



File 2. Figure S1. Boxplots summarizing quantitative trait results for *S. aethnensis*, *S. chrysanthemifolius*, and a reciprocal F₂ mapping family that were included in the quantitative trait locus analysis.

Trait numbers in title correspond to the trait numbering system of Table 1. Bold horizontal lines indicate median values. Boxes indicate 25 to 75 percentile range. Lines indicate the range of values within 1.5 times the upper and lower quartiles, respectively. Points indicate values more extreme than 1.5 times the upper and lower quartiles. Asterisks indicate the trait values of the mapping family parents. No mapping family parental values were available for flowering time as these individuals were vegetatively propagated for comparison with their progeny.

File 3. Figure S2. Genetic map of a reciprocal F₂ *S. aethnensis* and *S. chrysanthemifolius* mapping family showing quantitative trait loci identified by composite interval mapping and marker loci that were significantly divergent or convergent between species.

Map distances in Kosambi centiMorgans are shown in the scale bar to the left of linkage groups. Linkage groups are represented by vertical bars with mapped locus positions

indicated with horizontal lines. Weakly linked linkage groups (< 4 LOD or > 20 cM) that probably belong to the same chromosome are aligned vertically. Grey shading on linkage groups indicates regions exhibiting significant transmission ratio distortion (TRDLs). Locus names are listed to the left of linkage groups and mapped QTLs are listed to the right. “c” or “d” listed to the left of locus names indicates if that locus was identified as significantly convergent or divergent based on genetic differentiation analysis across sample populations; while > symbol to the left of locus names indicates if the locus was included in QTL analysis. QTLs were identified by composite interval mapping with significance determined if the LOD score exceeded the 0.95 quantile of 1000 data permutations. QTLs 2-LOD interval ranges are indicated with vertical lines with a bold horizontal line indicating the highest LOD score position. QTL summary information includes; trait names, “a” or “d” each followed by “+” or “-” indicating additive or dominance effects and their direction of effect supporting or opposing the observed species difference respectively, and the percent mapping family variance explained.

