



Supplementary Figure 19. Coalescent analyses of 76 genes and 78 taxa (77+GE). Numbers above the branches are supported based on the ASTRAL methods. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 20. Coalescent analyses of 76 genes and 78 taxa (77+EA). Numbers above the branches are supported based on the ASTRAL methods. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 21. Coalescent analyses of 76 genes and 78 taxa (77+RG). Numbers above the branches are supported based on the ASTRAL methods. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 22. Coalescent analyses of 76 genes and 79 taxa. Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 23. Coalescent tree from 76 genes for 80 taxa. Numbers above the branches are supported based on the ASTRAL methods. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 24. Concatenated analyses (maximum likelihood) of 39 genes and 77 taxa. Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 25. Concatenated analyses (maximum likelihood) of 39 genes and 78 taxa (77+GE). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 26. Concatenated analyses (maximum likelihood) of 39 genes and 78 taxa (77+EA). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 27. Concatenated analyses (maximum likelihood) of 39 genes and 79 taxa (77+EA+GE). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 28. Concatenated tree from 39 genes for 80 taxa. Numbers above the branches ML bootstrap percentages. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 29. Concatenated analyses (maximum likelihood) of 76 genes and 77 taxa (Maximum Likelihood). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 30. Concatenated analyses (maximum likelihood) of 76 genes and 78 taxa (77+GE). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 31. Concatenated analyses (maximum likelihood) of 76 genes and 78 taxa (77+EA). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 32. Concatenated analyses (maximum likelihood) of 76 genes and 79 taxa (77+GE+EA). Numbers above the branches are supported of ML. Yellow indicates taxa with high amounts of non-randomly distributed missing data.

Supplementary Figure 33. Bayesian inference (concatenated analyses) of 76 genes and 80 taxa (77+GE+EA+RG). Numbers above/below the branches are supported of BI. Yellow indicates taxa with high amounts of non-randomly distributed missing data. Red indicates long branches. Blue indicates short branches.

Figure S1

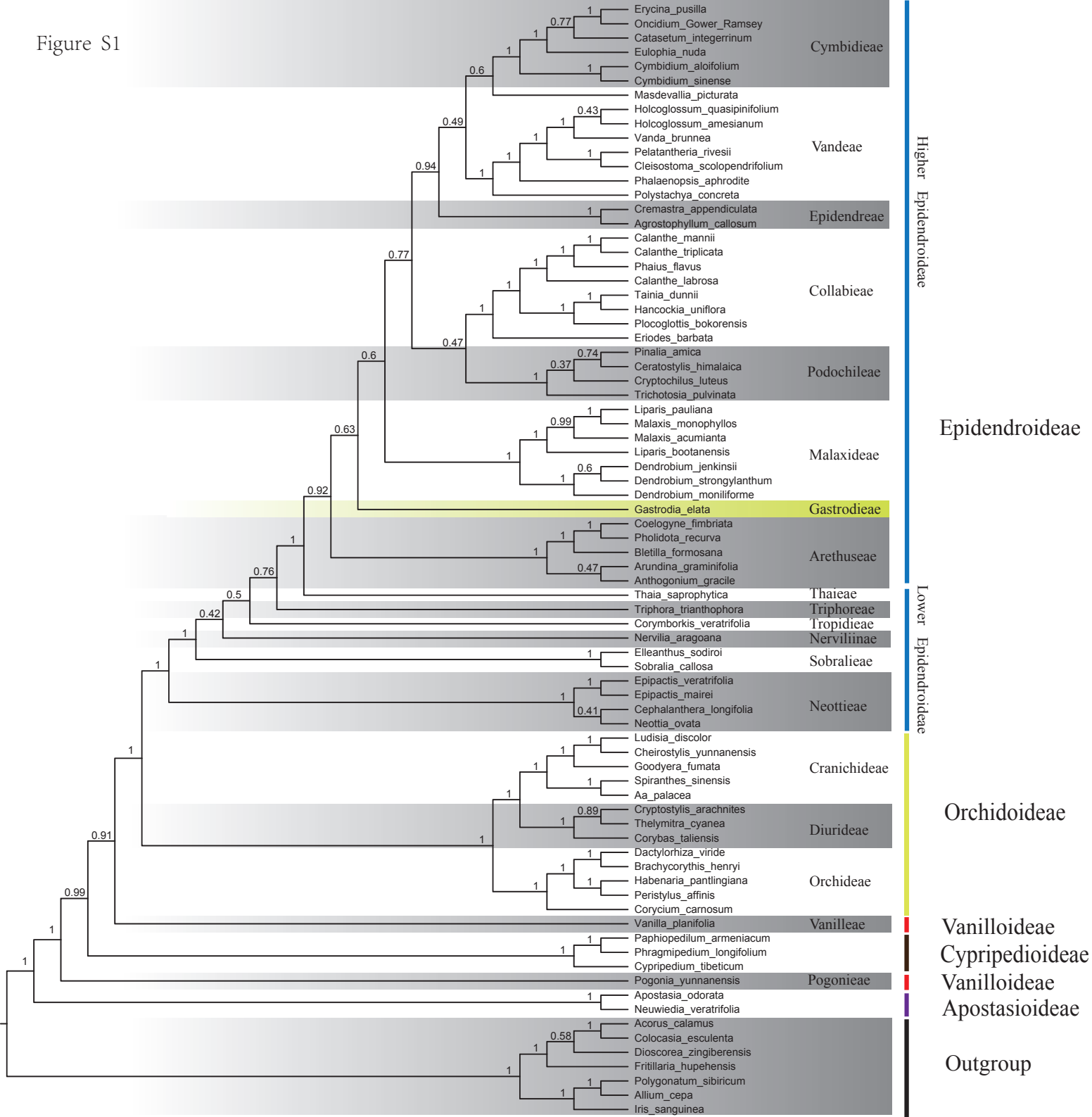


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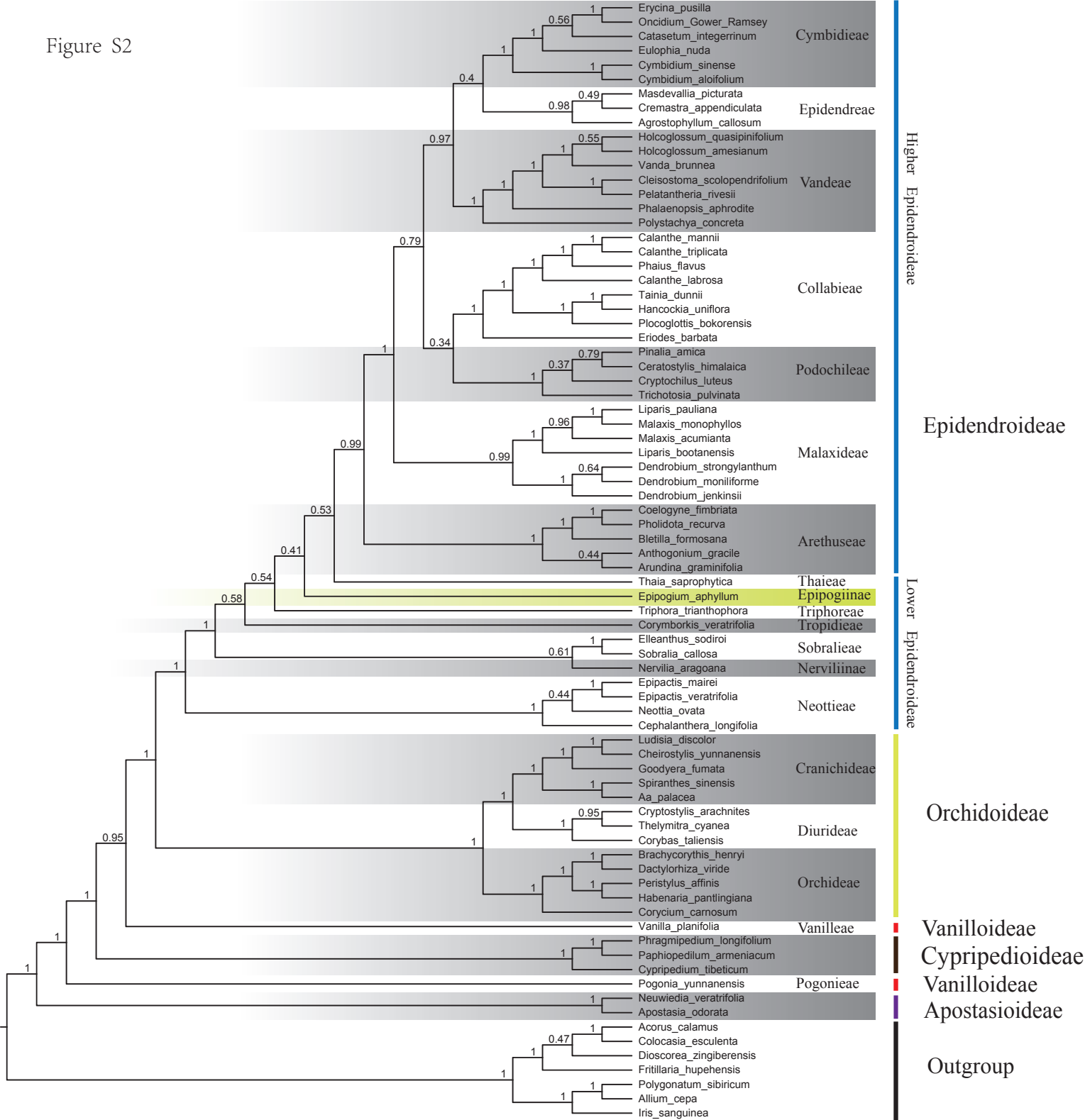


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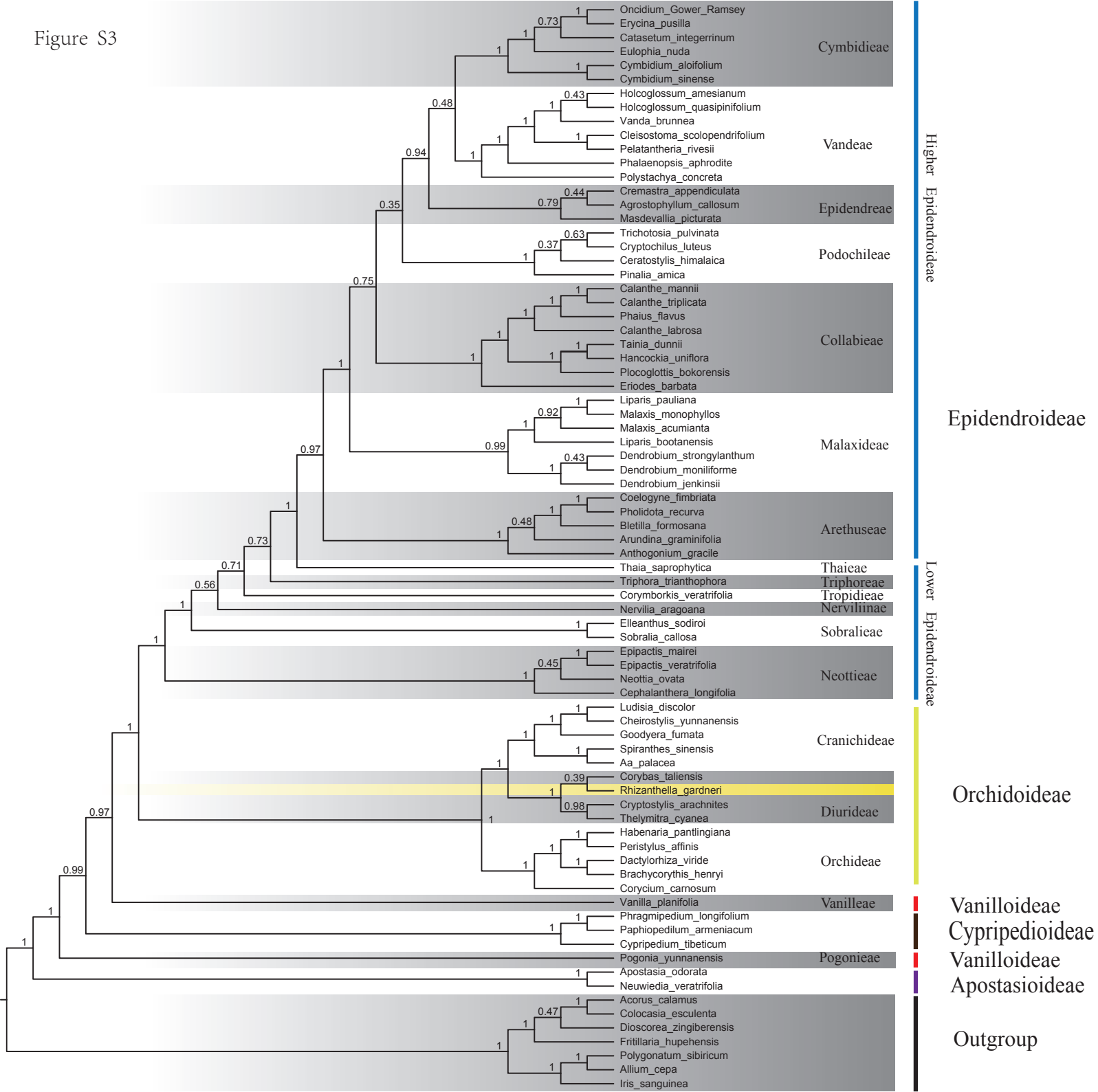


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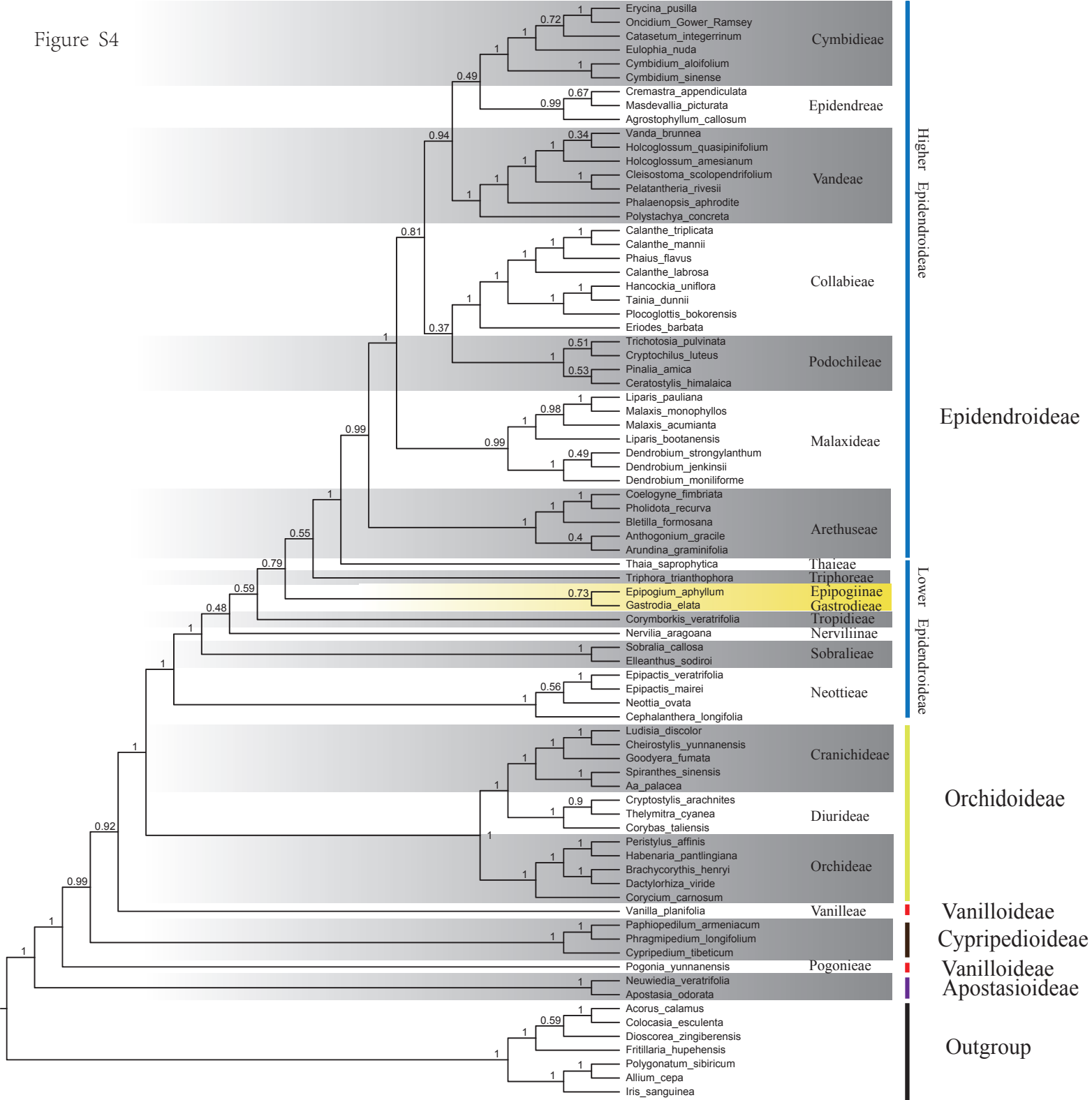


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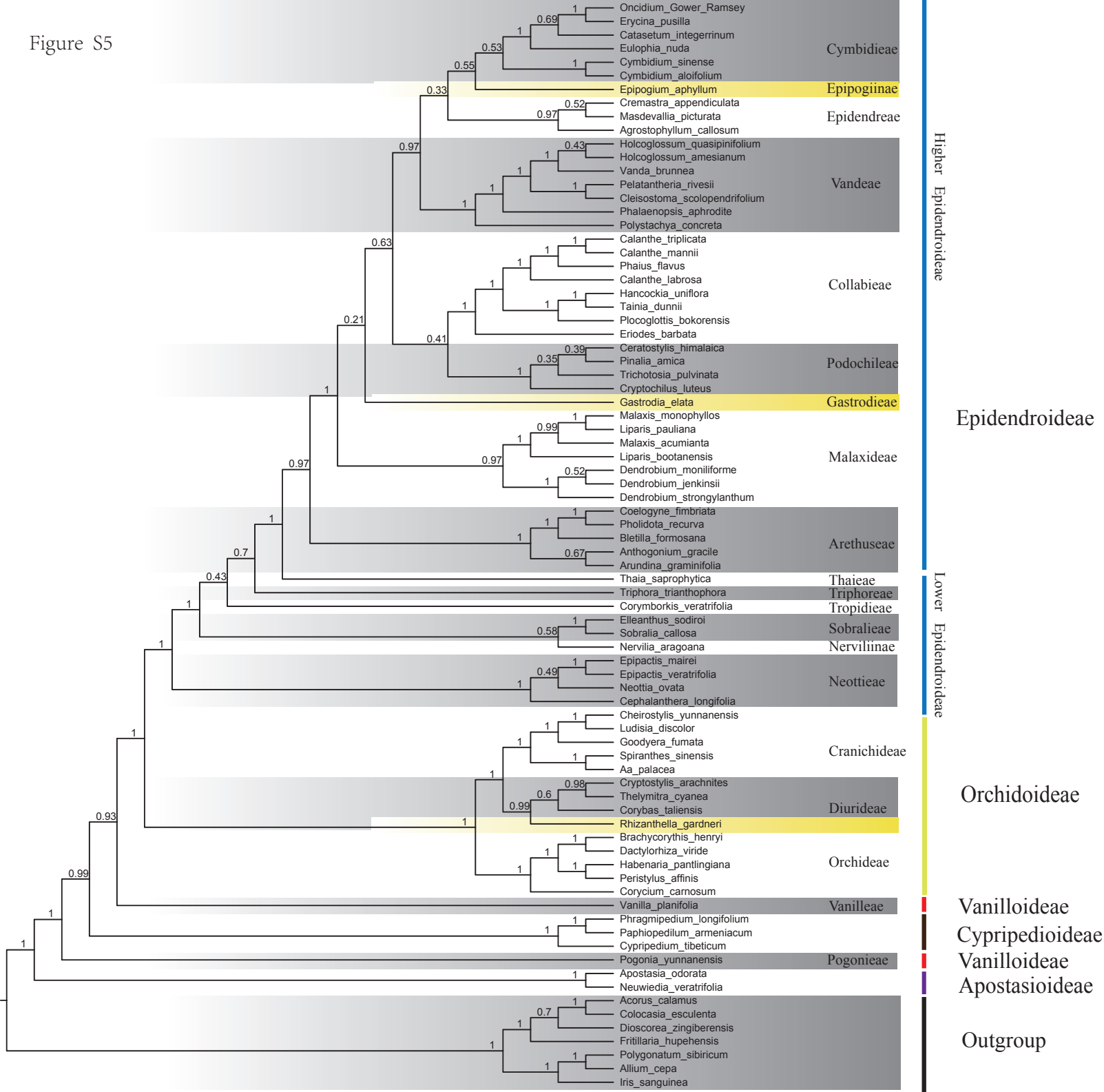


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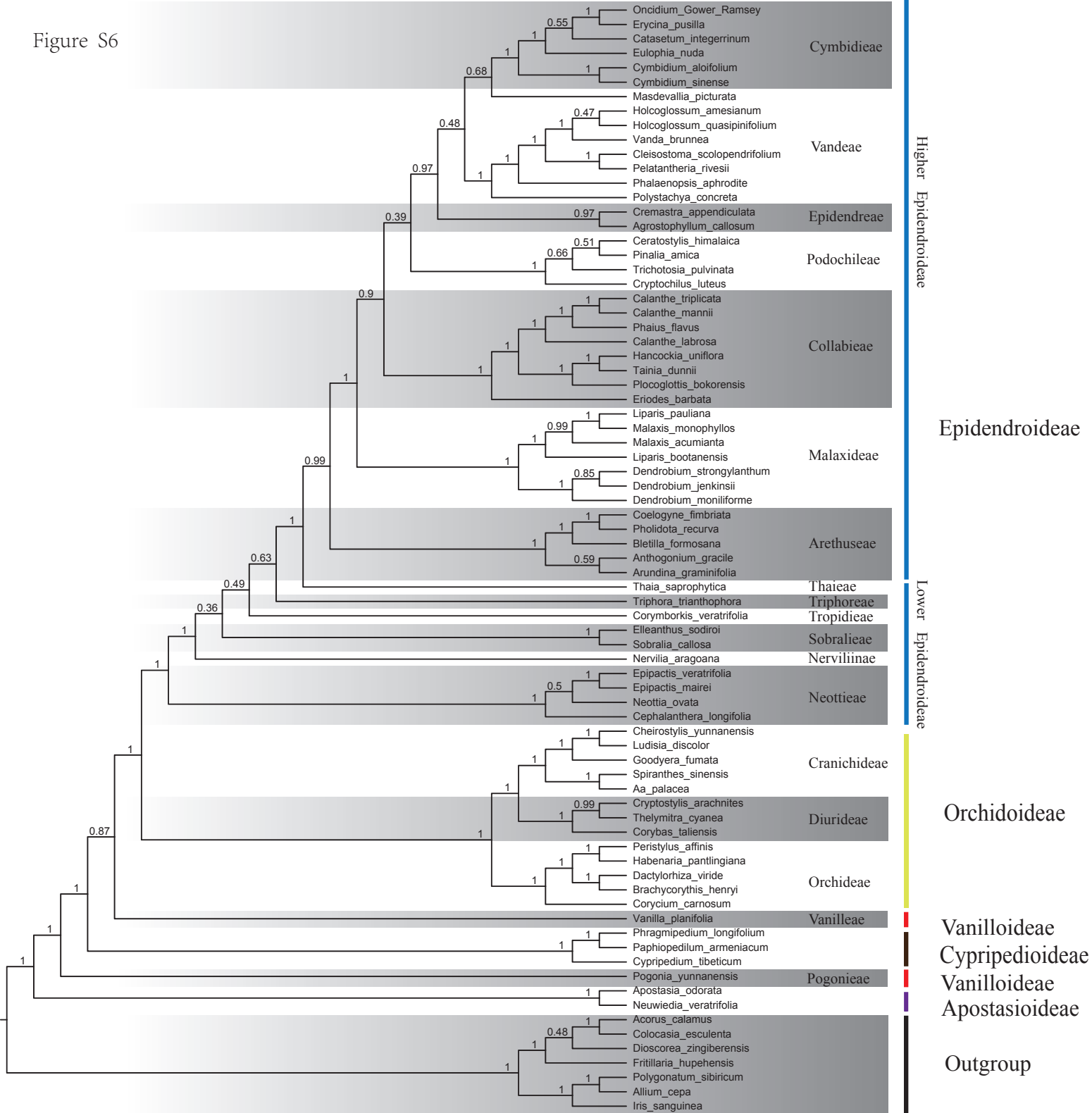


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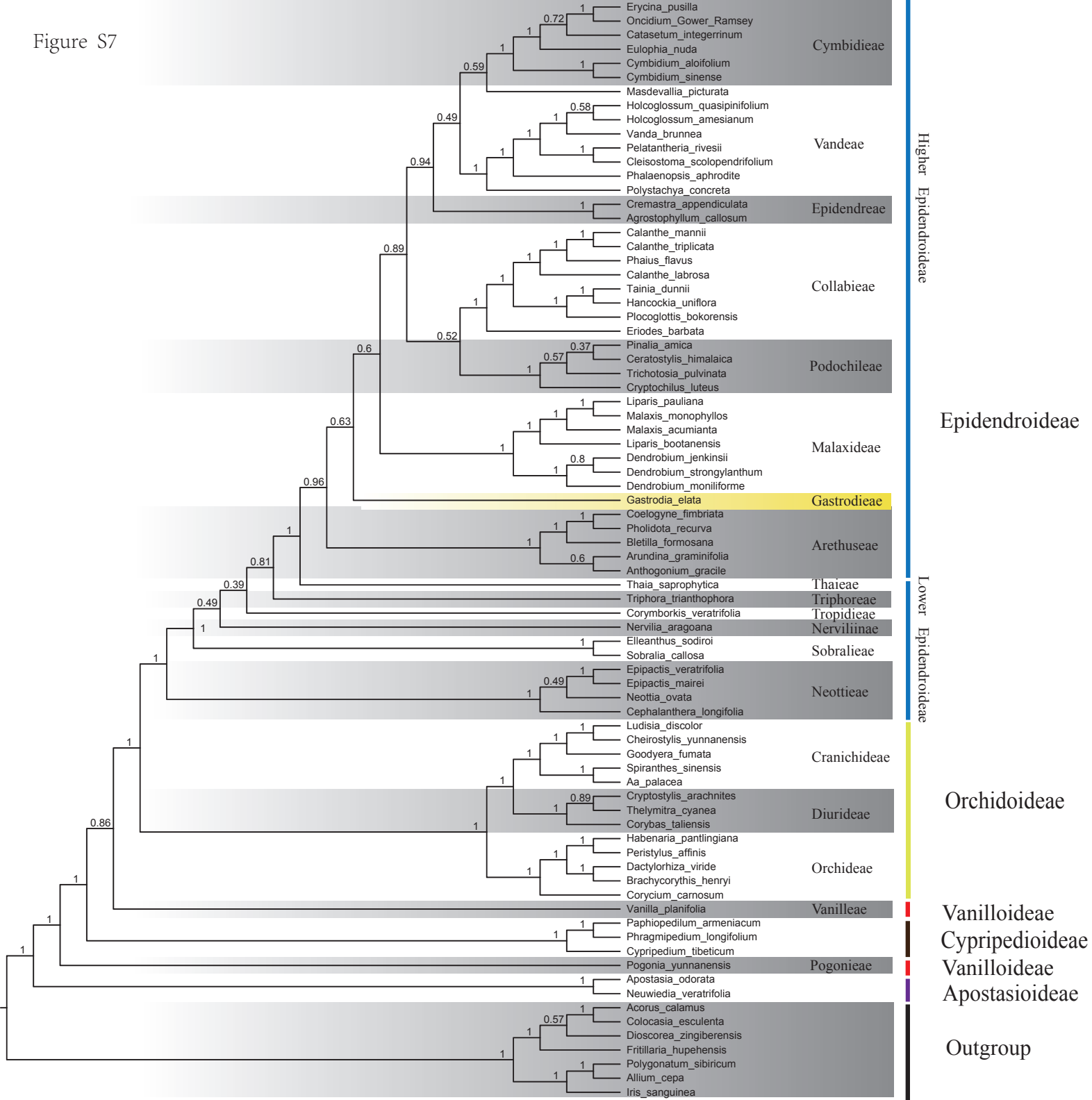


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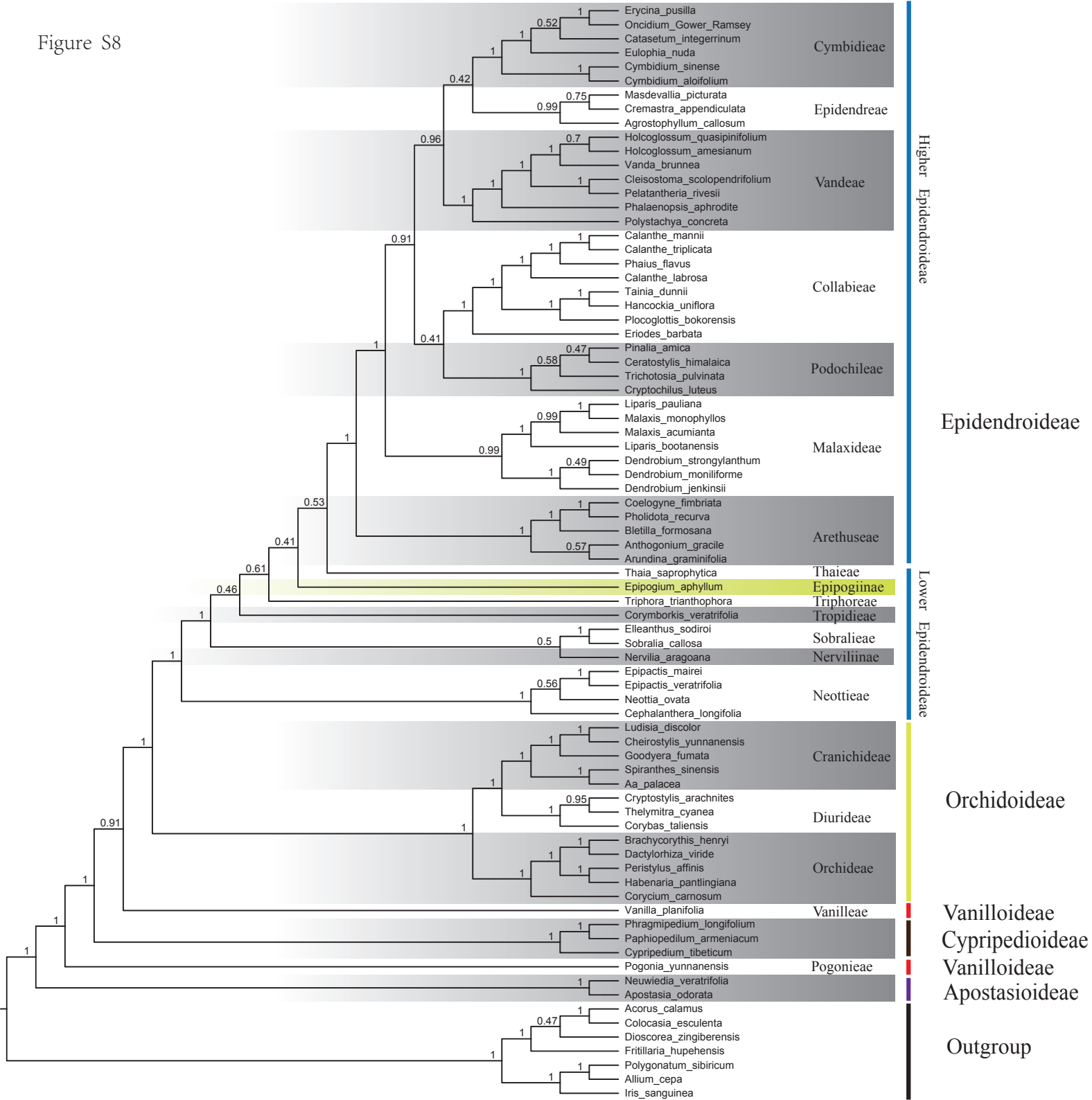


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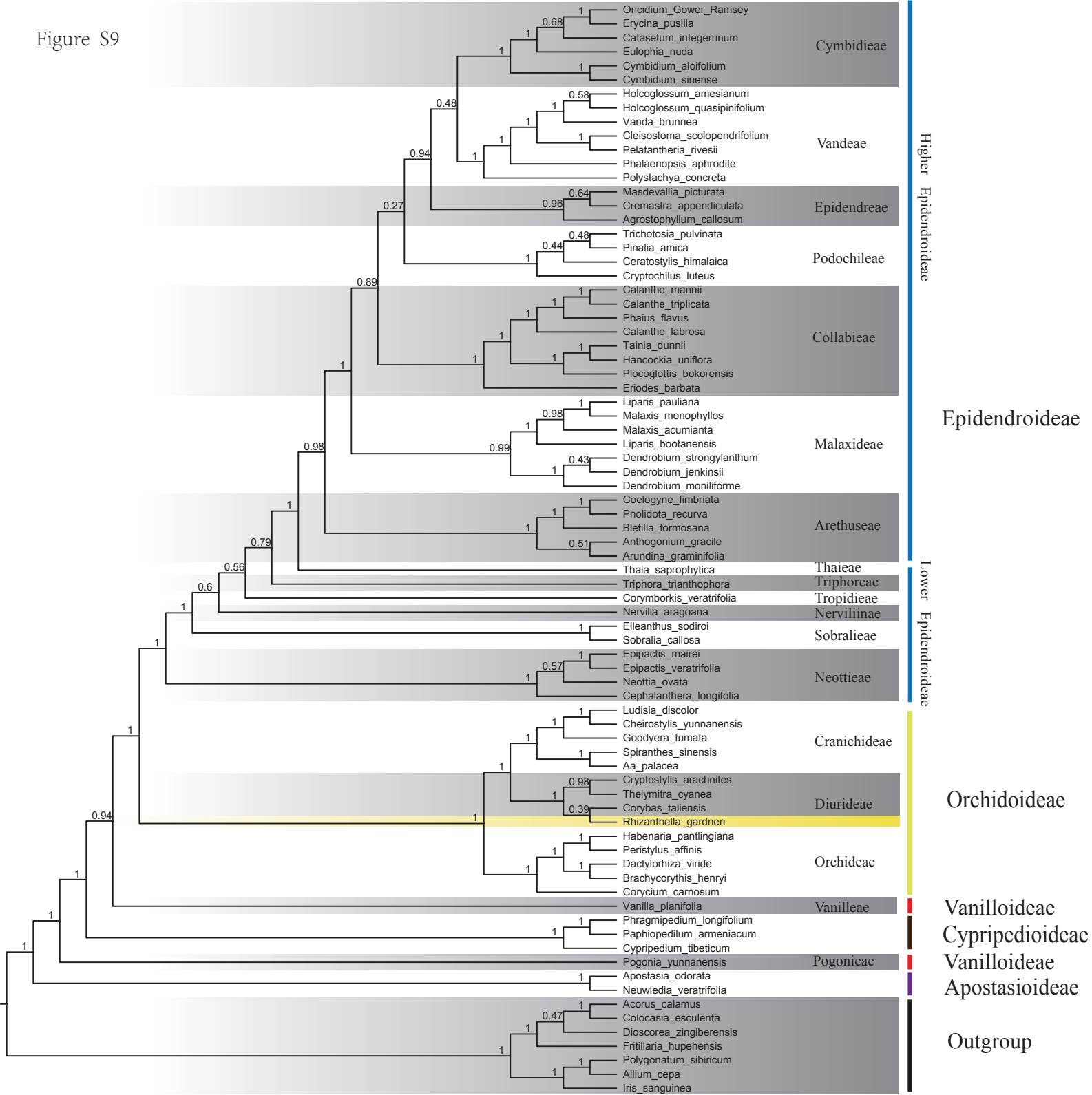


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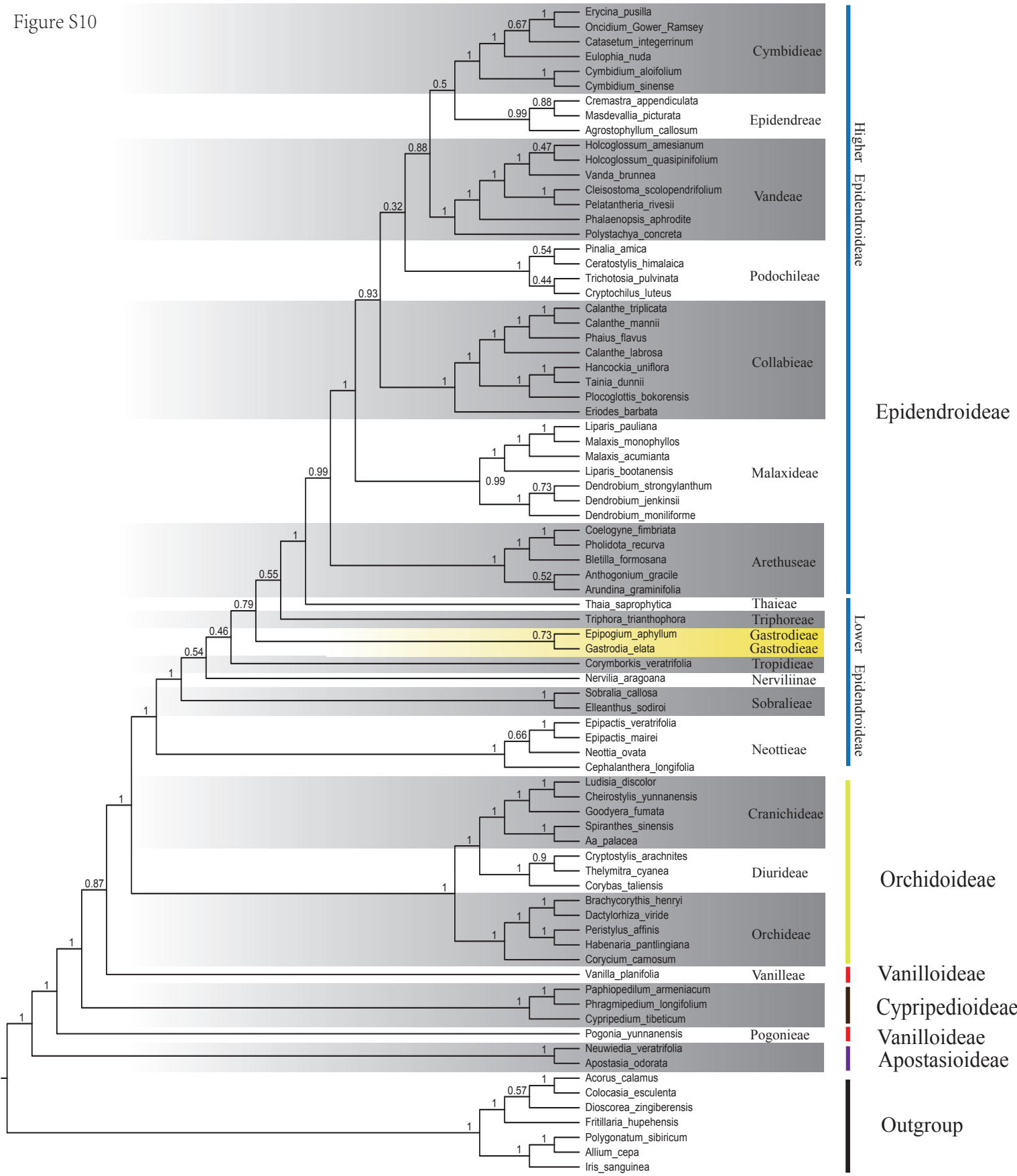


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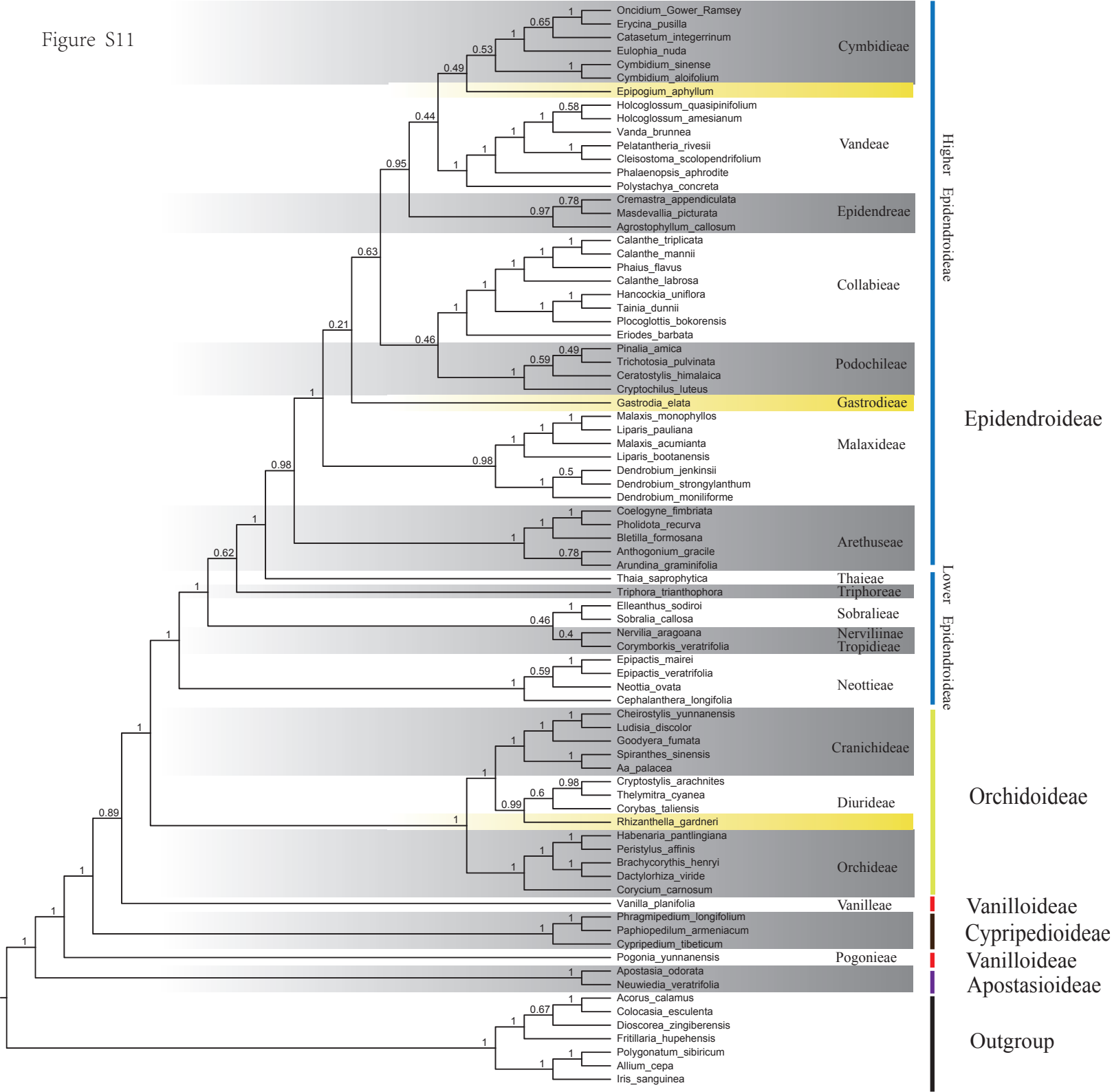


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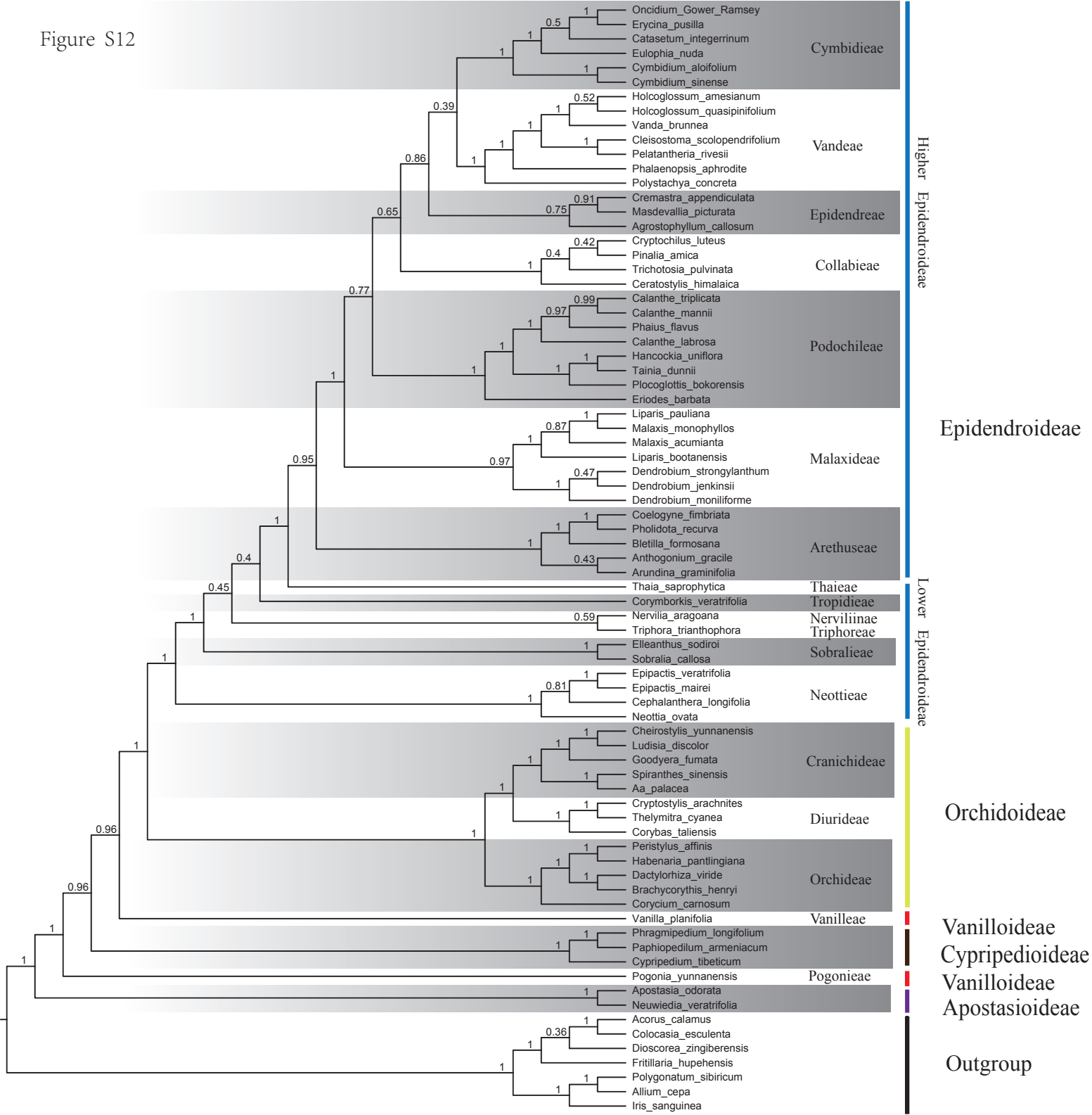


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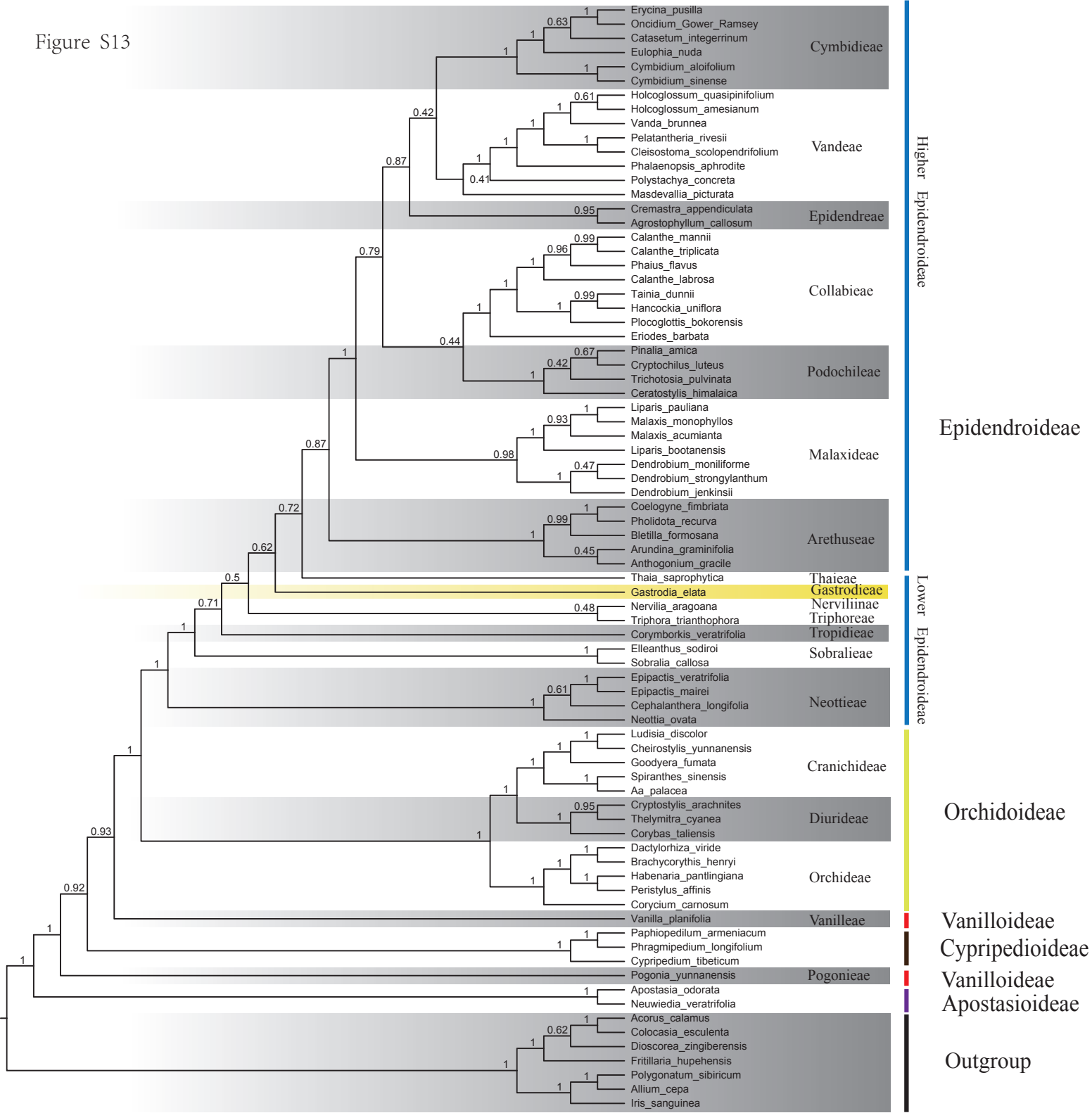


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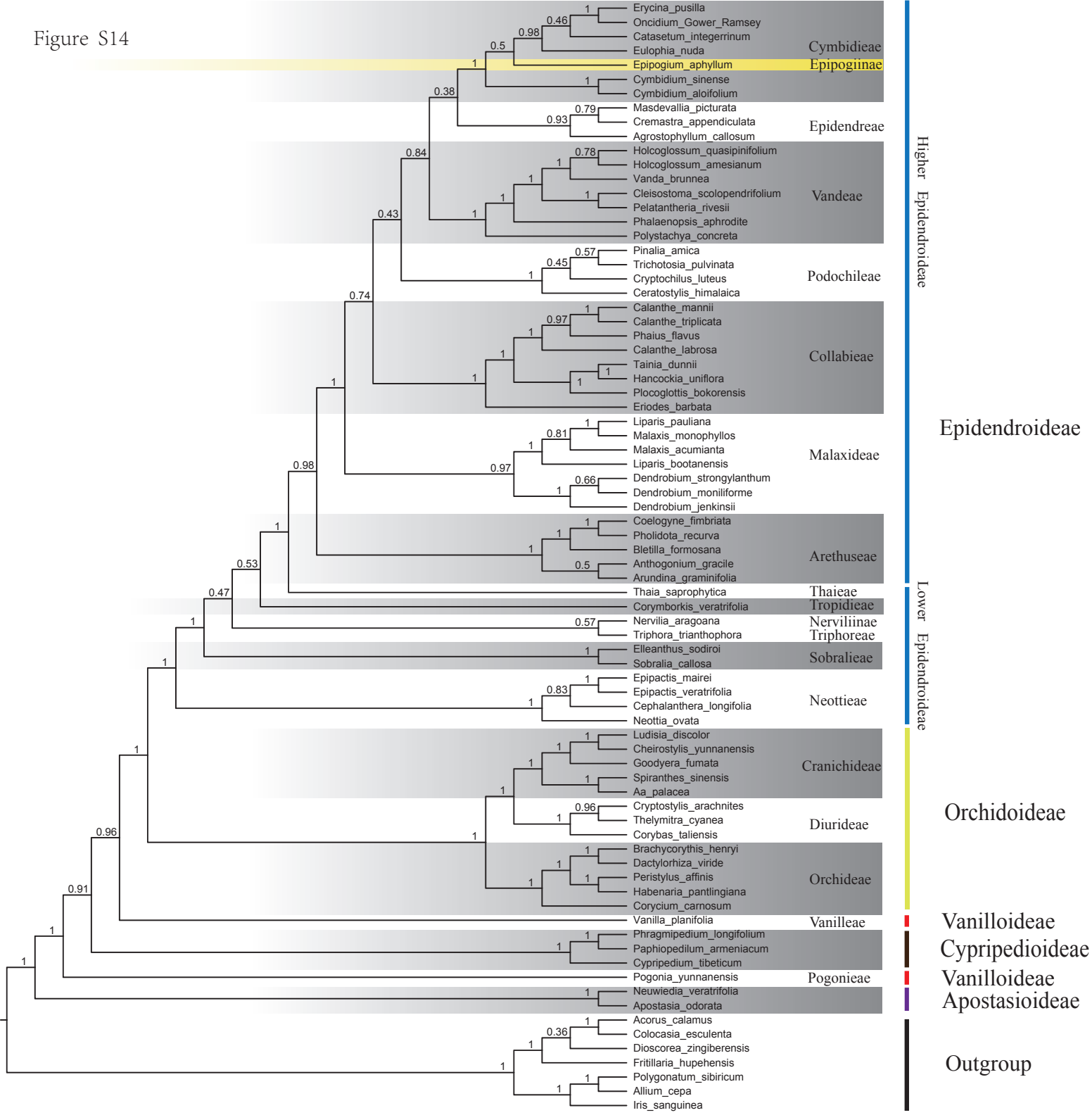


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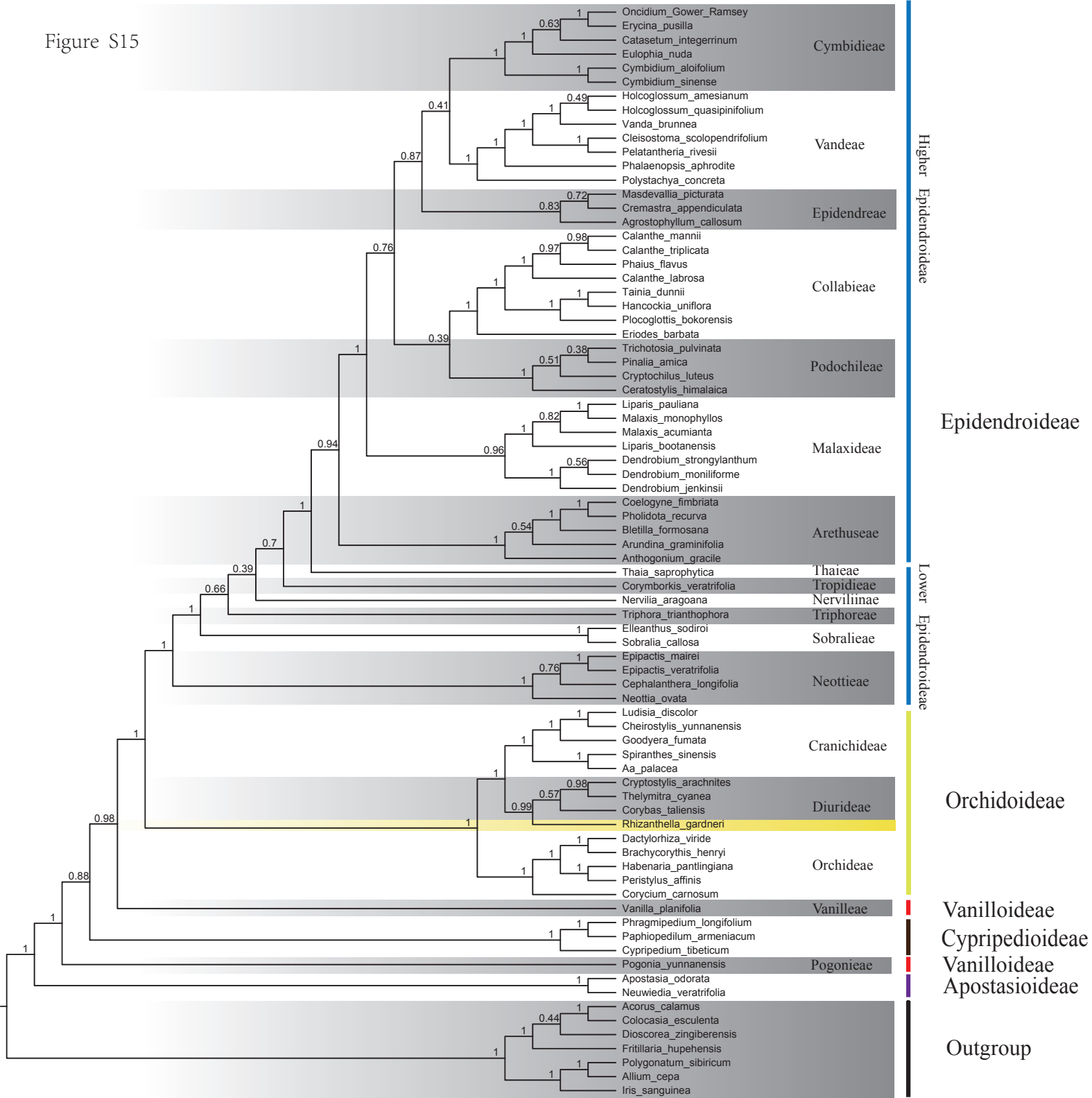


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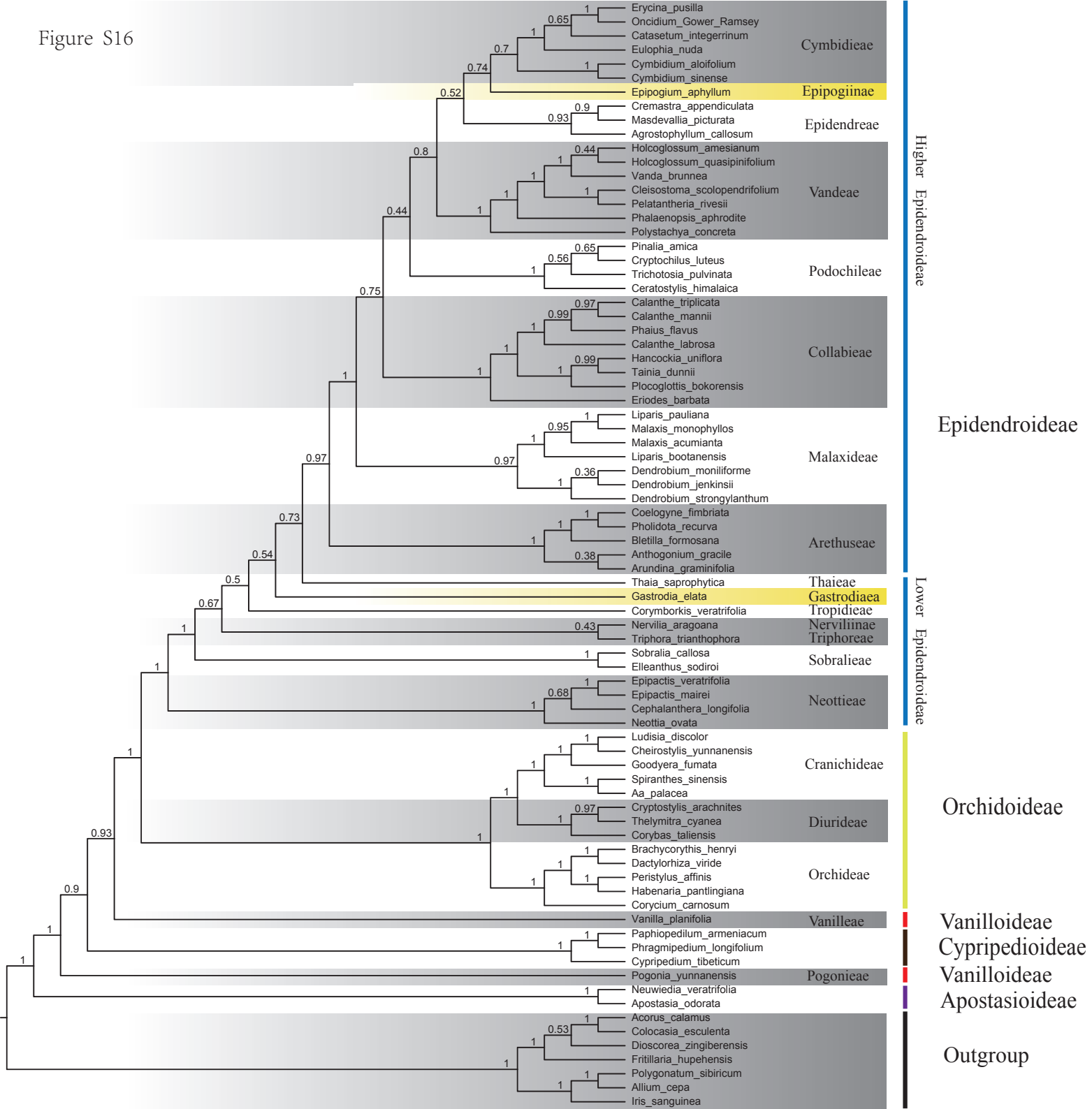


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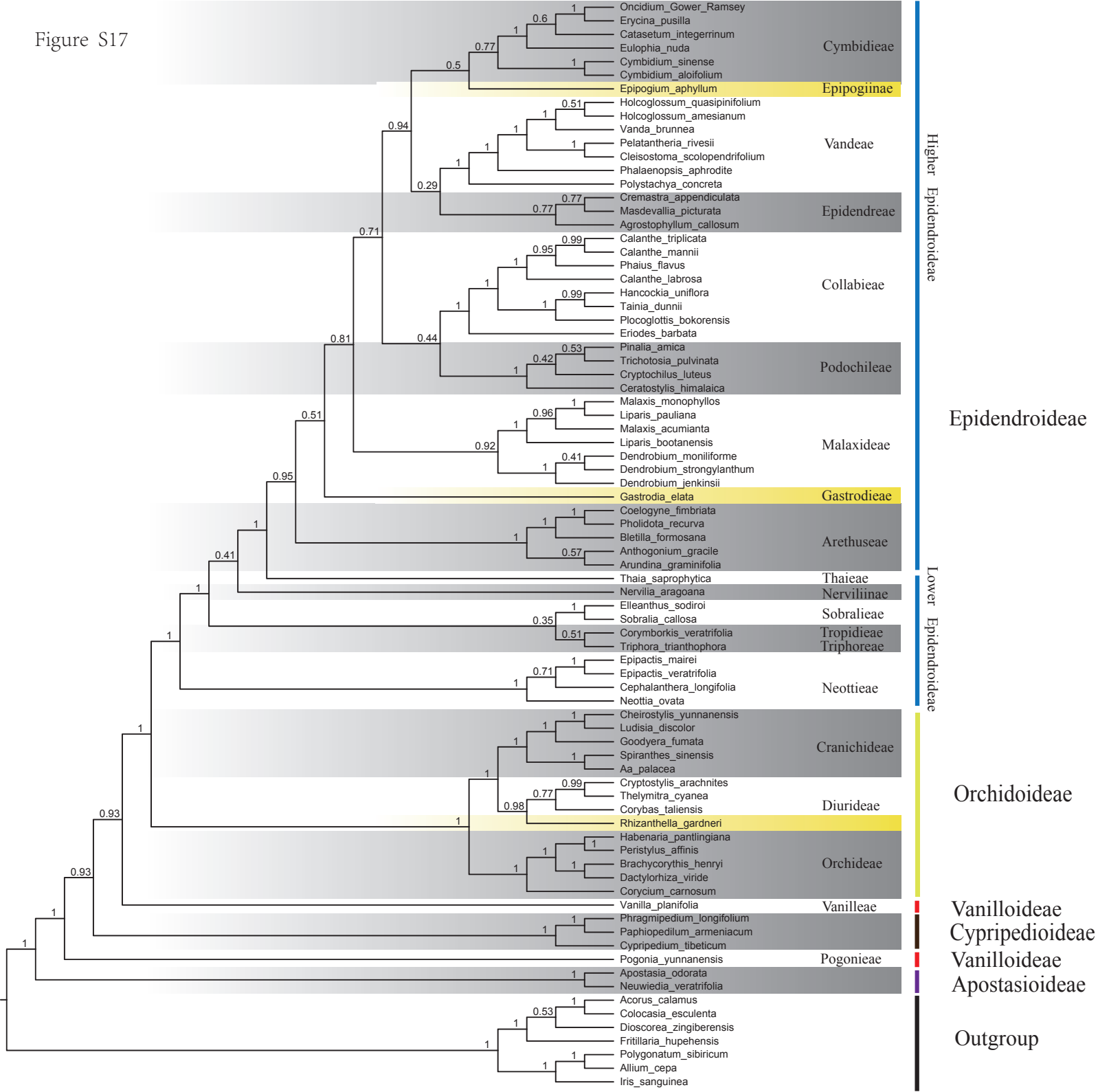


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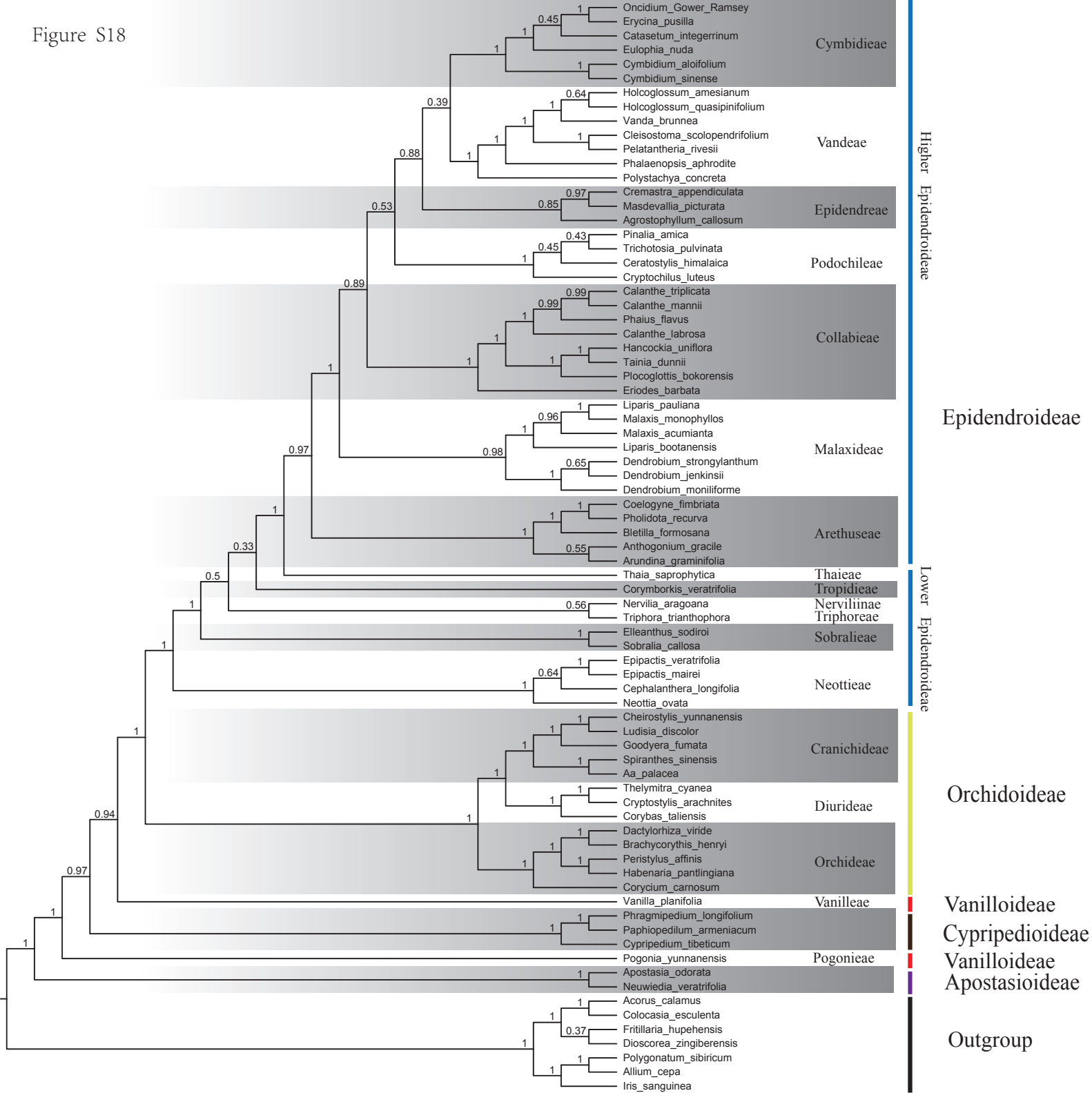


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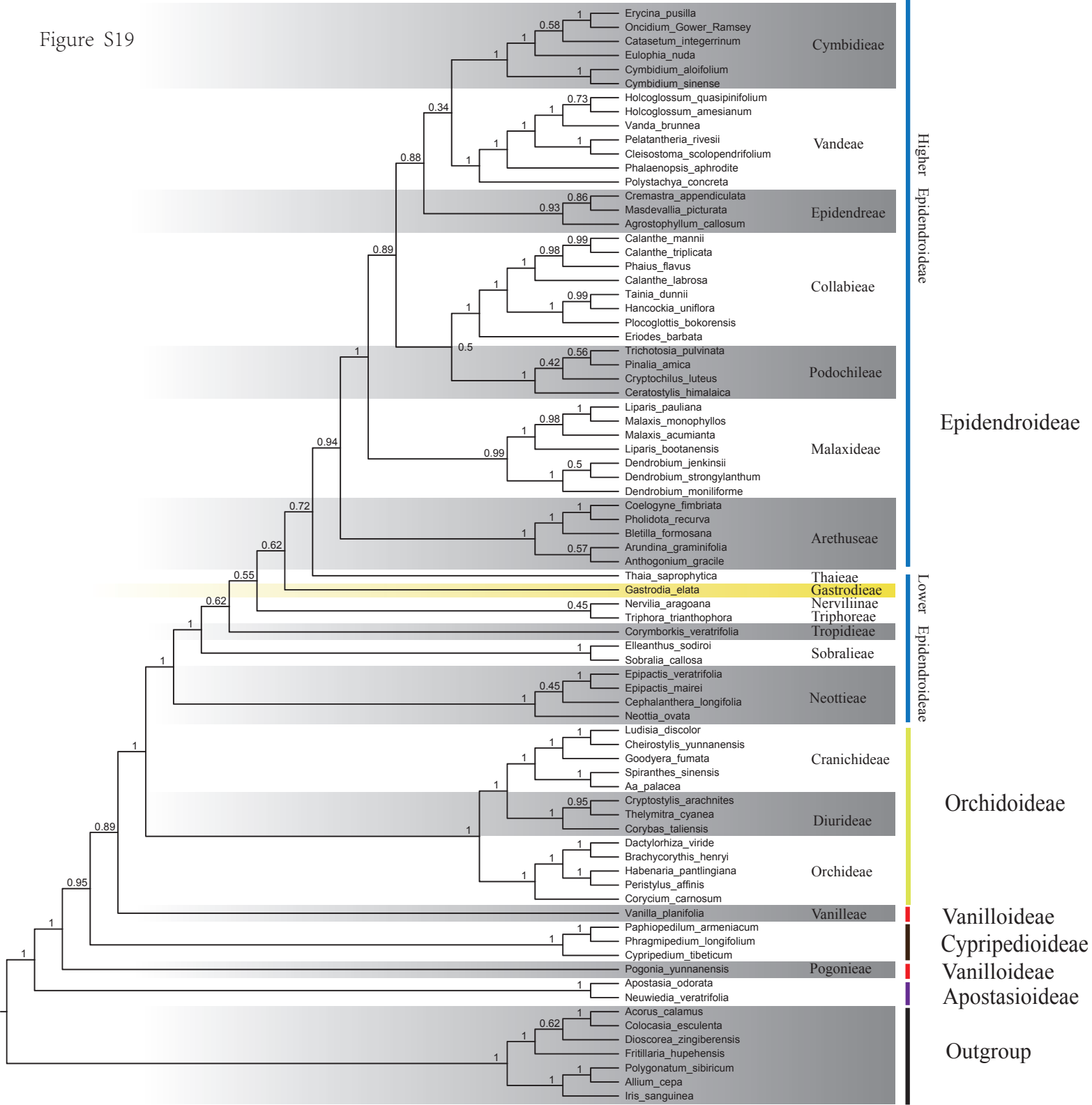


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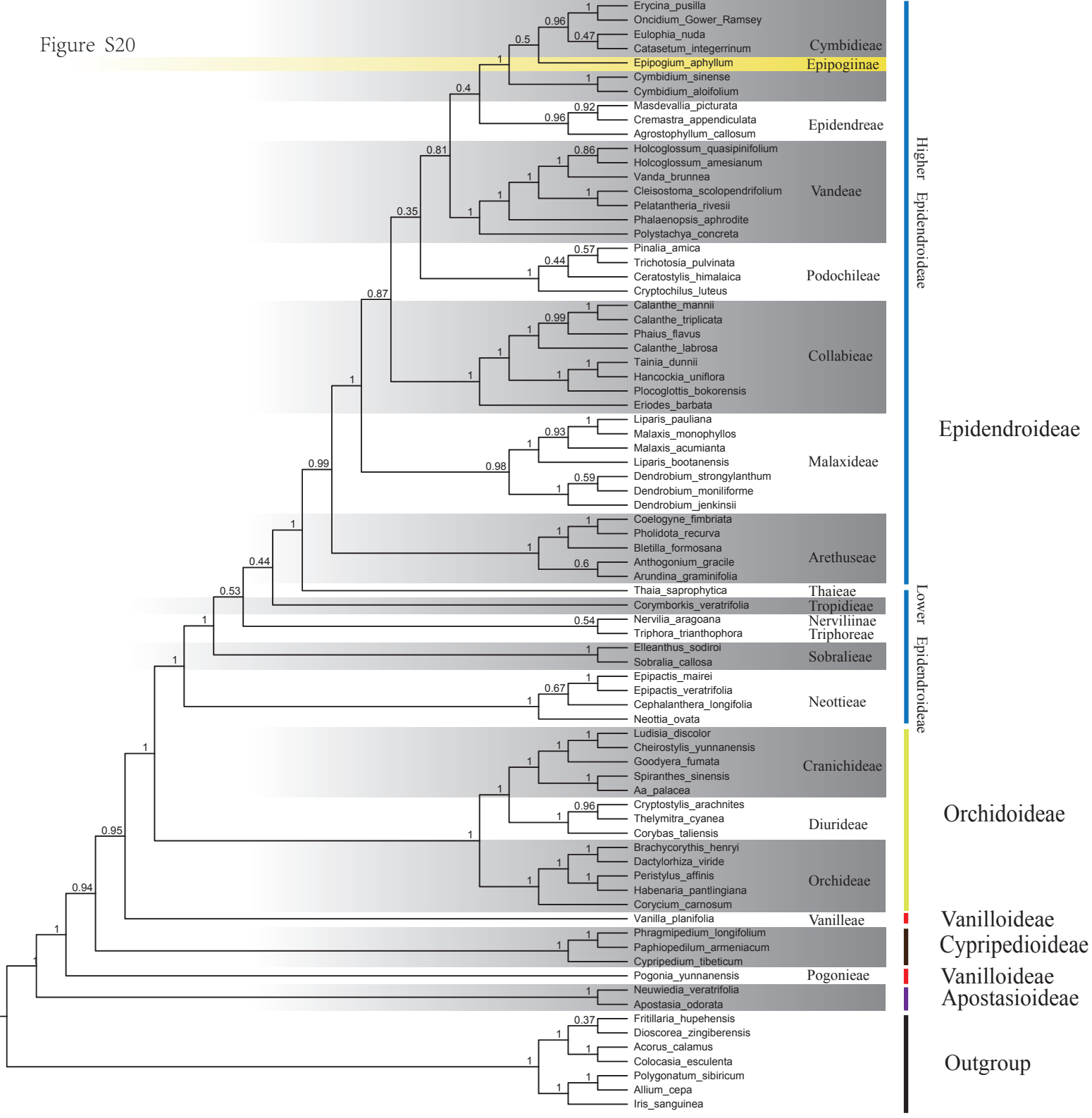


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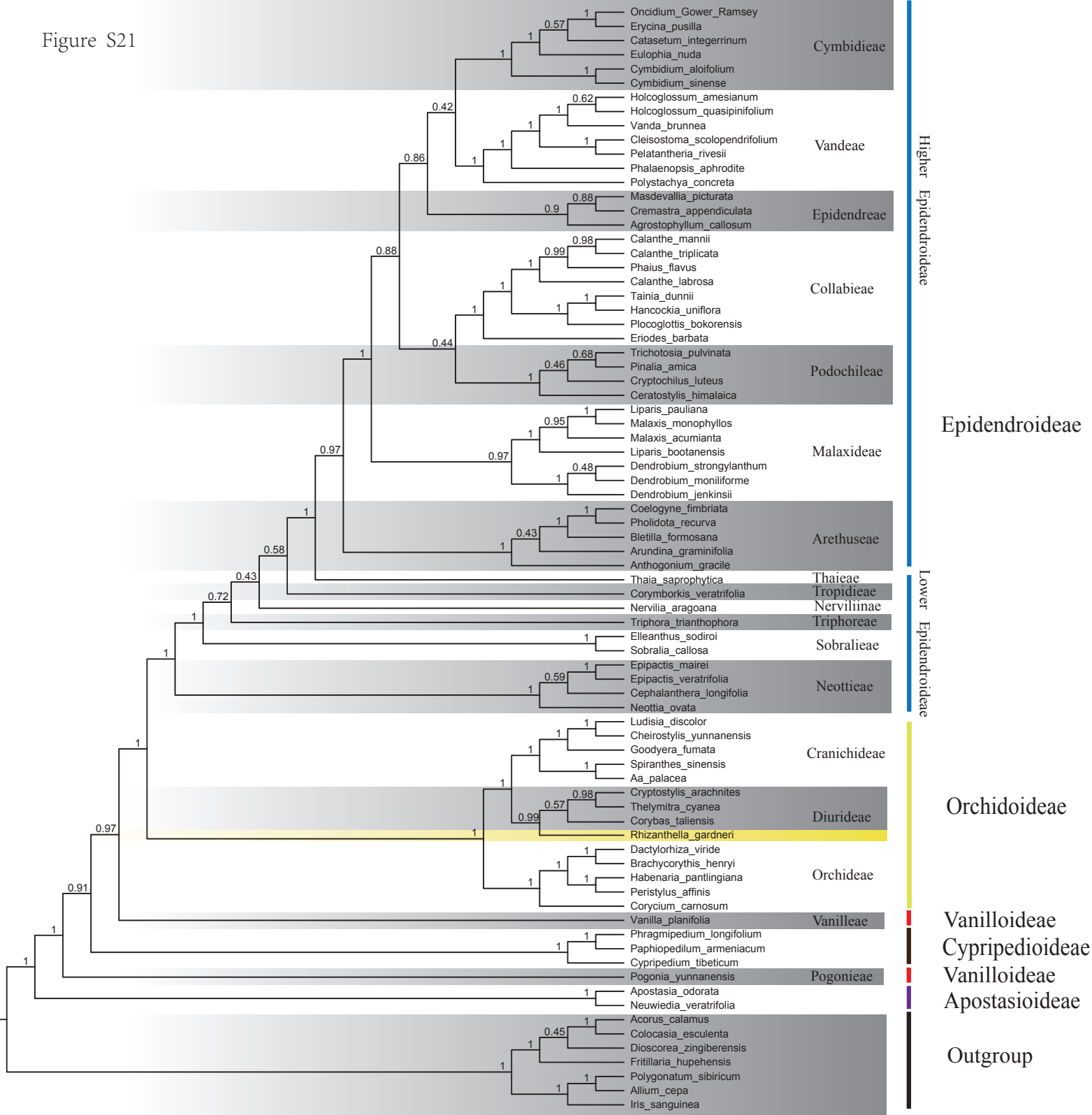


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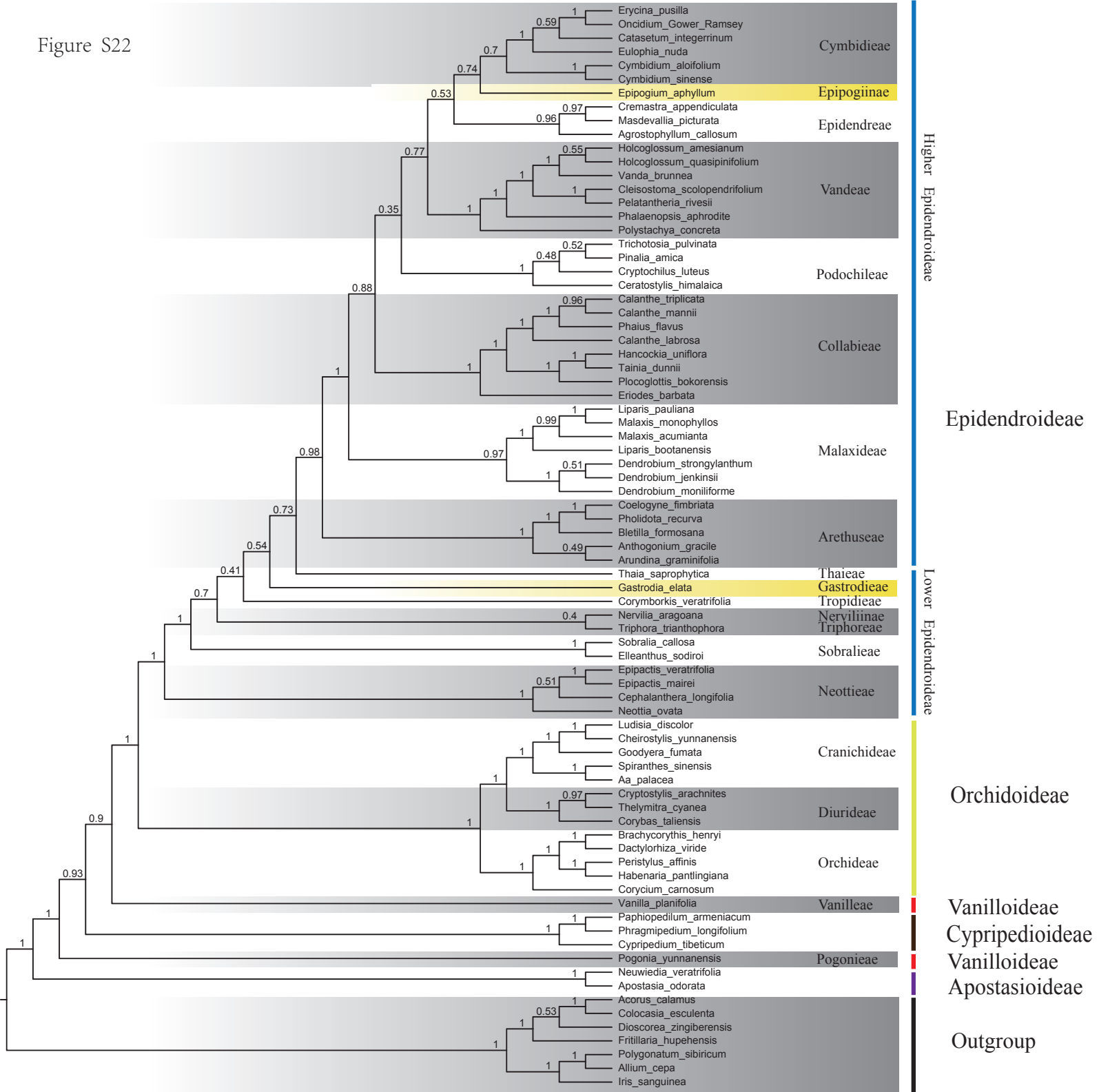


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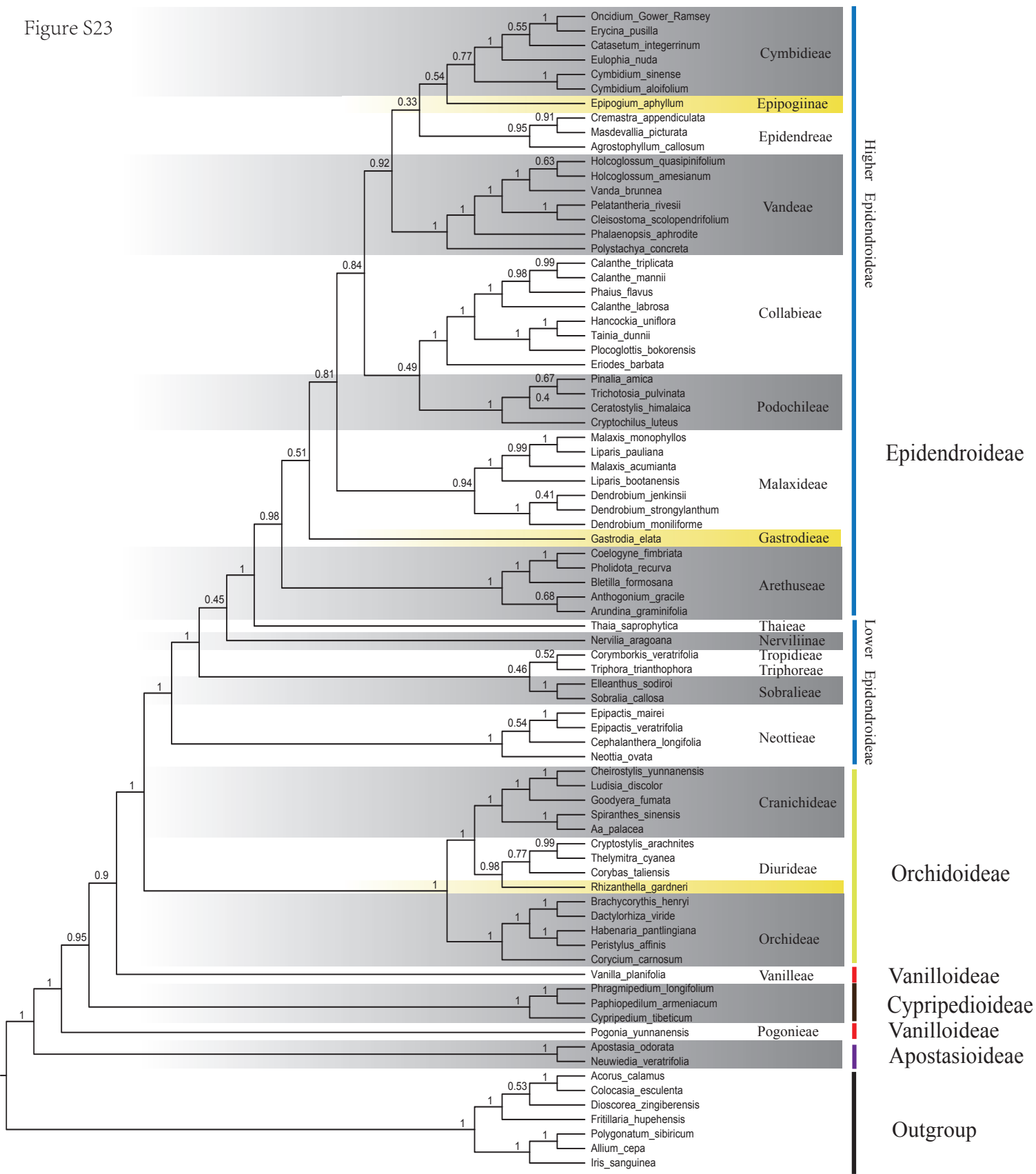


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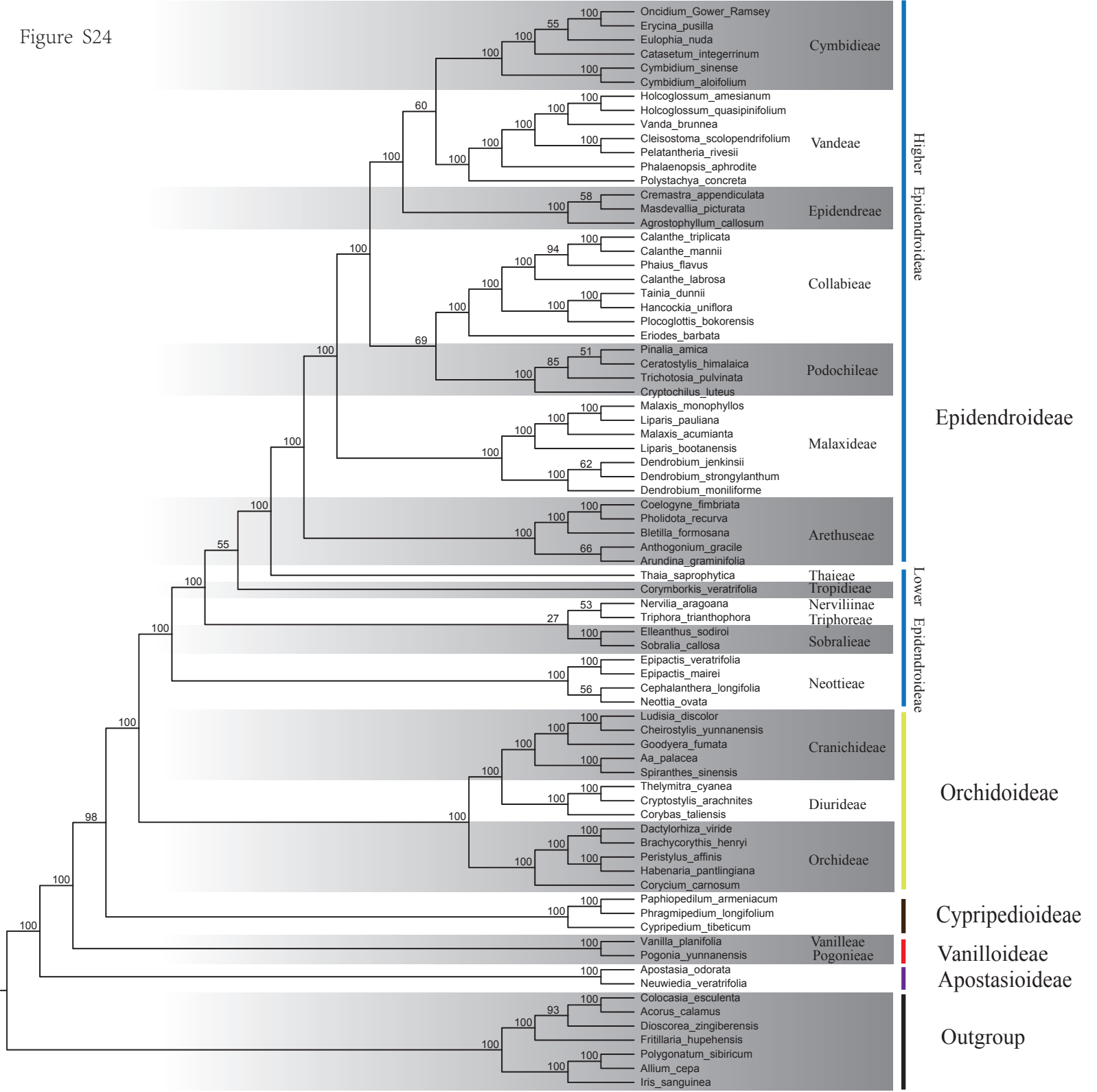


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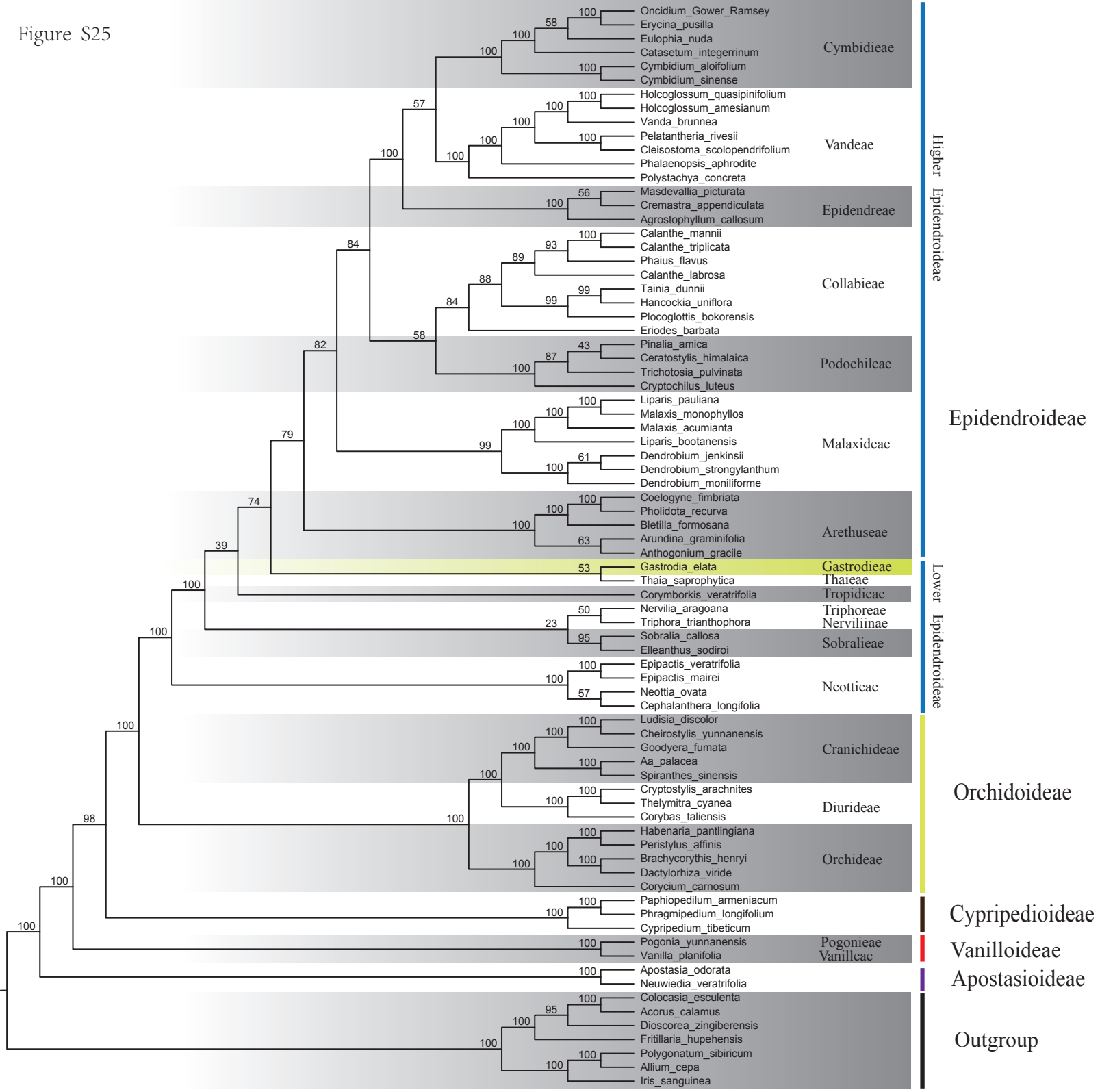


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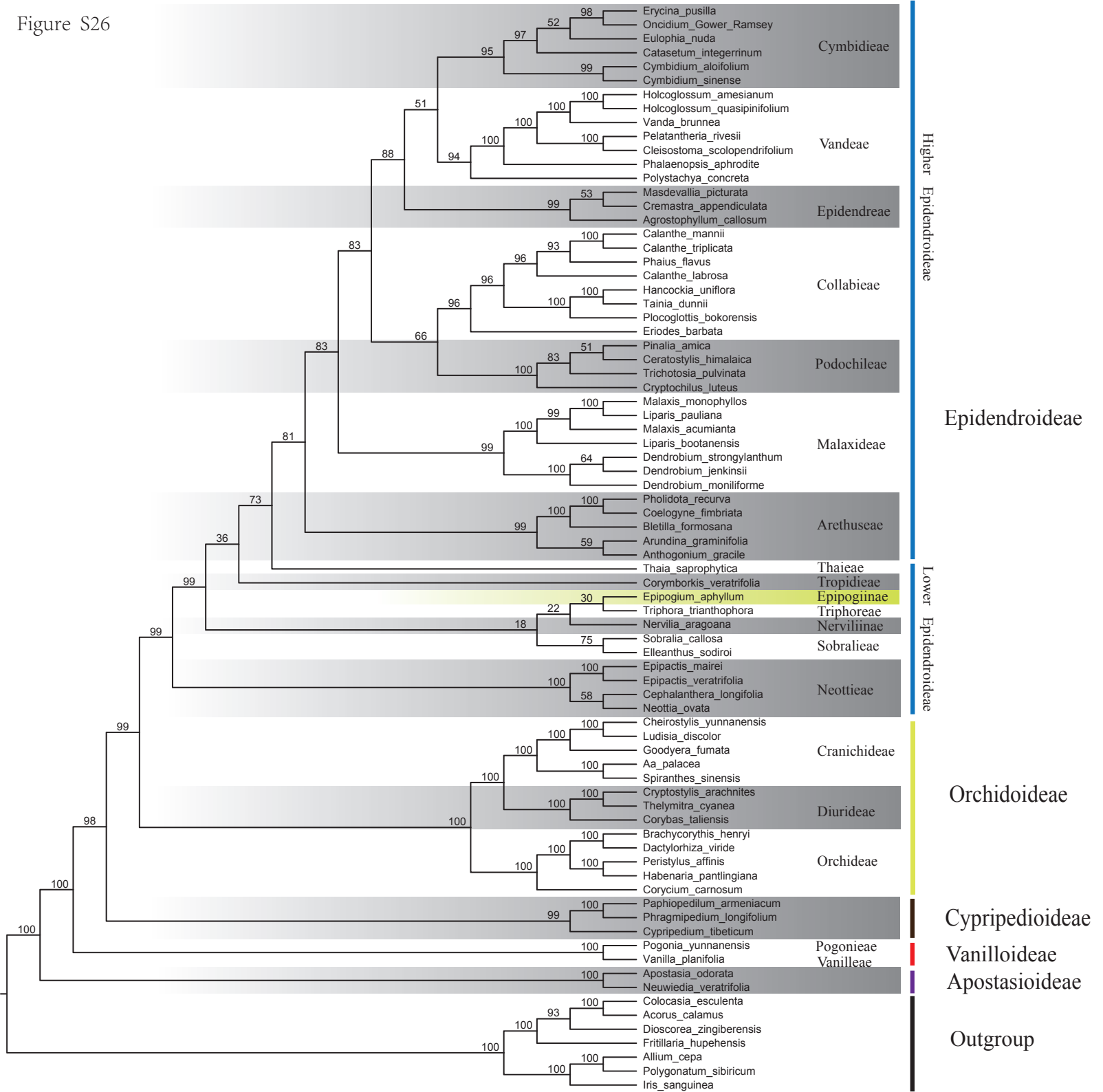
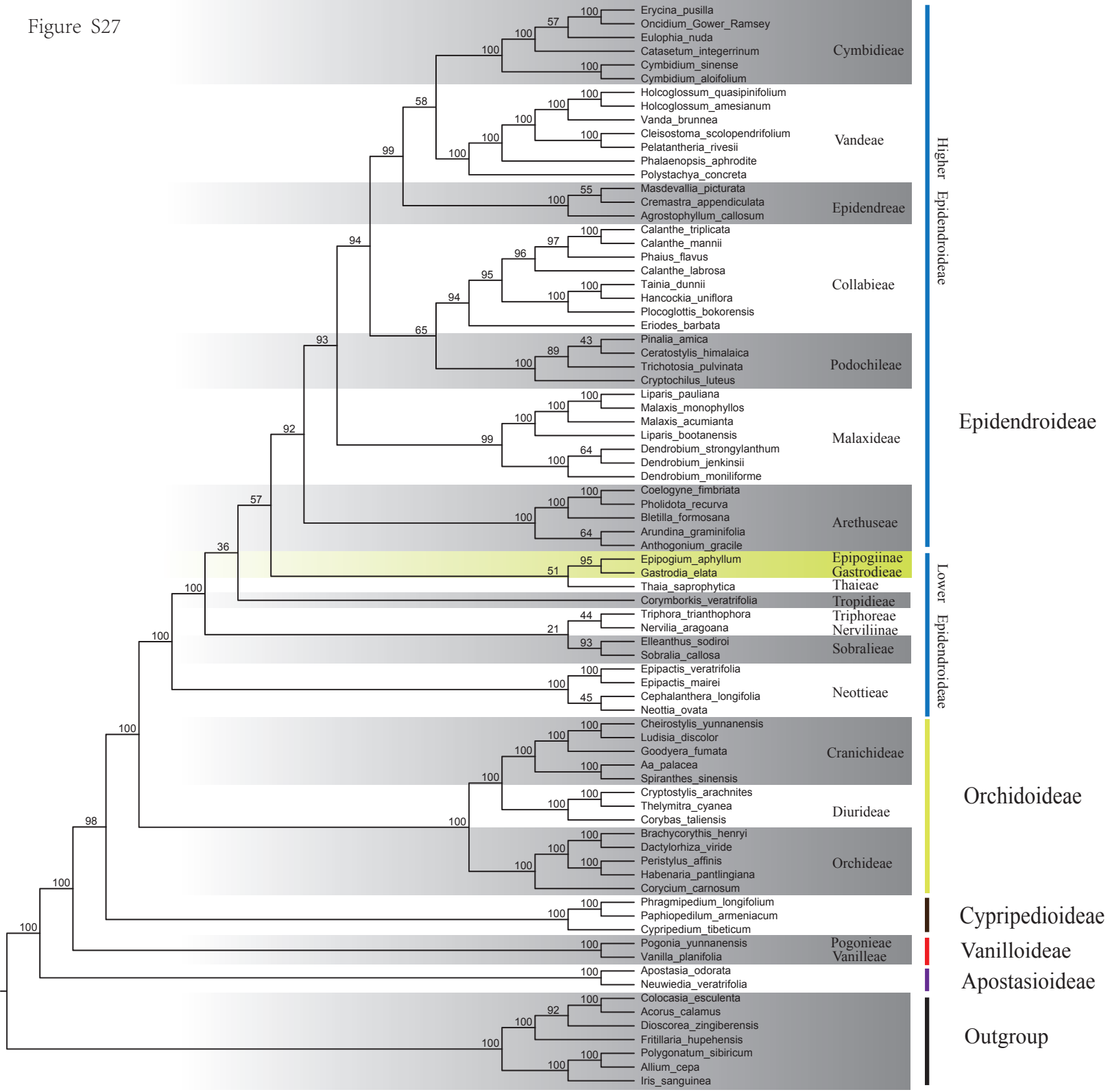


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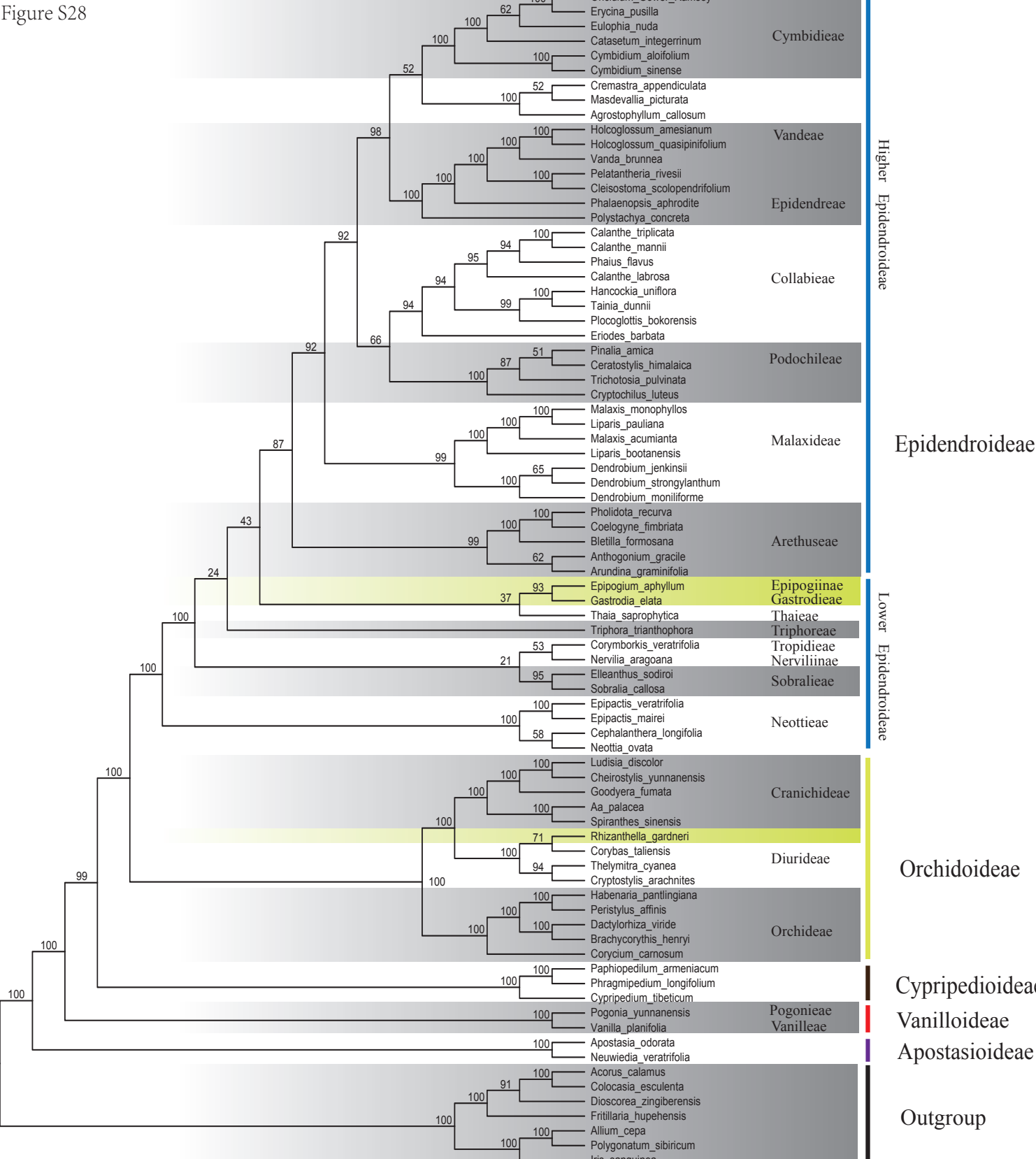


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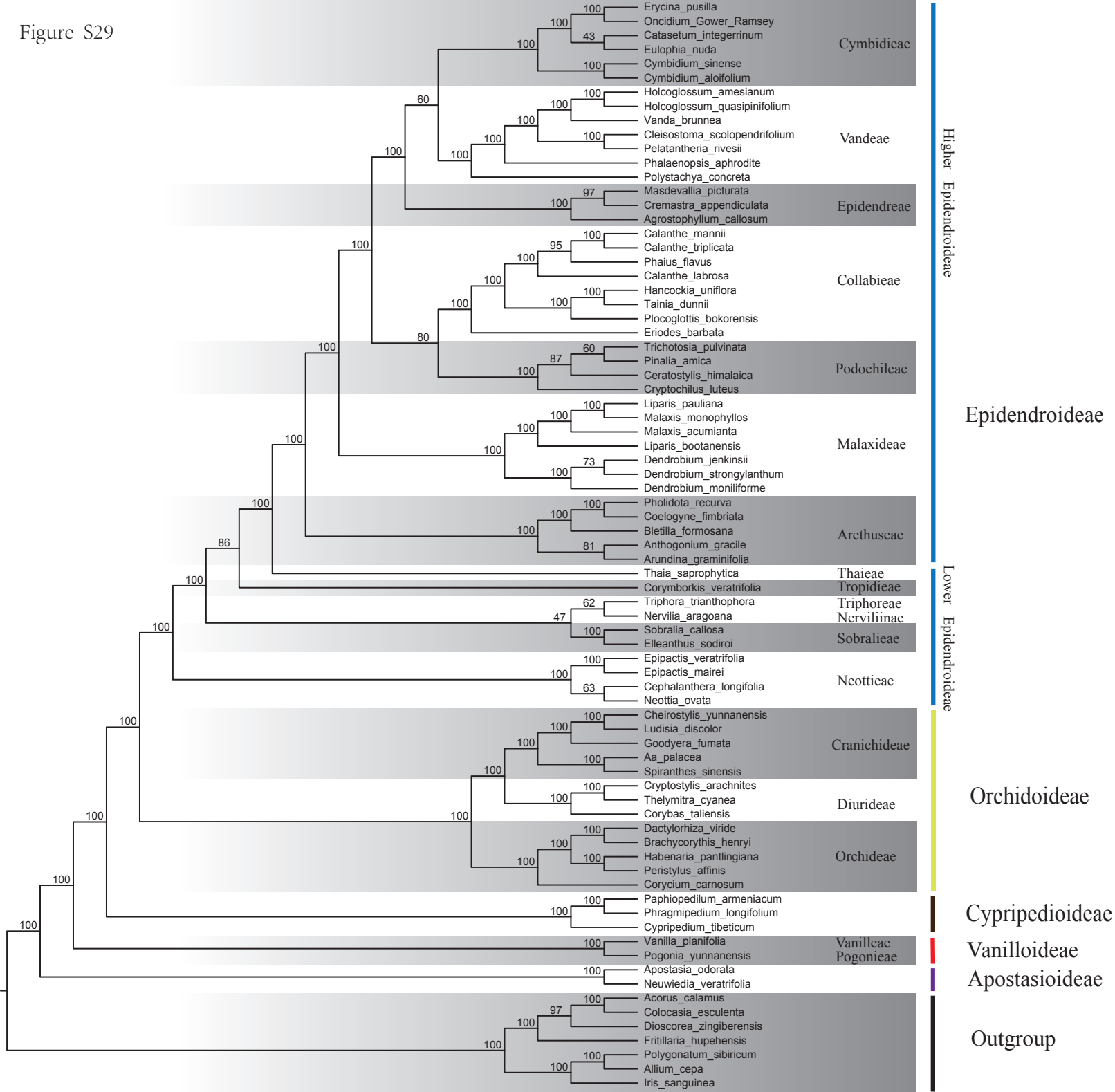


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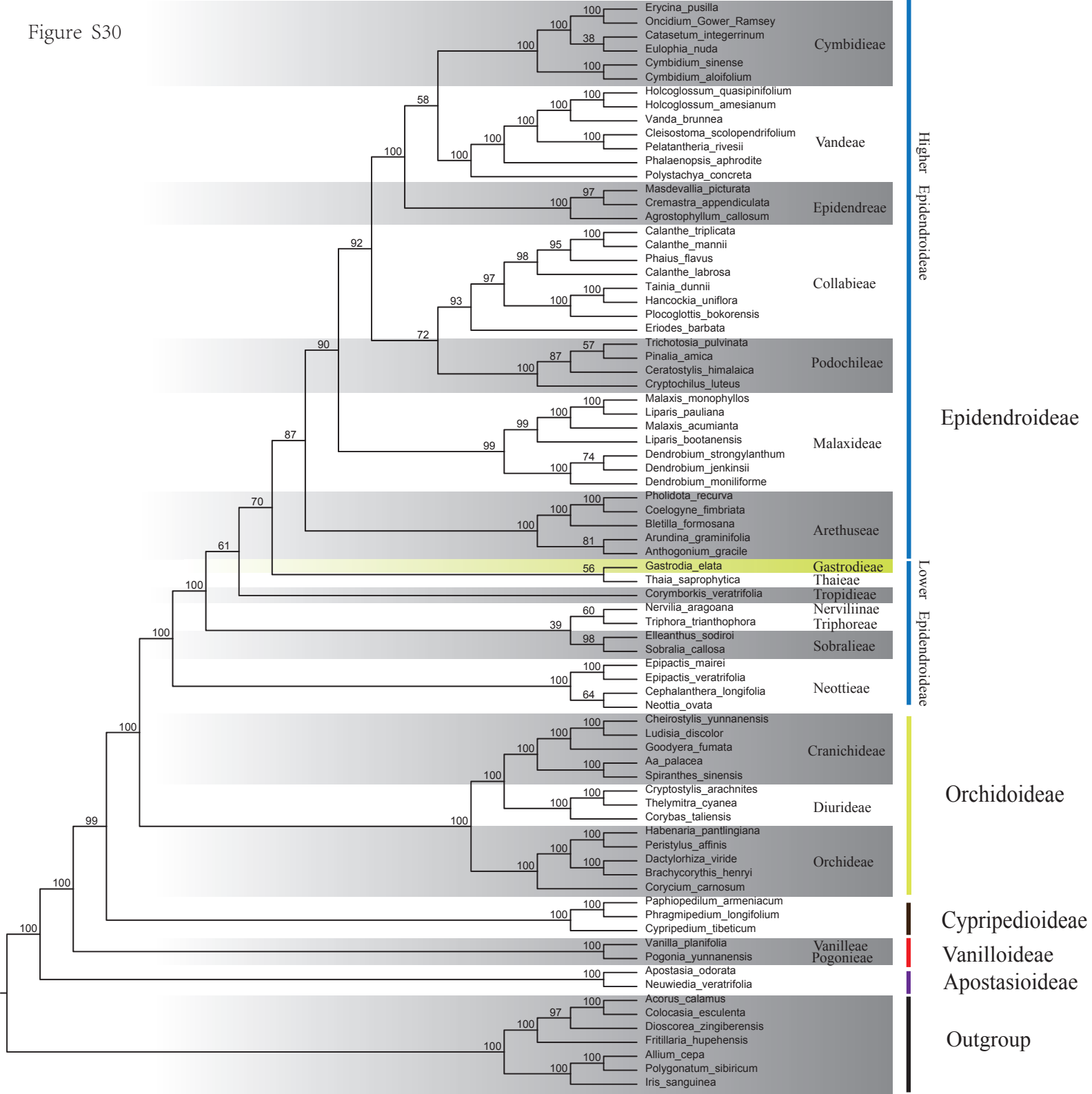


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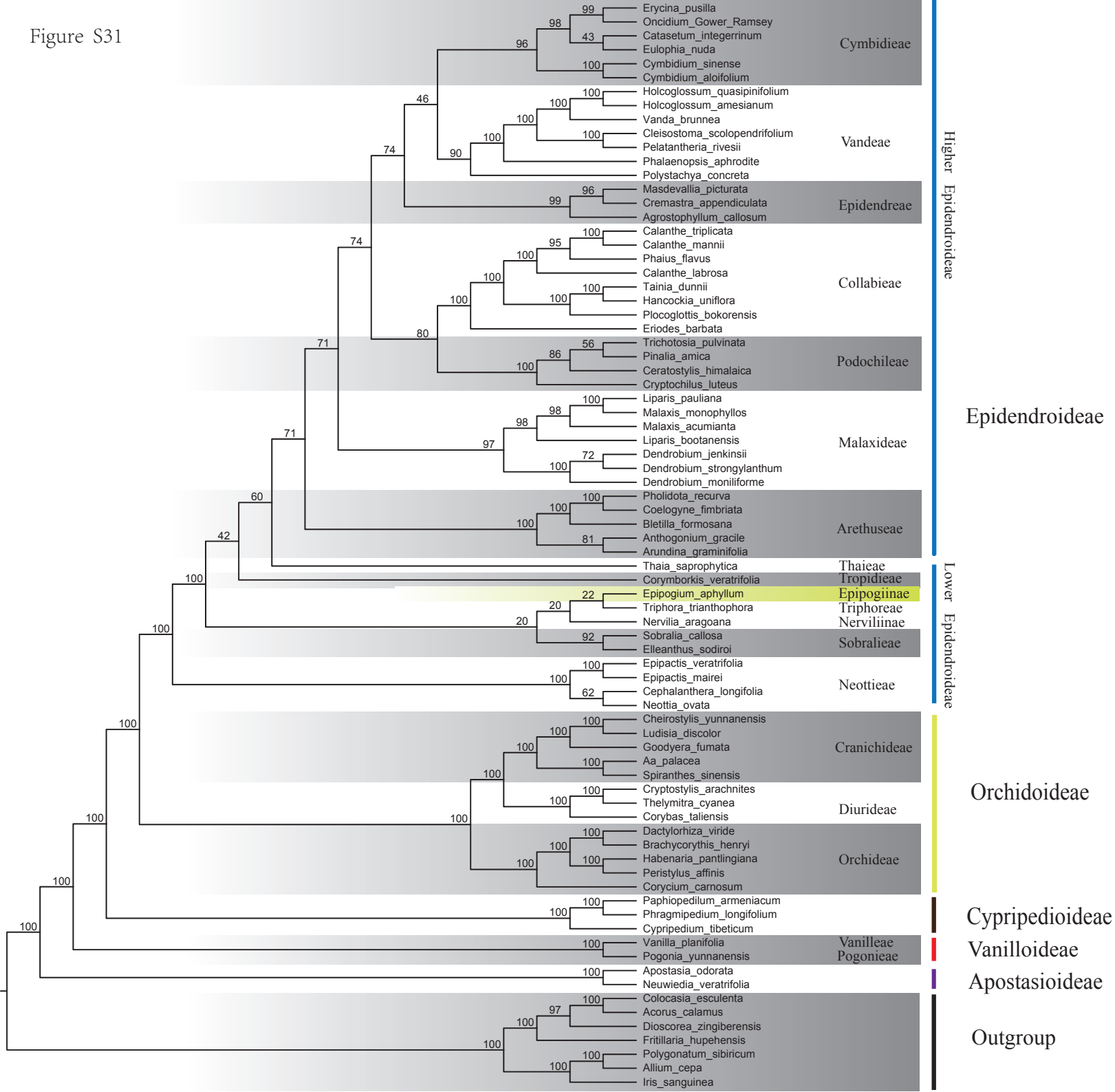


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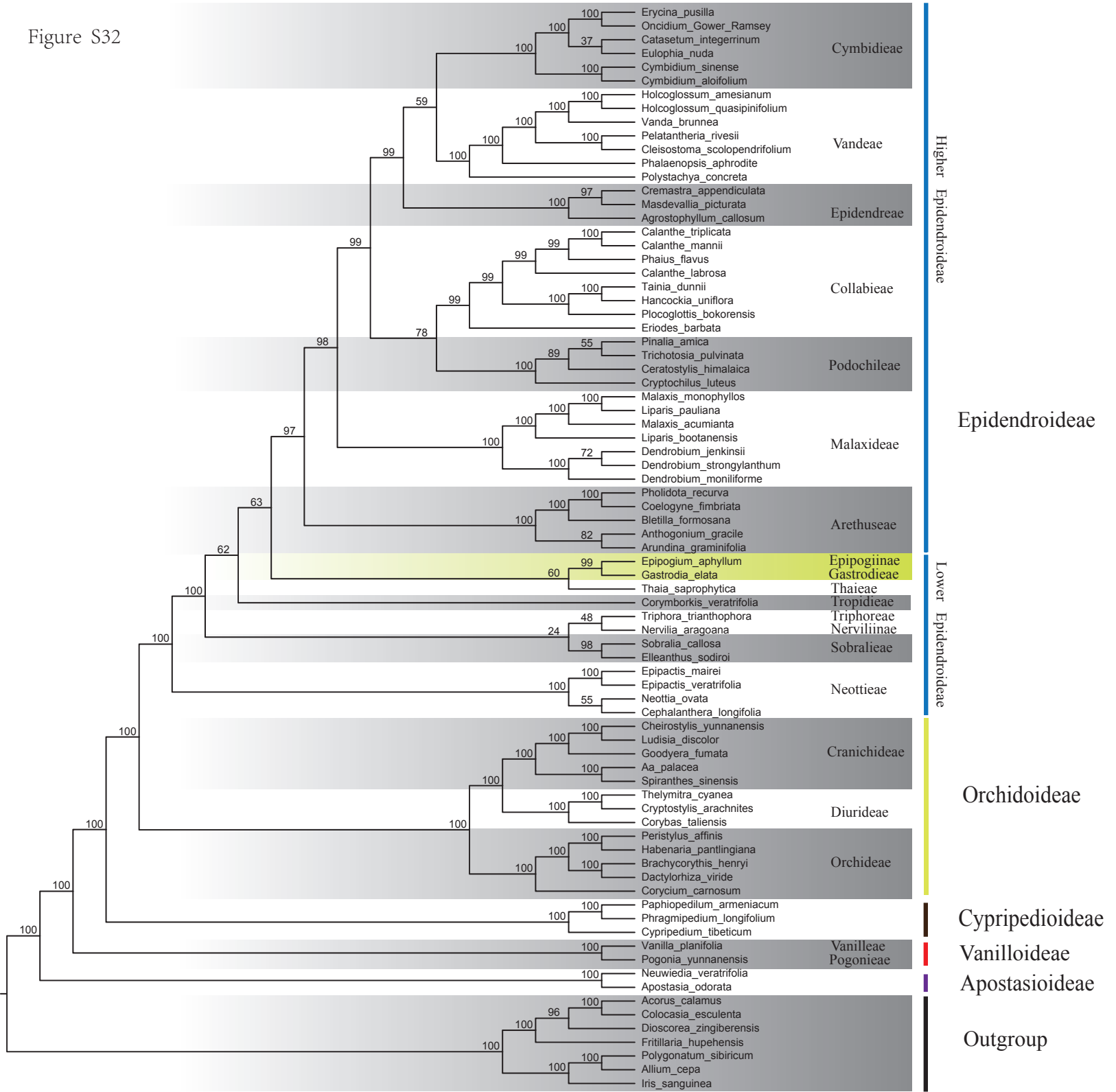


Figure S33

