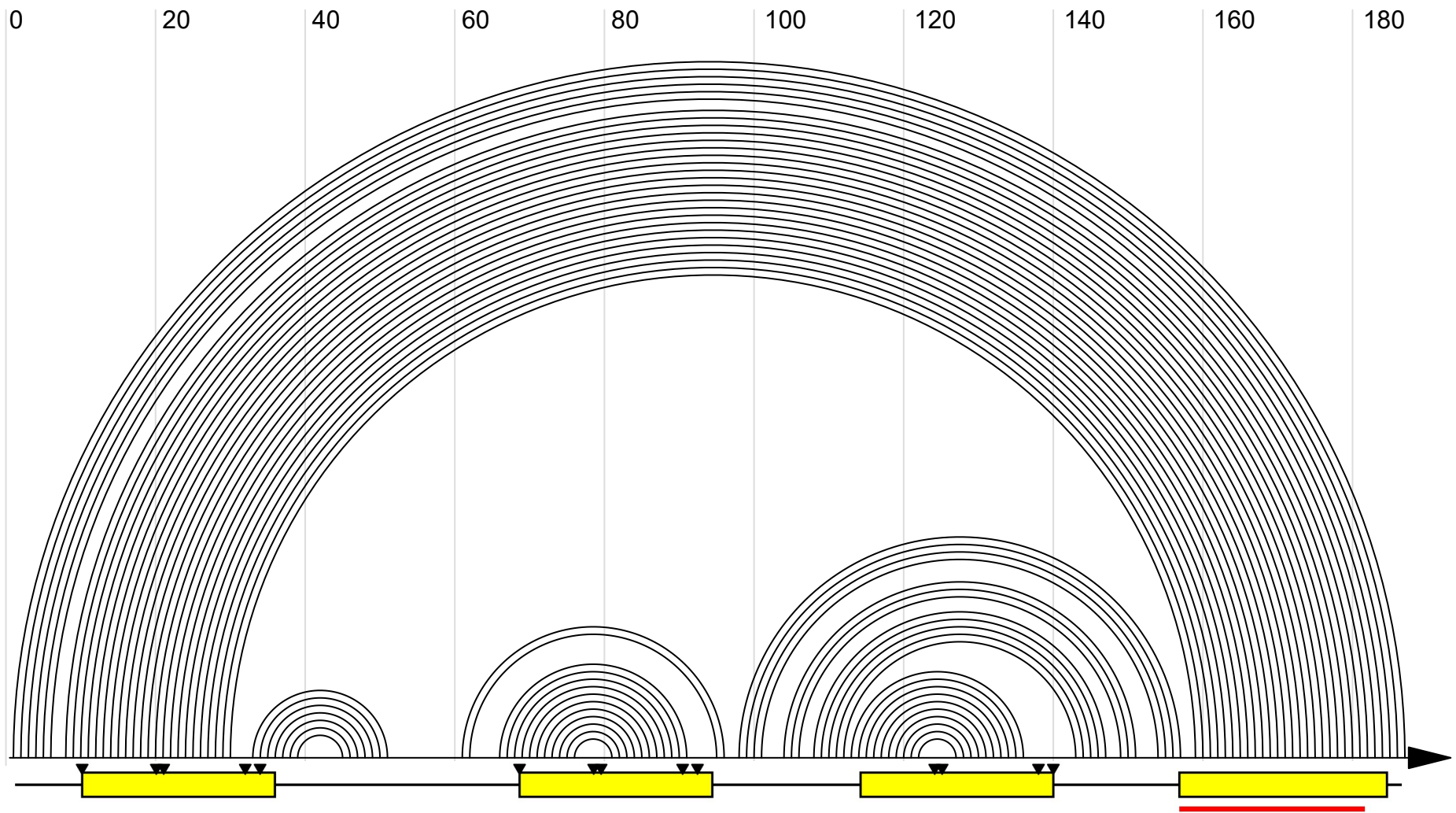
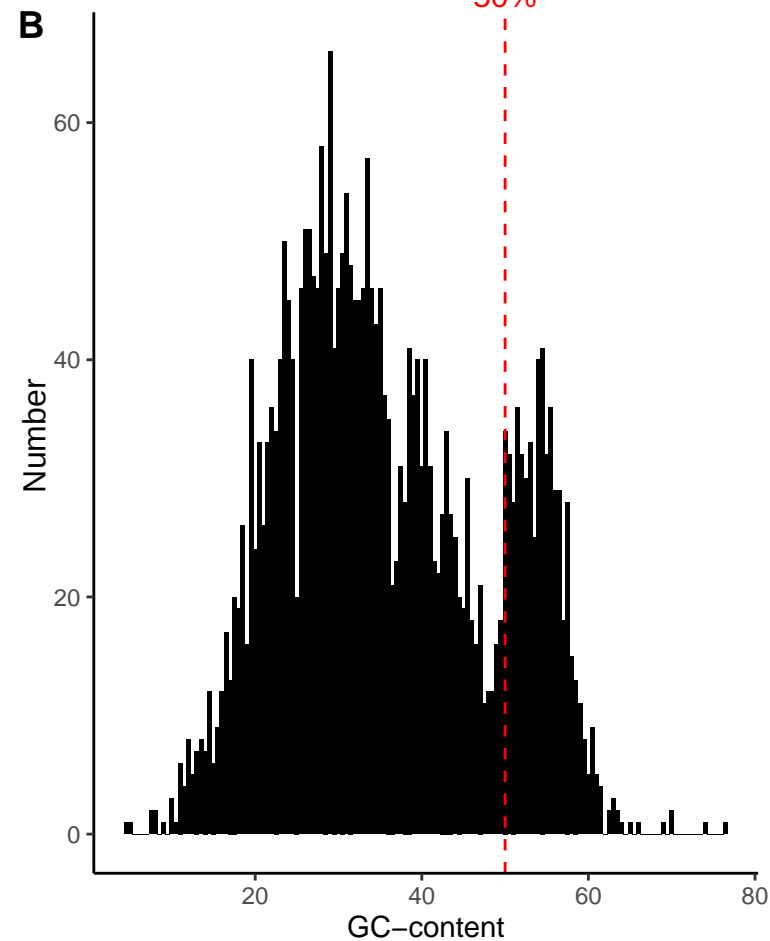
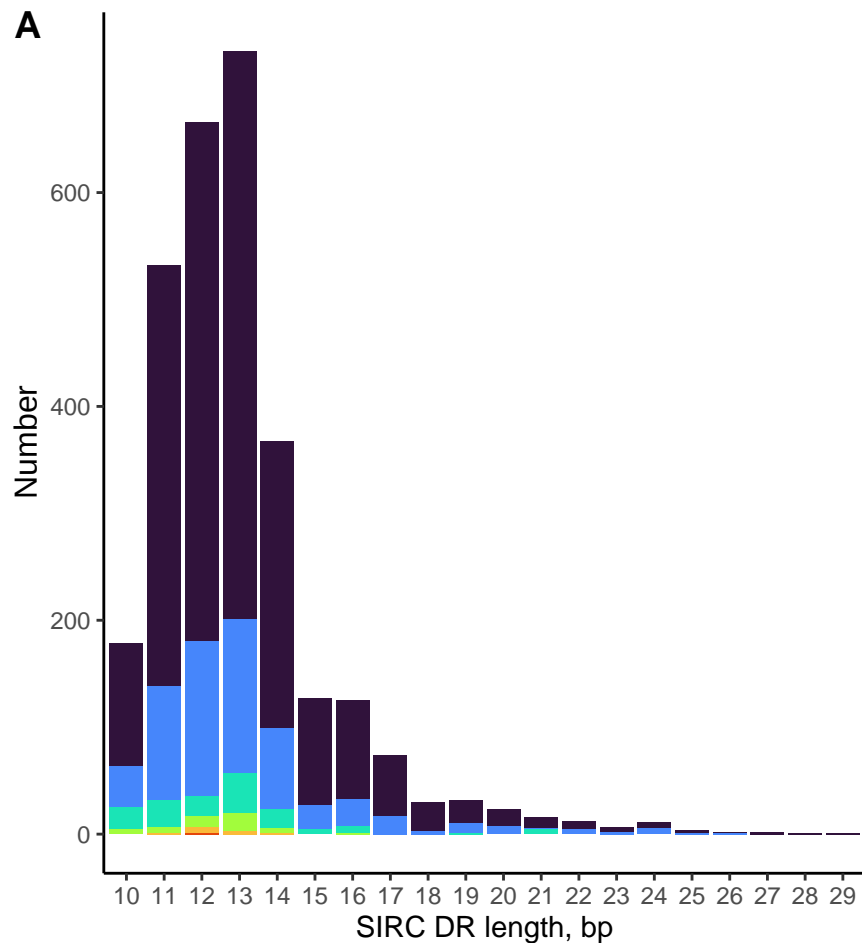


Supplementary Figure S1.
The secondary structure of miRNA ath-MIRf10275 primary transcript. Yellow rectangles are direct repeats. Red line is mature miRNA. Black marks are repeats mismatches (comparing with last repeat). Arcs are base pairs.



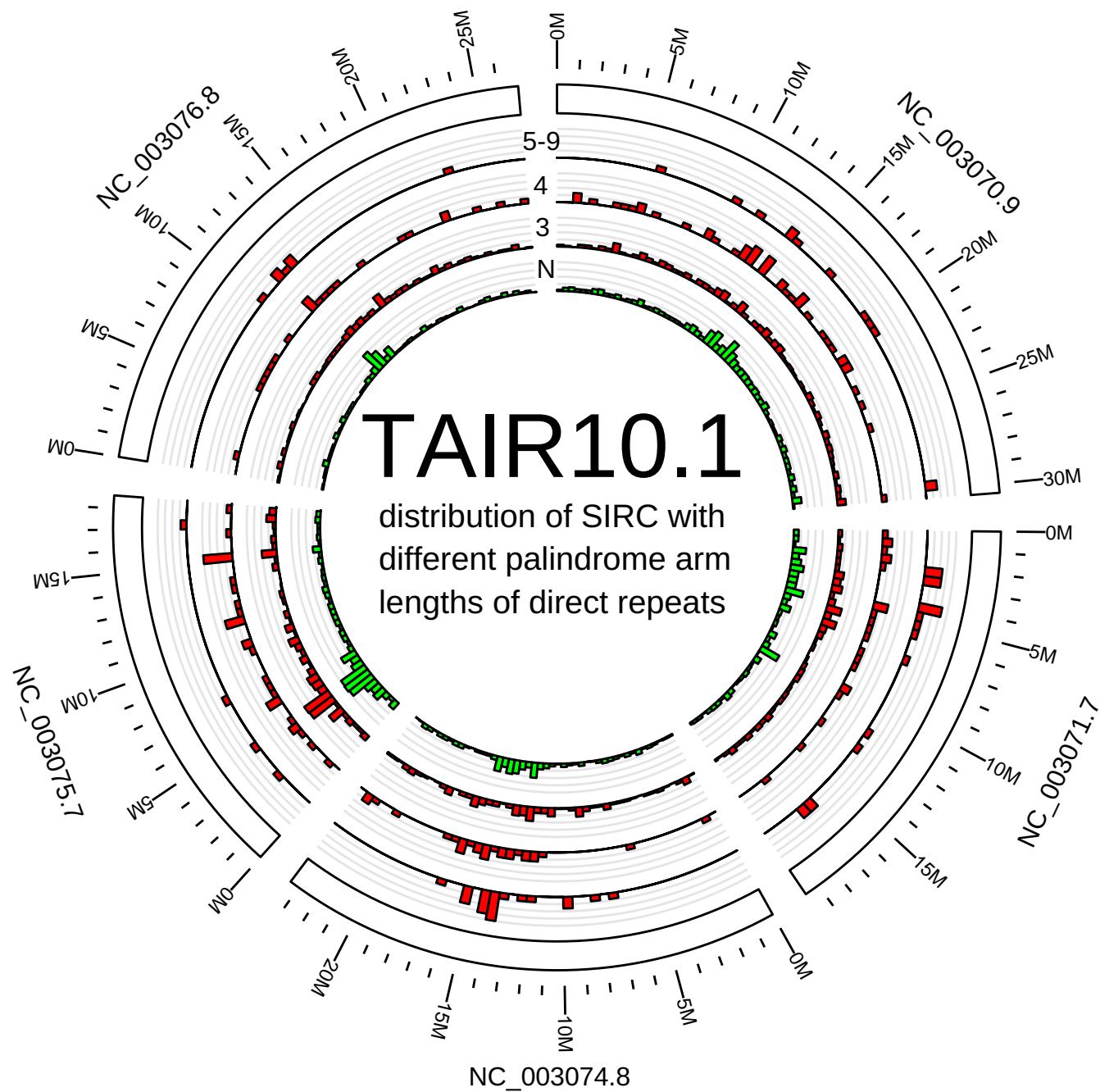
Supplementary Figure S2.

A: Statistics of SIRC DR lengths with spacer numbers; B: GC-content of full SIRC sequences

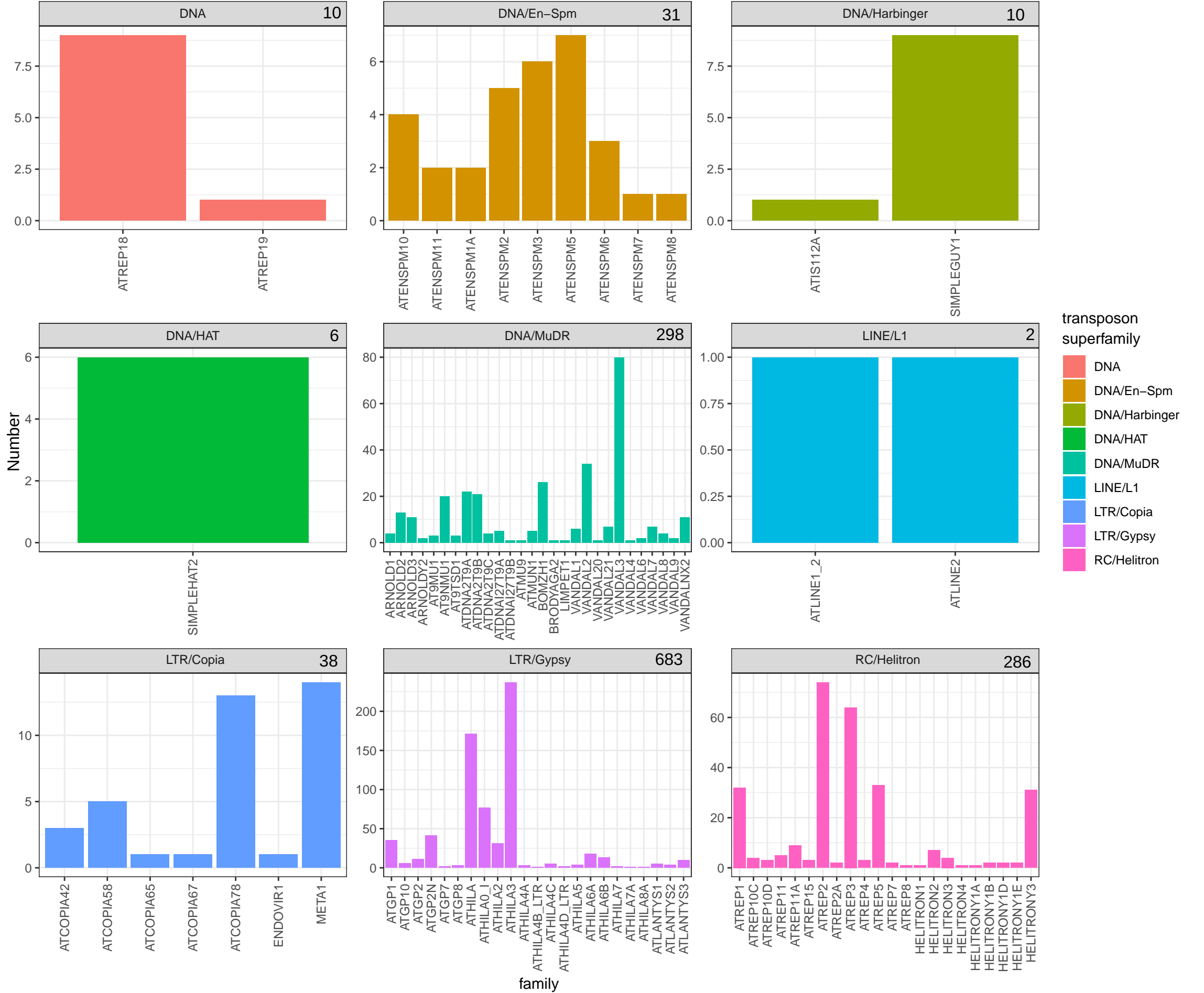


Supplementary Figure S4.

Distribution of SIRC possessing palindromes in DRs with different arm lengths across Arabidopsis genome (N stands for no palindromes).

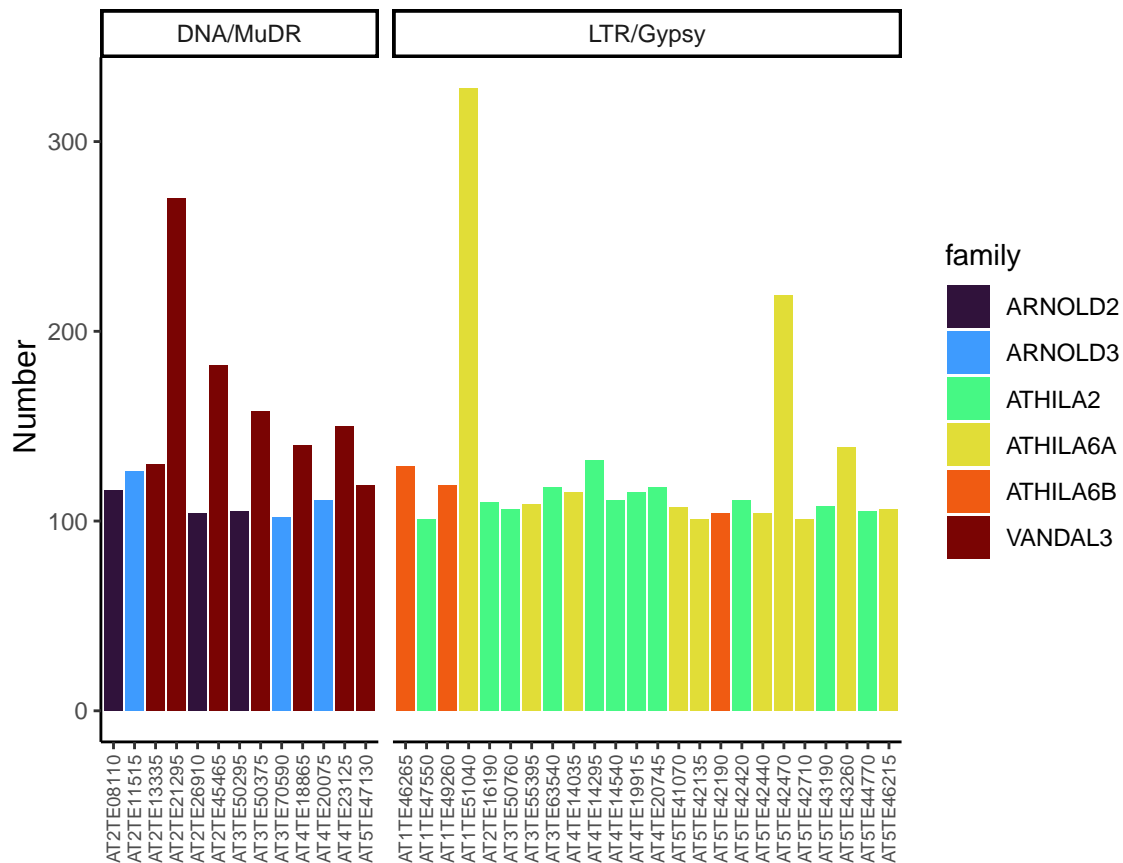


Supplementary Figure S8.
Statistics of Non-MITE mobile genetic containing SIRC hidden copies. The numbers in upper right corner of the frames represents the total number of transposon superfamily members that contain at least 1 hidden copy of SIRC.

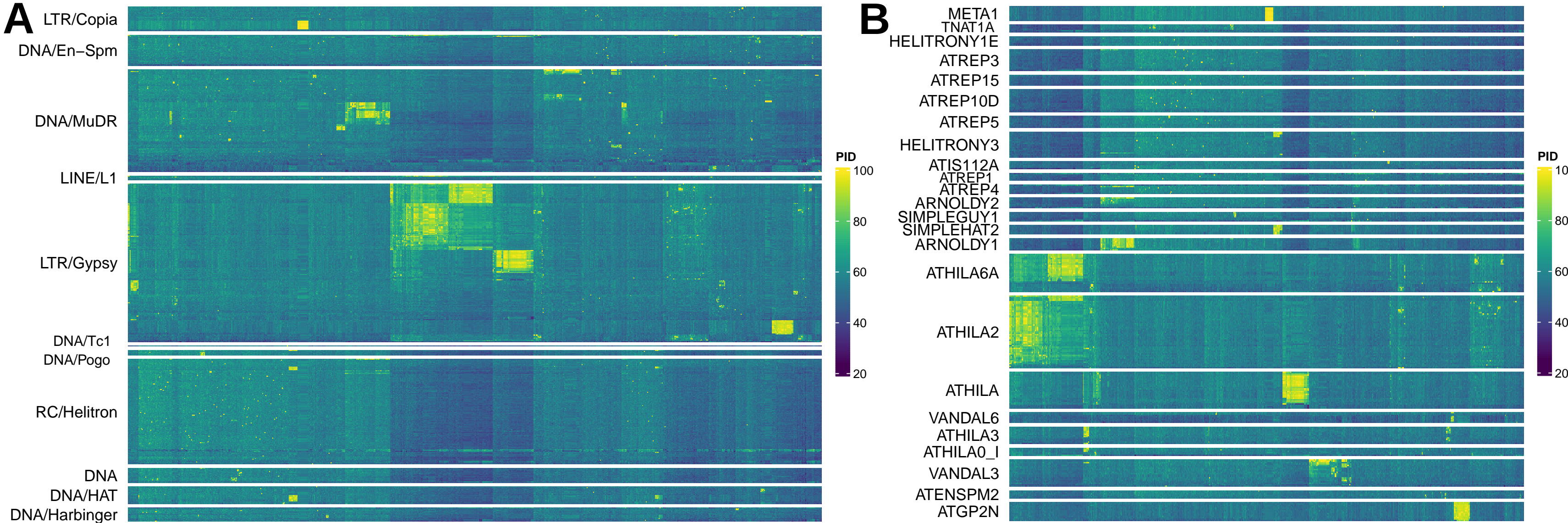


Supplementary Figure S10.

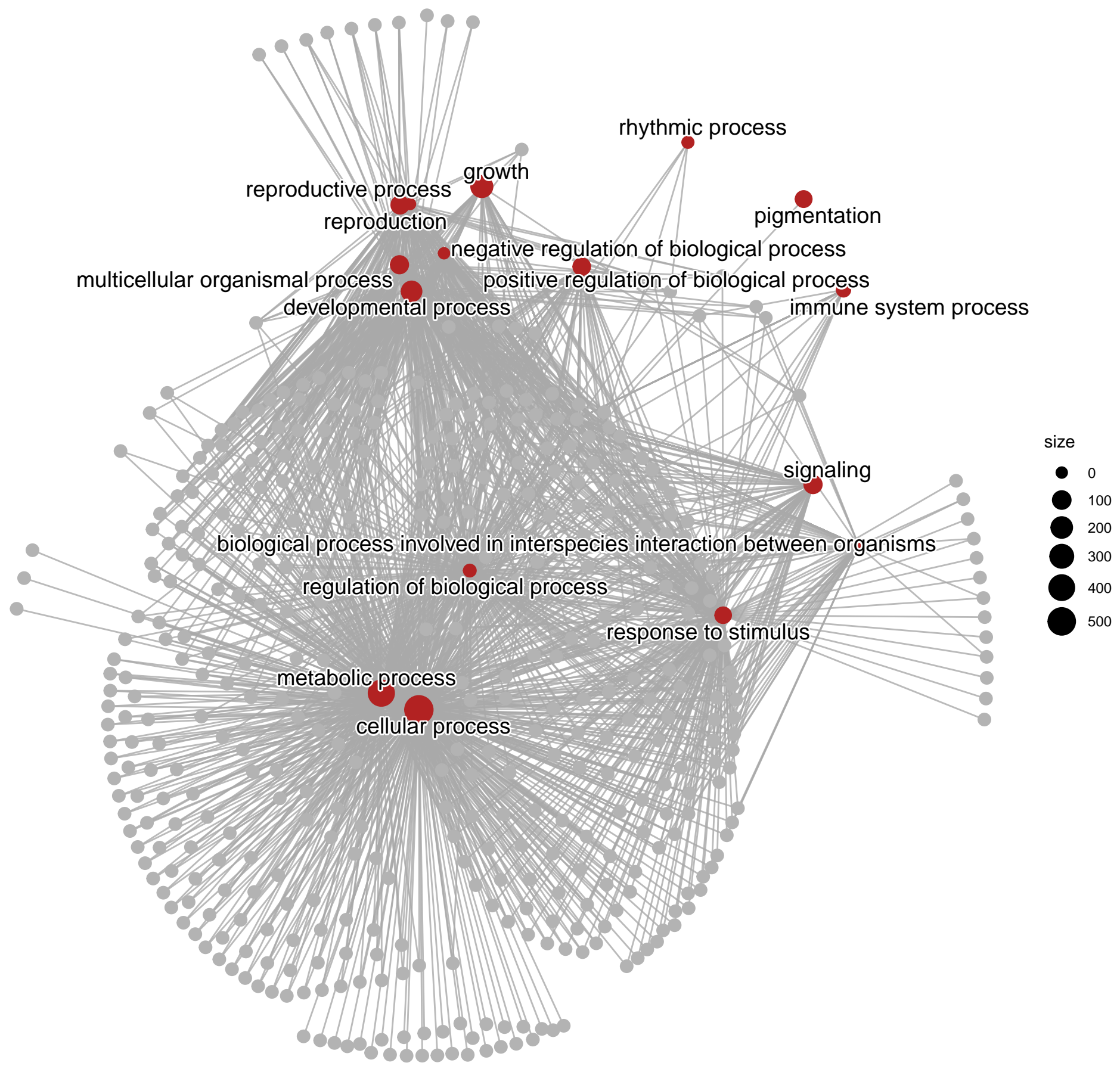
Particular mobile genetic elements that contain 100+ exact copies of different SIRC DRs.



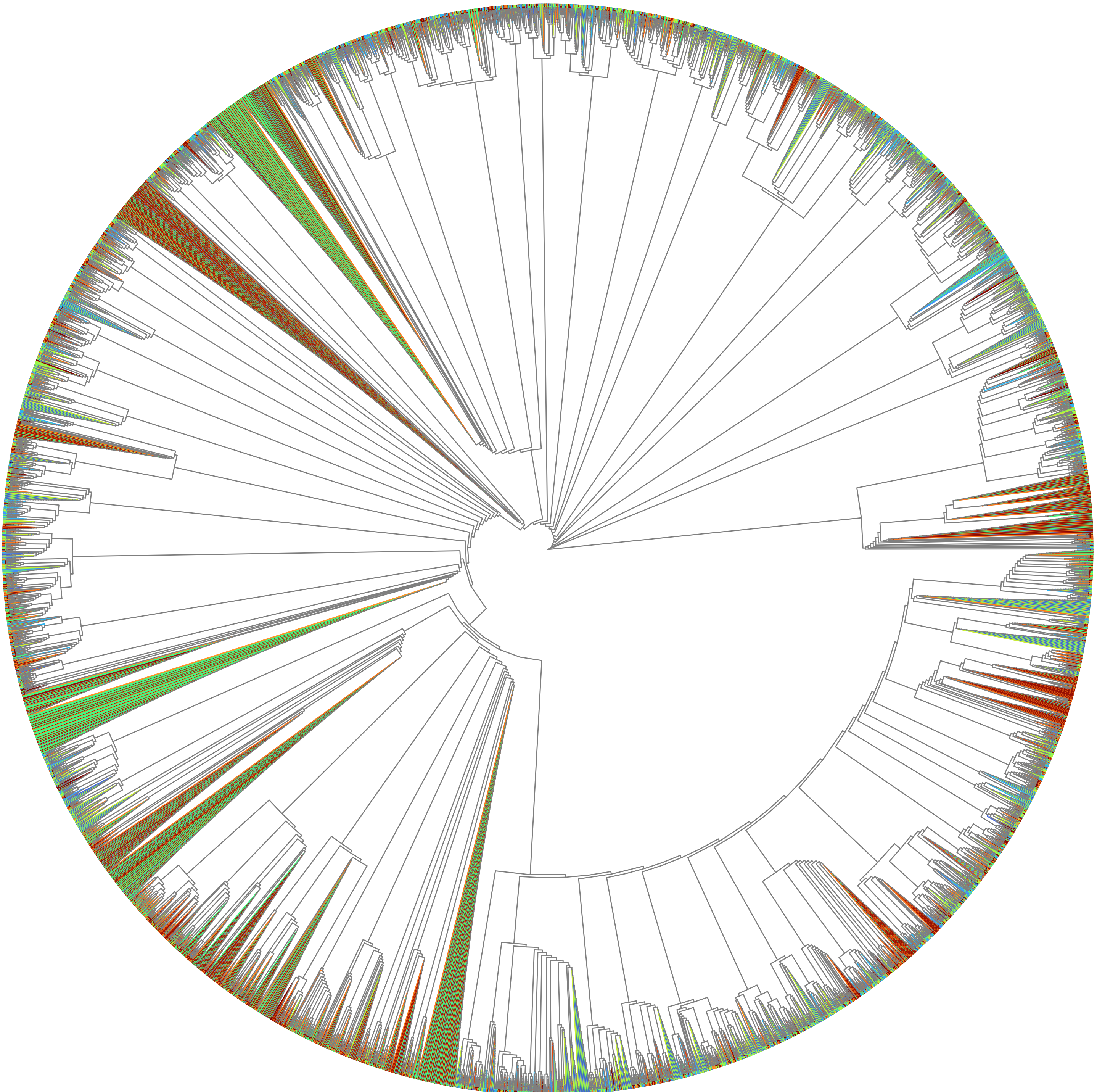
Supplementary Figure S11.
Heatmaps of percentages of identities of global-local pairwise alignments of MGE-located SIRC sequences vs full MGE sequences. A: grouped by MGE superfamilies; B: grouped by MGE families.



Supplementary Figure S12.
GO group analysis of products of SIRC-associated genes



Supplementary Figure S13.
A tree of cluster analysis (method "complete") of tetranucleotide frequencies of direct repeats consensuses of SIRC, grouped by overlapped annotations.



SIRC-associated genomic feature

- antisense lncRNA
- antisense RNA
- CDS
- enhancer
- exon
- 5'UTR
- intergenic spacer
- gene
- lncRNA
- miRNA primary transcript
- MITE
- mRNA
- ncRNA
- TE-derived origin
- protein
- pseudogene
- pseudogenic exon
- pseudogenic transcript
- regulatory inverted repeats
- smallRNA
- snoRNA
- 3'UTR
- transcript region
- transposable element
- transposable element gene
- transposon fragment

Supplementary Figure S16.
the principal workflow scheme

