Figure S4  A maximum likelihood phylogeny of MIXTA-like proteins based on an alignment of the R2R3 MYB domains. Phylogenetic analyses were conducted using RAxML 7.0.4 (Stamatakis 2006), with the BLOSUM62 amino acid substitution matrix and CAT approximation. Bootstrap values greater than 50% are indicated along the branches. *Mimulus lewisii* sequences have been deposited in GenBank (KC139356, KC692454-KC692460). *M. guttatus* sequences were retrieved from Scoville et al. (2011). Information on other sequences was given in Figure S3.