**FIGURE S2.**—Comparison of mitochondrial substitution rates between *Silene latifolia* and *Beta vulgaris*, using *Arabidopsis thaliana* as an outgroup. (A) The trees depict rates of synonymous (left) and non-synonymous (right) substitution based on a concatenated dataset of all protein genes. The values above each branch indicate branch length in terms of number of substitutions per site, which were estimated using codeml (PAML) as described previously (Sloan et al. 2009). The rate difference between *S. latifolia* and *B. vulgaris* for the concatenated dataset was highly significant based on both a molecular clock test implemented in codeml (\(\chi^2_{df=1} = 24.75; p < 0.0001\)) and a relative rate test implemented in MEGA (\(\chi^2_{df=1} = 23.96; p < 0.0001\)). These tests included both synonymous and non-synonymous sites. The branch lengths estimated in this 3-species analysis are very similar to estimates from a larger phylogenetic analysis of fully sequenced seed plant mitochondrial genomes (data not shown). (B) The table summarizes the results of relative rate tests performed on individual protein genes in MEGA (including both synonymous and non-synonymous sites). Genes shown in bold exhibited a significant difference in rates between the two species at the \(p = 0.05\) threshold. No corrections for multiple tests were performed. For all analyses, codons that are edited in any of the three species were excluded to ensure that substitutions at RNA editing sites themselves do not account for estimated rate differences.