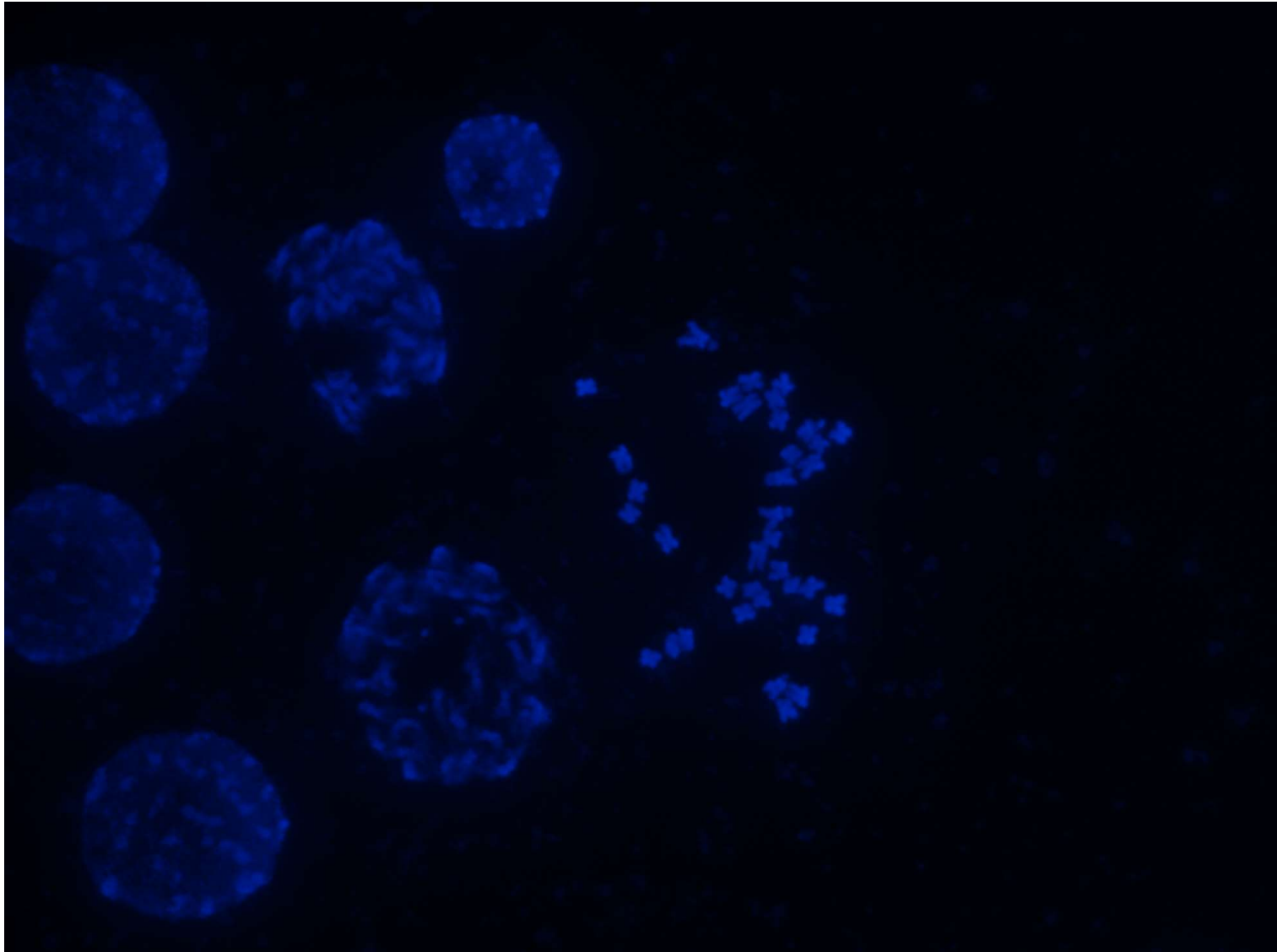


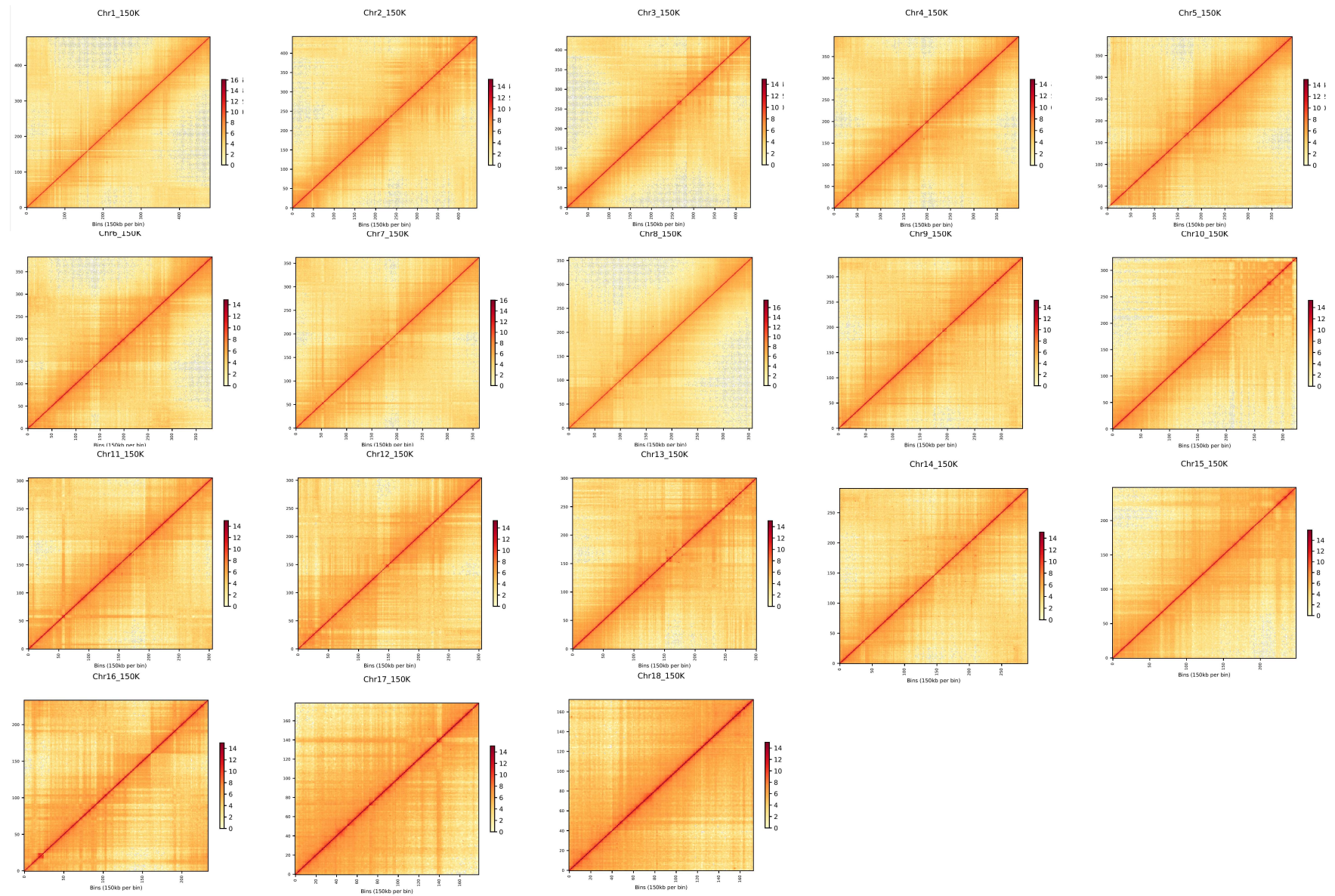
Supplementary Figure 1 The estimated genome size of *Hibiscus cannabinus* was 1000 Mb by flow cytometry .
 (a)The flow cytometry figure of *A. thaliana* leaf shown four peaks: 2C=25, 4C=50, 8C=102, 16C=200. (b) The flow cytometry figure shown the 2C peaks of *Hibiscus cannabinus* leaf : 2C=195. The genome size of *A. thaliana* is 125 MB.

(a) *Arabidopsis thaliana* 2C=25

(b) *Hibiscus cannabinus* 2C=195

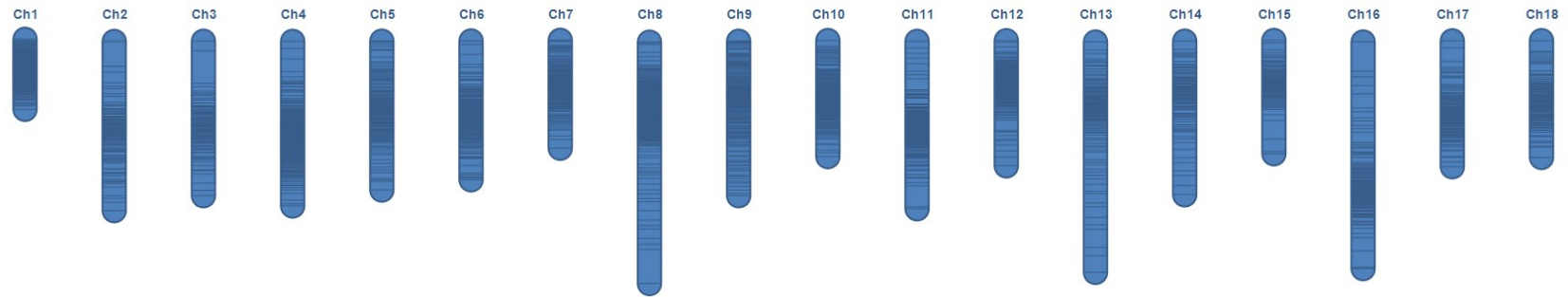
Supplementary Figure 2 karyotype analysis using FISH (fluorescence in situ hybridization) in *H. cannabinus*



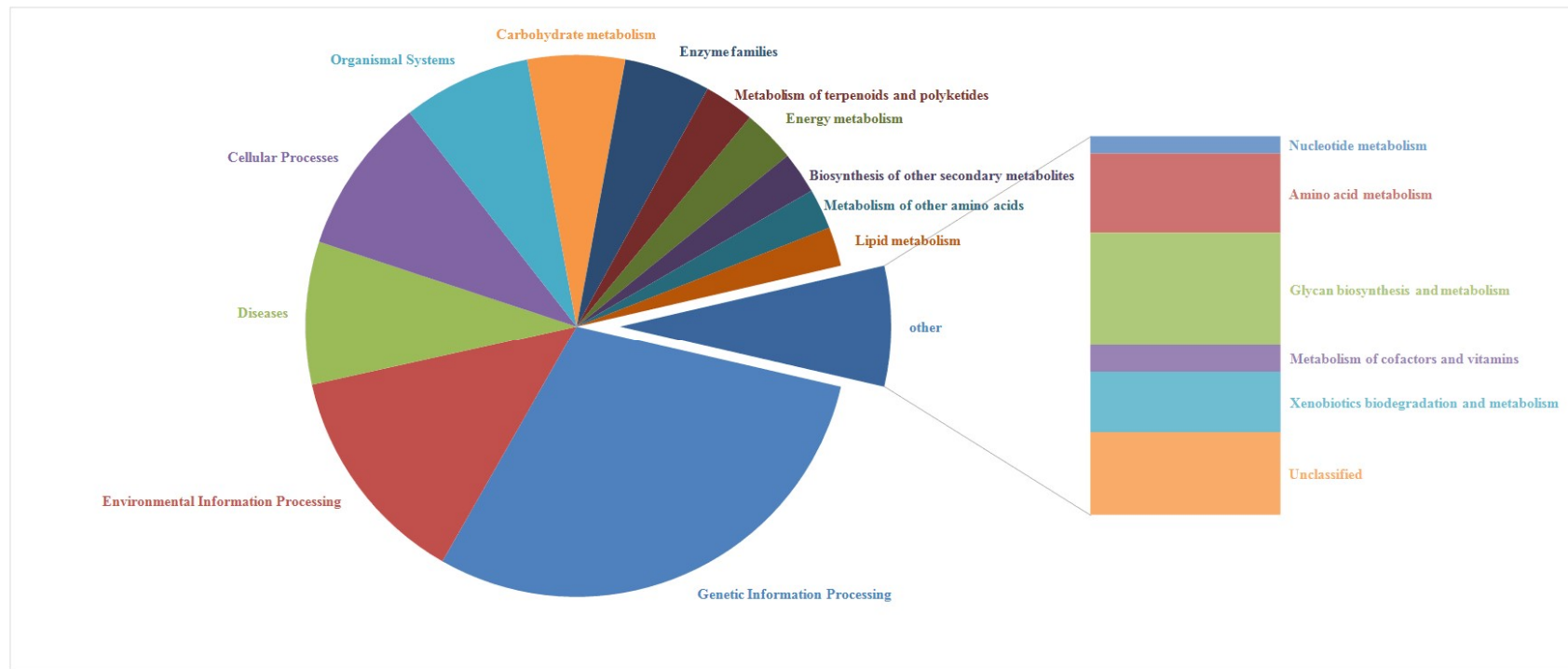


Supplementary Figure 3 HiC maps of 18 chromosomes using 150 k resolution in *H. cannabinus*

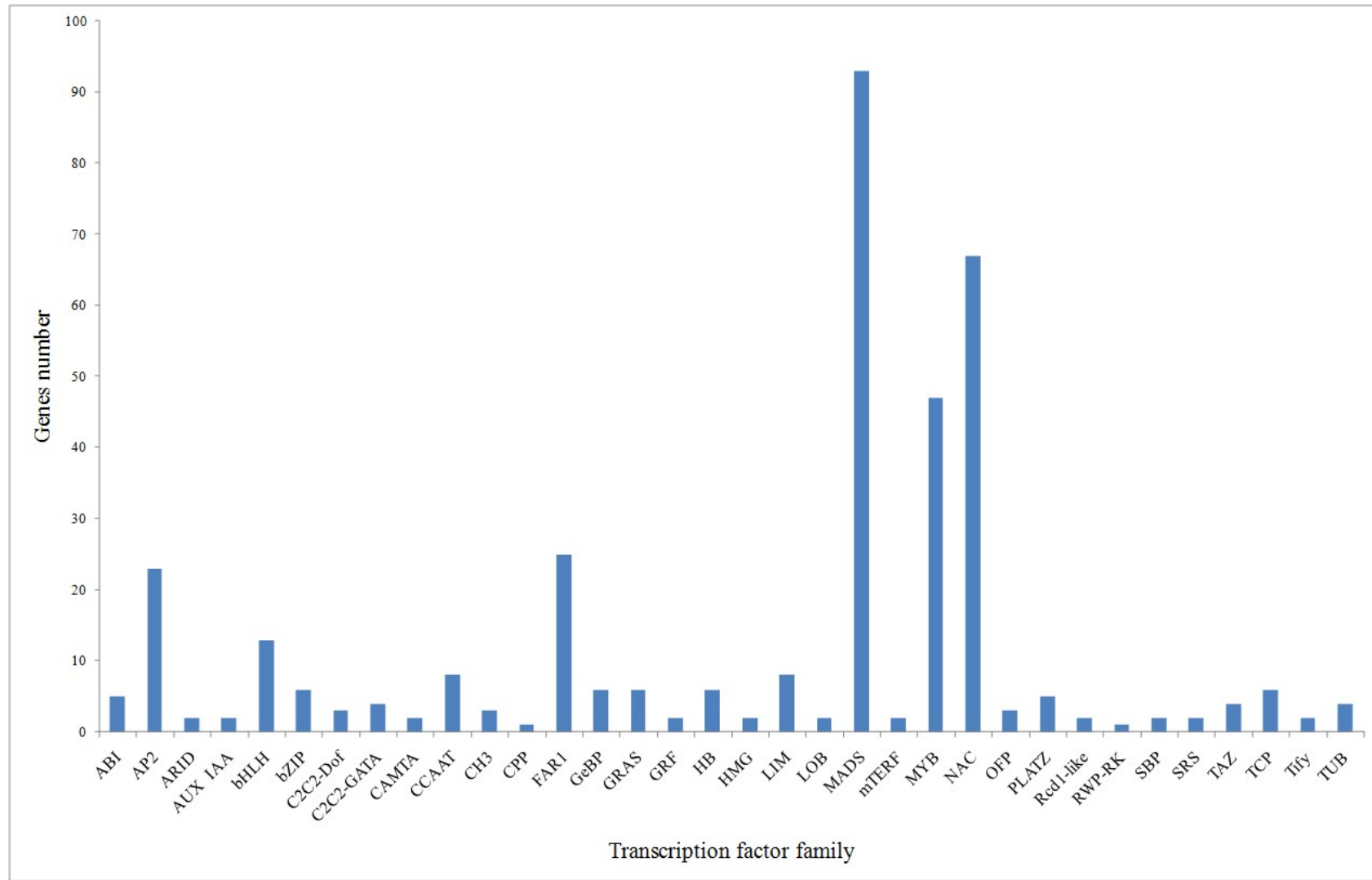
Supplementary Figure 4 High-resolution SNP genetic map based on a F2 population derived from a cross between 'Fuhong 952' and 'Zanyin No. 1' in *H. cannabinus*

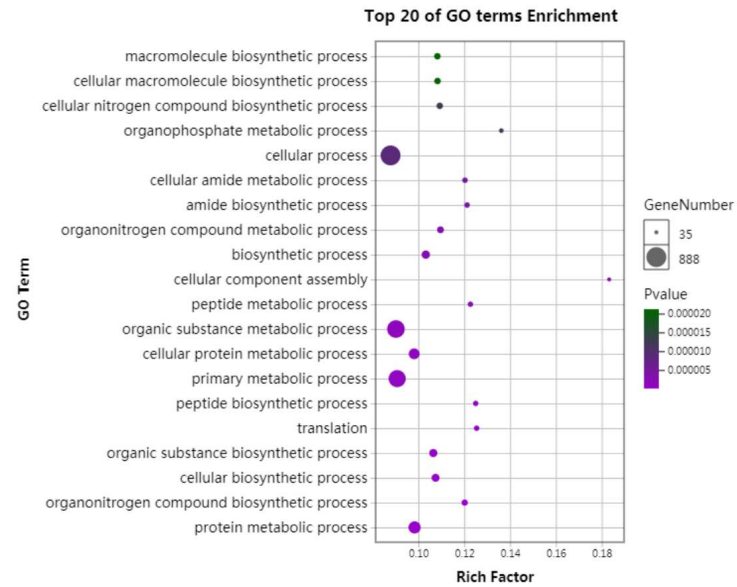


Supplementary Figure 5 Frequency of KEGG pathway for specific *H. cannabinus* genes



Supplementary Figure 6 Gene numbers of *H. cannabinus* transcription factors





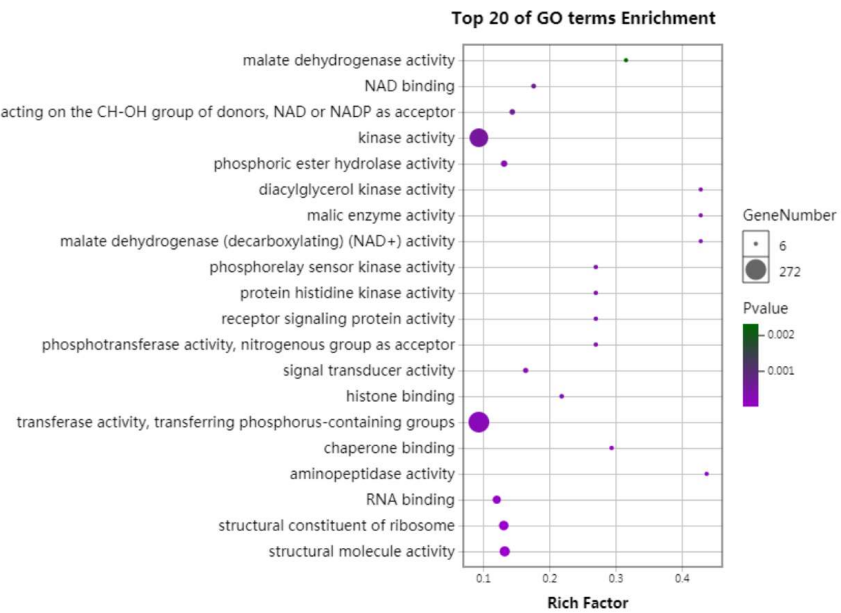
Biological process

oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor

Supplementary Figure 7

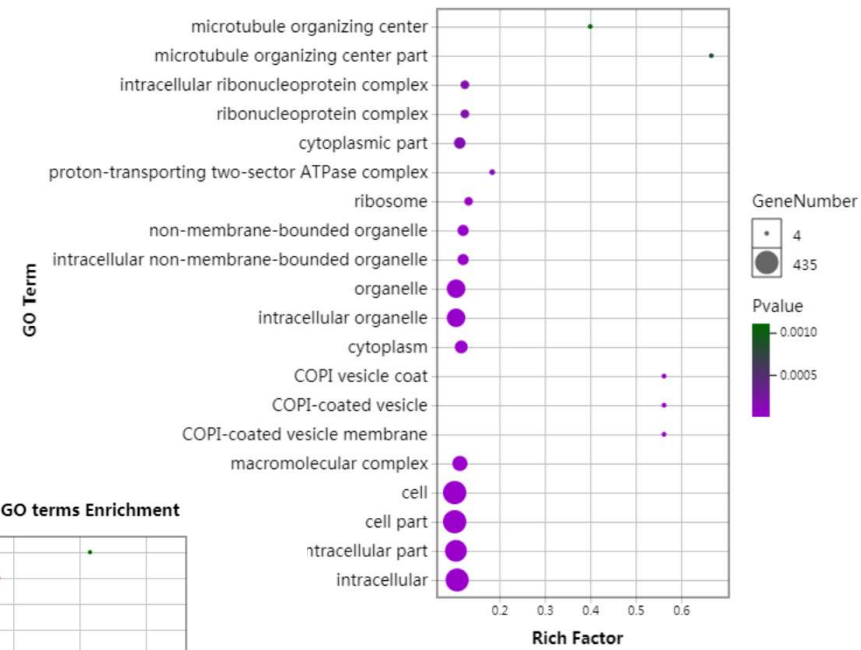
GO enrichments of duplicated genes after WGD in *H. cannabinus*

GO Term



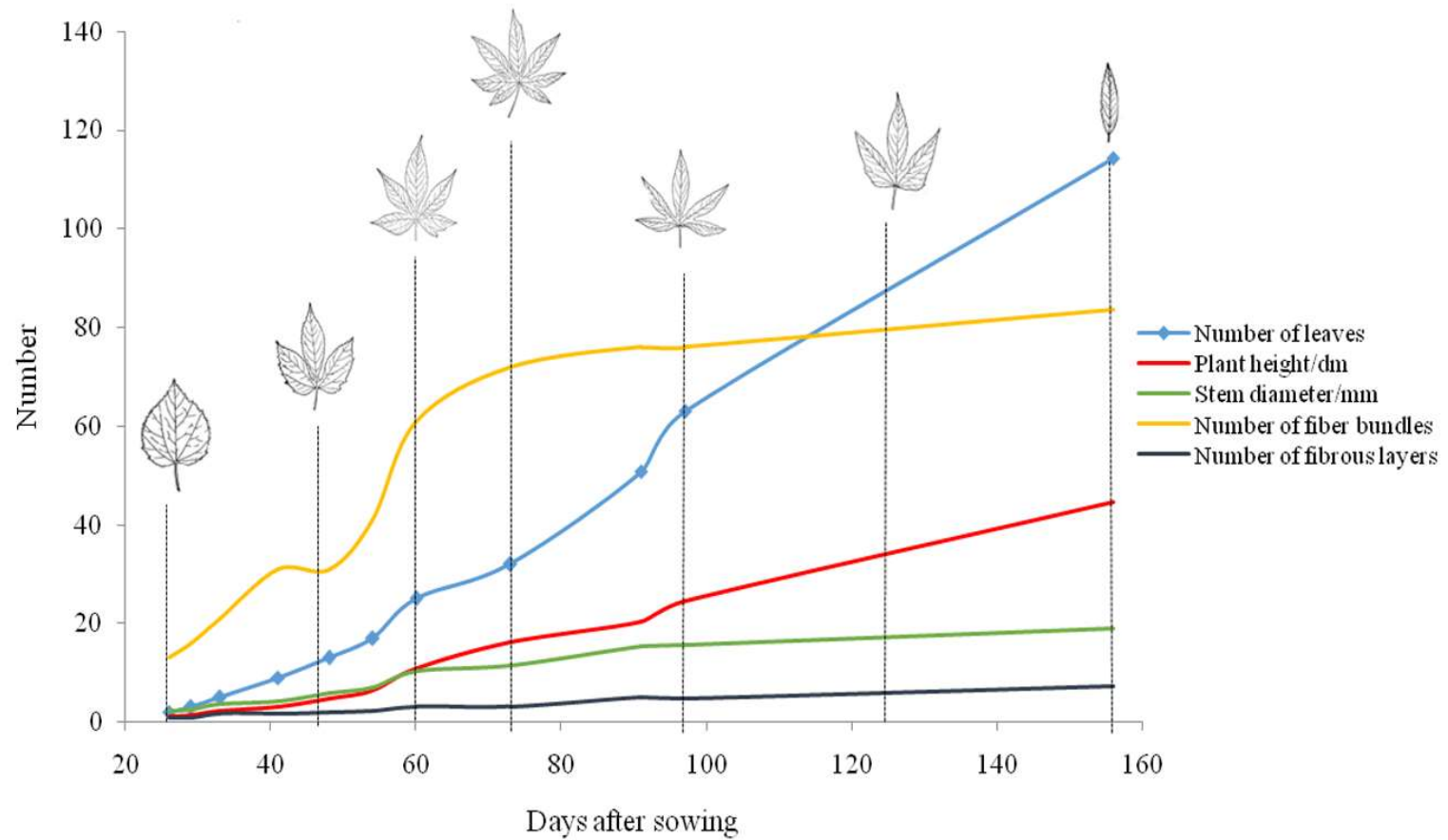
Molecular Function

Top 20 of GO terms Enrichment

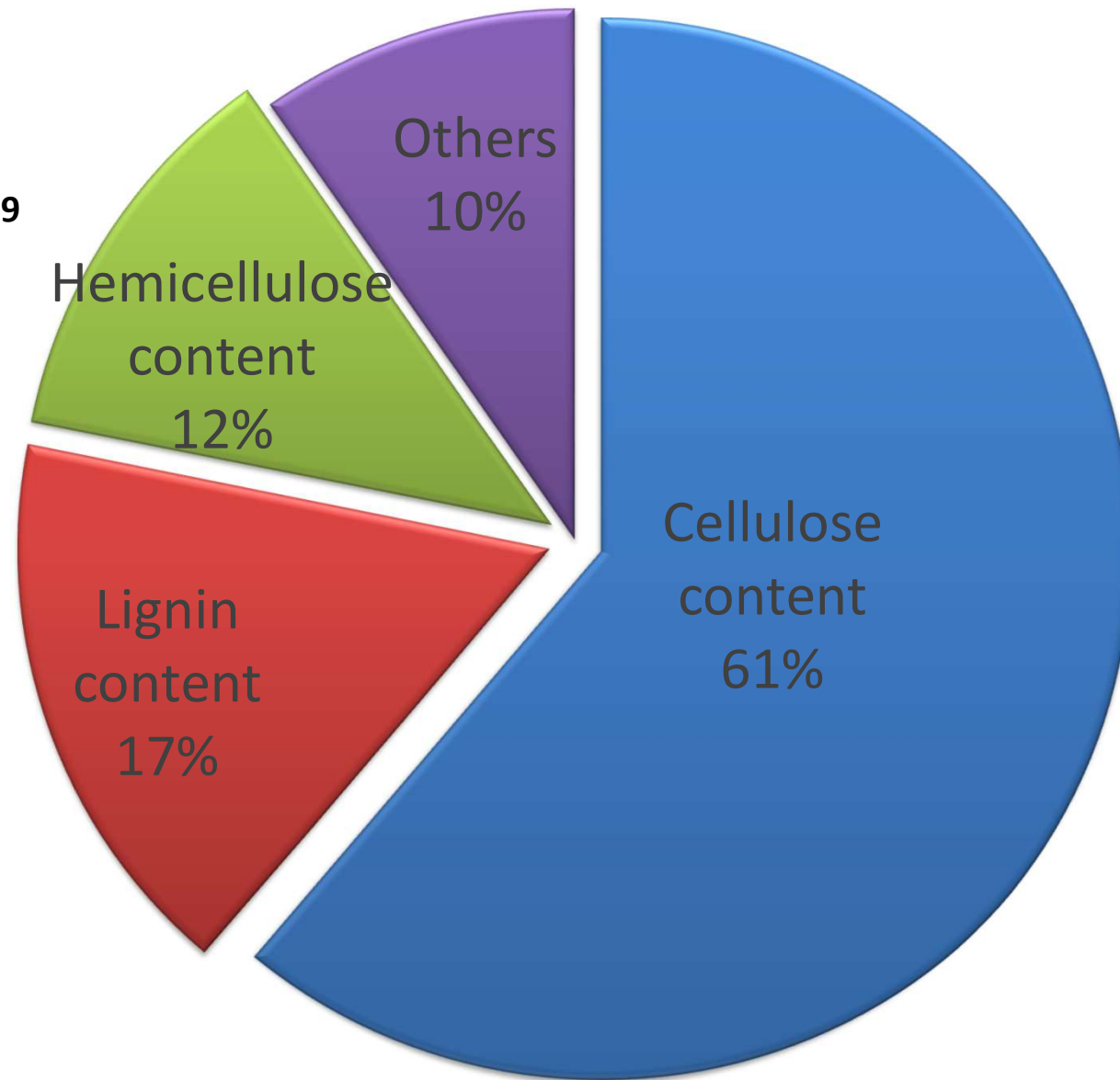


Cellular component

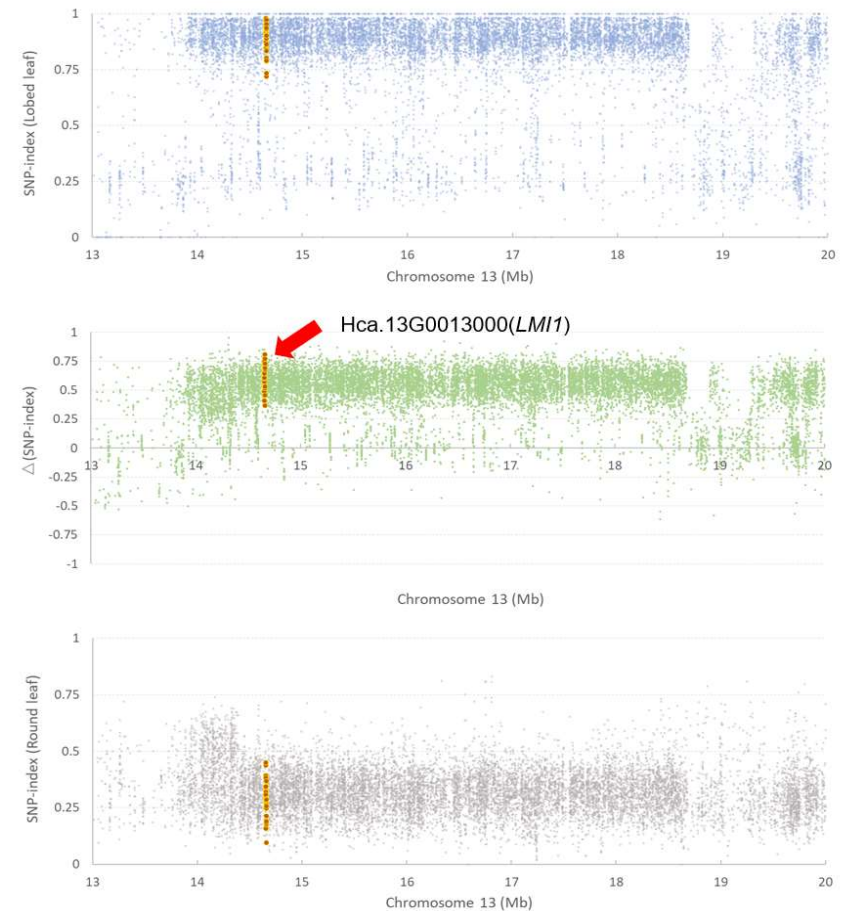
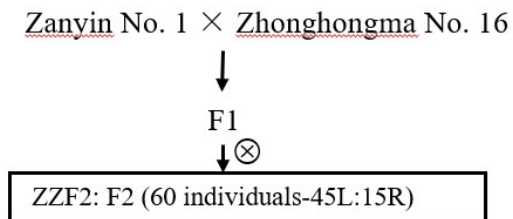
Supplementary Figure 8 Relationship between leaf shape and fiber accumulation at the different stages of growth.



Supplementary Figure 9
Different chemical
components of bast
fiber in *H. cannabinus*.



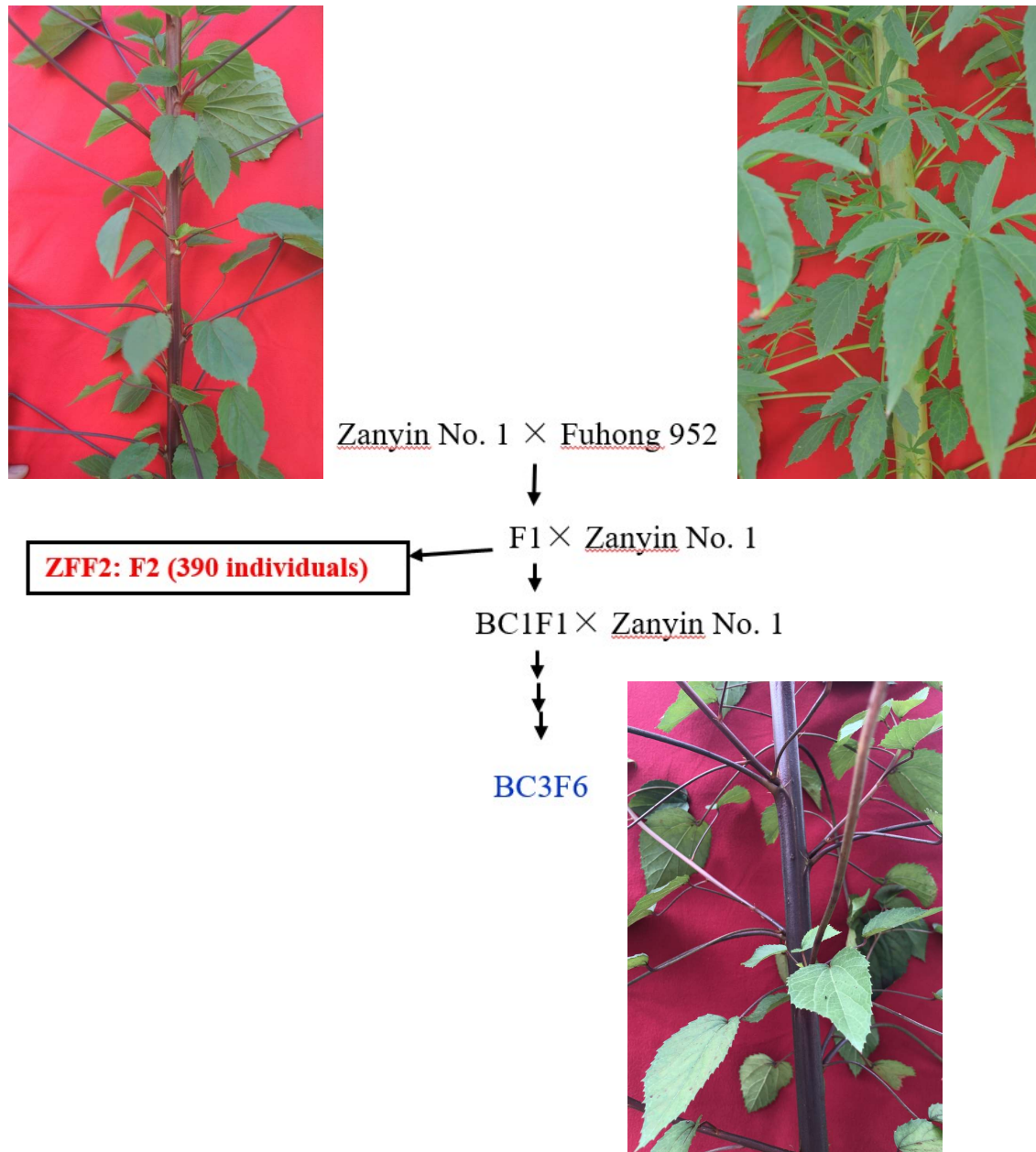
Supplementary Figure 10 BSA mapping of the candidate leaf shape gene (*HcLMI1*) in the population of ZZF2. BSA mapping showing the candidate leaf shape gene (*HcLMI1*) with a high Δ SNP-index value, a high SNP-index value in the bulked lobed-leaf sample, and a low SNP-index value in the bulked round-leaf sample in *H. cannabinus*

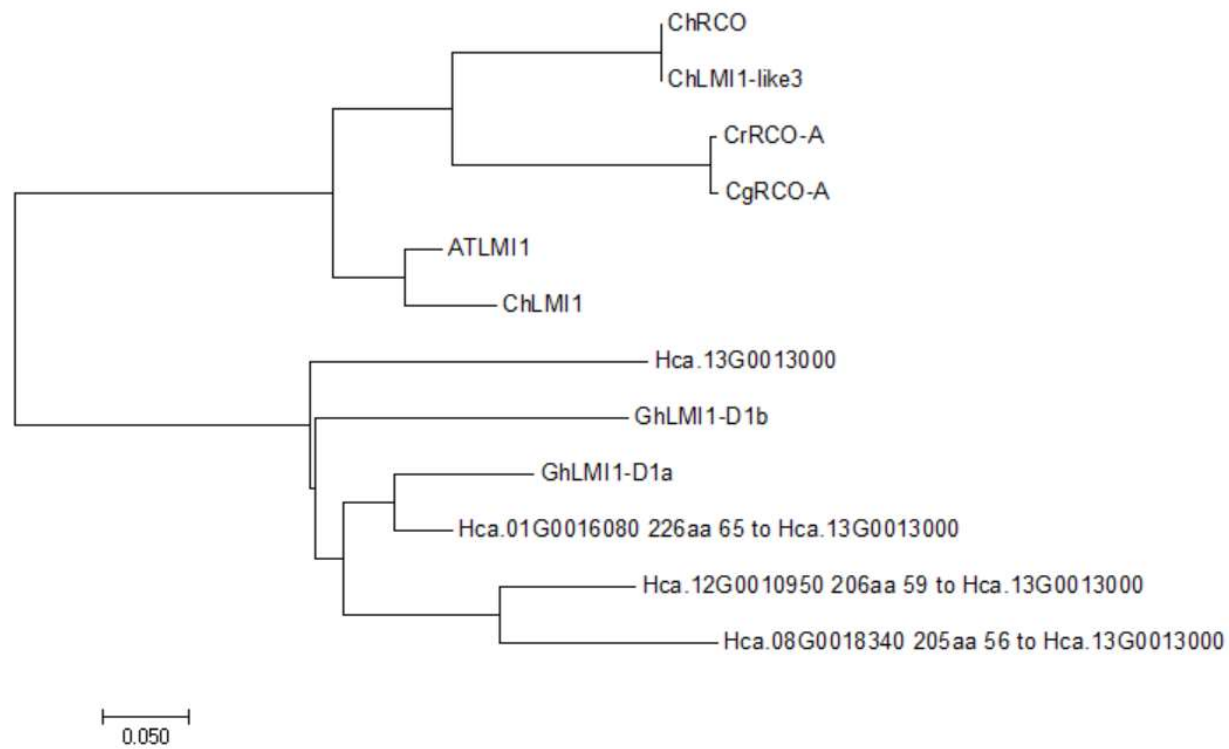


Supplementary

Figure 11

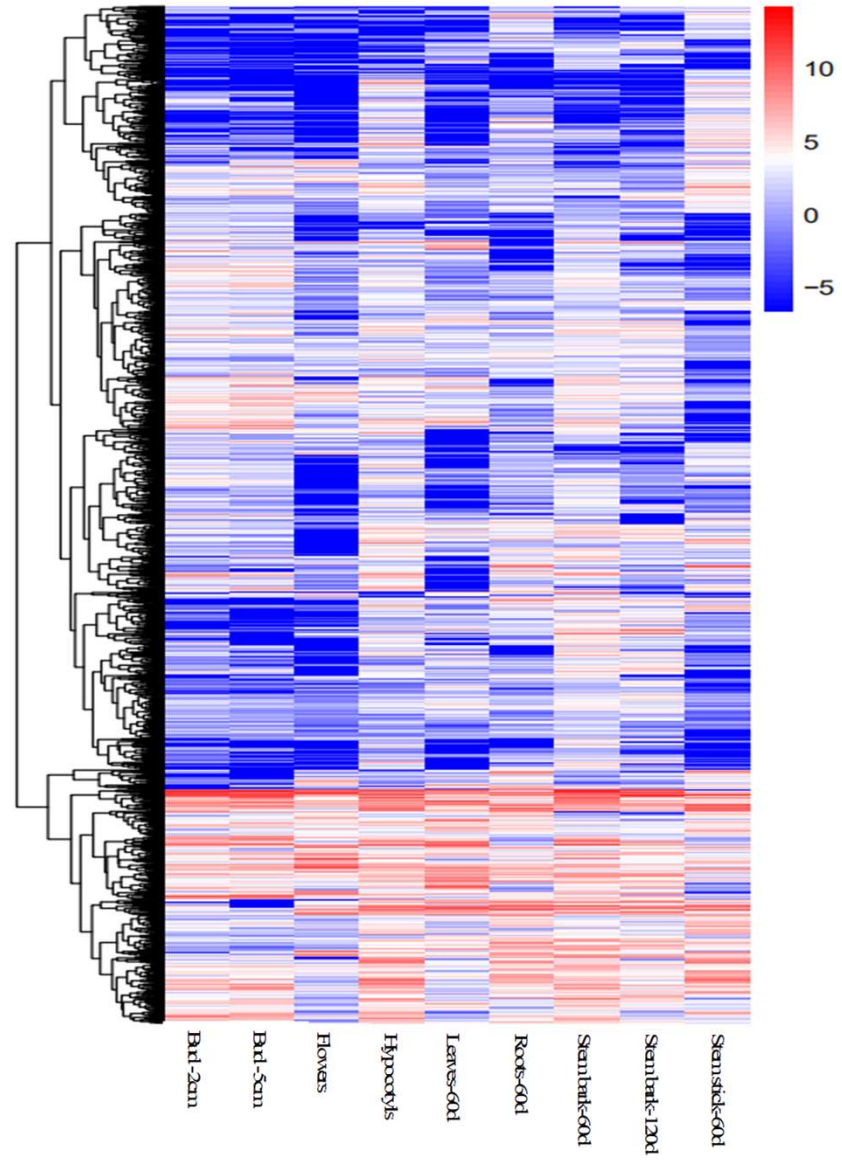
Development of near
iso-genic lines using
backcrosses



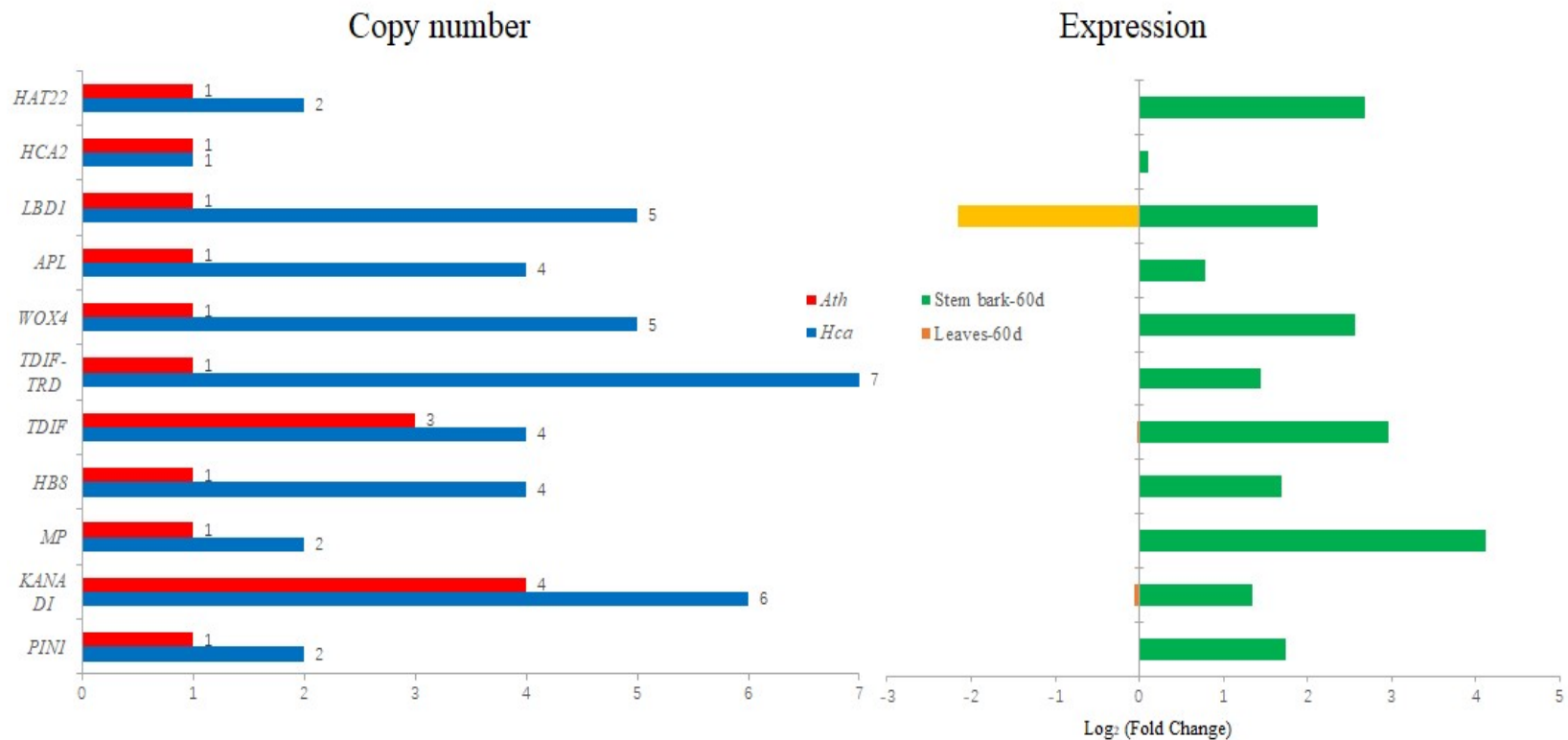


Supplementary Figure 12 Evolutionary relationships of *LMI1*. *Ch*: *Cardamine hirsuta*; *Cr*: *Capsella rubella*; *Cg*; *Capsella grandiflora*; *Gh*: *Gossypium hirsutum*.

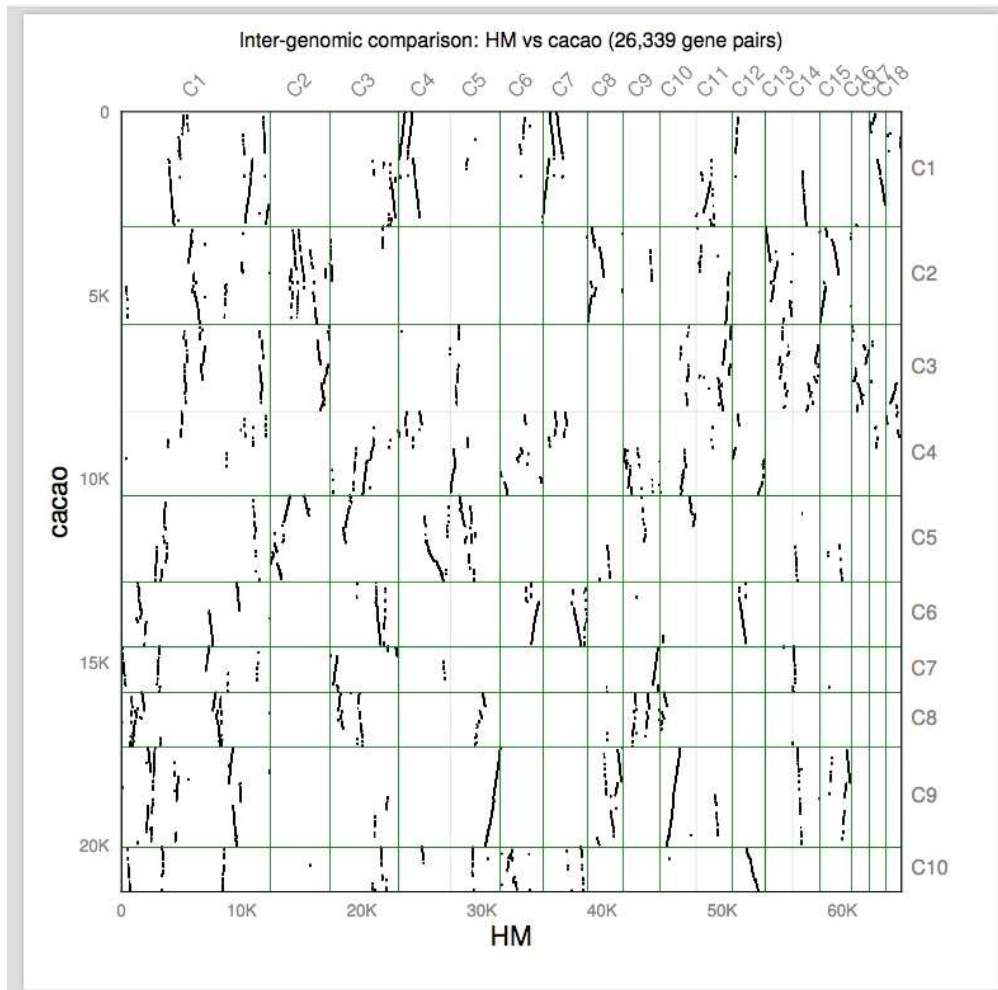
Supplementary Figure 13 Expression analysis of genes from different tissues at the various stages in *H. cannabinus*



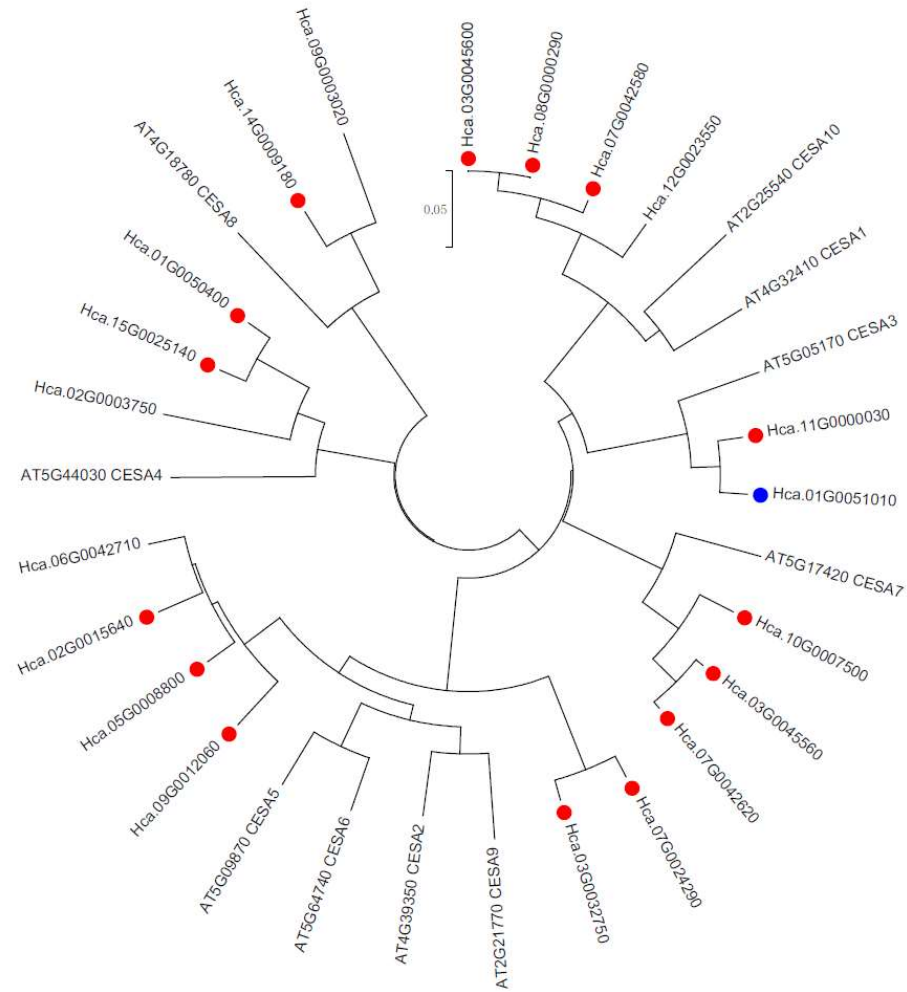
Supplementary Figure 14 Comparison of copy numbers of genes involved in secondary cell wall enzymes between *Hca* and *Ath*. Comparison of relative RNA-Seq expression of secondary cell wall enzymes in leaves.60d and stem bark.60d. *Hca*, *H. cannabinus*; *Ath*, *A. thaliana*.



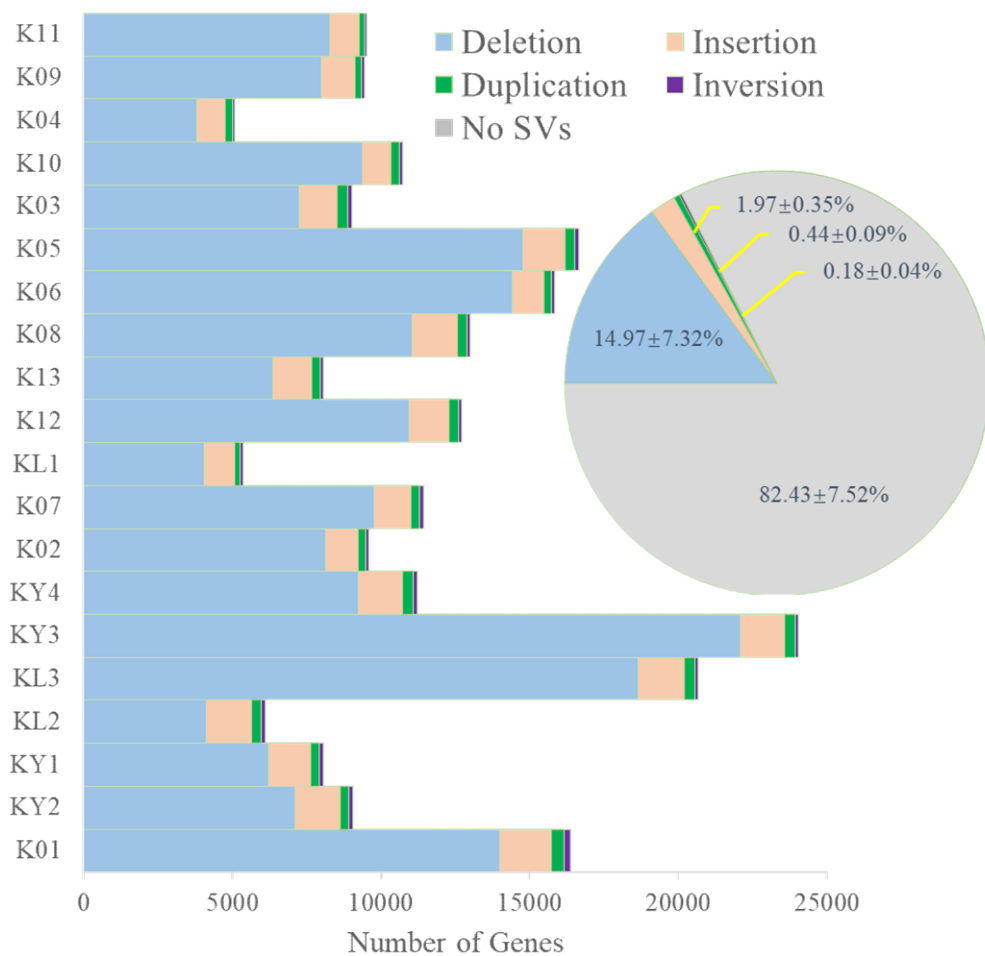
Supplementary Figure 15 Synthenic analysis between *H. cannabinus* and the close related species *T. cacao*



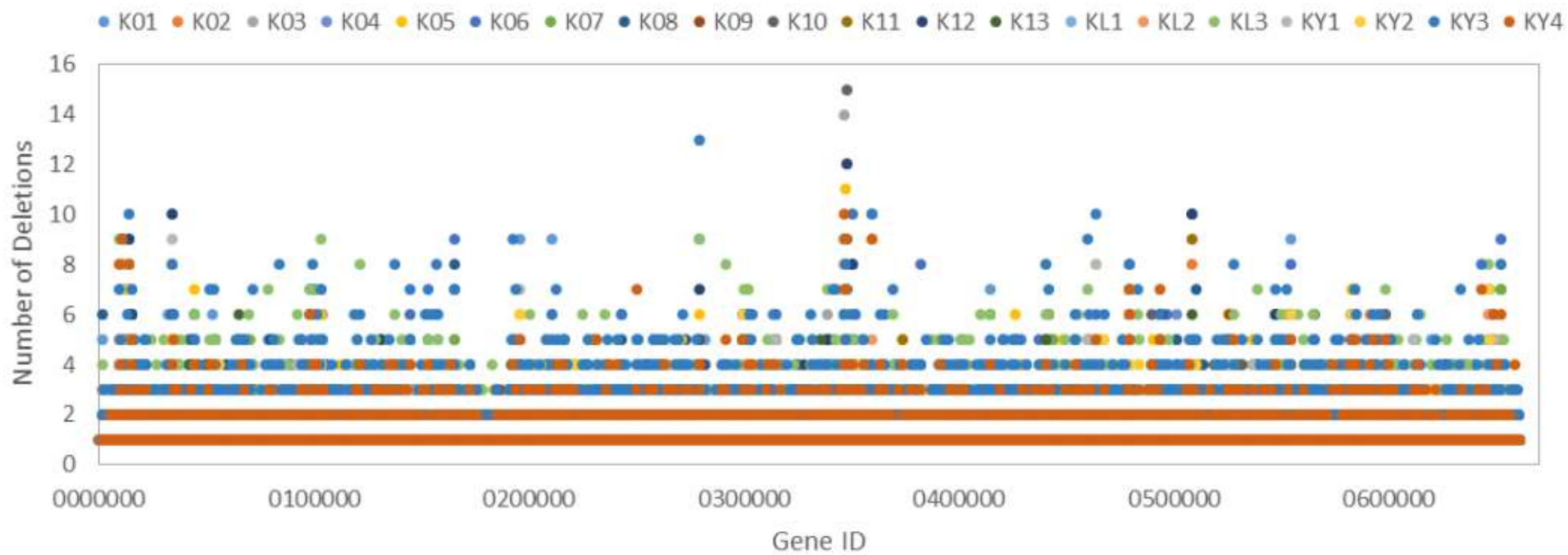
Supplementary Figure 16 Phylogenetic analysis of cellulose synthase A (*CesA*) genes in *Arabidopsis thaliana* and *H. cannabinus*. Red circles represent up-regulation at stem-bark-60d, while blue one indicates up-regulation at leaves-60d.



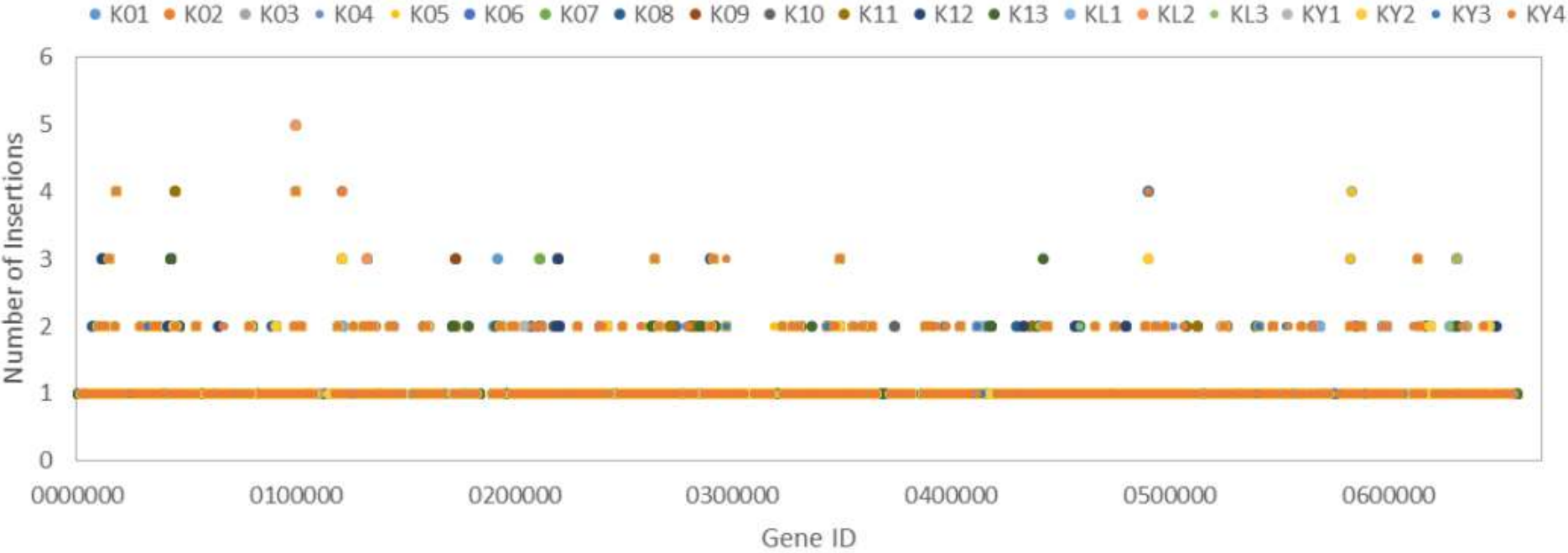
Supplementary Figure 17 Genetic diversity and structure variations among 20 core kenaf cultivars based on SNPs.



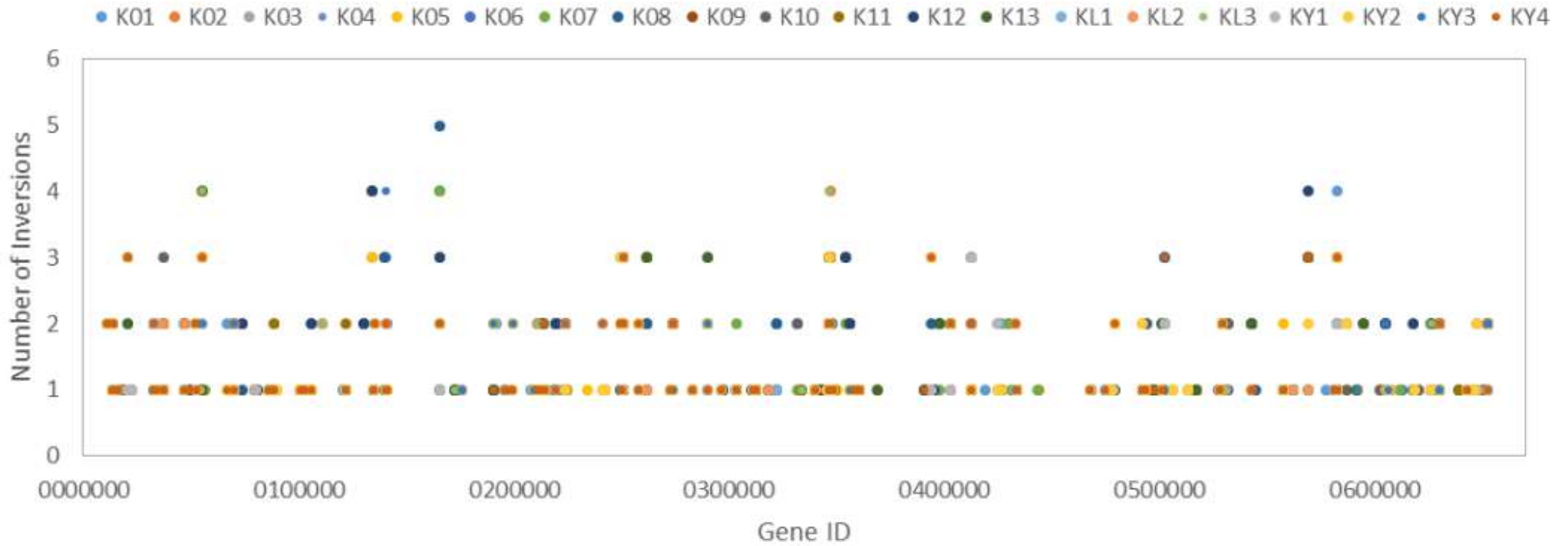
Supplementary Figure 18 Number of genes with deletions of 20 core *H. cannabinus* cultivars



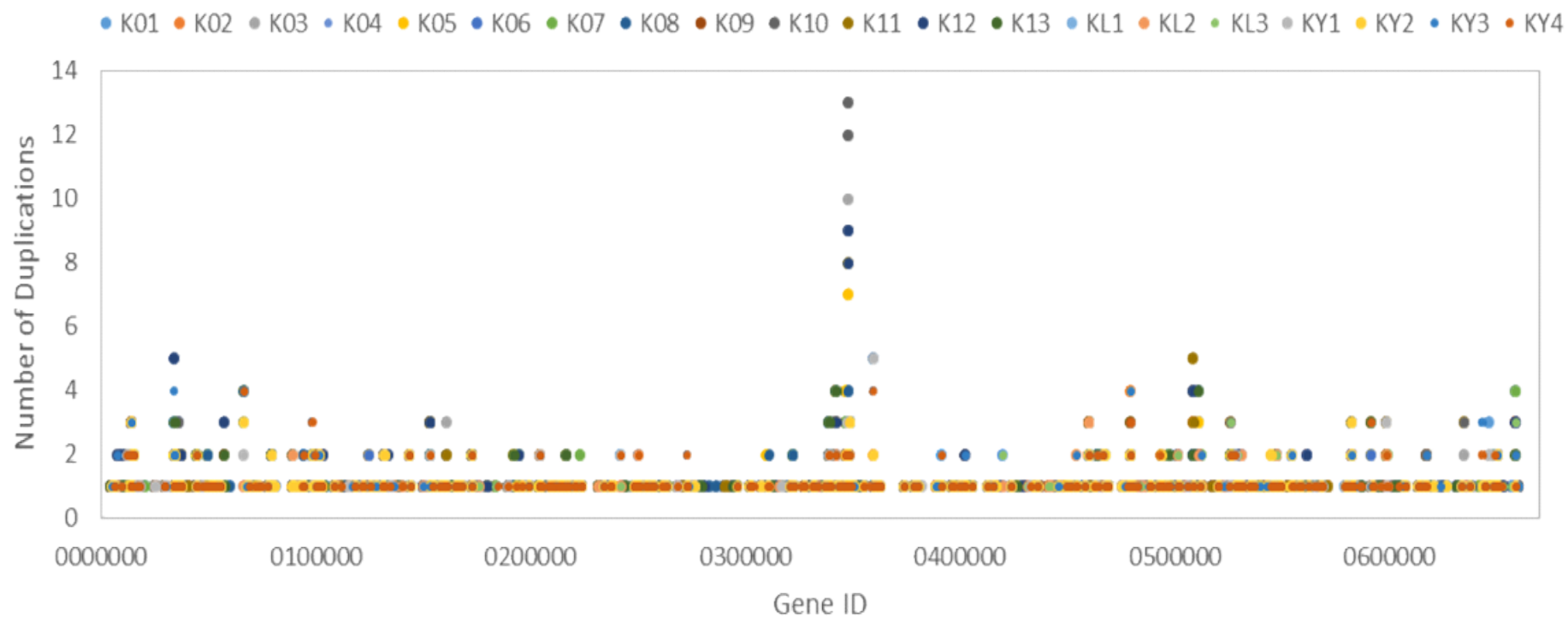
Supplementary Figure 19 Number of genes with insertions of 20 core *H. cannabinus* cultivars



Supplementary Figure 20 Number of genes with inversions of 20 core *H. cannabinus* cultivars

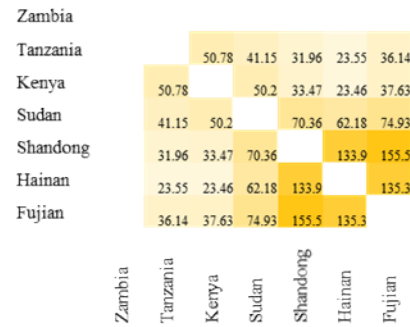


Supplementary Figure 21 Number of genes with tandem duplications of 20 core *H. cannabinus* cultivars

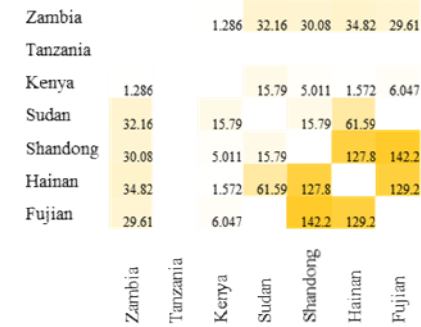


Supplementary Figure 22 Heat maps for introgression detection among different geographical regions. Introgression is significant if the Z-score is significantly negative.

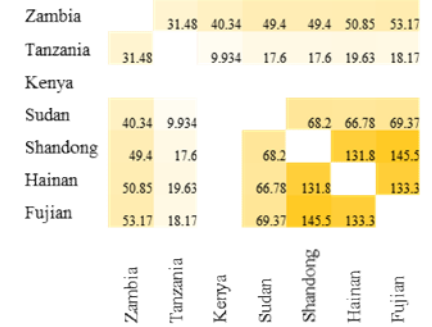
Zambia



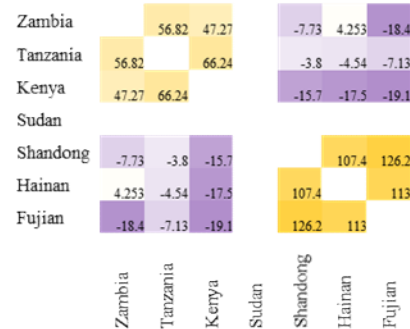
Tanzania



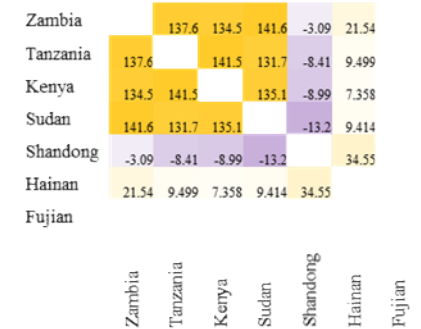
Kenya



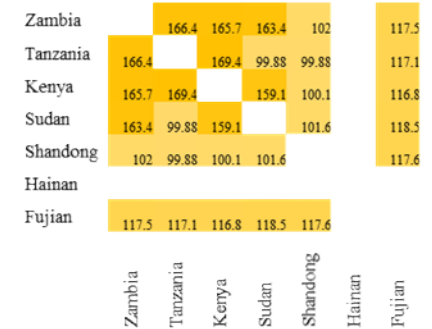
Sudan



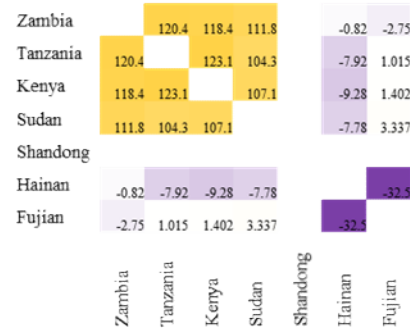
Fujian



Hainan

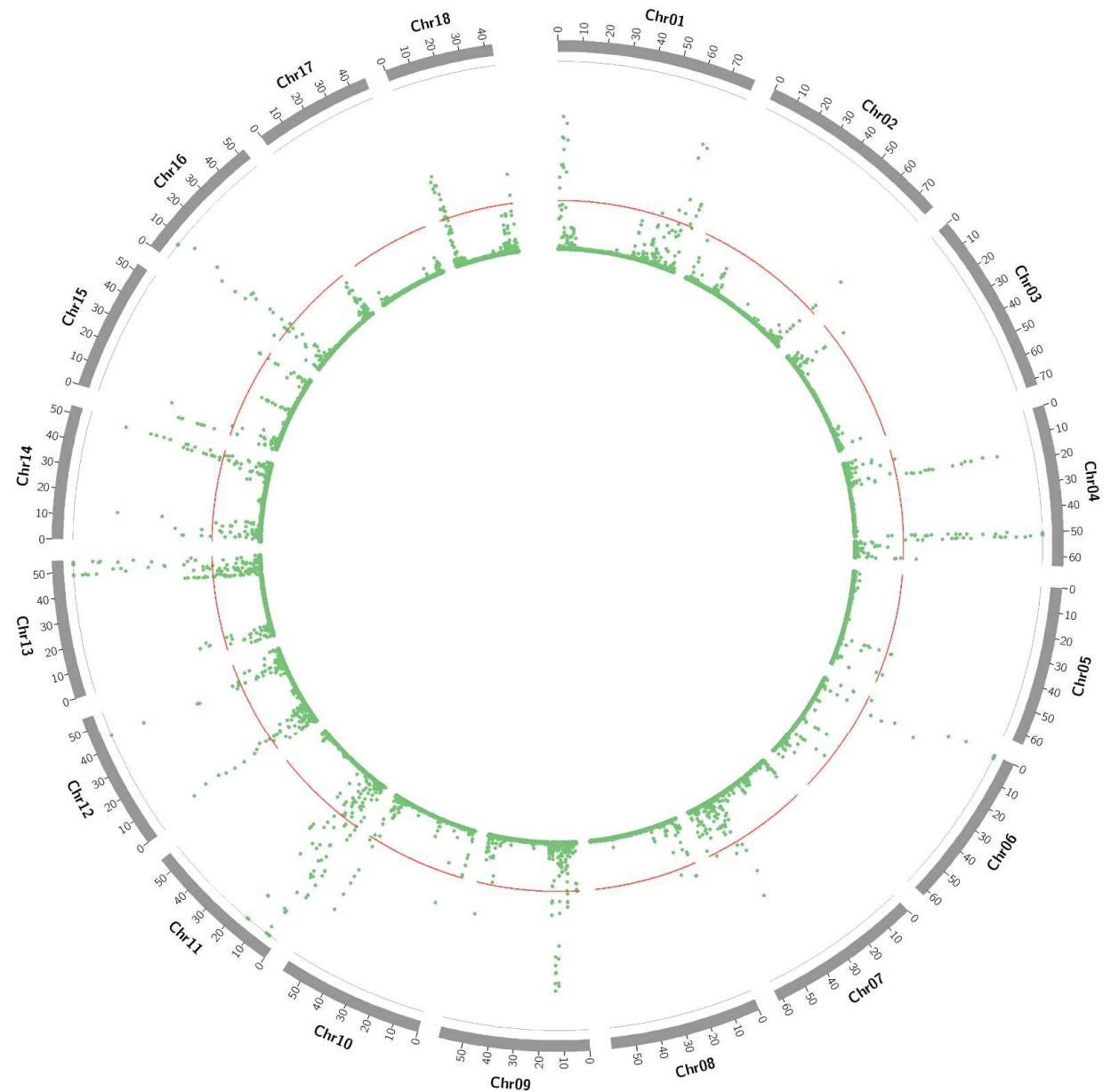


Shandong

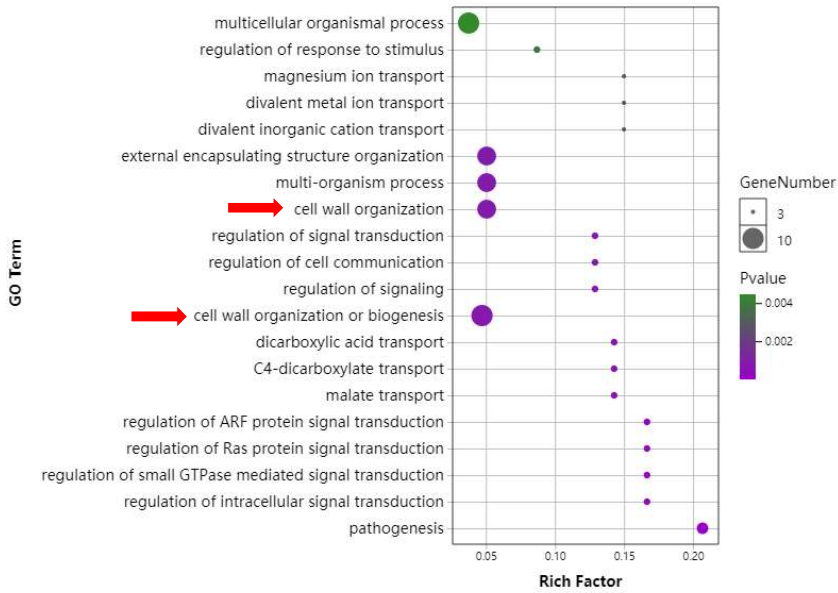


Supplementary Figure 23

Selective sweeps scanning in 20 core *H. cannabinus* cultivars. Identification of candidate regions by the composite likelihood ratio (CLR) score across kenaf genome. Each chromosome was divided into 2,000 windows, and each dot represents one window. The red solid line indicates the candidate regions above the 1% cutoff outlier with significant deviations from neutrality, indicating recent selective sweeps.

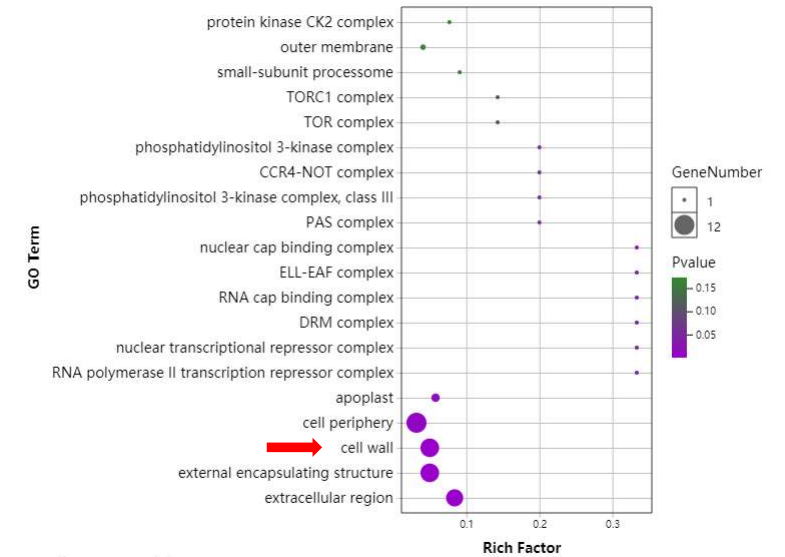


Top 20 of GO terms Enrichment



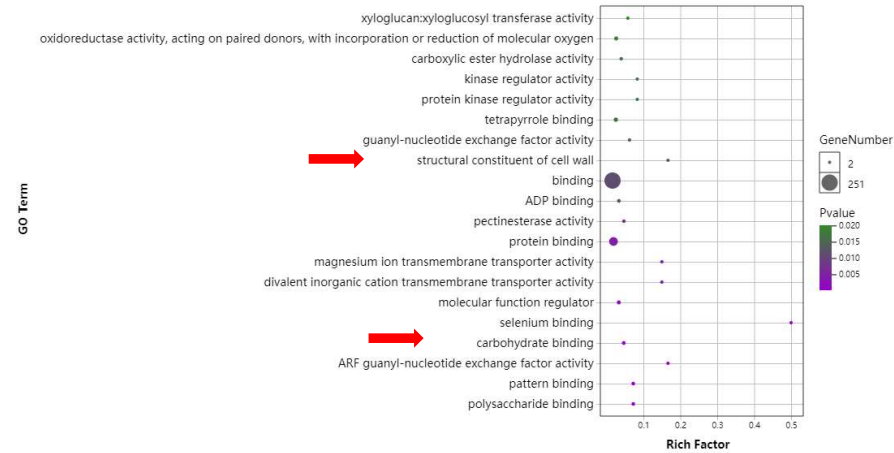
Biological process

Top 20 of GO terms Enrichment



Cellular component

Top 20 of GO terms Enrichment



Molecular Function

Supplementary Figure 24
GO enrichments of
selective swept genes in
20 core *H. cannabinus*
cultivars