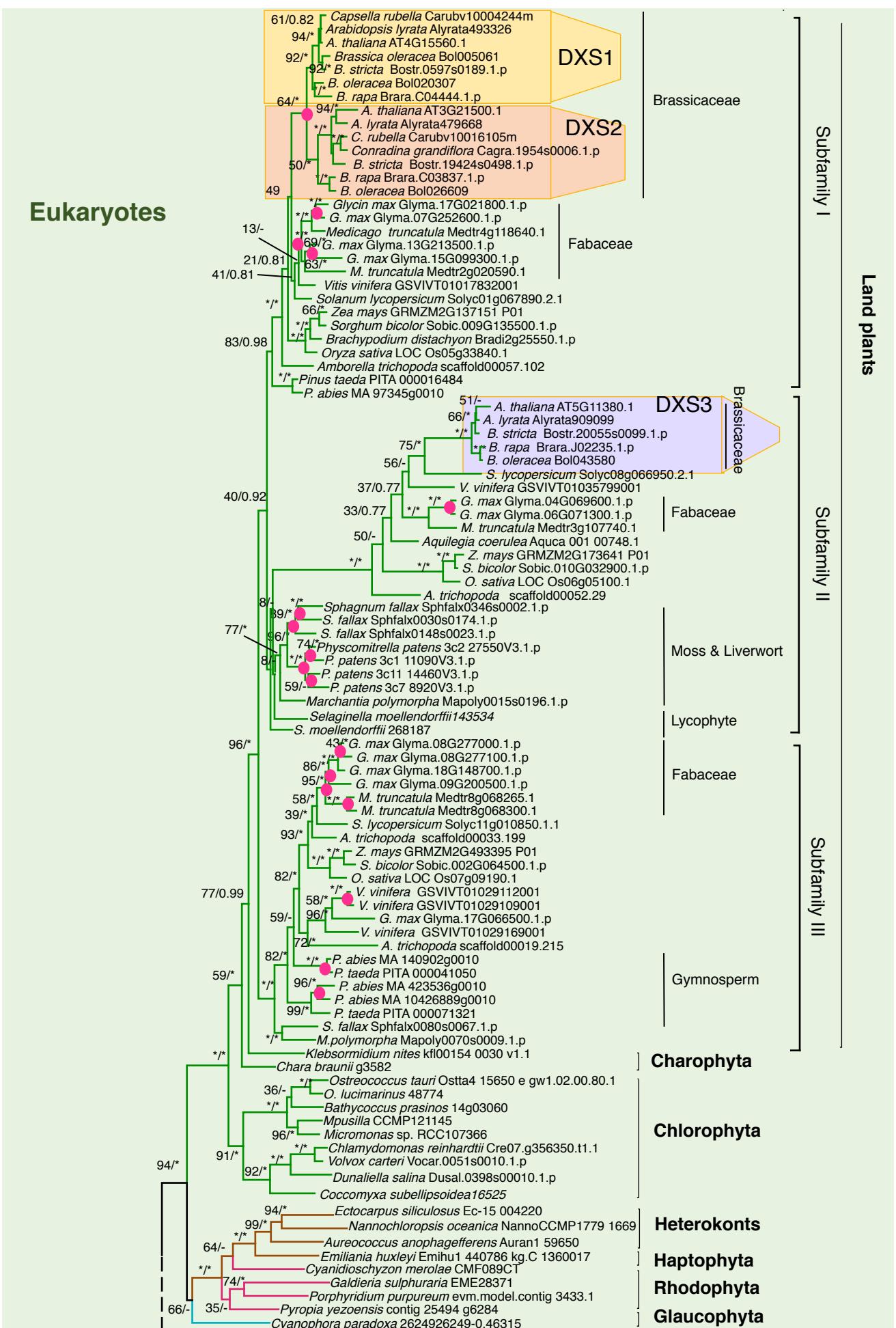


Eukaryotes



Continue to next page

Continued

Other-eubacteria

PVC group

Cyano-bacteria

Other eubacteria

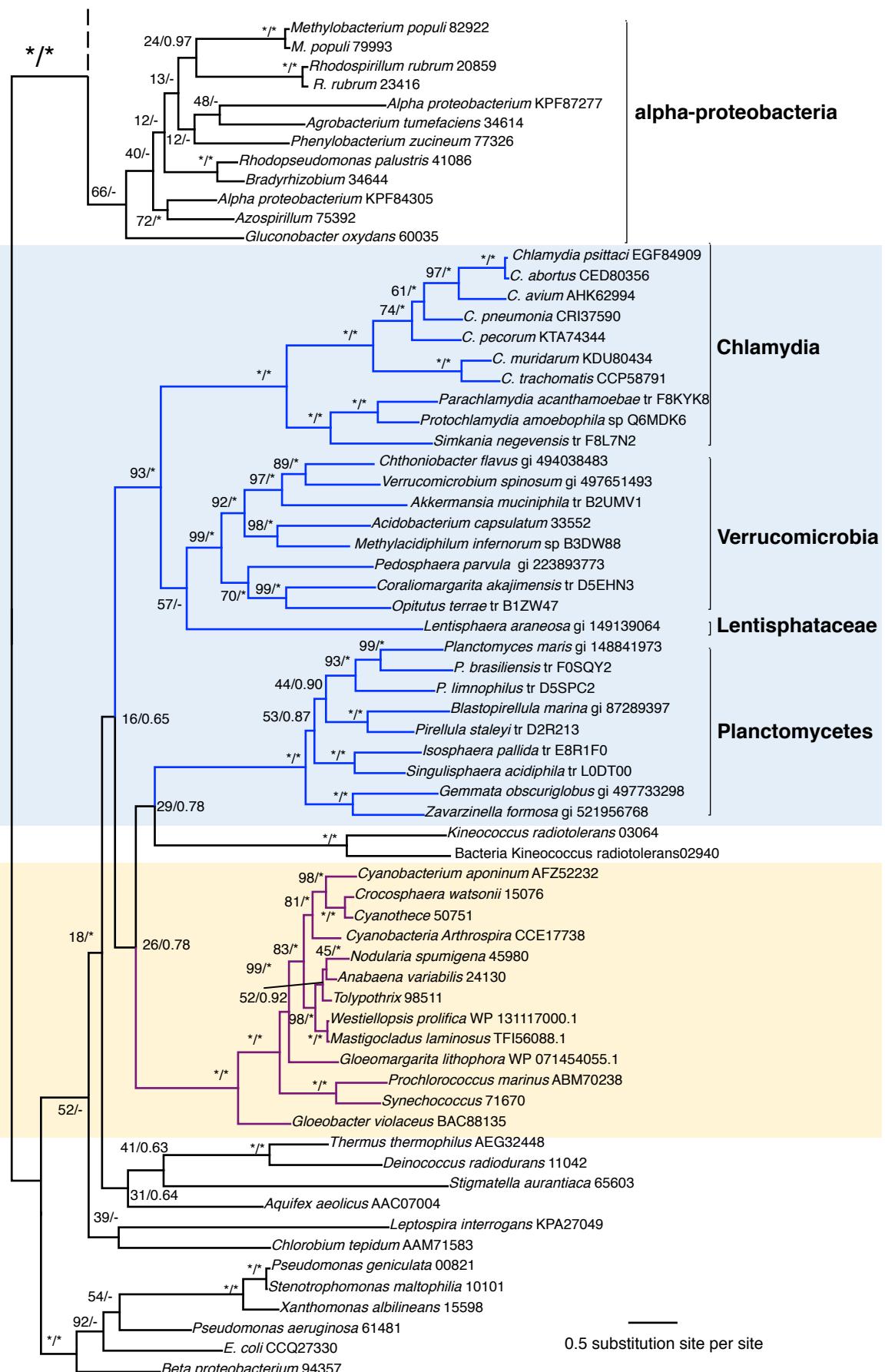
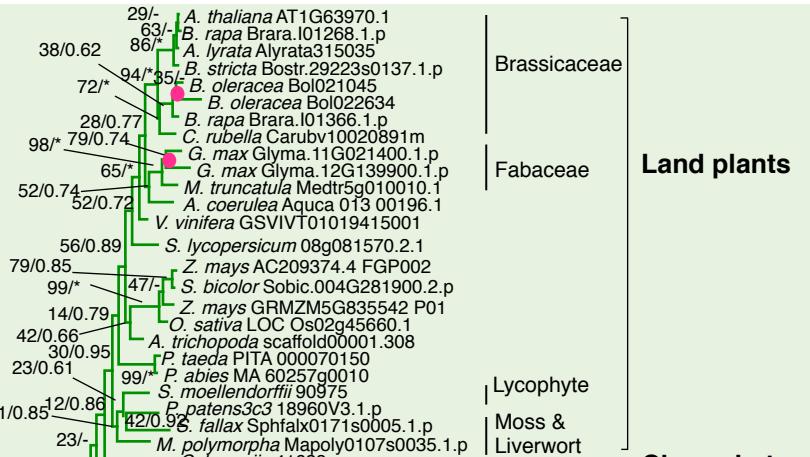


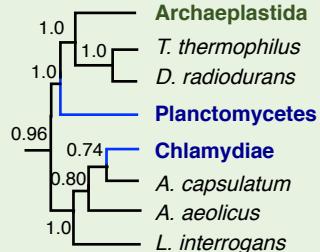
Figure S1. Phylogenetic tree of DXS. Numbers associated with branches are bootstrap values (BS, on the left) obtained by RAxML and the posterior probability (PP, on the right) obtain by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Pink-filled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

A



Eukaryotes

B



Other-eubacteria

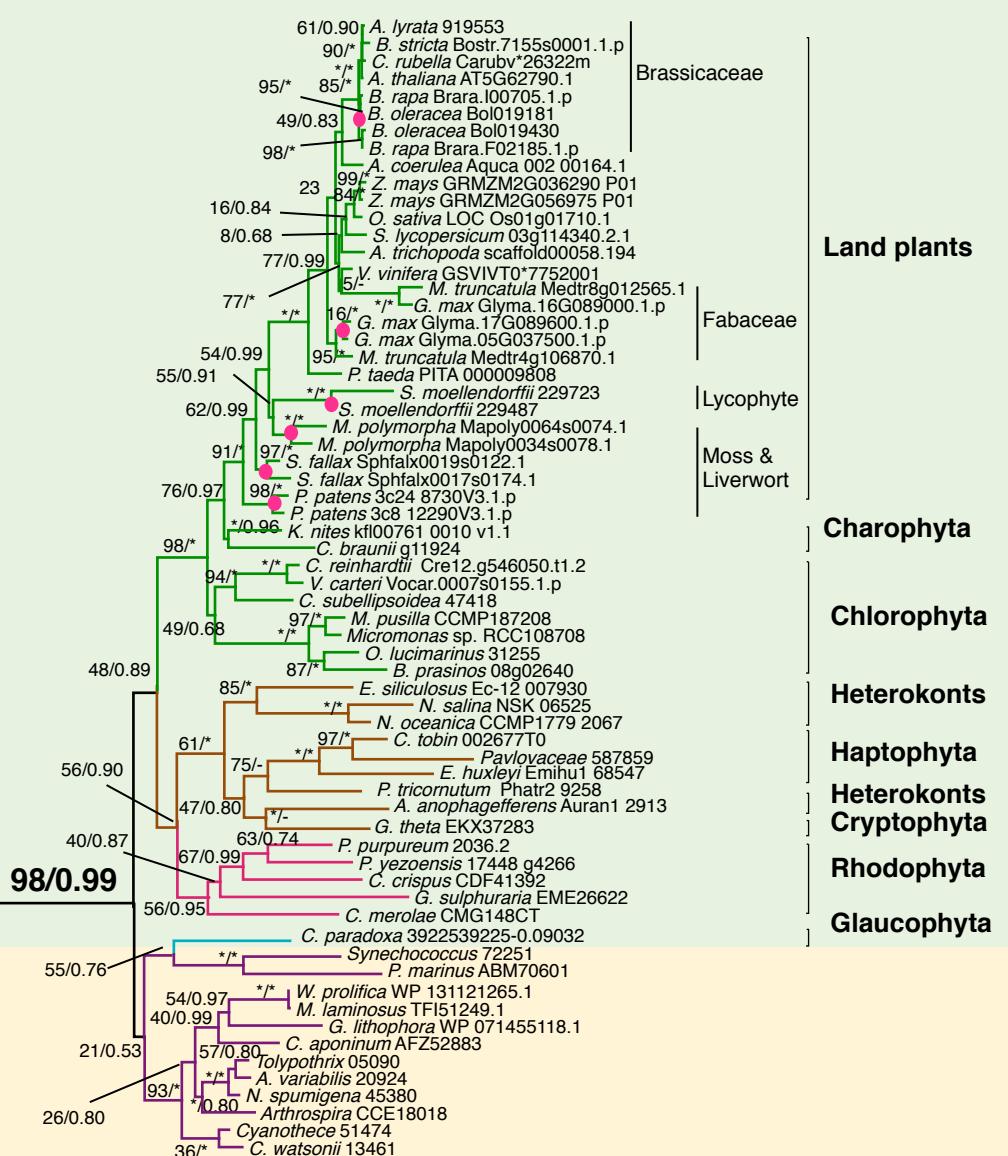
PVC group

Cyanobacteria

Other-eubacteria

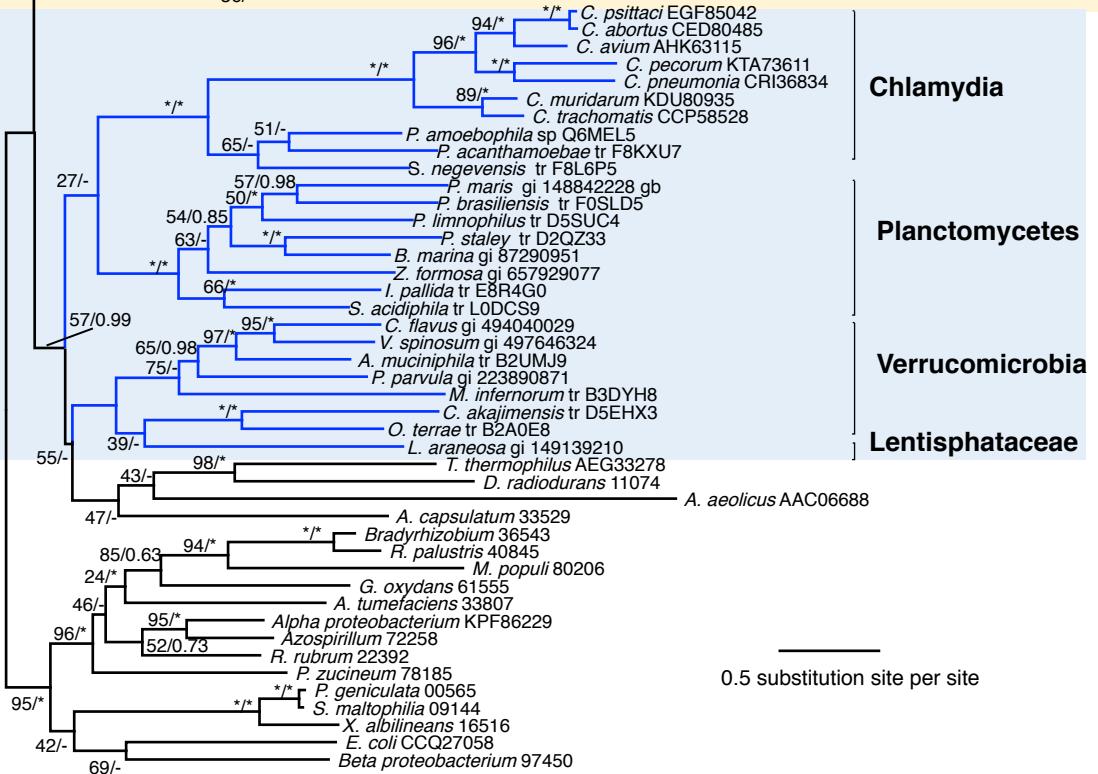
Figure S2. Phylogenetic tree of MDS. A. The detailed phylogenetic tree of RAxML and MrBayes. B. The simplified cladogram shows the different eubacteria species clustered with eukaryotes obtained from MrBayes comparing to RAxML shown in red rectangle. Numbers associated with branches are BS values (left) or PP values (right) obtained by RAxML and 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.

Eukaryotes



Cyanobacteria

PVC group

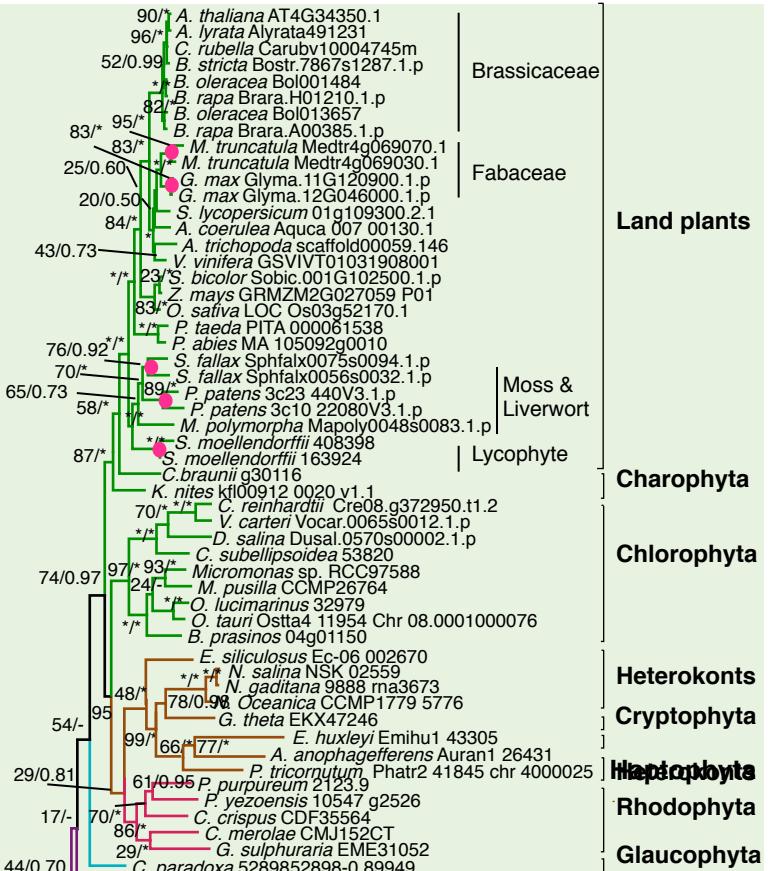


Other-eubacteria

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.

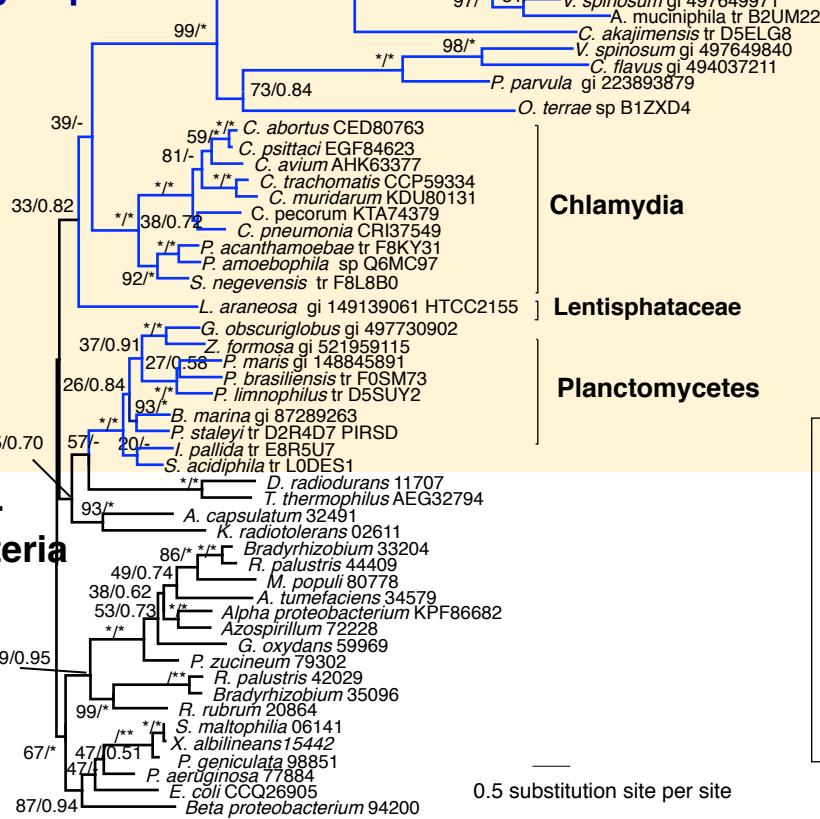
A

Eukaryotes



Cyanobacteria

PVC group



0.5 substitution site per site

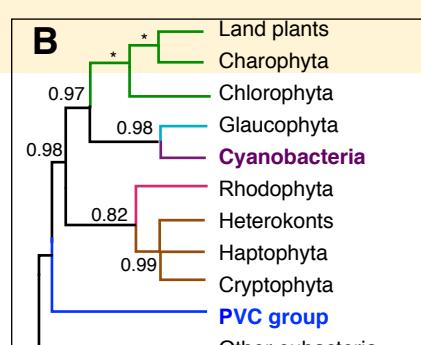


Figure S4. Phylogenetic tree of HDR. **A.** The detailed phylogenetic tree of RAxML and MrBayes. **B.** The simplified cladogram shows the different position of Cyanobacteria obtained from MrBayes. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtained by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Pink-filled circle indicates gene duplication. Dash means the topology is different between two methods.

Eukaryotes

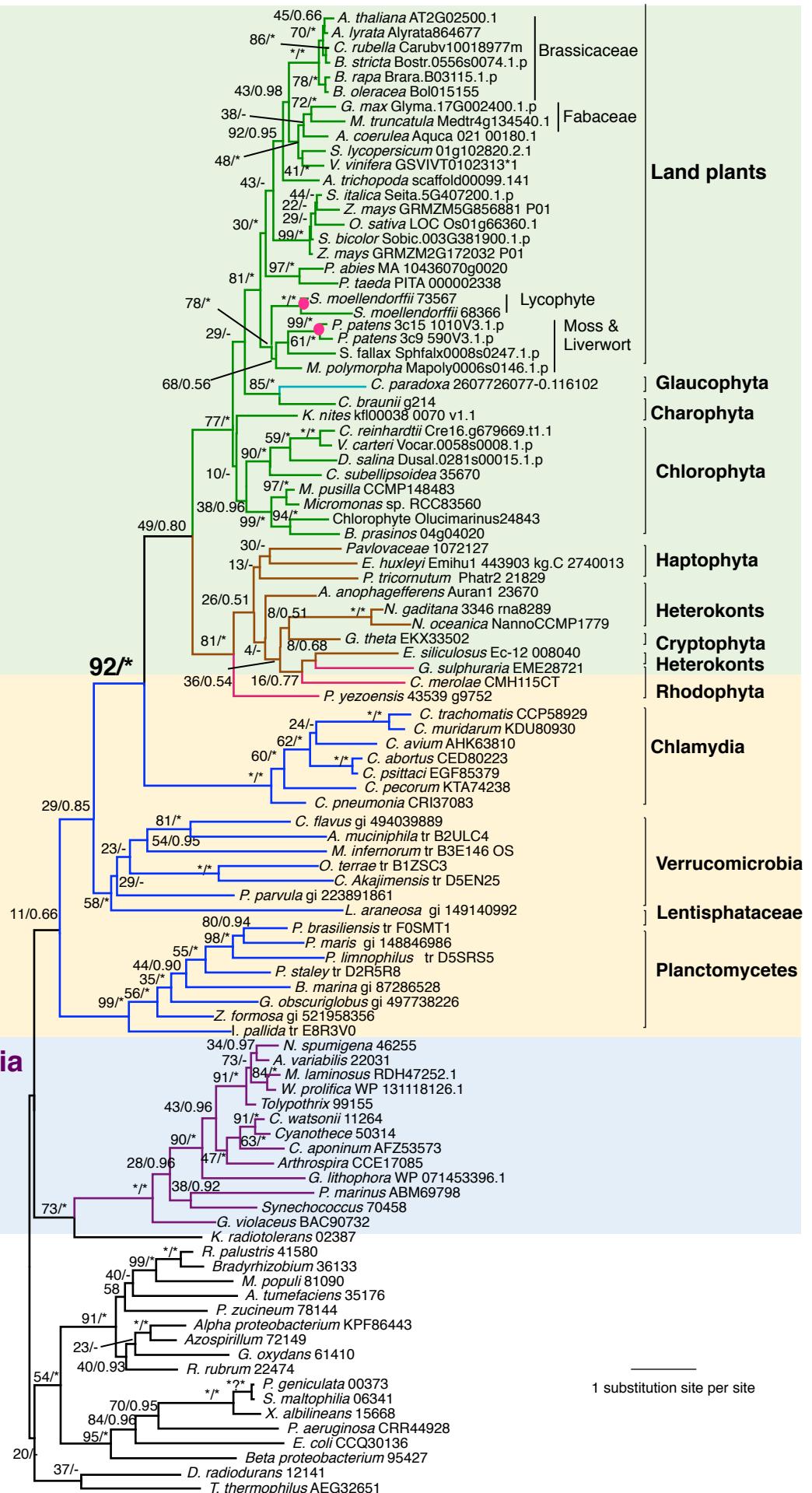
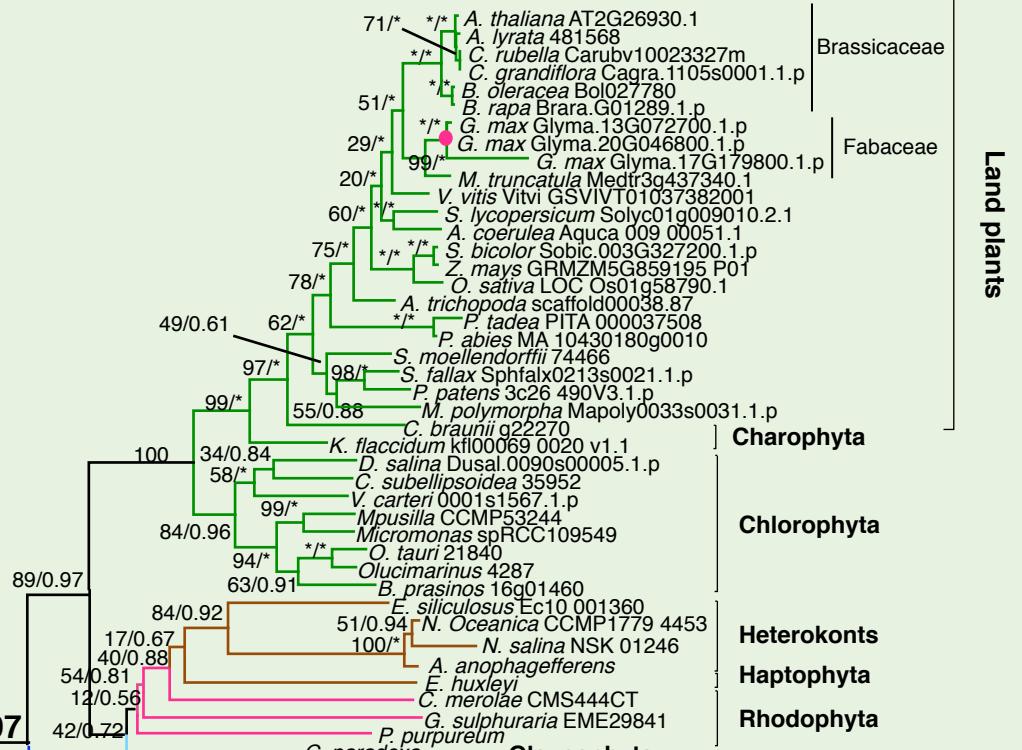


Figure S5. Phylogenetic tree of CMS. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtain by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. Dash means the topology is different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

Land plants

Eukaryotes



PVC group

91/0.97

82/0.97

Cyanobacteria

40/-

Other-eubacteria

32/-

1 substitution site per site

63

43/-

59/0.91

36/0.87

19/0.75

MVK-outgroup

90/-

68/-

49/-

80/0.95

33/0.5/

82/-

A. trichopoda scaffold00013.110

P. abies MA 10436220g0010

E. siliculosus 004360

Ochromonadaceae Clagr2 isotig04633

P. tricornutum 10004

G. sulphuraria EME30254

A. anophagefferens Auran1 12350

Figure S6. Phylogenetic tree of CMK. MVK sequences are set as the outgroup. Numbers associated with branches are BS values (values on the left) obtained by RAxML and the PP values (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. Dash means the topology is different between two methods.

Eukaryotes

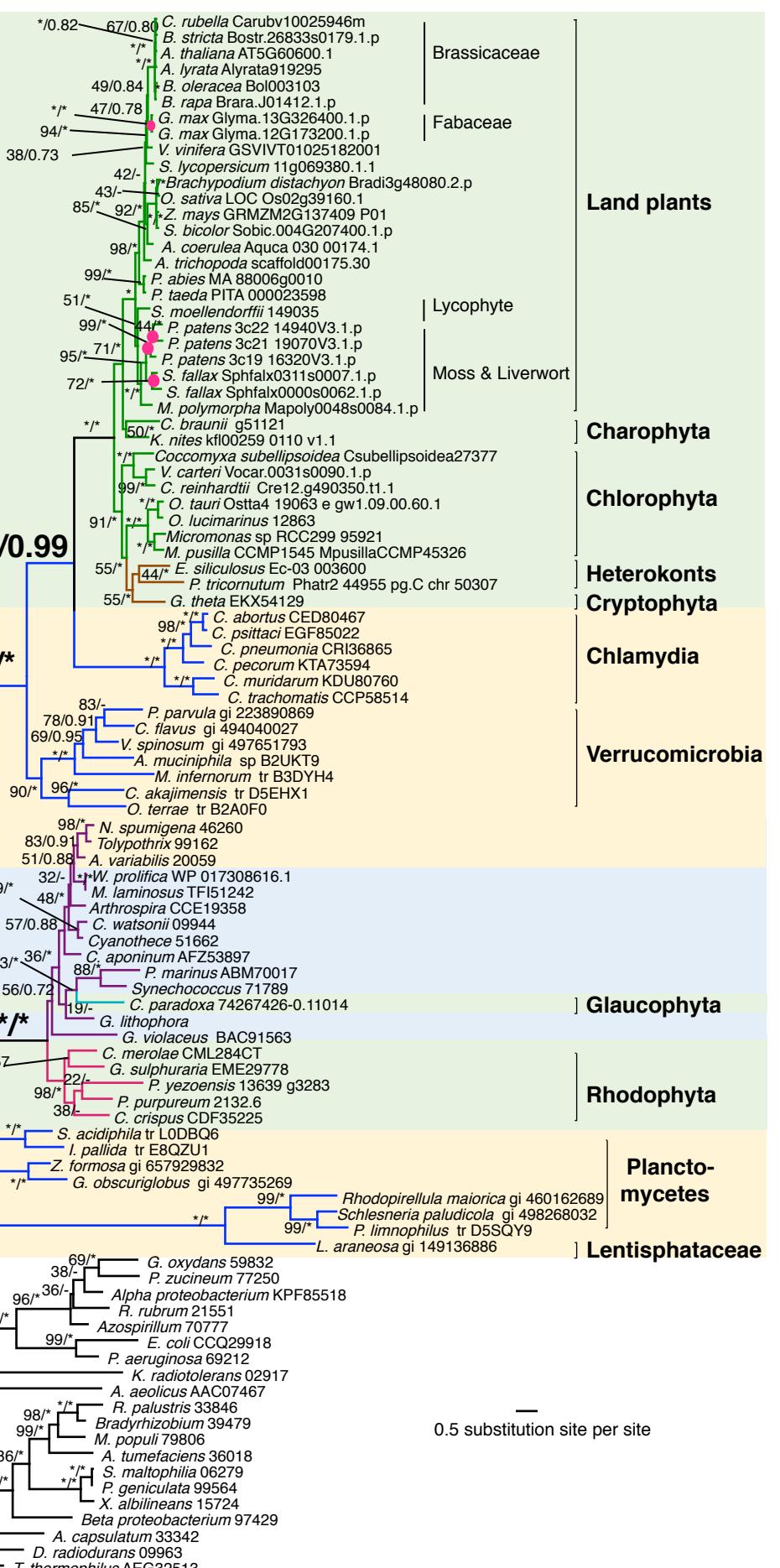


Figure S7. Phylogenetic tree of HDS. Numbers associated with branches are BS values (on the left) obtained by RAxML and the PP values (on the right) obtain by MrBayes. Taxa in different major groups are shaded in different colors. The star is the BS=100 or PP=1.0. The dash is the topology is different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