Supplementary Materials for

Identification of carnivory in the flowering plant *Saxifraga* via multidisciplinary evidence

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The PDF file includes:

Figs. S1 to S5

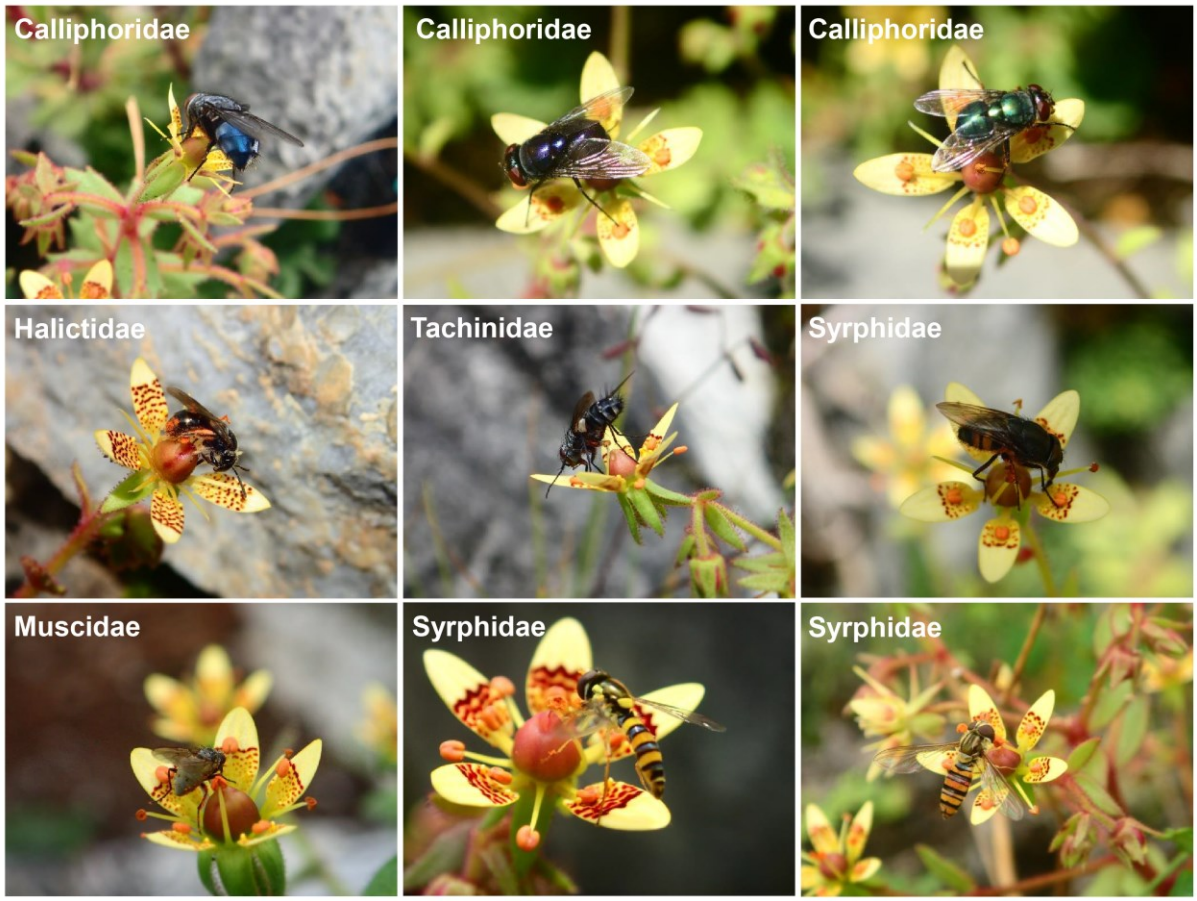

Fig. S1 Photographs of efficient pollinators of *Saxifraga candelabrum*. Voucher specimens are listed in Supplementary Data 1.

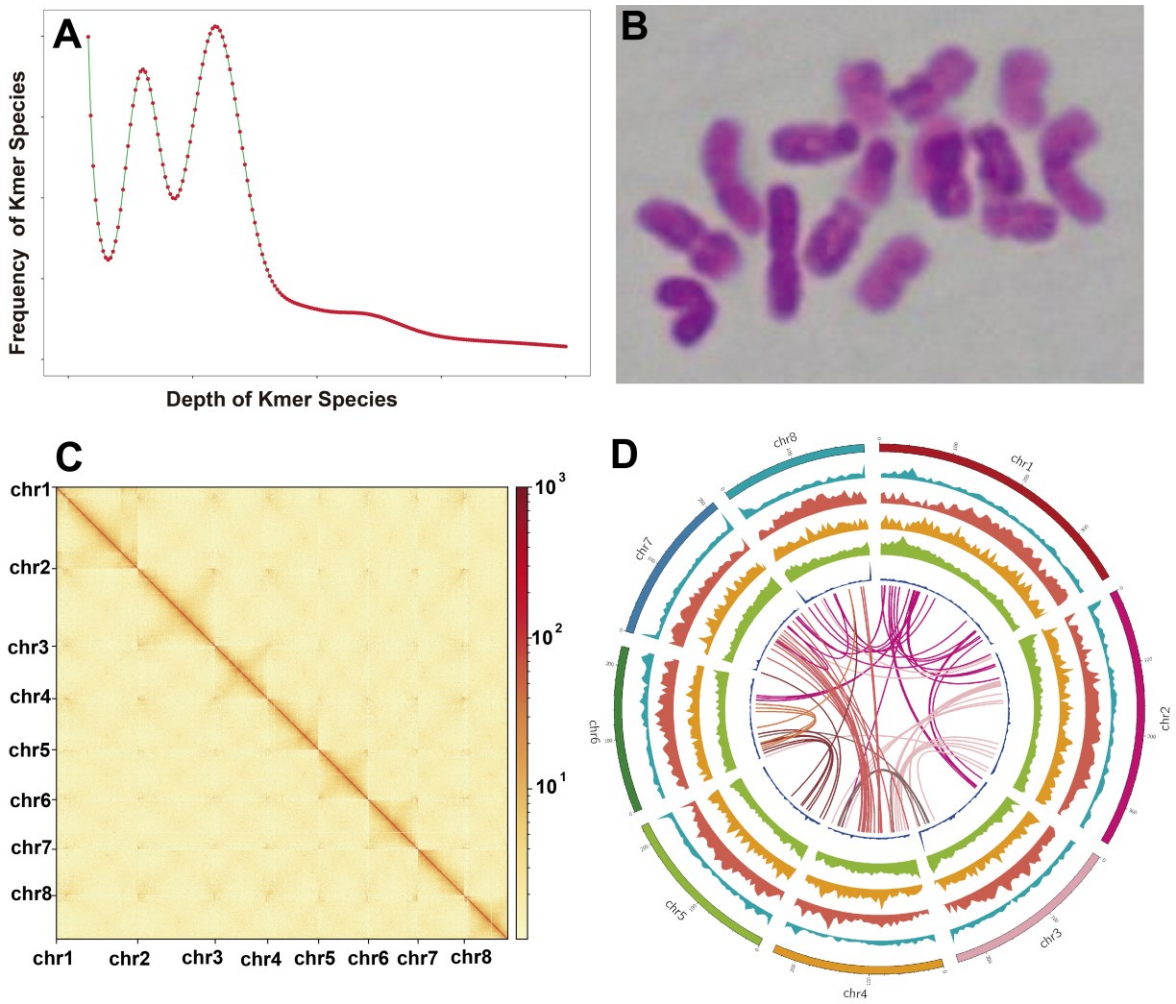

Fig. S2 *Saxifraga candelabrum* genome. (A) The 17-mer frequency distribution analysis for the genome size prediction; (B) Chromosome squash preparation ($2n = 2x = 16$) for *Saxifraga candelabrum*; (C) Hi-C contact map from all-by-all interactions of all 16 chromosomes; (D) The distribution of various repetitive sequences and gene density on each chromosome (chr1-chr8) in *Saxifraga candelabrum*. From the outer to the inner ring: the eight ($n = 8$) chromosomes, GC content, distribution of Class I TE, distribution of Class II TE, gene density, and collinear gene blocks, respectively.

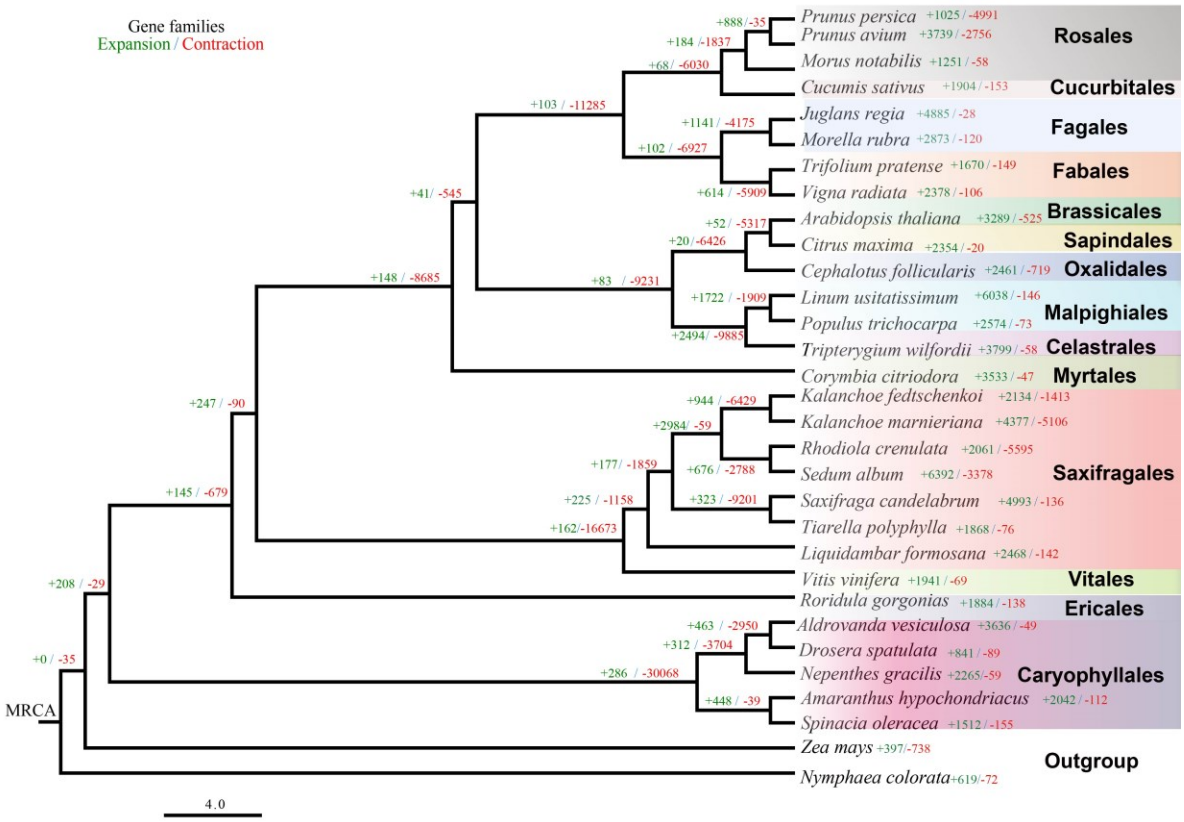

Fig. S3 Expansion and contraction of gene families for 31 species used in the current study. The ML tree was inferred from phylogenetic analysis based on orthologs obtained via OrthoFinder v2.4. Carnivorous plants are indicated by a symbol of an insect on the corresponding branch.

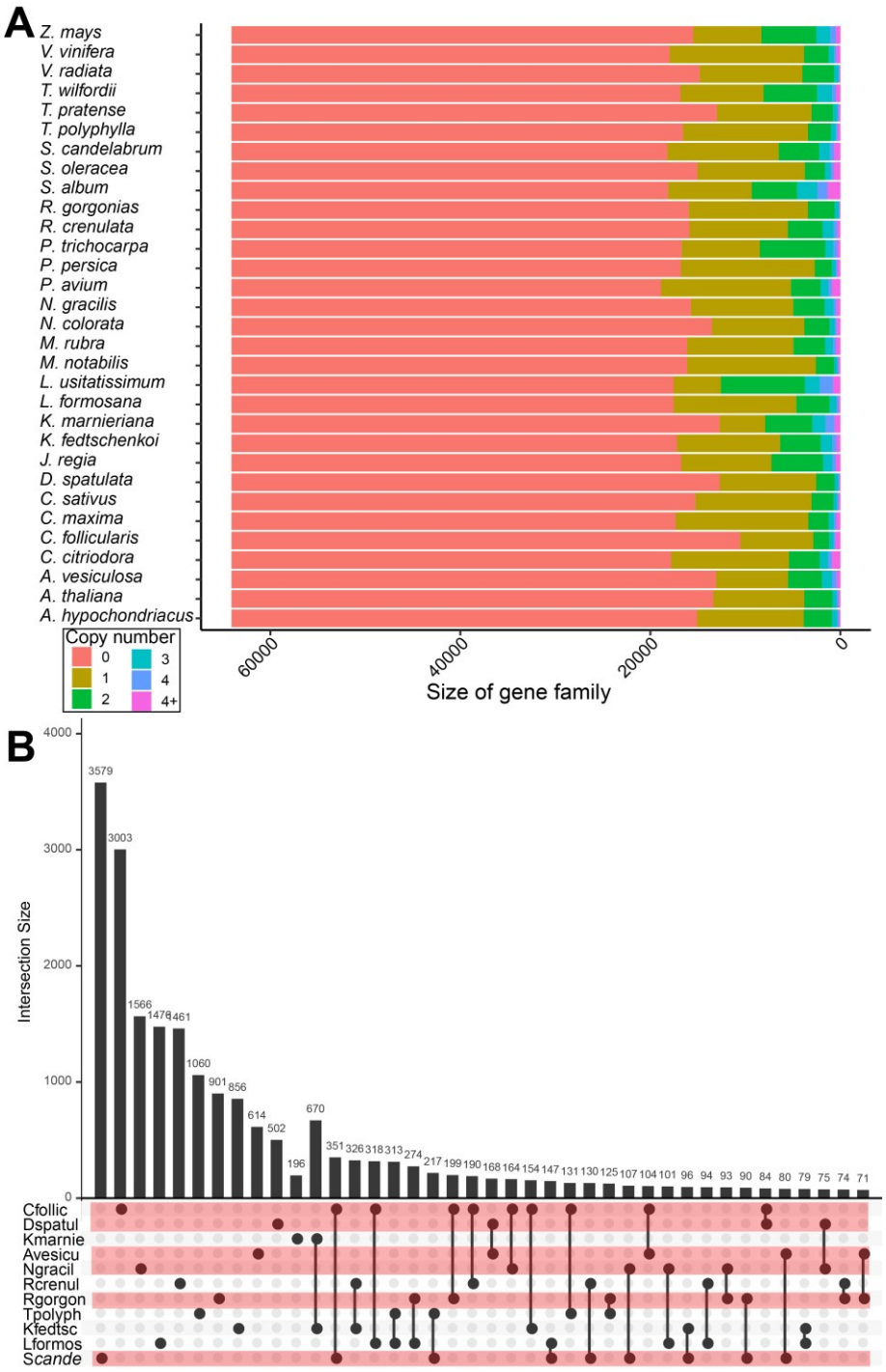

Fig. S4 (A) Gene family size of single-copy, multiple-copy, unique, and other genes identified in the *Saxifraga candelabrum* genome and other representative species. (B) Common and species-specific gene families in *Saxifraga candelabrum* and the other species examined.

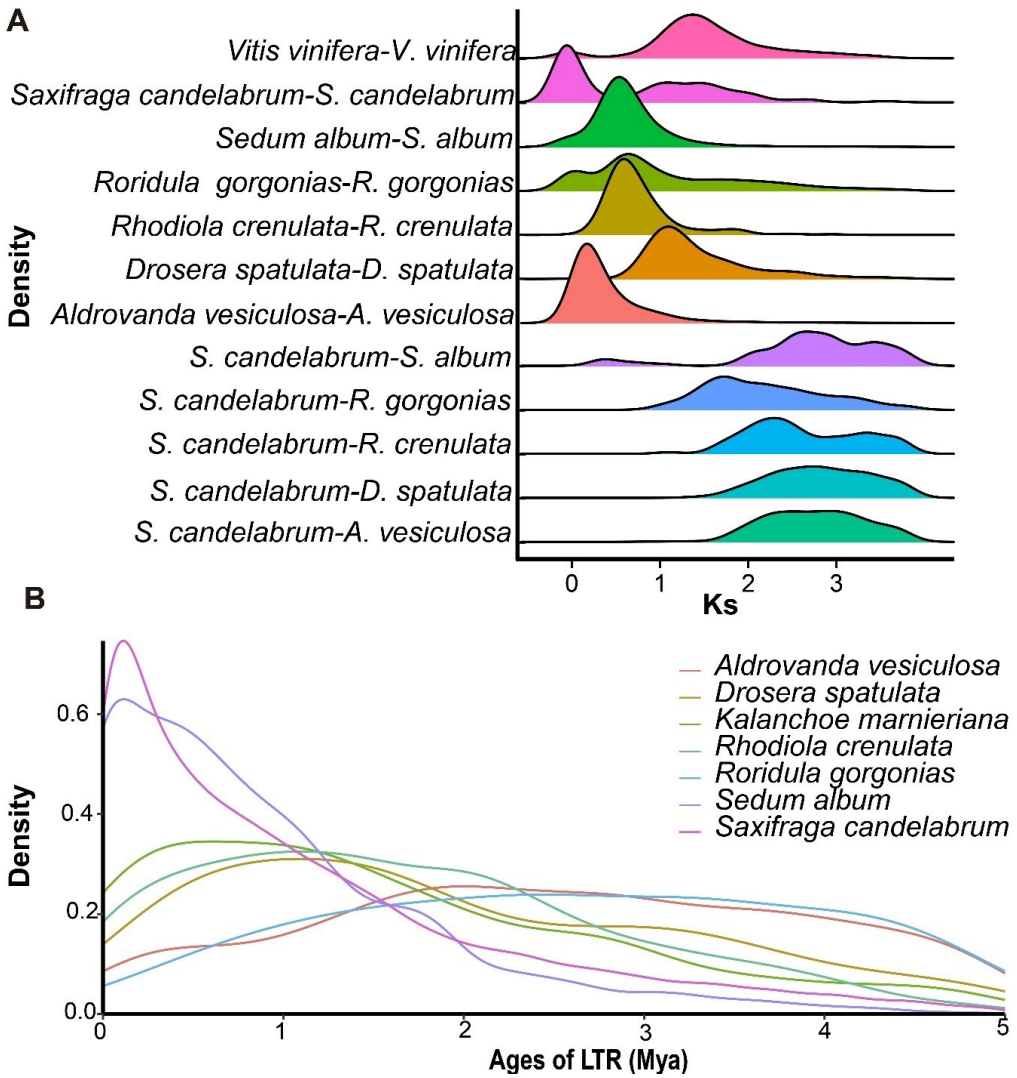

Fig. S5 Distribution of synonymous substitutions per synonymous site (Ks) and the estimated insertion time for LTR retrotransposons. (A) The distributions of synonymous substitutions per synonymous site (*K*s) across *Saxifraga candelabrum* and other related species. The peak close to Ks = 0 is a false indicator of a whole genome duplication event that is not supported by the chromosome collinearity analysis; (B) The insertion times were calculated for LTR retrotransposons in *Saxifraga candelabrum* and other related species based on the formula T = K/2r (T: insertion time, r: synonymous mutations/site/Myr, K: divergence between the two LTRs)