

# Small RNA profiling in *Pinus pinaster* reveals the transcriptome of developing seeds and highlights differences between zygotic and somatic embryos

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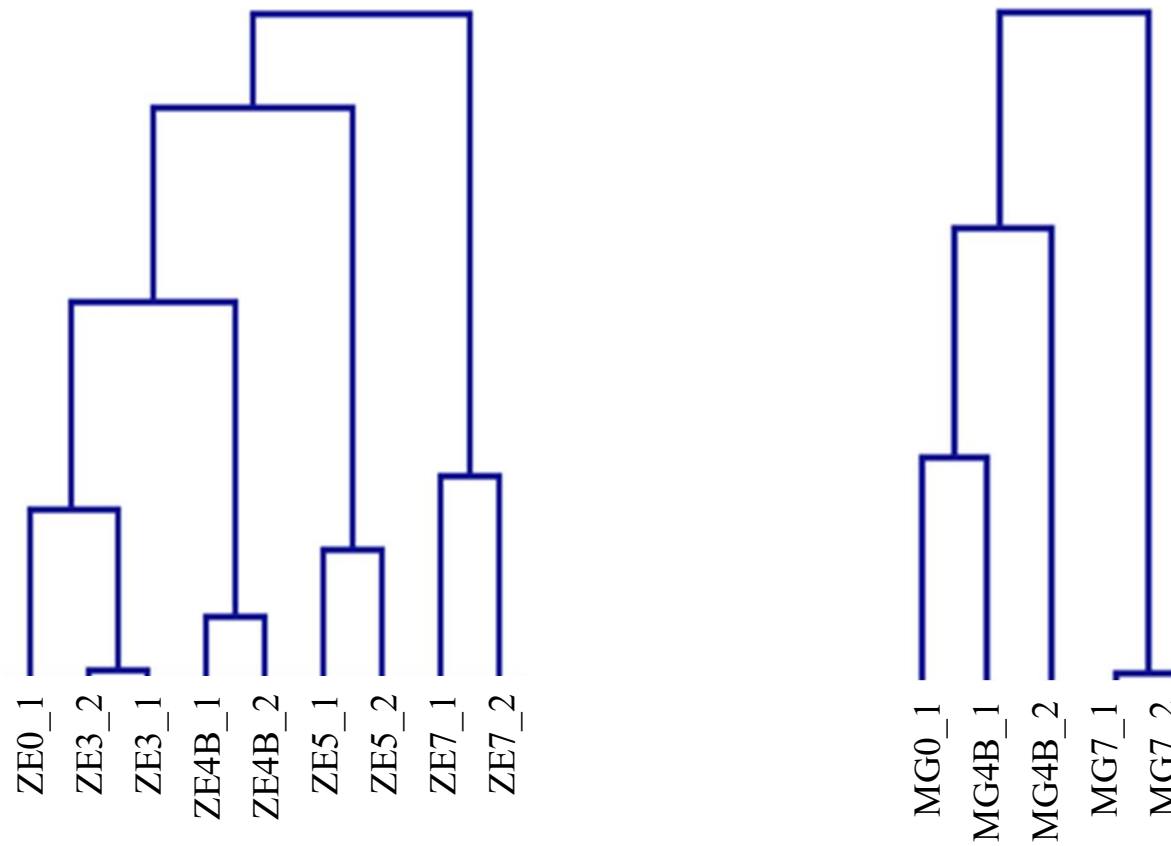
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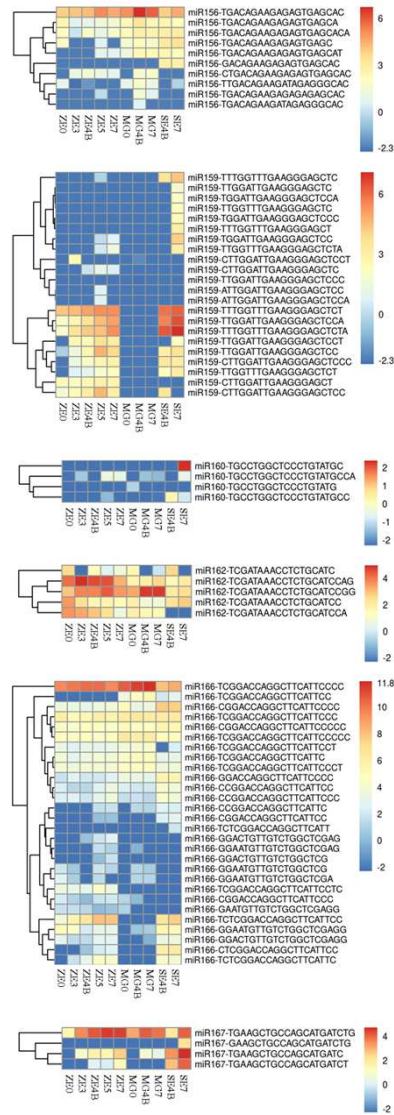
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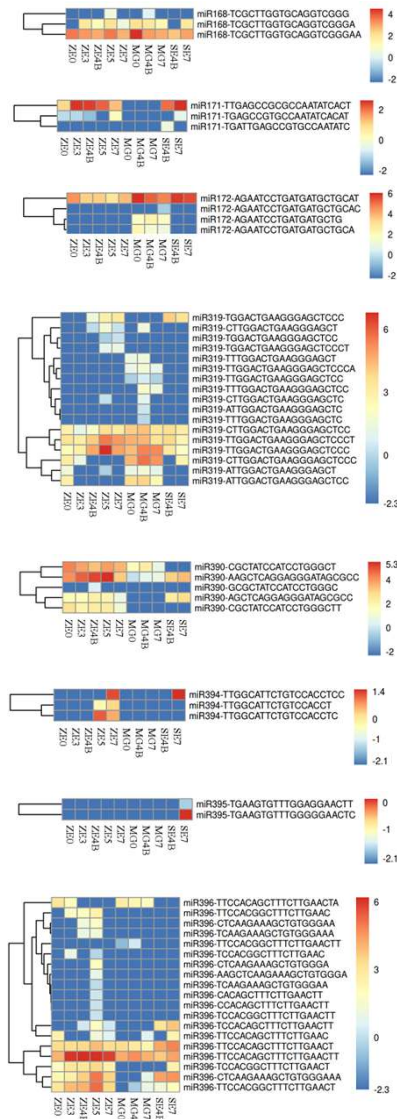
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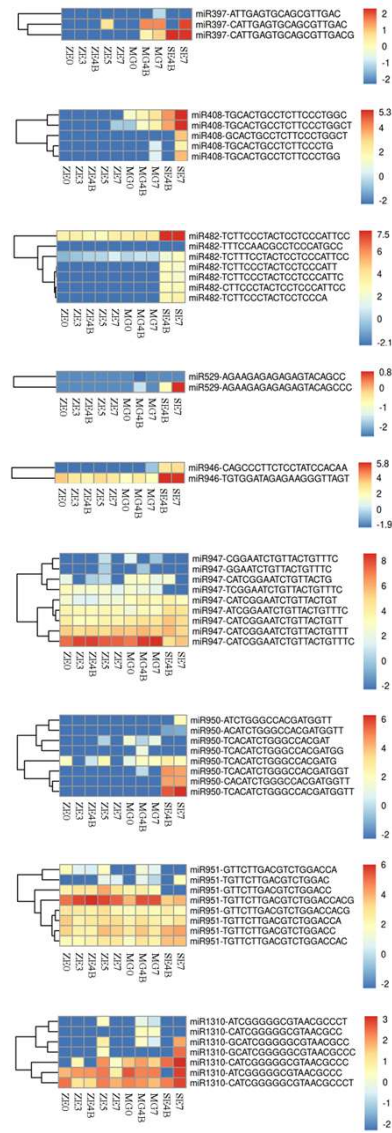
Supplementary Fig. S1 - Hierarchical cluster analysis of ZE and MG samples, using the ln(CPM) for each miRNA and a Kendall's Tau correlation.



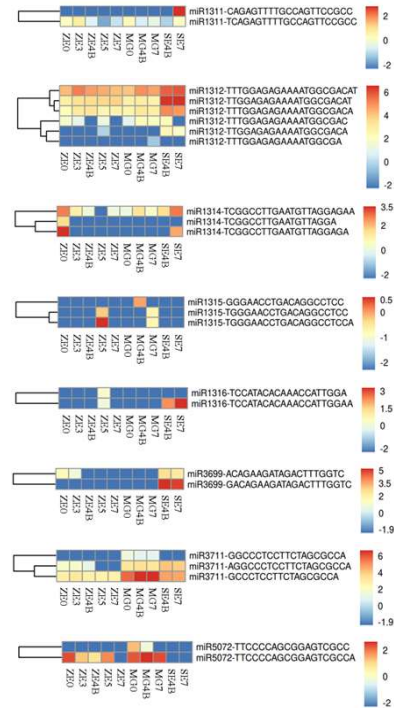
Supplementary Fig. S2 - Conserved miRNA isoforms detected across the distinct developmental stages within each tissue (ZE, MG and SE). The heatmaps represent the transformed expression values for each miRNA isoform, where miRNAs are grouped according to miRNA family and expression profiles across the biological samples.



Supplementary Fig. S2 (cont.) - Conserved miRNA isoforms detected across the distinct developmental stages within each tissue (ZE, MG and SE). The heatmaps represent the transformed expression values for each miRNA isoform, where miRNAs are grouped according to miRNA family and expression profiles across the biological samples.



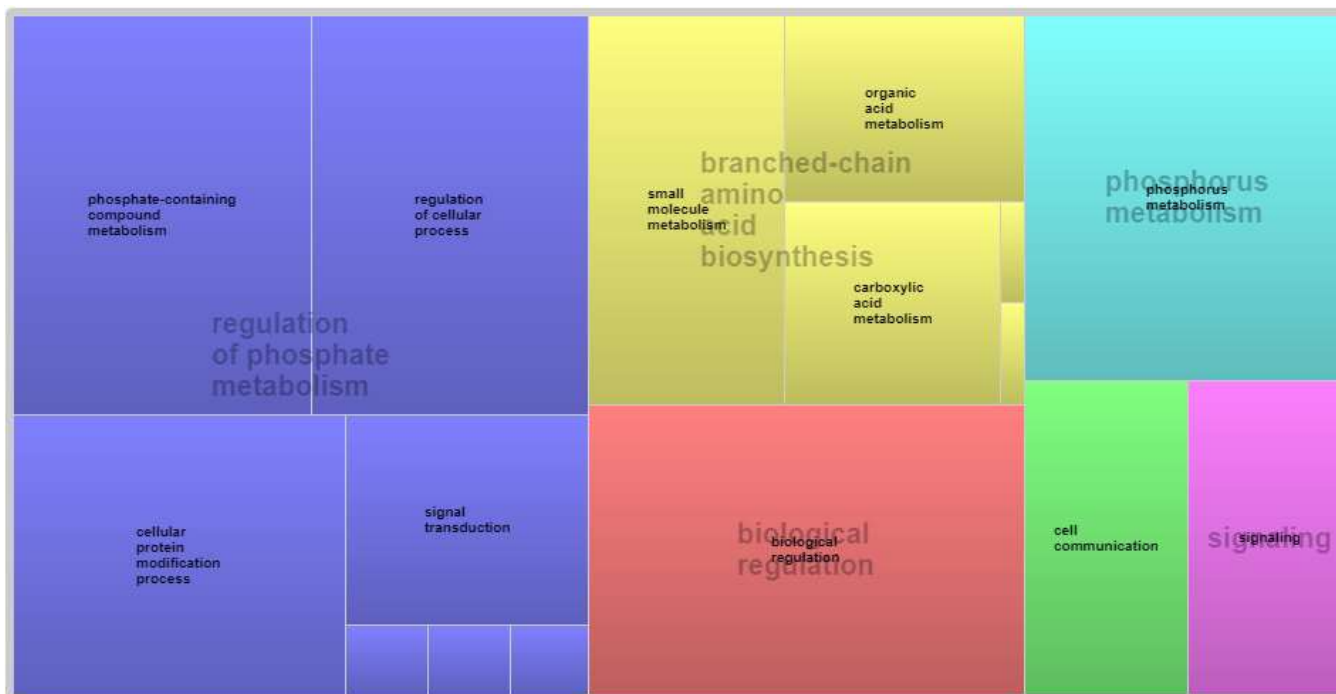
Supplementary Fig. S2 (cont.) - Conserved miRNA isoforms detected across the distinct developmental stages within each tissue (ZE, MG and SE). The heatmaps represent the transformed expression values for each miRNA isoform, where miRNAs are grouped according to miRNA family and expression profiles across the biological samples.



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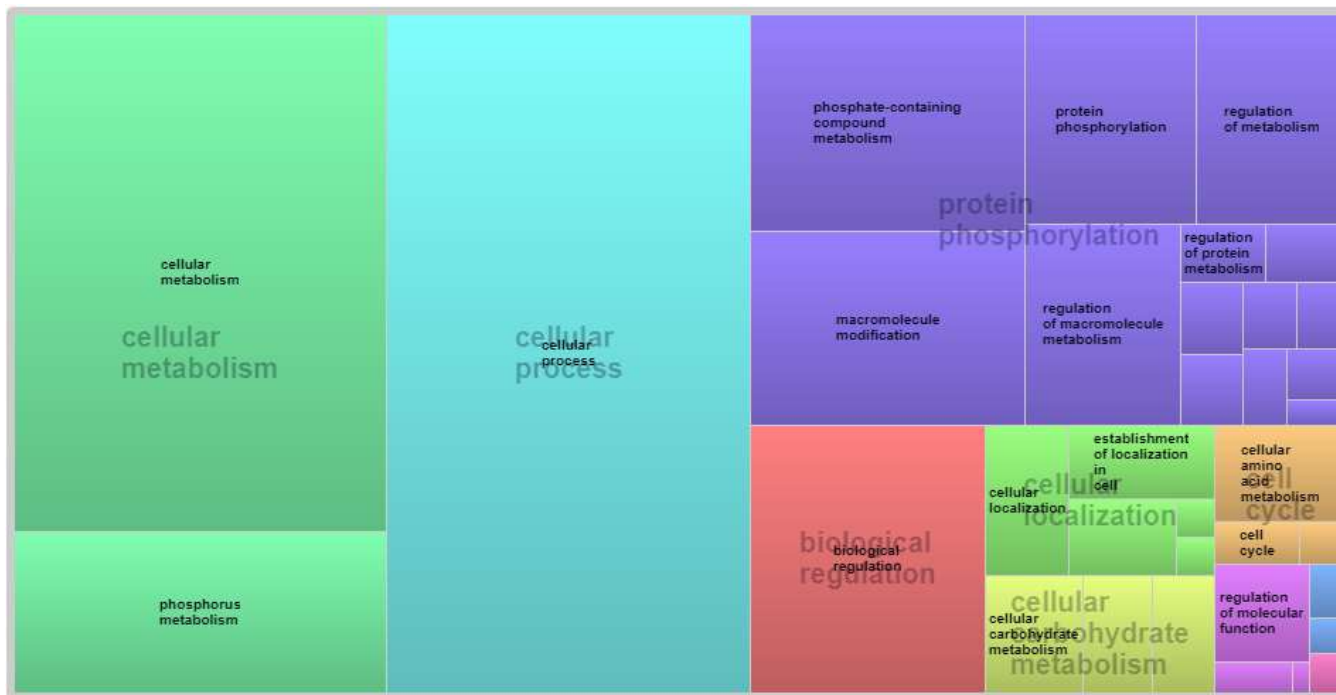


Supplementary Fig. S3 - REViGO TreeMap representation of the BP GO terms found enriched among the miRNAs' targets. The result refers to targets of the differentially expressed miRNAs that follow an expression profile along ZE development included in cluster 2.



Supplementary Fig. S4 - REViGO TreeMap representation of the BP GO terms found enriched among the miRNAs' targets. The result refers to targets of the differentially expressed miRNAs that follow an expression profile along ZE development included in cluster 4.





Supplementary Fig. S5 - REViGO TreeMap representation of the BP GO terms found enriched among the miRNAs' targets. The result refers to targets of the differentially expressed miRNAs that follow an expression profile along ZE development included in cluster 6.



Supplementary Fig. S6. REViGO TreeMap representation of the BP GO terms found enriched among the miRNAs' targets. The result refers to targets of the differentially expressed miRNAs that follow an expression profile along MG development included in cluster 2.