

Figure S1. Heatmap of correlation between samples under different chilling stress for *Sphagneticola calendulacea* (a), F1(b), and *S. trilobata* (c) using Pearson's correlation coefficient calculated from the log-transformed raw reads counting per transcripts; Hierarchical clustering dendrogram of expression levels for *S. calendulacea* (d), F1 (e), and *S. trilobata* (f) under different chilling stress. T1, T2, T3 represents 30°C, 16°C, 4°C indicated with red bar, yellow bar, and blue bar, respectively. *S. calendulacea* and *S. trilobata* abbreviated as *Spc*, and *Spt* respectively, and the following numbers mark different biological replicates.

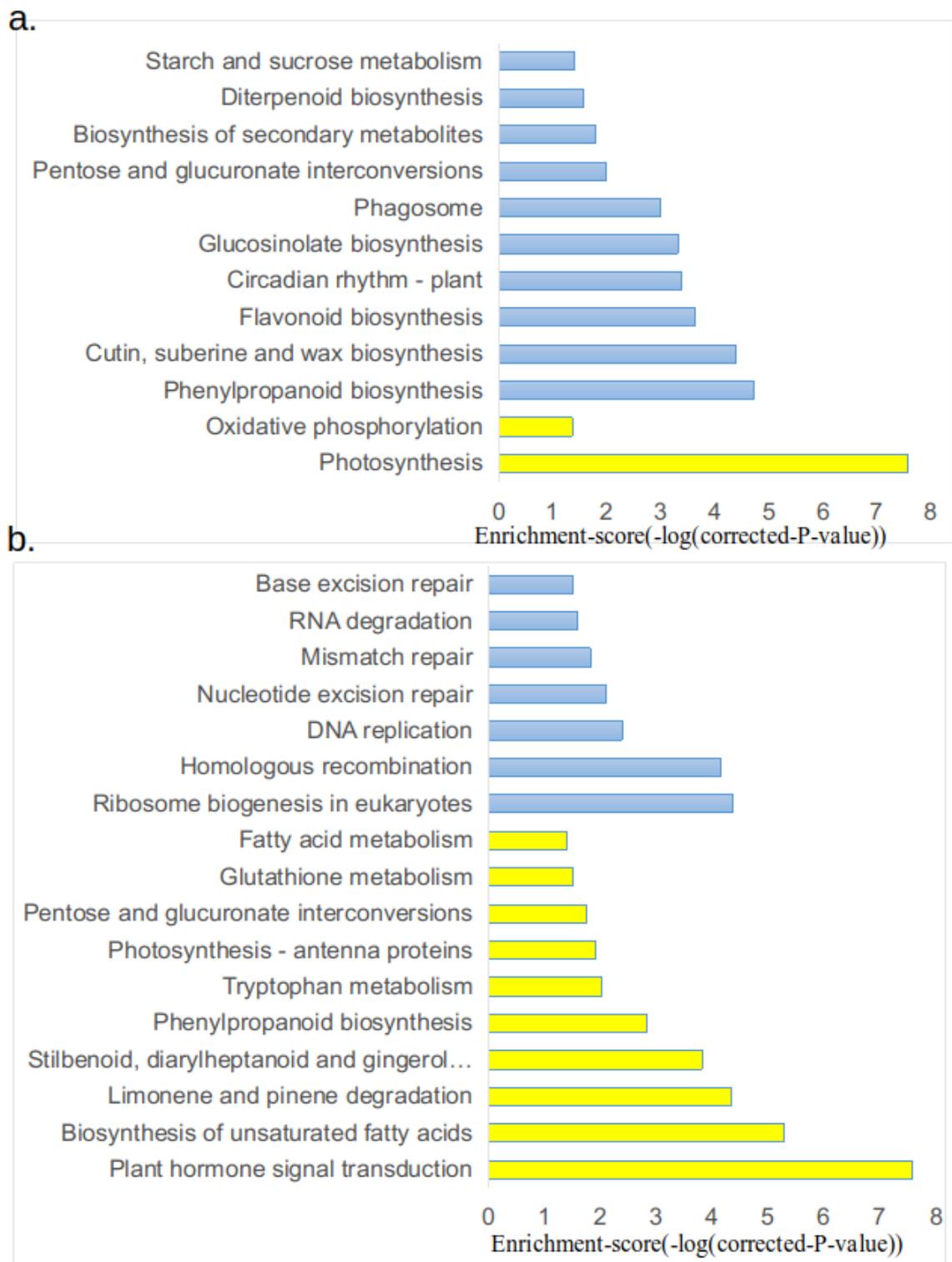


Figure S2. Significantly enriched KEGG pathways for the differentially expressed transcripts in *Sphagneticola calendulacea* under chilling stress from 30°C to 16°C (a) and 16°C and 4°C (b). The yellow bar and blue bar showed the enrichment scores of down-regulated pathways and up-regulated pathways respectively.

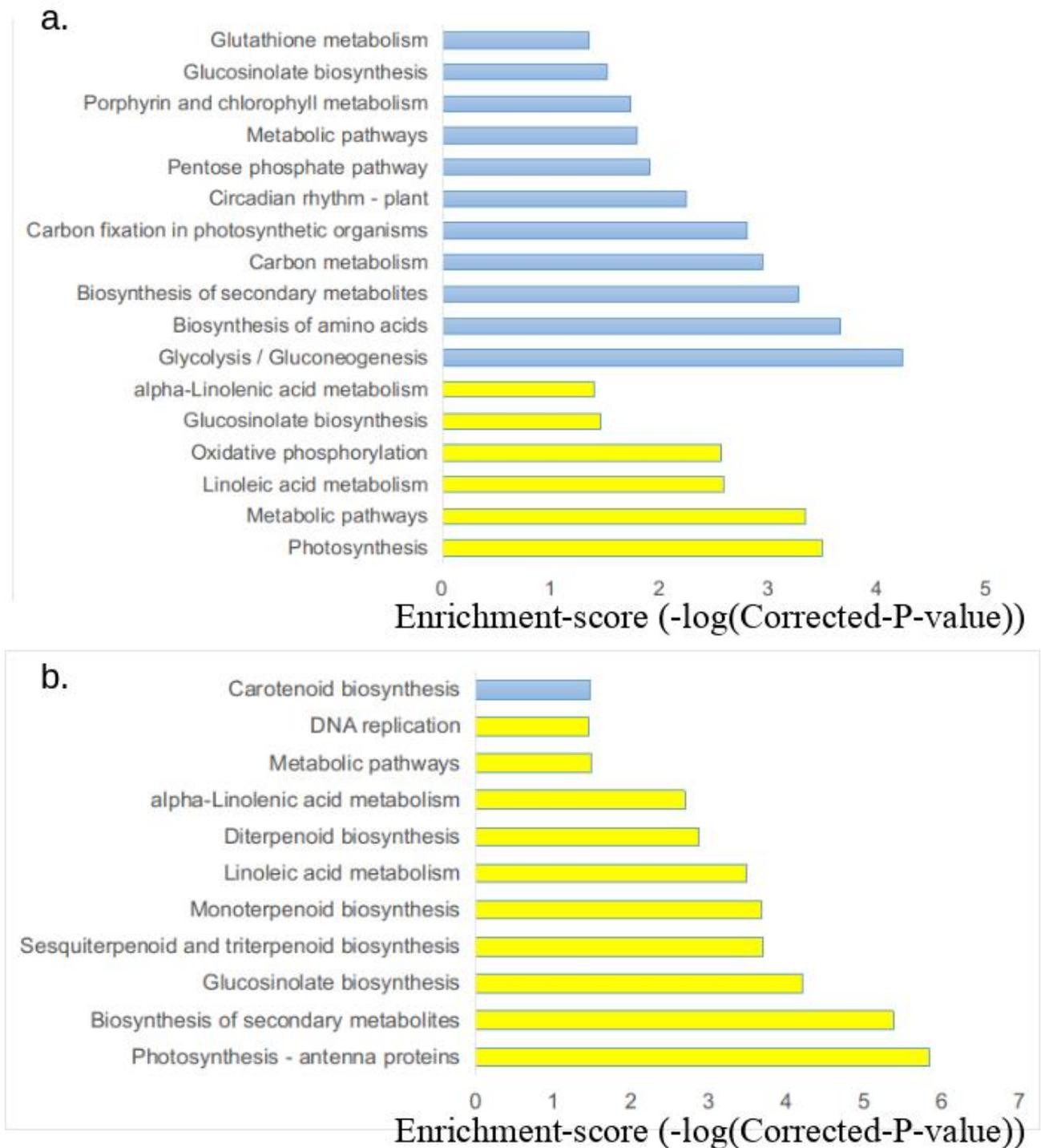


Figure S3. Significantly enriched KEGG pathways for the differentially expressed transcripts in *Sphagneticola trilobata* under chilling stress from 30°C to 16°C (a) and 16°C and 4°C (b). The yellow bar and blue bar showed the enrichment scores of down-regulated pathways and up-regulated pathways respectively.

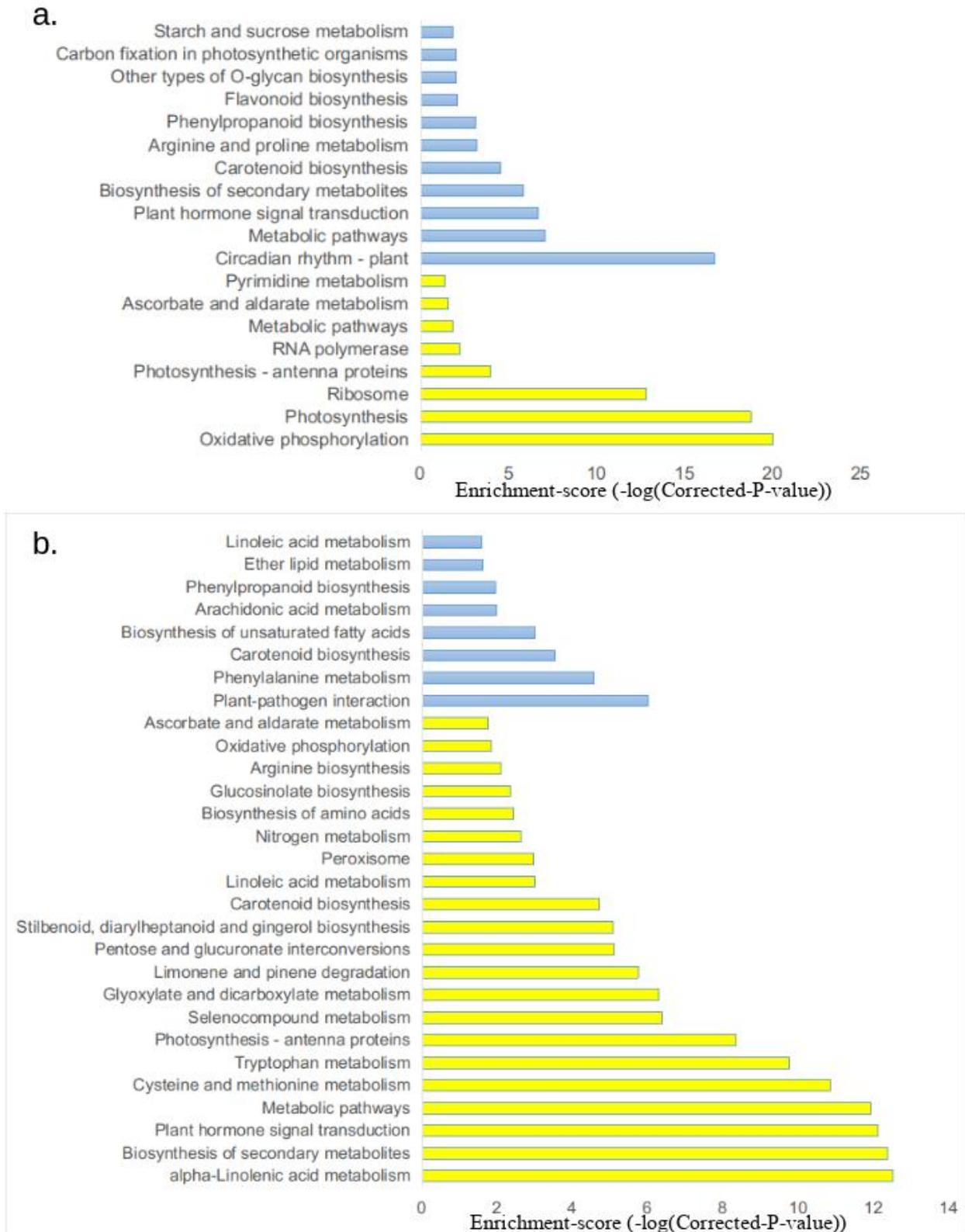


Figure S4. Significantly enriched KEGG pathways for the differentially expressed transcripts in F1s under chilling stress from 30°C to 16°C (a) and 16°C and 4°C (b). The yellow bar and blue bar showed the enrichment scores of down-regulated pathways and up-regulated pathways respectively.

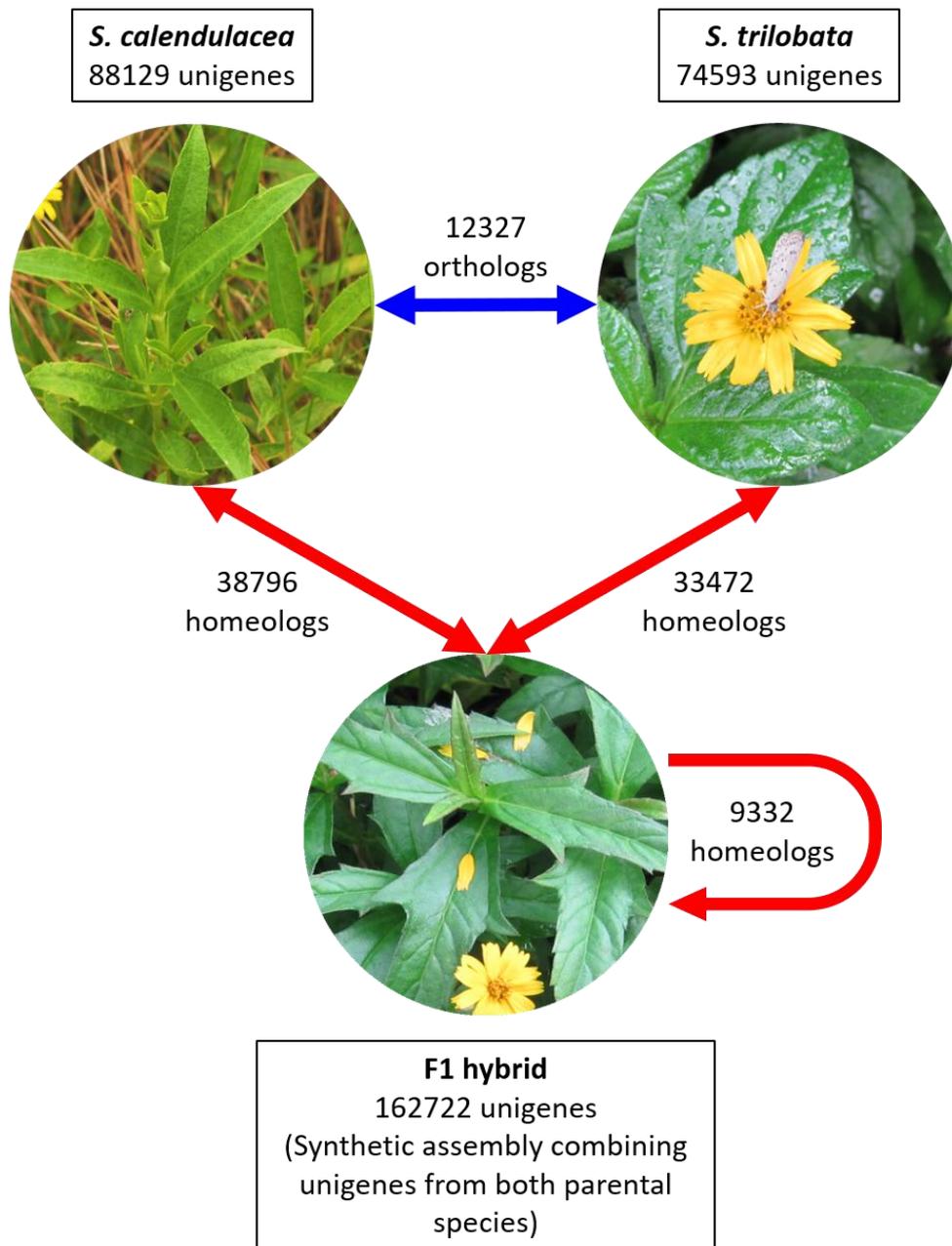


Figure S5. Relationships of orthologs and homeologs among the parental species and the F1 hybrid.