



Supplementary Materials

Genome-wide identification, comparison and expression analysis of transcription factors in ascidian *Styela clava*

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Citation: Zhang, J.; Wei, J.; Yu, H.; Dong, B. Genome-Wide Identification, Comparison, and Expression Analysis of Transcription Factors in Ascidian *Styela clava*. *Int. J. Mol. Sci.* **2021**, *22*, 4317.
<https://doi.org/10.3390/ijms22094317>

Academic Editors: Akira Ishihama, Igor Rogozin and Clifford Louime

Received: 15 January 2021

Accepted: 6 April 2021

Published: 21 April 2021

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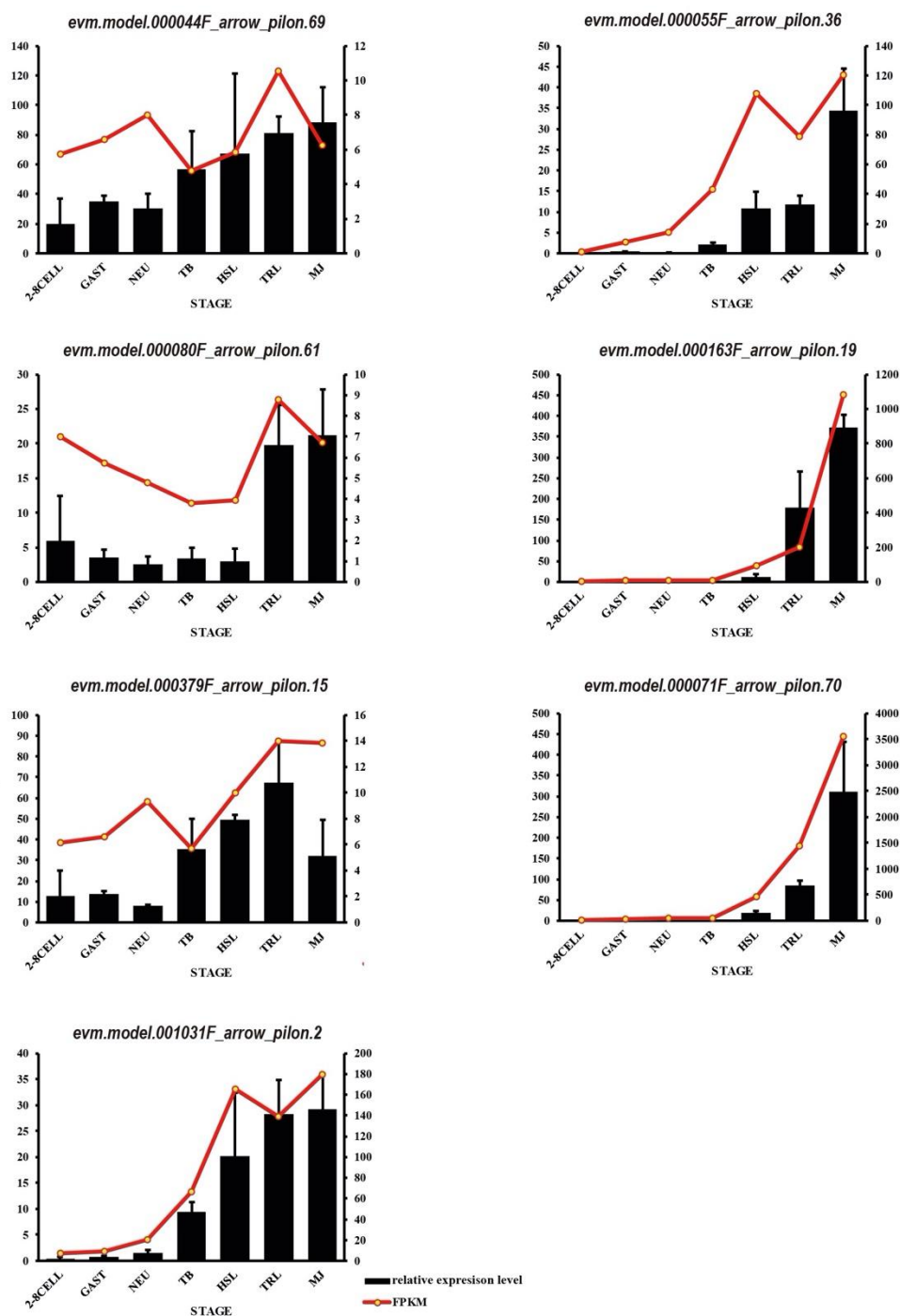


Figure 1. Expressions of partial TFs detected by RNA-Seq and quantitative real-time PCR (RT-qPCR). The black cylinders indicate the relative expression levels acquired through RT-qPCR. The red lines with yellow dots indicate the FPKM value from RNA-Seq. The left y-axis indicates the FPKM value and the right y-axis indicates the relative expression levels. Gene ID is shown on the top of each charts.



Figure 2. Phylogenetic tree of hox genes in *S. clava*, *C. robusta*, and *H. sapiens*. Phylogenetic tree of hox genes in *S. clava*, *C. robusta*, and *H. sapiens* constructed by the Maximum-Likelihood (ML) method using amino acid sequences. Black solid dots indicate *S. clava* proteins. The scale bar indicates an evolutionary distance of 0.1 amino acid substitutions per position.

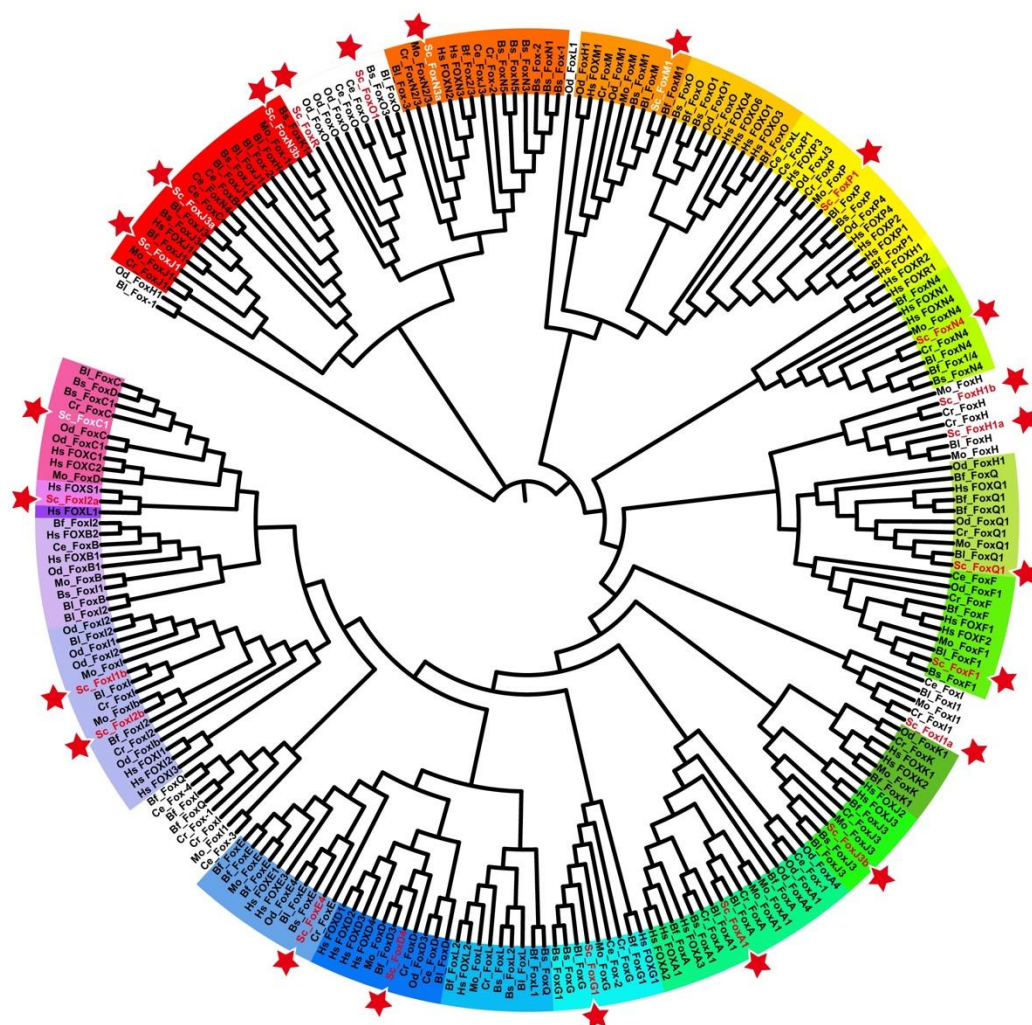


Figure 3. Function annotation of maternal TFs. The top 20 terms of GO enrichment analysis for maternal TFs. Y-axis indicates the GO term and x-axis indicates the Rich Factor. Size of points indicate the gene number, and the color of points indicate the q-value.

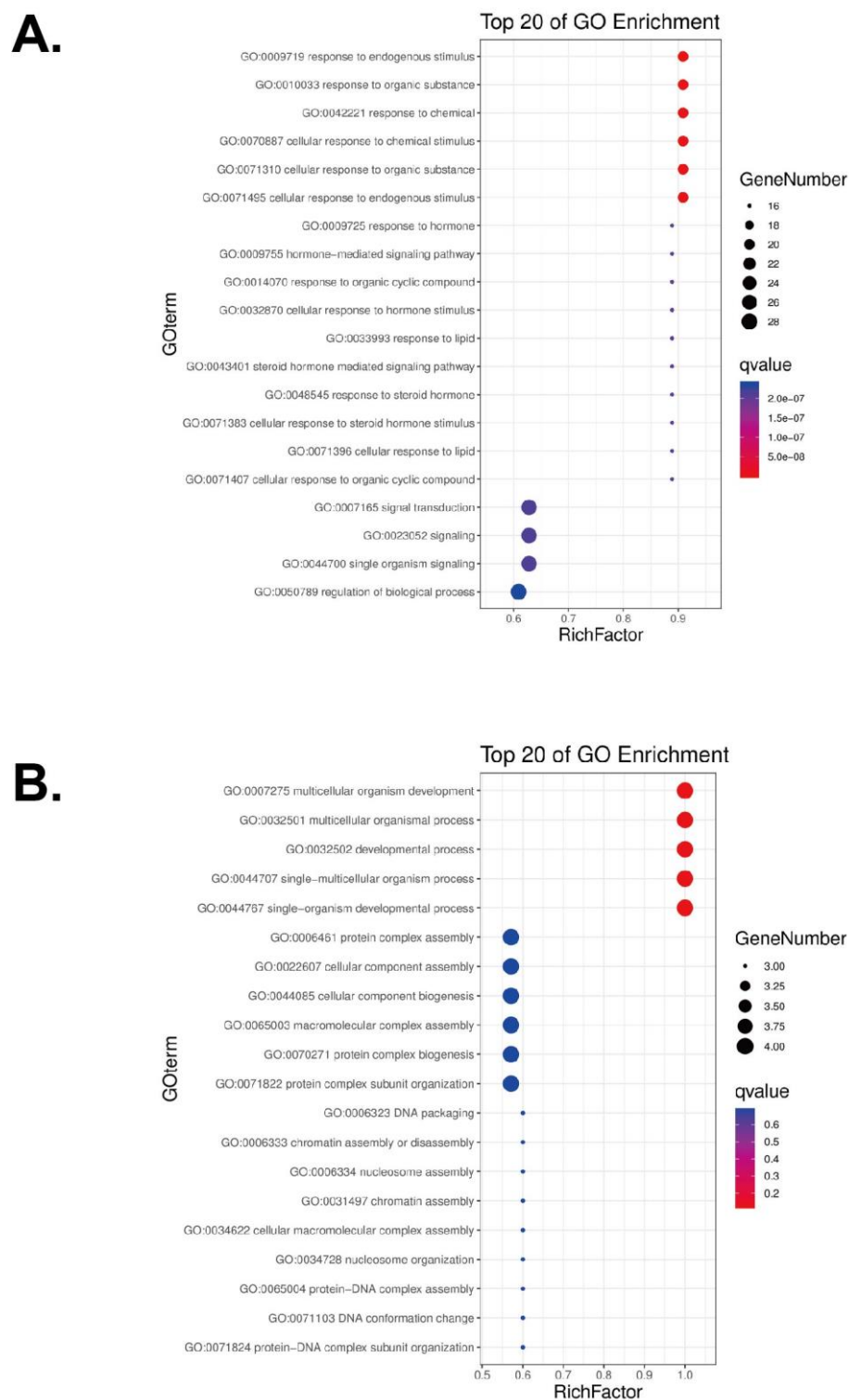


Figure 4. Function annotation of maternal expressed TFs and zygotically expressed TFs. (A) Function annotation of maternal expressed TFs. (B) Function annotation of zygotically expressed TFs. The top 20 terms of GO enrichment analysis for TFs. Y-axis indicates the GO term and x-axis indicates the Rich Factor. Rich Factor indicated the ratio of maternal TFs and all TFs in the GO annotation, implying the degree of enrichment. Size of points indicate the gene number, and the color of points indicate the q-value. .

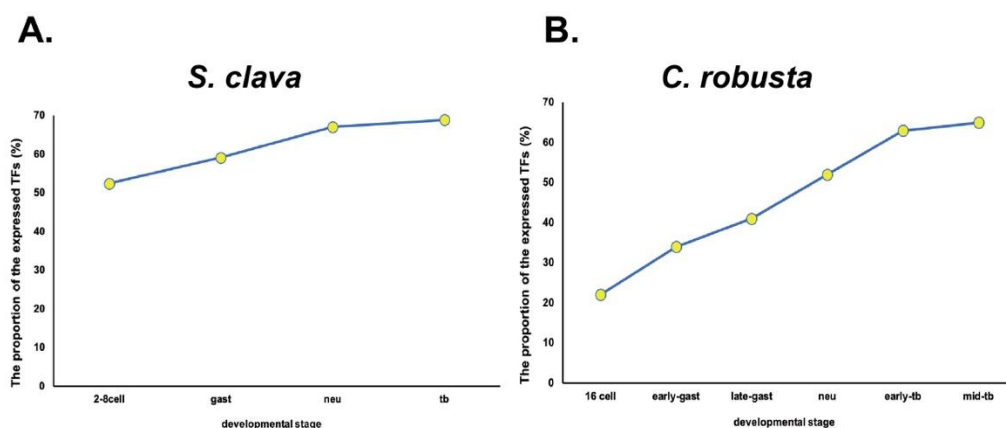


Figure 5. Proportion of the expressed TFs through early development of *S. clava* and *C. robusta*. (A) The proportion of the expressed TFs through early development of *S. clava*. (B) The proportion of the expressed TFs through early development of *C. robusta*. The y-axis was indicated the proportion of expressed TFs and the x-axis was indicated the developmental stage of *S. clava* and *C. robusta*.