

Supplementary figures

Fig. S1: Phylogenetic tree of ester synthases/diacylglycerol acyltransferases (WSD). The tree was constructed in IQ-Tree using the LG+F+R5 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 269 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. *Euglena gracilis* sequences are shown in green, *Rhabdomonas costata* sequences in blue.

Fig. S2: Phylogenetic tree of mitochondrial carrier family proteins. The tree was constructed in IQ-Tree using the LG+F+R4 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 226 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions.

Fig. S3: Phylogenetic tree of Hsp70 family proteins. The tree was constructed in IQ-Tree using the LG+I+G4 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 439 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The cytosolic, ER and mitochondrial paralogues of Hsp70 are shown in blue, brown and red branches respectively. *Rhabdomonas costata* sequences are indicated by blue names. Based on the position in the tree the transcripts RCo049920 and RCo045932 are considered as mitochondrial.

Fig. S4: Phylogenetic tree of 5-aminolevulinate synthase (ALAS). The tree was constructed in IQ-Tree using the LG+R6 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 341 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of euglenids are shown in red.

Fig. S5: Phylogenetic tree of porphobilinogen synthase (ALAD). The tree was constructed in IQ-Tree using the LG+R6 model selected by Bayesian information criterion from a trimmed and manually

inspected alignment containing 152 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of the plastidial C5 pathway are shown in green, enzymes of the C4 pathway are shown in red.

Fig. S6: Phylogenetic tree of porphobilinogen deaminase (PBGD). The tree was constructed in IQ-Tree using the LG+I+G4 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 269 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of the plastidial C5 pathway are shown in green, enzymes of the C4 pathway are shown in red.

Fig. S7: Phylogenetic tree of uroporphyrinogen synthase (UROS). The tree was constructed in IQ-Tree using the site heterogeneous PMSF model from a trimmed and manually inspected alignment containing 185 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The putative enzyme of the plastidial C5 pathway of *Euglena gracilis* is shown in green, enzymes of the C4 pathway are shown in red.

Fig. S8: Phylogenetic tree of uroporphyrinogen decarboxylase (UROD). The tree was constructed in IQ-Tree using the LG+R6 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 255 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of the plastidial C5 pathway are shown in green, enzymes of the C4 pathway are shown in red.

Fig. S9: Phylogenetic tree of coproporphyrinogen oxidase (CPOX). The tree was constructed in IQ-Tree using the LG+F+R6 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 237 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of euglenids are shown in red.

Fig. S10: Phylogenetic tree of protoporphyrinogen oxidase (PPOX). The tree was constructed in IQ-Tree using the LG+I+G4 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 314 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of the plastidial C5 pathway are shown in green, enzymes of the C4 pathway are shown in red.

Fig. S11: Phylogenetic tree of ferrochelatase (FECH). The tree was constructed in IQ-Tree using the LG+I+G4 model selected by Bayesian information criterion from a trimmed and manually inspected alignment containing 232 amino acid positions. The values at the nodes represent ultrafast bootstraps from 1,000 repetitions. The enzymes of the plastidial C5 pathway are shown in green, enzymes of the C4 pathway are shown in red.

Figure S1

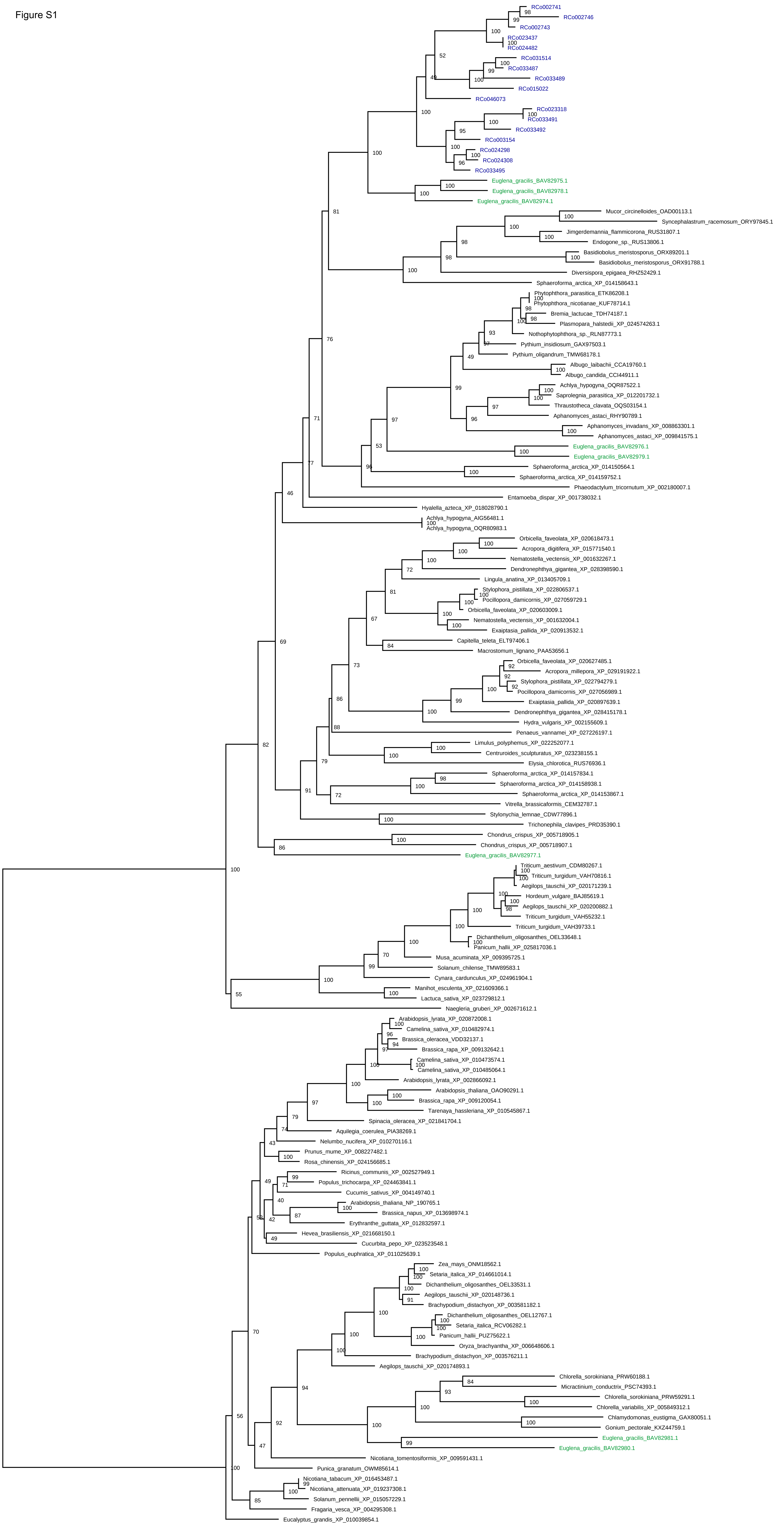
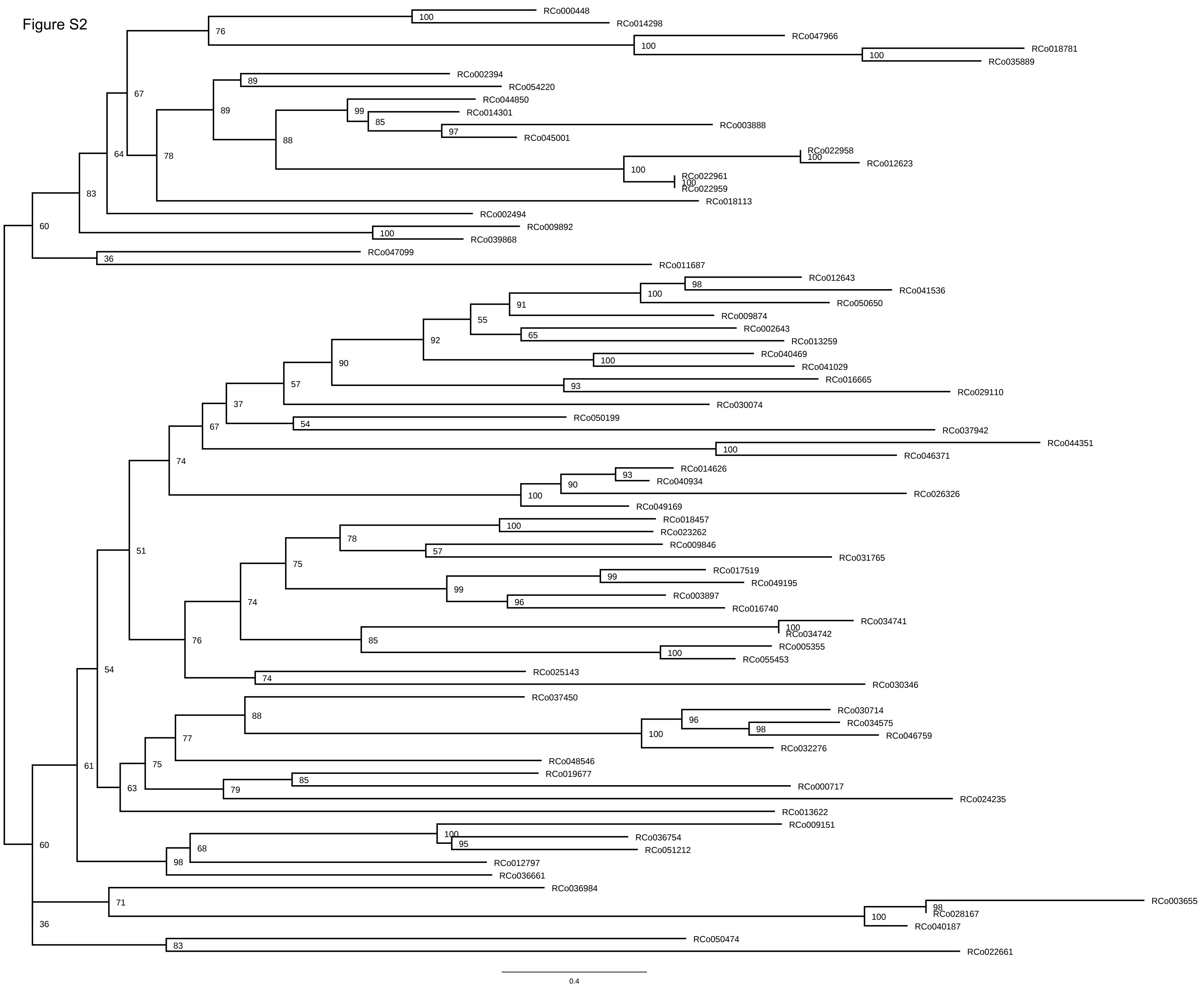


Figure S2



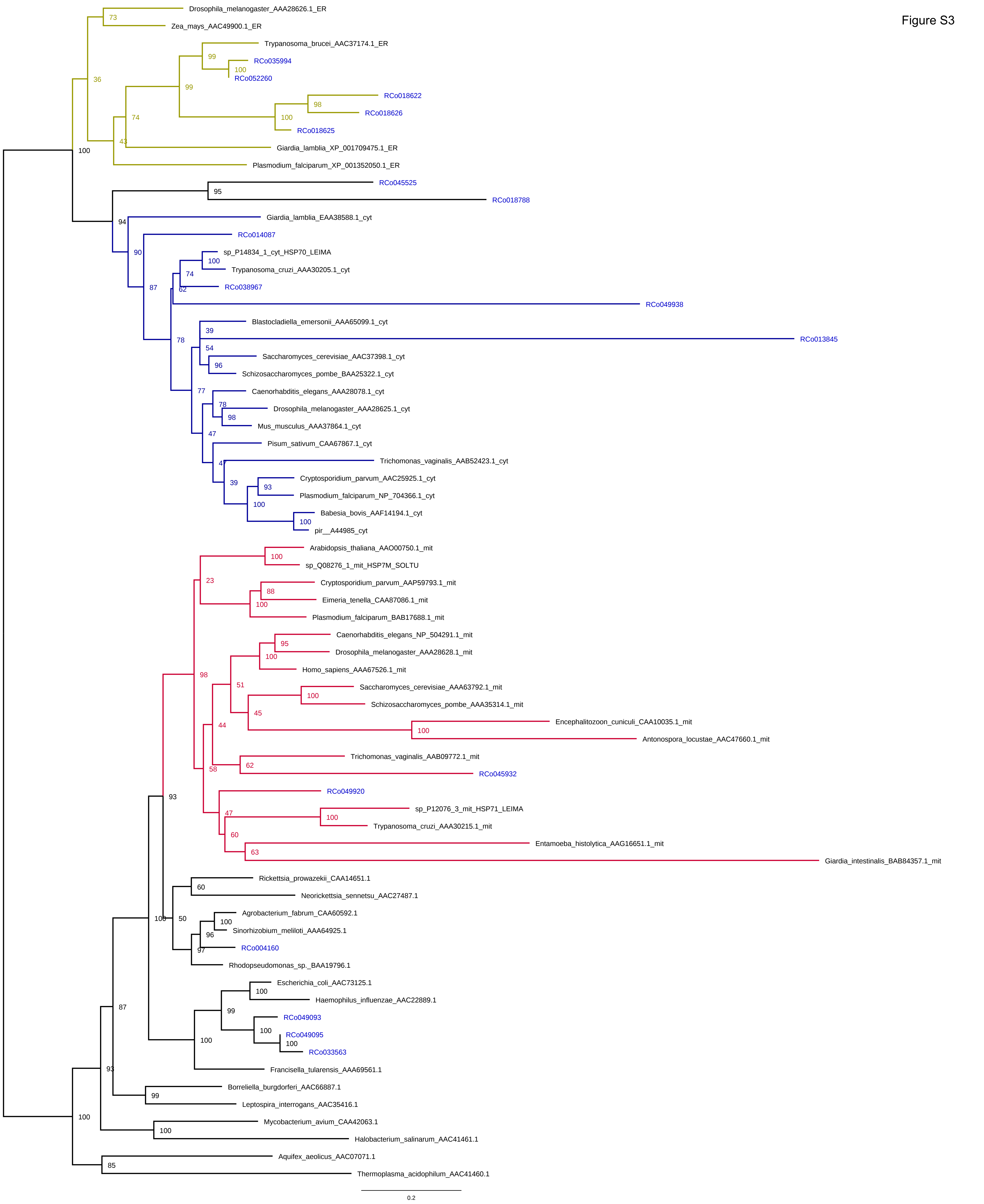


Figure S4

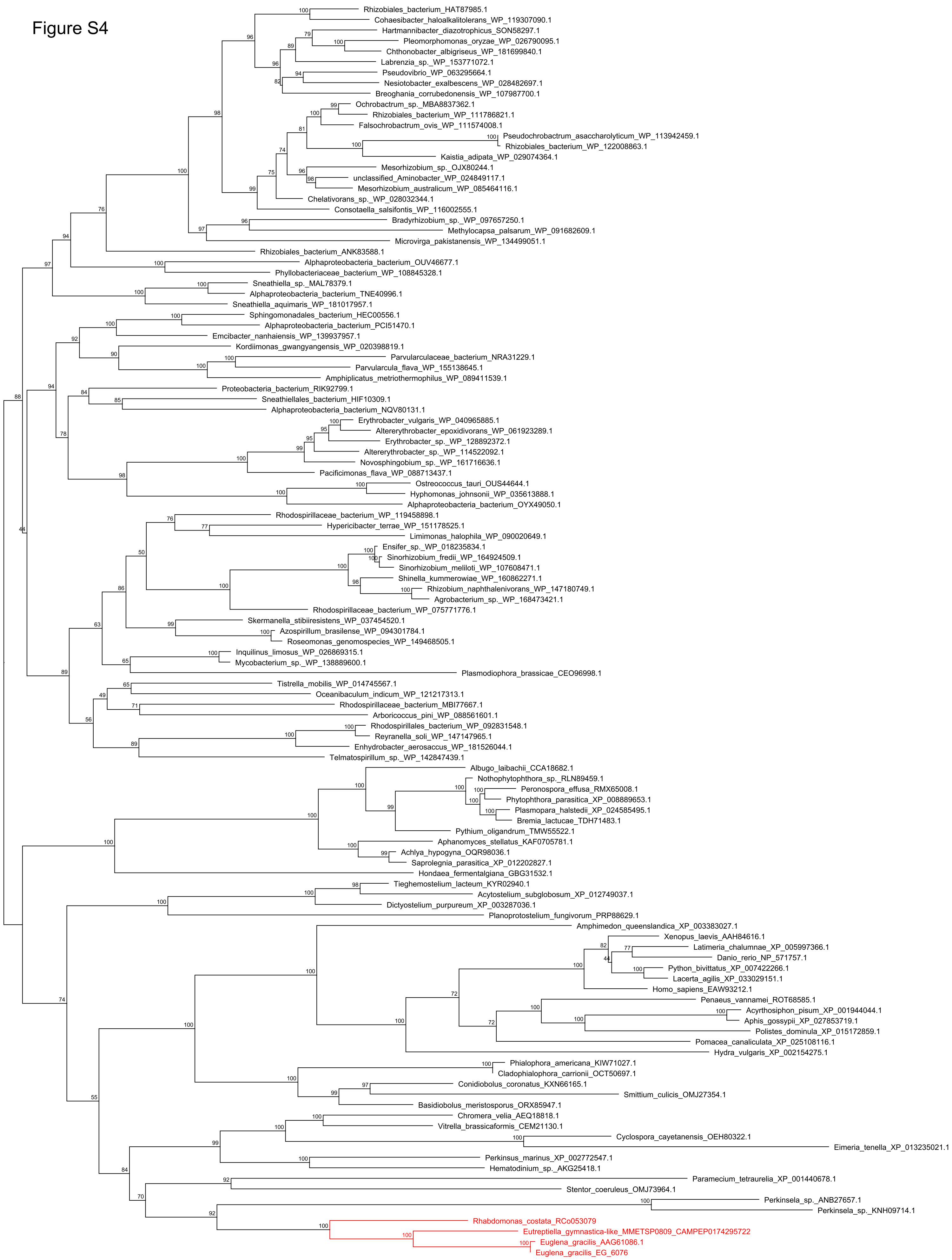


Figure S5

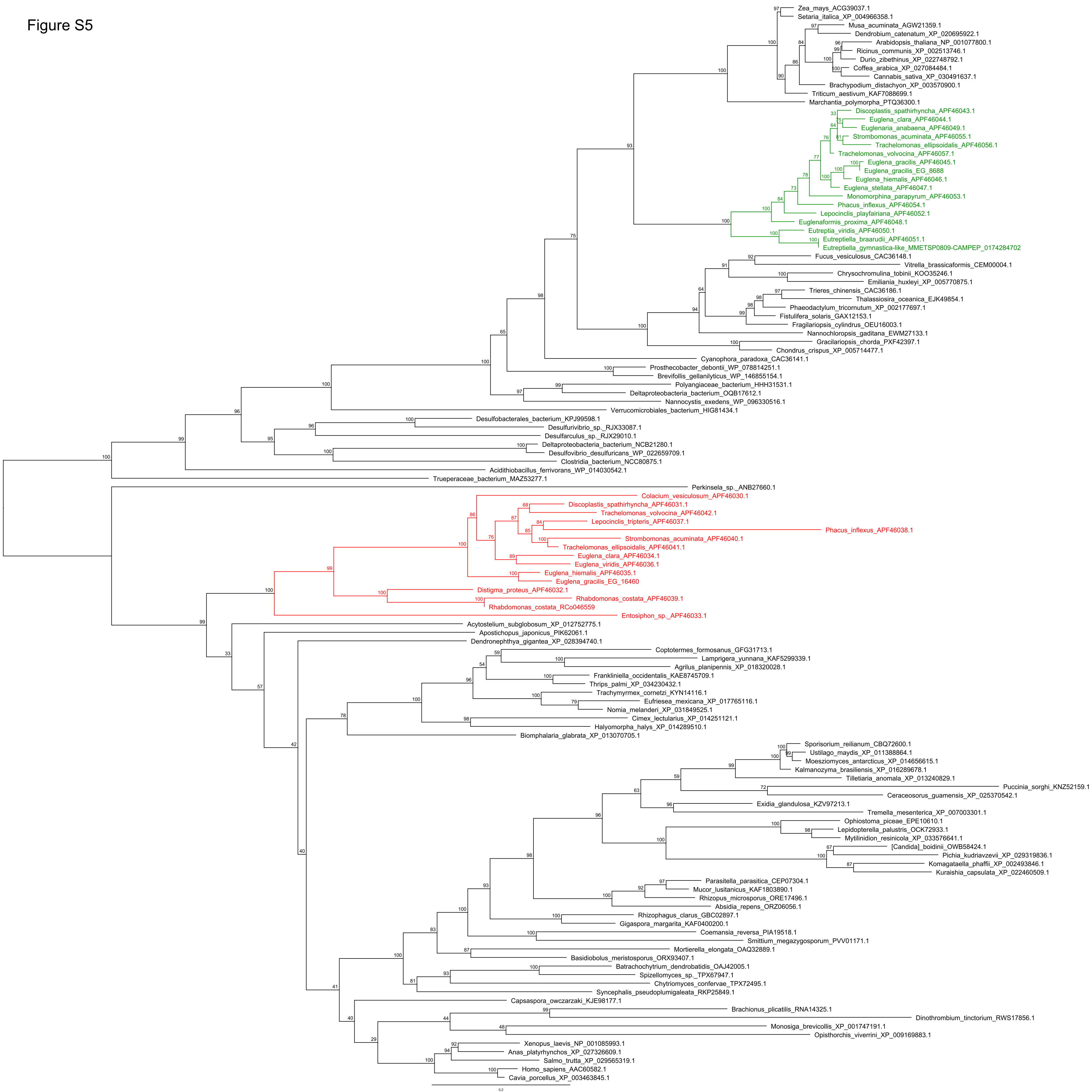


Figure S6

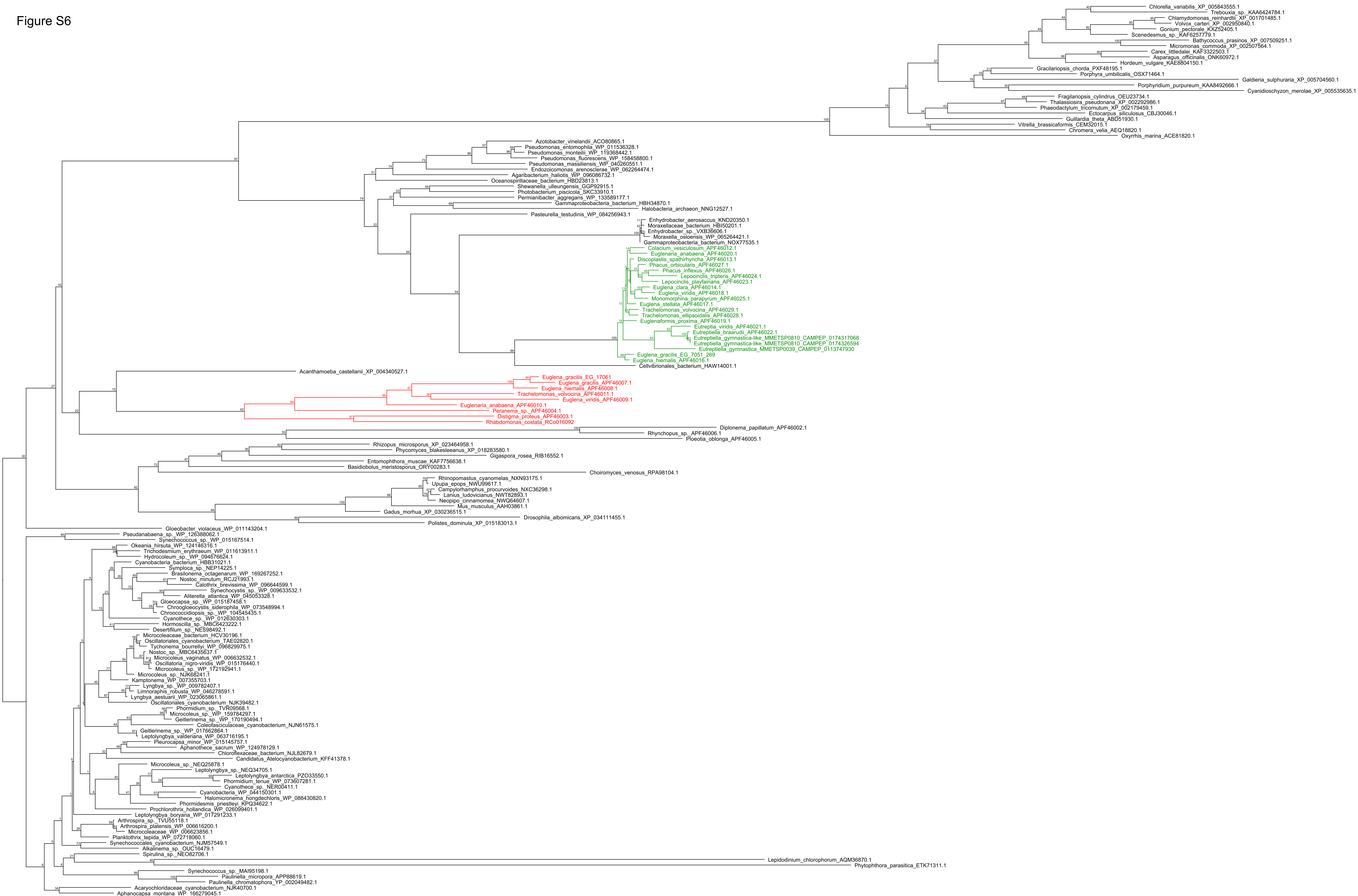


Figure S7



Figure S8

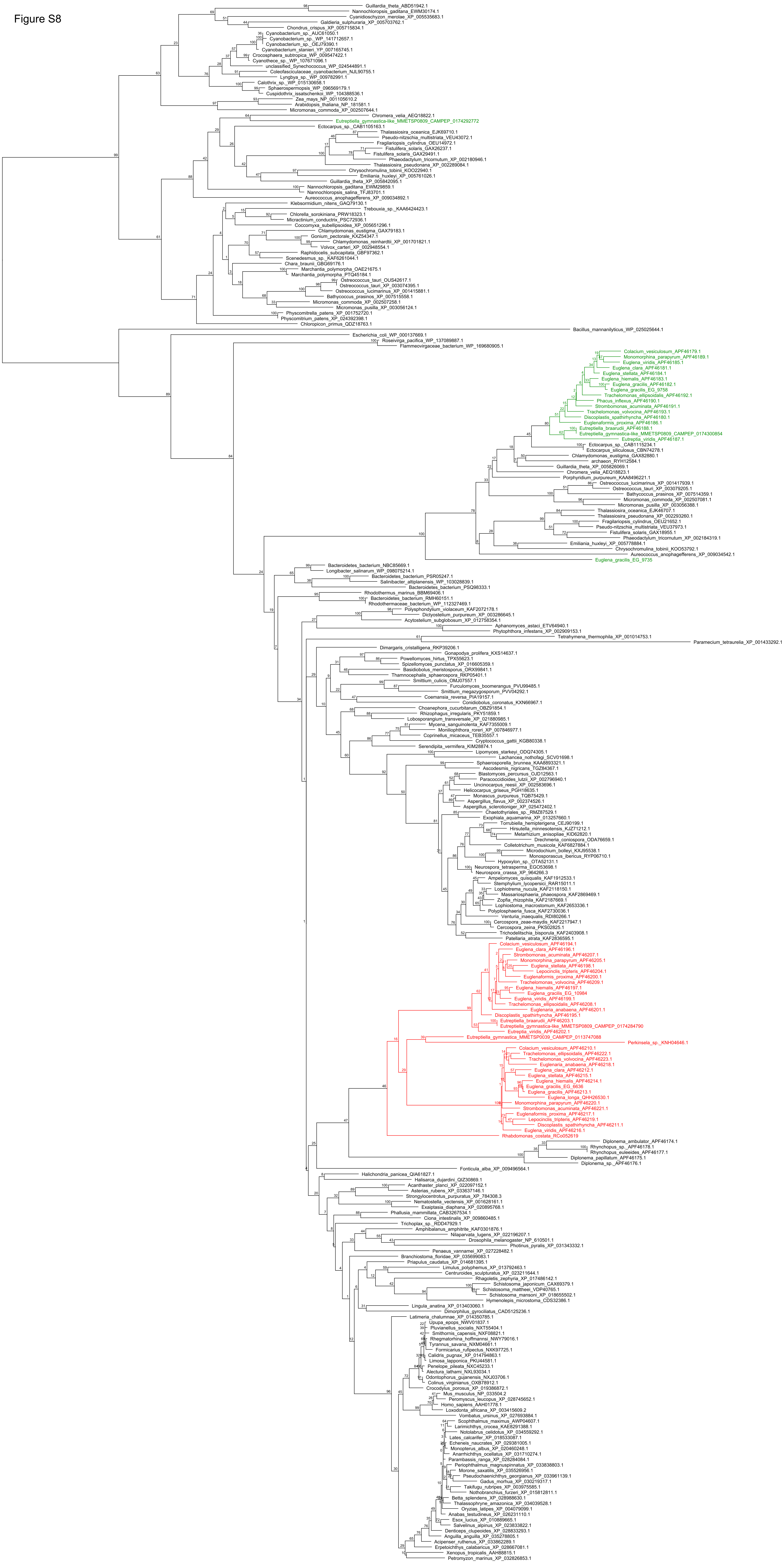


Figure S9



Figure S10

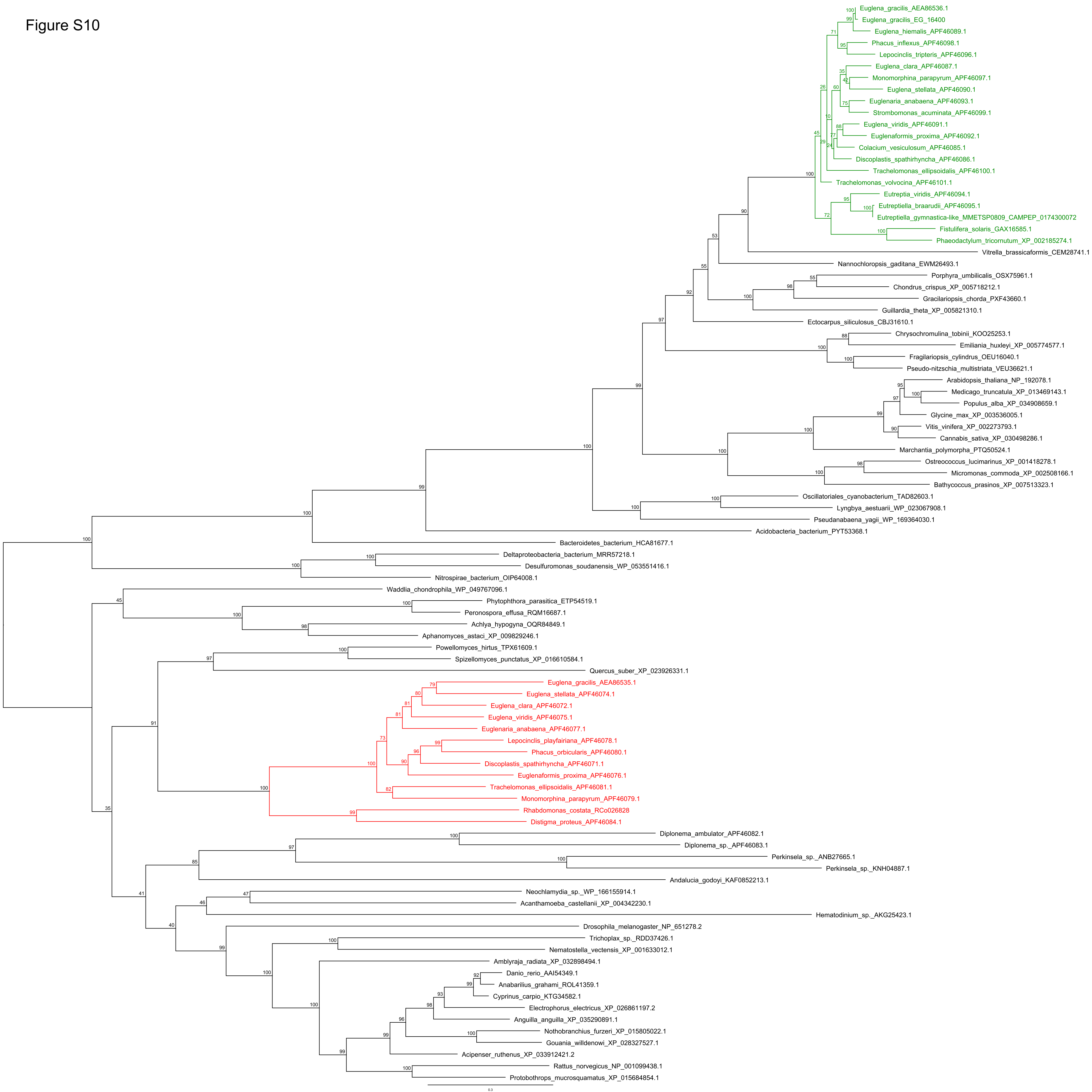


Figure S11

