

Descriptions of Additional Supplementary Data files

Supplementary Data 1 Detailed information for the insects found on glandular hairs and the flower-visiting insects of *Saxifraga candelabrum* based on field observations from the Qinghai-Tibet Plateau-Hengduan Mountains. Insects categorized as “prey” are flower visitors captured by glandular hairs, whereas “uncaptured visitors” are flower visitors not captured. All insect voucher specimens were deposited in the National Animal Collection Resource Center (NACRC), Institute of Zoology, Chinese Academy of Sciences. When the identity of the specimen was unclear, no genus or in some cases no species name is given. Insects were identified by Dr. Lishen Qian (Kunming Botanical Garden, Kunming Institute of Botany, Chinese Academy of Sciences) and Drs. Lili Shao and Kuiyan Zhang (Institute of Zoology, Chinese Academy of Sciences).

Supplementary Data 2 Number of prey insects adhering to glandular hairs on historical specimens of *Saxifraga candelabrum* from the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN). NA=Not available.

Supplementary Data 3 Floral volatile components detected in *Saxifraga candelabrum*. The volatile compounds listed were identified through GC-MS analysis and compared with the results from air samples and non-flowering *S. candelabrum* individuals. Only compounds with a match score (Qualitative) ≥ 80 were retained to ensure reliable compound identification. SC1–SC3 represent three individual plants of *S. candelabrum*, each with three technical replicates (-1 to -3).

Supplementary Data 4 Raw data of $\delta^{15}\text{N}$ values for all plant tissues measured in the isotopic experiments. Data include different species, organs, localities, treatment durations, and treatments with either ^{15}N -labeled or unlabeled *Drosophila* (as control). SC: *S. candelabrum*; NPH: Napahai; WFS: Wufeng Mountain; SZL: Songzanlin-Lamasery.

Supplementary Data 5 Species used for building genome dataset examined as part of the current study. The six carnivorous plants examined are indicated by an asterisk (*) following their species names. A total of 31 species were included in our study, consisting of *Saxifraga candelabrum* and 30 other species. We included *Saxifraga candelabrum* and all six available genomes from representative species from Saxifragales, 15 representative species from various clades of rosids, five available (published) representative carnivorous species, two non-carnivorous species in Caryophyllales and two species for outgroups (*Vitis vinifera* and *Zea mays*). The data resource was download from online genome databases. (*) indicates carnivorous plants)

Supplementary Data 6 Statistics of sequencing data obtained using the Illumina platform for assembly of the *Saxifraga candelabrum* genome.

Supplementary Data 7 Statistics of sequencing data for *Saxifraga candelabrum* generated using the PacBio HiFi platform.

Supplementary Data 8 Statistics of sequencing data for *Saxifraga candelabrum* generated using the PacBio Hi-C platform.

Supplementary Data 9 The assembled length and contig number of each chromosome of the *Saxifraga candelabrum* genome.

Supplementary Data 10 The statistics map_rate and read coverage of the *Saxifraga candelabrum* genome.

Supplementary Data 11 The summary of BUSCO assessment of the *Saxifraga candelabrum* genome.

Supplementary Data 12 The statistics of the repeat sequence classification of the *Saxifraga candelabrum* genome.

Supplementary Data 13 Summary of gene prediction of the *Saxifraga candelabrum* genome from three approaches: De novo prediction (D), Homology-based annotation (H), and Transcriptome evidence (S).

Supplementary Data 14 Statistics of gene functional annotations of the *Saxifraga candelabrum* genome.

Supplementary Data 15 Gene family statistics in *Saxifraga candelabrum* and other plant genomes used in this study. The six carnivorous plants examined are indicated by an asterisk (*) following their species names. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 16 Enriched GO terms of convergently expanded gene families in three carnivorous plants with “flypaper” traps (*Saxifraga candelabrum*, *Drosera spatulata*, and *Roridula gorgonias*). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 17 Enriched GO terms of convergently expanded gene families in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Drosera spatulata* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 18 Enriched GO terms of convergently expanded gene families in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Roridula gorgonias* (Roridulaceae). BP, MF and CC are corresponding to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 19 Enriched GO terms of convergently expanded gene families in *Saxifraga candelabrum* and a carnivorous plant with a pitcher trap, *Cephalotus follicularis* (Cephalotaceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was

assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 20 Enriched GO terms of convergently expanded gene families in *Saxifraga candelabrum* and a carnivorous plant with a pitcher trap, *Nepenthes gracilis* (Nepenthaceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 21 Enriched GO terms of convergently expanded gene families in *Saxifraga candelabrum* and a carnivorous plant with a snap trap, *Aldrovanda vesiculosa* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 22 List of Gene Ontology (GO) terms of genes under convergent acceleration in three carnivorous plants with “flypaper” traps (*Saxifraga candelabrum*, *Drosera spatulata*, and *Roridula gorgonias*). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 23 Enriched GO terms of genes under convergently accelerated rate evolution in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Drosera spatulata* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 24 Enriched GO terms of genes under convergently accelerated rate evolution in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Roridula gorgonias* (Roridulaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 25 Enriched GO terms of genes under convergently accelerated rate evolution in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Cephalotus follicularis* (Cephalotaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 26 Enriched GO terms of genes under convergently accelerated rate evolution in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Nepenthes gracilis* (Nepenthaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was

assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 27 Enriched GO terms of genes under convergently accelerated rate evolution in *Saxifraga candelabrum* and another carnivorous plant with a snap trap, *Aldrovanda vesiculosa* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 28 List of Gene Ontology (GO) terms of genes under convergently accelerated rate evolution in all six carnivorous species. BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 29 List of Gene Ontology (GO) terms for genes experiencing positive selection in three carnivorous plants with “flypaper” traps (*Saxifraga candelabrum*, *Drosera spatulate*, and *Roridula gorgonias*). BP, MF and CC are corresponds to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 30 List of Gene Ontology (GO) terms for genes experiencing positive selection in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Drosera spatulata* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 31 List of Gene Ontology (GO) terms for genes experiencing positive selection in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Roridula gorgonias* (Roridulaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 32 List of Gene Ontology (GO) terms for genes experiencing positive selection in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Cephalotus follicularis* (Cephalotaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 33 List of Gene Ontology (GO) terms for genes experiencing positive selection in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Nepenthes gracilis* (Nepenthaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively.

Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 34 List of Gene Ontology (GO) terms for genes experiencing positive selection in *Saxifraga candelabrum* and another carnivorous plant with a snap trap, *Aldrovanda vesiculosa* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 35 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in three carnivorous plants with a “flypaper” trap (*Saxifraga candelabrum*, *Drosera spatulata*, and *Roridula gorgonias*). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 36 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Drosera spatulata* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 37 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Roridula gorgonias* (Roridulaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 38 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Cephalotus follicularis* (Cephalotaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 39 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Nepenthes gracilis* (Nepenthaceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 40 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in *Saxifraga candelabrum* and another carnivorous plant with a snap trap, *Aldrovanda vesiculosa* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 41 List of Gene Ontology (GO) terms for genes suggested by FADE (FUBAR Approach to Directional Evolution) with convergent amino acid substitutions in all six carnivorous species. BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 42 List of Gene Ontology (GO) terms for gene families convergently contracted in three carnivorous plants with “flypaper” traps (*Saxifraga candelabrum*, *Drosera spatulata*, and *Roridula gorgonias*). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 43 List of Gene Ontology (GO) terms for genes convergently contracted in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Drosera spatulata* (Droseraceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 44 List of Gene Ontology (GO) terms for gene families convergently contracted in *Saxifraga candelabrum* and another carnivorous plant with a “flypaper” trap, *Roridula gorgonias* (Roridulaceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 45 List of Gene Ontology (GO) terms for gene families convergently contracted in *Saxifraga candelabrum* and another carnivorous plant with a pitcher trap, *Cephalotus follicularis* (Cephalotaceae). BP, MF and CC correspond to biological process, molecular function and cellular component, respectively. Enrichment significance was assessed using a one-sided hypergeometric test, with p-values adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Supplementary Data 46 List of convergently lost genes in six carnivorous species; genes are putatively related to root development, photosynthesis, and kinetochore formation.

Supplementary Data 47 Previously published genomic datasets used in this study.