



Figure S 4: Phylogenetic tree visualizing the calculated branch lengths used in phylogenetic signal detection. Branch lengths were estimated using dnaml from a MAFFT v7.205 alignment of *rps16*, *atp2*, *18s*, *26s* and *SMC1* (FASTA file of sequences available in File S3). The tree topology reported by the *Arabidopsis* Genome Project (2013) was used. Branch lengths represent site changes converted to relative age of branches using the R package ape.