

Figure S1. Distribution of SSR motifs: (a) motif types, (b) repeat number, and (c) motif length.

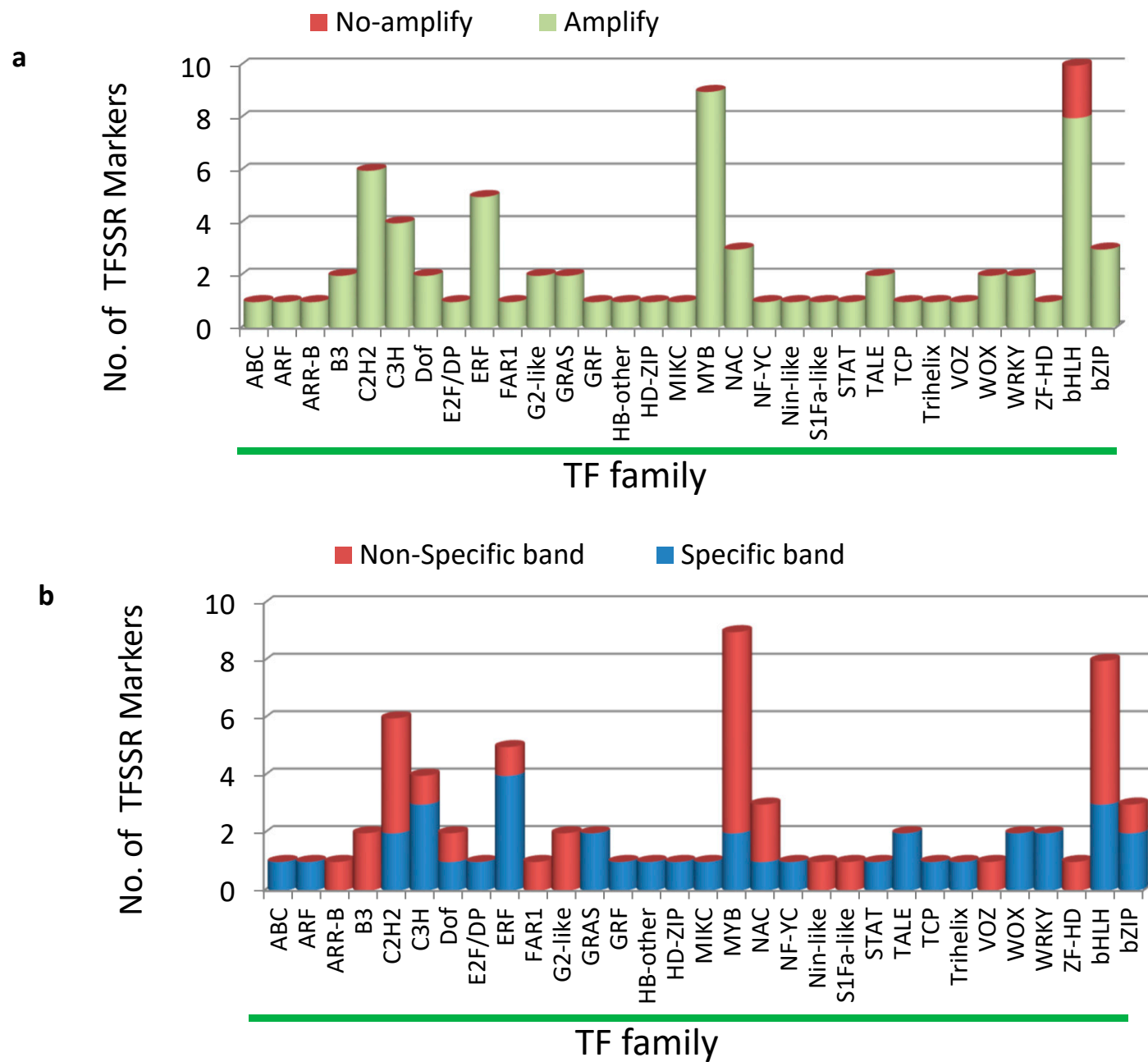


Figure S2. Evaluation of TFSSR markers based on wet lab of 31 TF families (a) based on nPCR amplification and (b) based on band specificity.

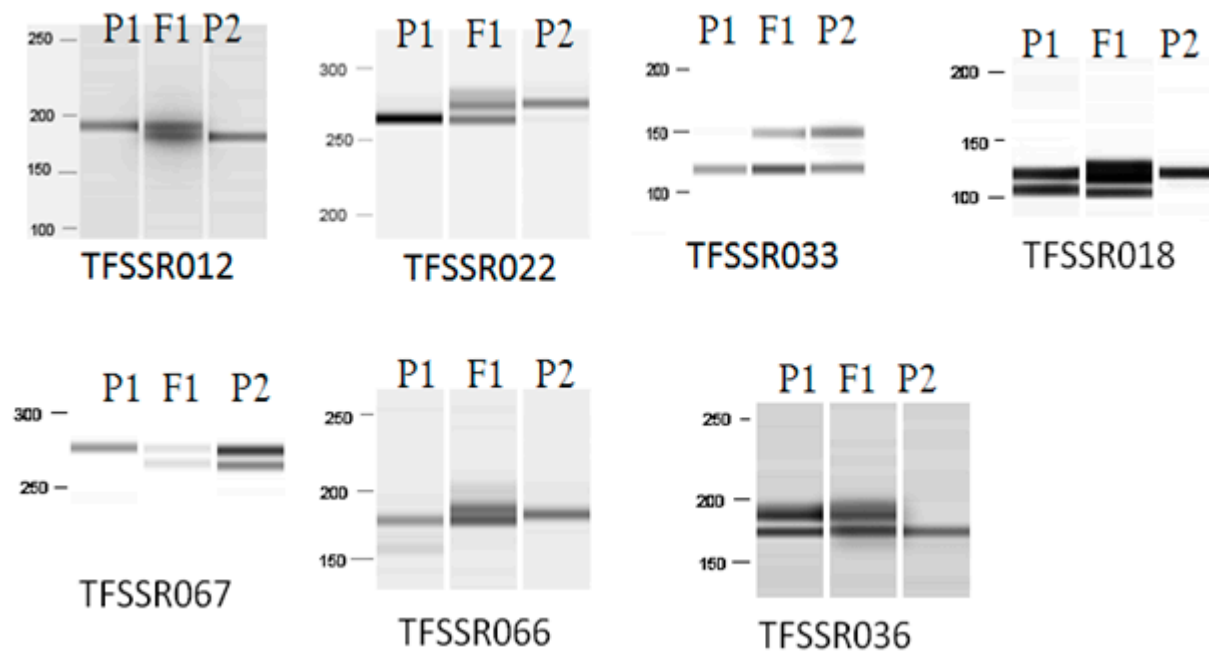


Figure S3. Banding profile of the 7 TFSSR markers able to identify hybrid crosses between inbred lines *Lilium longiflorum* (**Easter lily**) L2-4 and *Lilium longiflorum* (**Easter lily**) L2-28. [P1= L2-4 P2= L2-28 and F1= L2-4X L2-28].

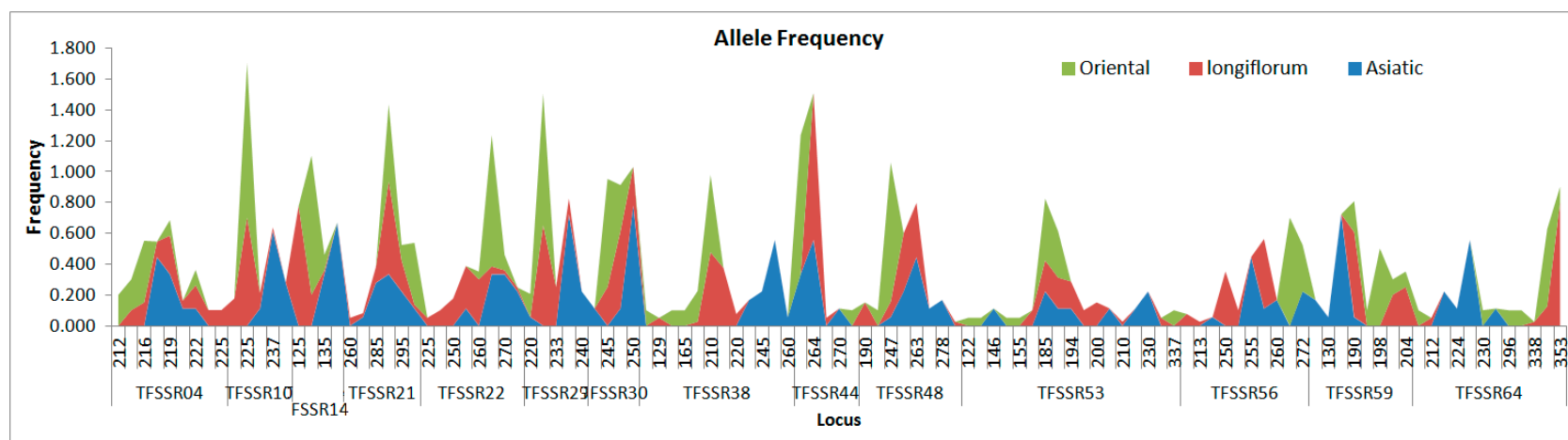


Figure S4. Allele frequencies by population.

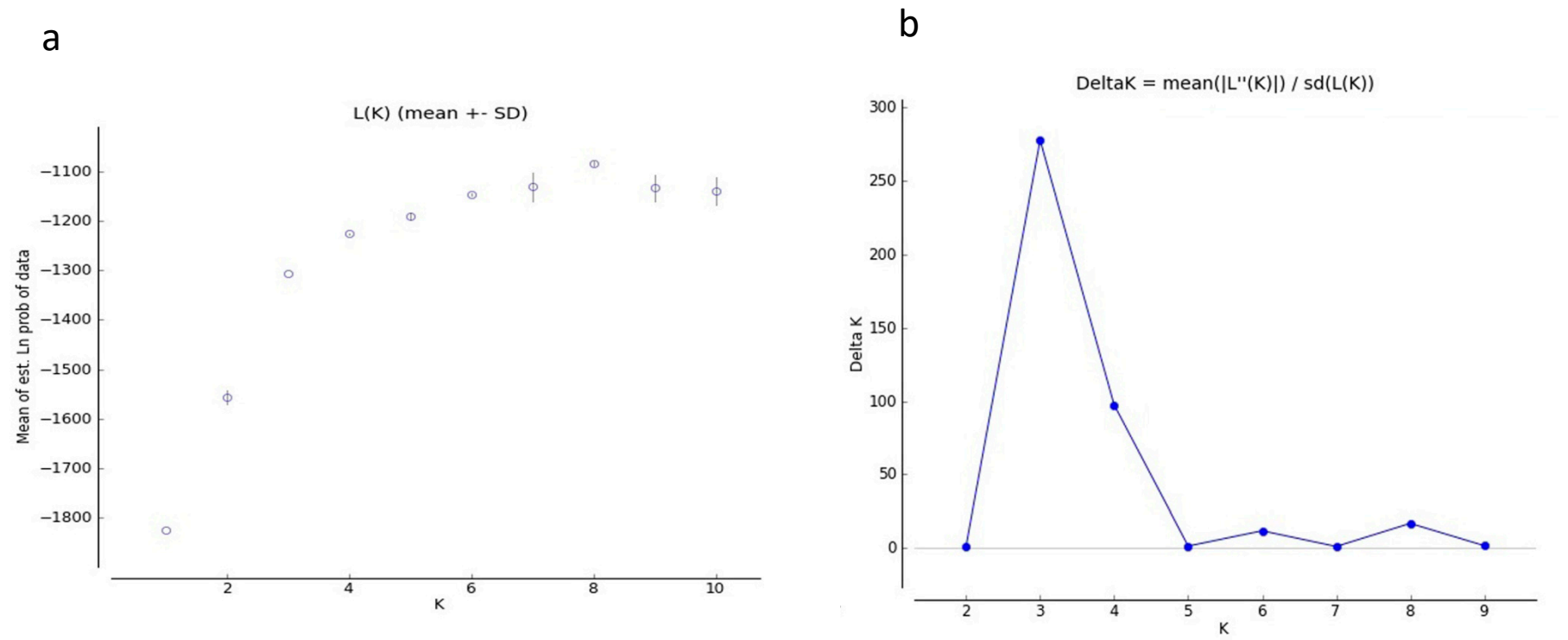


Figure S5. (a) Estimated log likelihood of the data; $\text{LnP}(D)$ over 10 repeats of STRUCTURE analysis and (b) the true value of K was obtained following the delta-K method of Evanno et al. [37].