Data collection

To encompass a broad range of *Asteraceae* species, we compiled 132 genome assembly datasets from 74 species sourced primarily from the National Center for Biotechnology Information (NCBI) (1), National Genomics Data Center (NGDC) (2), and European Bioinformatics Institute (EBI) (3). These include well-known species like sunflower (4), lettuce (5), cultivated *Chrysanthemum* (6), and *Artemisia annua* (7), with 76 genomes assembled at the chromosome level. Additionally, we collected 3,897 RNA-seq libraries for 44 species from NCBI’s SRA database, which were utilized for genetic variation analysis and co-expression network construction.

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