

Supplementary Figure 1 - Caryophyllaceae phylogeny and divergence times. (a) Phylogeny of Caryophyllaceae and sister families (Amaranthaceae, Achatocarpaceae) resulting from a maximum likelihood analysis of the chloroplast *matK* gene using a GTR+G+I model in PAUP*. The five taxa at bottom were defined as the outgroup. Numbers above each node represent bootstrap values from 100 replicates. Only values above 50% are shown. (b) Chronogram of Caryophyllaceae resulting from a penalized likelihood analysis of the *matK* ML tree shown in (a) using the program r8s. To calibrate the tree, a divergence time of 38 Myr was used for the split between Caryophyllaceae and the sister families Amaranthaceae and Achatocarpaceae (Wikstrom et al., 2001). S. = *Silene*.

Supplementary Figure 2 - Unconstrained survey of synonymous sequence divergence. Shown are the d_S trees from unconstrained analyses of the *atp1* data set used in Figure 1, the *cox1* data set used in Figure 2, and the *matR* data set used in Figure 3. Taxa with long branches that were labeled in Figures 1–3 are also labeled here for comparison.

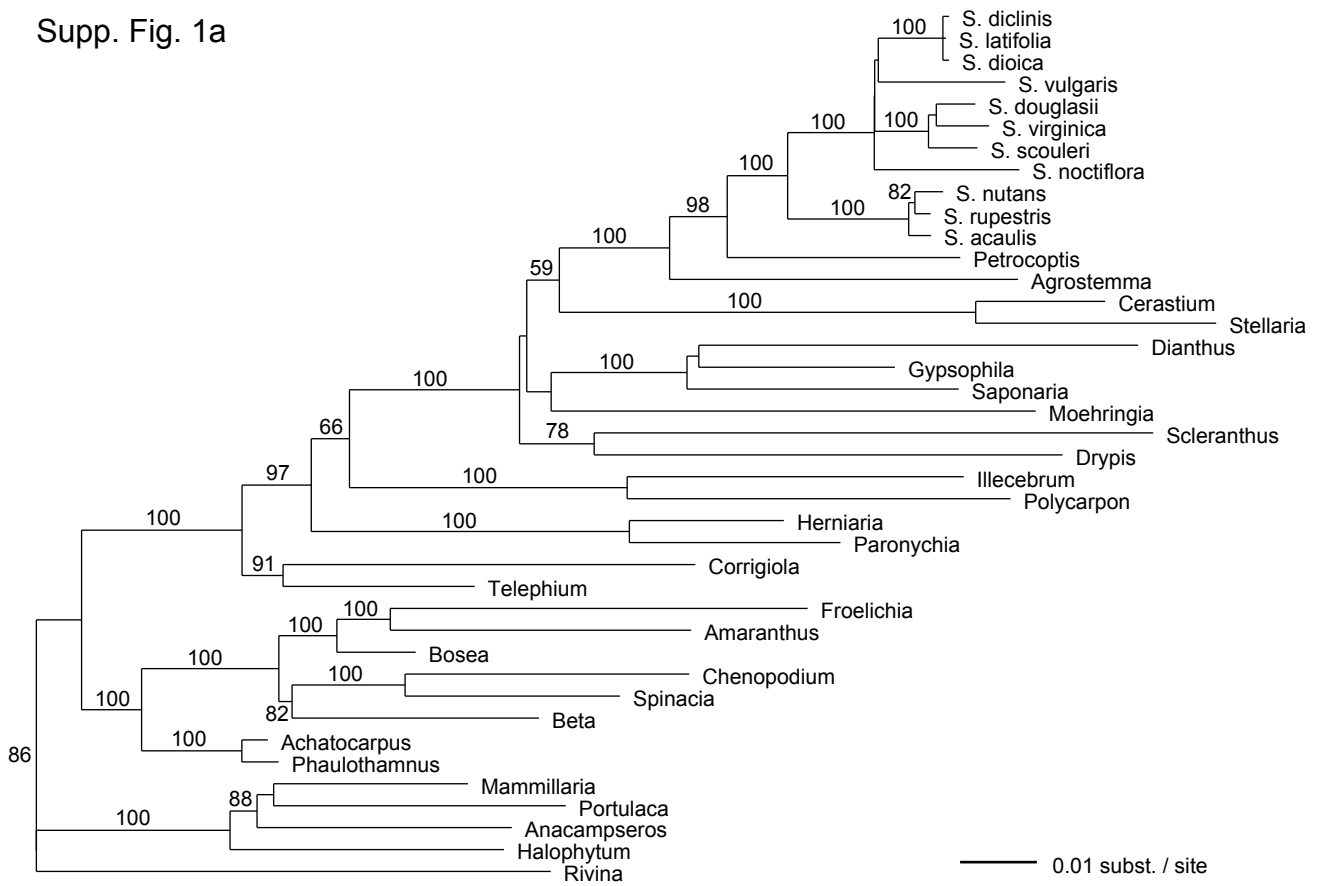
Supplementary Figure 3 - Unconstrained multigene analysis of synonymous and nonsynonymous sequence divergence. Shown are the d_S (left) and d_N (right) trees from an unconstrained analysis of the combined 5-gene data set used in Figure 4. P. = *Plantago*; S. = *Silene*.

Supplementary Figure 4 - d_S tree for mitochondrial *atp1* at expanded scale. Shown is the d_S tree from Figure 1 of the main text, except that all taxa are labeled and all non-*Plantago* and non-*Pelargonium* branch lengths are drawn at an expanded scale. Compressed branches for *Plantago* and *Pelargonium* are shown as thickened lines.

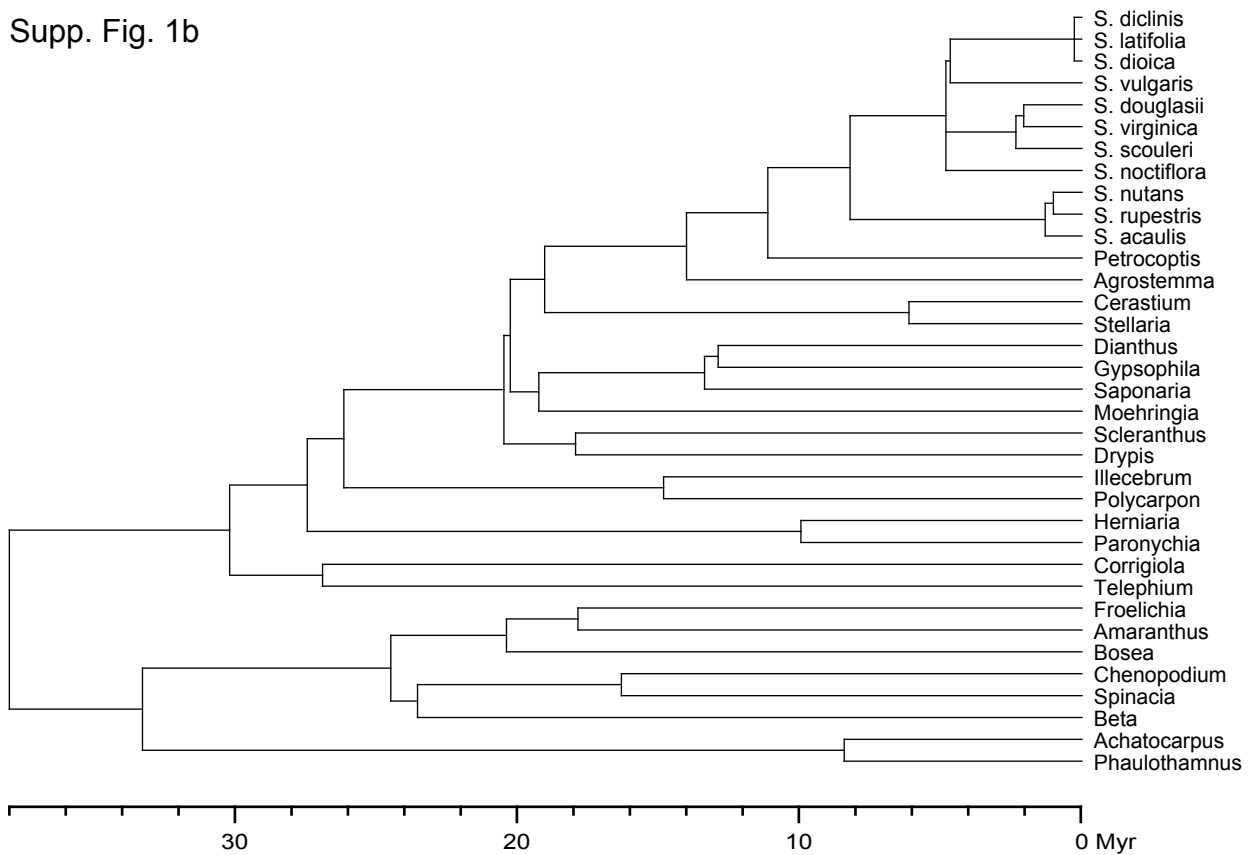
Supplementary Figure 5 - d_S tree for mitochondrial *cox1* at expanded scale. Shown is the d_S tree from Figure 2 of the main text, except that all taxa are labeled and all non-*Plantago* and non-*Pelargonium* branch lengths are drawn at an expanded scale. Compressed branches for *Plantago* and *Pelargonium* are shown as thickened lines.

Supplementary Figure 6 - d_S tree for mitochondrial *matR* at expanded scale. Shown is the d_S tree from Figure 3 of the main text, except that all taxa are labeled and all branch lengths are drawn at an expanded scale.

Supp. Fig. 1a

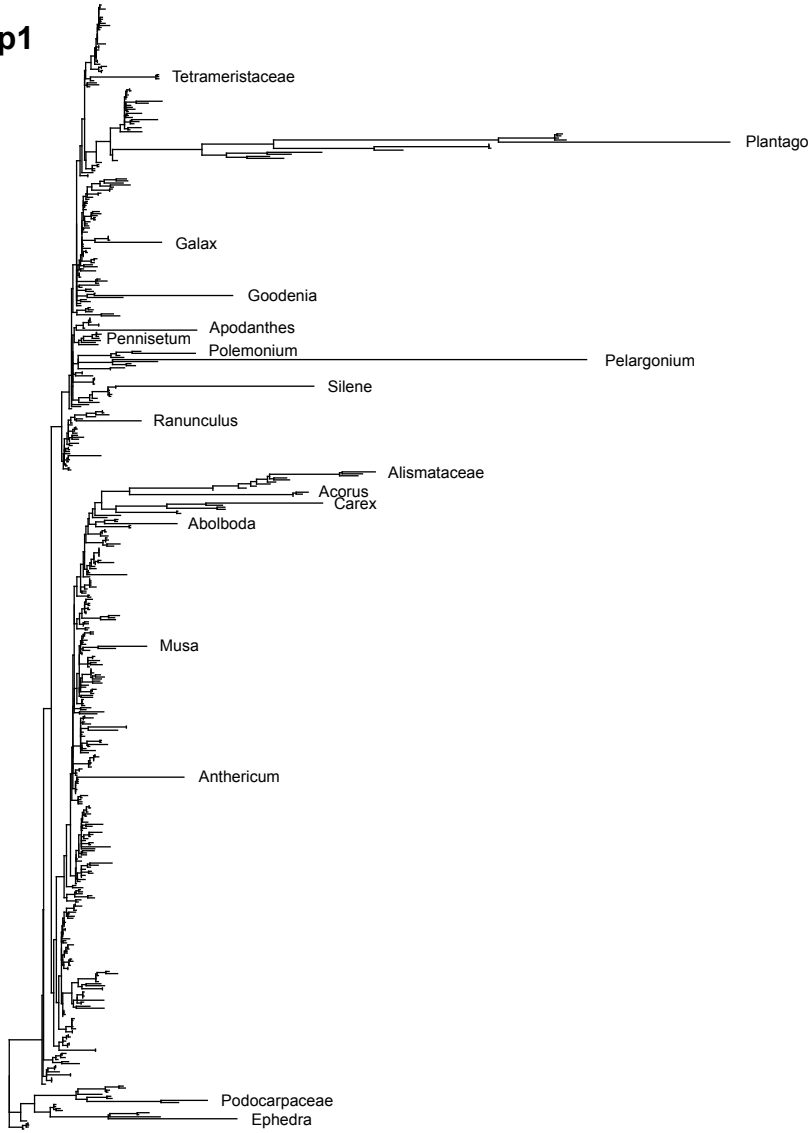


Supp. Fig. 1b

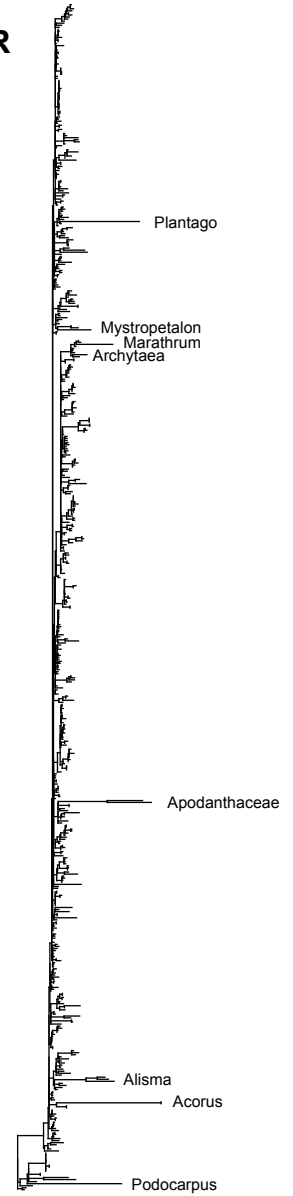


Supp. Fig. 2

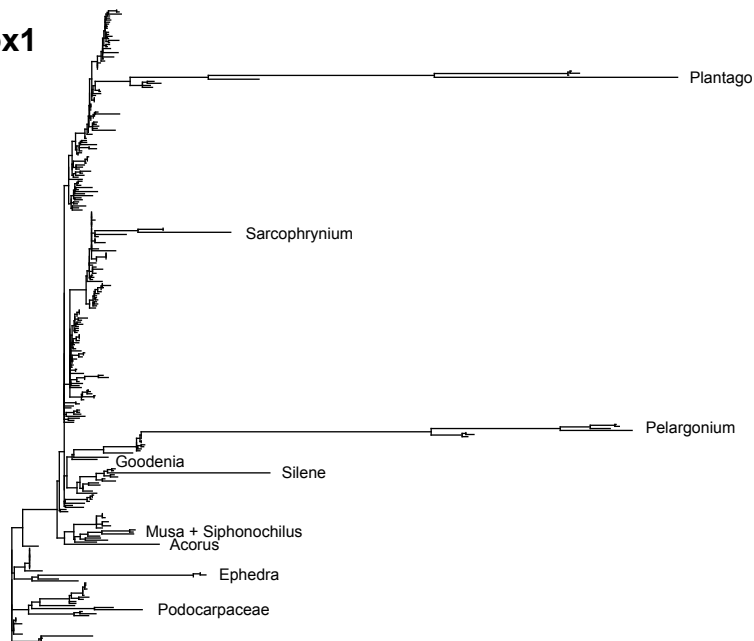
atp1



matR

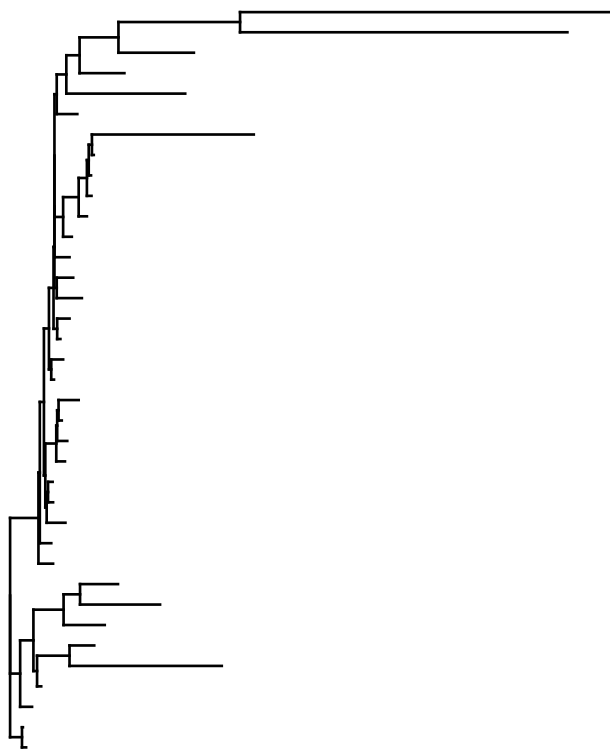


cox1



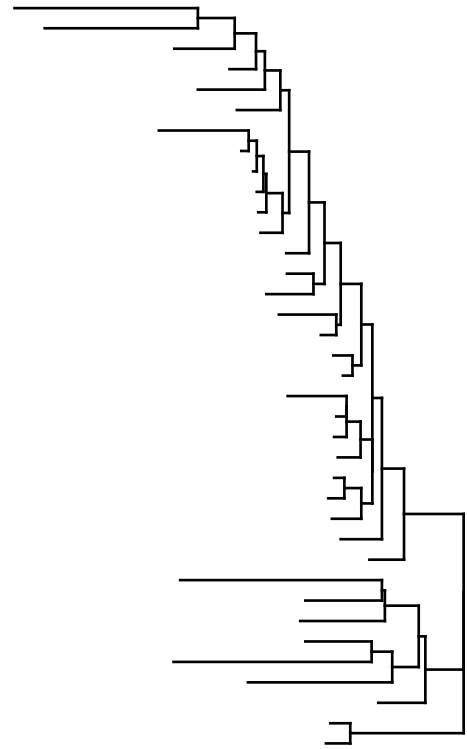
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Supp. Fig. 3



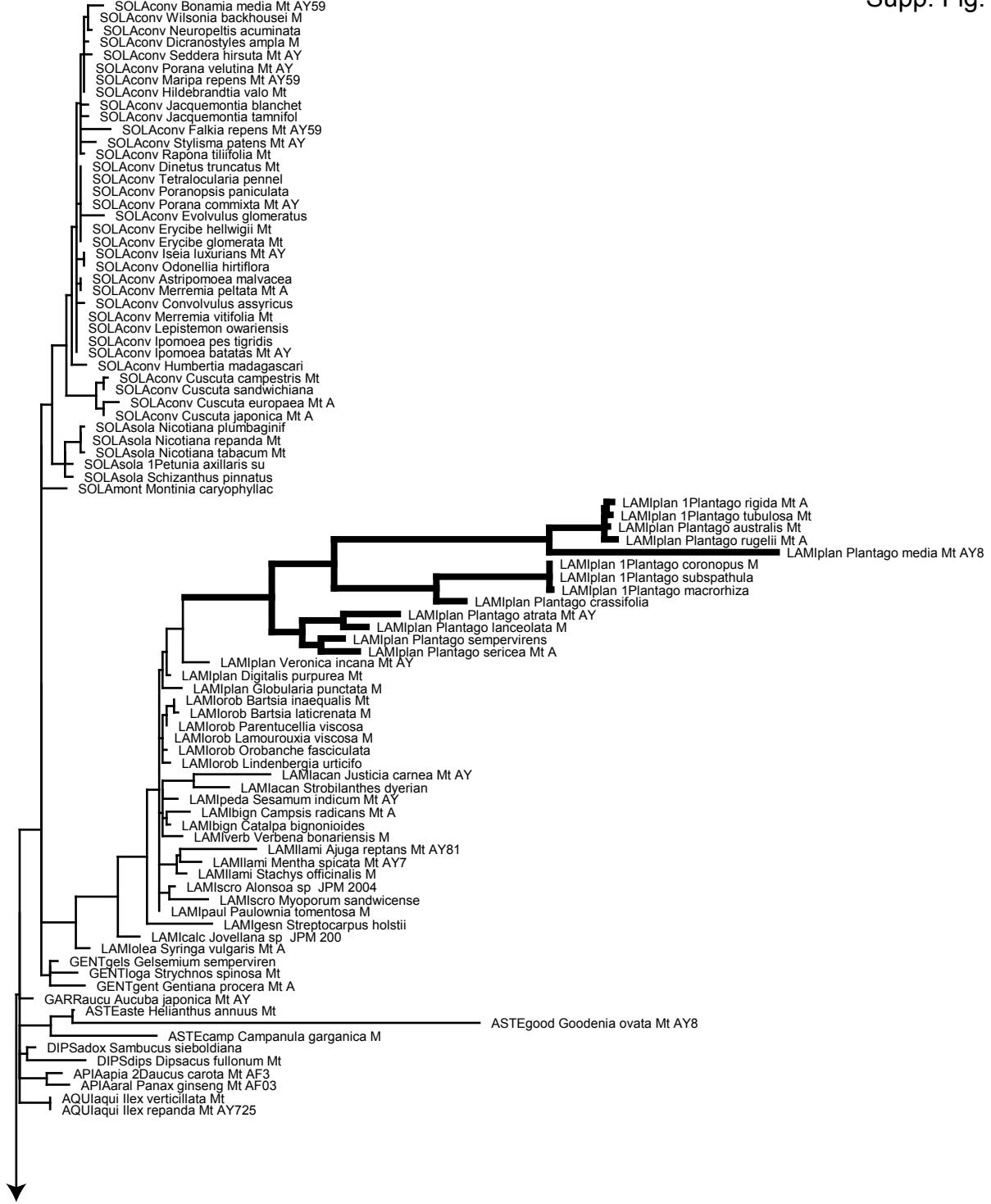
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Pelargonium
P. rugelii
P. lanceolata
Erodium
Acorus
Arabidopsis
S. noctiflora
S. acaulis
S. latifolia
Stellaria
Beta
Nepenthes
Nicotiana
Pisum
Oenothera
Daucus
Sambucus
Mahonia
Platanus
Oryza
Phoenix
Eichhornia
Philodendron
Liriodendron
Laurus
Piper
Amborella
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Juniperus
Podocarpus
Araucaria
Gnetum
Ephedra
Pinus
Ginkgo
Cycas
Zamia



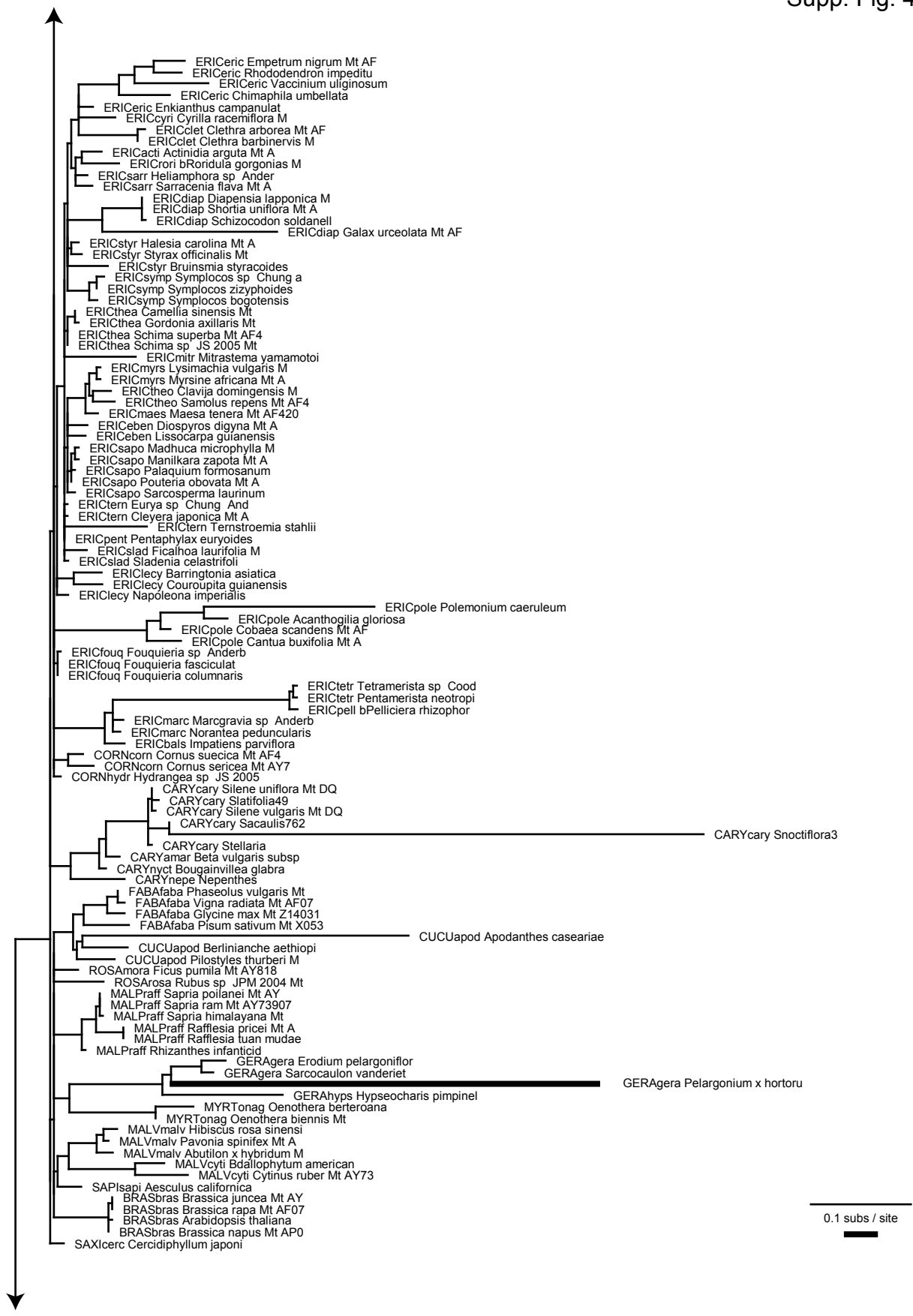
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Supp. Fig. 4a

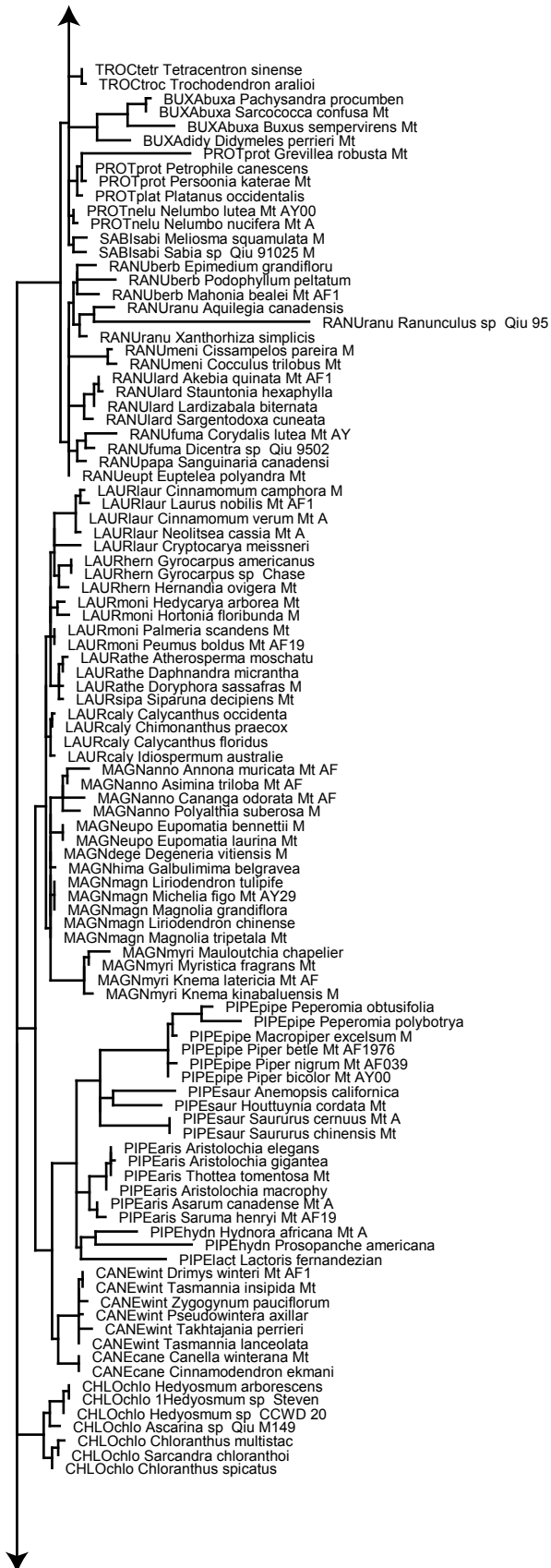


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Supp. Fig. 4b



Supp. Fig. 4c

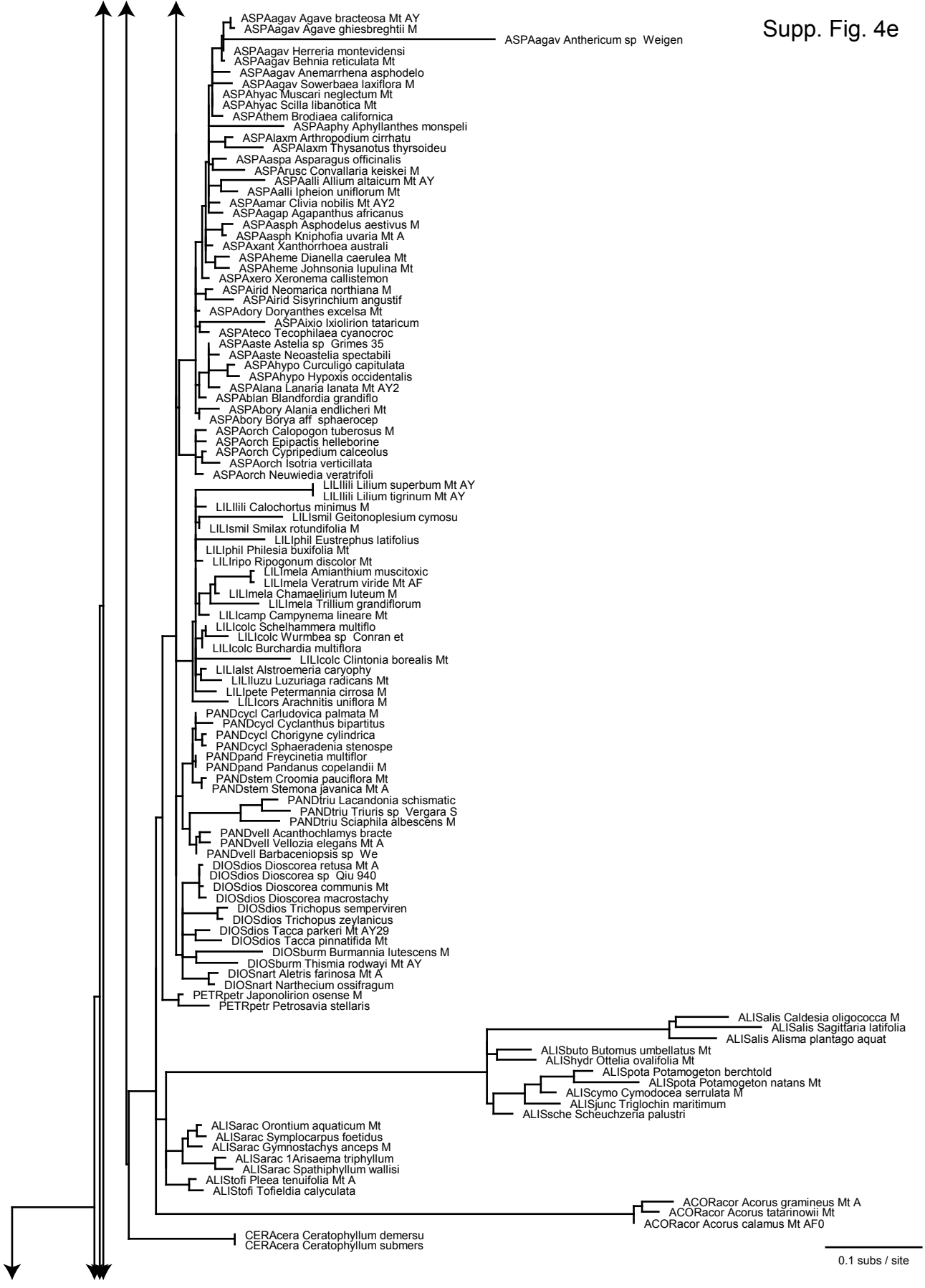


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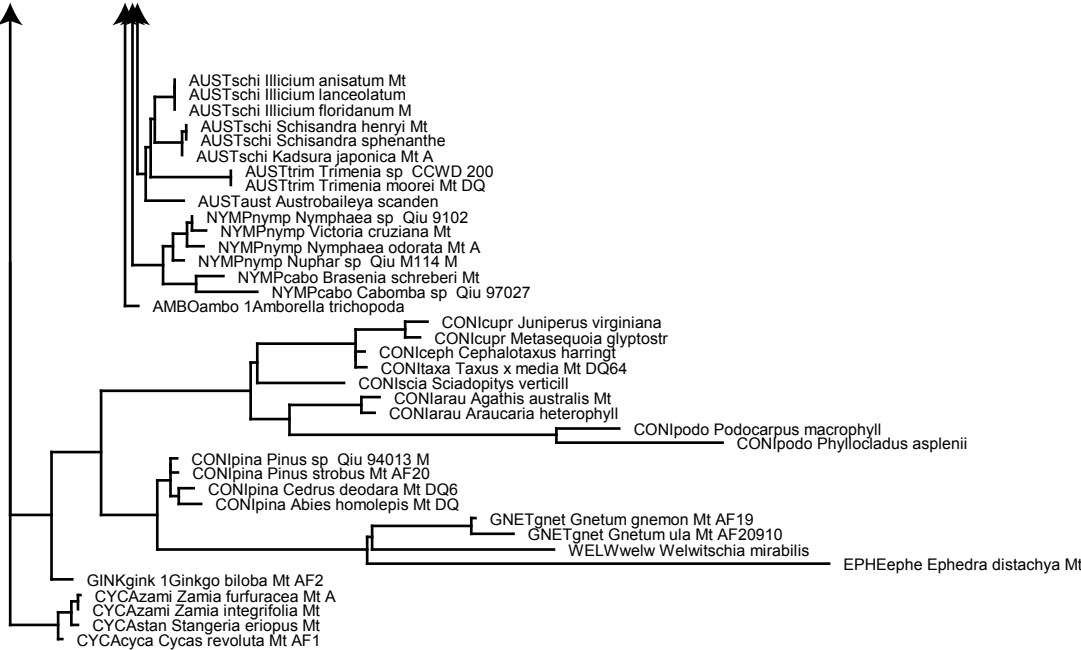
Supp. Fig. 4d



Supp. Fig. 4e

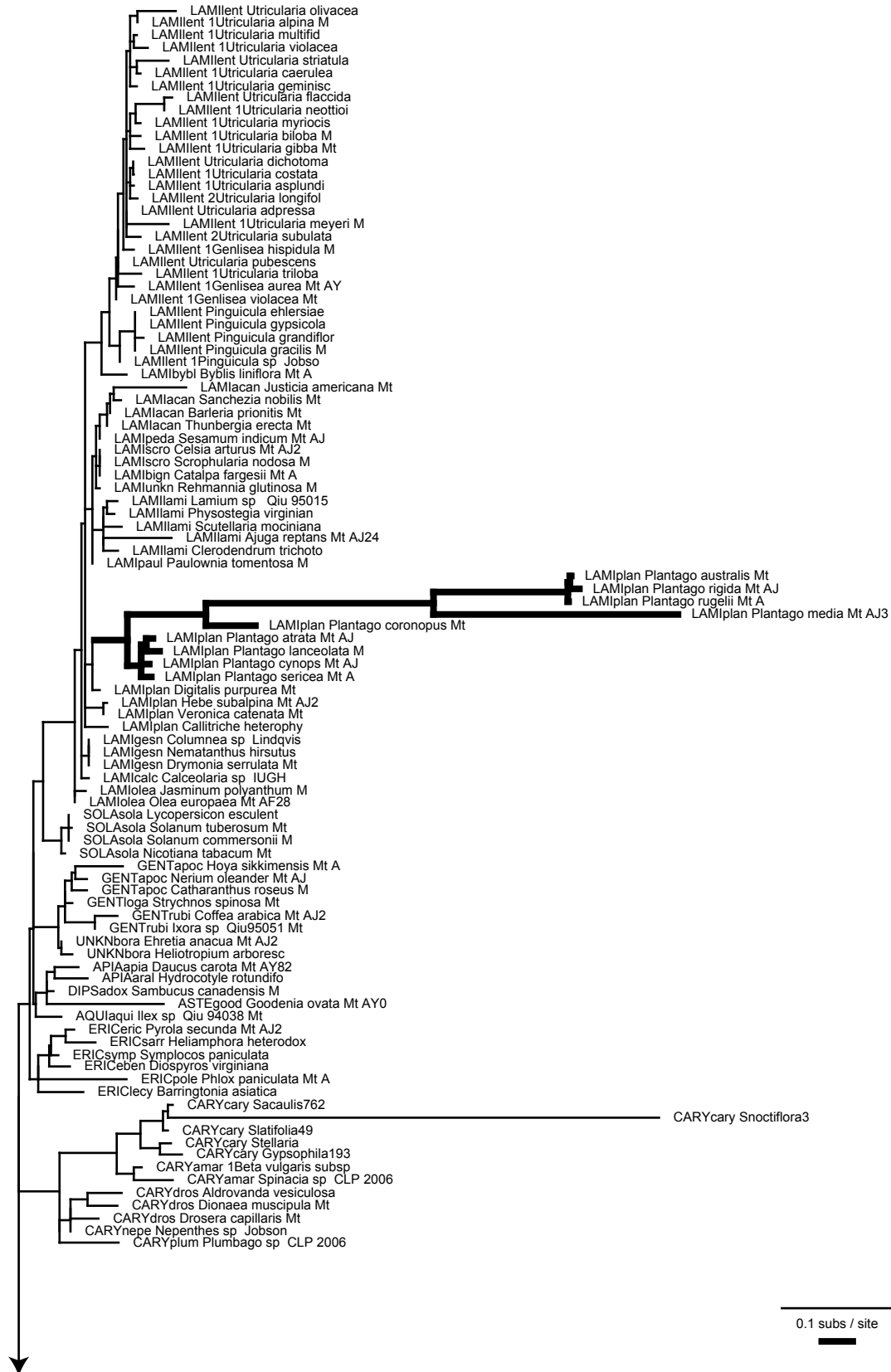


Supp. Fig. 4f

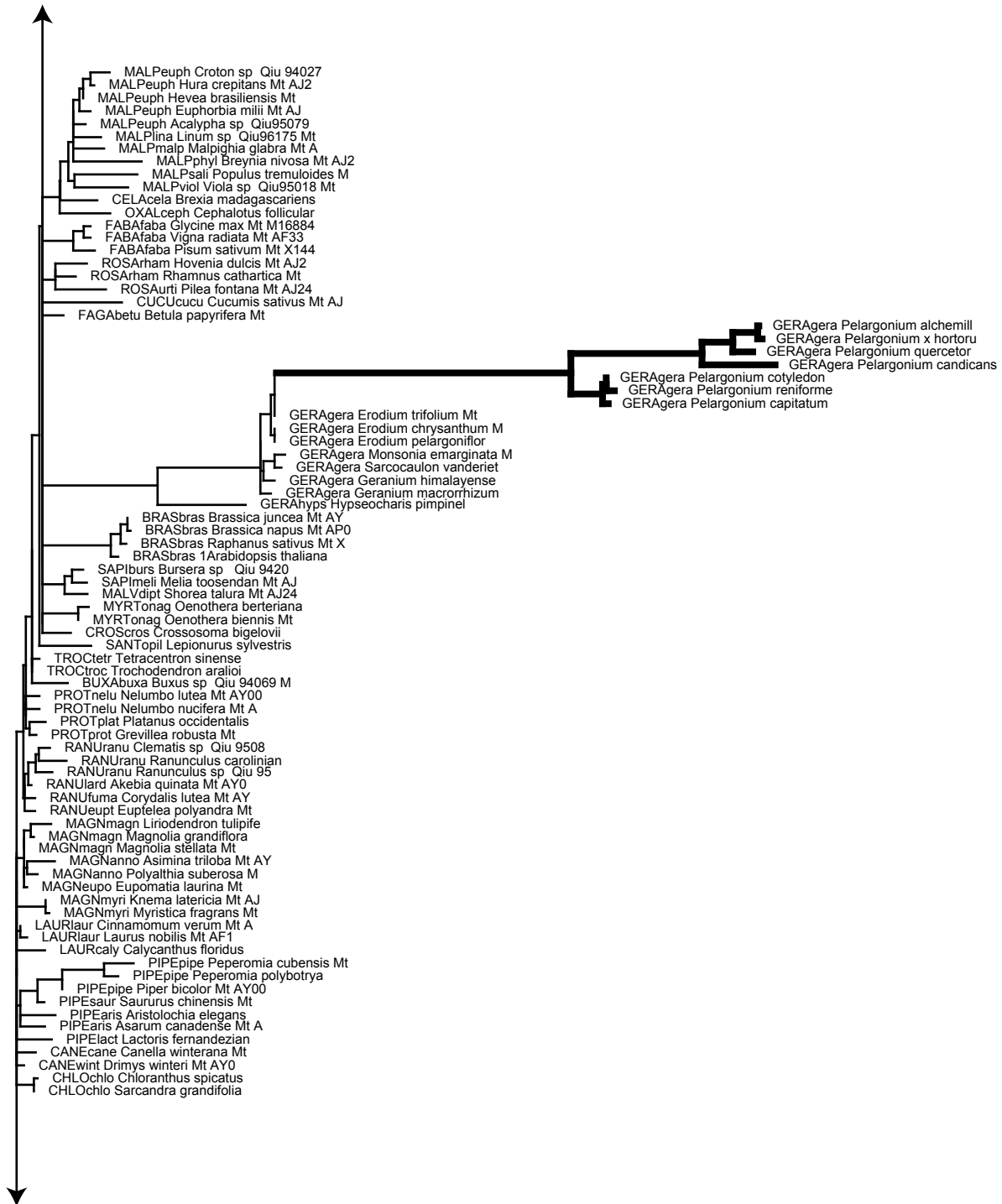


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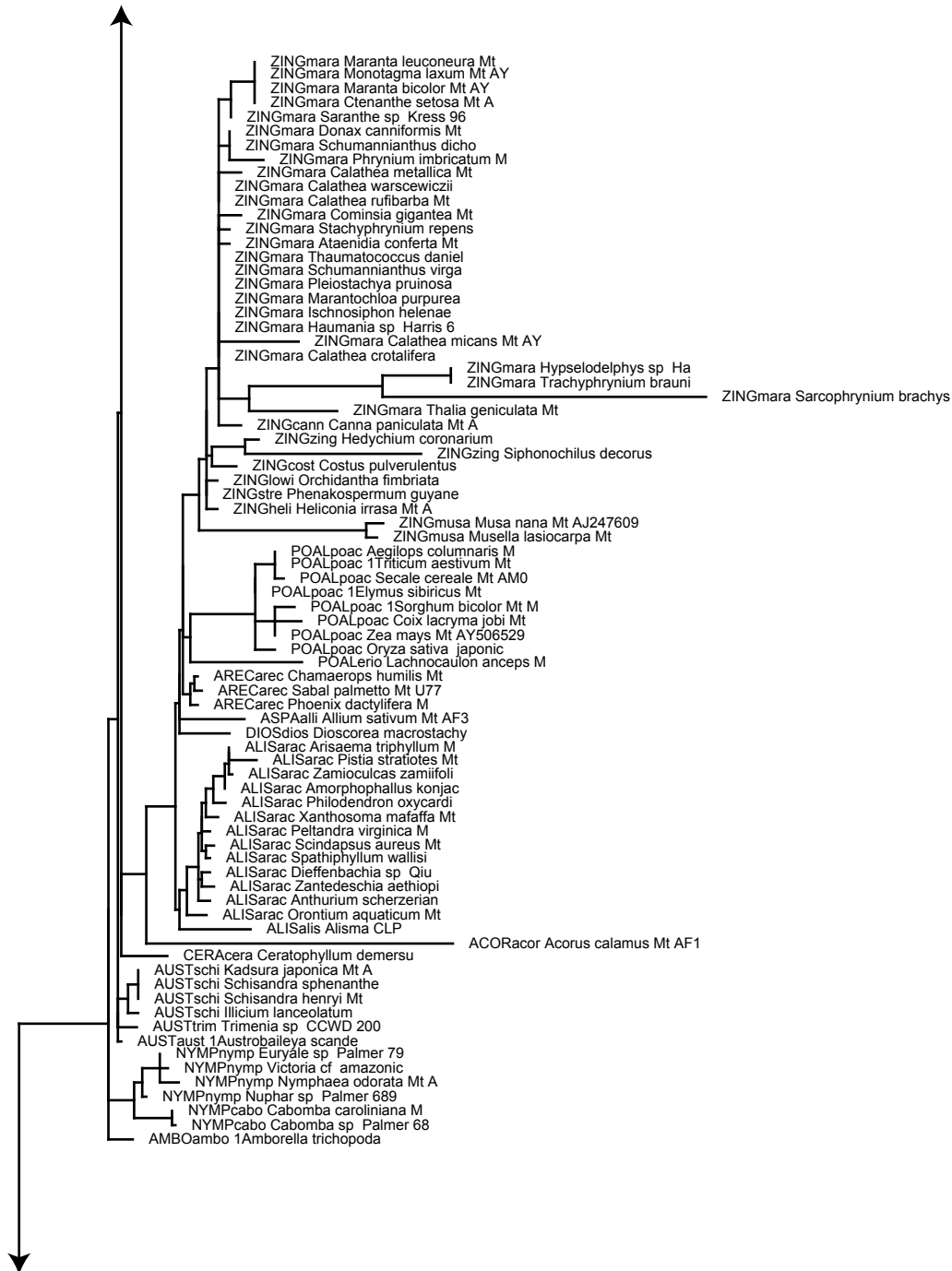
Supp. Fig. 5a



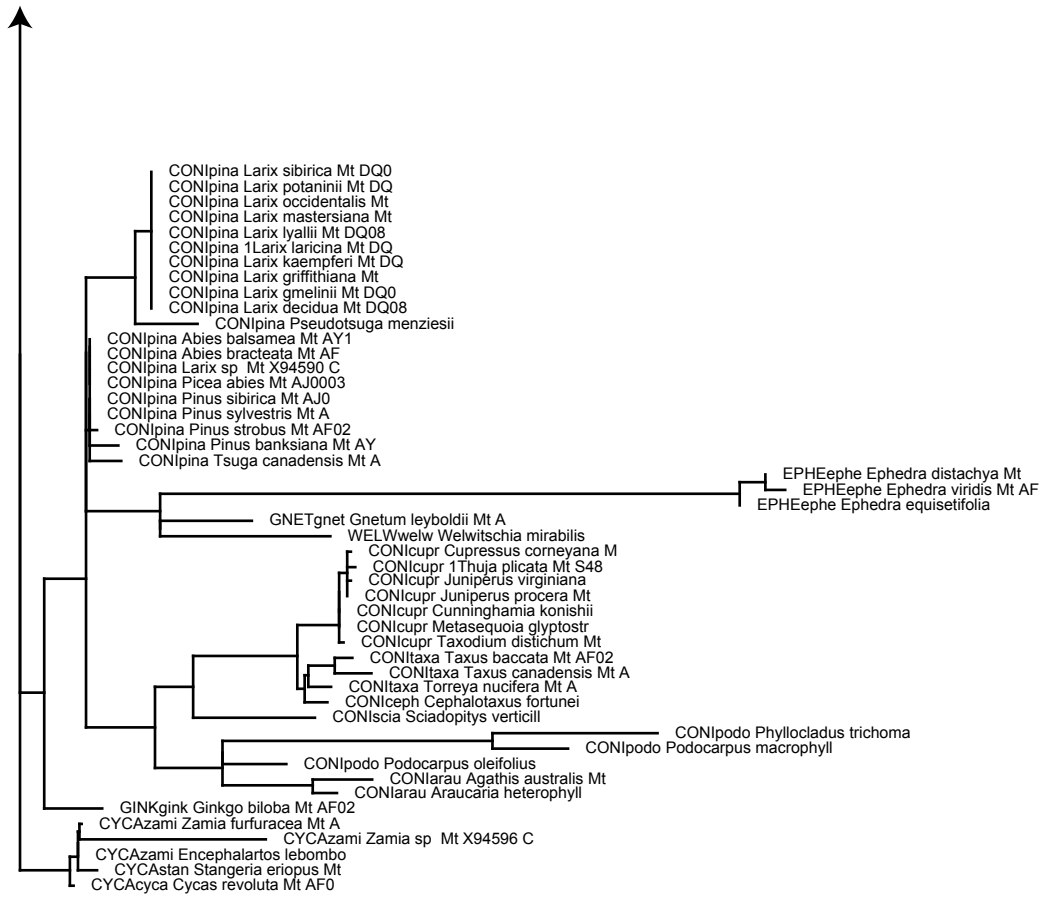
Supp. Fig. 5b



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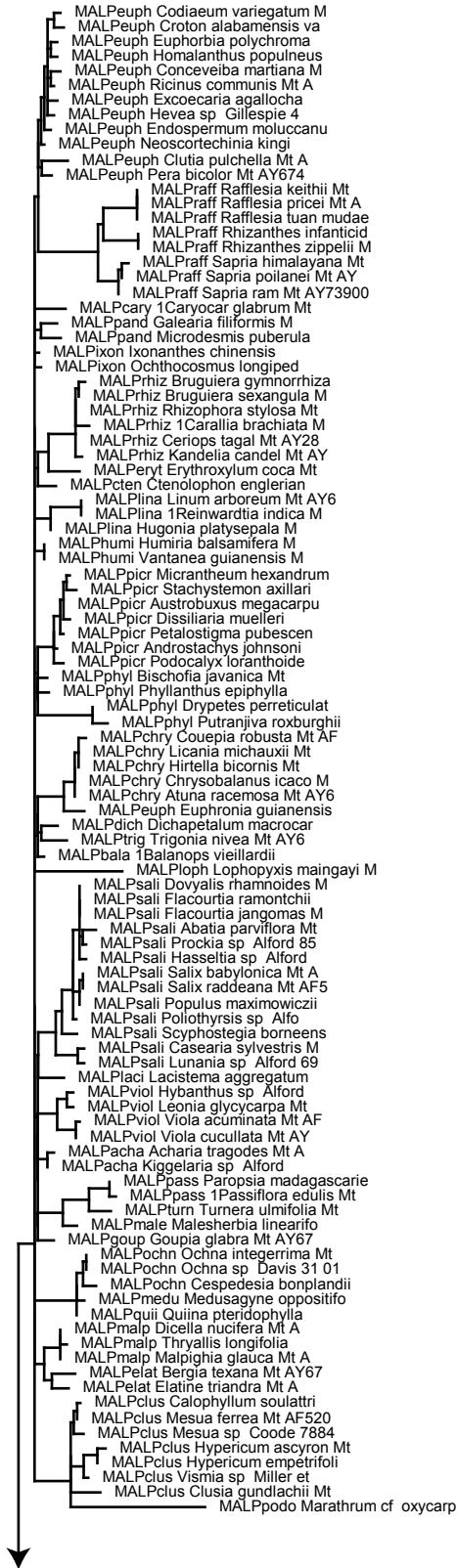


Supp. Fig. 5d

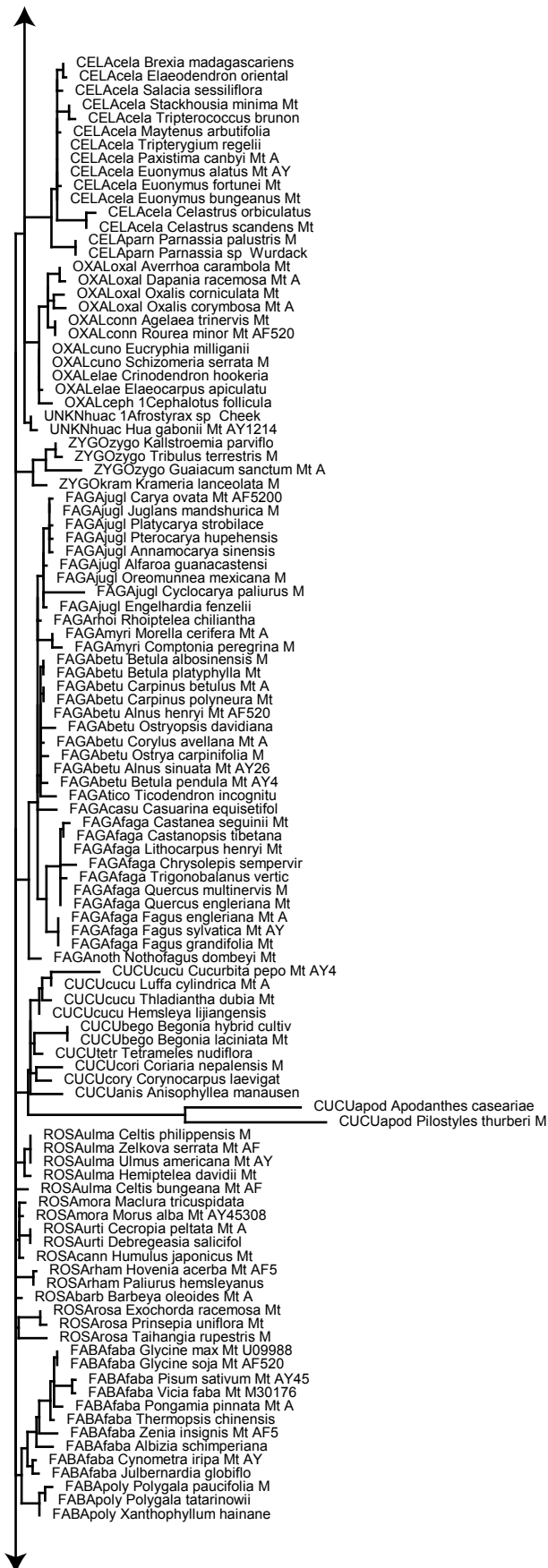


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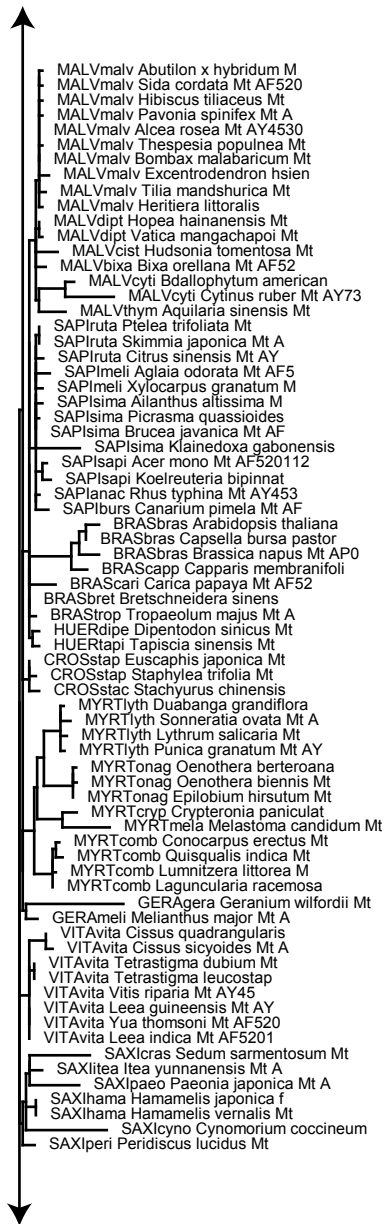
Supp. Fig. 6a



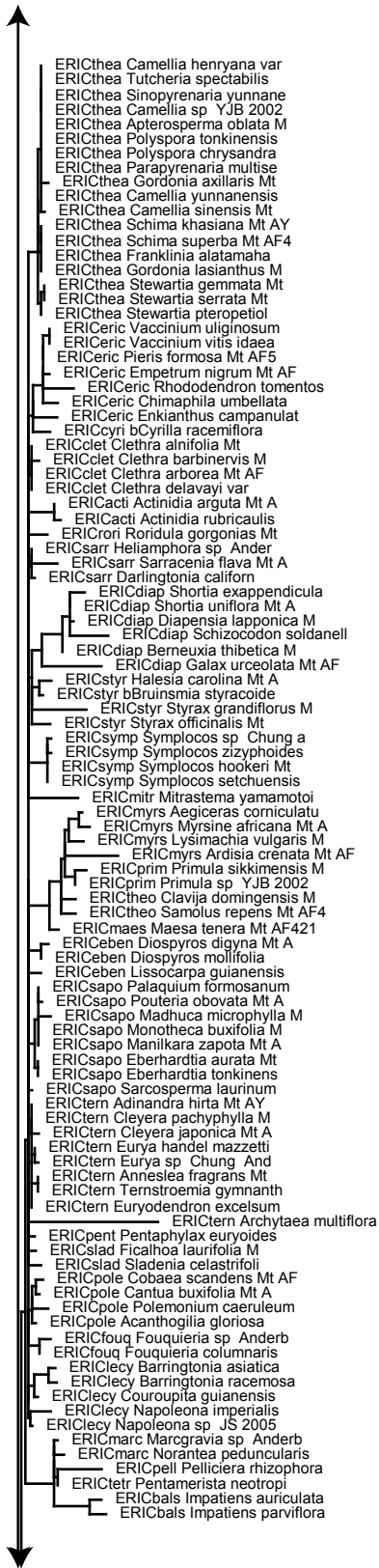
Supp. Fig. 6b



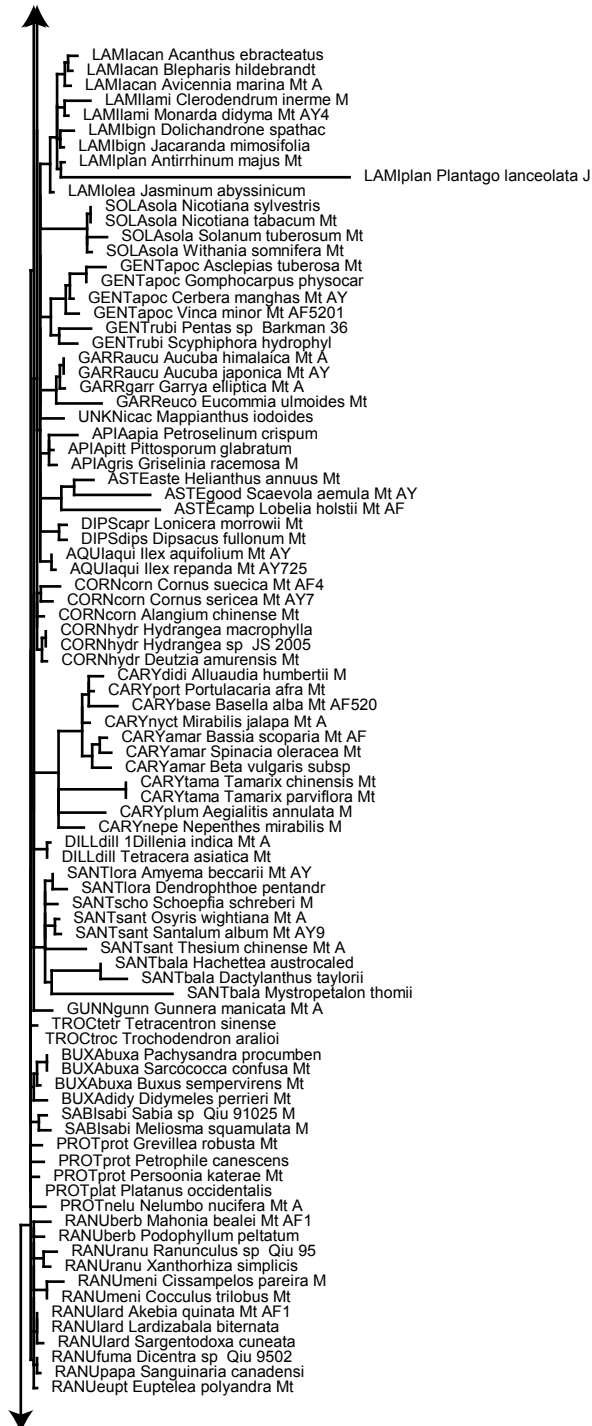
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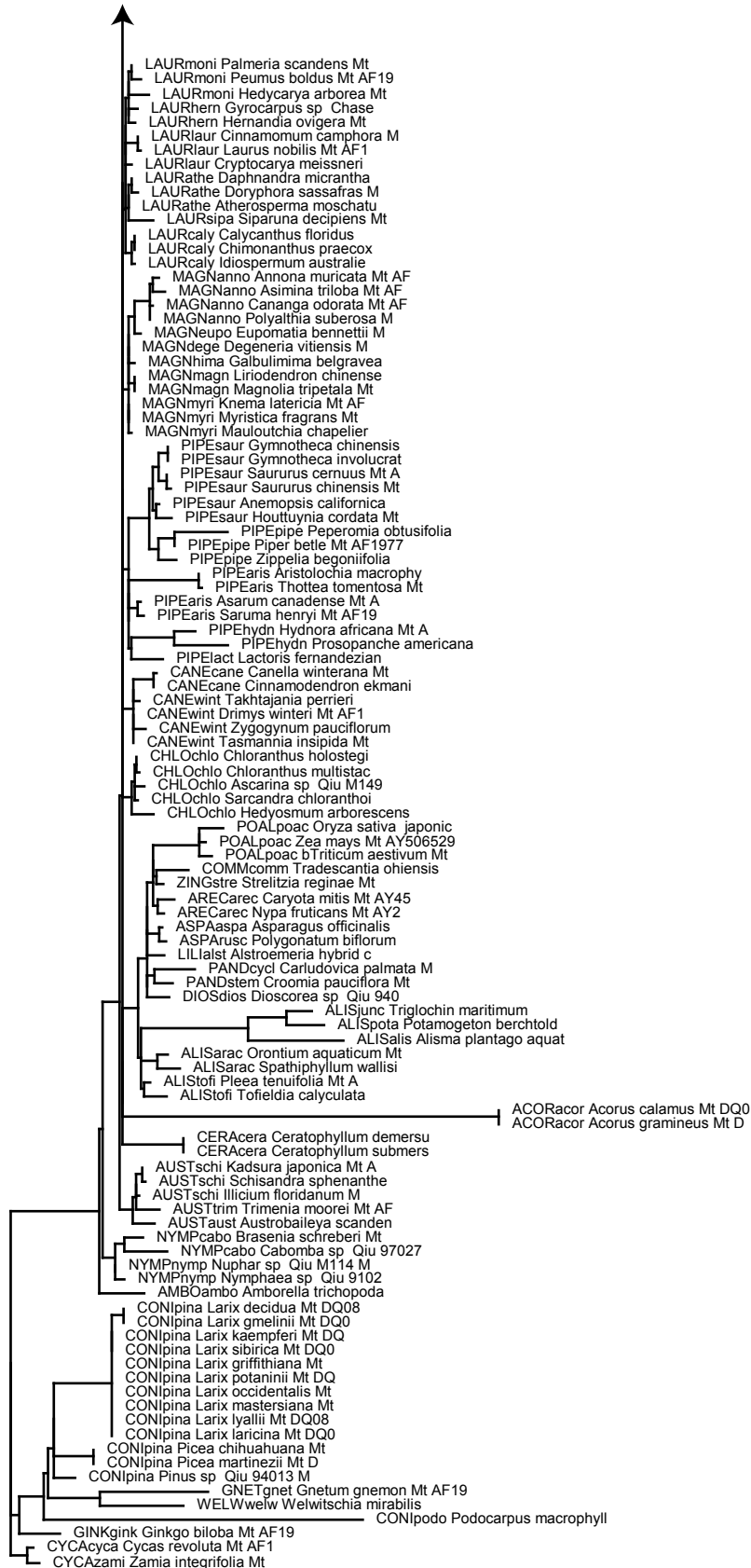
Supp. Fig. 6d



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Supp. Fig. 6f



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