

Deciphering shared attributes of plant long non-coding RNAs through a comparative computational approach

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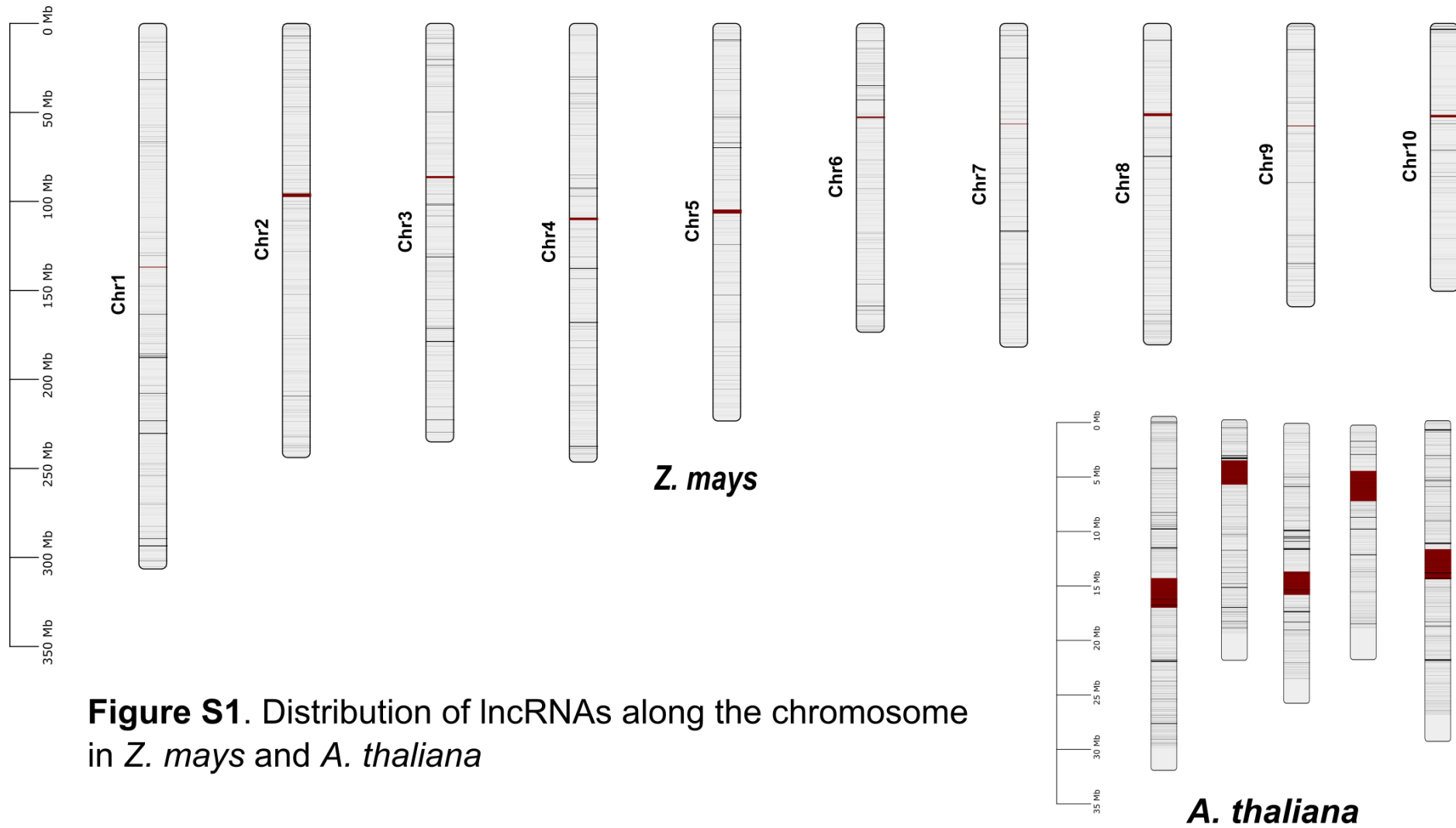
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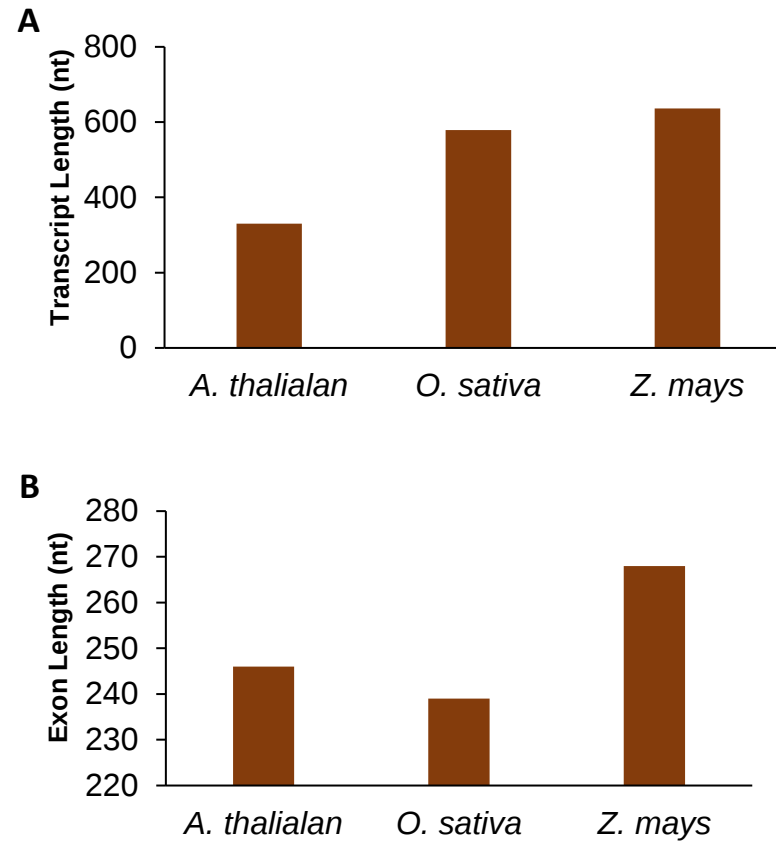


Figure S2. (A) The median size of full-length transcript of in *A. thaliana*, *O. sativa*, and *Z. mays*, respectively. **(B)** The median length of exon in *A. thaliana*, *O. sativa* and *Z. mays*, respectively.

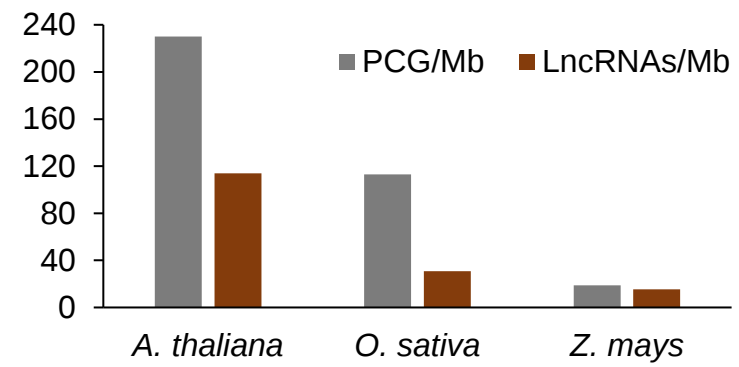


Figure S3. Bar graph showing the density of LncRNAs and protein coding genes per Mb of the genome.

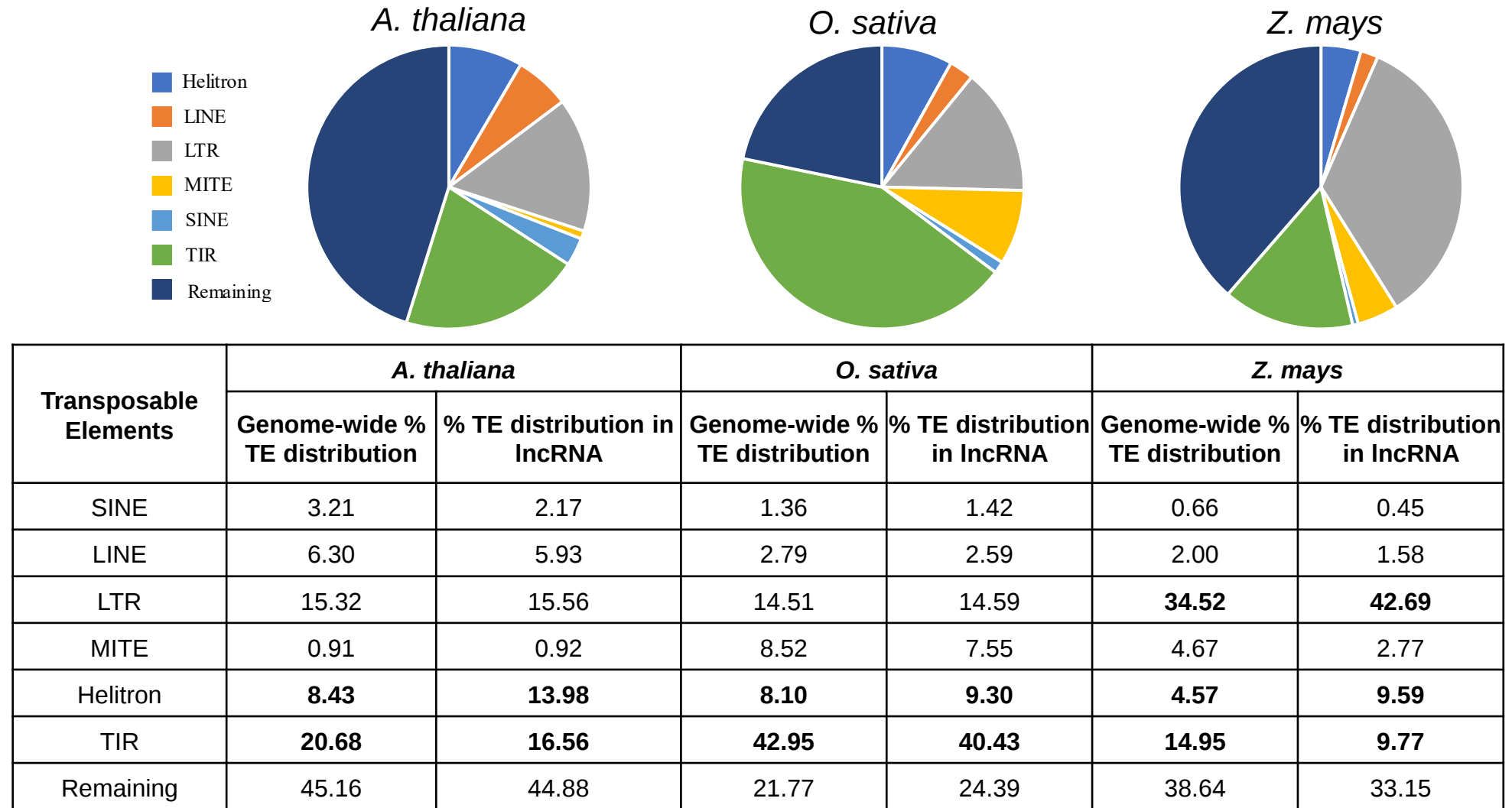


Figure S4. (A) Distribution of different classes of TEs in the genome of *A. thaliana*, *O. sativa* and *Z. mays*. (B) Comparative table of TEs distribution in Genome and lncRNA transcribing regions

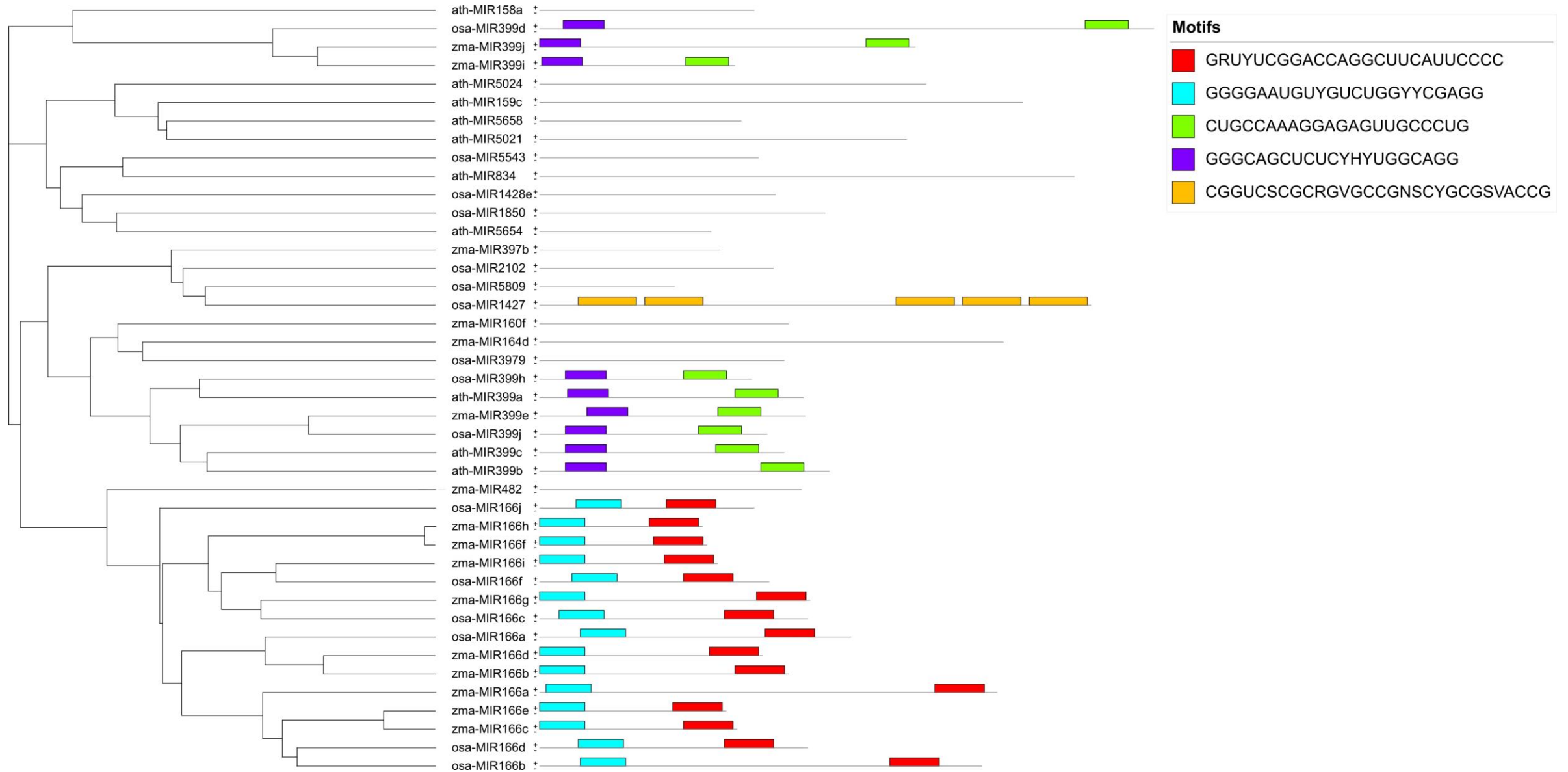


Figure S5: The cladogram showing the relatedness of miRNA targeted by lncRNA endogenous mimics among the *A. thaliana*, *O. sativa*, and *Z. mays*. The lncRNAs possessing the endogenous target mimic revealed conserved motifs in *A. thaliana*, *O. sativa*, and *Z. mays* lncRNAs, as determined by MEME.

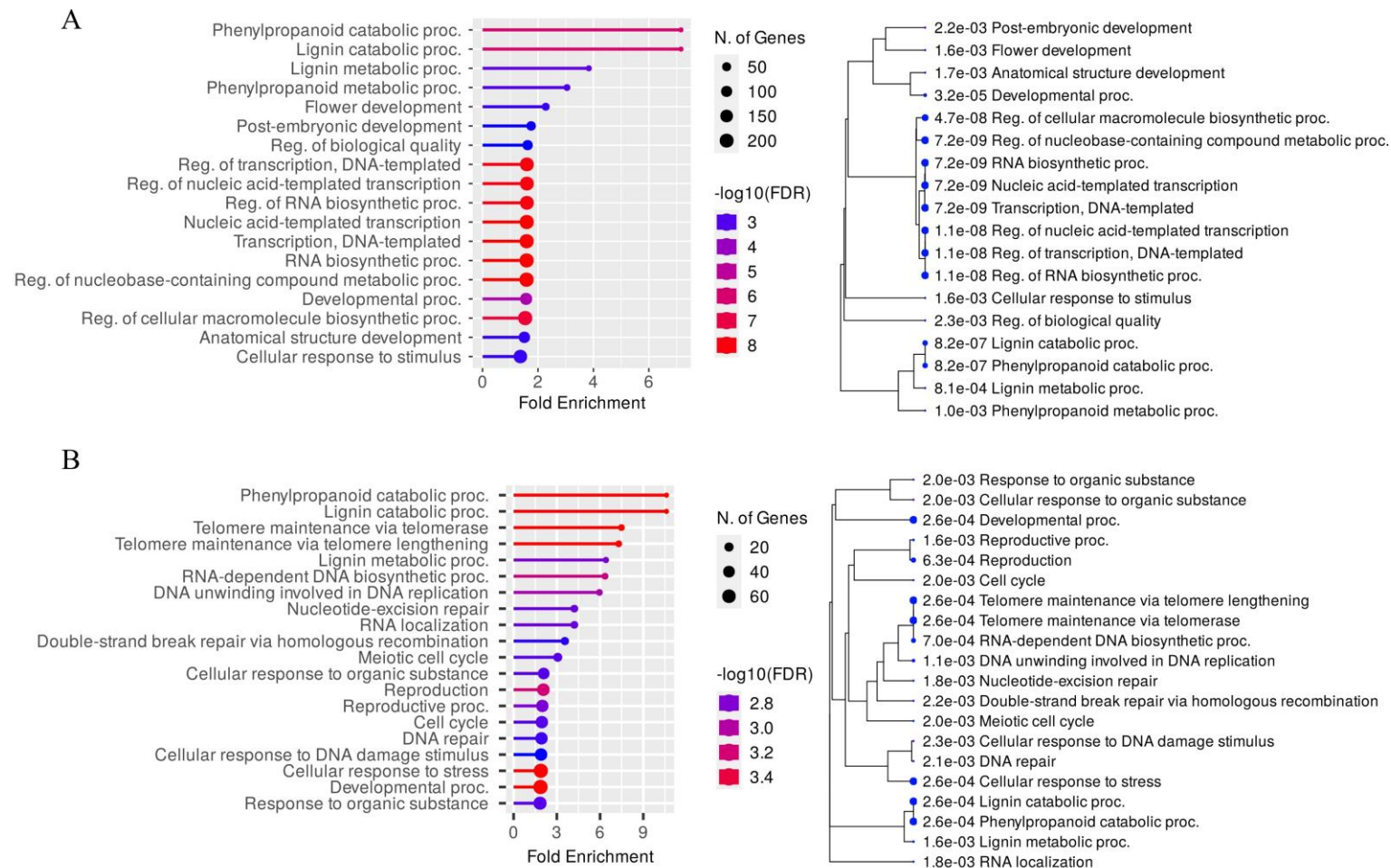


Figure S6: GO enrichment analysis showing the top 20 biological processes derived from lncRNA-associated miRNA-targeted genes in (A) *O. Sativa* and (B) *Z. mays*. The significant GO enrichment plots at $p < 0.05$ were depicted using ShinyGO v0.76. The fold enrichment of GO terms represents how drastically a particular pathway's genes are overrepresented.

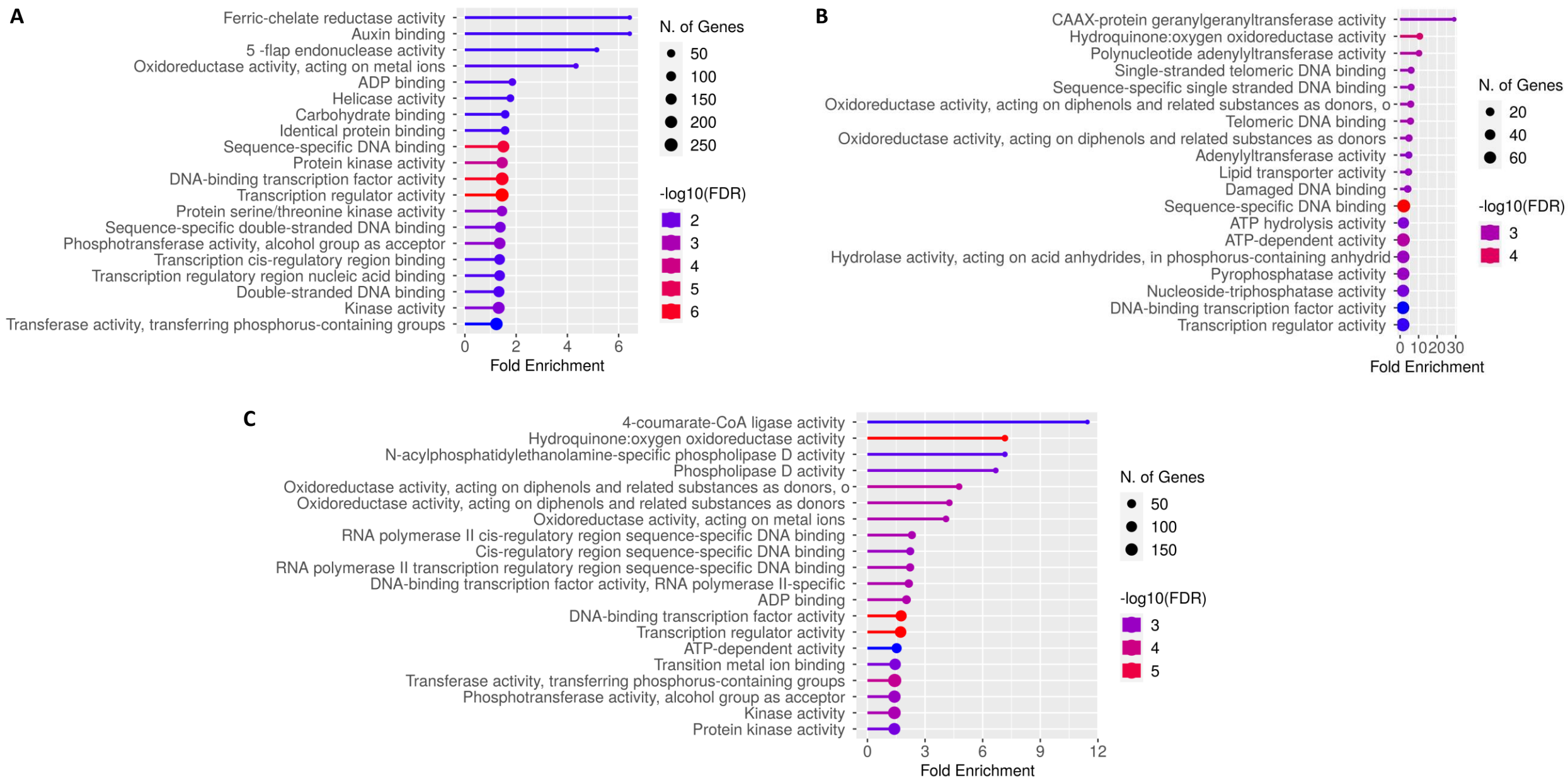


Figure S7: GO enrichment analysis showing the top 20 molecular function derived from lncRNA-associated miRNA-targeted genes in (A) *A. thaliana* (B) *Z. mays* and (C) *O. Sativa*.

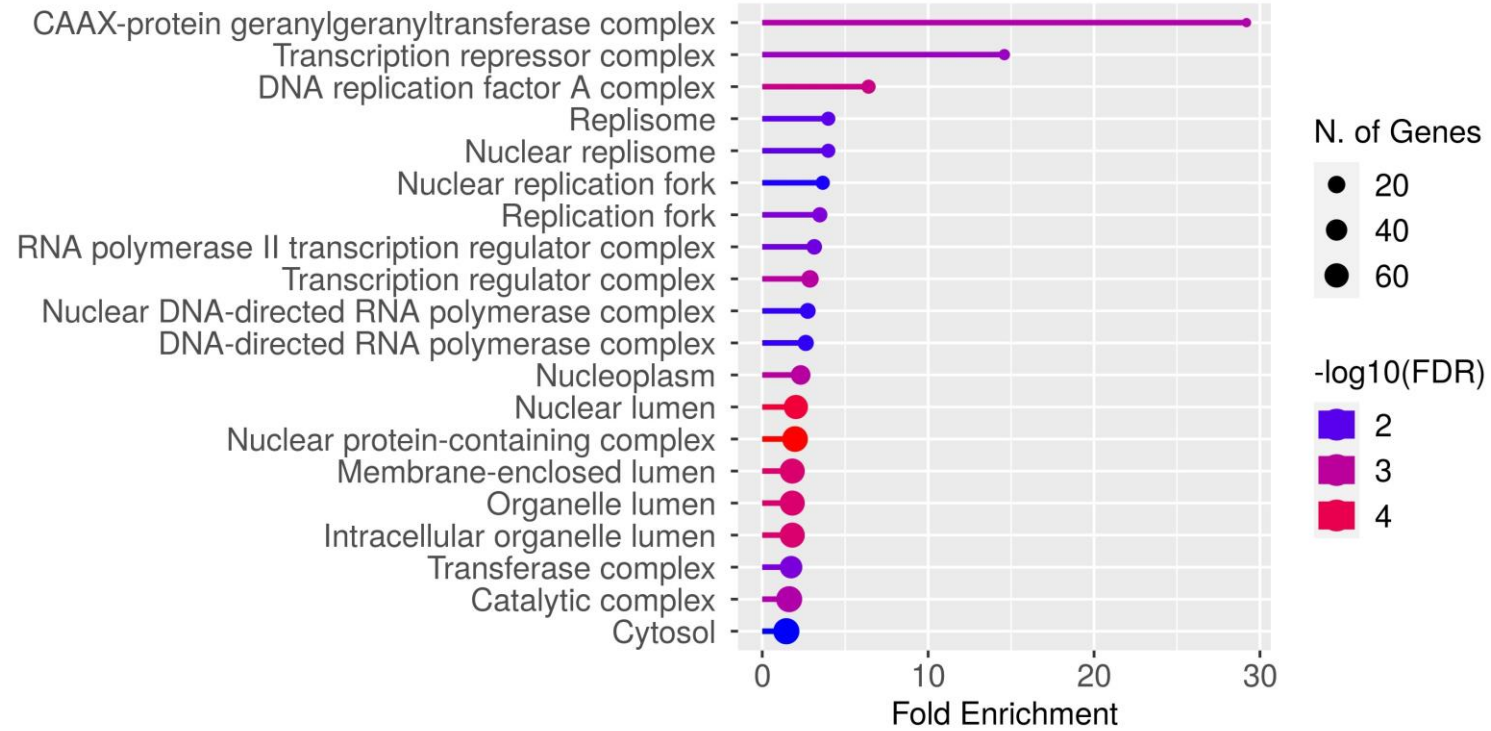


Figure S8: GO enrichment analysis showing the top 20 cellular component derived from lncRNA-associated miRNA-targeted genes in *Z. mays*

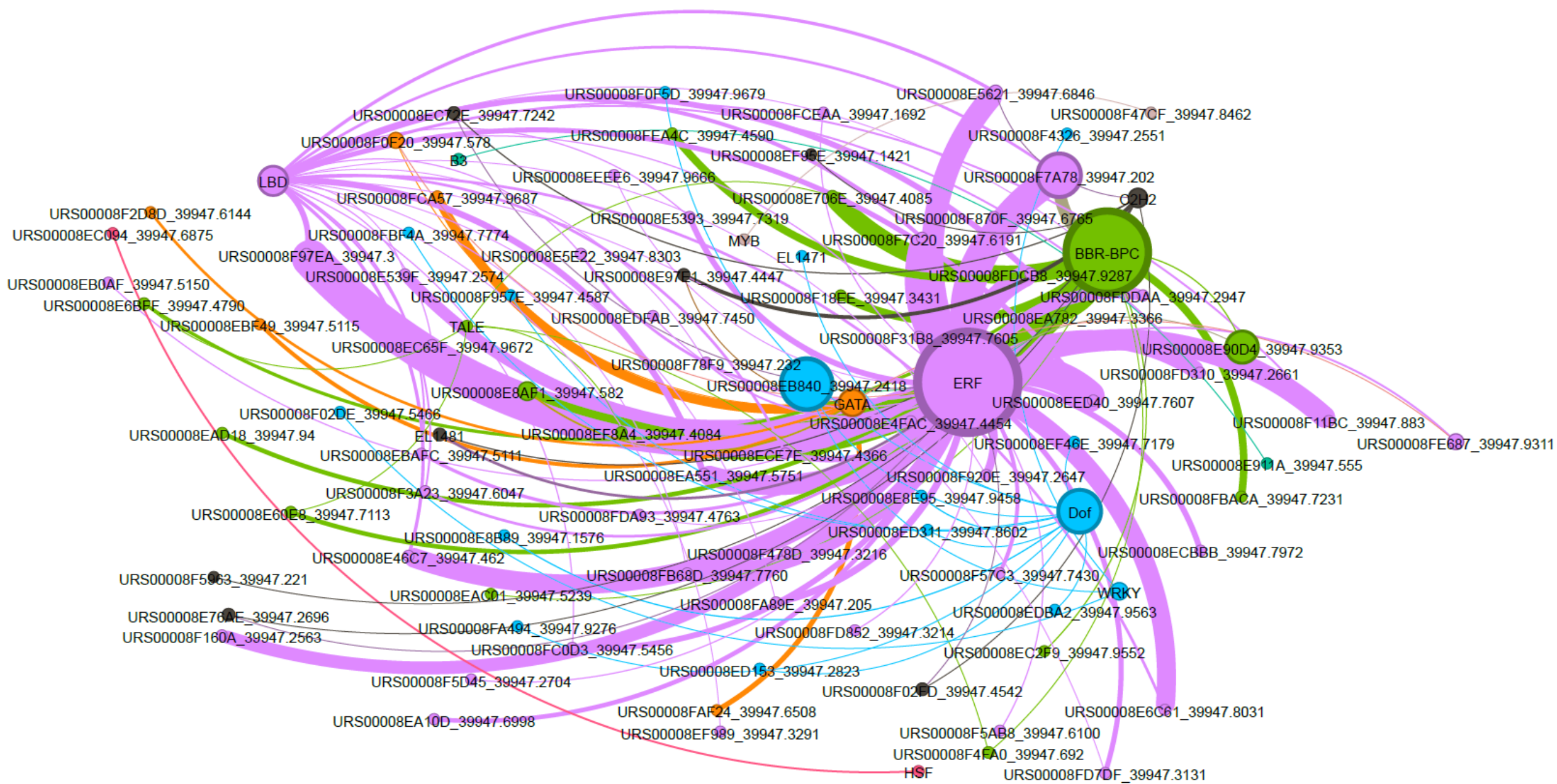


Figure S9B. Interaction network showing association of lncRNAs with transcription factors in *O. sativa*. Nodes represent transcription factors and edges represents lncRNA. Node size is proportional to the number of interactions. Thick edge showed interaction occur together more often than those with a thinner edge.

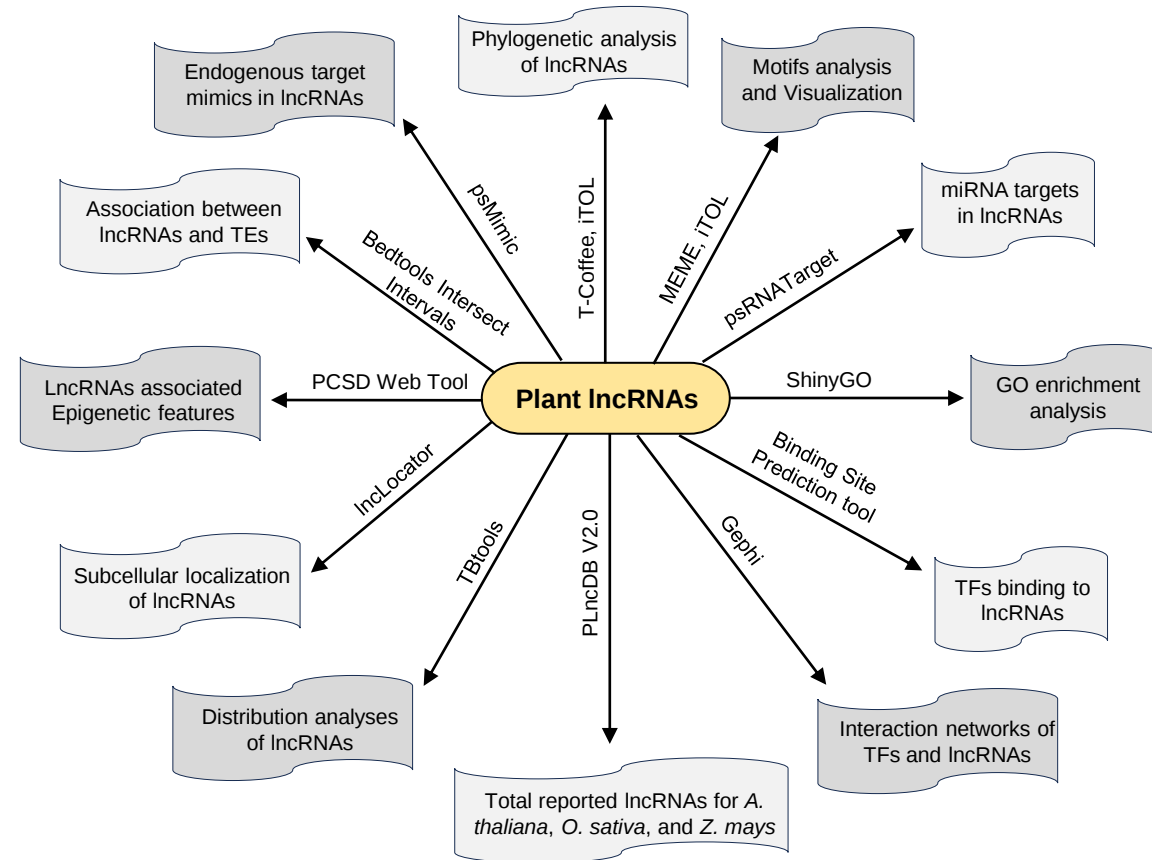


Figure S10. Schematic diagram showing an overview of computational tools used to study the characteristics and conserved features associated with plant lncRNAs.