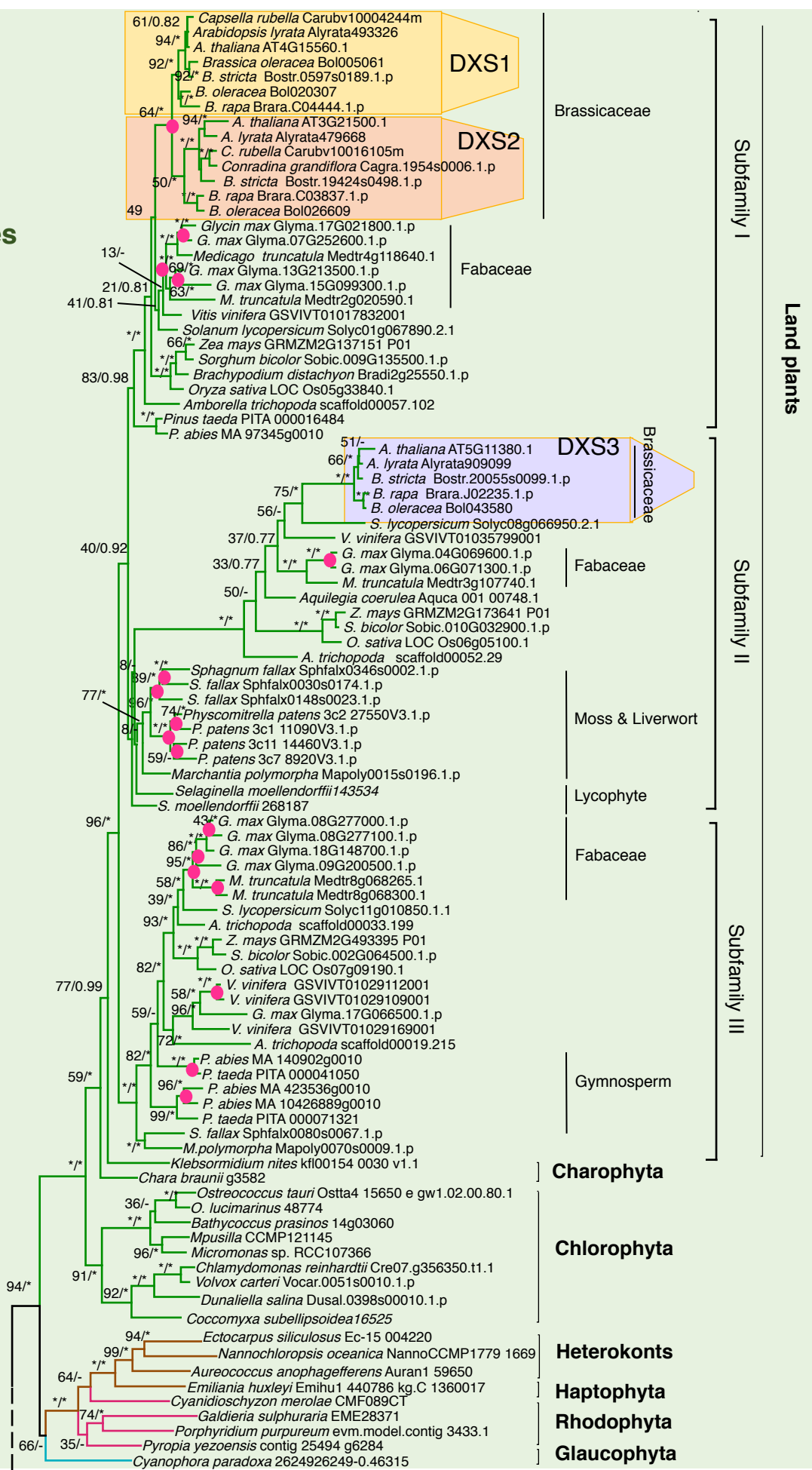


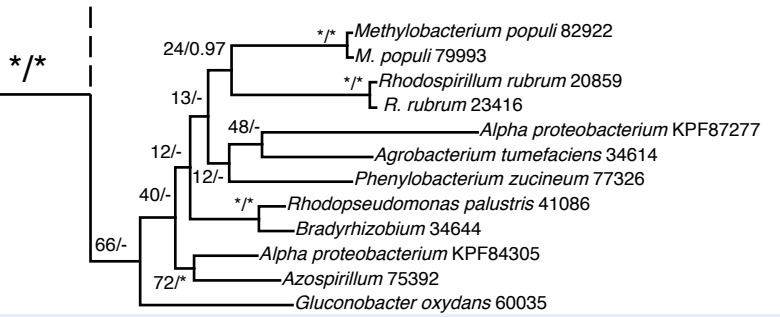
Eukaryotes



Continue to next page

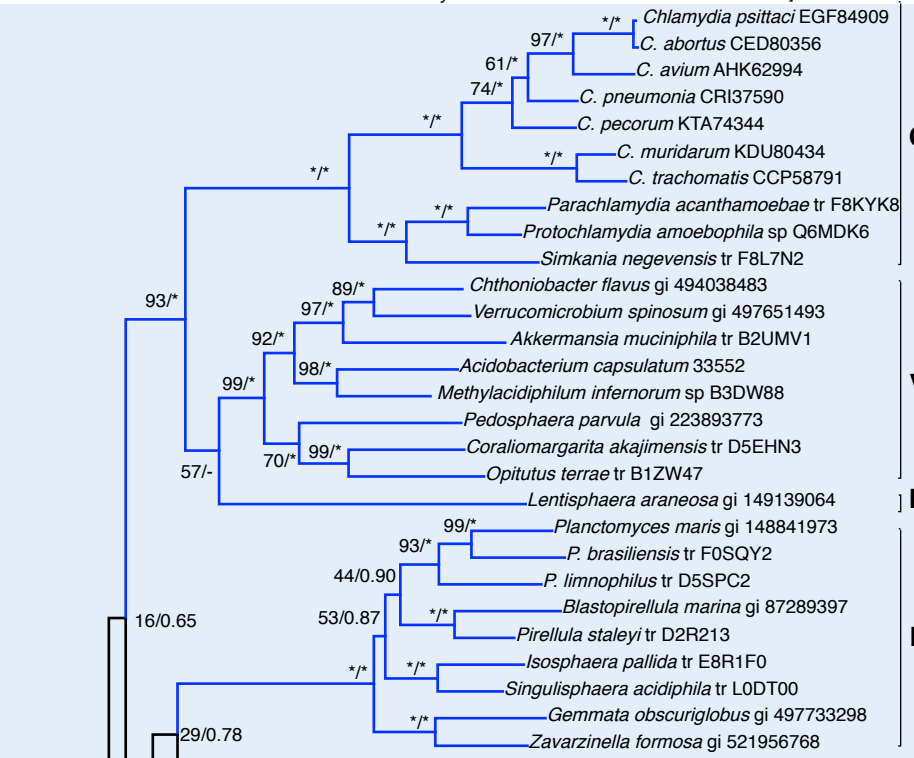
Continued

Other-eubacteria



alpha-proteobacteria

PVC group



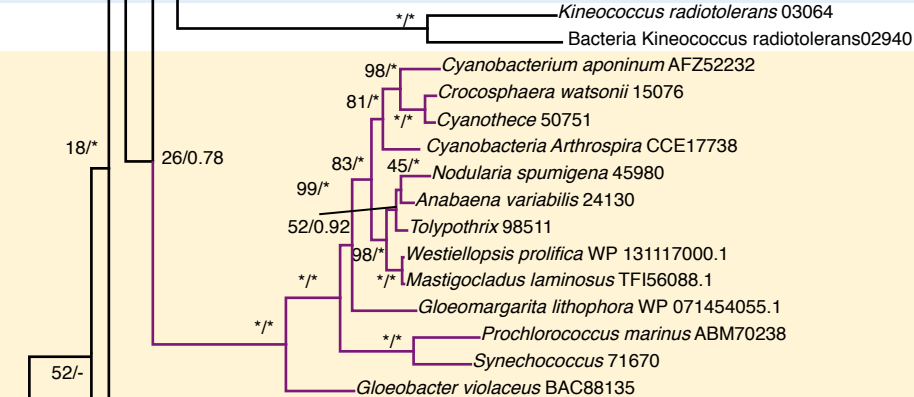
Chlamydia

Verrucomicrobia

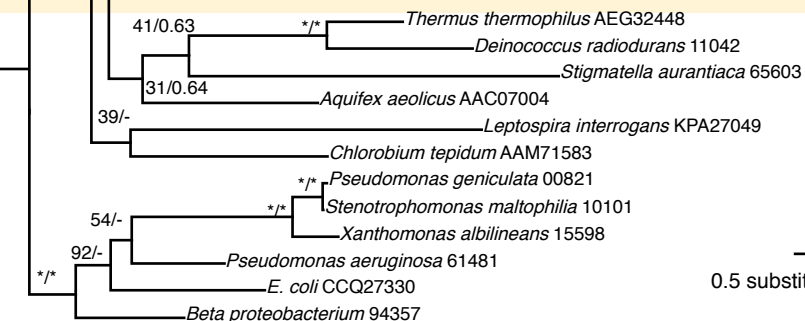
Lentisphaetae

Planctomycetes

Cyano-bacteria

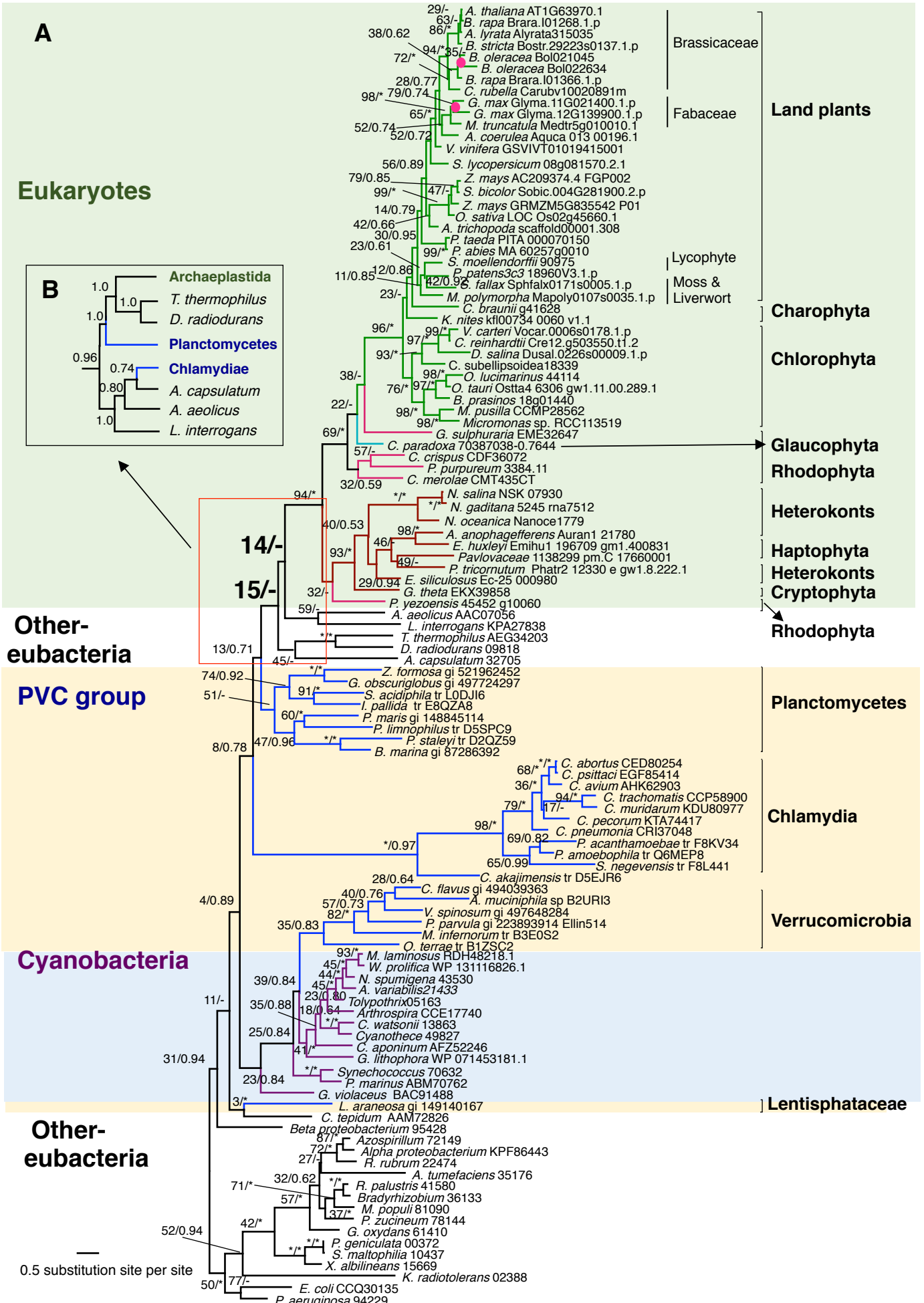


Other eubacteria



0.5 substitution site per site

Figure S1. Phylogenetic tree of DXS. Numbers associated with branches are bootstrap values (BS, on the left) obtained by RAxML and the posterior probability (PP, on the right) obtain by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Pink-filled circle indicates gene duplication. Dash means the topology is different between two methods.



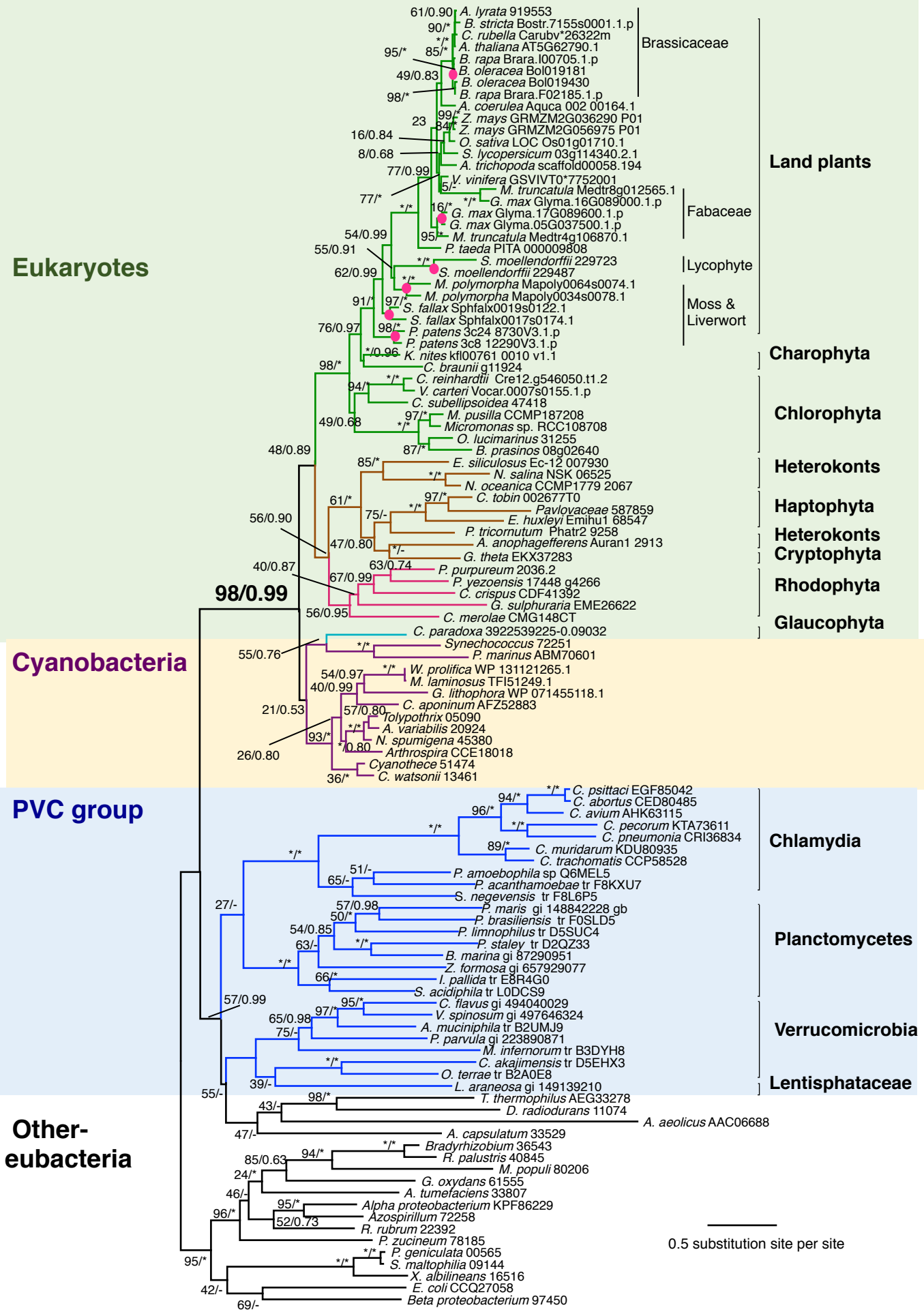
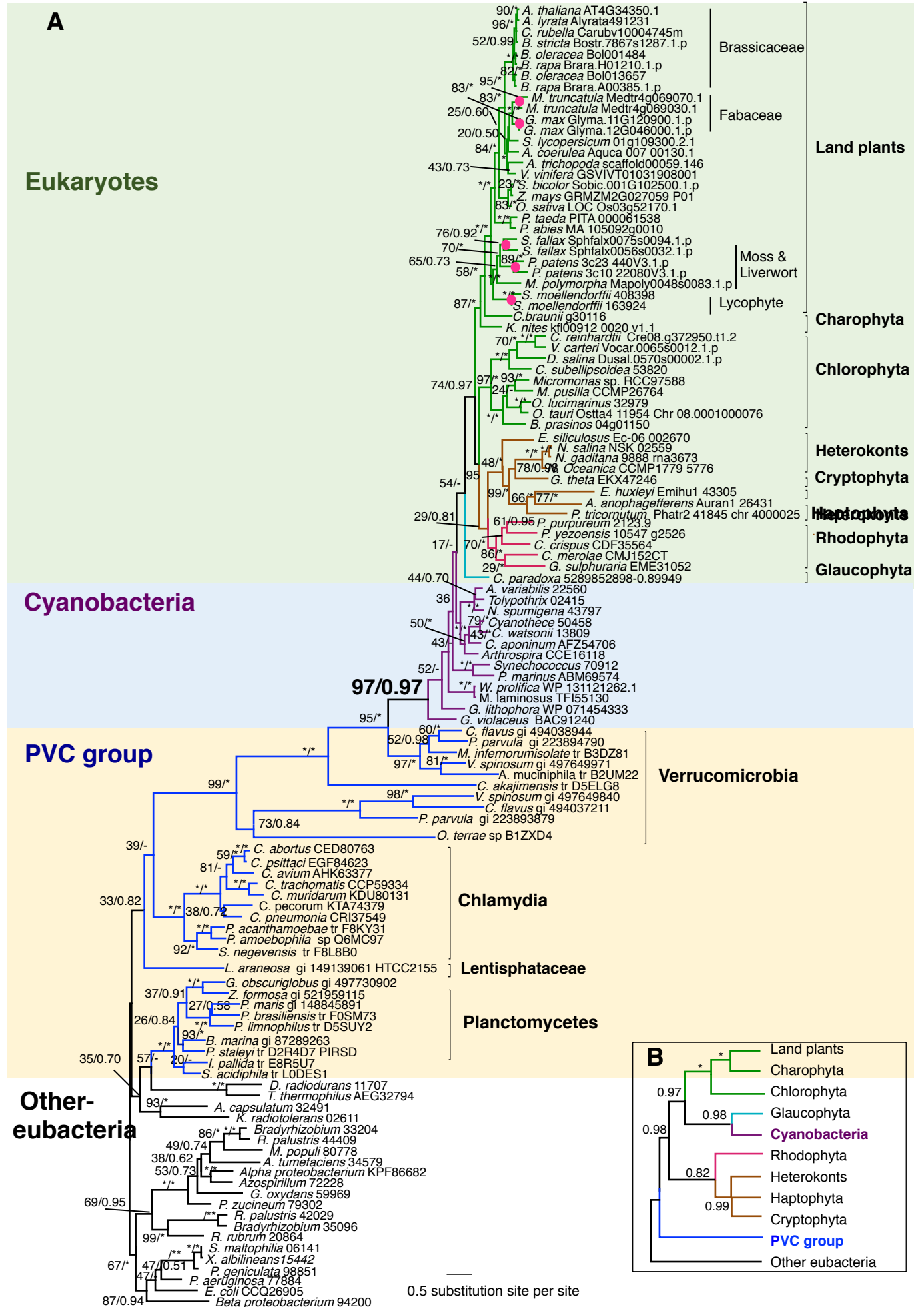


Figure S3. Phylogenetic tree of DXR. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtain by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Pink-filled circle indicates gene duplication. Dash means the topology is different between two methods.



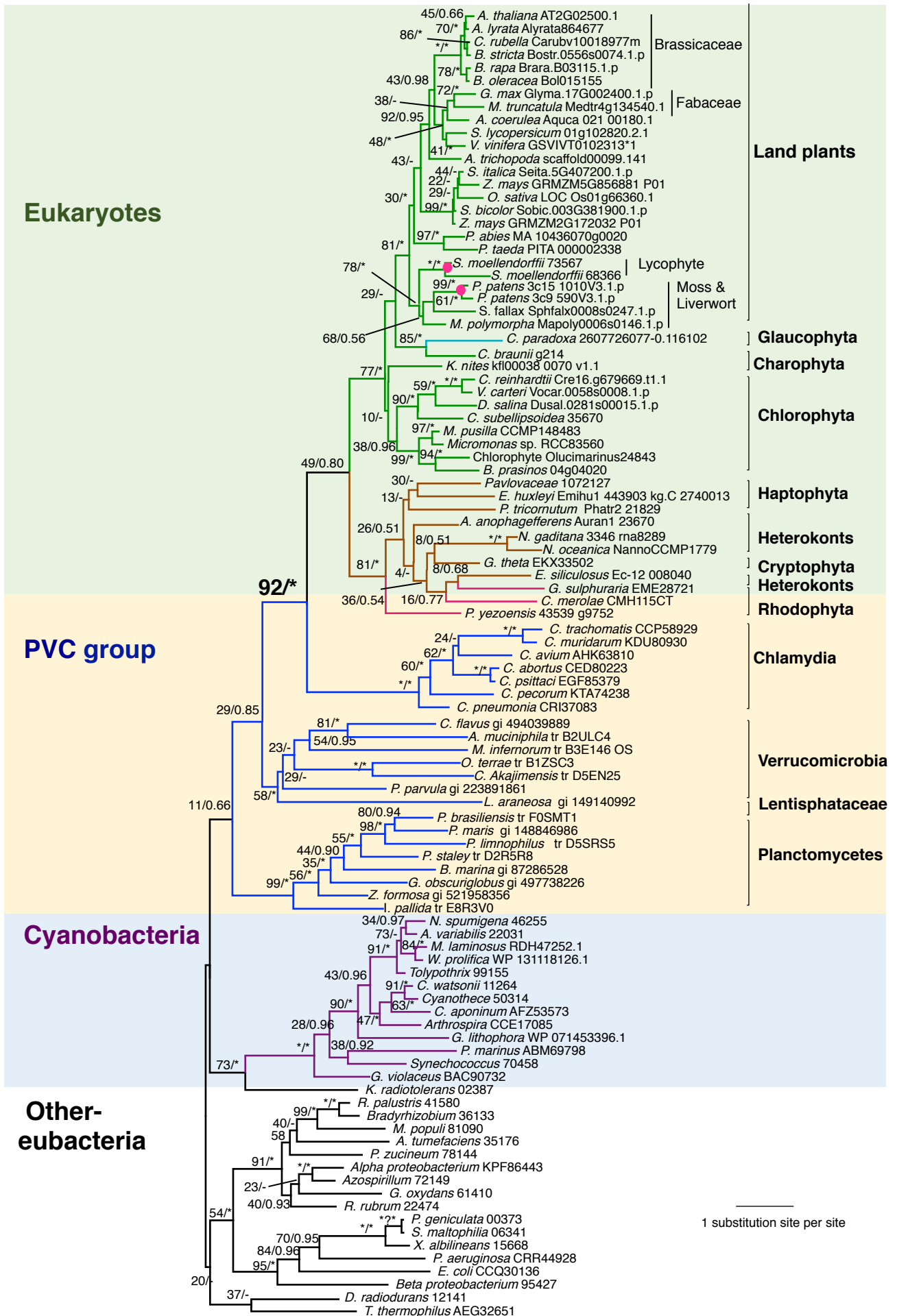
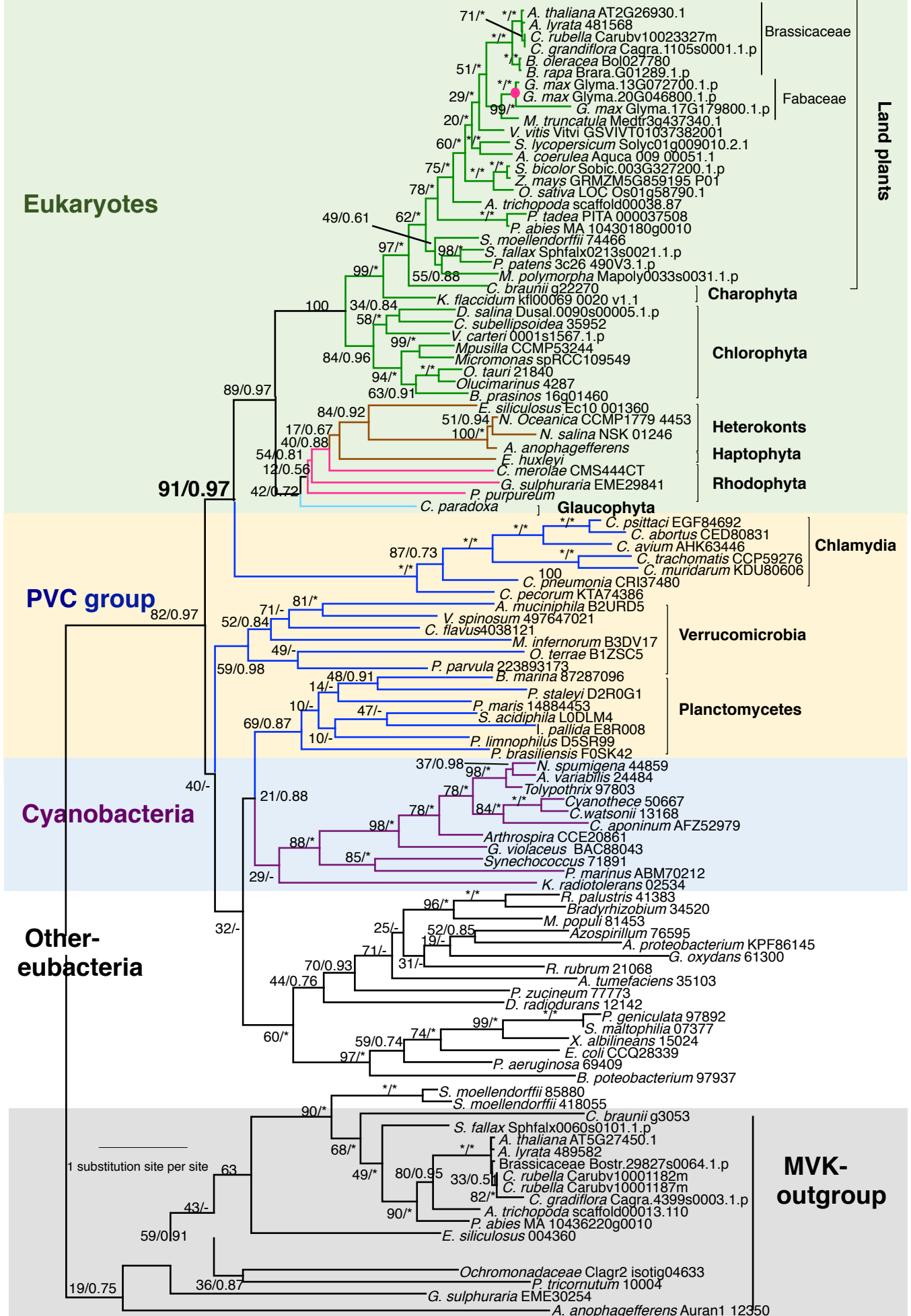


Figure S5. Phylogenetic tree of CMS. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtained by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Dash means the topology is different between two methods.



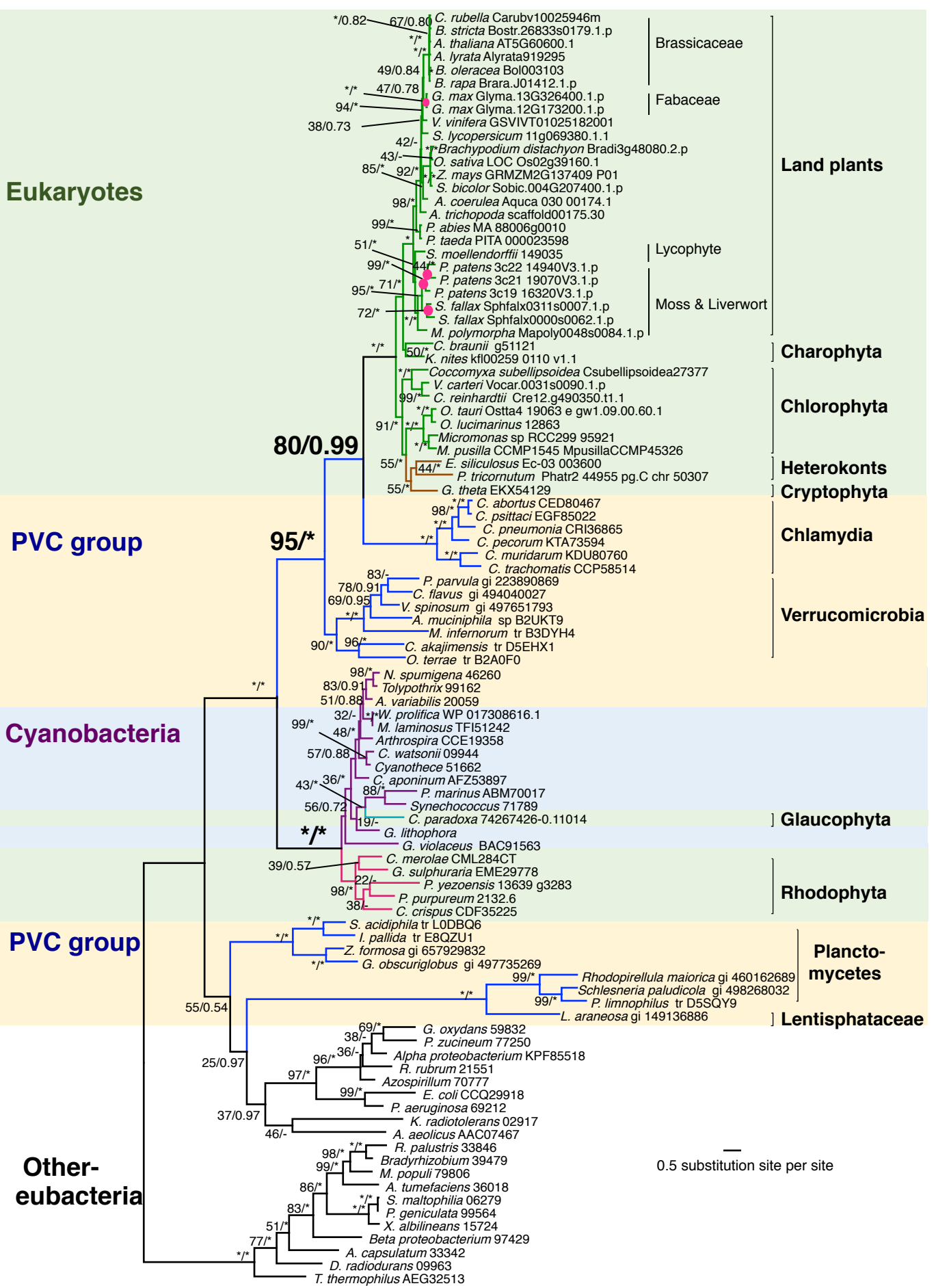


Figure S7. Phylogenetic tree of HDS. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtained by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. The dash is the topology is different obtained by MrBayes. Pink-filled circle indicates gene duplication. Dash means the topology is different between two methods.