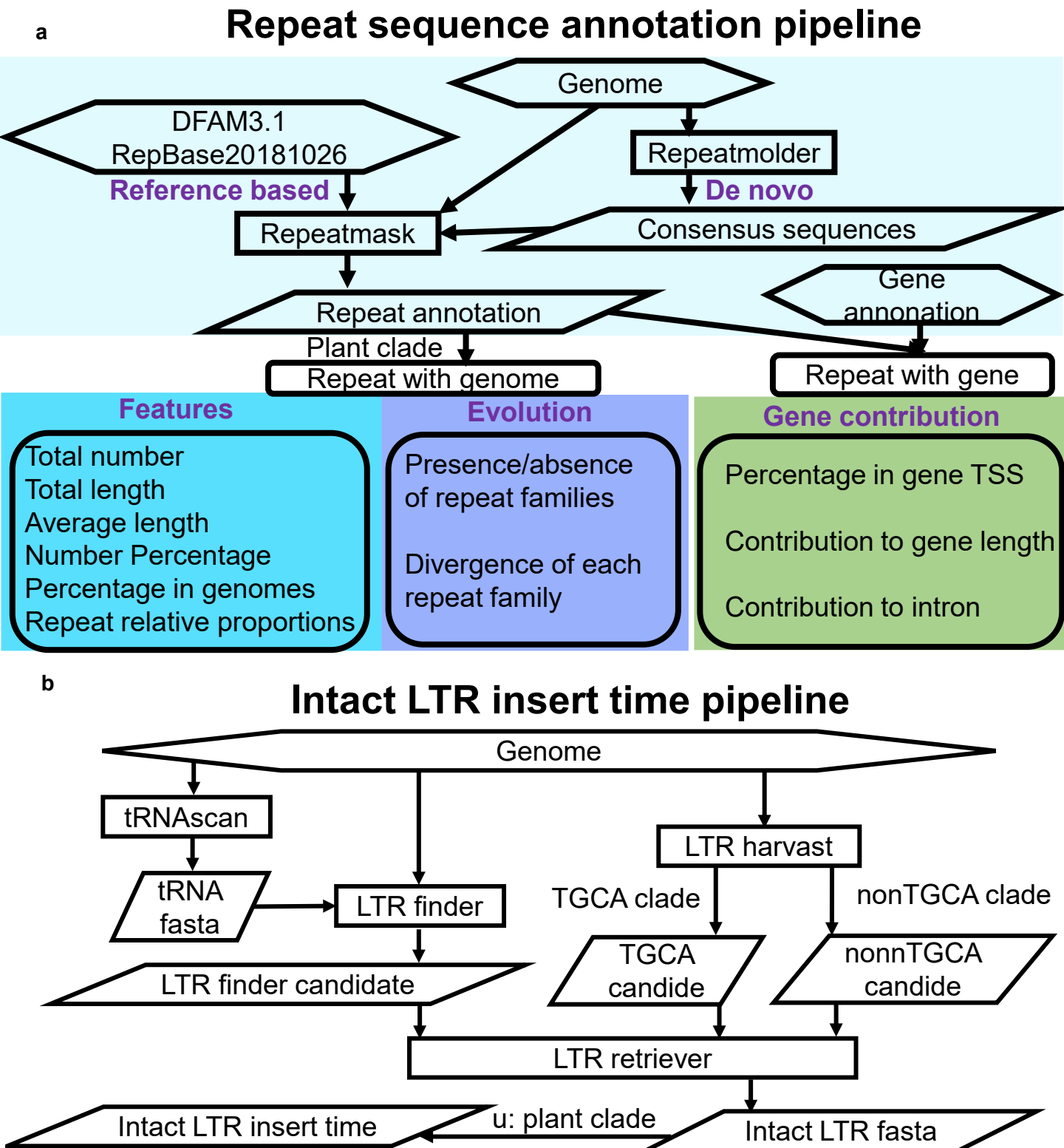
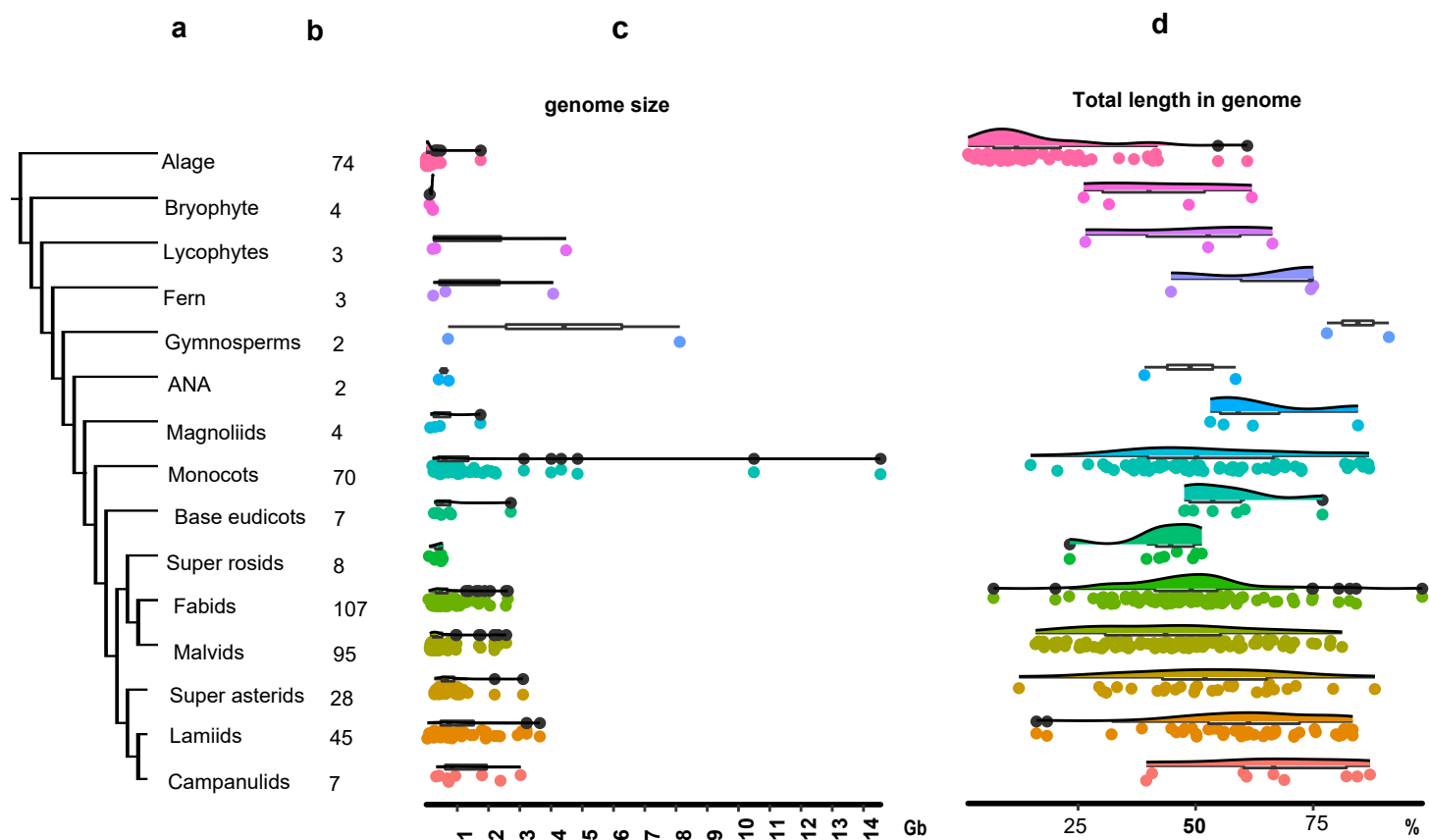
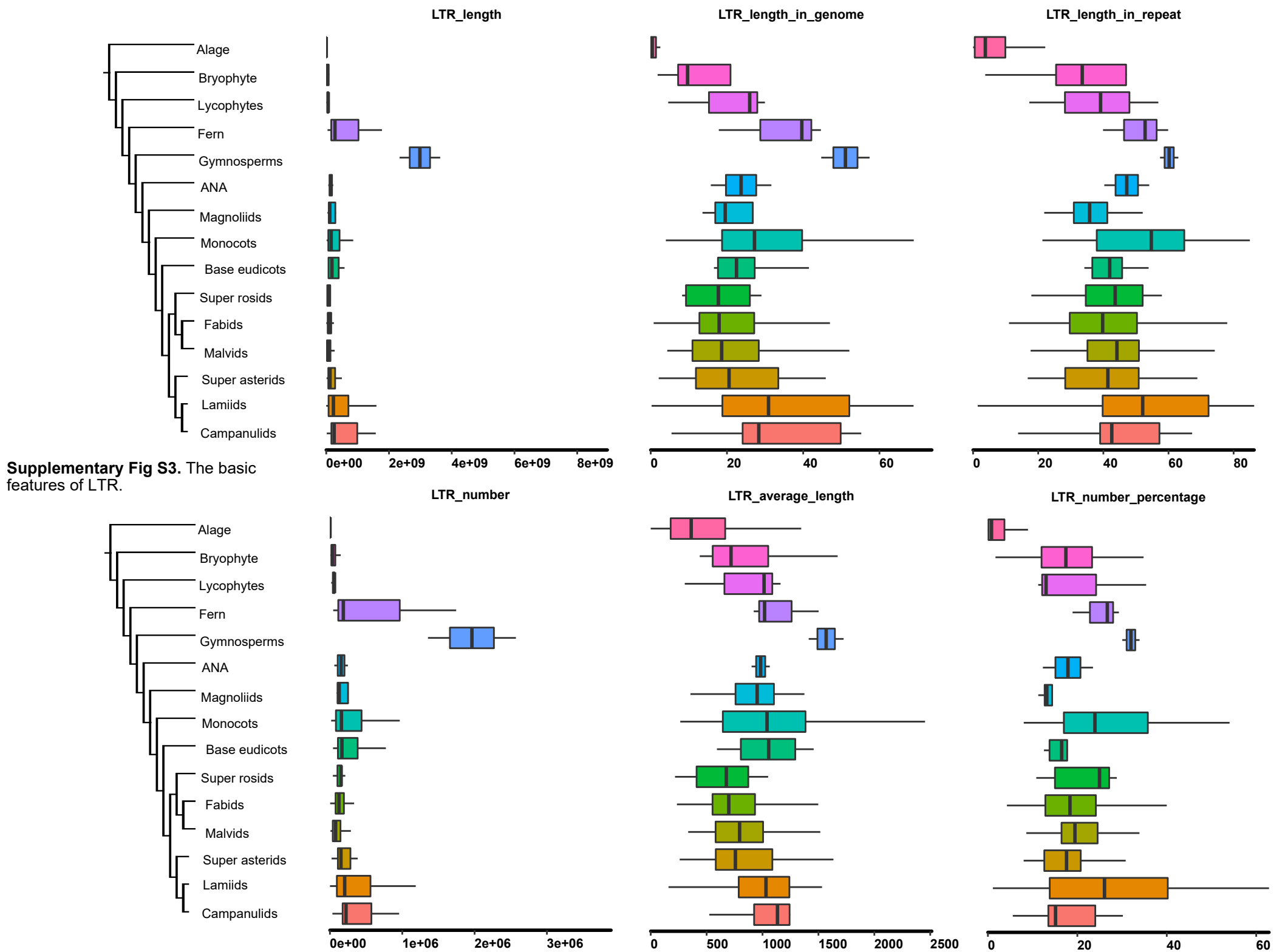


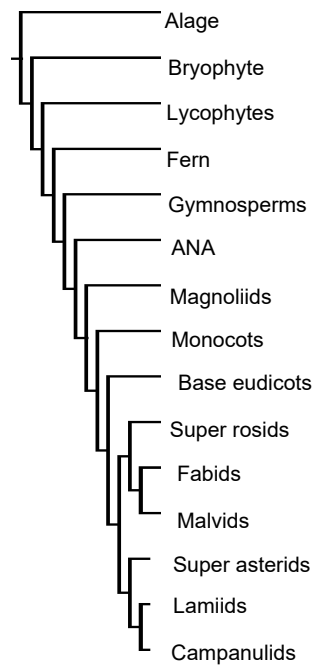


Supplementary Fig S1. The analyse pipeline of repeat sequence. (a) The analyse pipeline of genome repeat sequence. The upper is repeat annonation pipeline, the down is repeat feature, repeat evolution analyse and the repeat contribution to gene. (b) The analyse pipeline of intact LTR insert time.

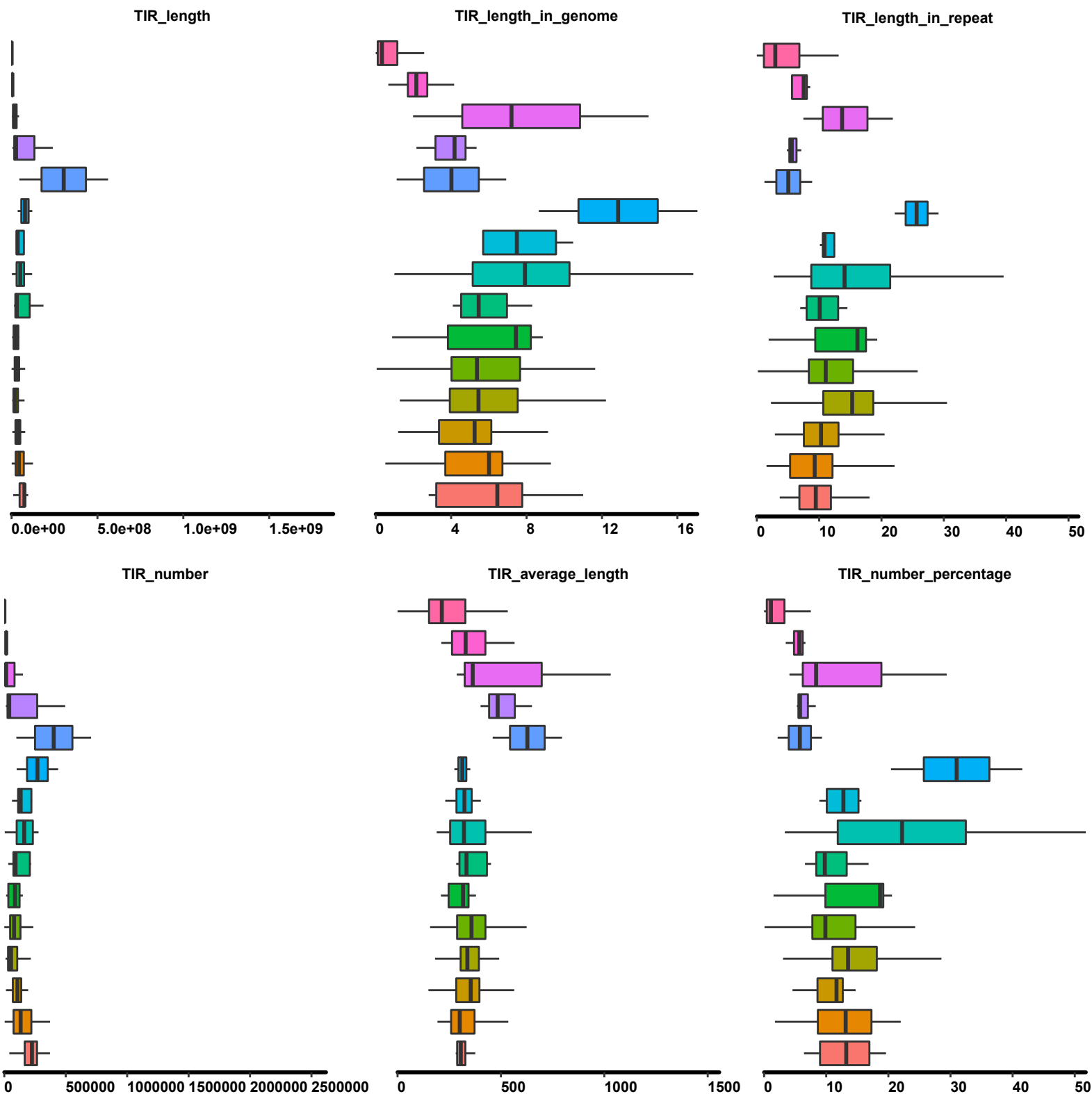


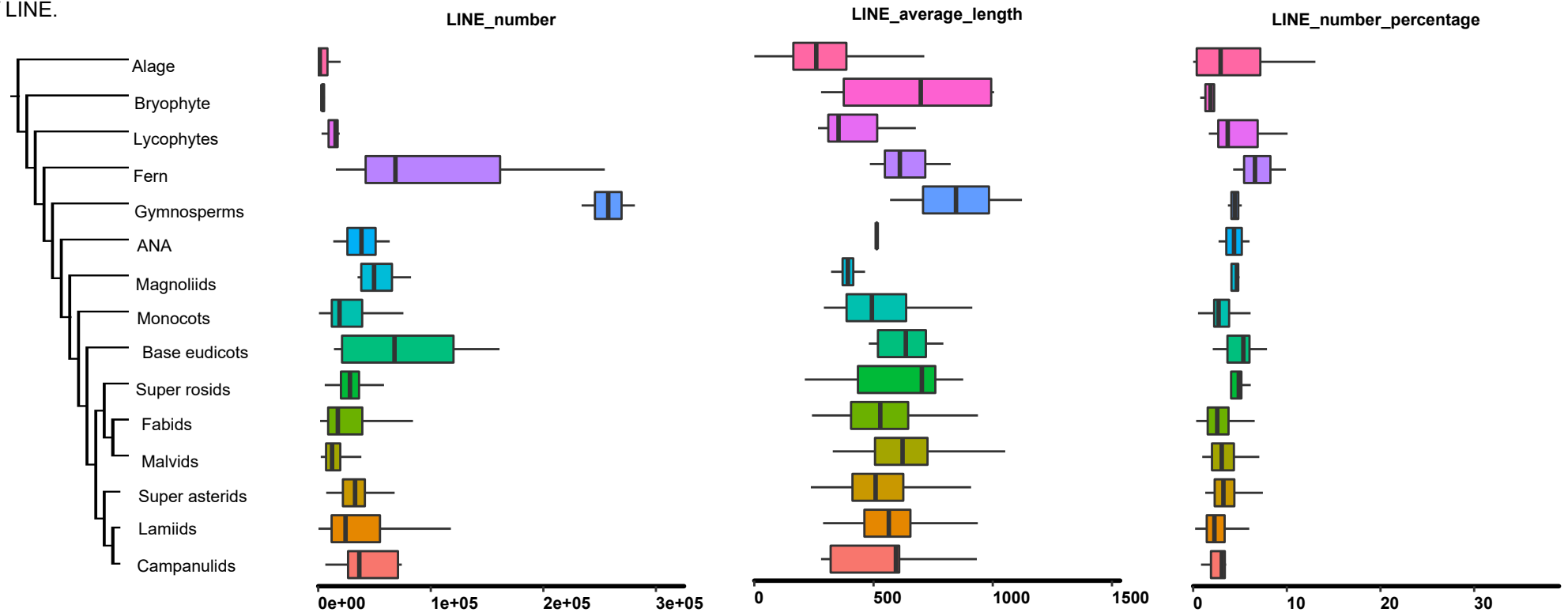
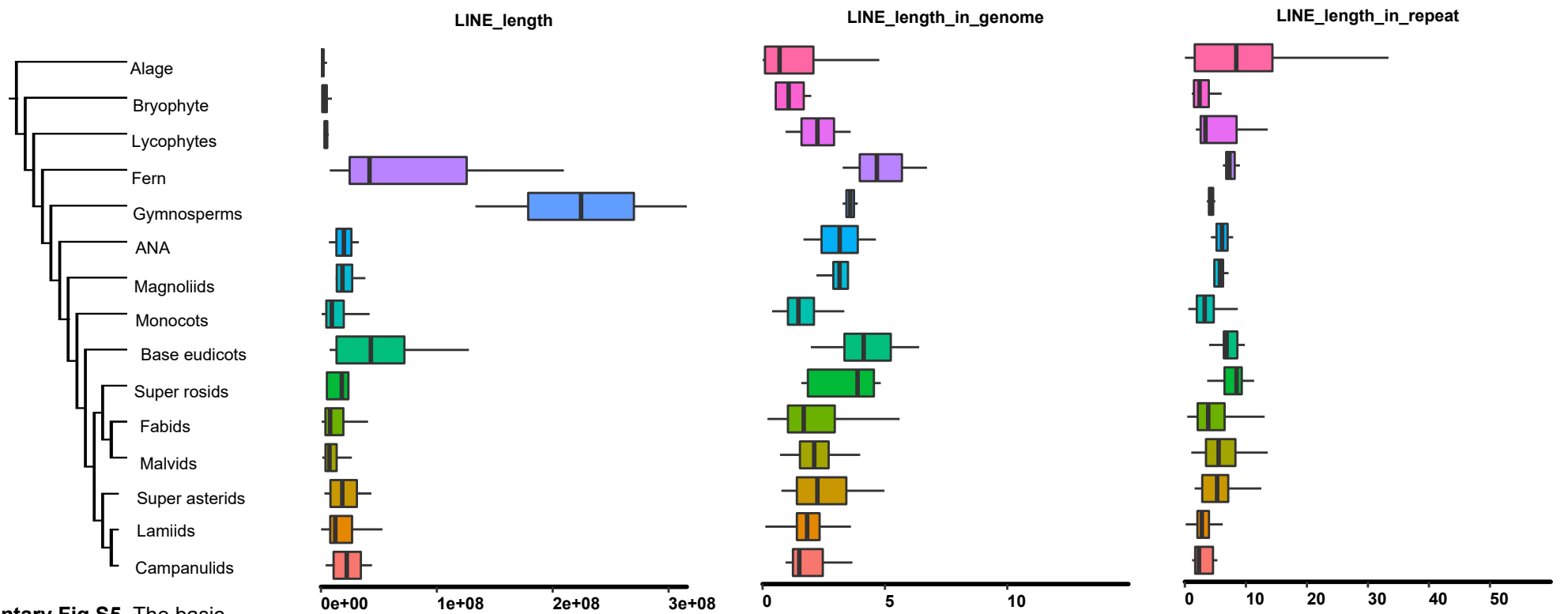
Supplementary Fig S2. The plant repeat information. (a) The phylogenetic tree in green plant kingdom with 15 plant phylogenetic branches from early Algae to eudicots. (b)The species number of each phylogenetic branches. (c)The plant genome size of each phylogenetic branches. (d)The repeat length percentage in each species.

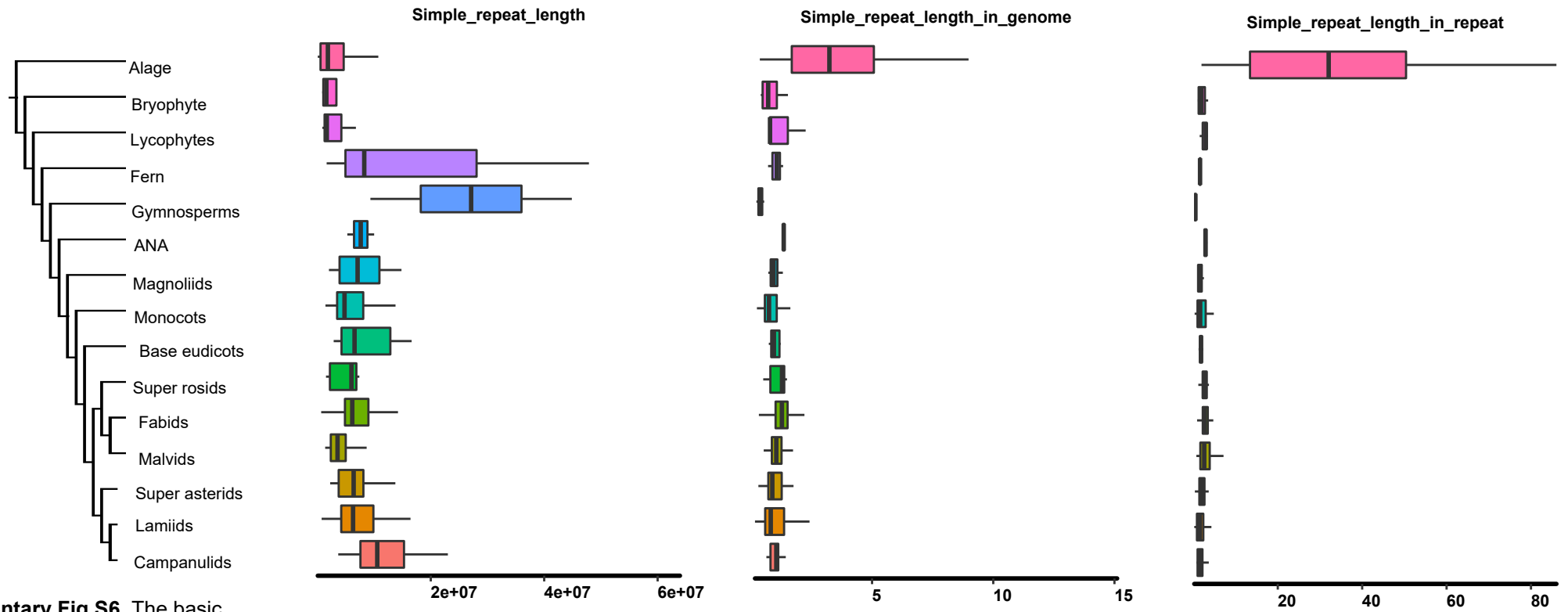




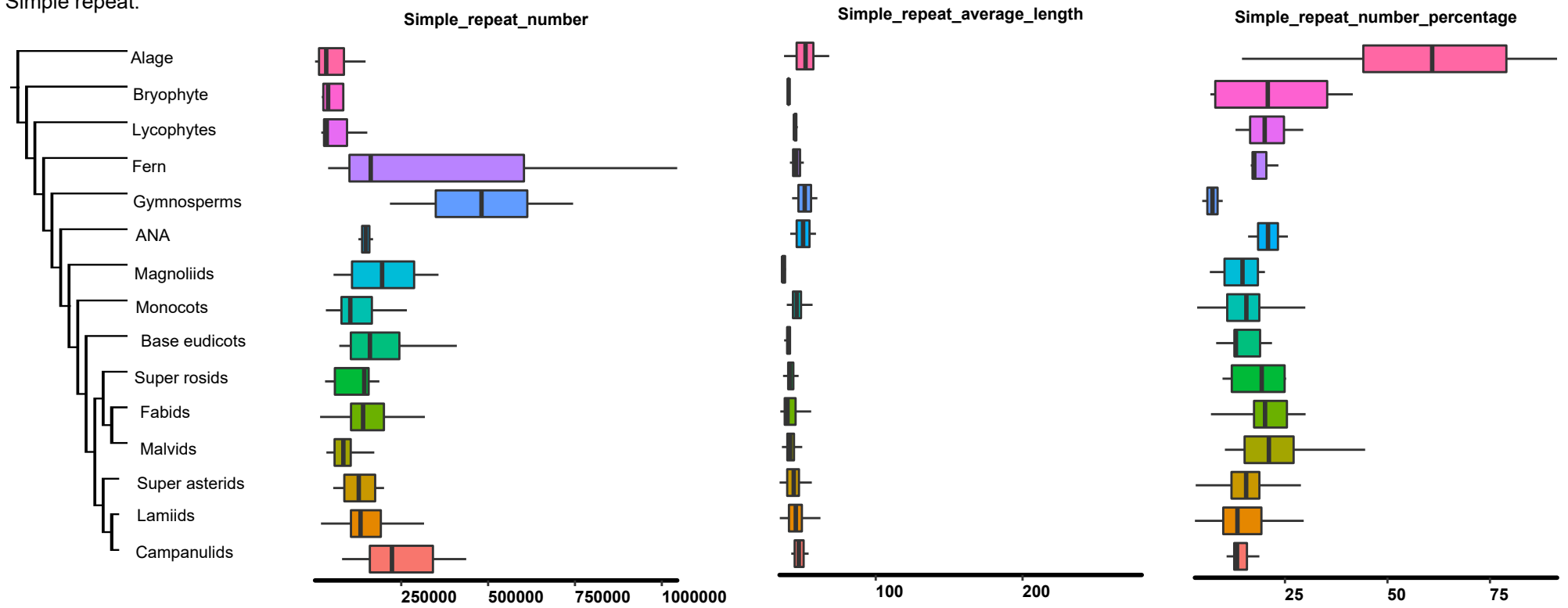
Supplementary Fig S4. The basic features of TIR.



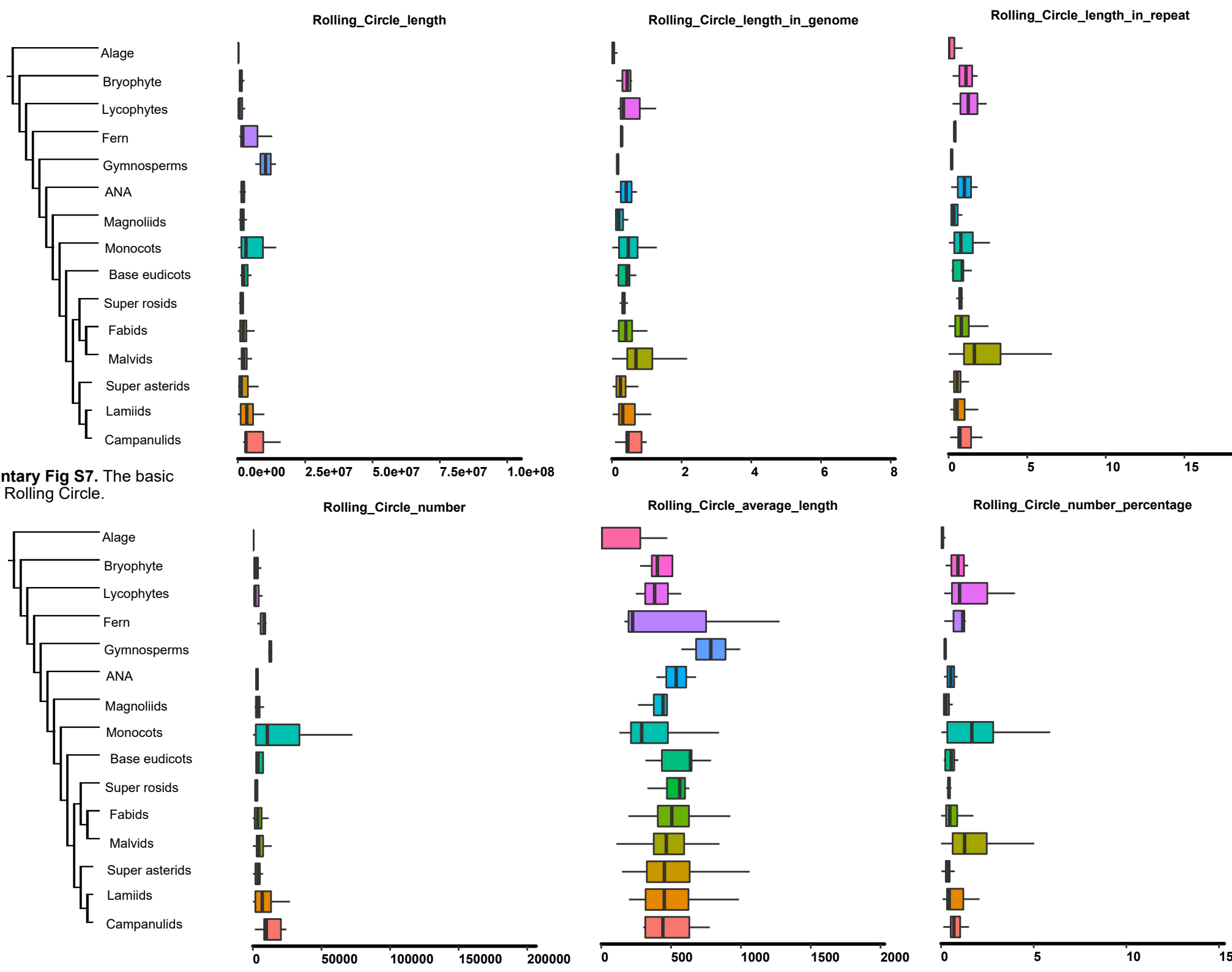


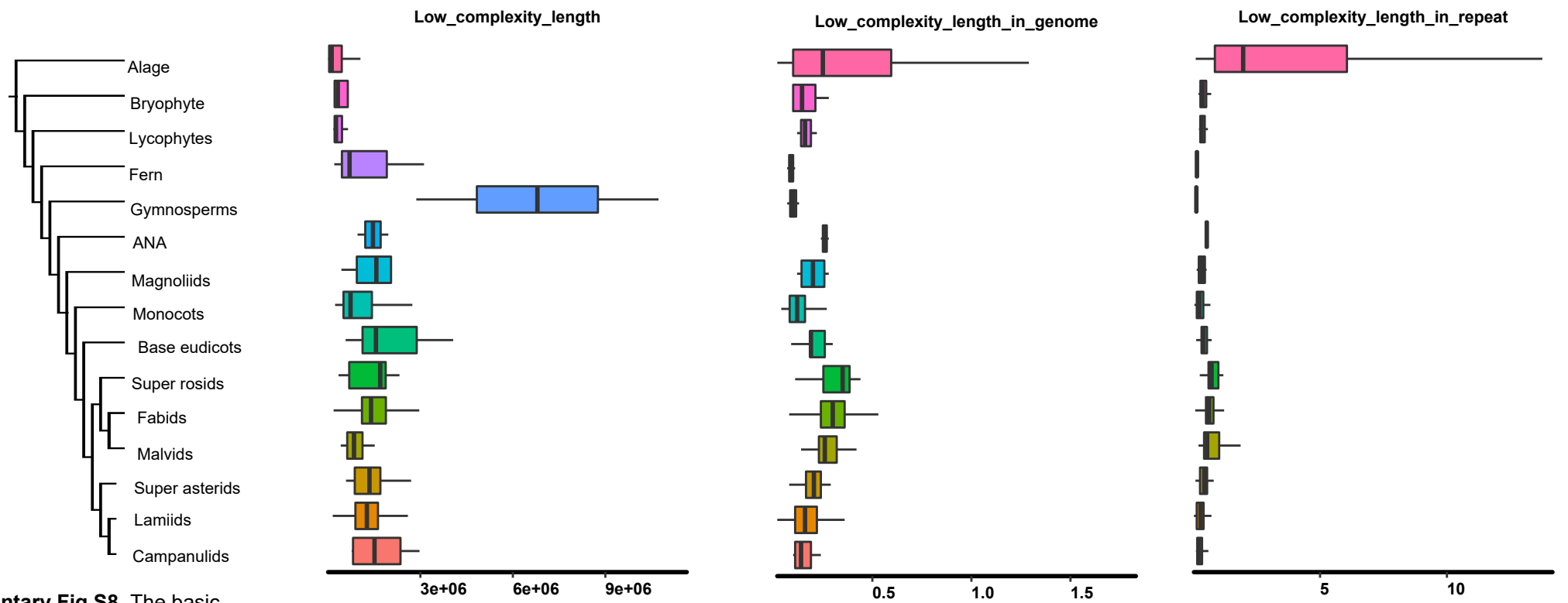


Supplementary Fig S6. The basic features of Simple repeat.



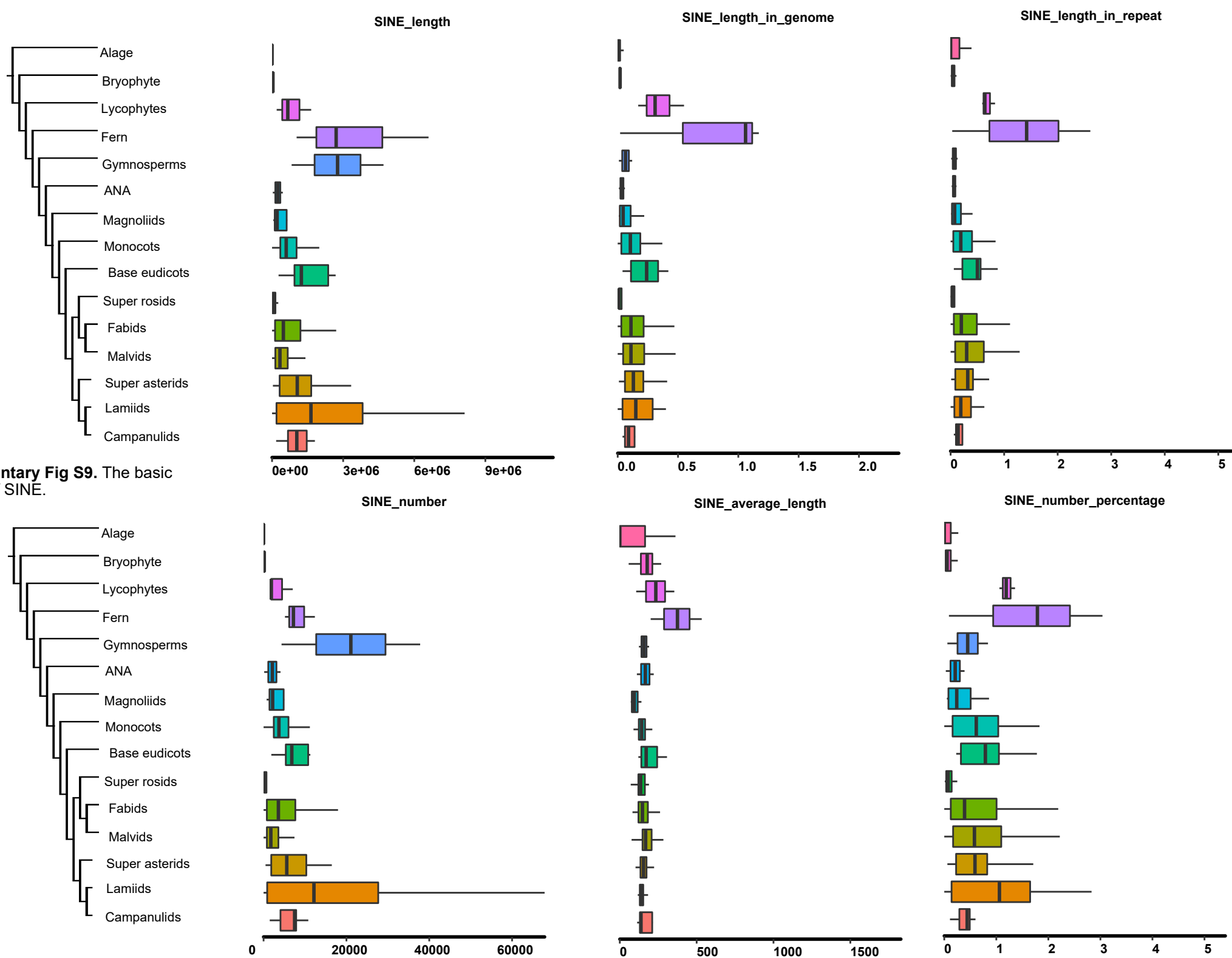
Supplementary Fig S7. The basic features of Rolling Circle.



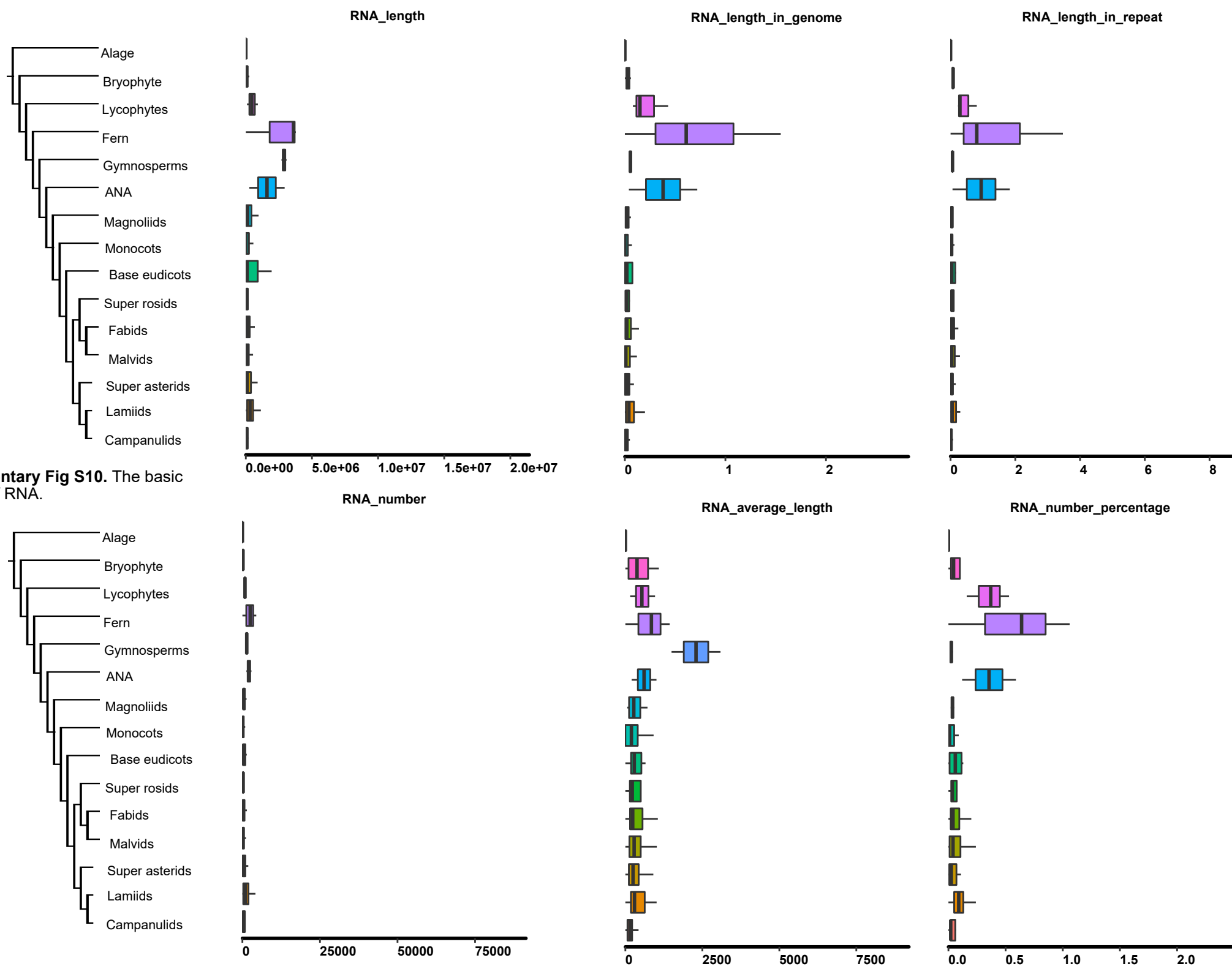


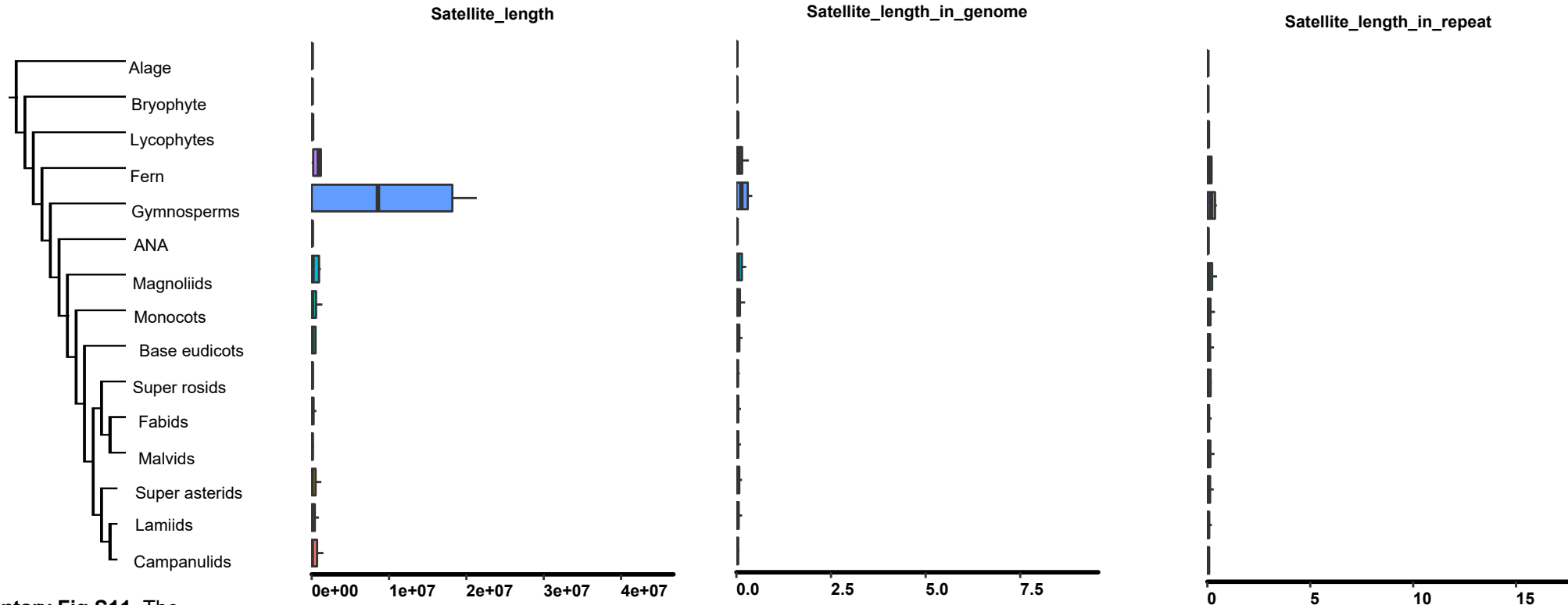
Supplementary Fig S8. The basic features of Low complexity.

Supplementary Fig S9. The basic features of SINE.

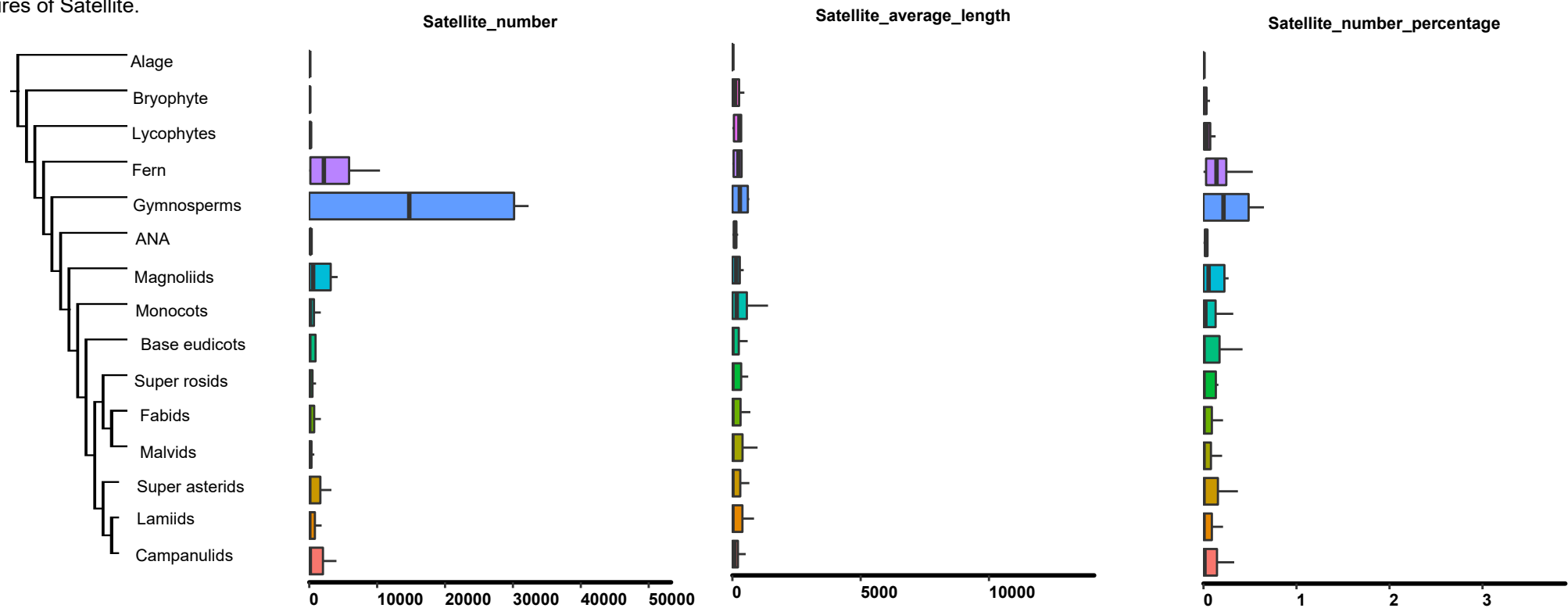


Supplementary Fig S10. The basic features of RNA.





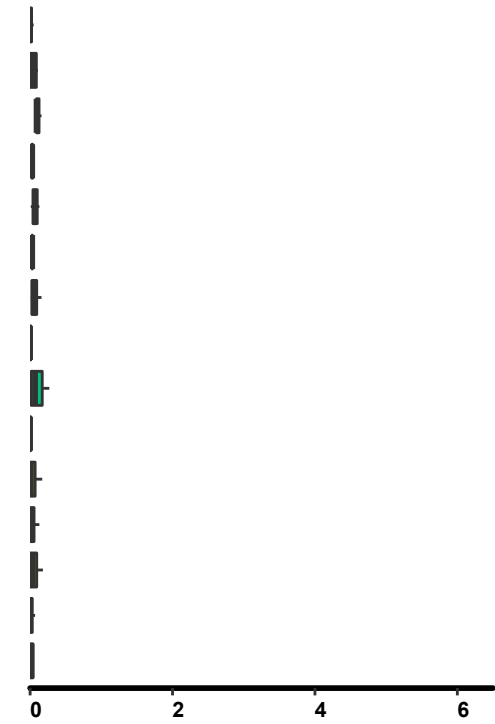
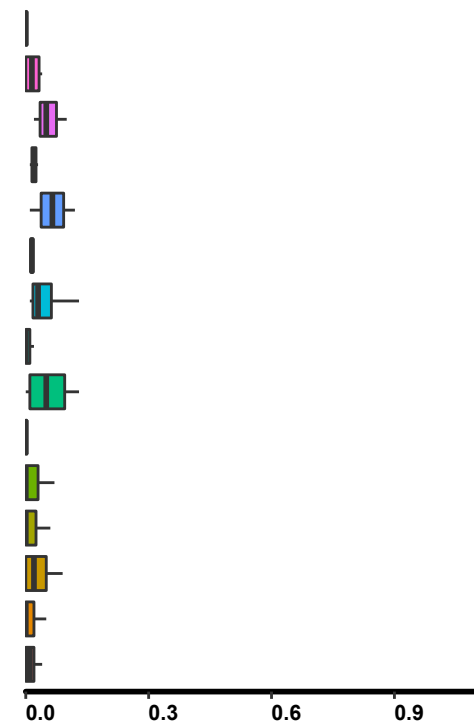
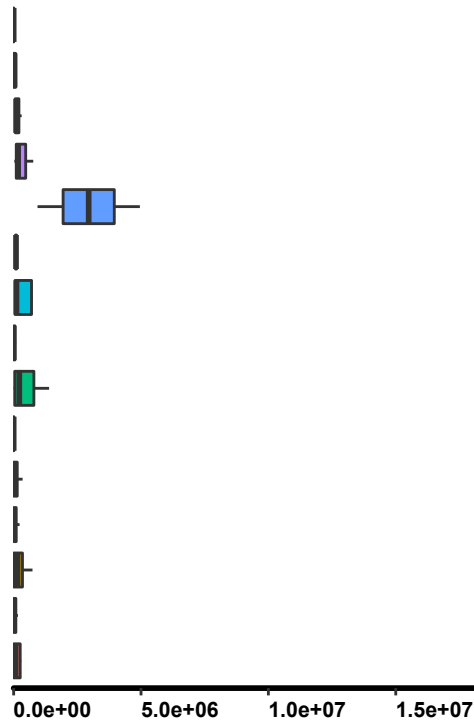
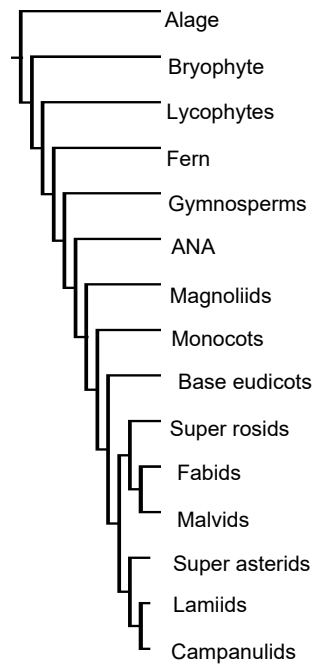
Supplementary Fig S11. The basic features of Satellite.



DNA_Polymerase_length

DNA_Polymerase_length_in_genome

DNA_Polymerase_length_in_repeat

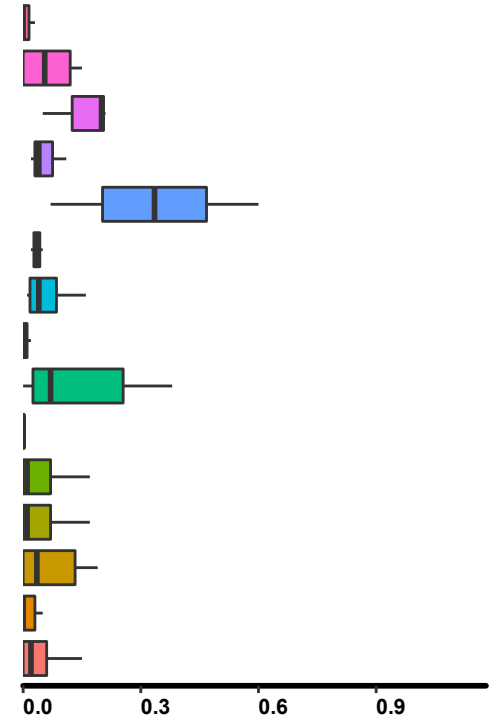
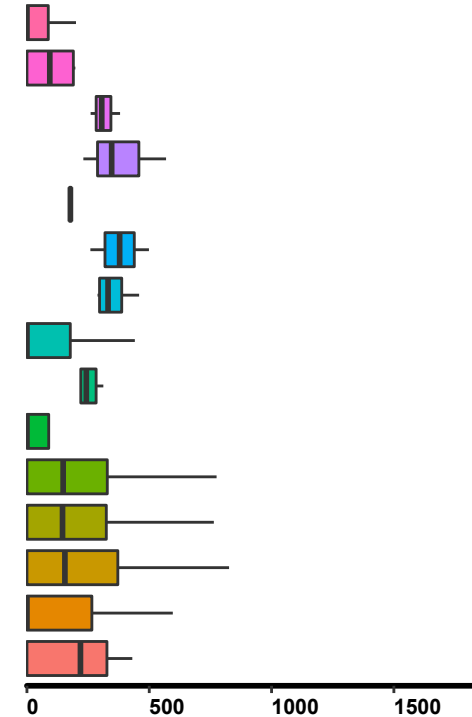
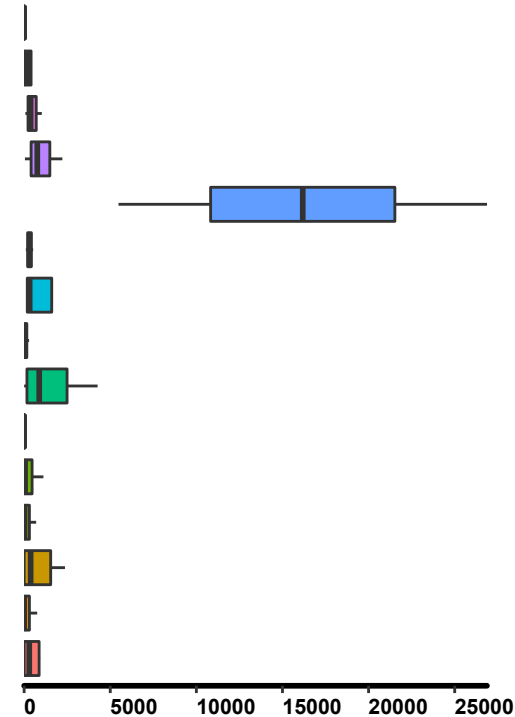
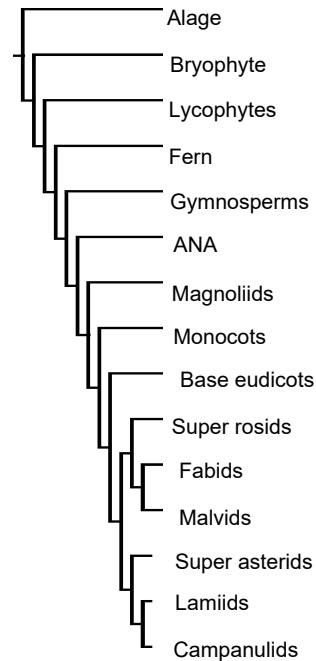


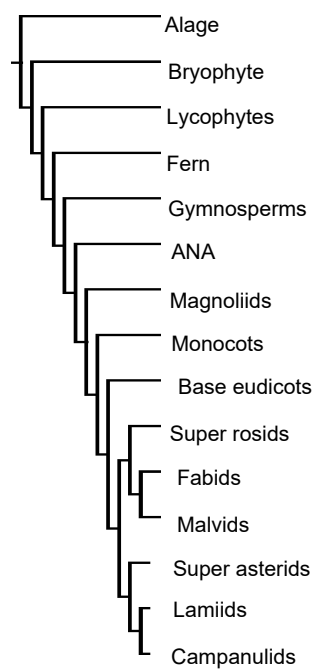
Supplementary Fig S12. The basic features of DNA Polymerase.

DNA_Polymerase_number

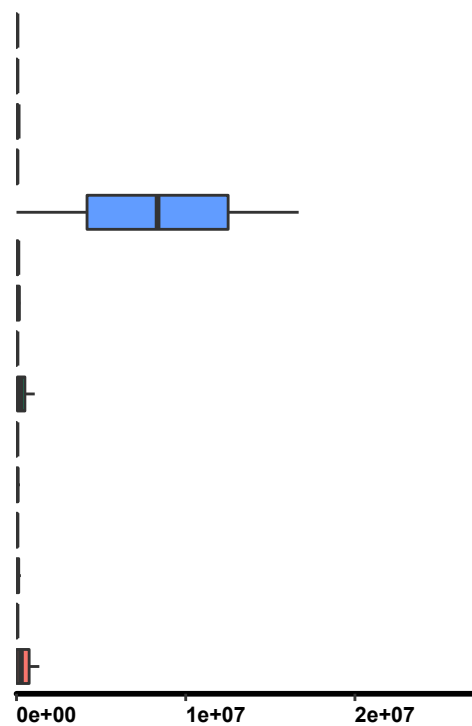
DNA_Polymerase_average_length

DNA_Polymerase_number_percentage

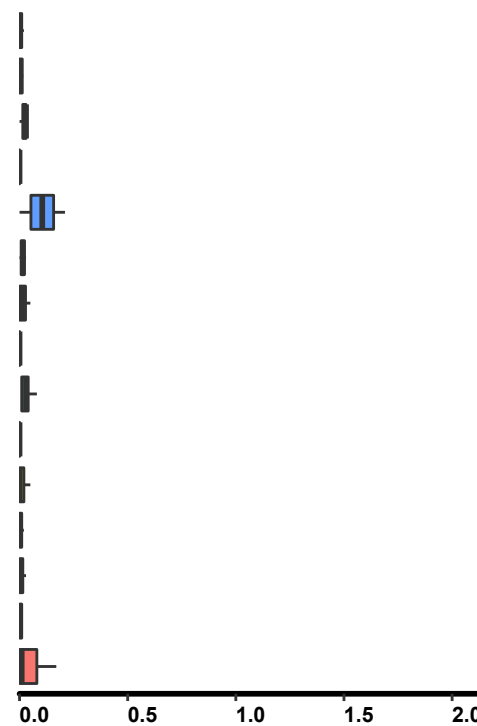




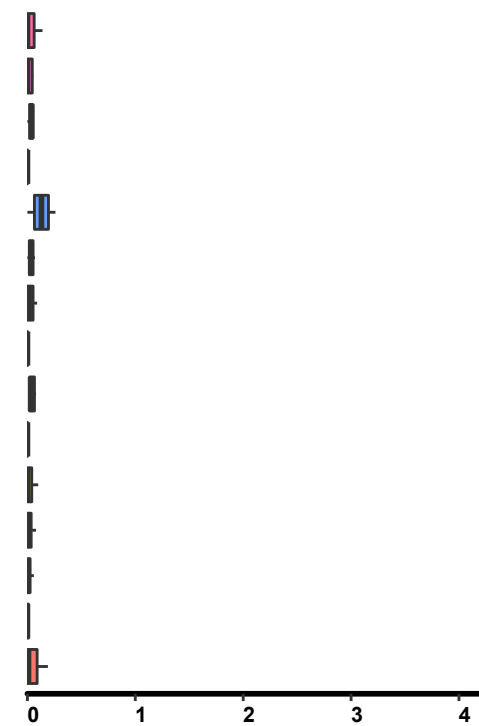
Circular_dsDNA_length



Circular_dsDNA_length_in_genome

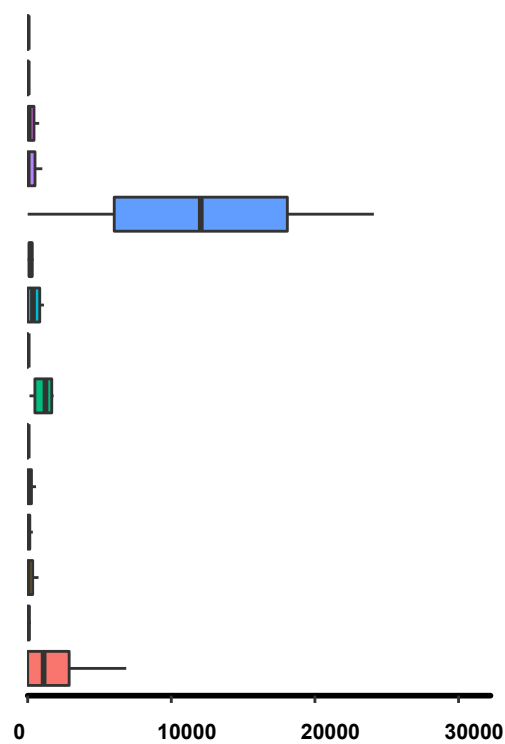


Circular_dsDNA_length_in_repeat

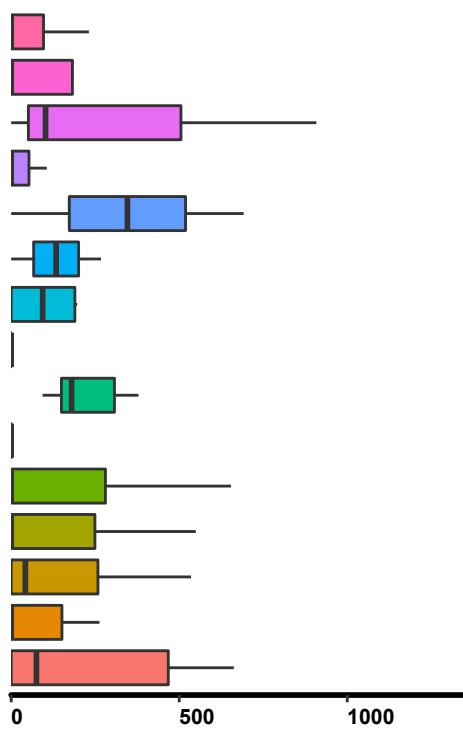


Supplementary Fig S13. The basic features of Circular dsDNA.

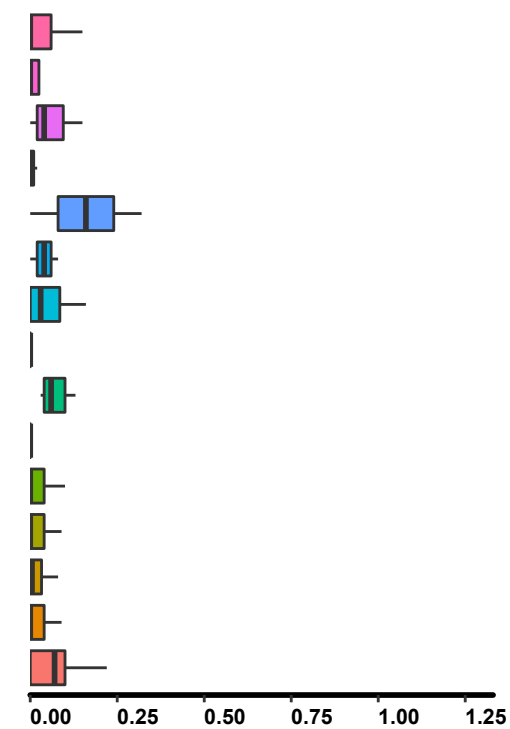
Circular_dsDNA_number

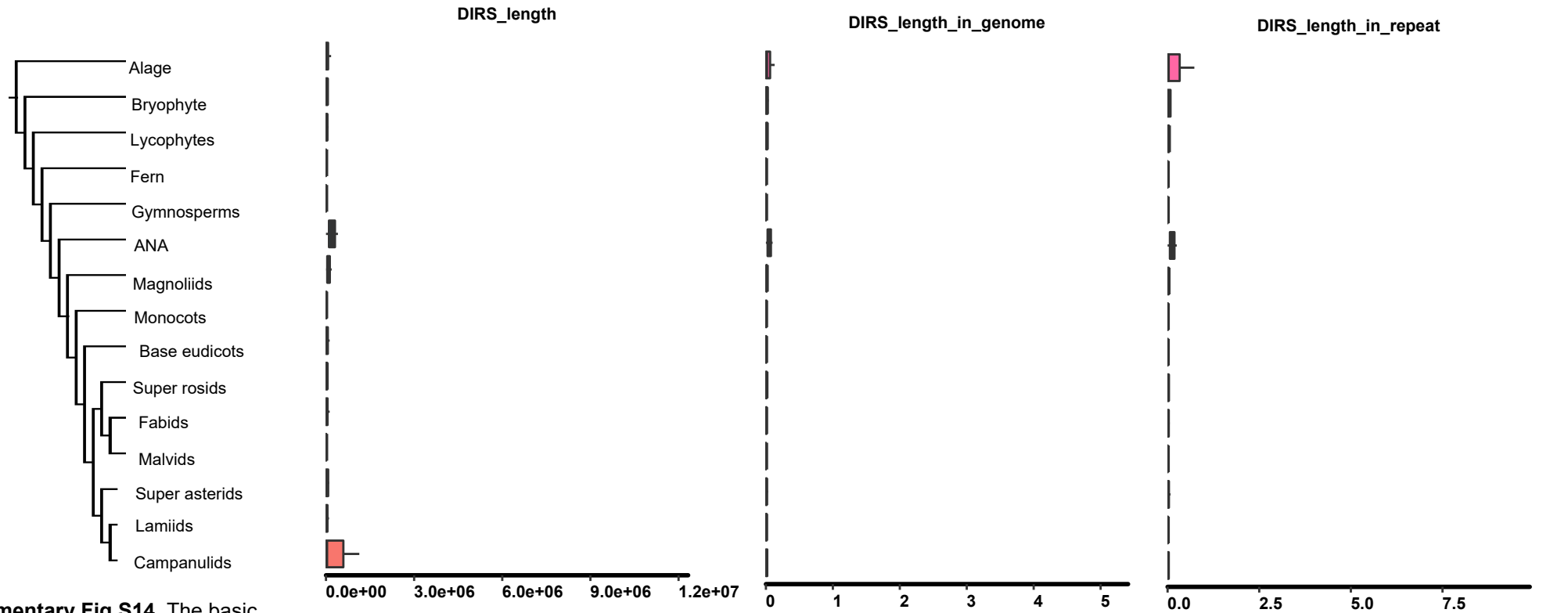


Circular_dsDNA_average_length

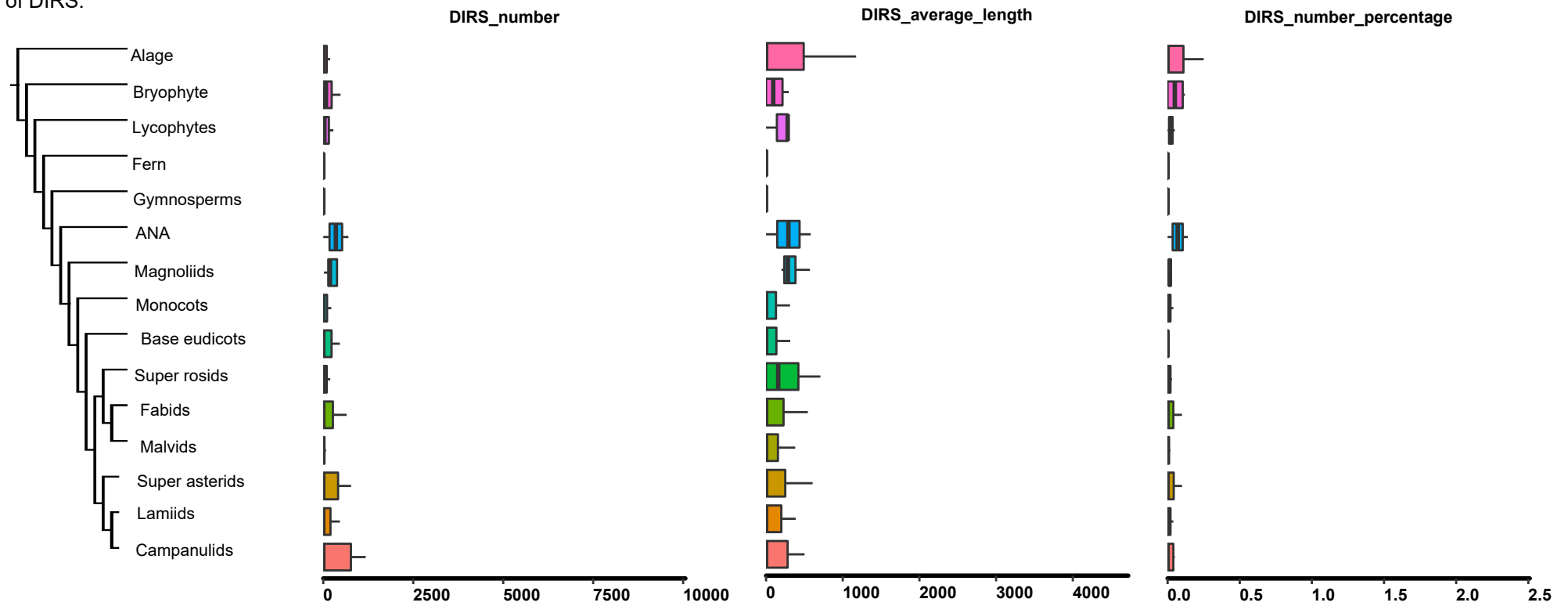


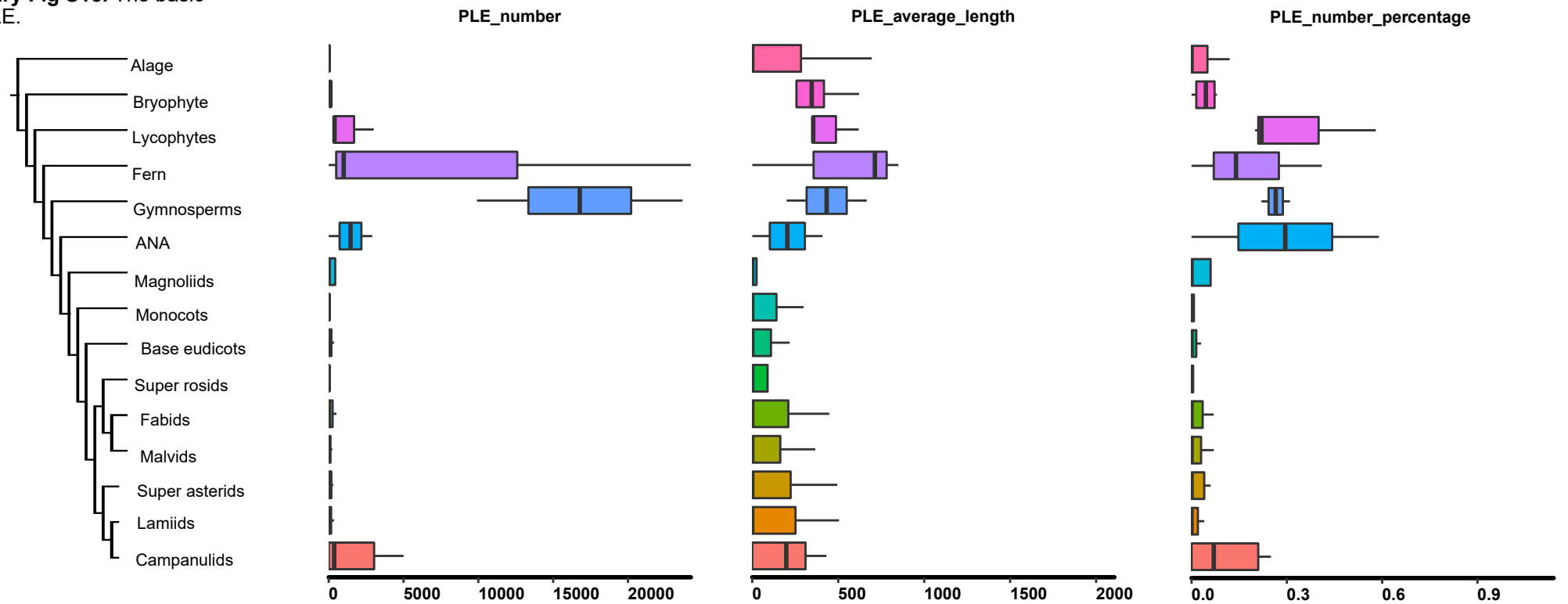
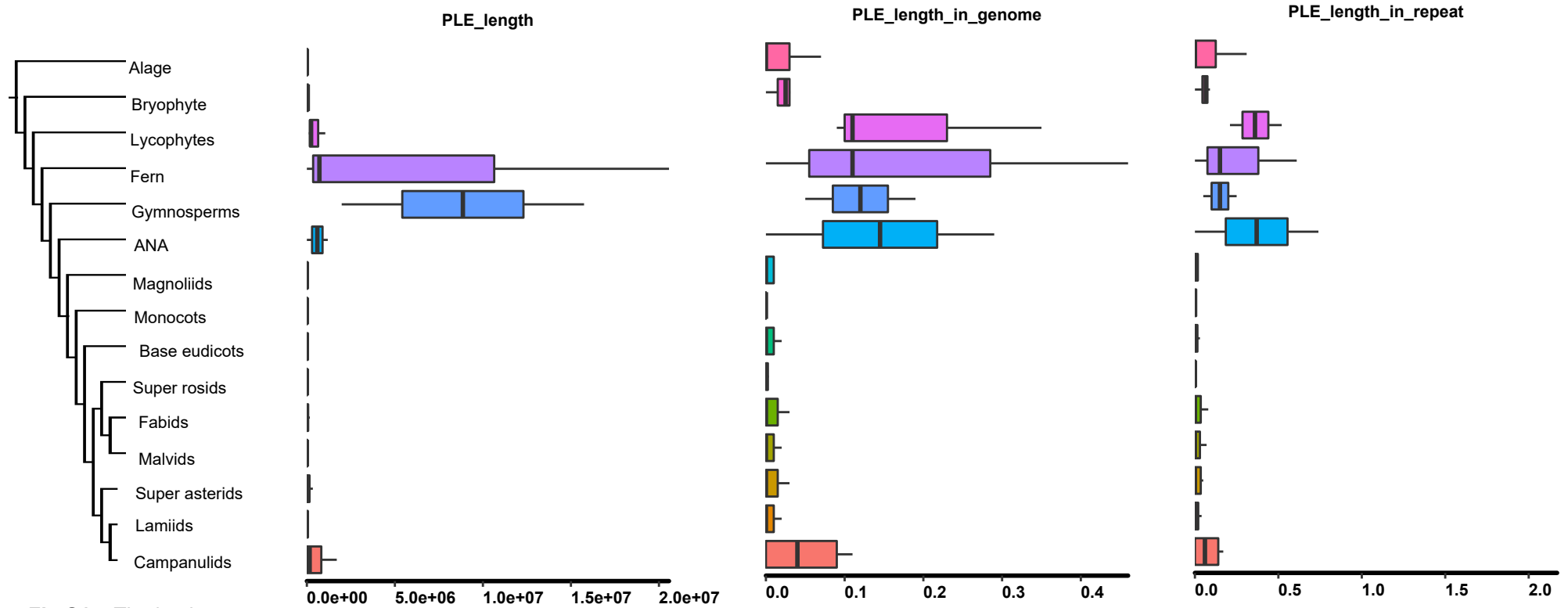
Circular_dsDNA_number_percentage



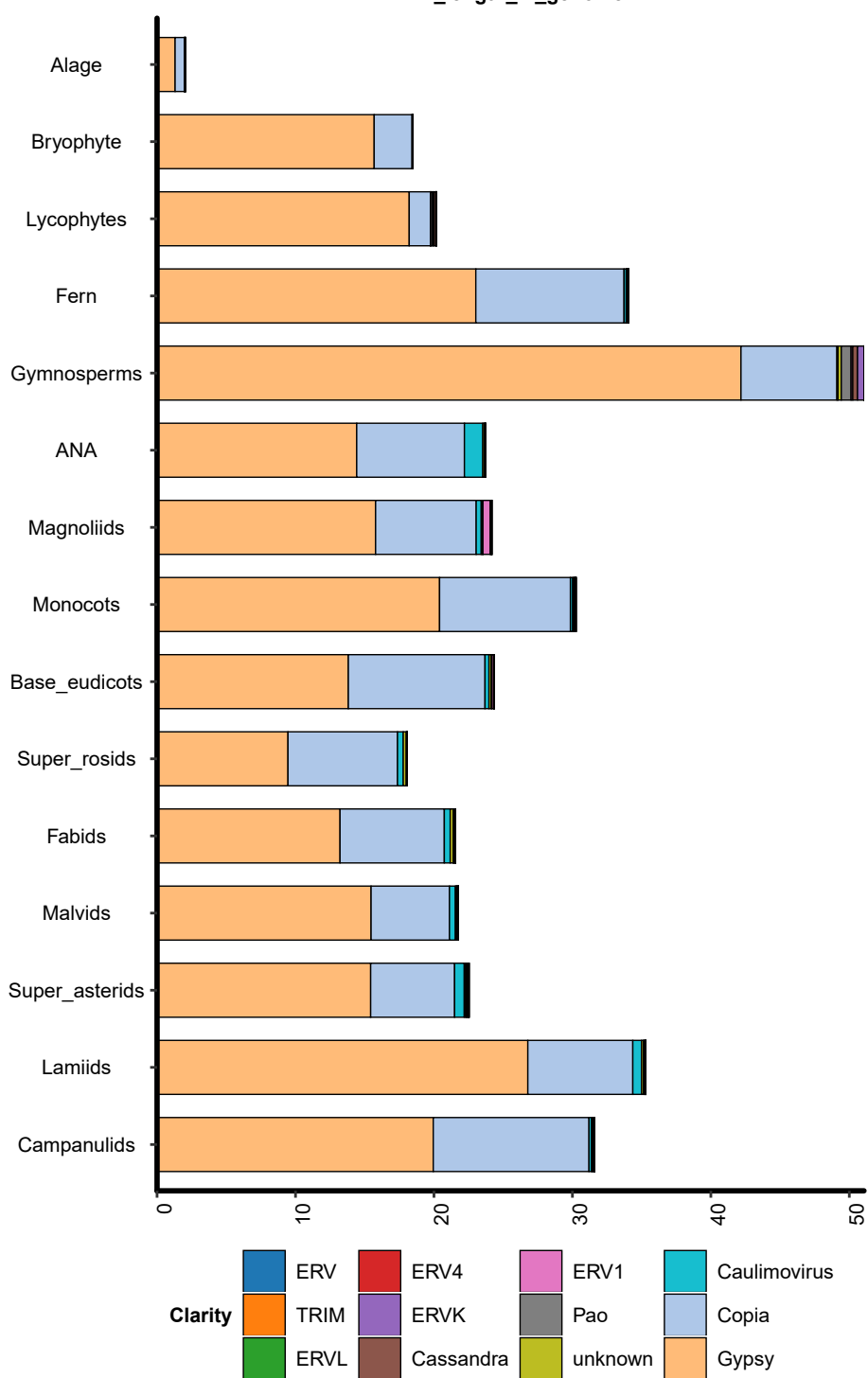


Supplementary Fig S14. The basic features of DIRS.

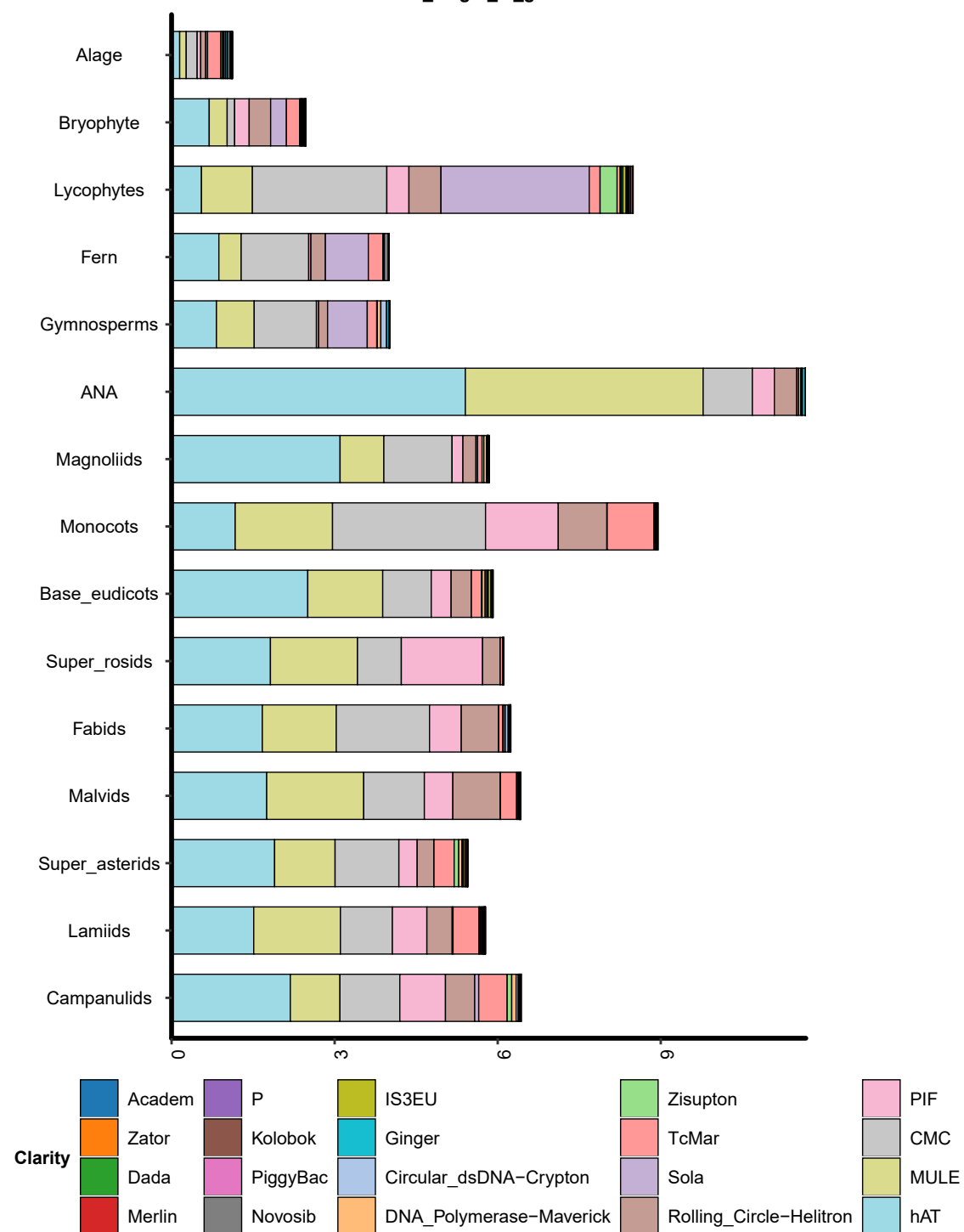




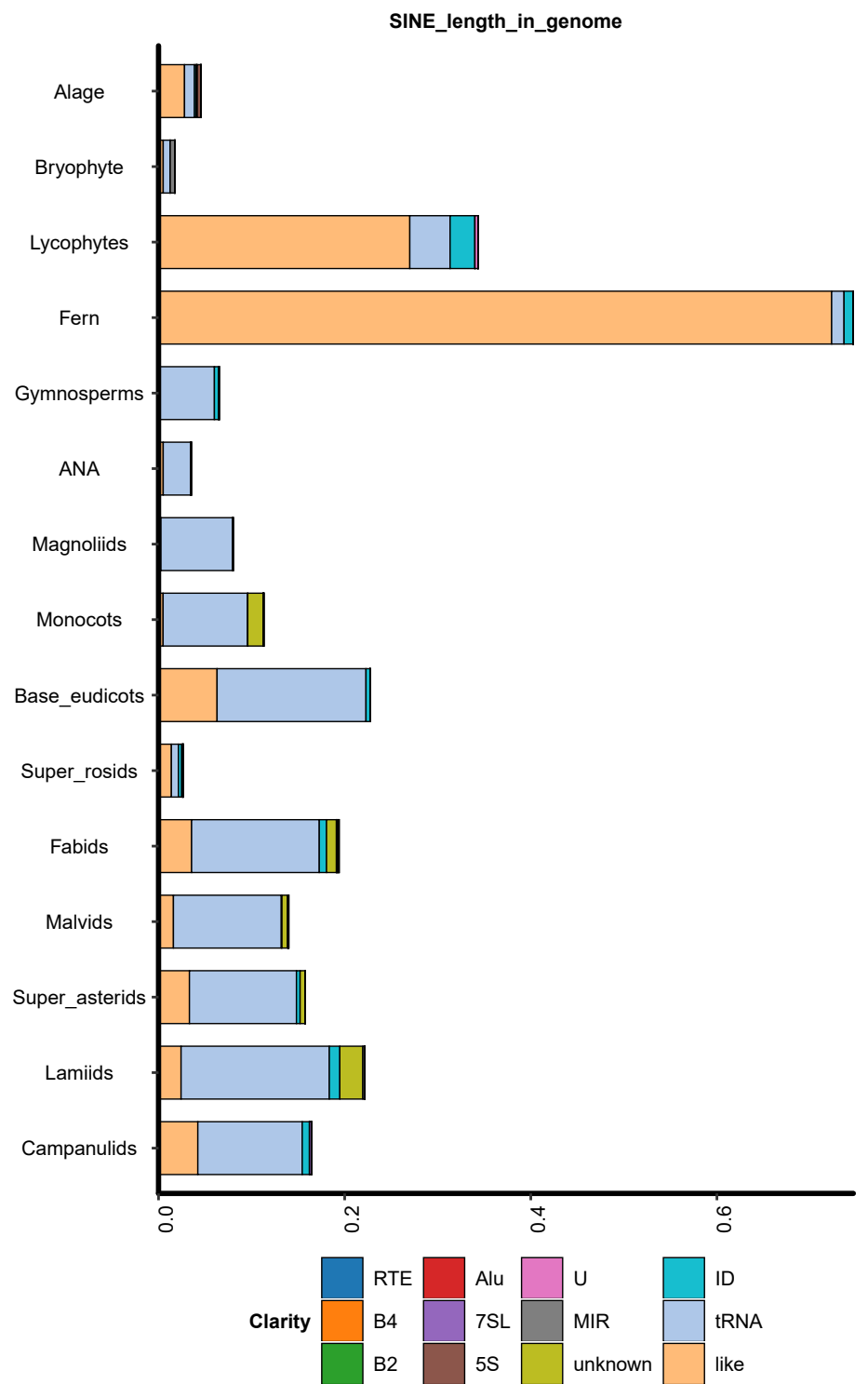
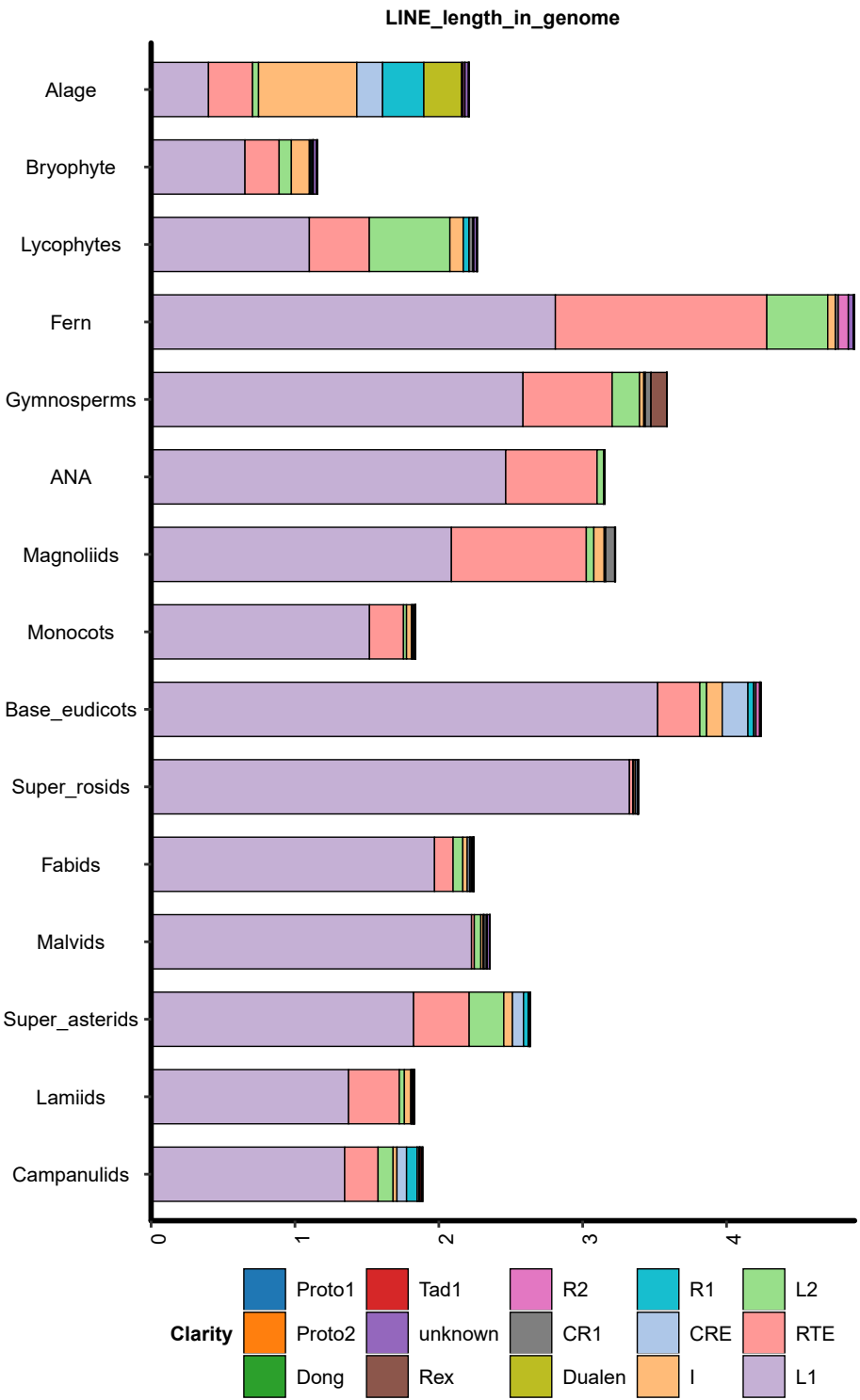
LTR_length_in_genome



DNA_length_in_genome



Supplementary Fig S16. (a)Proportion of the length of LTR superfamily in plant genome. **(b)**Proportion of the length of DNA transposon superfamily in plant genome.



Supplementary Fig S17. (a)Proportion of the length of LINE superfamily in plant genome. (b)Proportion of the length of SINE superfamily in plant genome.

Intact LTR insert time

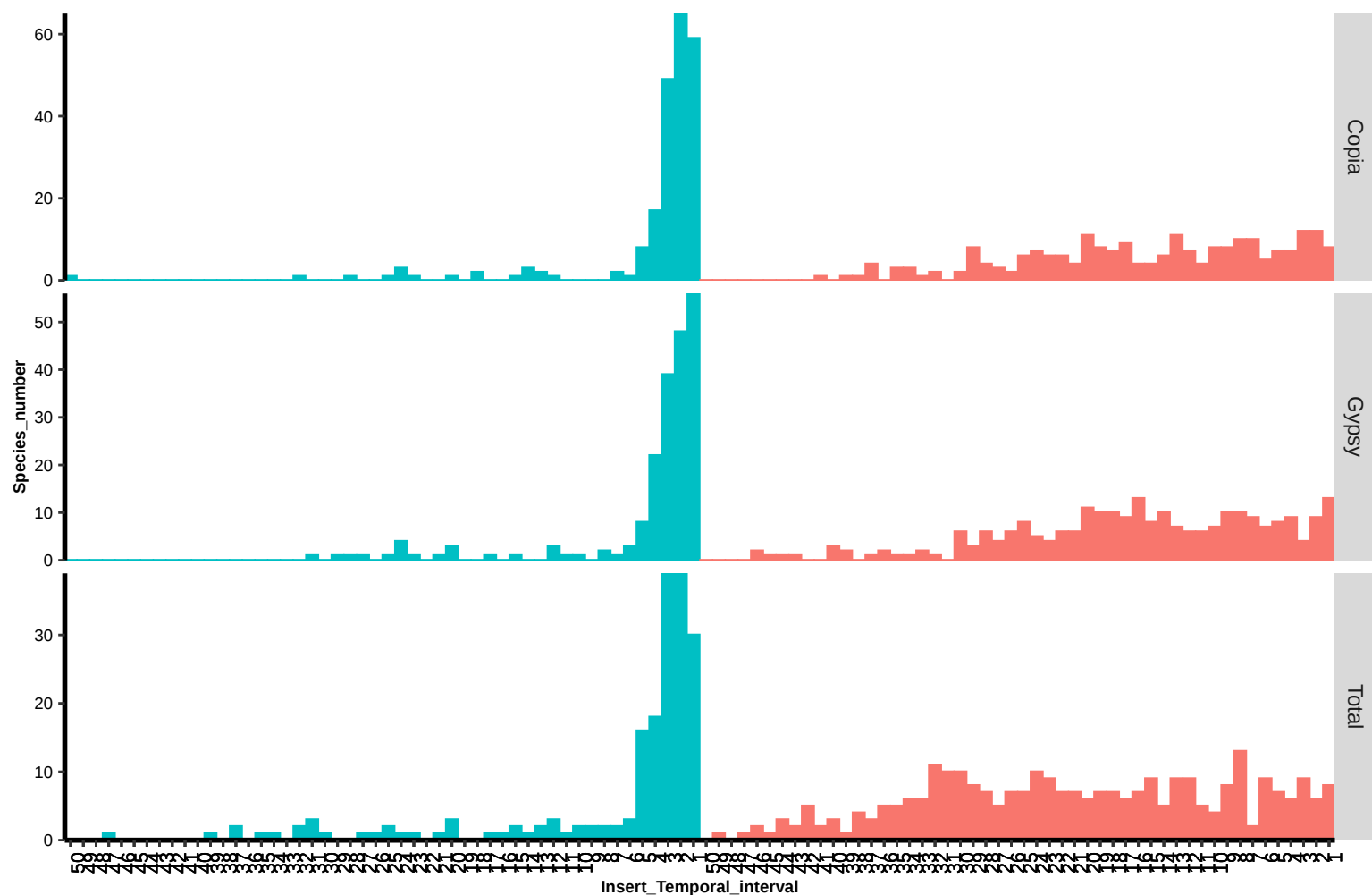
Temporal



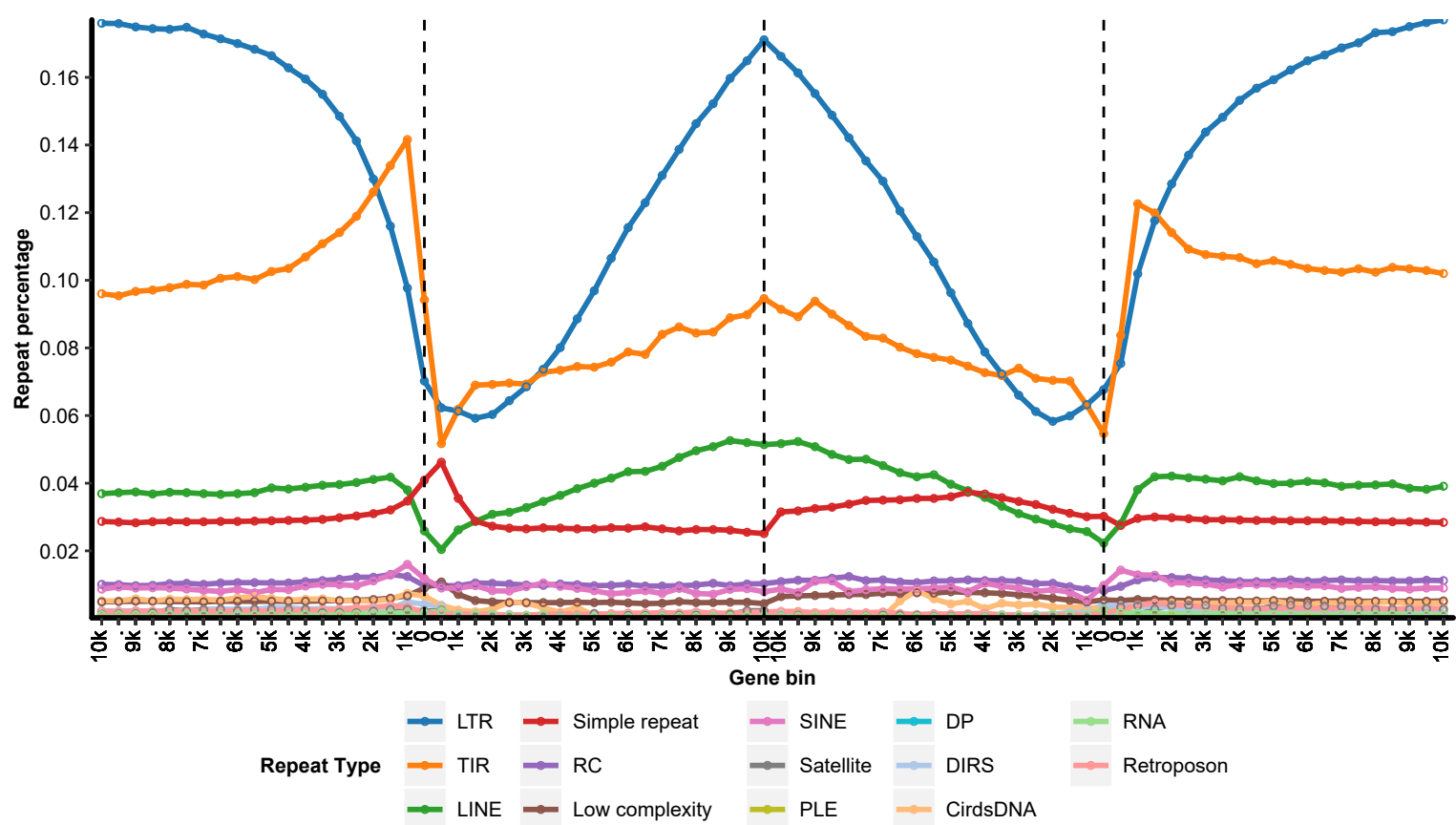
Million year



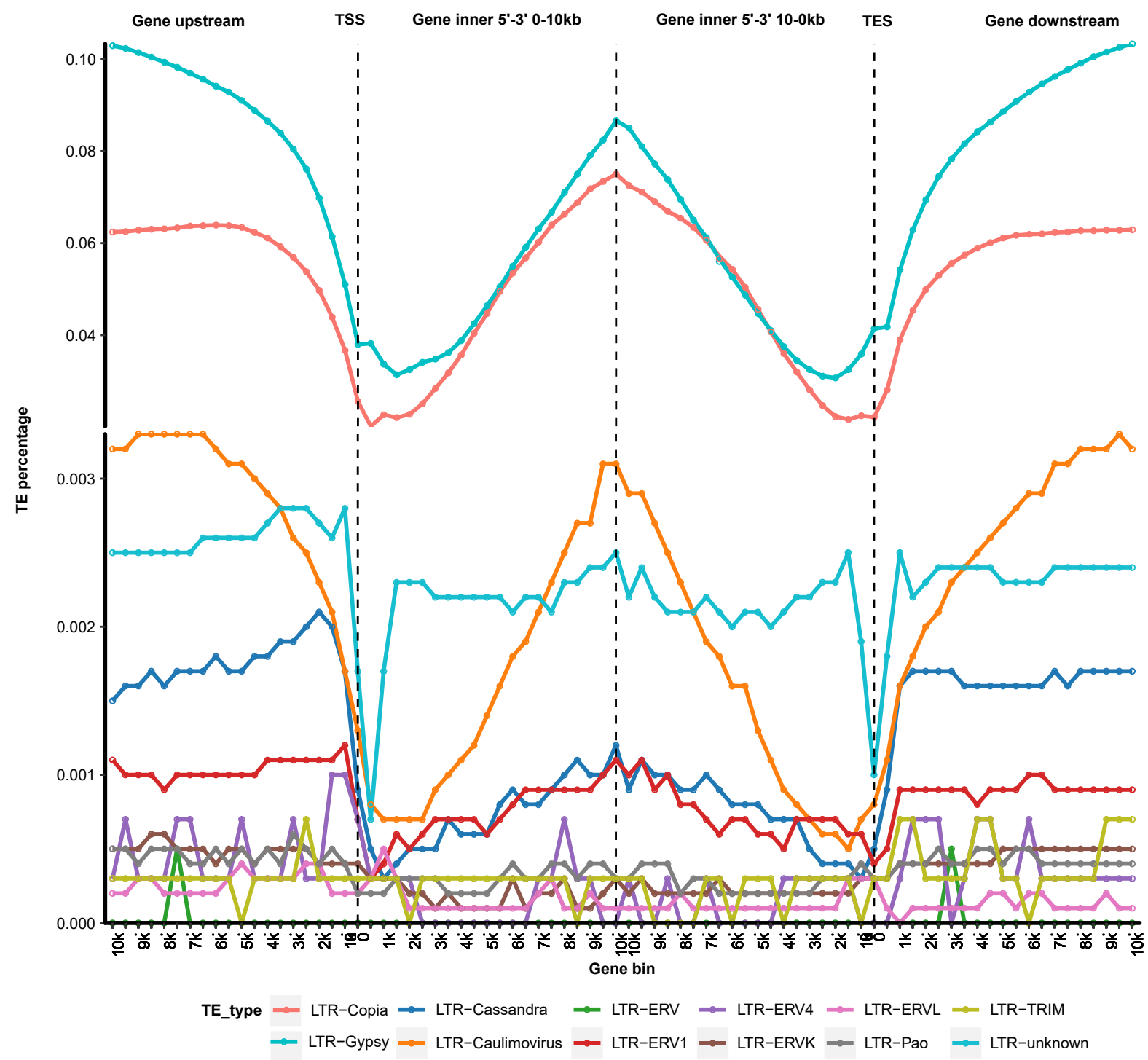
Hundred_thousand year



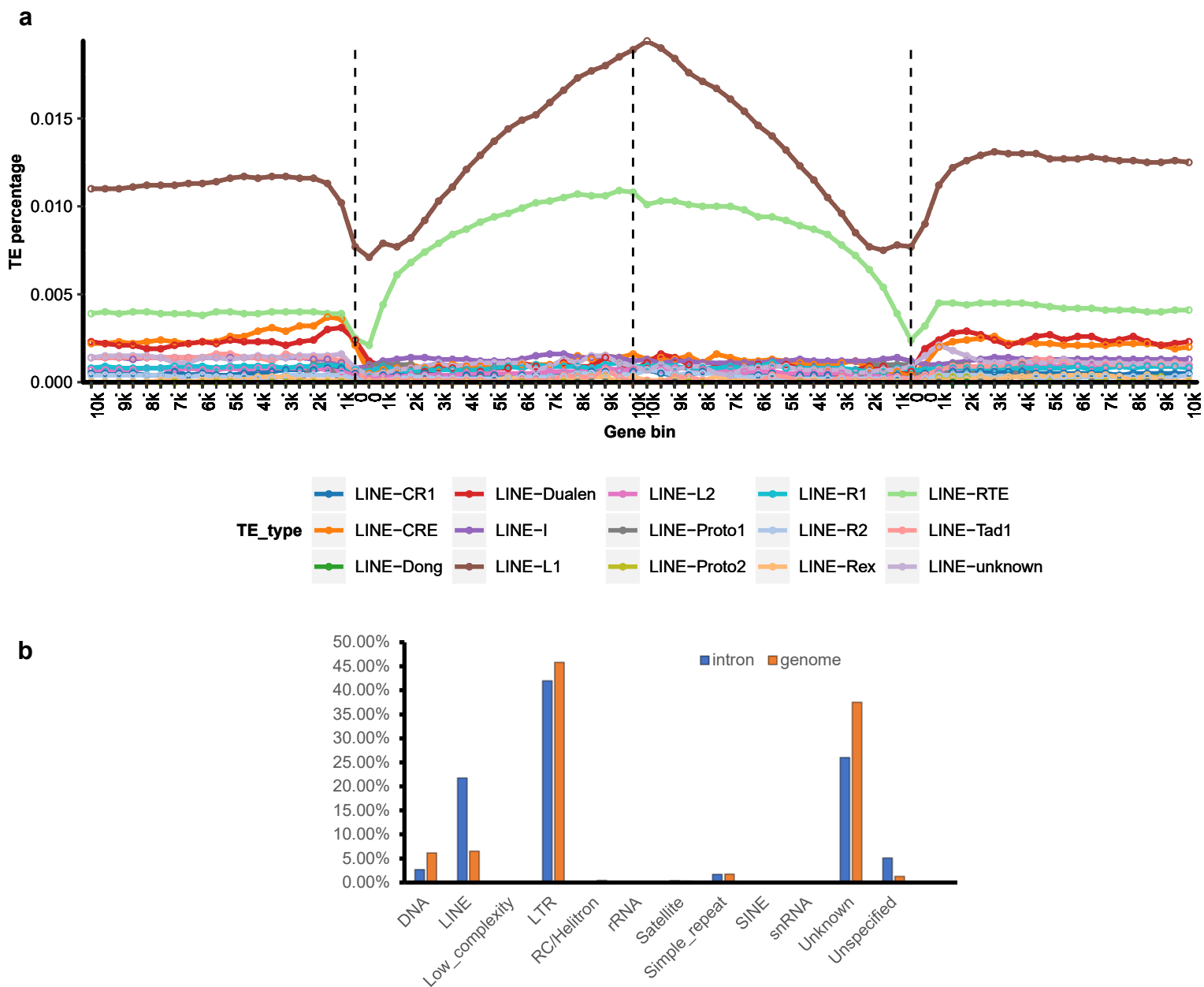
Supplementary Fig S18. The intact LTR insert time of every species.



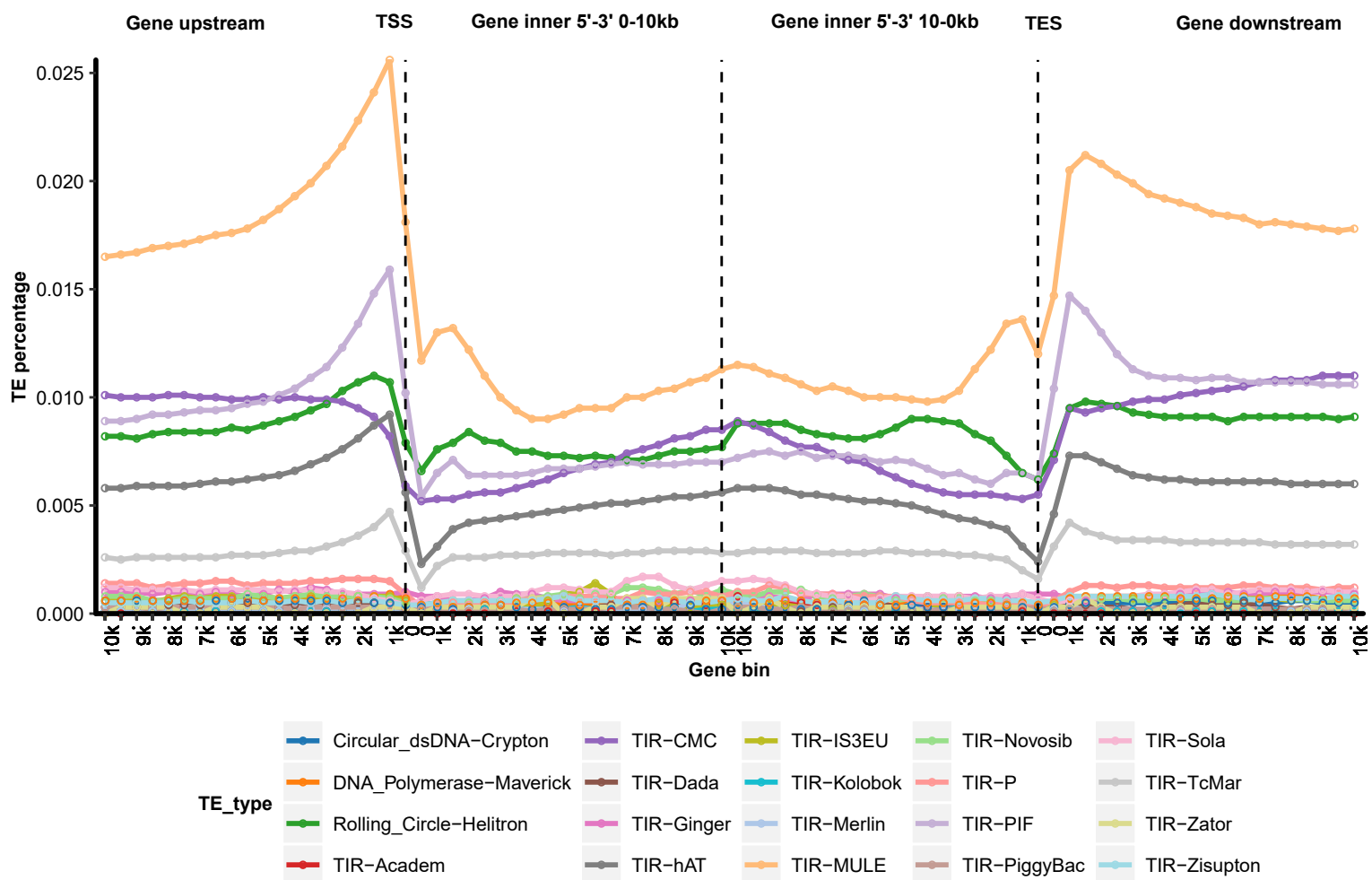
Supplementary Fig S19. Distributions of repeat sequences across gene bodies and flanking regions. The percentage of repeats were calculated for each 0.5kb window. TSS, transcription start site; TES, transcription end site.



Supplementary Fig S20. Distributions of LTR across gene bodies and flanking regions. The percentage of repeats were calculated for each 0.5kb window. TSS, transcription start site; TES, transcription end site.



Supplementary Fig S21. (a) Distributions of LINE across gene bodies and flanking regions. The percentage of repeats were calculated for each 0.5kb window. TSS, transcription start site; TES, transcription end site. **(b)** *Adiantum capillus* repeat sequences in the genome and repeat sequences in intron.



Supplementary Fig S22. Distributions of DNA transposon across gene bodies and flanking regions. The percentage of repeats were calculated for each 0.5kb window. TSS, transcription start site; TES, transcription end site.