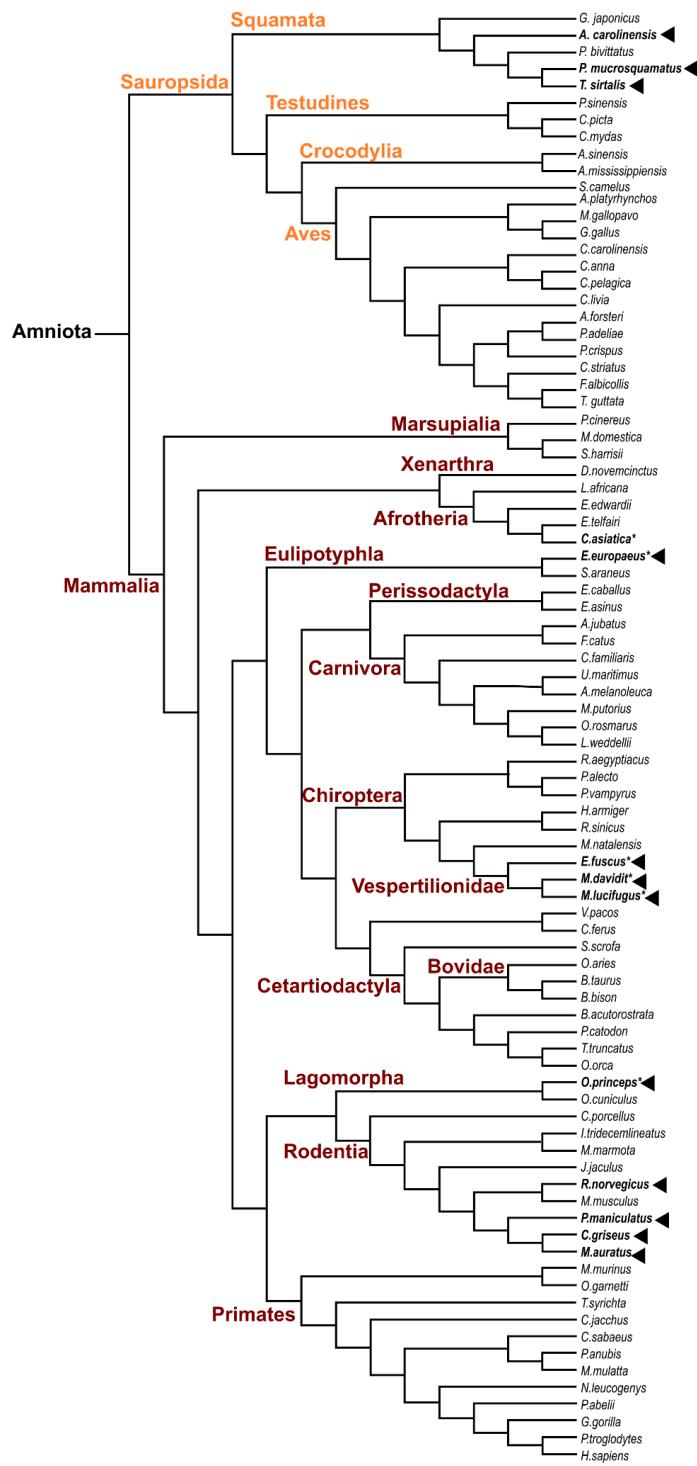


Supplementary Figures

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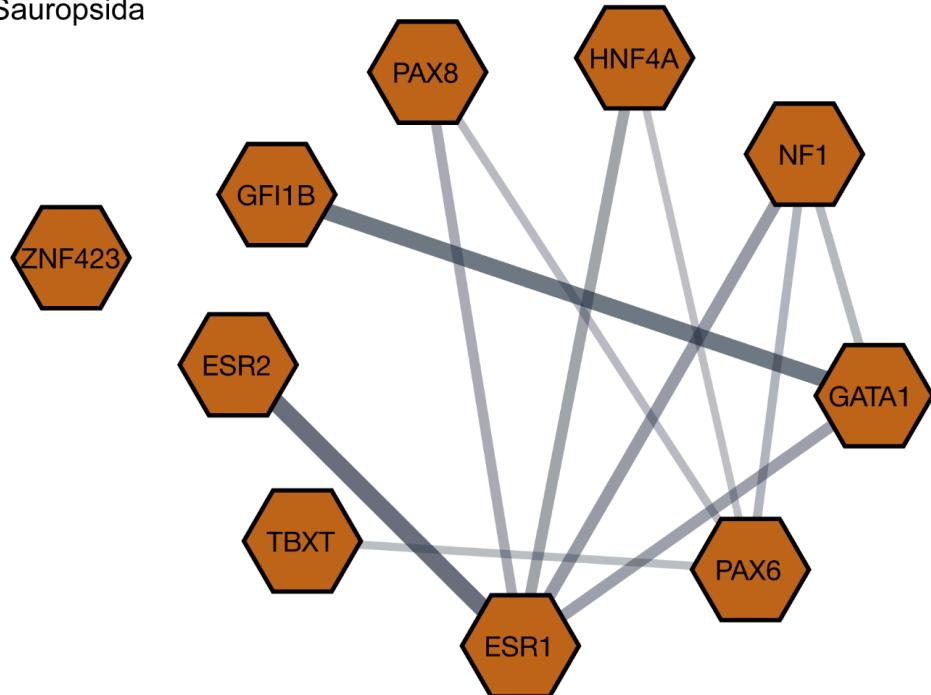
Supplementary Figure S1



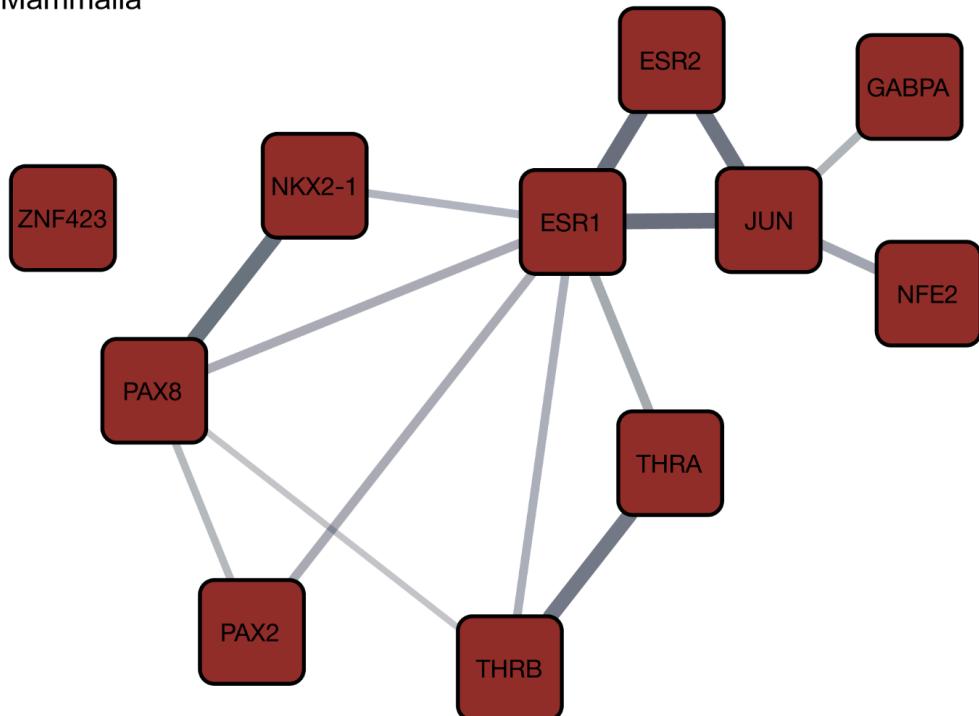
Supplemental Figure S1. Outliers found in intraclade conservation analysis of MSTN promoter/enhancer sequence. The species name in bold represents red dots in Figure 1B. An asterisk (*) indicates the entire promoter and an arrowhead indicates the core promoter.

Supplementary Figure S2

A Sauropsida



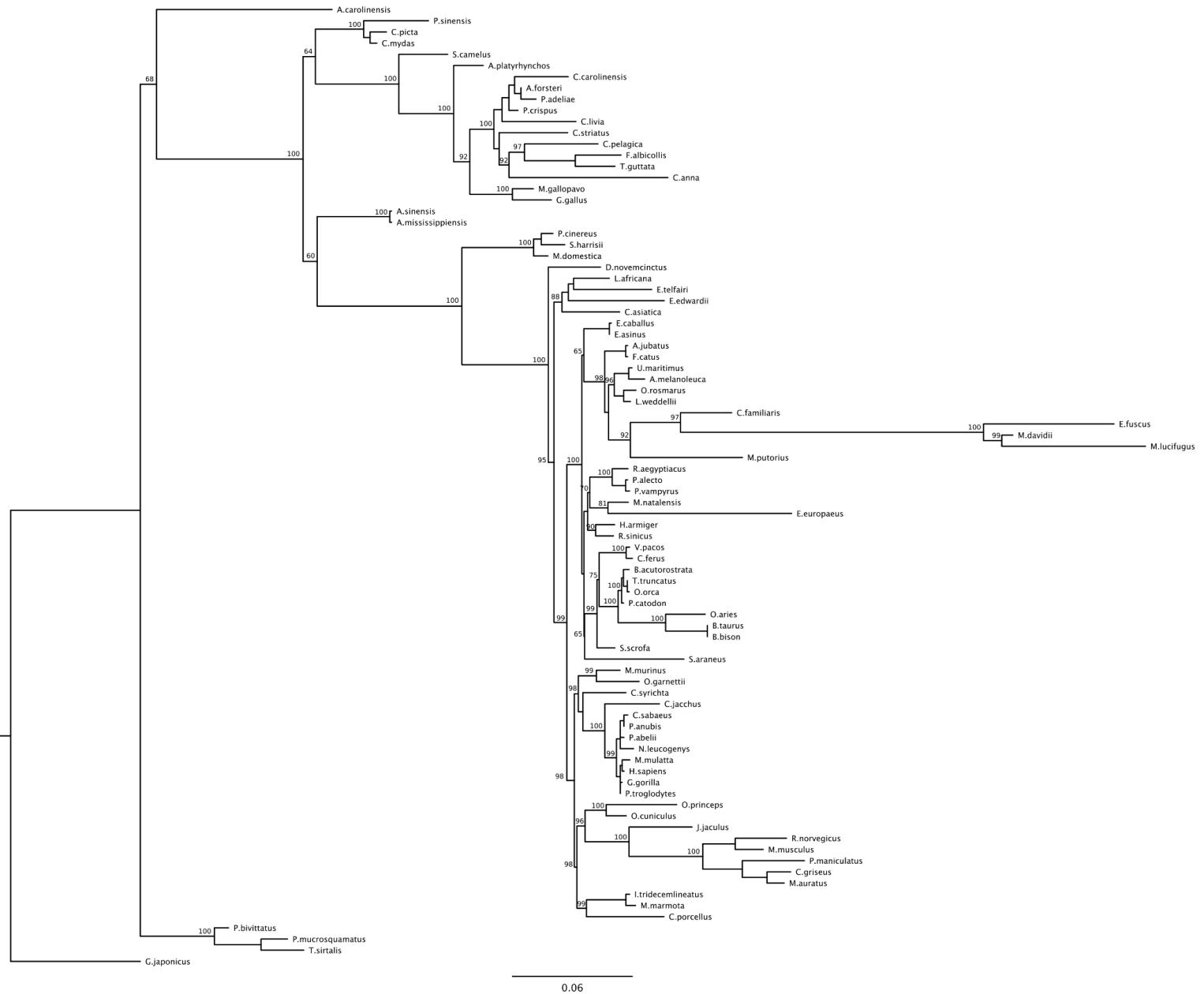
B Mammalia



Supplemental Figure S2. Protein-protein interaction (PPI) networks generated from the list of transcription factors predicted to bind to the overlapping sites in the PAX8 module. (A) PPI network of Sauropsida clade. (B) PPI network of Mammalia clade.

Supplementary Figure S3

CDS tree



Supplemental Figure S3. MSTN promoter/enhancer molecular evolution analysis.

Vertebrate phylogenetic tree evidencing the rate of MSTN P/E evolution resulted by phyloP software analysis. Longer stem branches indicate an accelerated rate of MSTN P/E evolution.