



**Fig. S4** Majority-rule consensus trees obtained from maximum parsimony analyses of the *LFY* and *DDB2* datasets. Numbers associated with branches are bootstrap percentages of MP and ML greater than 50%. Bold lines indicate Bayesian posterior probabilities greater than 0.90. Diploids are in black, and tetraploids are in color. Green, *E. glauca*, *E. intermedia* and *E. sinica*; Red, *E. gerardiana*, *E. likiangensis*, *E. saxatilis* and *E. saxatilis* var. *mairei*; Purple, *E. regeliana* and *E. przewalskii*. The combinations of letters and numbers following species names represent different clones.