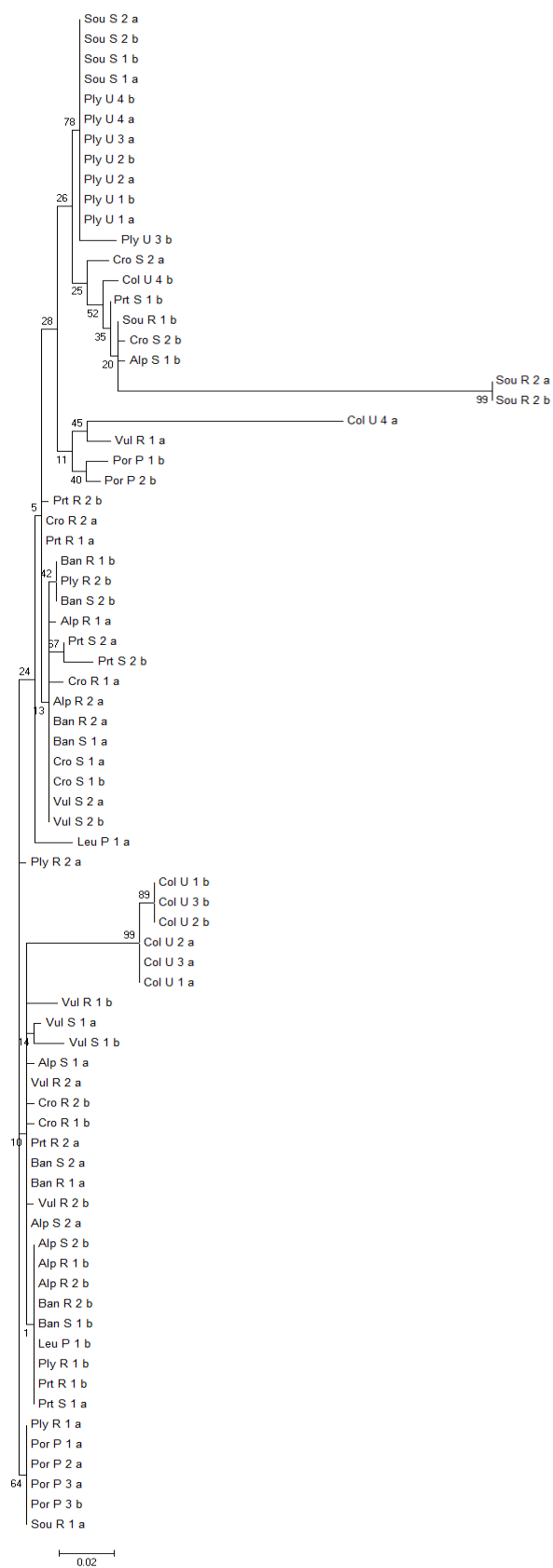


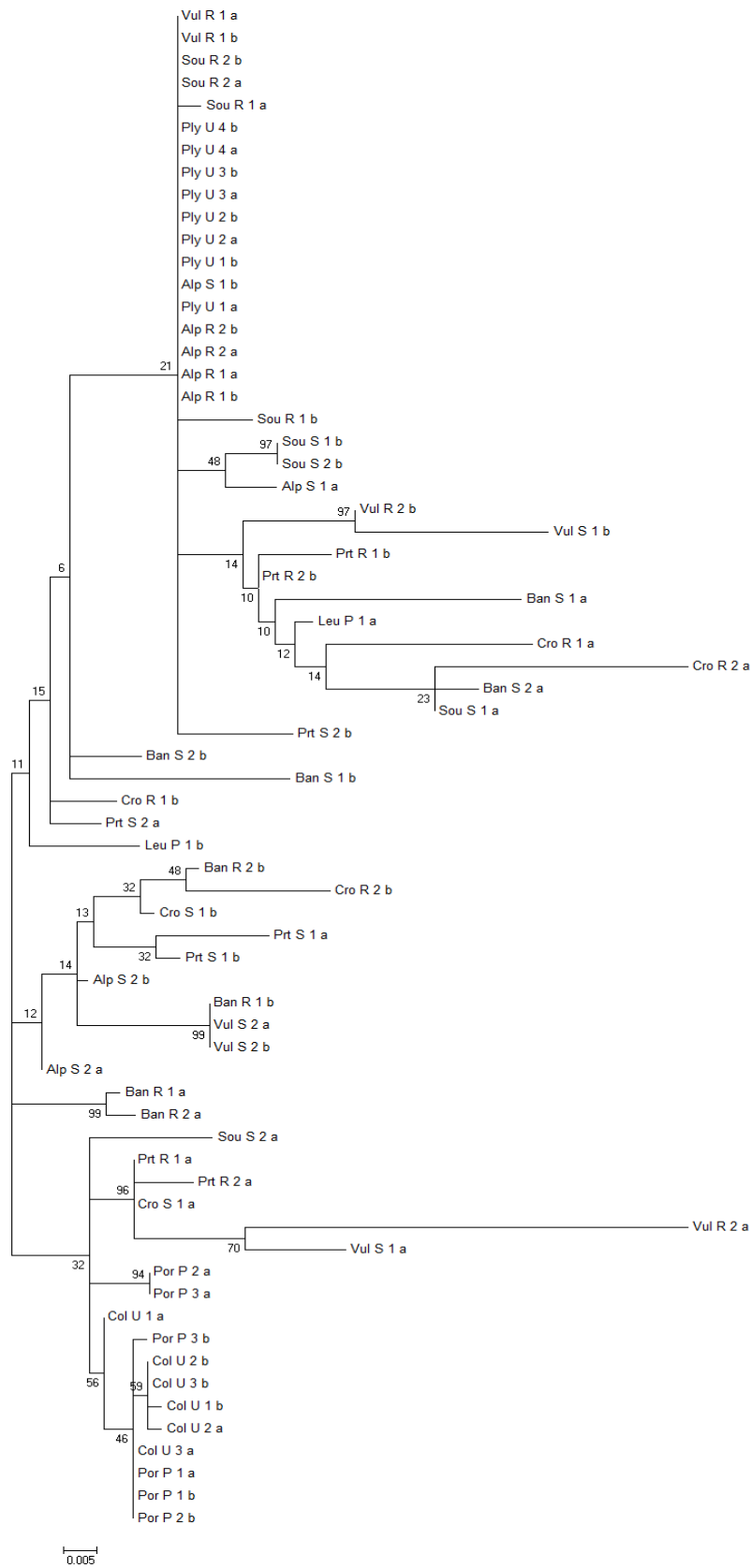
Supplementary figure S1 Maximum Likelihood phylogenies

For each locus a ML tree was built using the best substitution model as defined in MEGA6. These models were JC (Sym32), JC+I (CA2m), T92+ Γ (TyrK, RNAbinding5), T92+ Γ +I (DUF140). Each allele for each individual is designated in the tree as follows: Site (3 letters, see table 1) + morph (1 letter, see table 1) + individual ID number + allele (a or b).

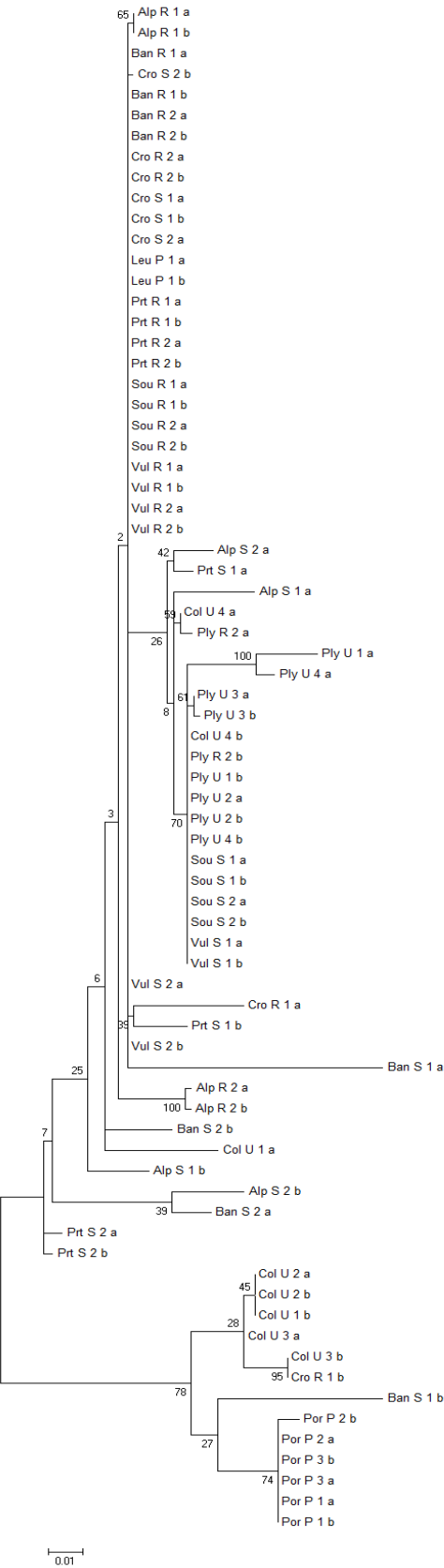


TyrK

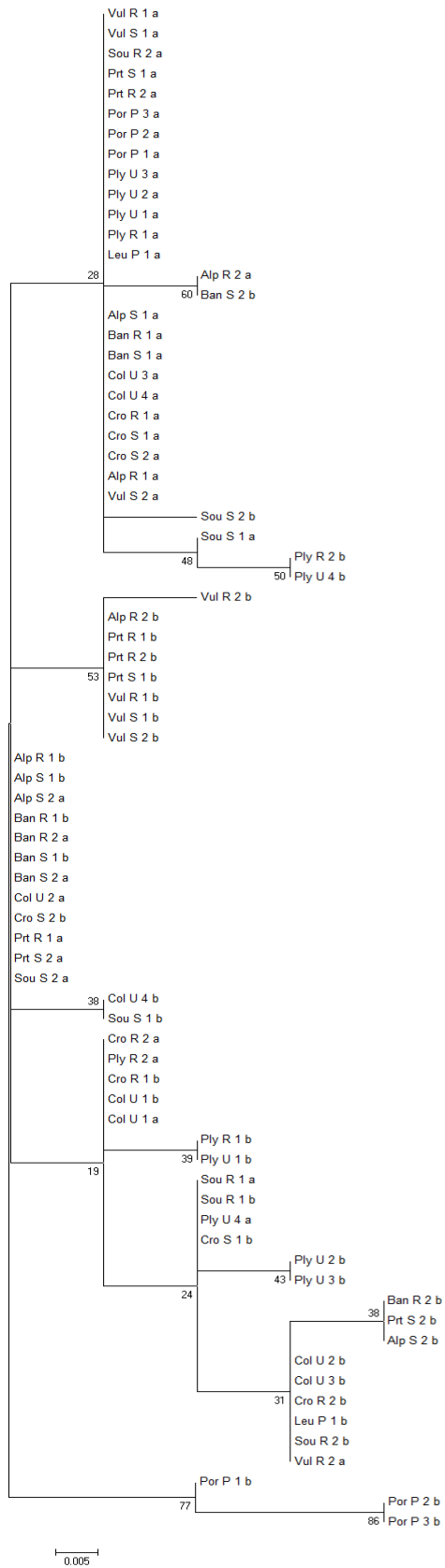
DUF140



RNAbinding5



CA2m



Sym32

