Fig. S1. Phylogenies of *Bacidia* s.s. resulting from the analysis of the concatenated multilocus dataset with a minimum of two loci included (out of nrITS, nrLSU, mtSSU, RPB1 and RPB2). Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S2. Phylogenies of *Bacidia* s.s. resulting from the analysis of the concatenated multilocus dataset with a minimum of three loci included (out of nrITS, nrLSU, mtSSU, RPB1 and RPB2). Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S3. Phylogenies of *Bacidia heterochroa* s.l. resulting from the analysis of the nrITS dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S4. Phylogenies of *Bacidia* s.s. resulting from the analysis of the nrITS dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S5. Phylogenies of *Bacidia* s.s. resulting from the analysis of the nrLSU dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S6. Phylogenies of *Bacidia* s.s. resulting from the analysis of the mtSSU dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S7. Phylogenies of *Bacidia* s.s. resulting from the analysis of the RPB1 dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

Fig. S8. Phylogenies of *Bacidia* s.s. resulting from the analysis of the RPB2 dataset. Clade branches that received BSr ≥ 70%, PP ≥ 0.95 or BSi ≥ 80%, respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

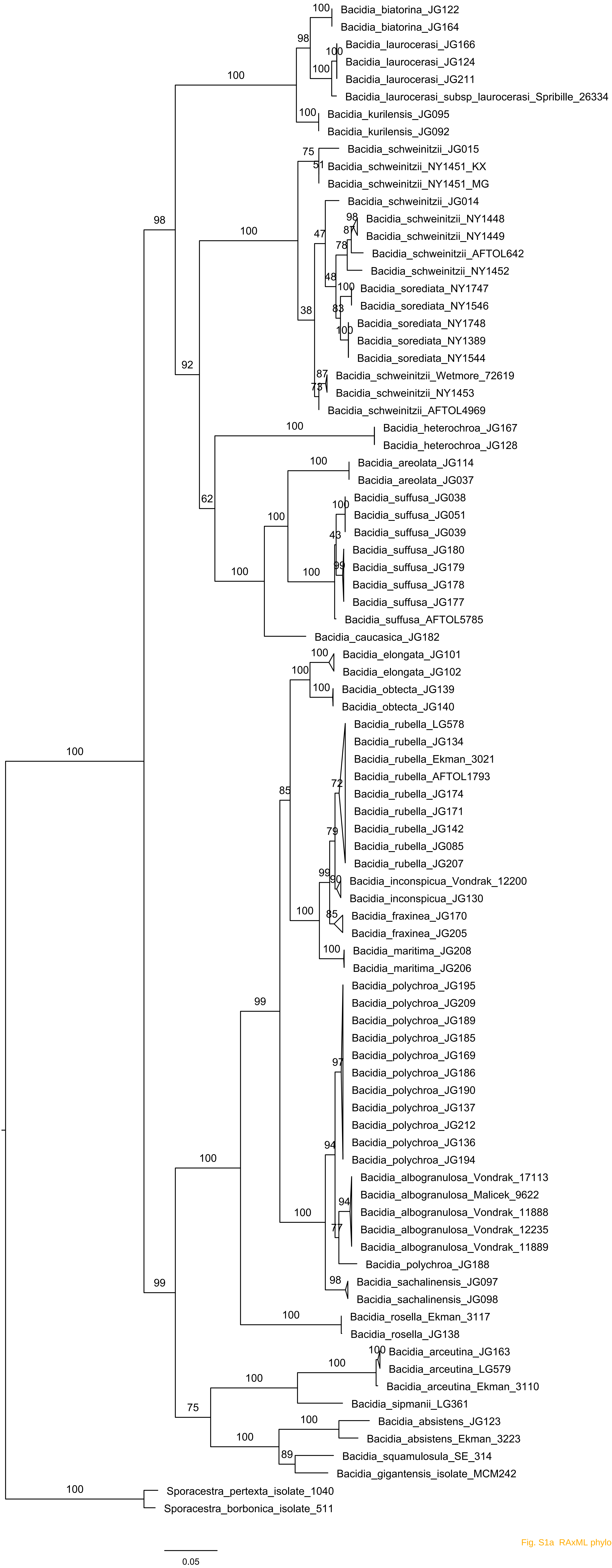

Fig. S1a RAxML phylogeny

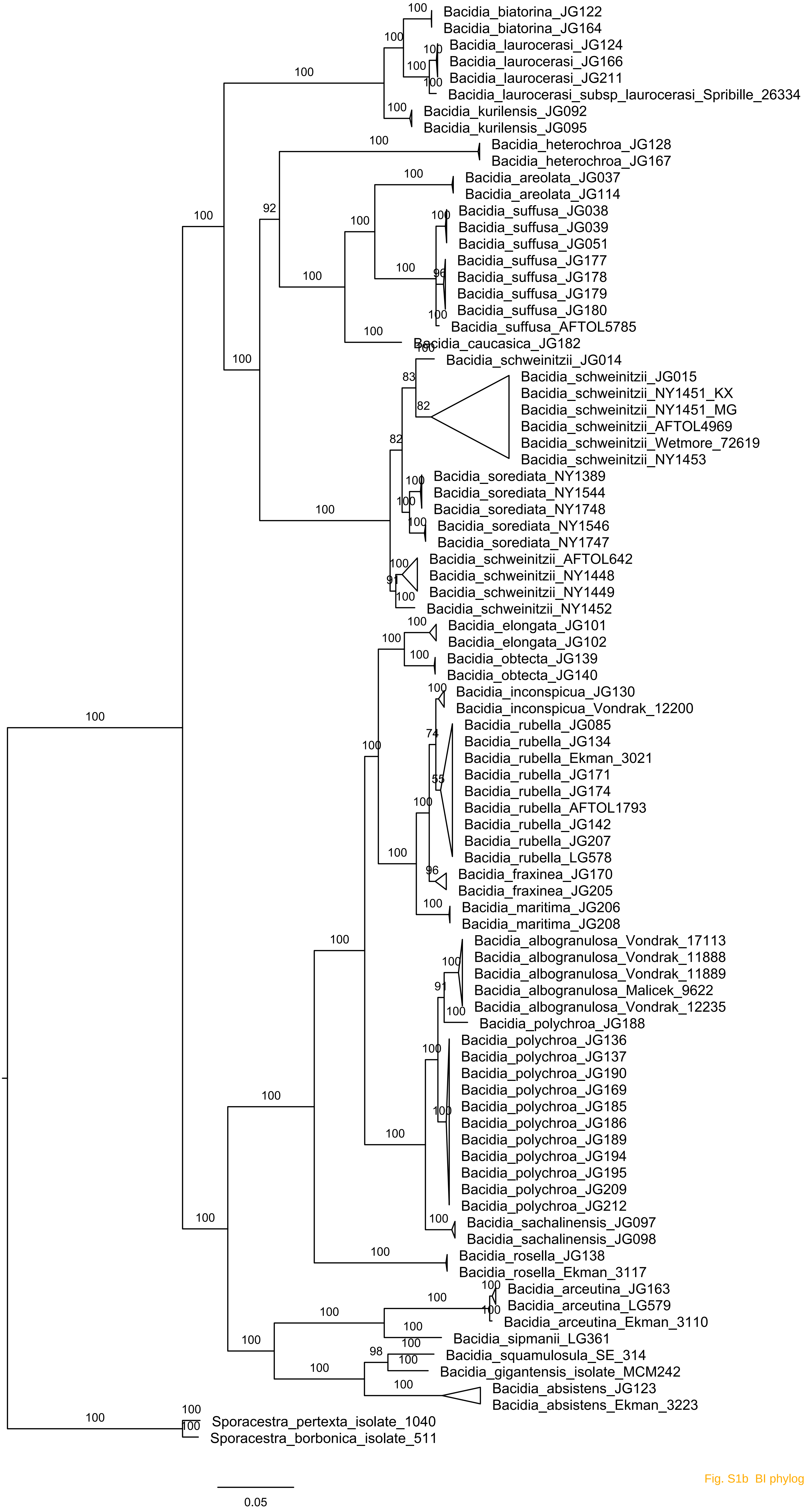

Fig. S1b BI phylogeny

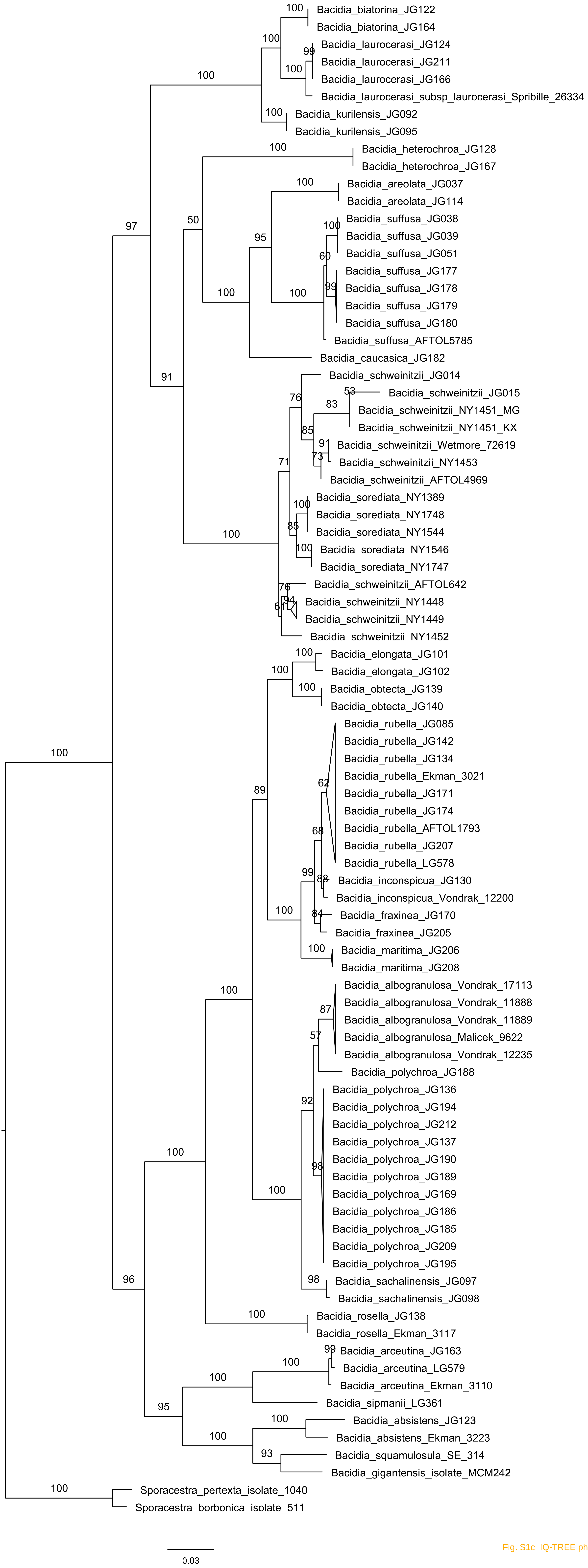

Fig. S1c IQ-TREE phylogeny

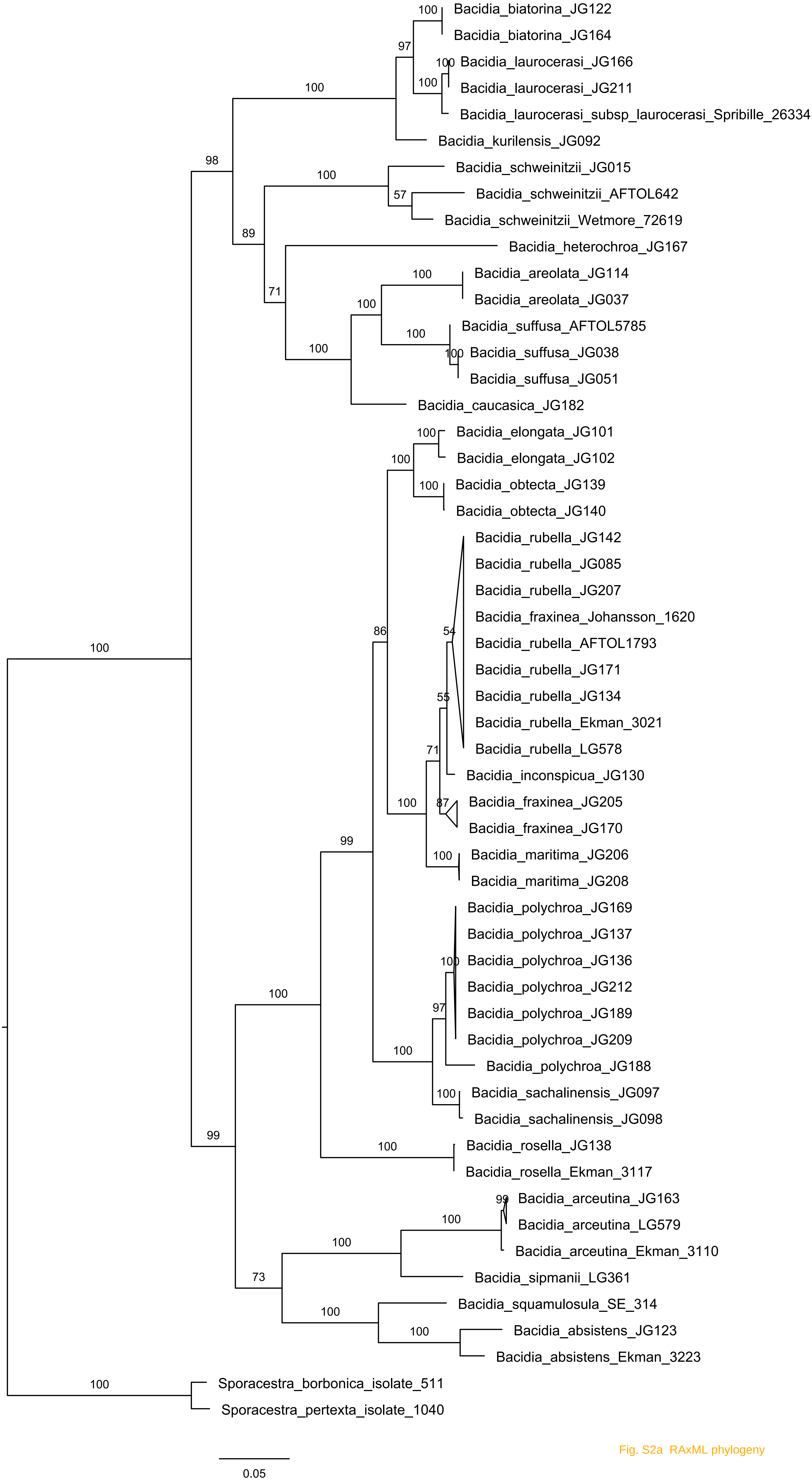

Fig. S2a RAxML phylogeny

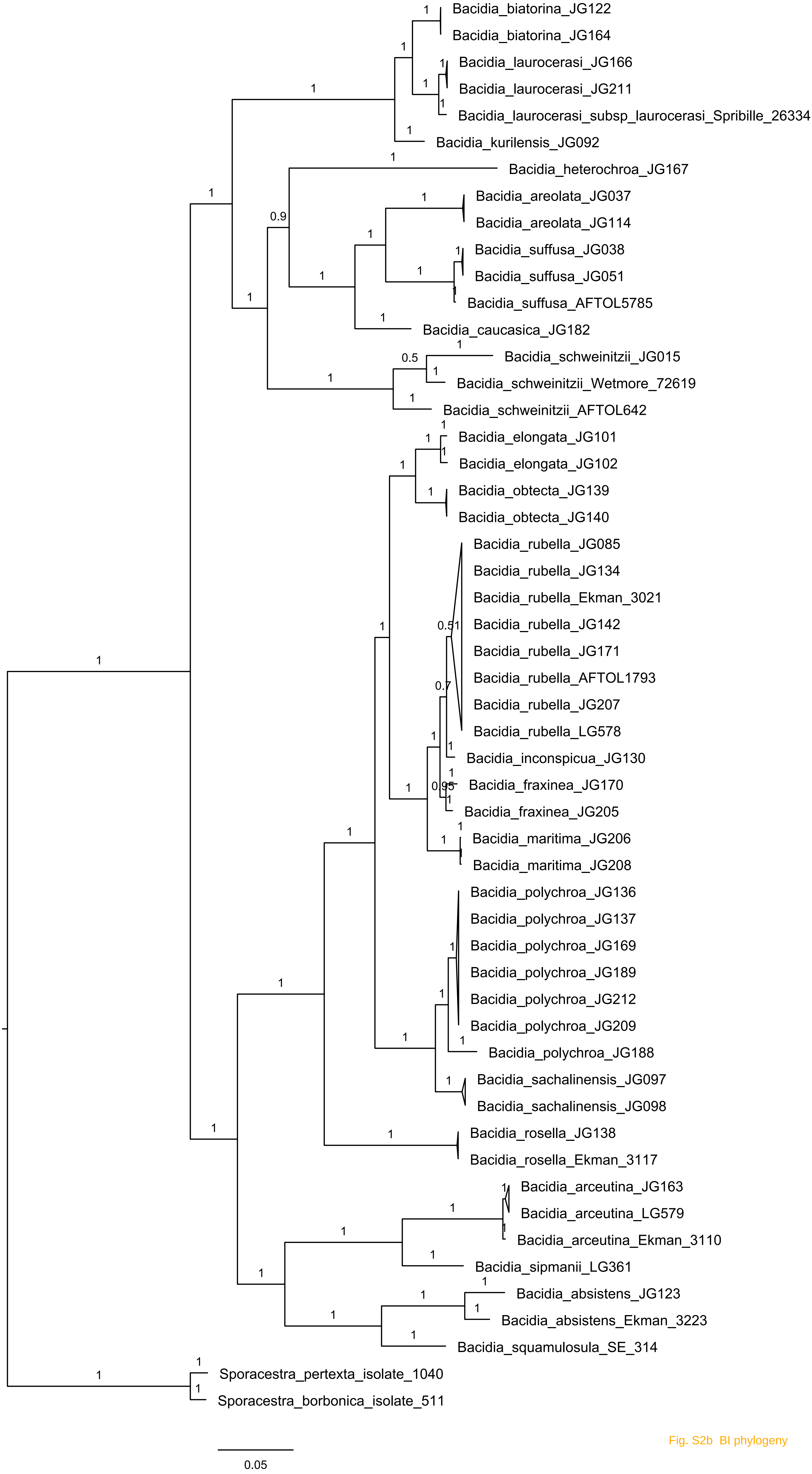

Fig. S2b BI phylogeny

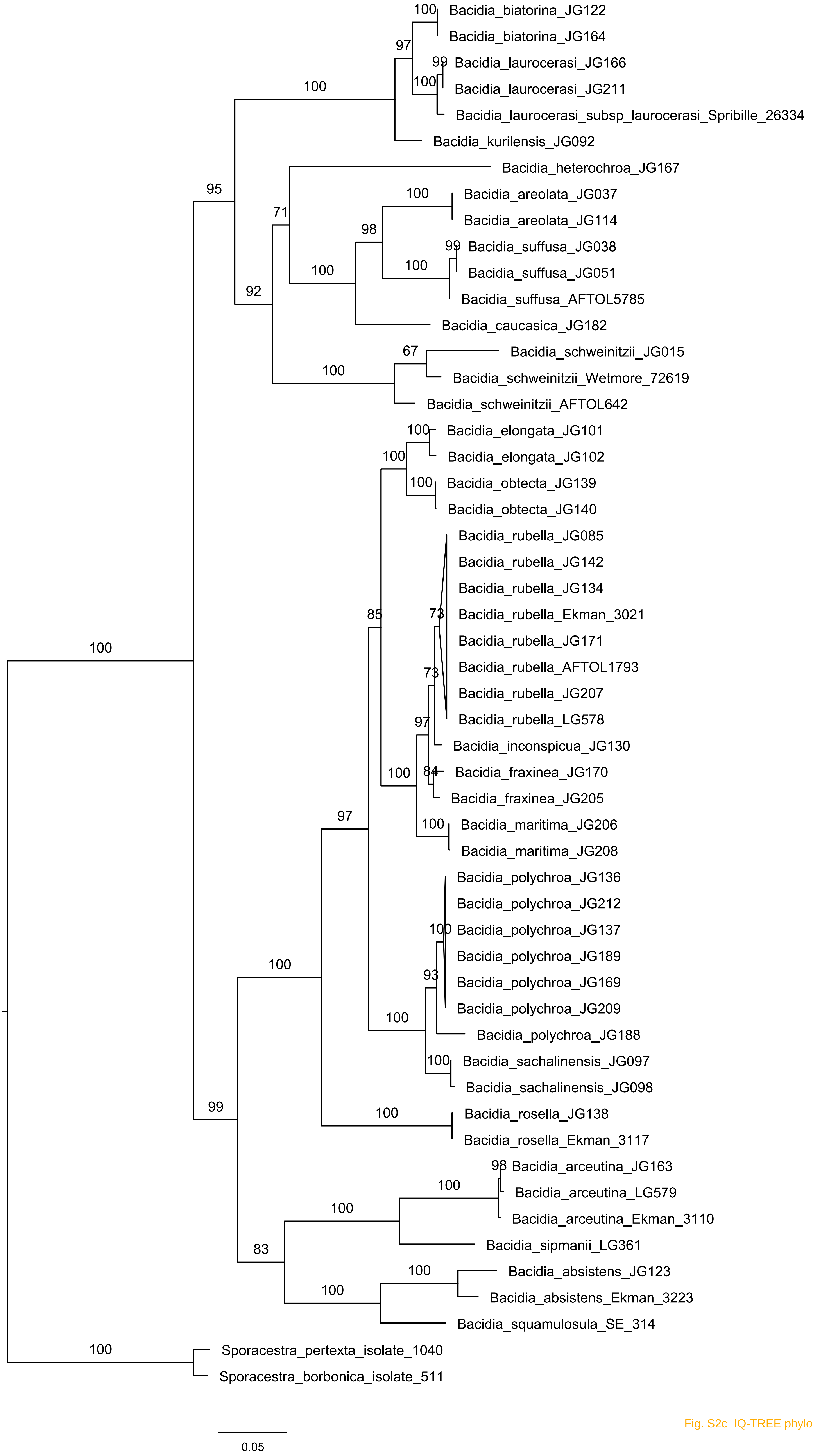

Fig. S2c IQ-TREE phylogeny

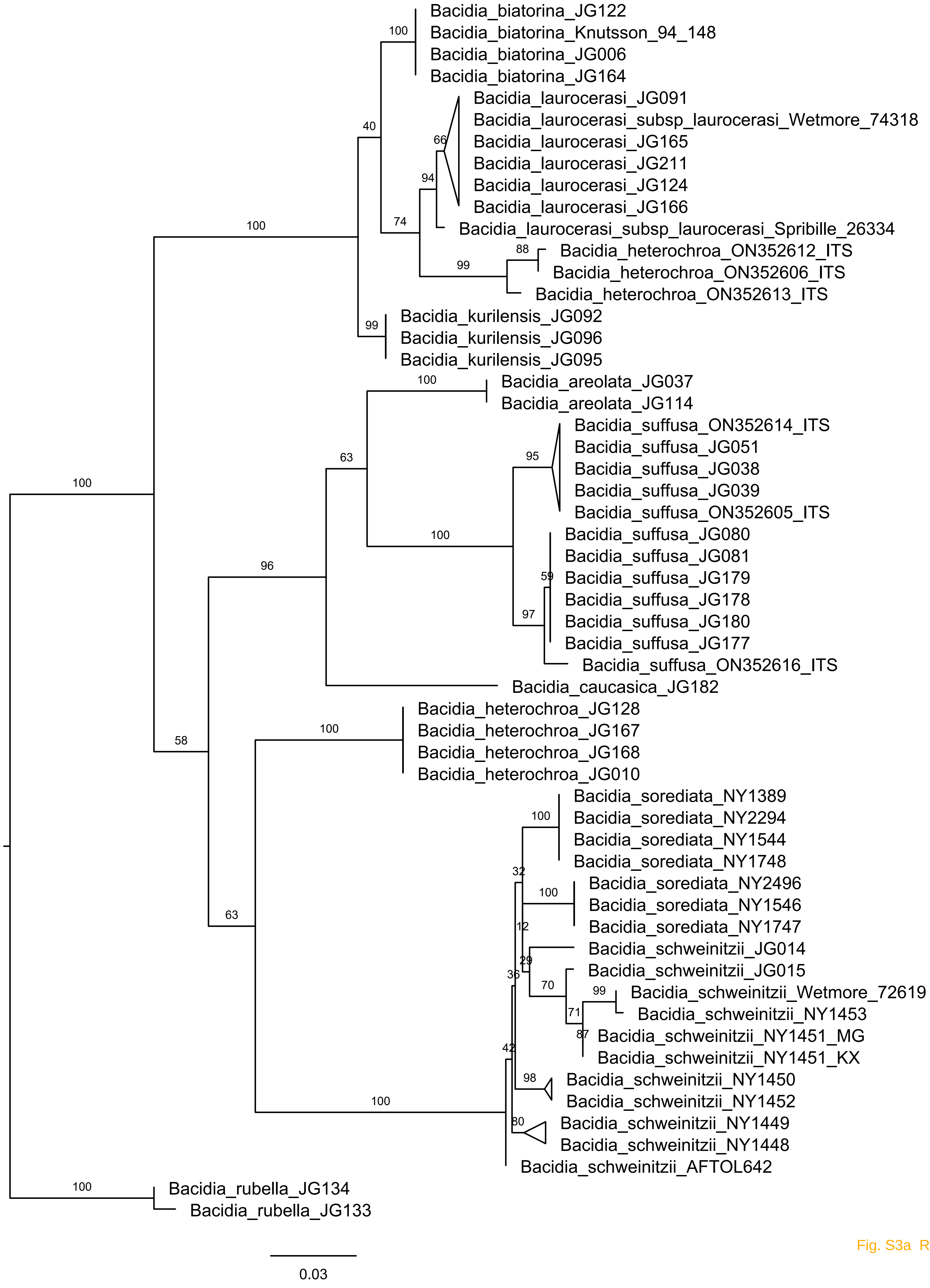

Fig. S3a RAxML phylogeny

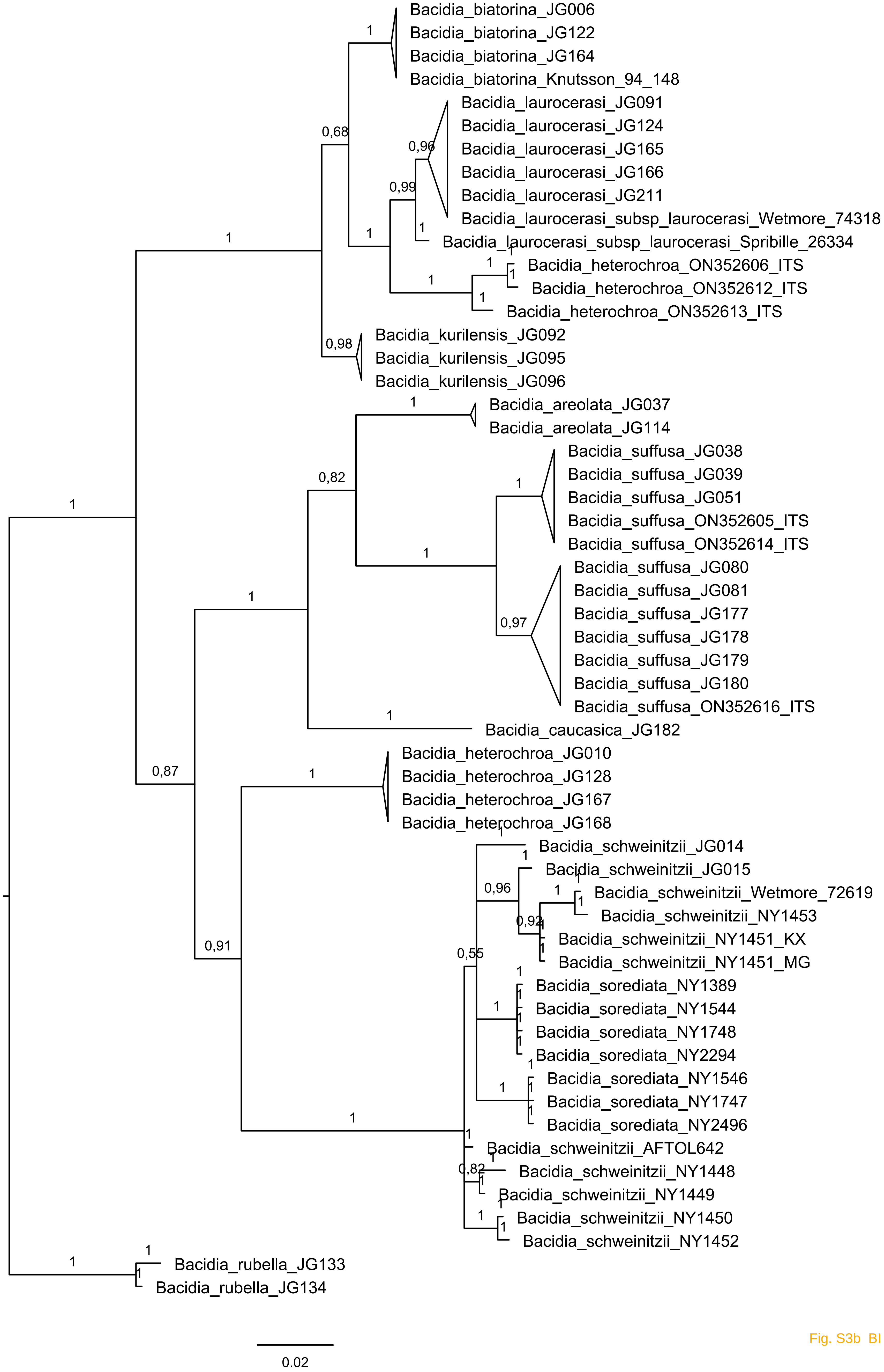

Fig. S3b BI phylogeny

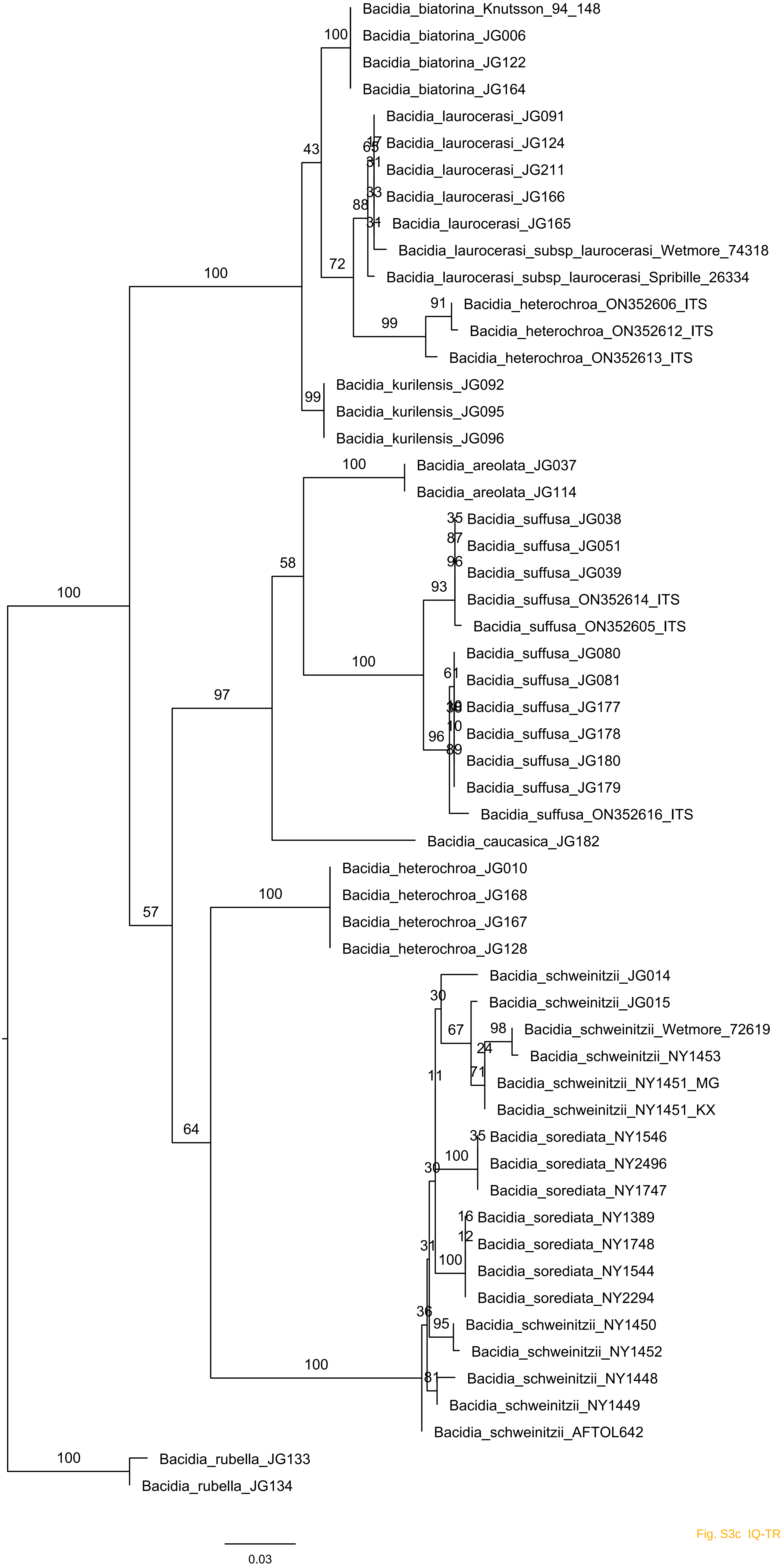

Fig. S3c IQ-TREE phylogeny

Fig. S4a RAxML phylogeny

Fig. S4b BI phylogeny

Fig. S4c IQ-TREE phylogeny

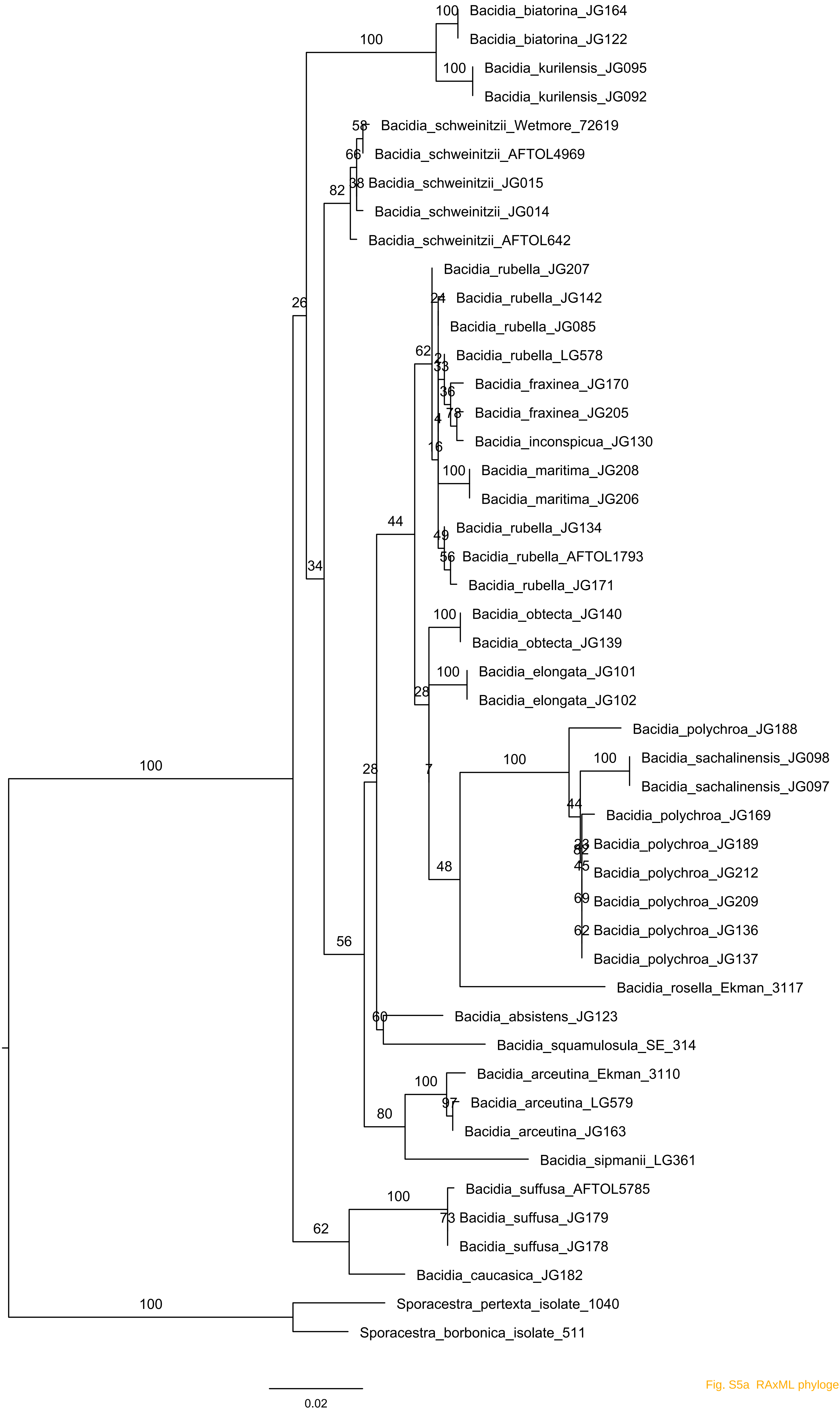

Fig. S5a RAxML phylogeny

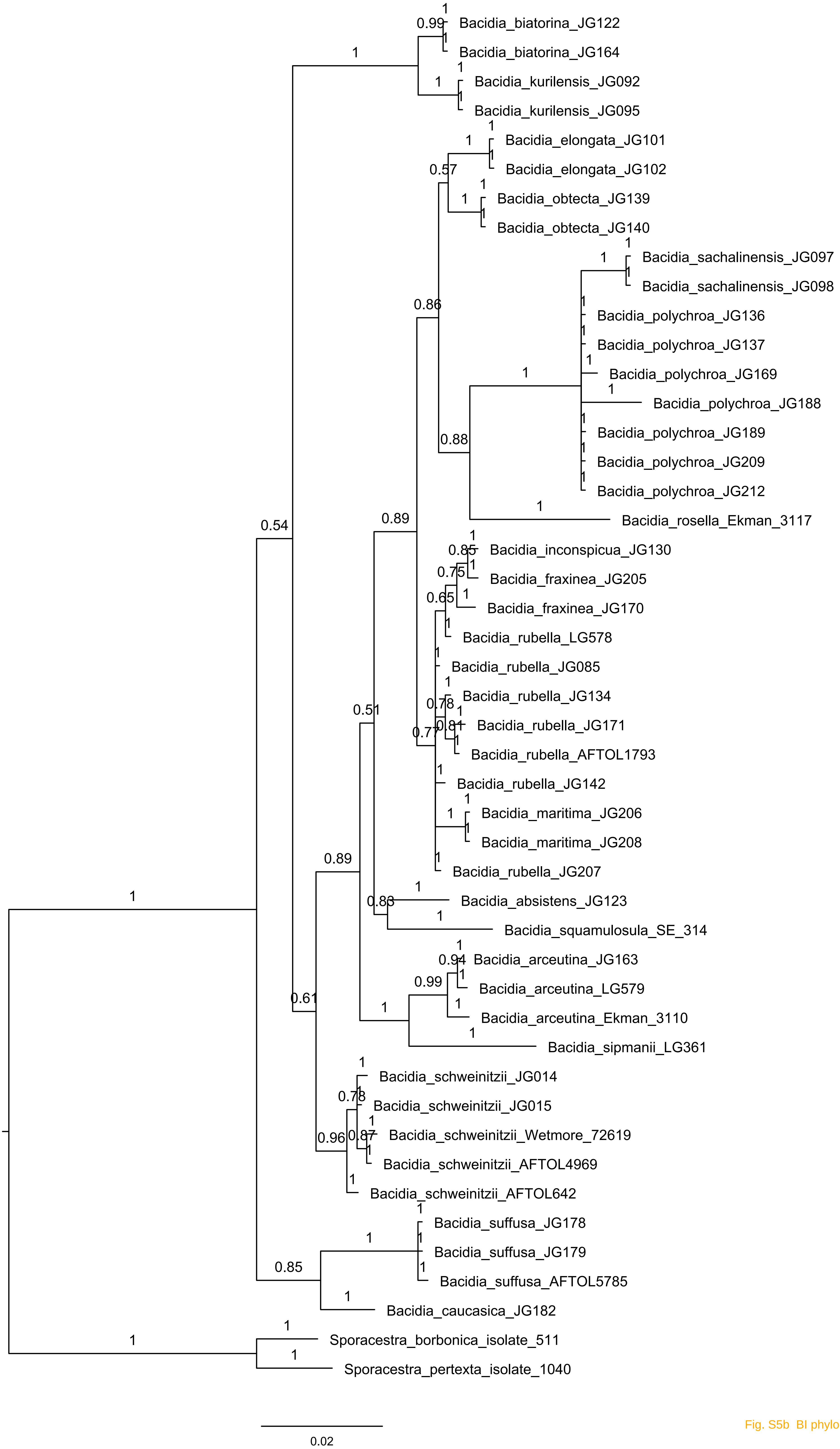

Fig. S5b BI phylogeny

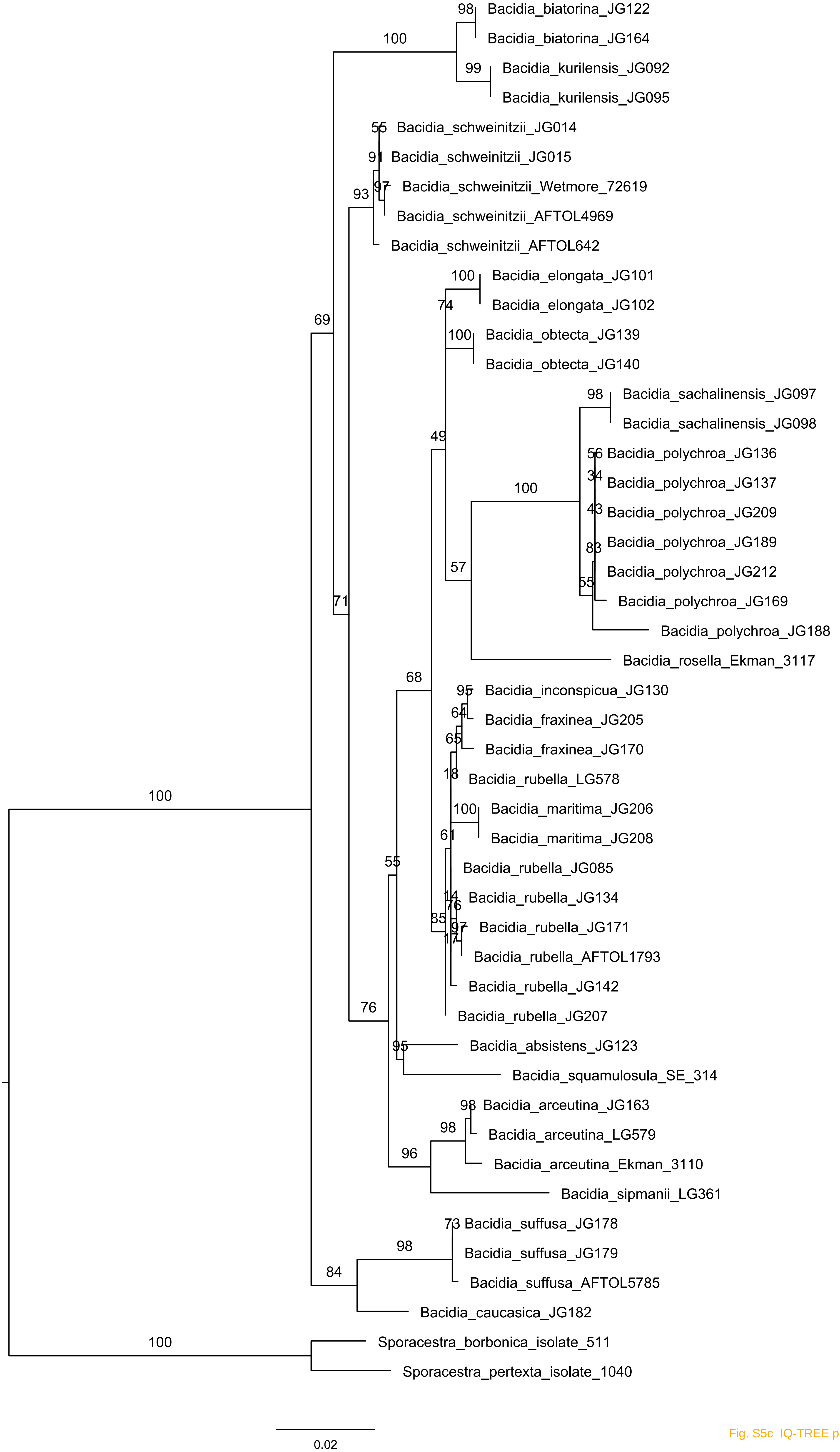

Fig. S5c IQ-TREE phylogeny

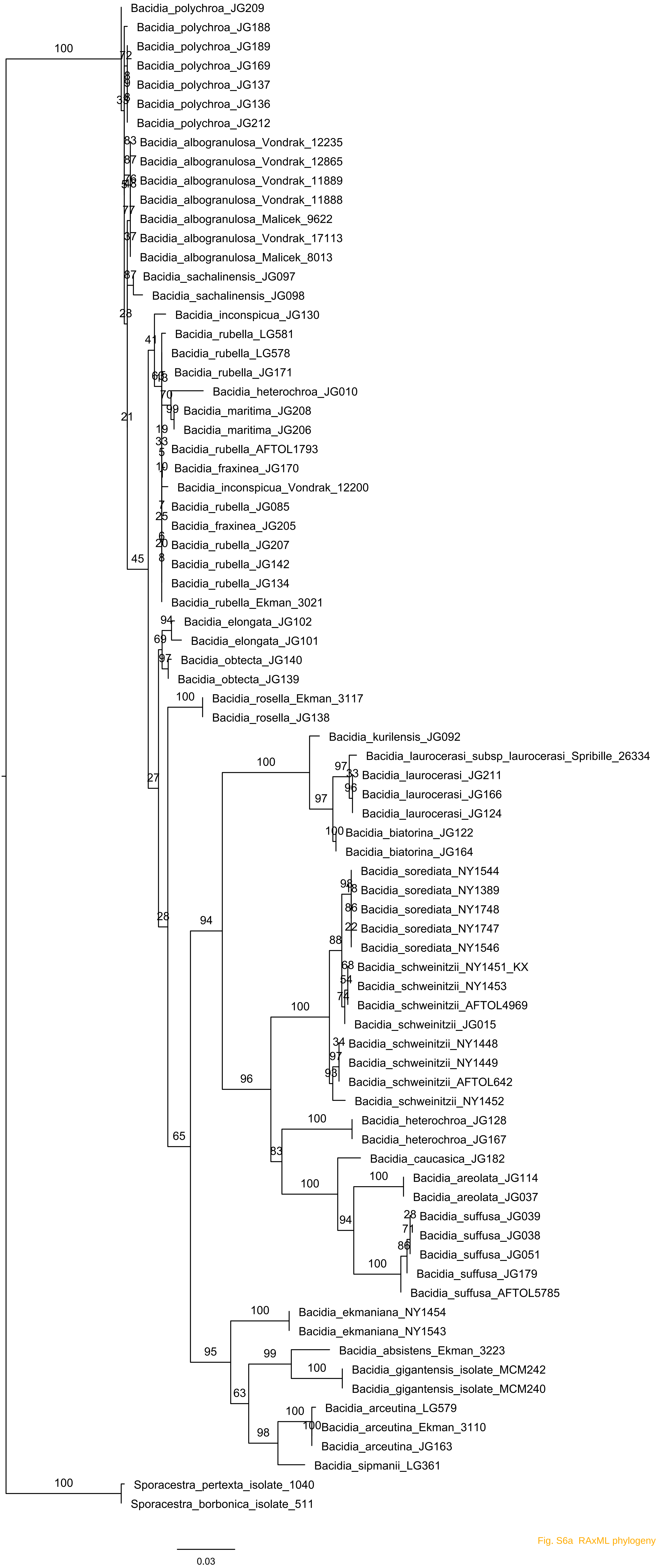

Fig. S6a RAxML phylogeny

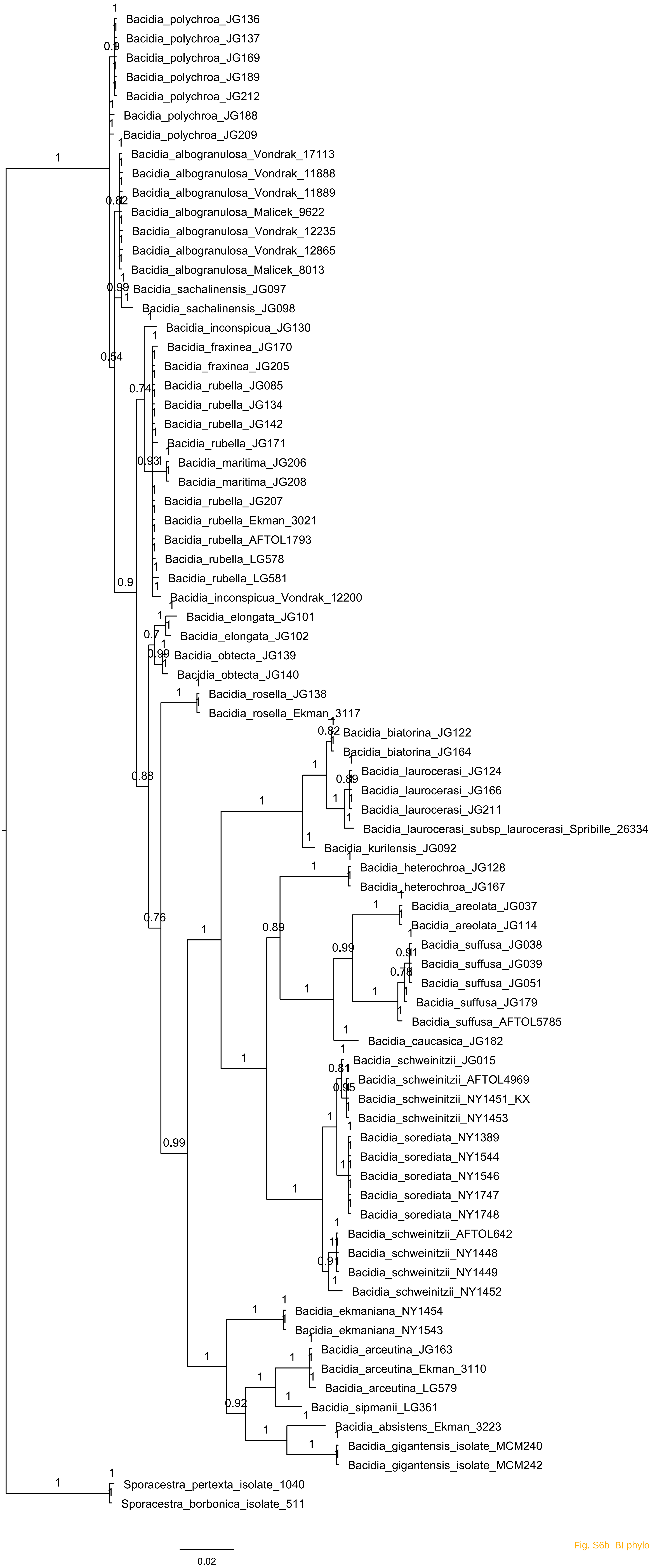

Fig. S6b BI phylogeny

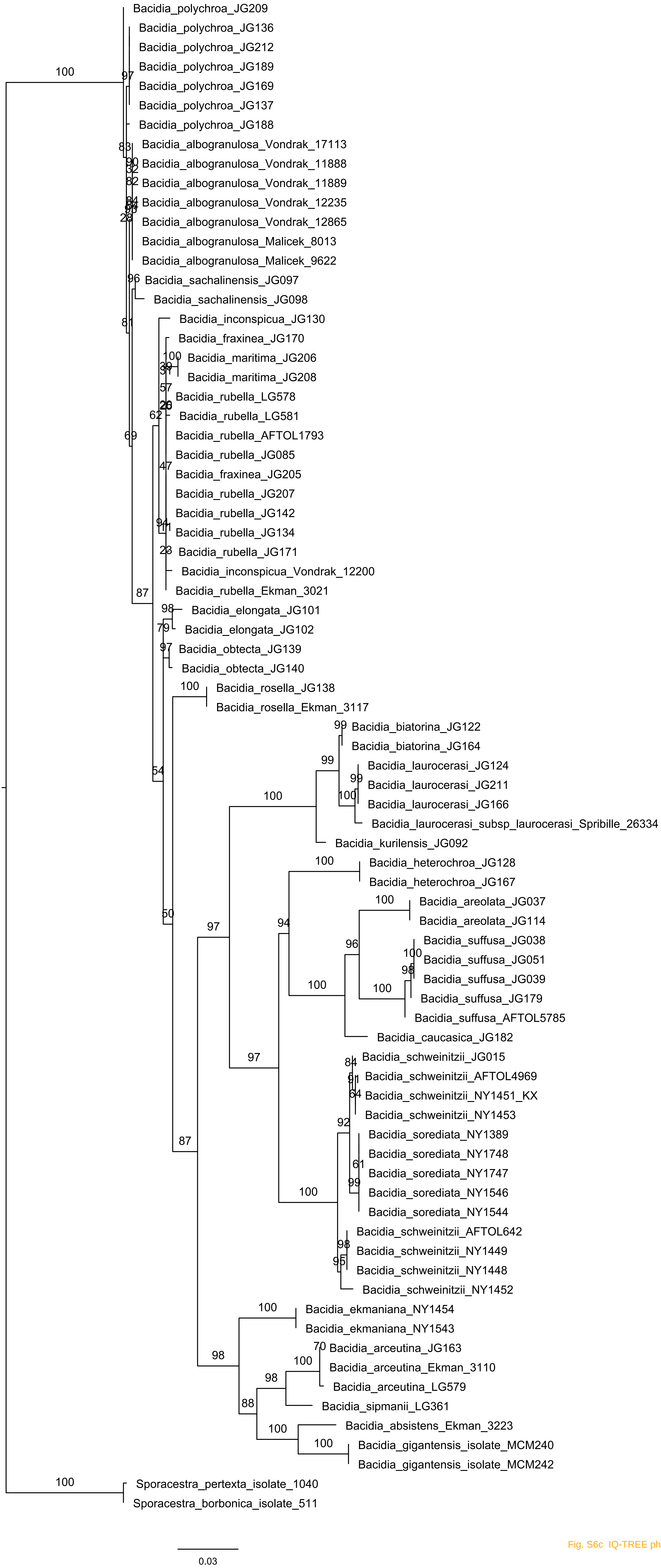

Fig. S6c IQ-TREE phylogeny

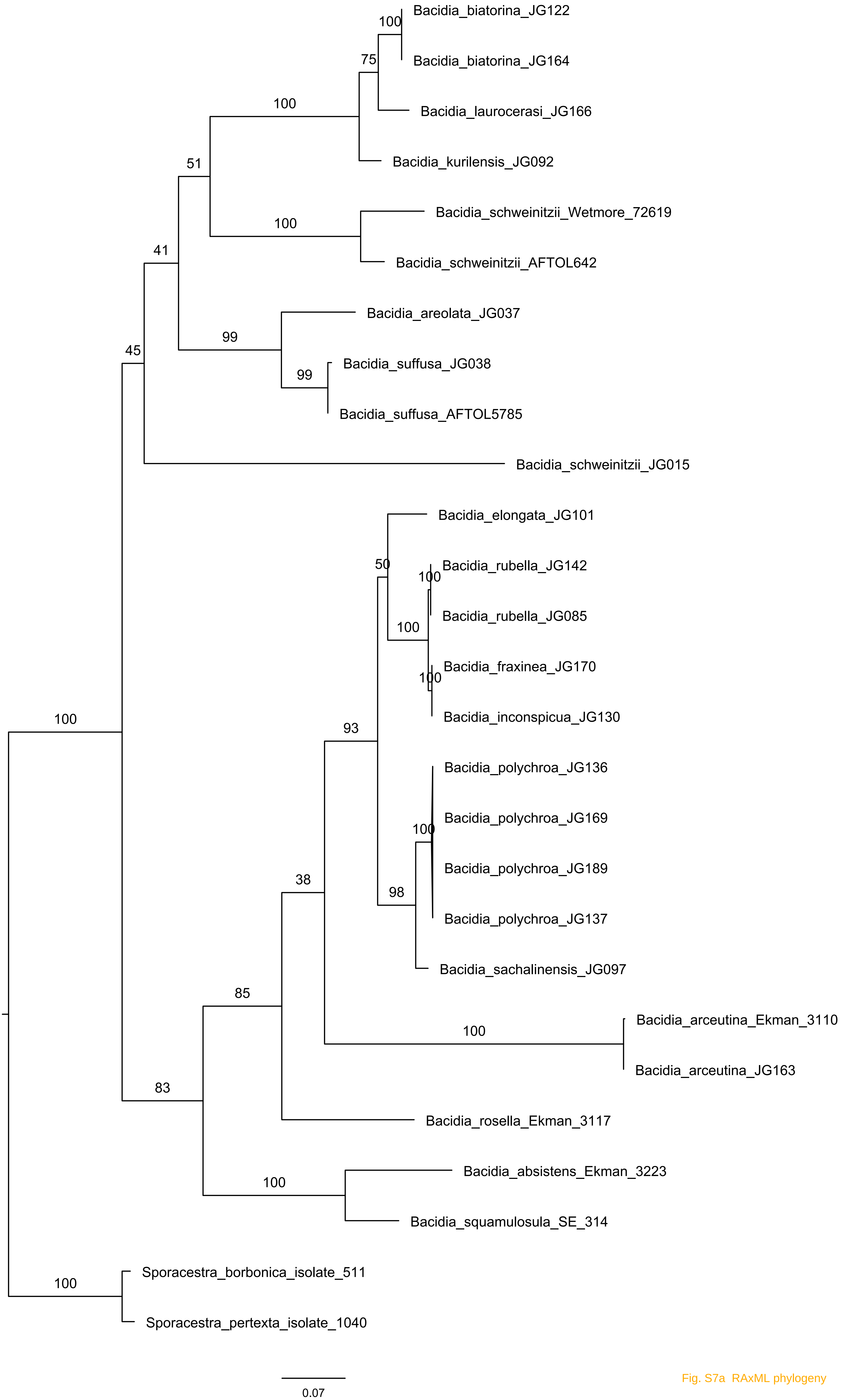

Fig. S7a RAxML phylogeny

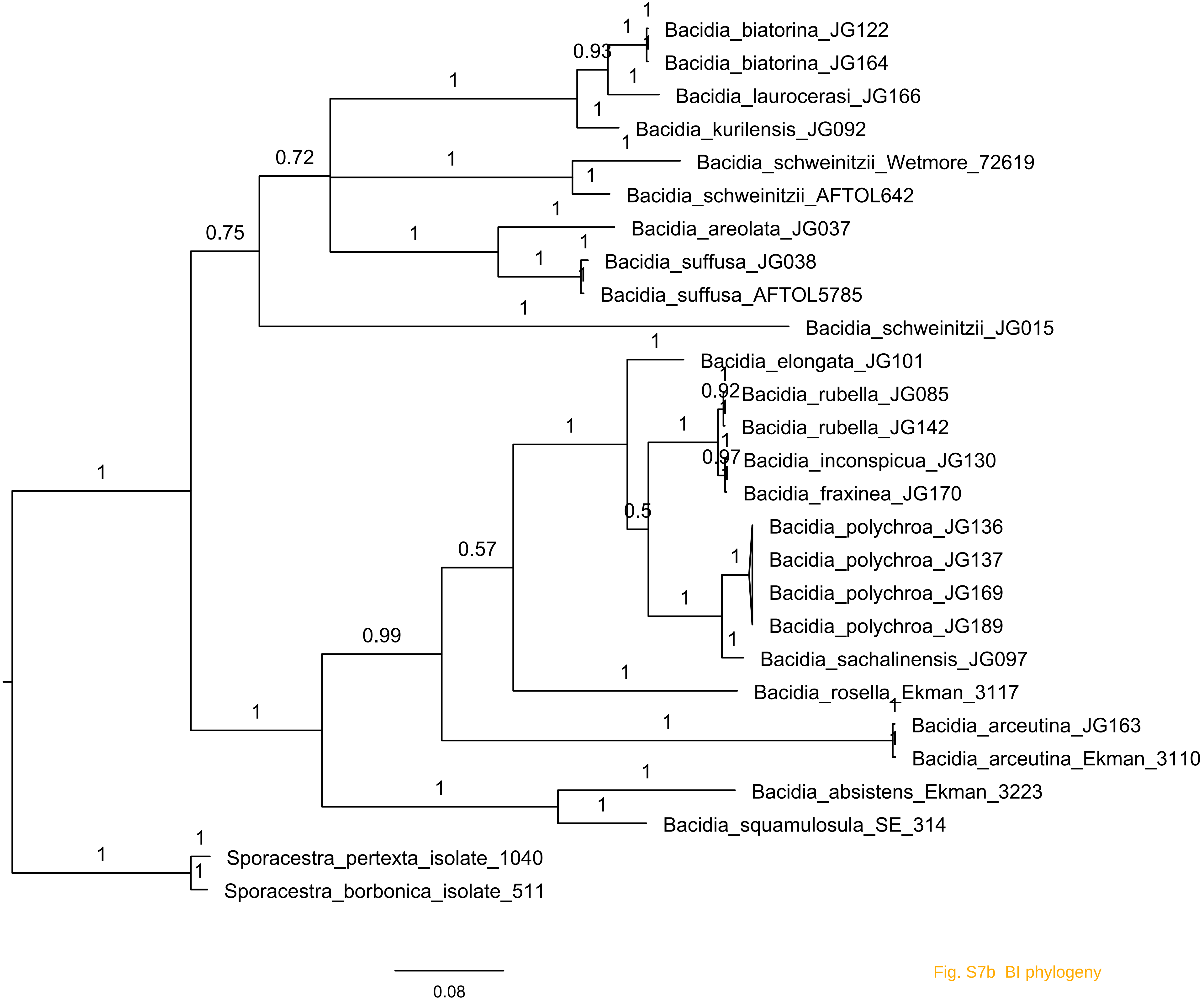

Fig. S7b BI phylogeny

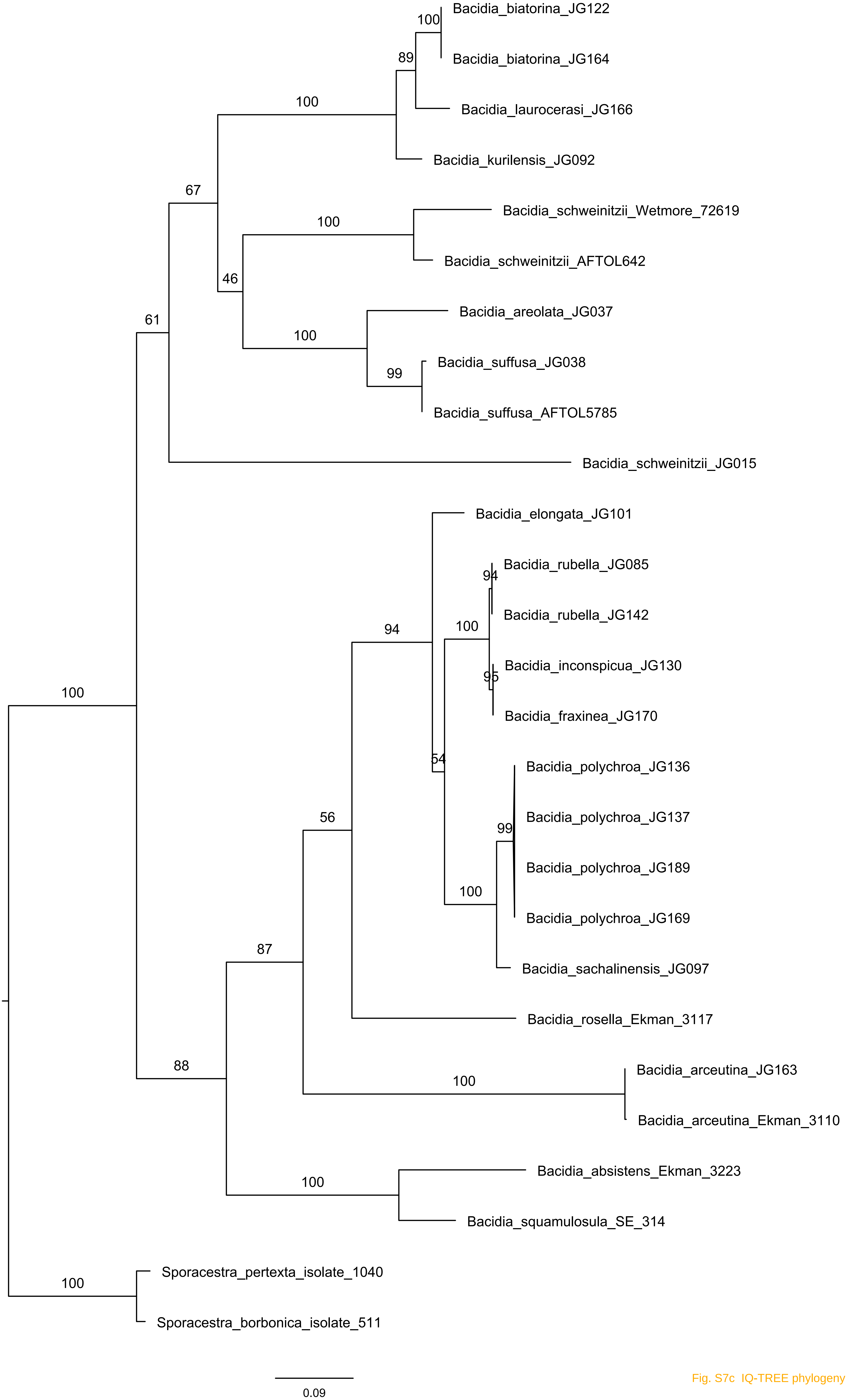

Fig. S7c IQ-TREE phylogeny

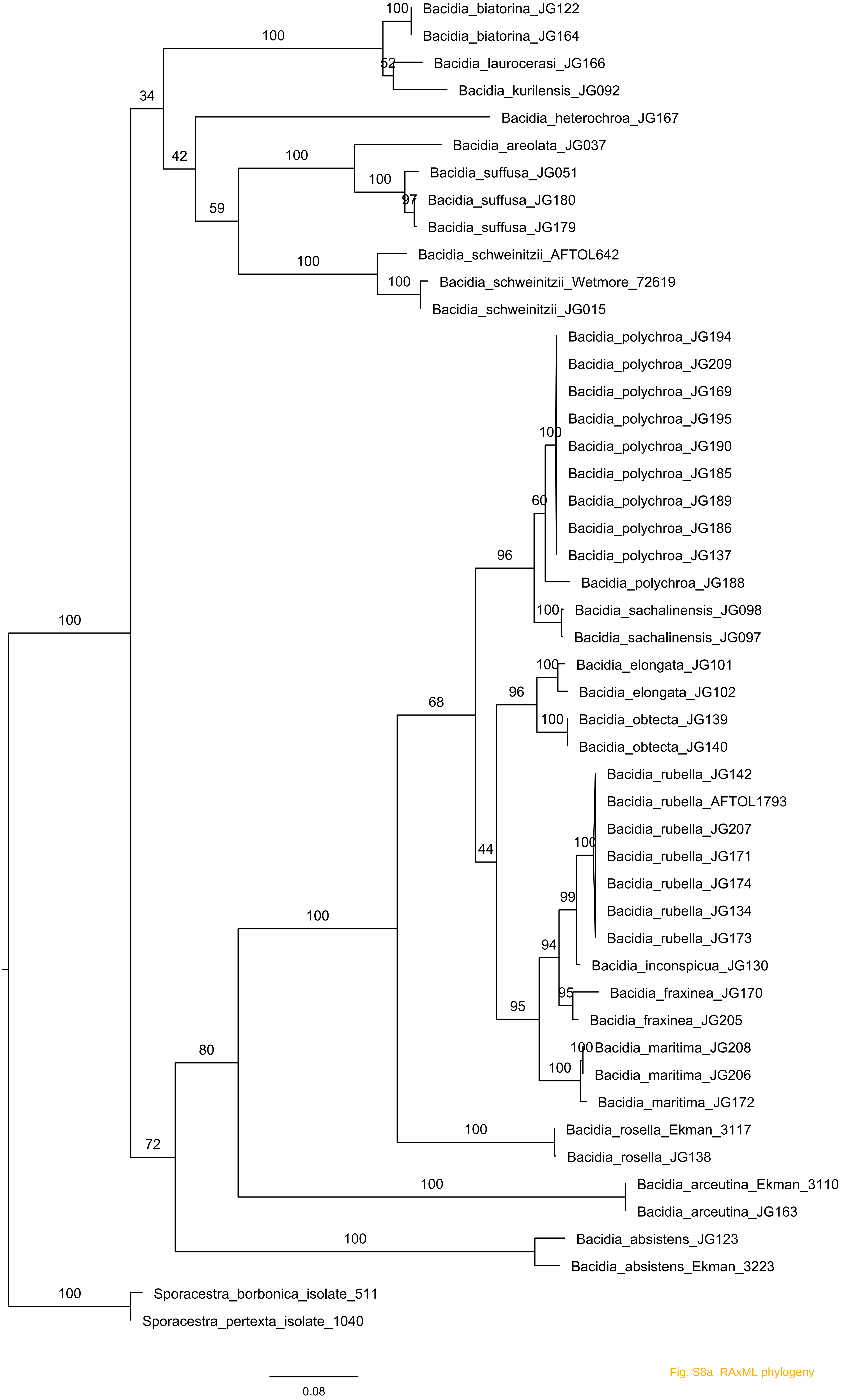

Fig. S8a RAxML phylogeny

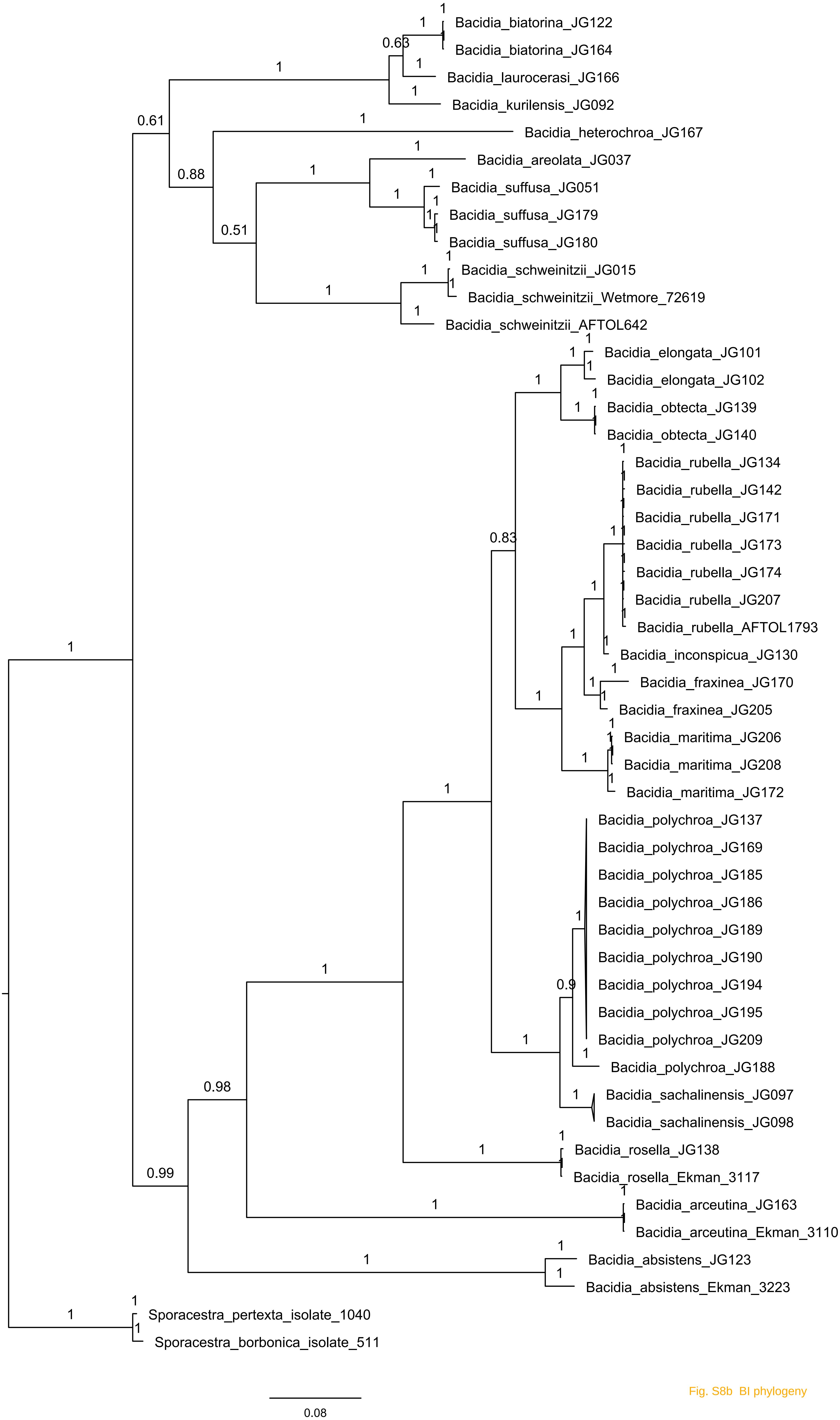

Fig. S8b BI phylogeny

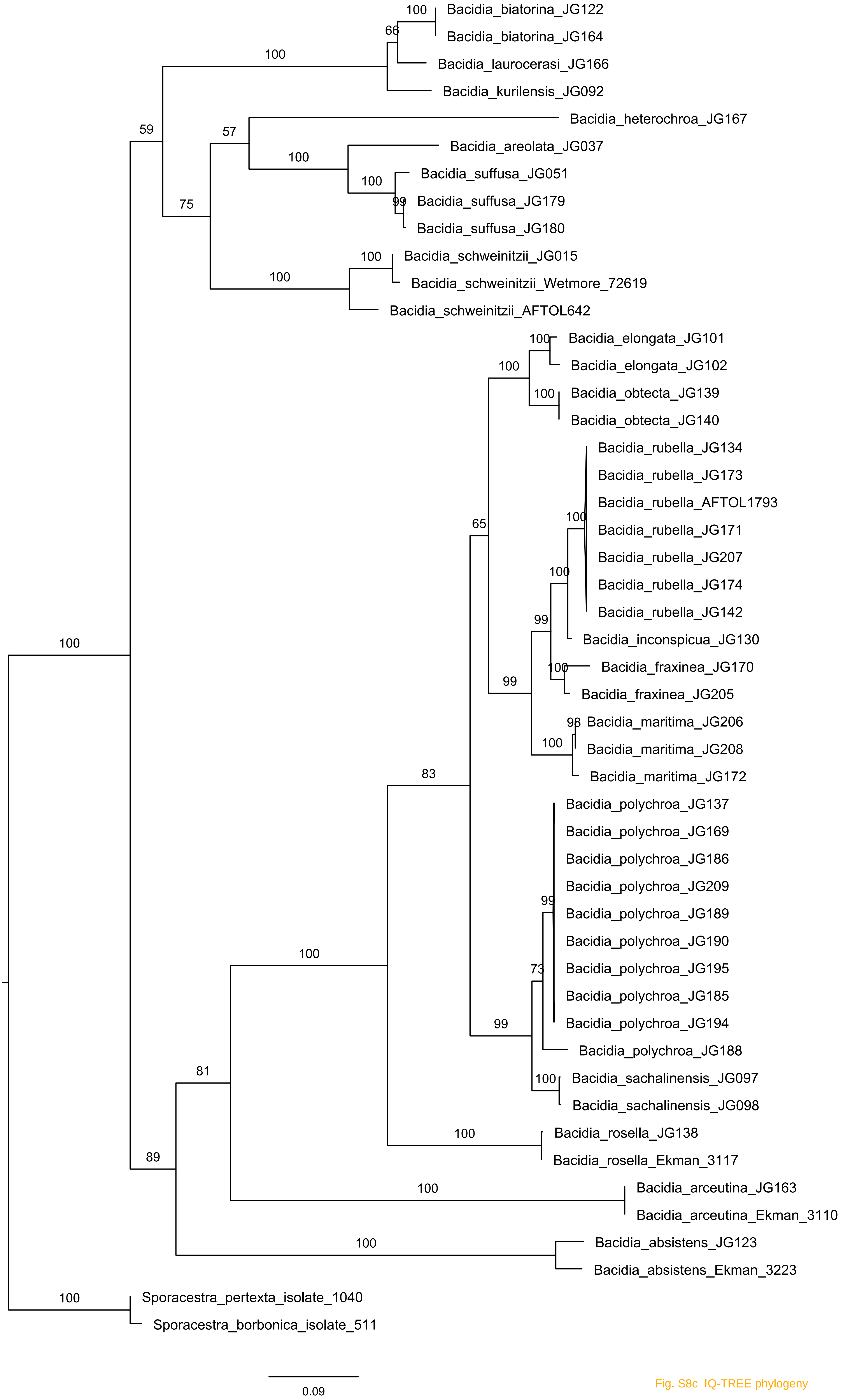

Fig. S8c IQ-TREE phylogeny