

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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , 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  $BSr \geq 70\%$ ,  $PP \geq 0.95$  or  $BSi \geq 80\%$ , respectively, were considered highly supported and given in bold. a) RAxML analysis, b) BI analysis, c) IQ-TREE analysis.

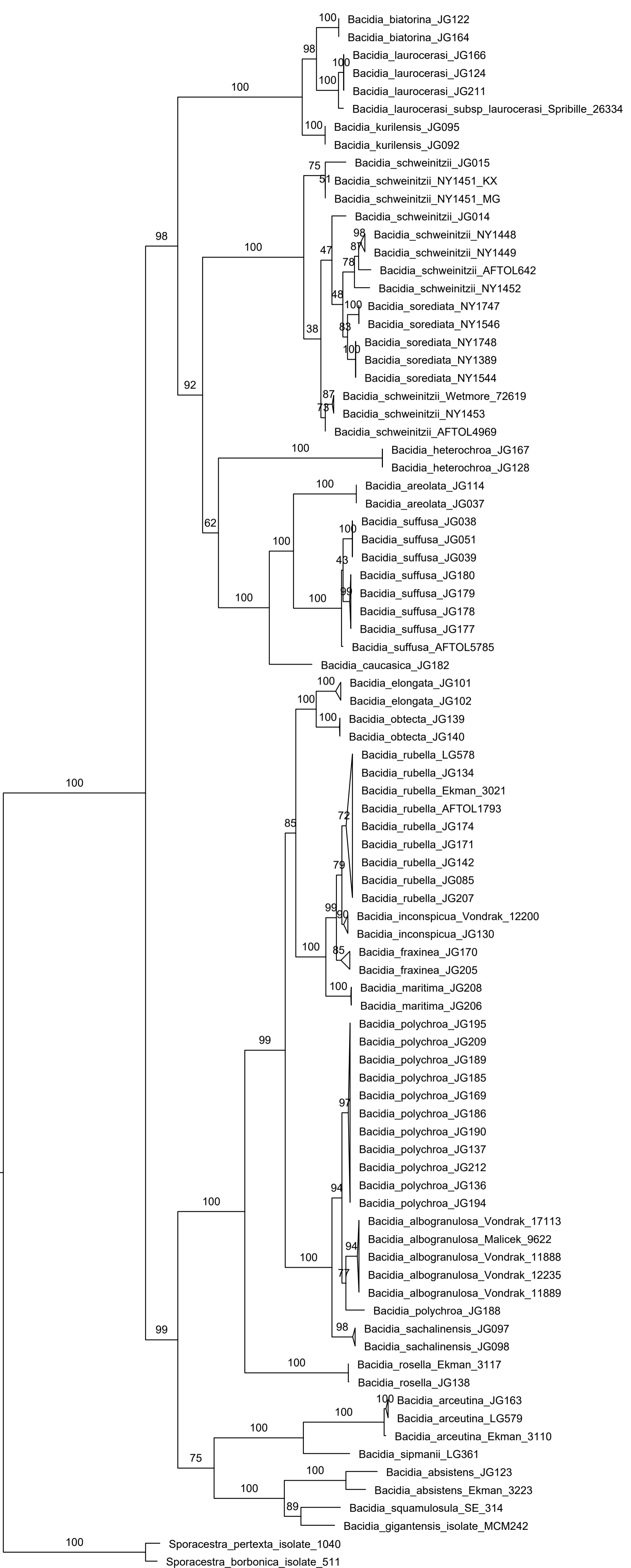


Fig. S1a RAxML phylogeny

0.05

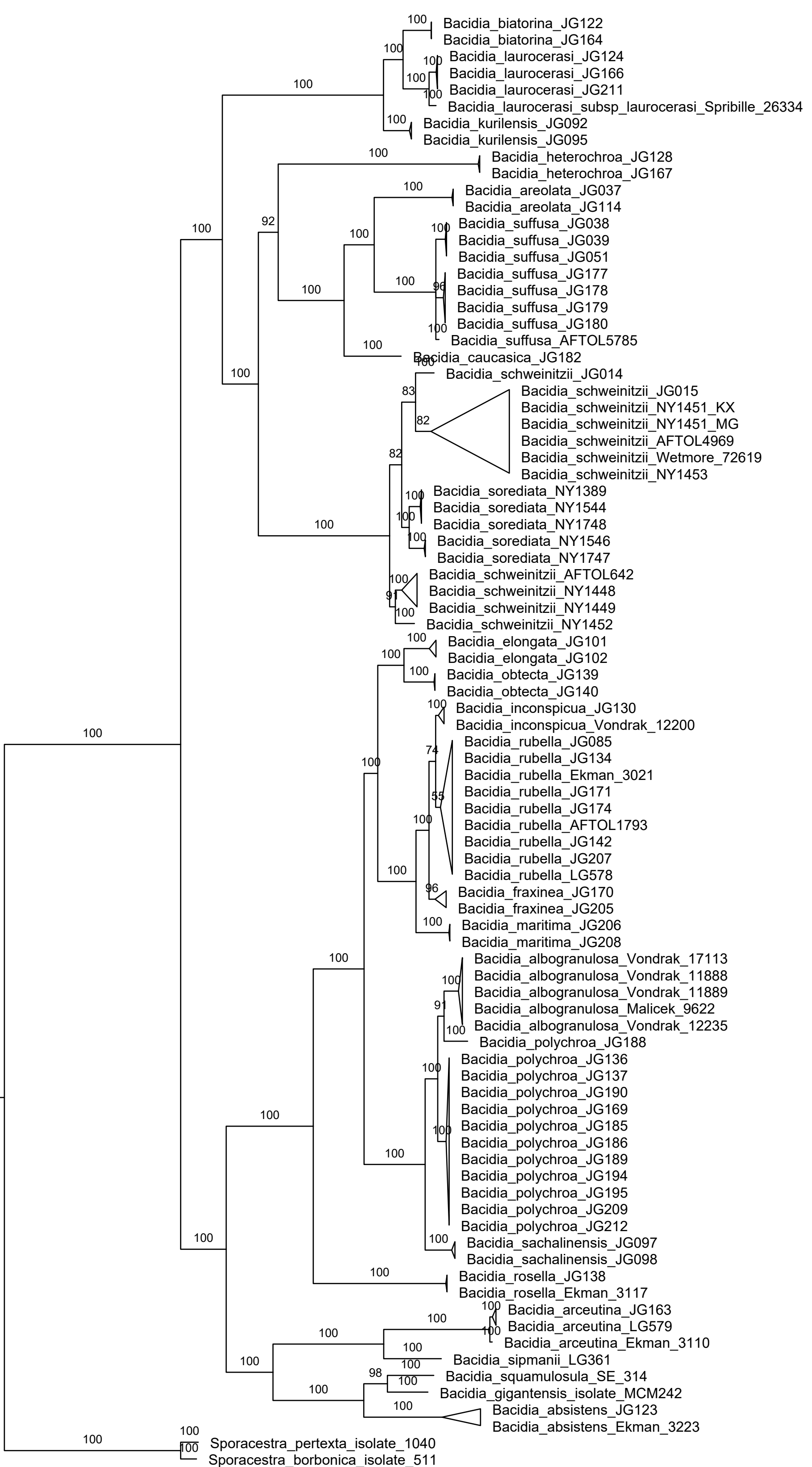


Fig. S1b BI phylogeny

0.05

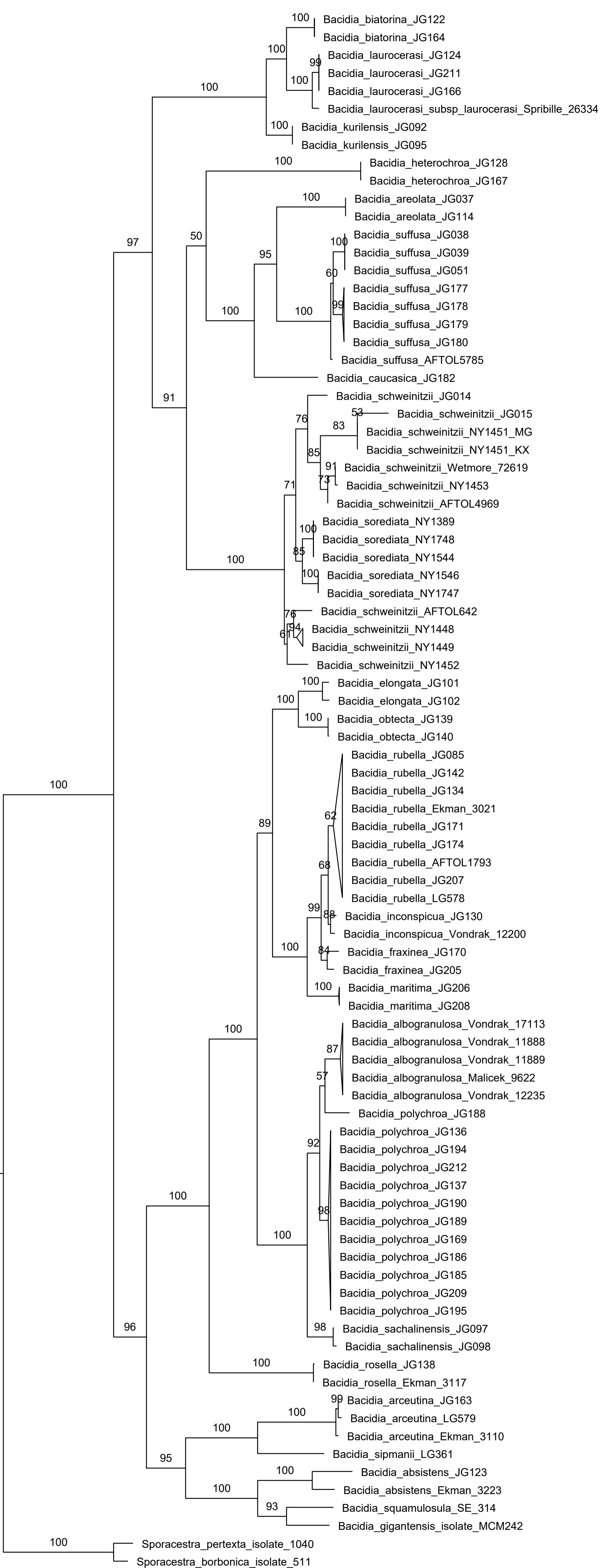


Fig. S1c IQ-TREE phylogeny

0.03

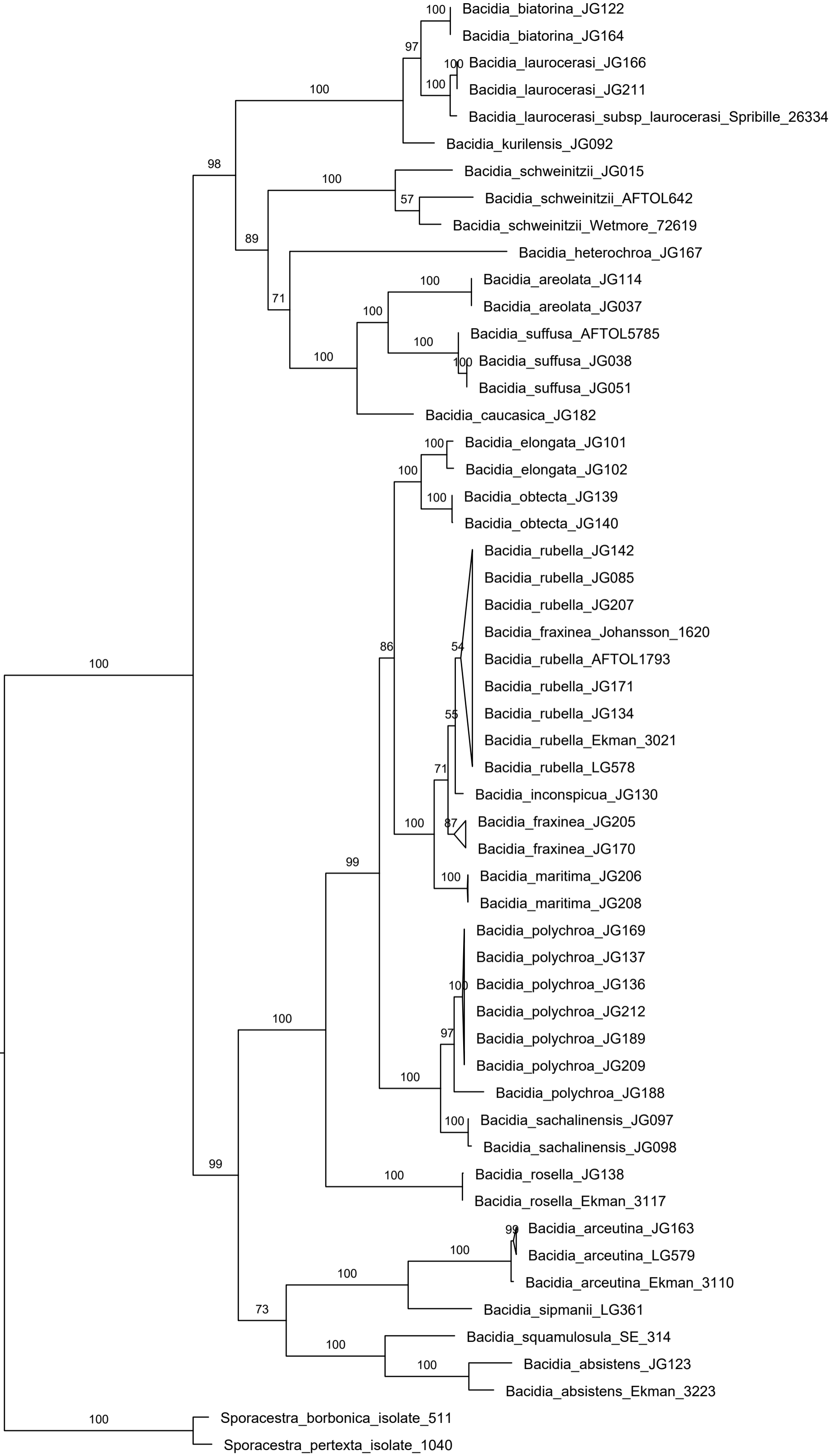
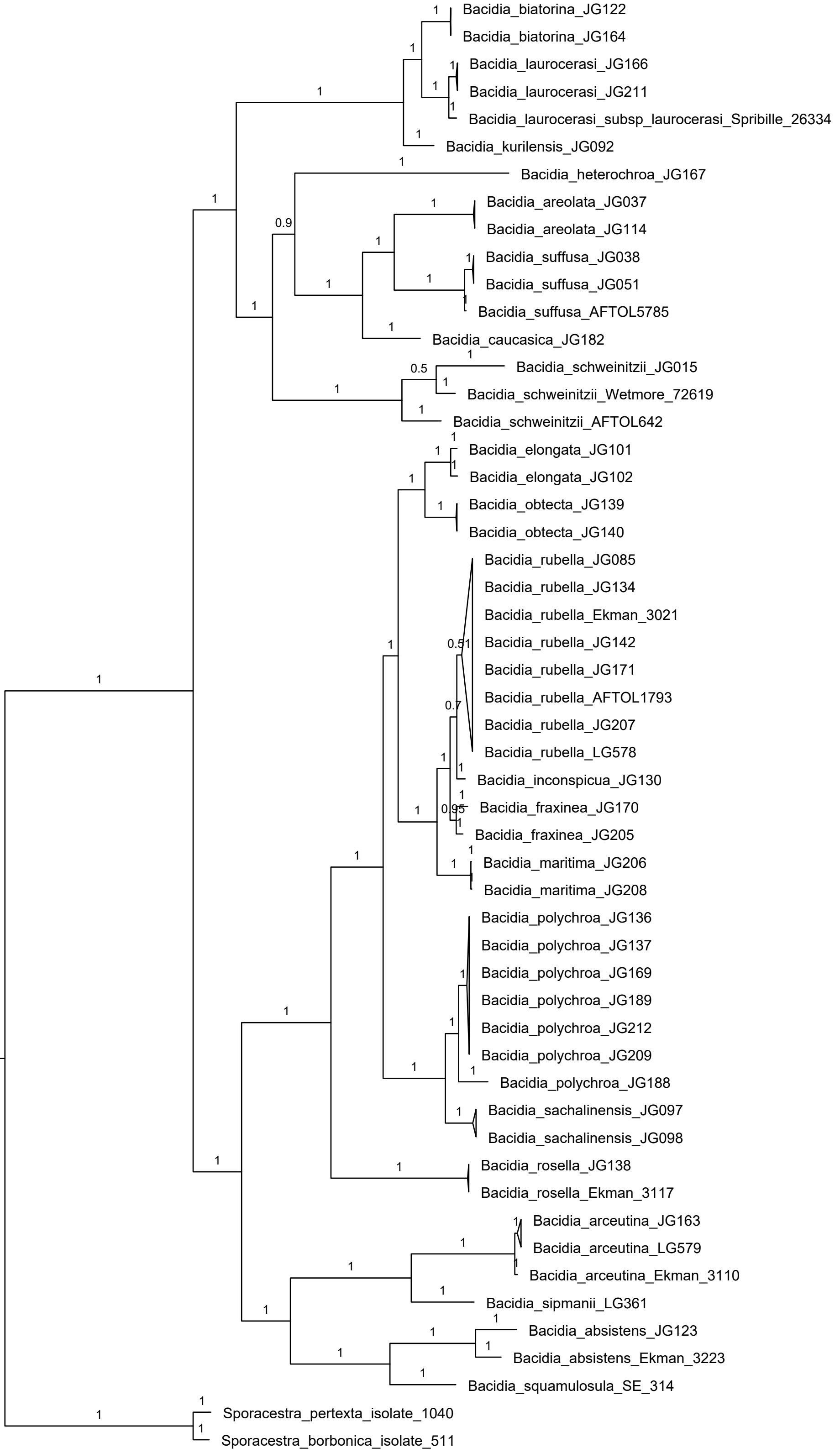


Fig. S2a RAxML phylogeny

0.05





0.05

Fig. S2b BI phylogeny

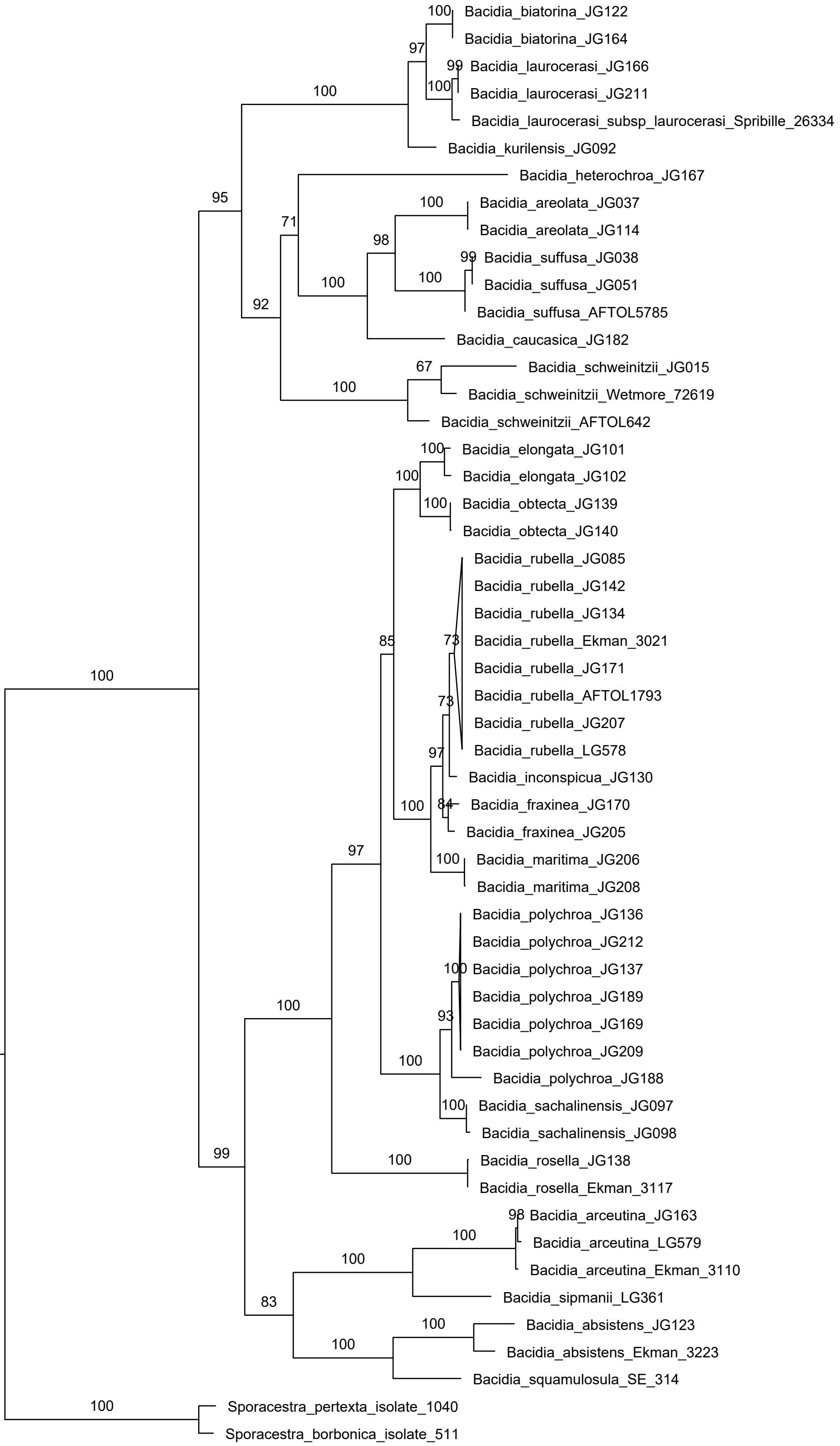
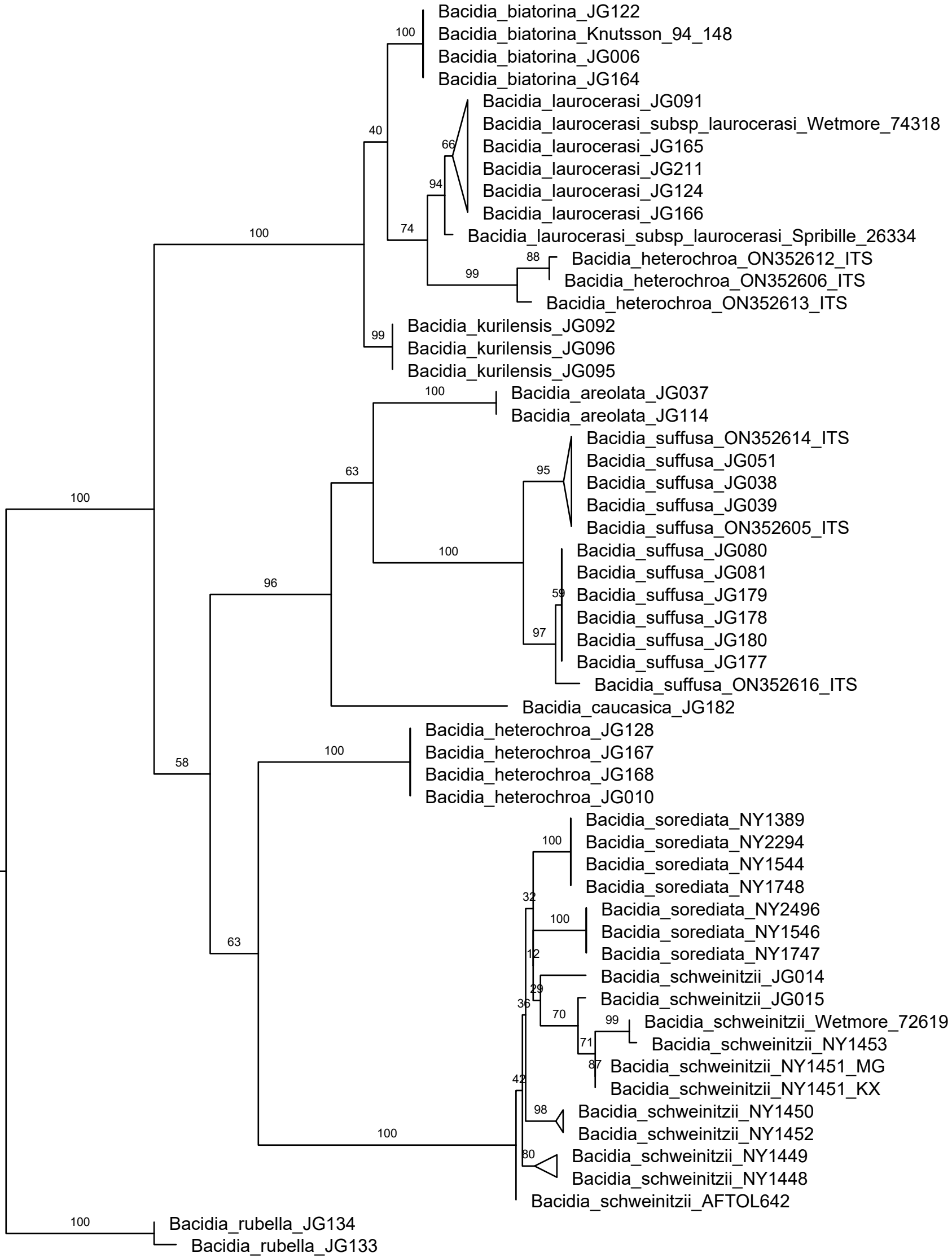


Fig. S2c IQ-TREE phylogeny

0.05



0.03

Fig. S3a RAxML phylogeny



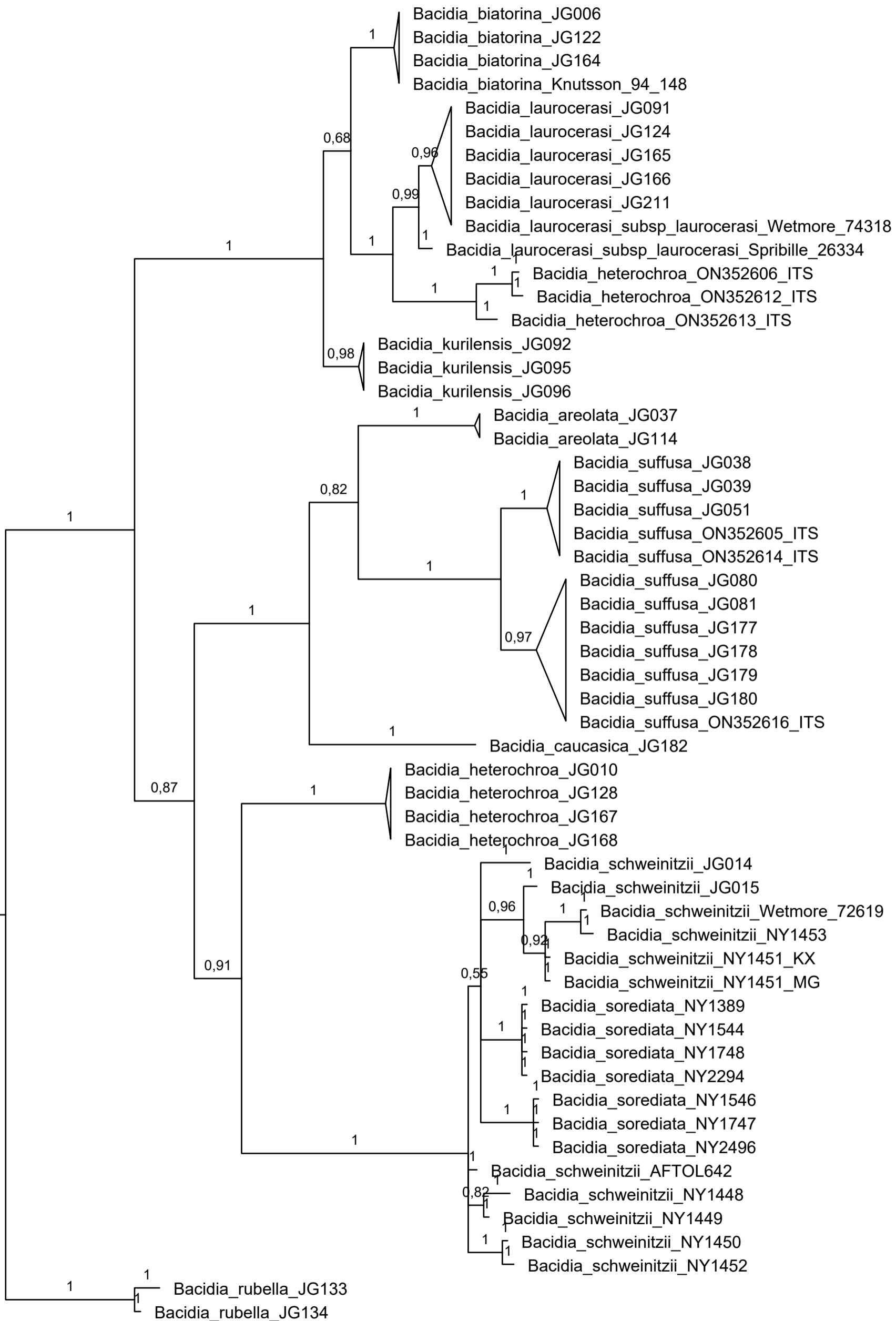


Fig. S3b BI phylogeny

0.02

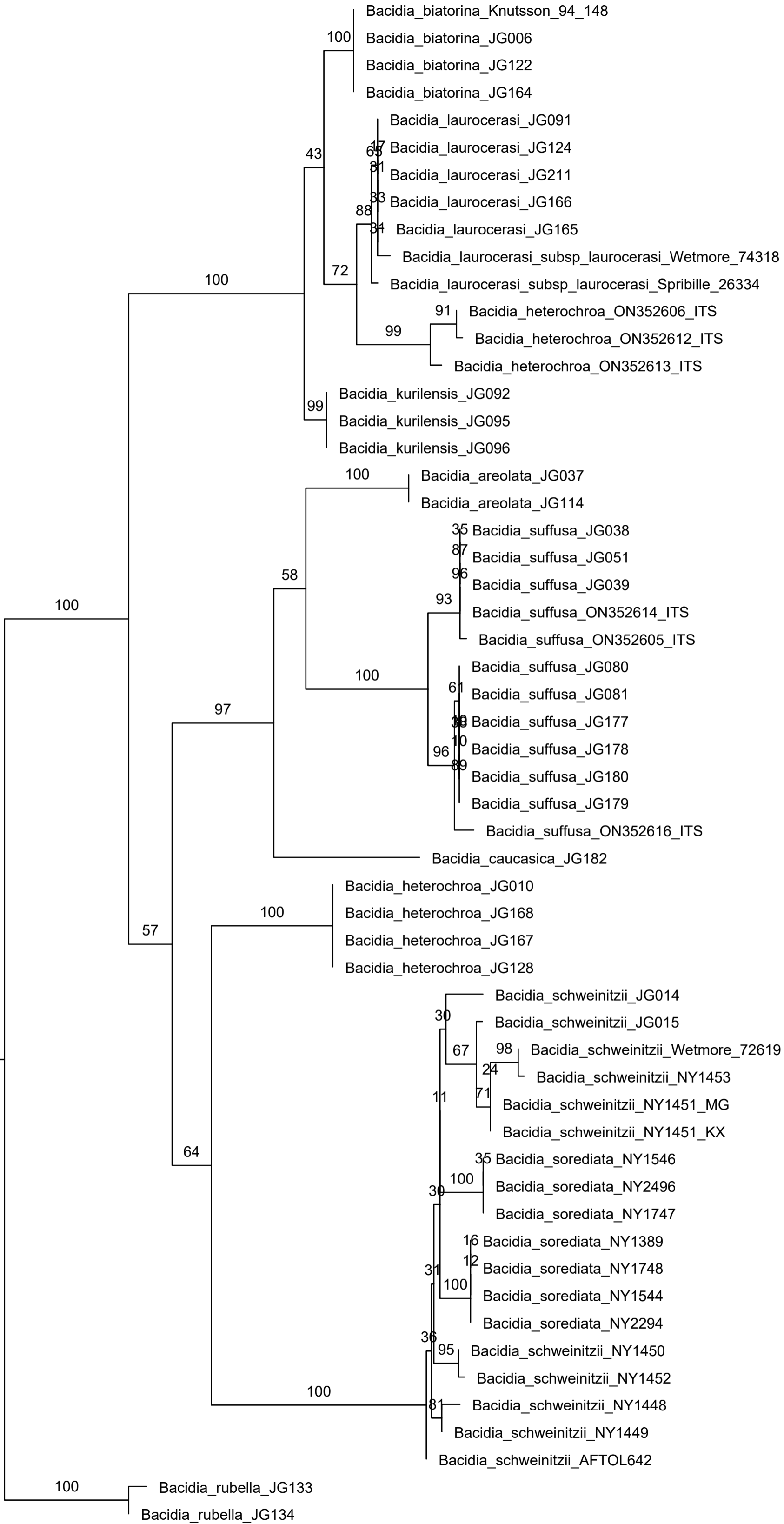


Fig. S3c IQ-TREE phylogeny

0.03

100

Sporacestra\_borbonica\_isolate\_511

Sporacestra\_pertexta\_isolate\_1040

Bacidia\_biatorina\_JG006

100 Bacidia\_biatorina\_Knutsson\_94\_148

Bacidia\_biatorina\_JG164

Bacidia\_biatorina\_JG122

Bacidia\_laurocerasi\_JG091

30 Bacidia\_laurocerasi\_subsp\_laurocerasi\_Wetmore\_74318

Bacidia\_laurocerasi\_JG165

90 Bacidia\_laurocerasi\_JG211

92 Bacidia\_laurocerasi\_JG124

Bacidia\_laurocerasi\_JG166

93 Bacidia\_laurocerasi\_subsp\_laurocerasi\_Spribille\_26334

100 Bacidia\_heterochroa\_ON352613\_ITS

89 Bacidia\_heterochroa\_ON352606\_ITS

Bacidia\_heterochroa\_ON352612\_ITS

98 Bacidia\_kurilensis\_JG096

Bacidia\_kurilensis\_JG092

Bacidia\_kurilensis\_JG095

100 Bacidia\_areolata\_JG037

Bacidia\_areolata\_JG114

Bacidia\_suffusa\_ON352605\_ITS

49 Bacidia\_suffusa\_JG038

92 Bacidia\_suffusa\_JG051

Bacidia\_suffusa\_JG039

100 Bacidia\_suffusa\_ON352614\_ITS

Bacidia\_suffusa\_ON352616\_ITS

Bacidia\_suffusa\_JG080

96 Bacidia\_suffusa\_JG081

Bacidia\_suffusa\_JG177

Bacidia\_suffusa\_JG179

Bacidia\_suffusa\_JG180

Bacidia\_suffusa\_JG178

Bacidia\_caucasica\_JG182

41 Bacidia\_heterochroa\_JG128

100 Bacidia\_heterochroa\_JG010

Bacidia\_heterochroa\_JG167

Bacidia\_heterochroa\_JG168

Bacidia\_schweinitzii\_JG014

56 Bacidia\_schweinitzii\_JG015

61 Bacidia\_schweinitzii\_NY1451\_KX

75 Bacidia\_schweinitzii\_NY1451\_MG

100 Bacidia\_schweinitzii\_Wetmore\_72619

Bacidia\_schweinitzii\_NY1453

59 Bacidia\_schweinitzii\_NY1452

99 Bacidia\_schweinitzii\_NY1450

40 Bacidia\_schweinitzii\_NY1448

91 Bacidia\_schweinitzii\_NY1449

58 Bacidia\_sorediata\_NY2496

100 Bacidia\_sorediata\_NY1546

47 Bacidia\_sorediata\_NY1747

100 Bacidia\_sorediata\_NY1748

Bacidia\_sorediata\_NY1544

Bacidia\_sorediata\_NY2294

Bacidia\_sorediata\_NY1389

Bacidia\_schweinitzii\_AFTOL642

60 Bacidia\_lutescens\_Ekman\_L1161

64 Bacidia\_hostheleoides\_1996\_Seaward

100 Bacidia\_fuscopallida\_ON352607\_ITS

Bacidia\_fuscopallida\_ON352608\_ITS

Bacidia\_arceutina\_JG163

100 Bacidia\_arceutina\_JG126

99 Bacidia\_arceutina\_LG579

98 Bacidia\_arceutina\_Ekman\_3110

40 Bacidia\_arceutina\_FR799125\_genomic

98 Bacidia\_arceutina\_FR799126\_genomic

Bacidia\_scopulicola\_Ekman\_3106

Bacidia\_sipmanii\_LG361

94 Bacidia\_absistens\_JG123

58 Bacidia\_absistens\_Ekman\_3223

69 Bacidia\_squamulosula\_SE\_314

Bacidia\_gigantensis\_isolate\_MCM242

99 Bacidia\_elongata\_JG102

Bacidia\_elongata\_JG007

57 Bacidia\_elongata\_JG101

99 Bacidia\_obtecta\_JG140

Bacidia\_obtecta\_JG141

Bacidia\_obtecta\_JG139

31 Bacidia\_rubella\_JG171

94 Bacidia\_rubella\_AFTOL1793

Bacidia\_rubella\_JG174

Bacidia\_rubella\_JG207

36 Bacidia\_inconspicua\_JG130

Bacidia\_inconspicua\_Vondrak\_12200

42 Bacidia\_rubella\_JG133

45 Bacidia\_rubella\_LIFU076\_16

38 Bacidia\_rubella\_LG578

Bacidia\_fraxinea\_JG170

Bacidia\_rubella\_JG142

22 Bacidia\_rubella\_JG085

36 Bacidia\_fraxinea\_JG049

76 Bacidia\_fraxinea\_JG205

83 Bacidia\_rubella\_Ekman\_3021

59 Bacidia\_rubella\_JG134

Bacidia\_rubella\_HurH06122

Bacidia\_maritima\_JG208

96 Bacidia\_maritima\_JG131

Bacidia\_maritima\_JG206

Bacidia\_fraxinea\_Johansson\_1620

96 Bacidia\_suffusa\_Wetmore\_74771

70 Bacidia\_diffRACTA\_Wetmore\_26401

Bacidia\_diffRACTA\_JG083

Bacidia\_albgranulosa\_Vondrak\_11888

100 Bacidia\_albgranulosa\_Malicek\_9622

56 Bacidia\_albgranulosa\_Vondrak\_11889

89 Bacidia\_albgranulosa\_Vondrak\_17113

Bacidia\_polychroa\_JG188

Bacidia\_polychroa\_JG195

67 Bacidia\_polychroa\_JG190

Bacidia\_polychroa\_JG137

Bacidia\_polychroa\_JG209

Bacidia\_polychroa\_JG189

97 Bacidia\_polychroa\_JG185

93 Bacidia\_polychroa\_JG186

Bacidia\_polychroa\_JG194

Bacidia\_polychroa\_JG169

Bacidia\_polychroa\_JG136

Bacidia\_polychroa\_Knutsson\_91\_215

Bacidia\_polychroa\_JG212

Bacidia\_sachalinensis\_JG099

100 Bacidia\_sachalinensis\_JG082

Bacidia\_sachalinensis\_JG097

Bacidia\_sachalinensis\_JG098

100 Bacidia\_rosella\_Ekman\_3117

Bacidia\_rosella\_JG138

100

0.08

Fig. S4a RAxML phylogeny

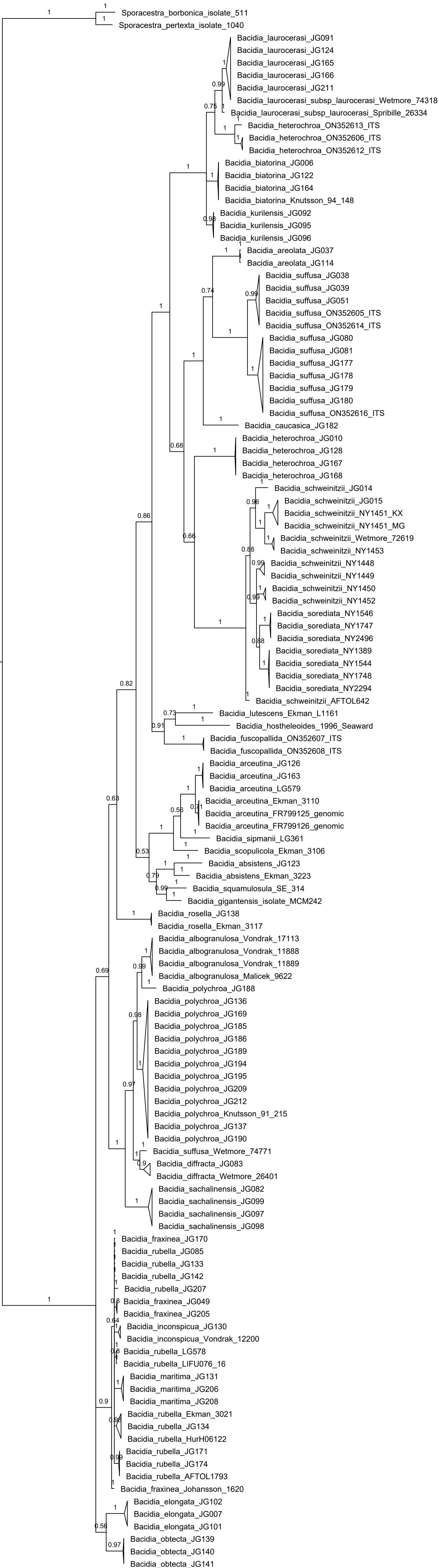


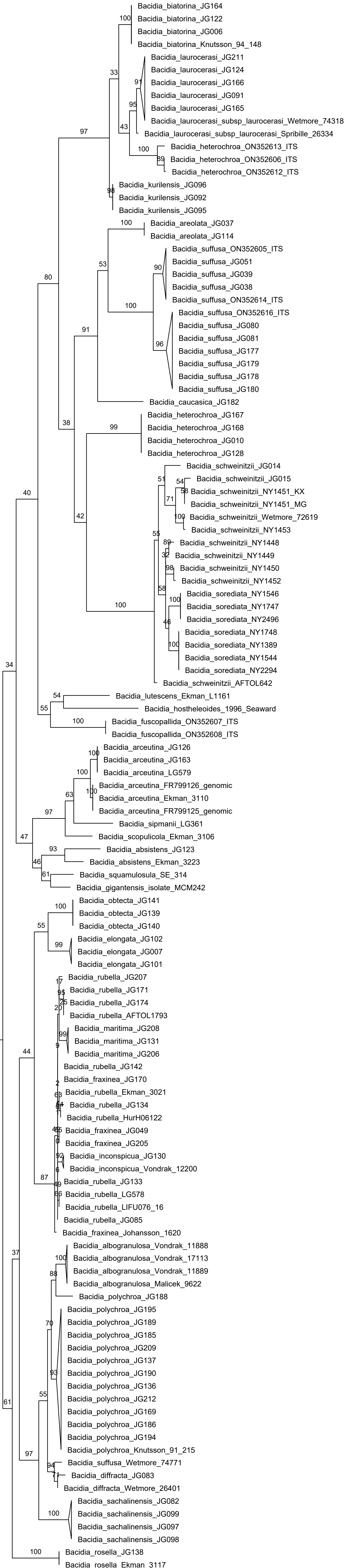
Fig. S4b BI phylogeny

0.05



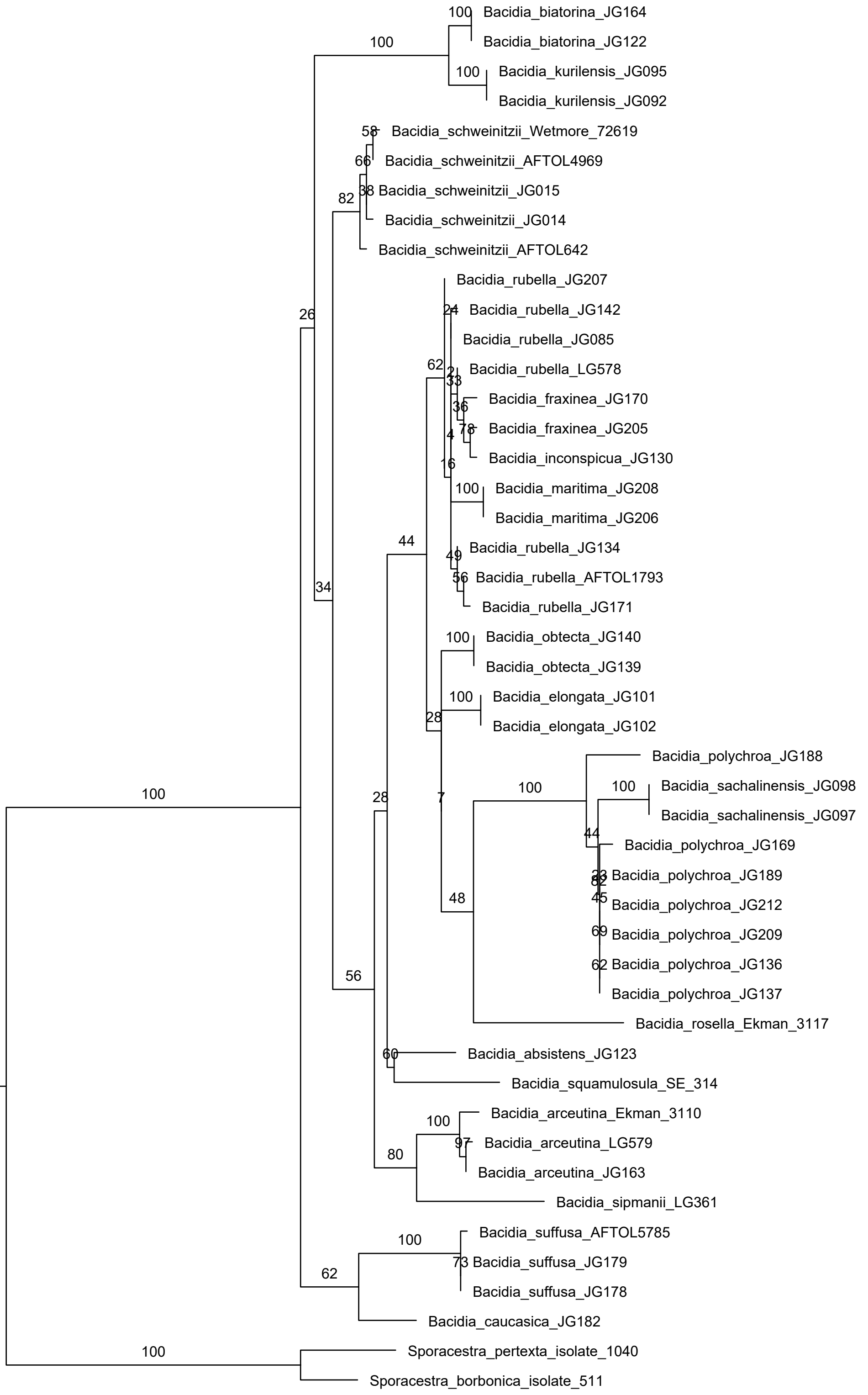
100

Sporacestra\_borbonica\_isolate\_511  
Sporacestra\_pertexta\_isolate\_1040



100





0.02

Fig. S5a RAxML phylogeny

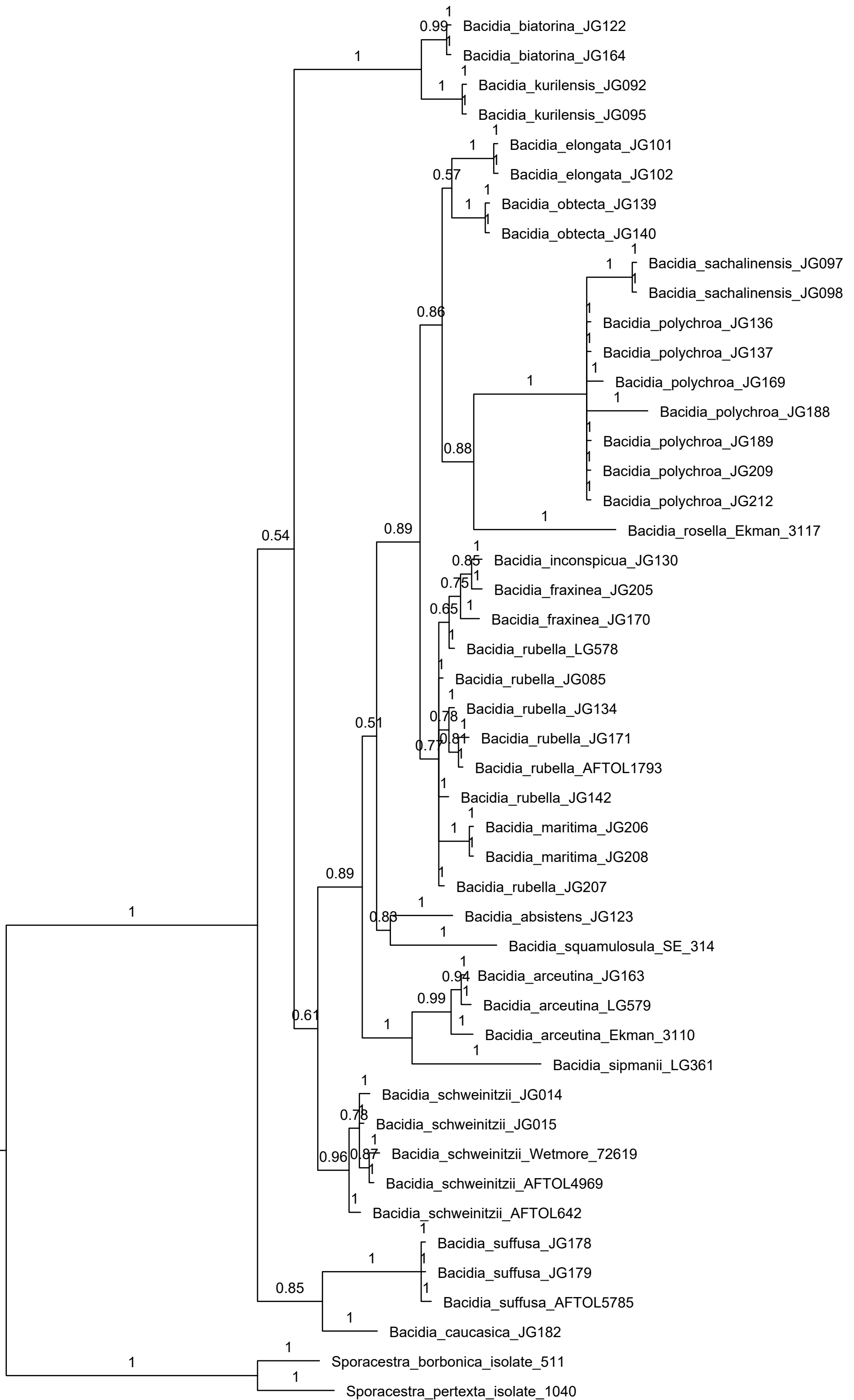
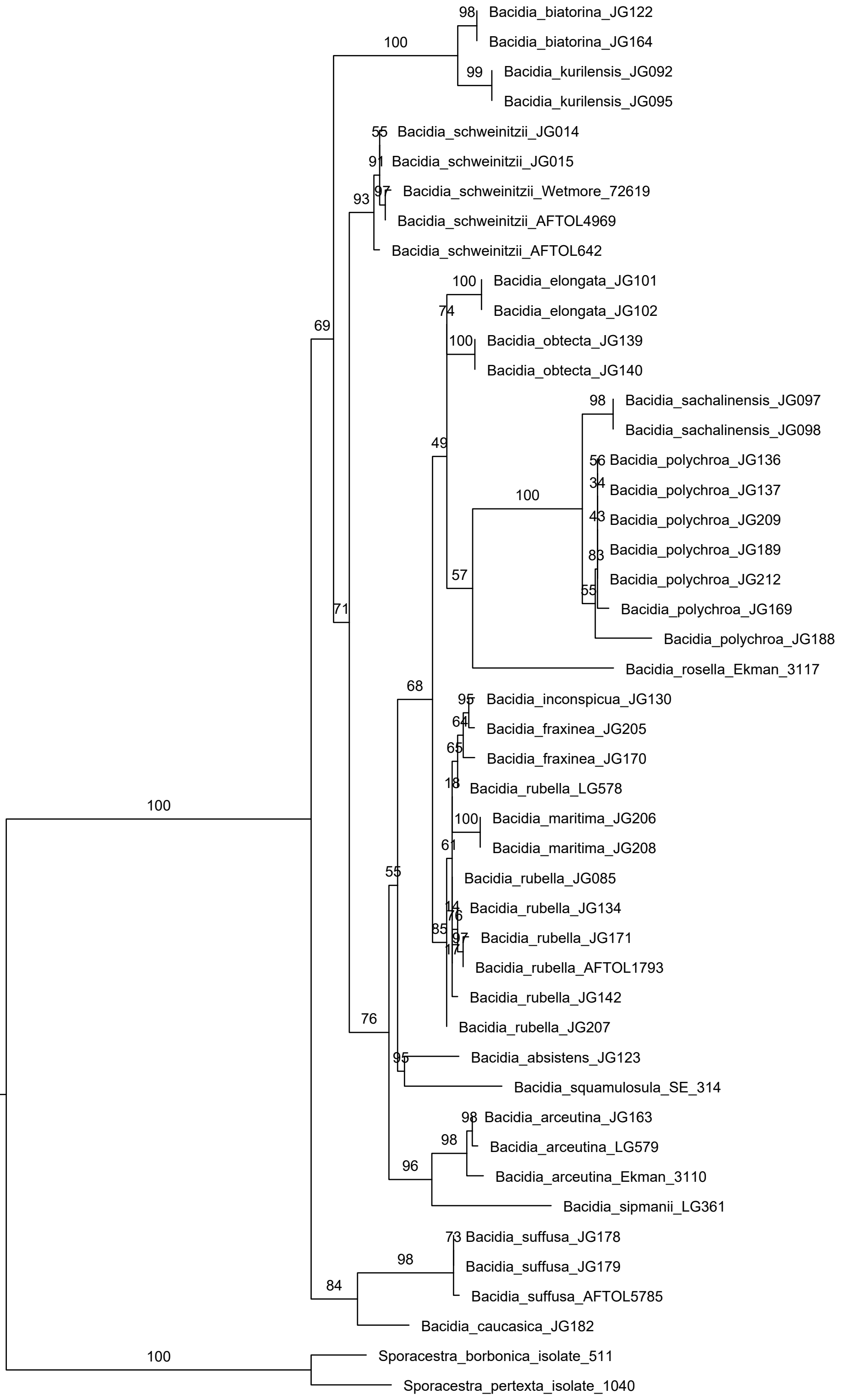


Fig. S5b BI phylogeny

0.02



0.02

Fig. S5c IQ-TREE phylogeny

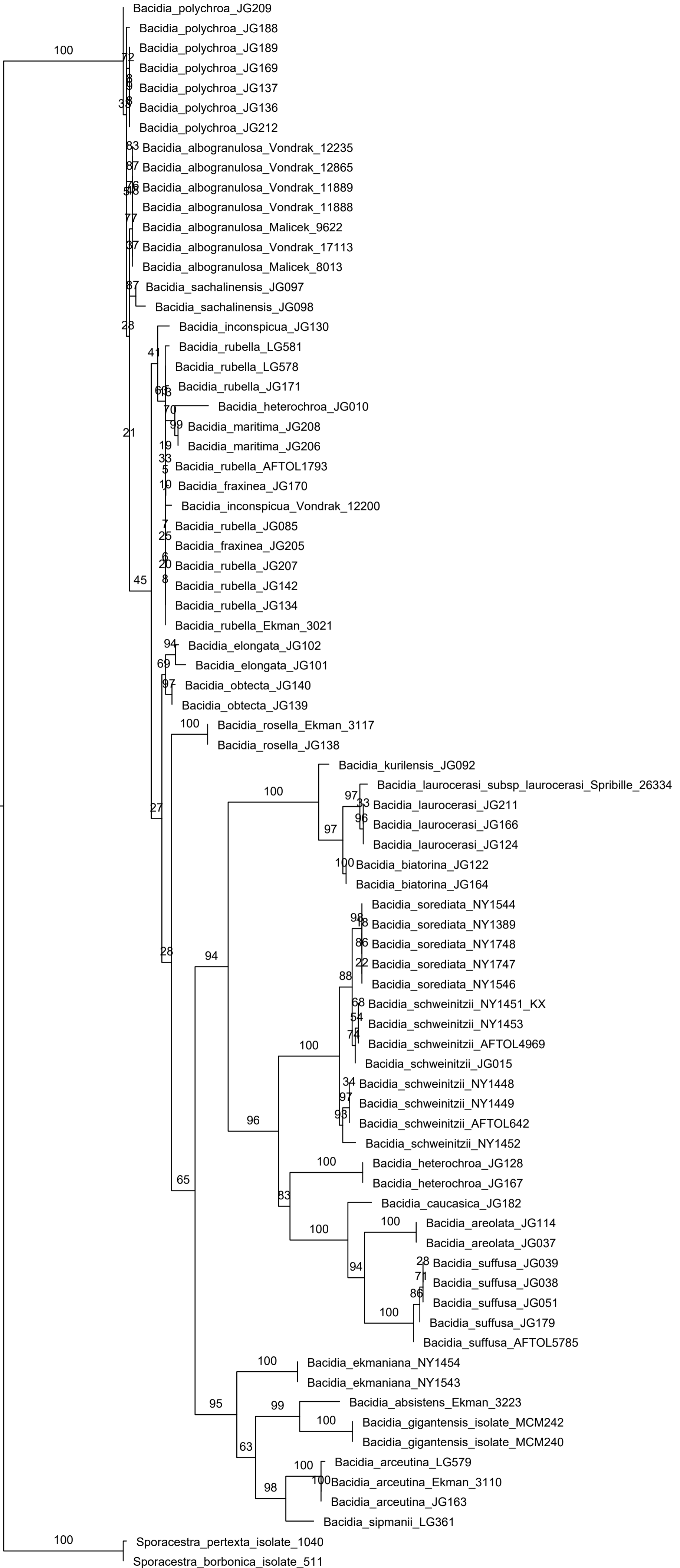


Fig. S6a RAxML phylogeny

0.03

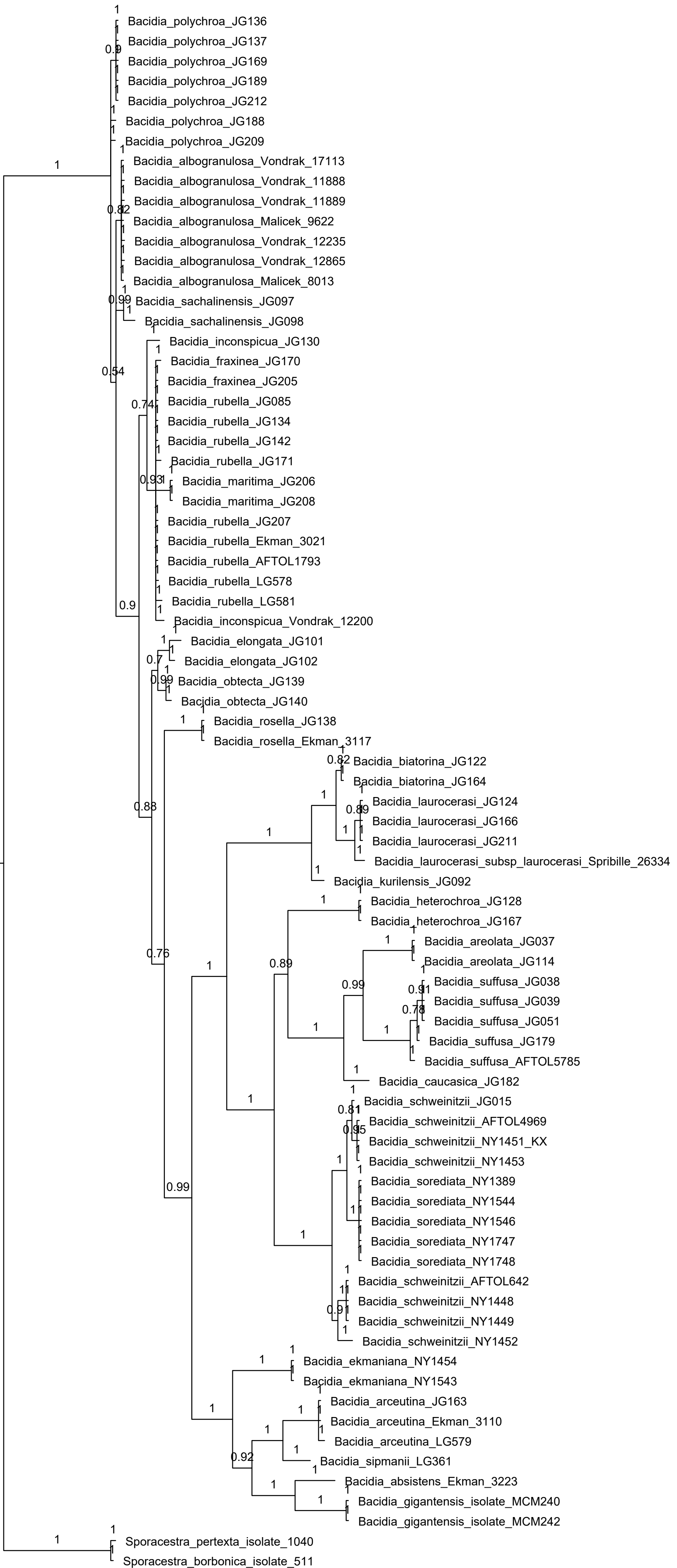


Fig. S6b BI phylogeny

0.02



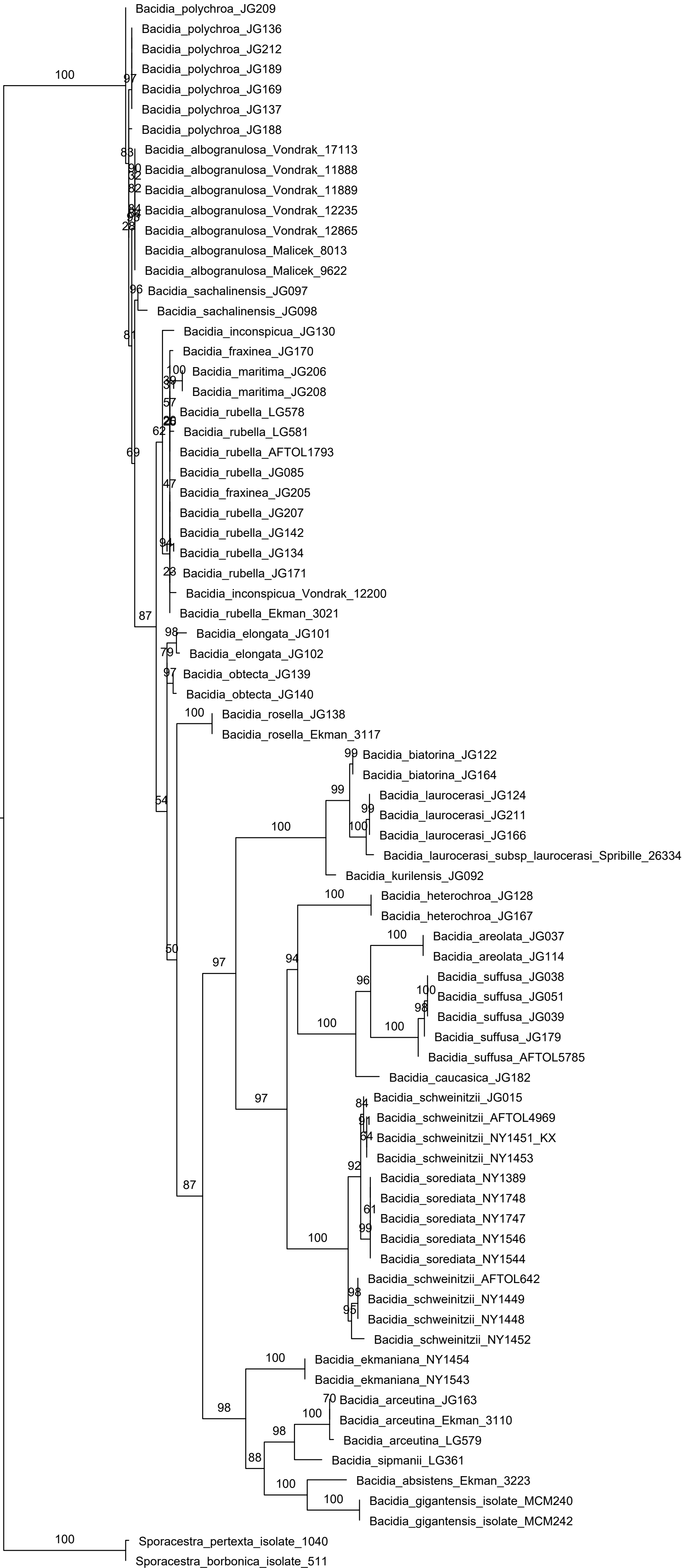
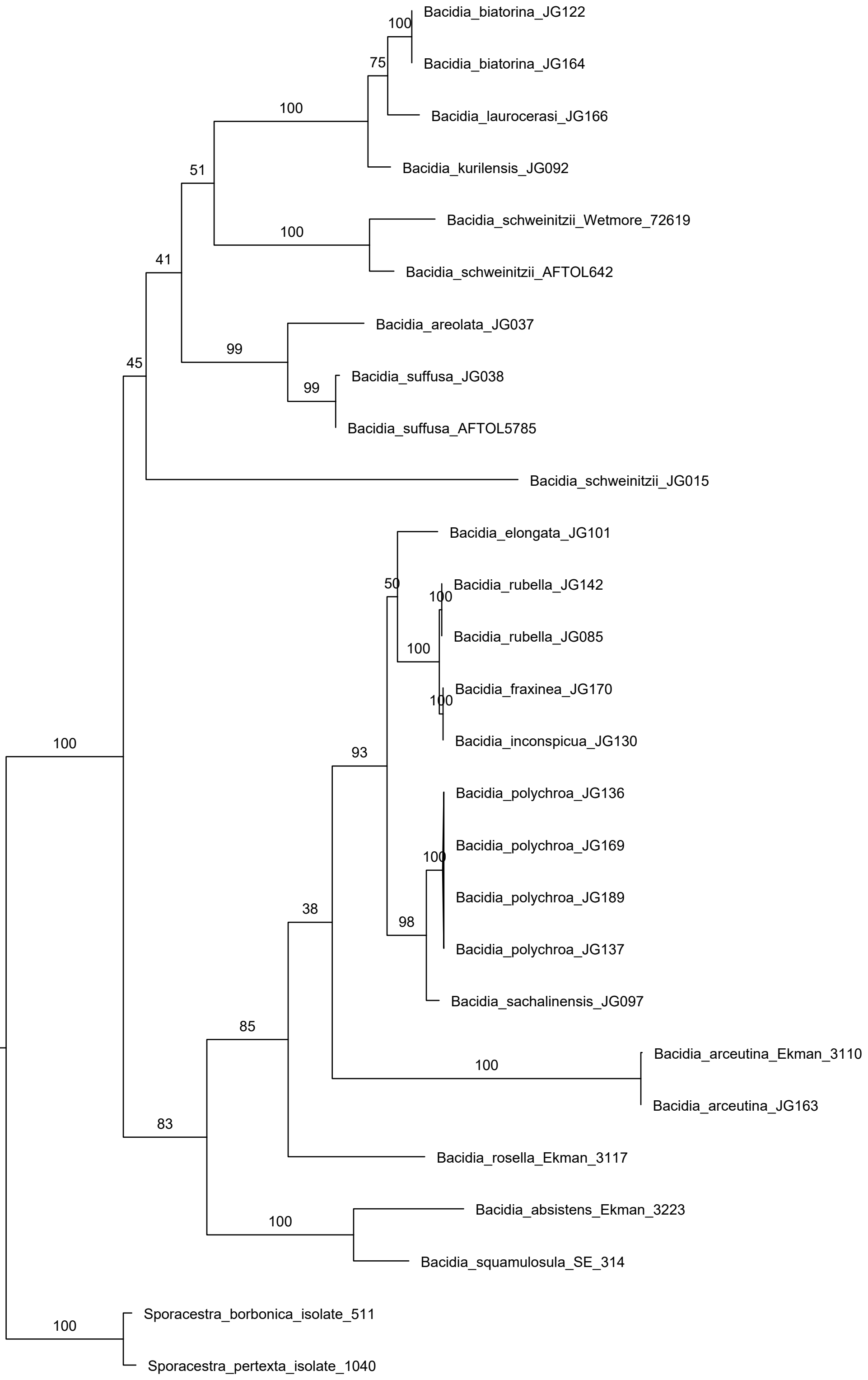


Fig. S6c IQ-TREE phylogeny

0.03



0.07

Fig. S7a RAxML phylogeny

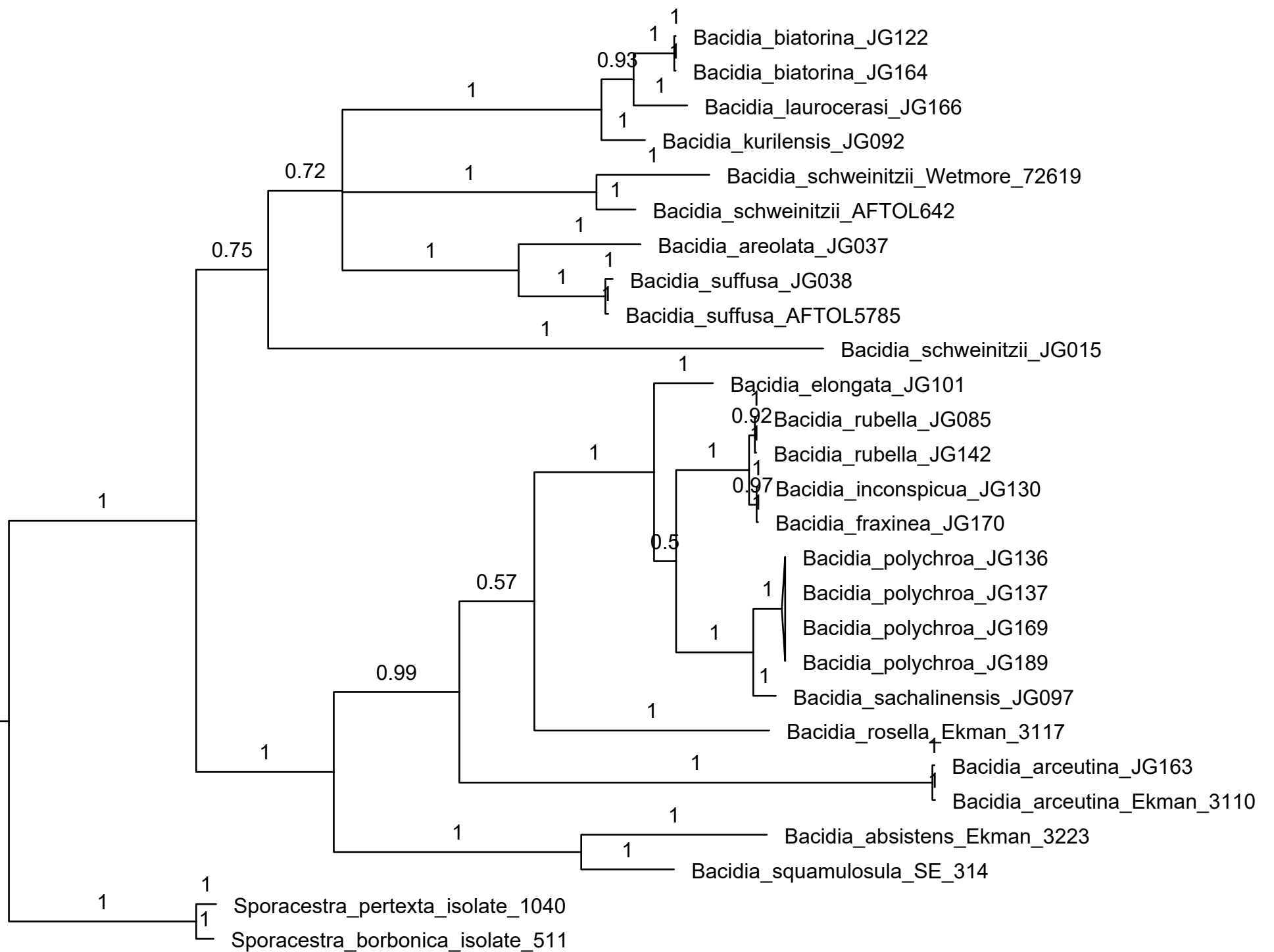
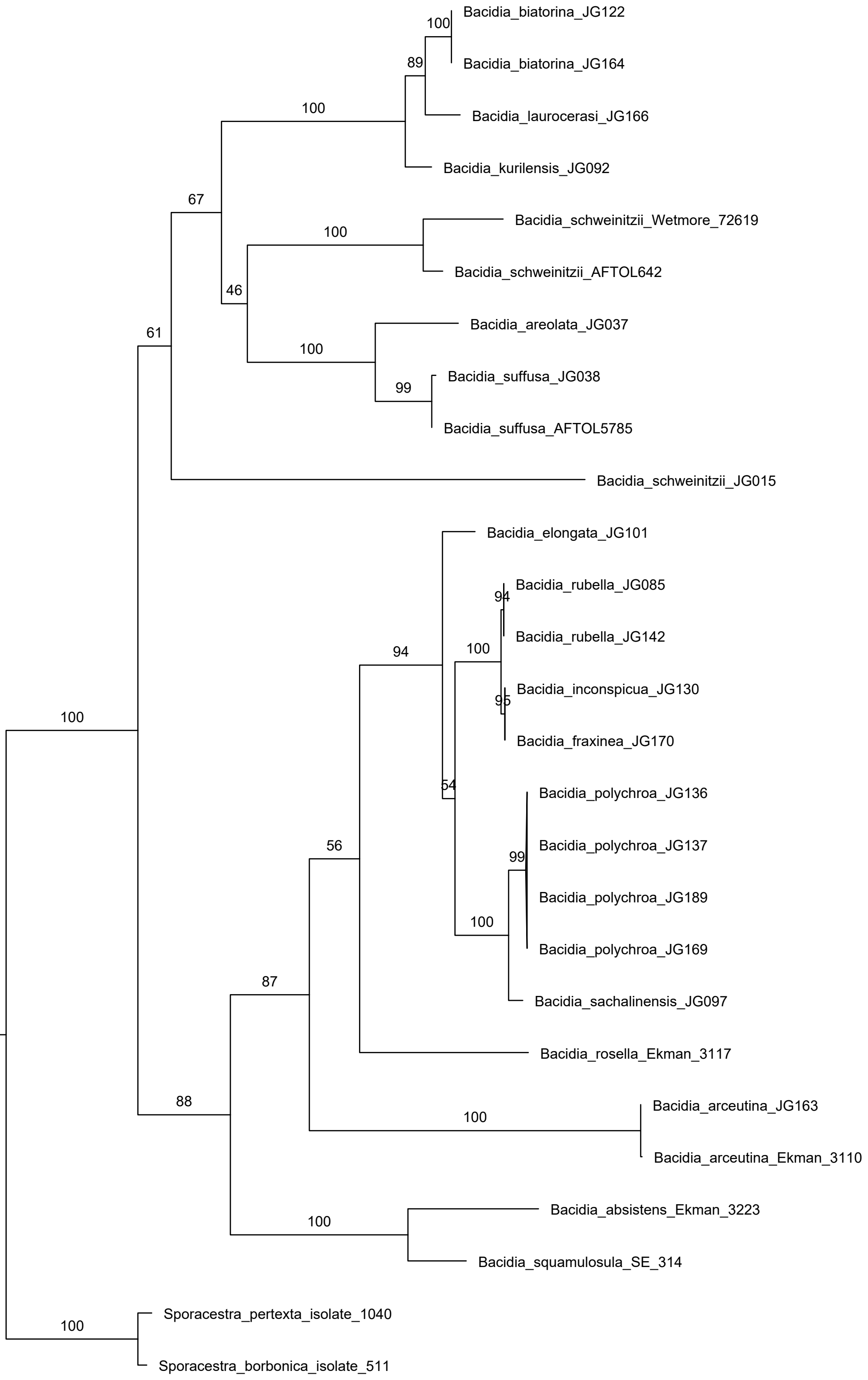


Fig. S7b BI phylogeny



0.09

Fig. S7c IQ-TREE phylogeny

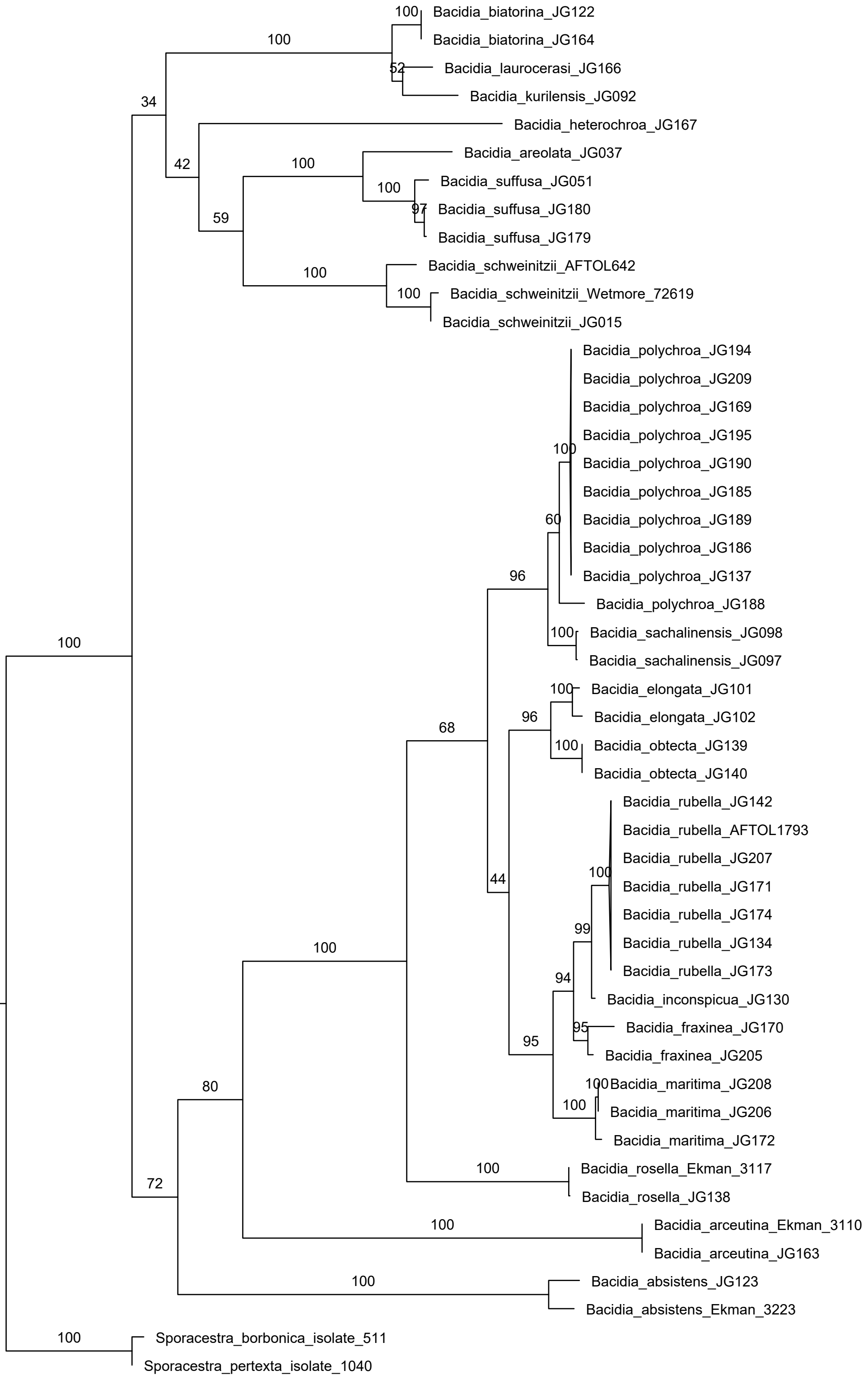
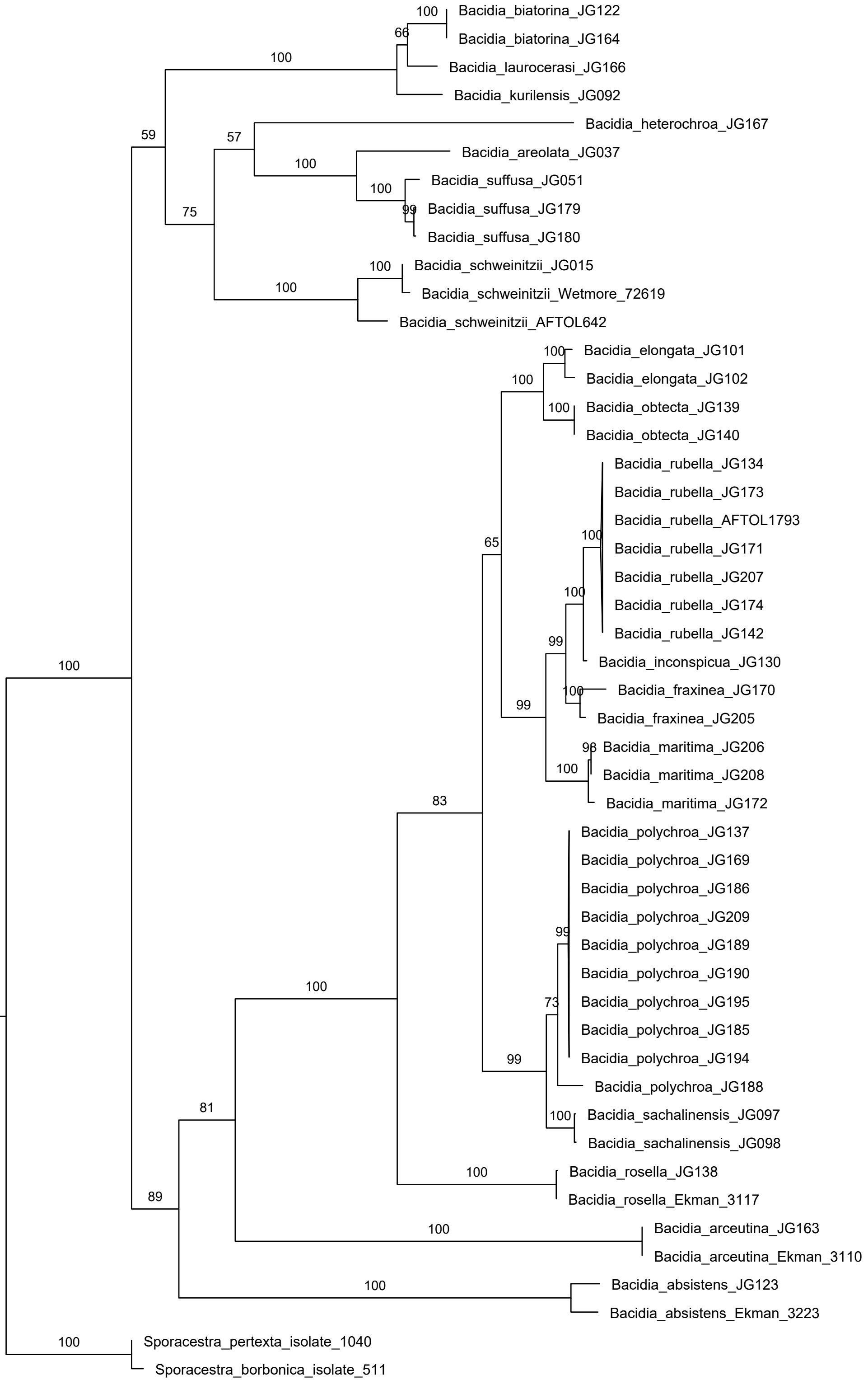


Fig. S8a RAxML phylogeny

0.08







0.09

Fig. S8c IQ-TREE phylogeny