

Figure S4. Azolla MIKC^C phylogenetic analysis and response to far-red light (FR). The Azolla MIKC^C gene model encoded by Azfi_s0028.g024032 was annotated manually: the TF was not expressed in sporophytes yet automated annotation relied on sporophyte RNAsequencing. Sequences extracted from the genome browsers of each species were aligned with MAFFT einsl (Kato et al., 2019), then trimmed with trimAl (Capella-Gutiérrez et al., 2009). Phylogenetic inferences were computed with IQTREE (Nguyen et al., 2015) and its internal model fitter; 2000 bootstrap determined by SH-aLRT (Kalyaanamoorthy et al., 2017). The tree was rooted using the sequence of Chara globulosa MIKC^C (cgMADS1). Nodes with bootstrap support equal or greater than 80% SH-aLRT are indicated. The lower branches of the tree were typically poorly supported by bootstrapping. Branches are color coded as per their plant lineage. Fold-change in response to FR, AND Base Mean were calculated by DESeq2 (Love et al., 2014); yellow stars mark significant changes of Padj <0.1.

