

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Statistics of the enriched gene ontology (GO) terms based on the retention genes in the triplicated genomic regions of different species

File Name: Supplementary Data 2

Description: Statistics of the preferential retention genes in the triplicated genomic regions of *Lactuca sativa* var. *angustana*

File Name: Supplementary Data 3

Description: Statistics of the preferential retention genes in the triplicated genomic regions of *Cynara*

File Name: Supplementary Data 4

Description: Statistics of the preferential retention genes in the triplicated genomic regions of *Helianthus annuus*

File Name: Supplementary Data 5

Description: Statistics of the preferential retention genes in the triplicated genomic regions of *Mikania*

File Name: Supplementary Data 6

Description: Statistics of the LTR retrotransposons identified in the surveyed genomes

File Name: Supplementary Data 7

Description: Statistics of the enriched InterPro entries associated with repetitive DNA elements in the Asteraceae species

File Name: Supplementary Data 8

Description: Prediction of genes inserted with repeat sequences in the Asteraceae family

File Name: Supplementary Data 9

Description: Prediction of transcription factor binding site (TFBS) introduced by repeat sequences in the Asteraceae family

File Name: Supplementary Data 10

Description: Statistics of the transcription factor binding site (TFBS) introduced by repeat sequences with top ten occurrence

File Name: Supplementary Data 11

Description: Statistics of the enriched Interpro entries in Asteraceae

File Name: Supplementary Data 12

Description: Statistics of lineage-specific orthogroups in Asteraceae

File Name: Supplementary Data 13

Description: The lineage-specific genes of Asteraceae family related to stress-related genes

File Name: Supplementary Data 14

Description: Distribution of PII gene in all the species in OneKP project

File Name: Supplementary Data 15

Description: Summary of the primer sequences used in this study