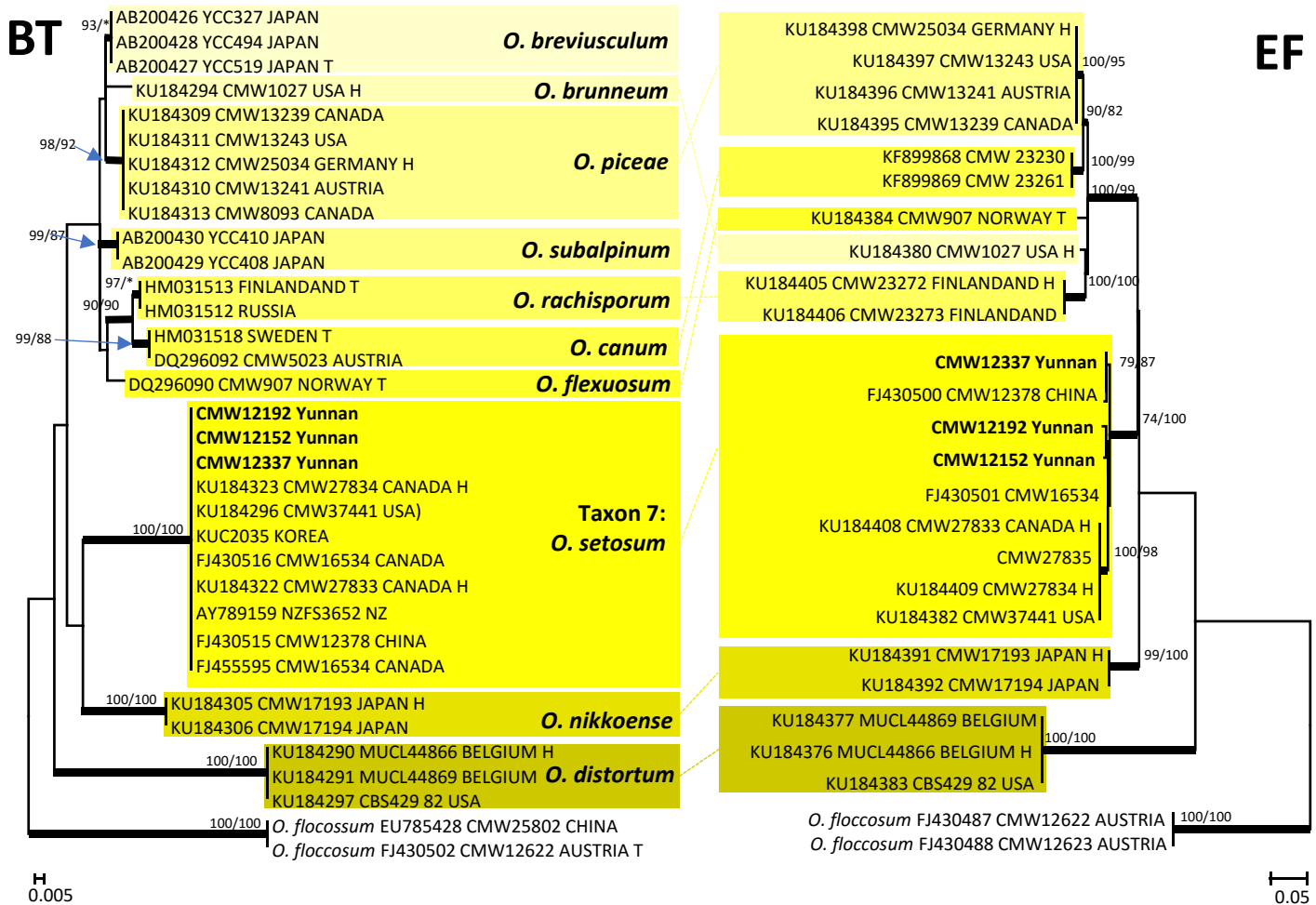
**Figure S2.** ML trees of the genus *Graphium* generated from DNA sequences of the ITS and BT regions. *Bold* branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.



**Figure S3.** ML trees of the genus *Sporothrix* generated from DNA sequences of ITS and BT regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.



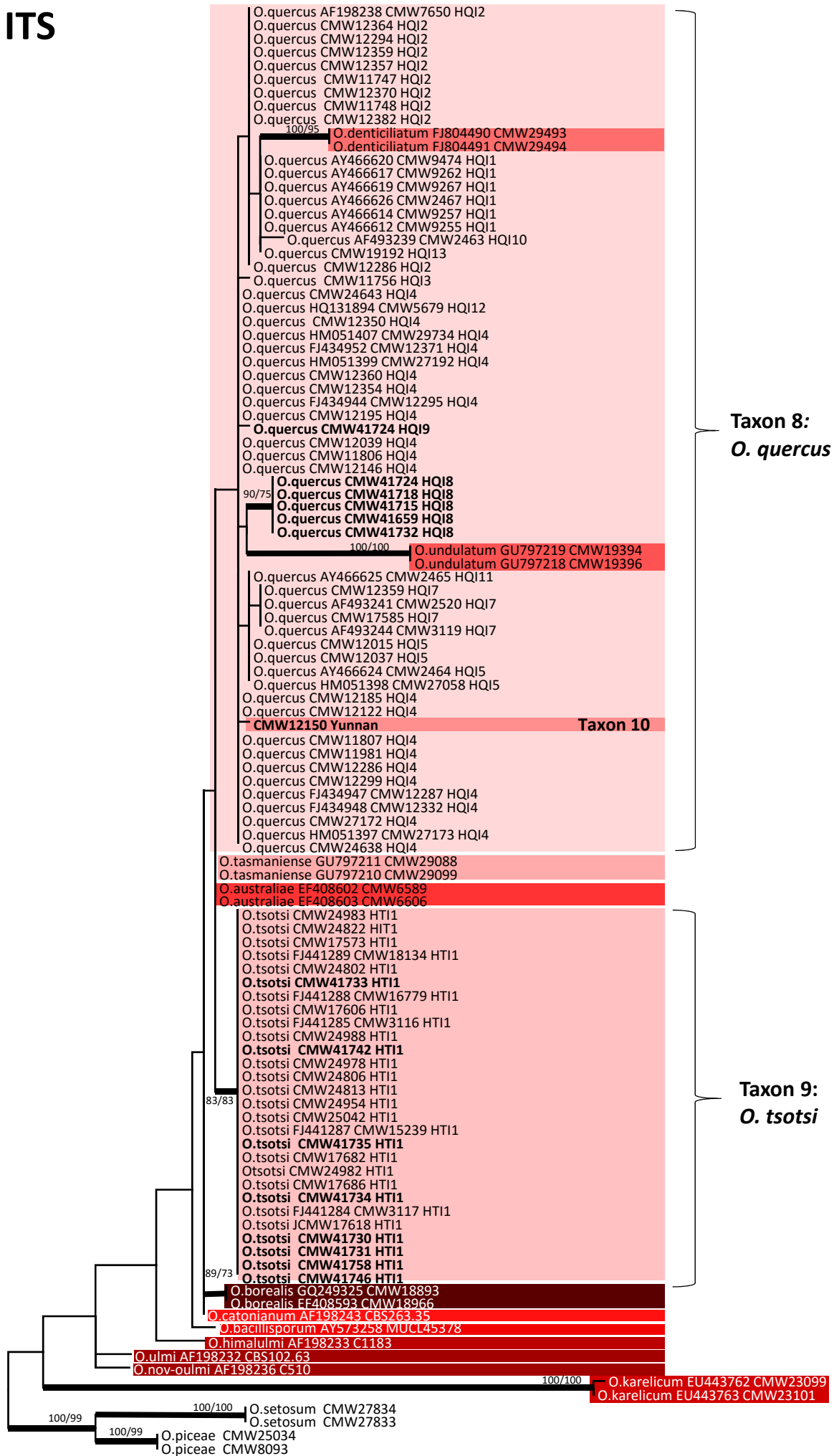
**Figure S4.** ML trees of the *O. ips* complex generated from DNA sequences of ITS and BT regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.



**Figure S5.** ML trees of the *O. piceae* complex generated from DNA sequences of BT and EF regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.

**Figure S6.** ML tree of the *O. quercus* complex generated from DNA sequences of ITS region. *Bold* branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.

ITS

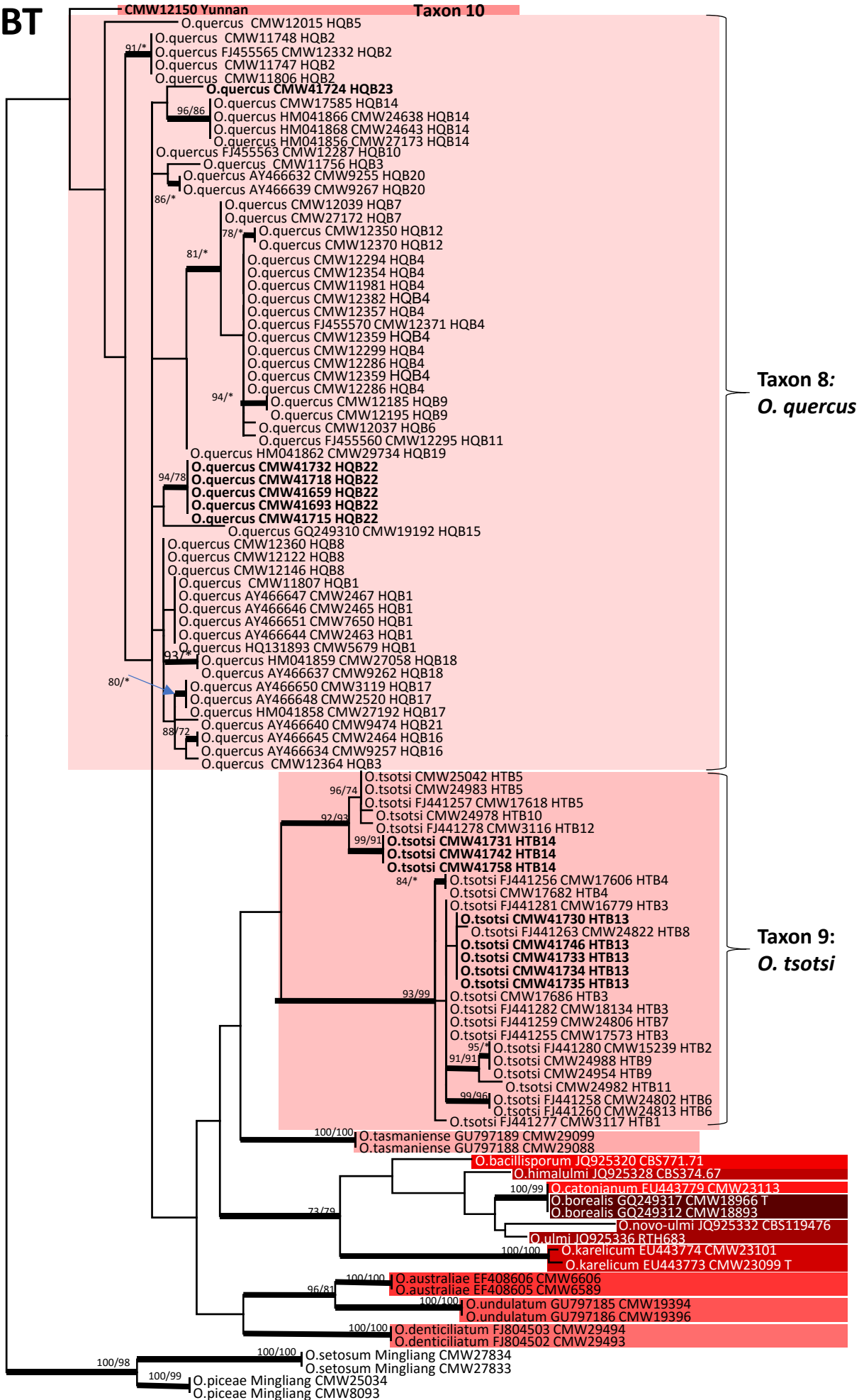


0.001

**Figure S7.** ML tree of the *O. quercus* complex generated from DNA sequences of BT region. *Bold* branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.

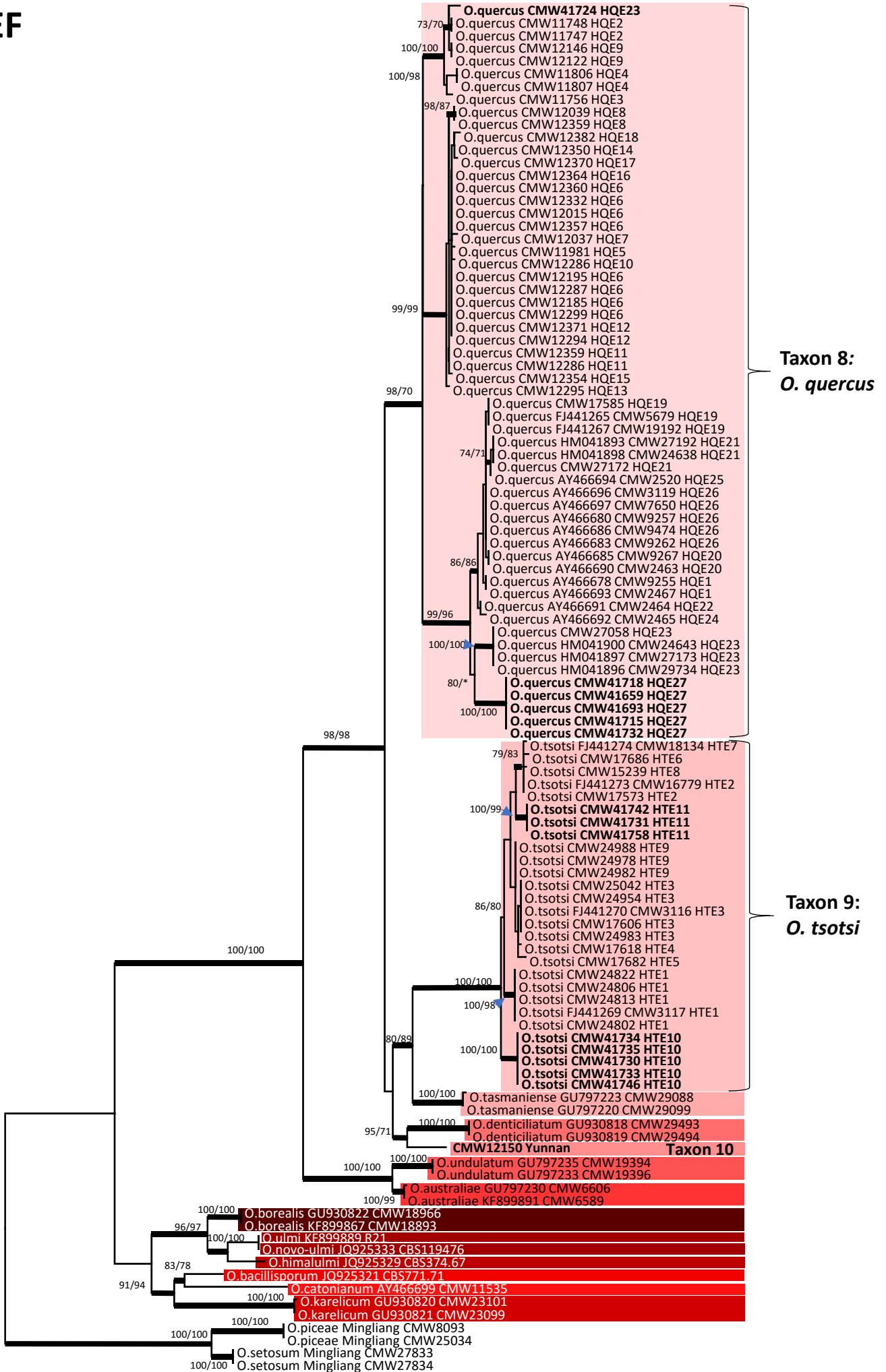


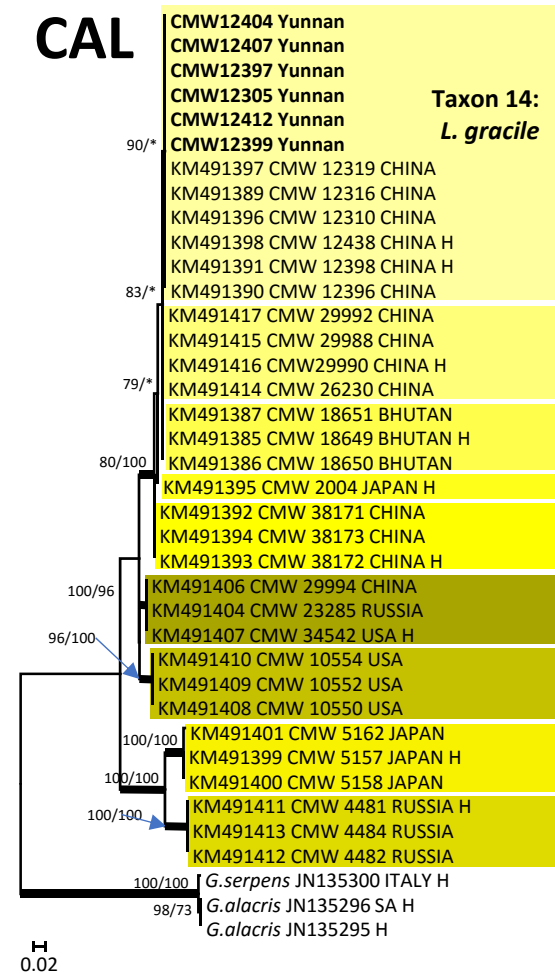
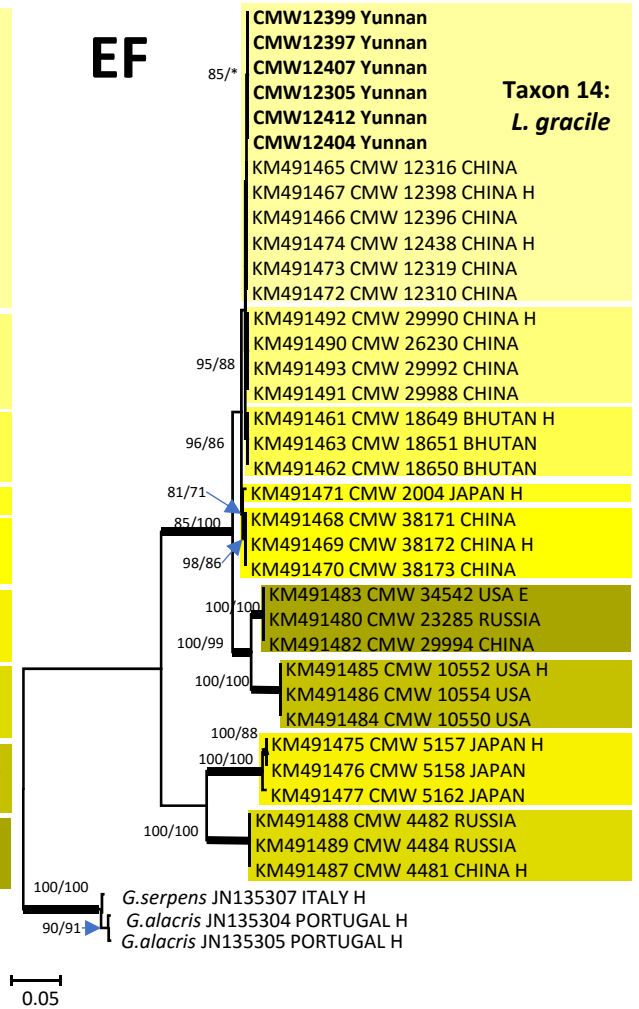
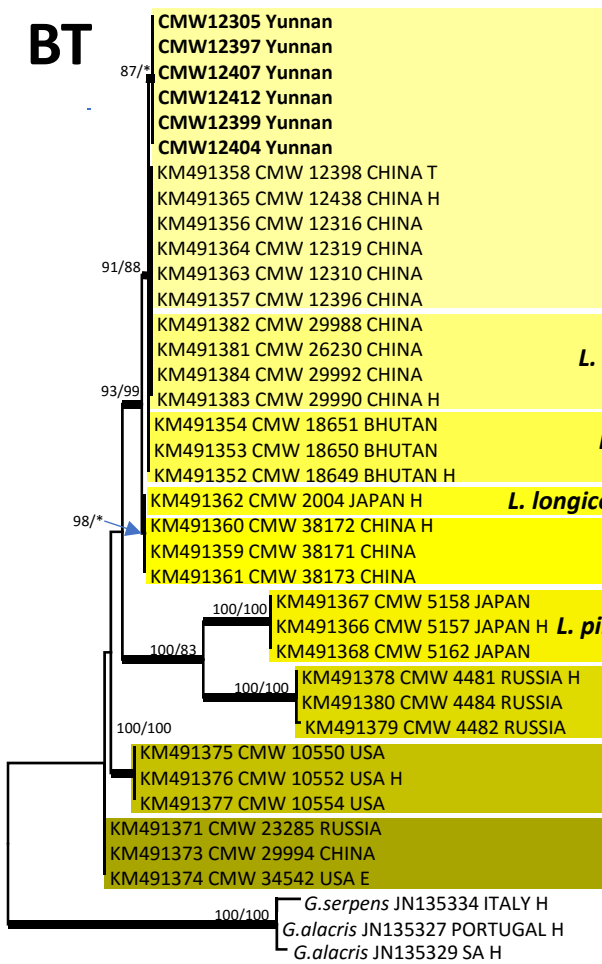
BT



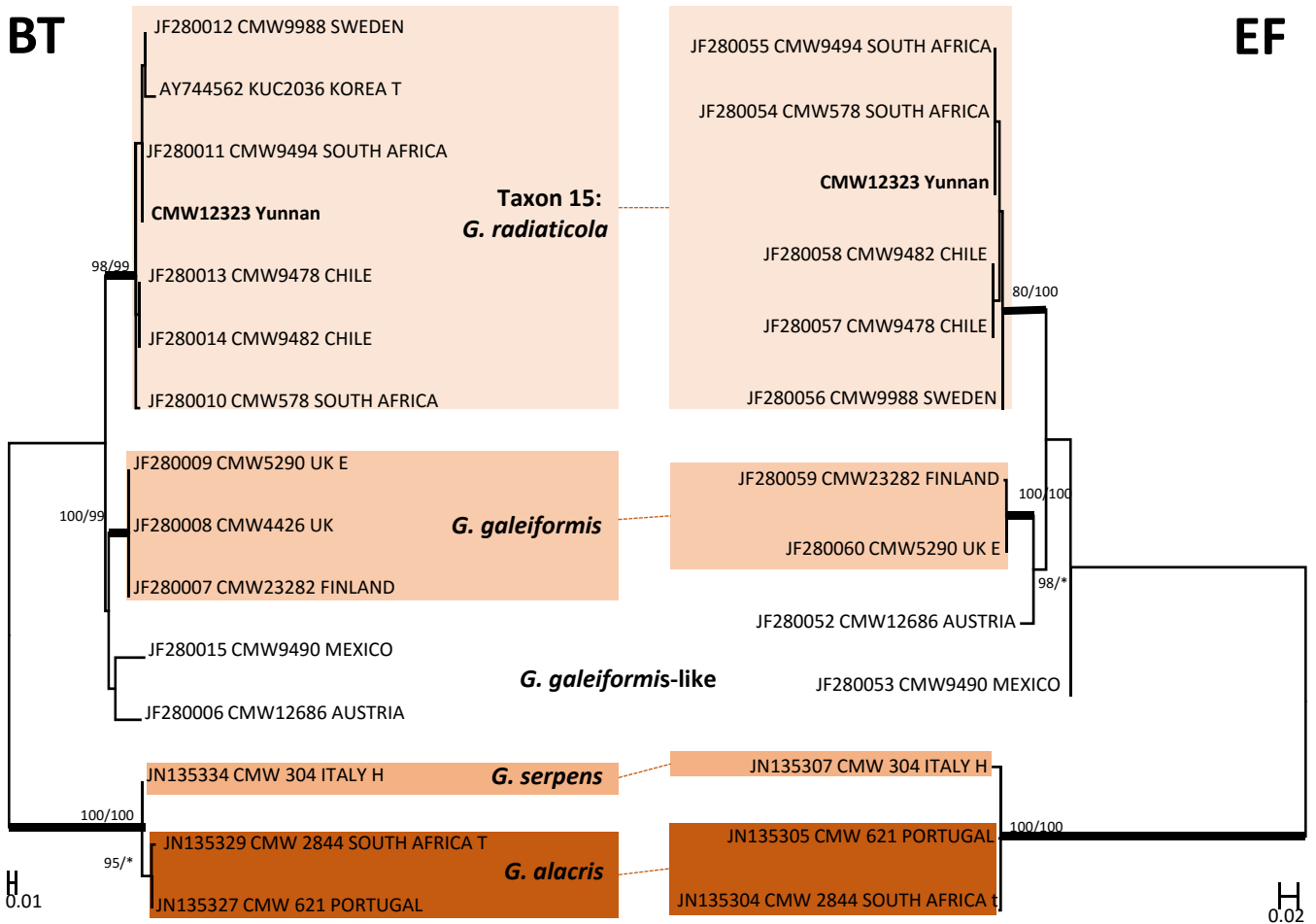
**Figure S8.** ML tree of the *O. quercus* complex generated from DNA sequences of EF region. *Bold* branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.

EF

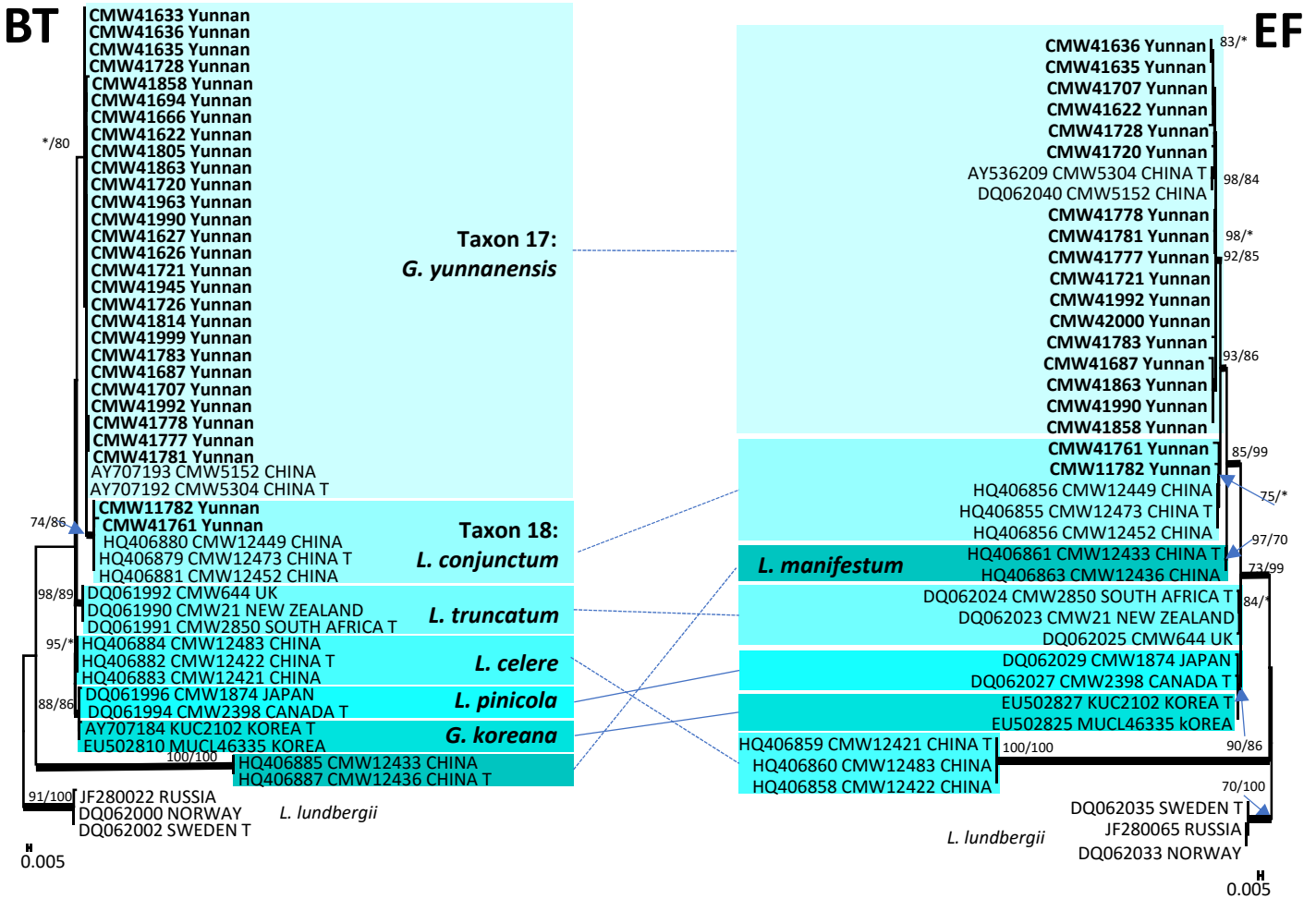




**Figure S9.** ML trees of the *L. procerum* complex generated from DNA sequences of BT, EF and CAL regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.



**Figure S10.** ML trees of the *G. galeiformis* complex generated from DNA sequences of BT and EF regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.



**Figure S11.** ML trees of the *L. lundbergii* complex generated from DNA sequences of BT and EF regions. **Bold** branches indicate posterior probabilities values  $\geq 0.95$ . Bootstrap values  $\geq 70\%$  are recorded at nodes as ML/MP. T = ex-type isolates.