

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Comparisons of genome assemblies and annotations among sequenced Asteraceae species.

File Name: Supplementary Data 2

Description: General statistics of predicted protein-coding genes.

File Name: Supplementary Data 3

Description: The detailed genome information of 15 species used for comparative genomic analysis in this study.

File Name: Supplementary Data 4

Description: Enriched GO terms and KEGG pathways for gene families expanded in *C. morifolium*.

File Name: Supplementary Data 5

Description: Summary of the mapping ratio of 12 *Chrysanthemum* wild species.

File Name: Supplementary Data 6

Description: Genomic similarity of cultivated chrysanthemum and 12 *Chrysanthemum* wild species by identify score analysis.

File Name: Supplementary Data 7

Description: Gene retention ratios between *C. nankingense* and *C. seticuspe* in the *C. morifolium* genome.

File Name: Supplementary Data 8

Description: Oligonucleotide probes used for FISH analysis in this study

File Name: Supplementary Data 9

Description: Enriched GO terms for balanced genes in *C. morifolium* genome.

File Name: Supplementary Data 10

Description: List of 105 MADS-box genes identified in *C. morifolium*.

File Name: Supplementary Data 11

Description: Consensus QTLs for petal type via BSA-seq analysis.

File Name: Supplementary Data 12

Description: The identified auxin related genes via BSA-seq and WGCNA analyses.

File Name: Supplementary Data 13

Description: Enriched GO terms for genes within hot spots SNP distribution regions in *C. morifolium* genome.