

#### **Additional File 4 – Additional phylogenetic analyses.**

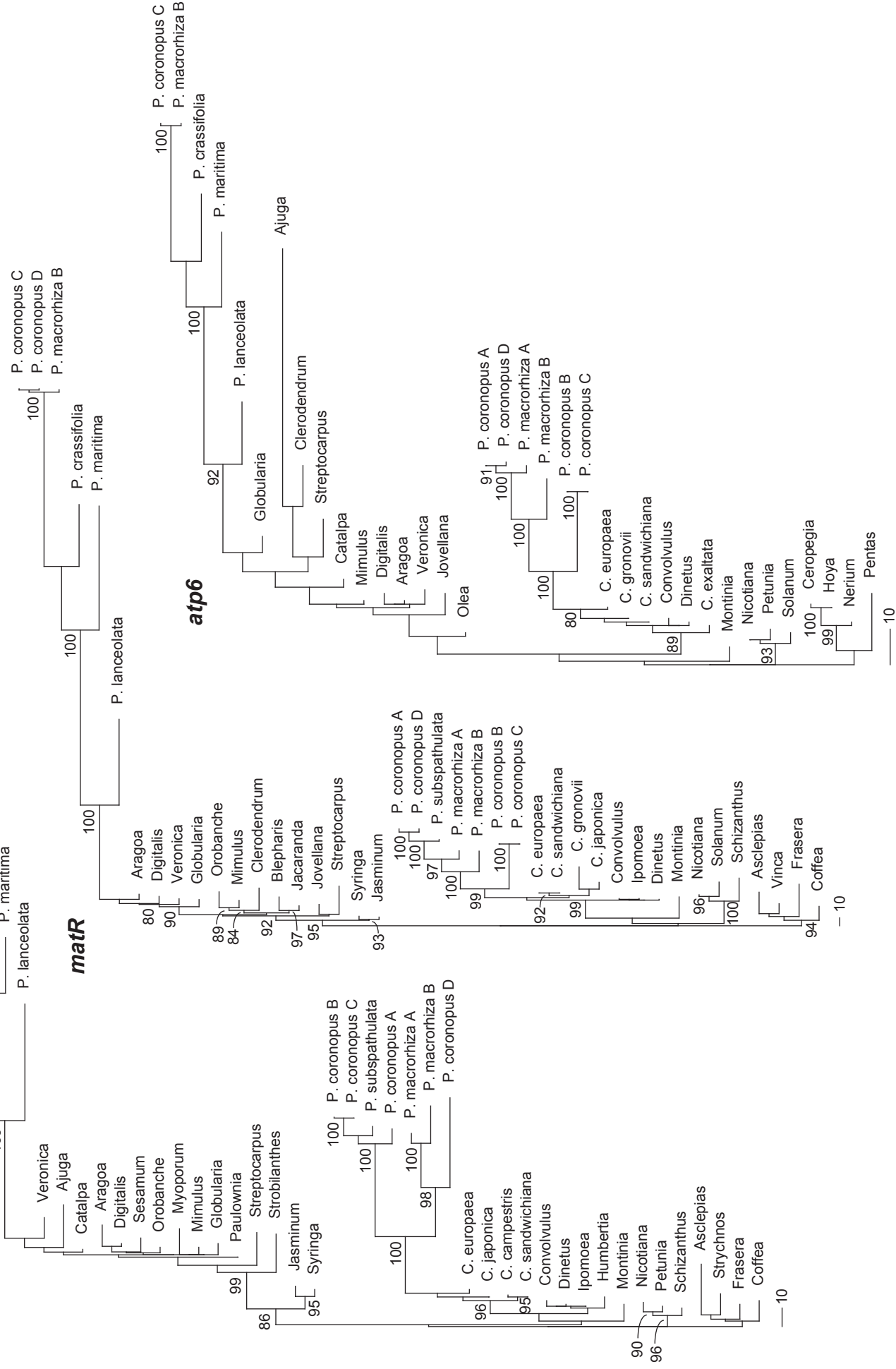
The *atp1*, *atp6*, and *matR* data sets were re-evaluated in several ways. (A) Neighbor joining was performed using MEGA version 4.0.2 [85] on the original data sets. The analysis used the maximum composite likelihood model, pairwise deletion of gaps, gamma-distributed rate variation among sites, and 500 replicates of bootstrapping. (B) Parsimony was also performed using MEGA on the original data sets. For this analysis, gaps and missing data were not excluded from the data sets, tree space was searched using 10 replicates of random starting trees and the close-neighbor interchange (level=1) heuristic search, and 500 replicates of bootstrapping were performed. (C) Edit sites and codons affected by gene conversion were eliminated from the data sets, and then maximum likelihood was performed as described in the main text. (D) The native functional copies from all *Plantago* species were removed from the original data sets and then evaluated by maximum likelihood. (E) Additional representatives from asterids, caryophyllids, and rosids were added to the original data sets and then evaluated by maximum likelihood.

### Additional File 4A Neighbor Joining

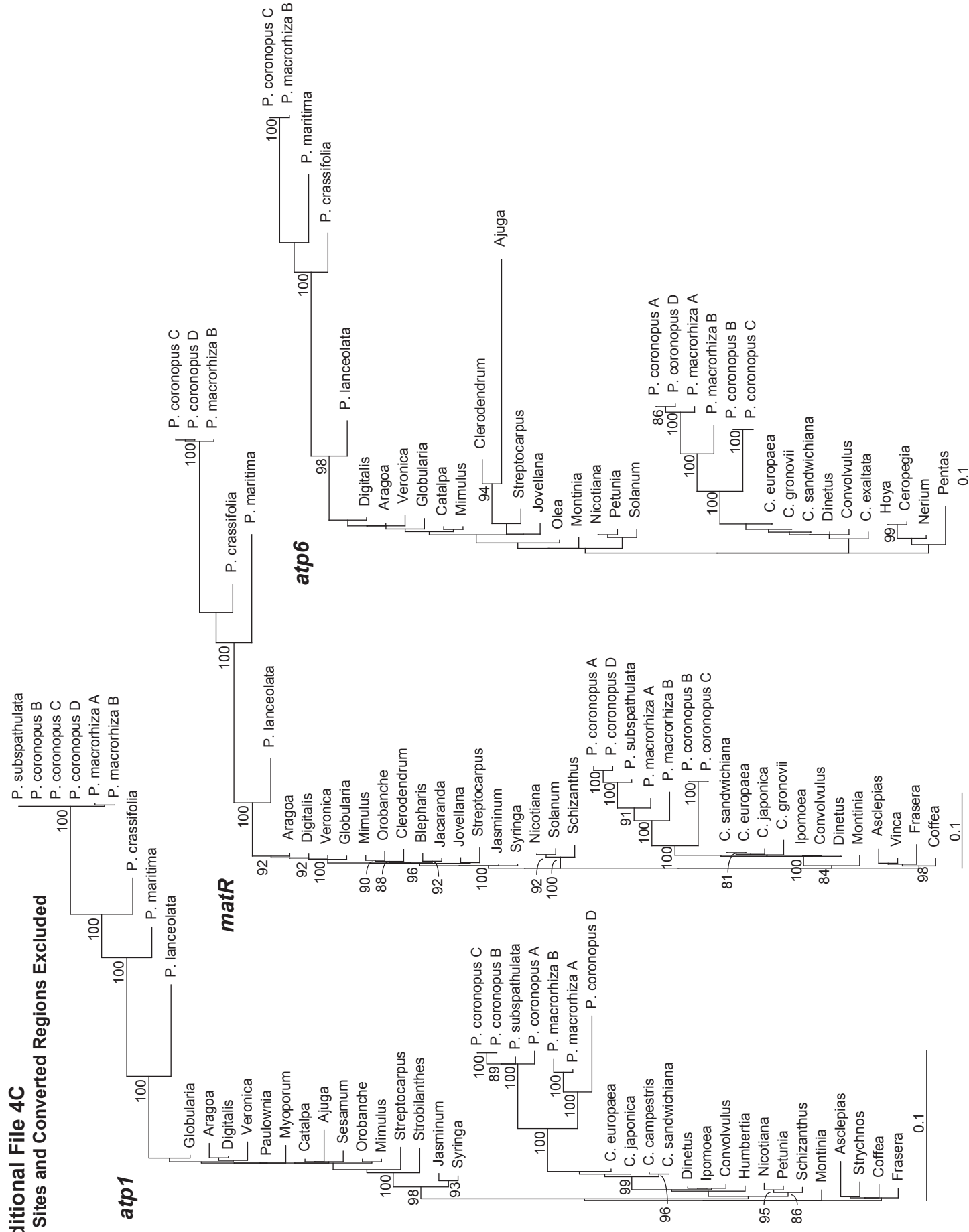


Phylogenetic tree showing relationships between *P. subspatulata*, *P. coronopus* B, *P. coronopus* C, *P. coronopus* D, *P. macrorrhiza* A, and *P. macrorrhiza* B. The tree has a scale bar of 100 and a bootstrap value of 8 at the base.

P. crassifolia



## Additional File 4C

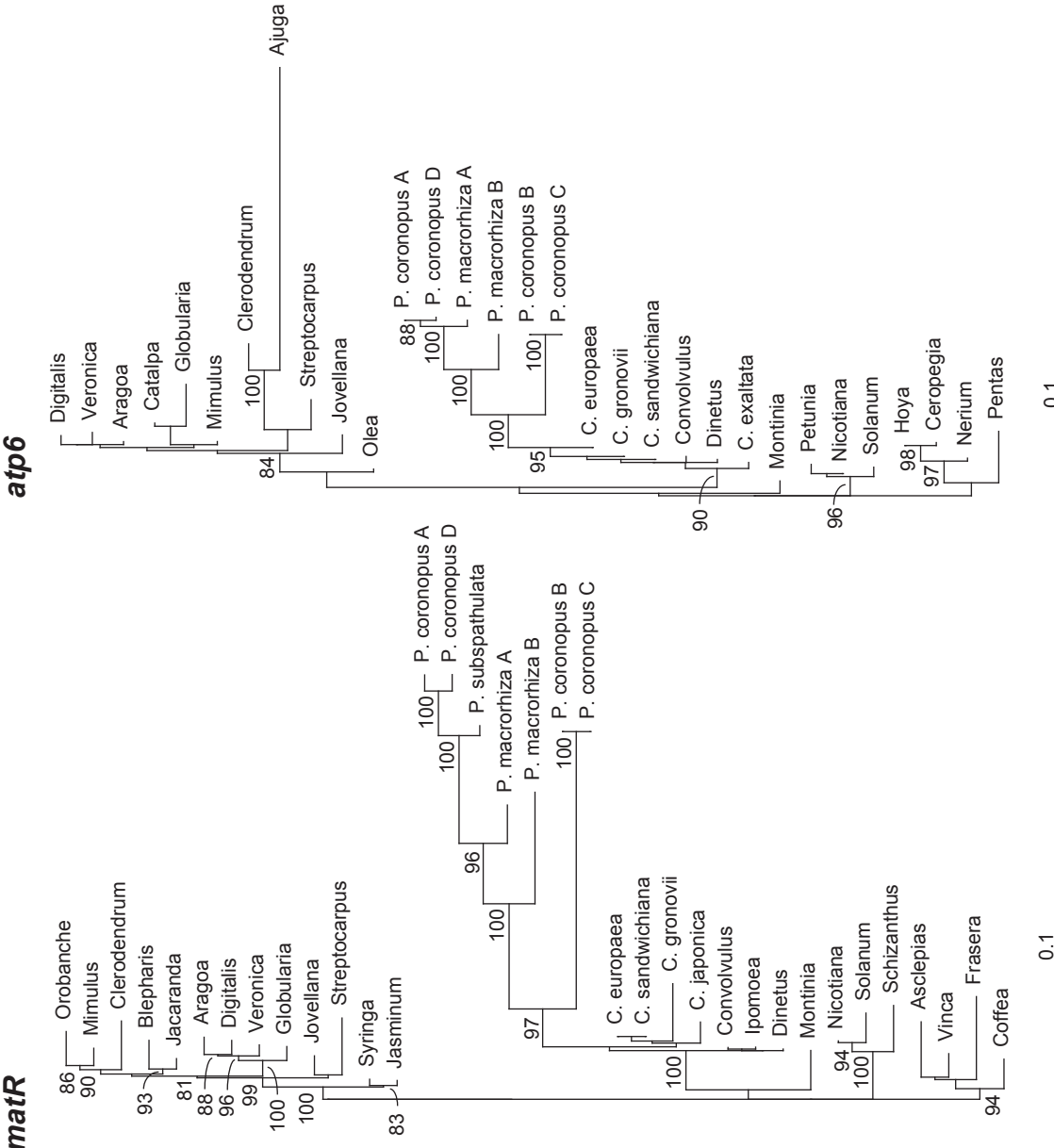


# Plantago Native Copies Excluded

# atp1



# matR



**atp6**

Additional File 4E  
Expanded Taxon Set

