Specificity landscapes of 40 R2R3-MYBs reveal how paralogs target different *cis*-elements by homodimeric binding

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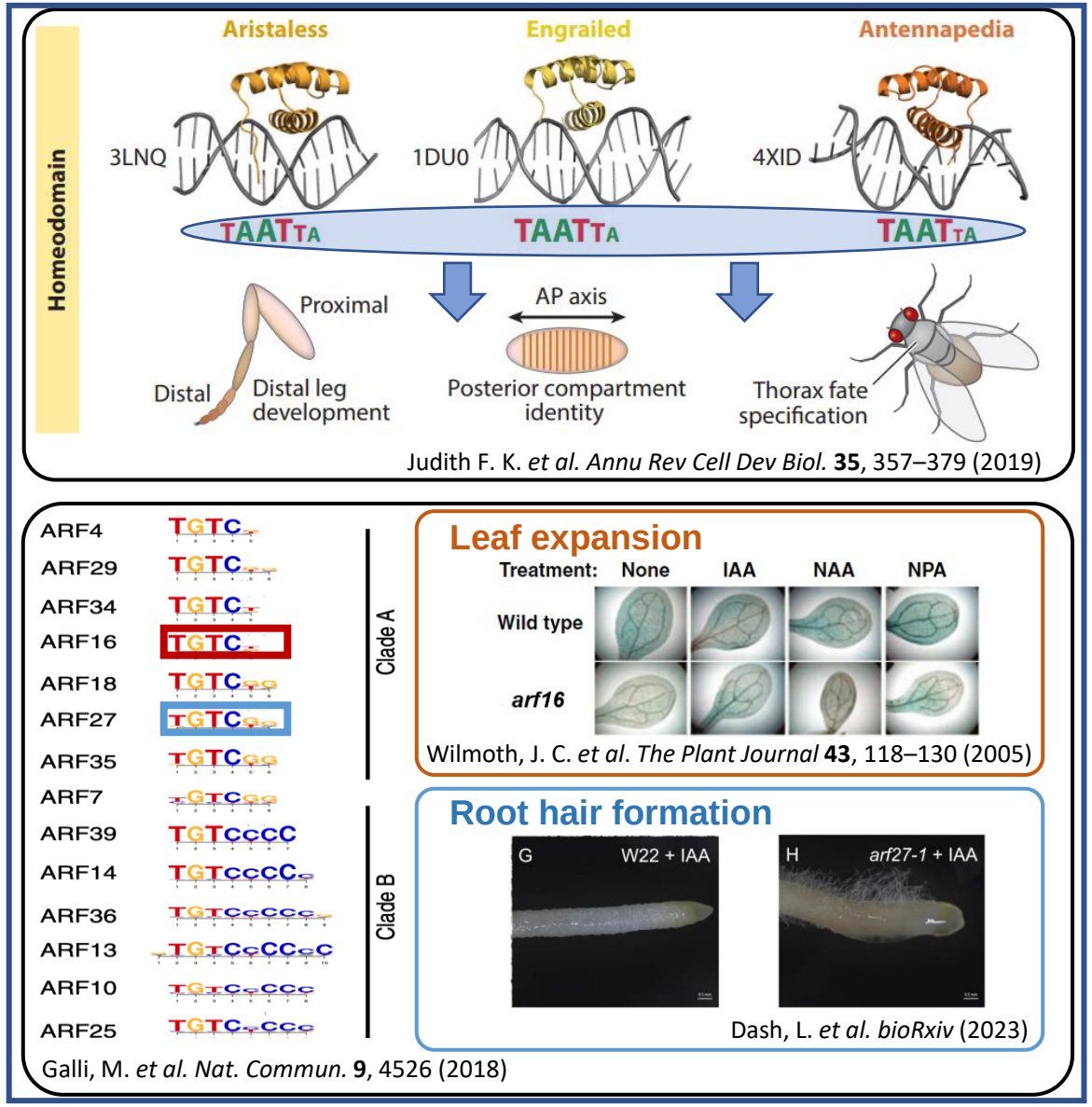
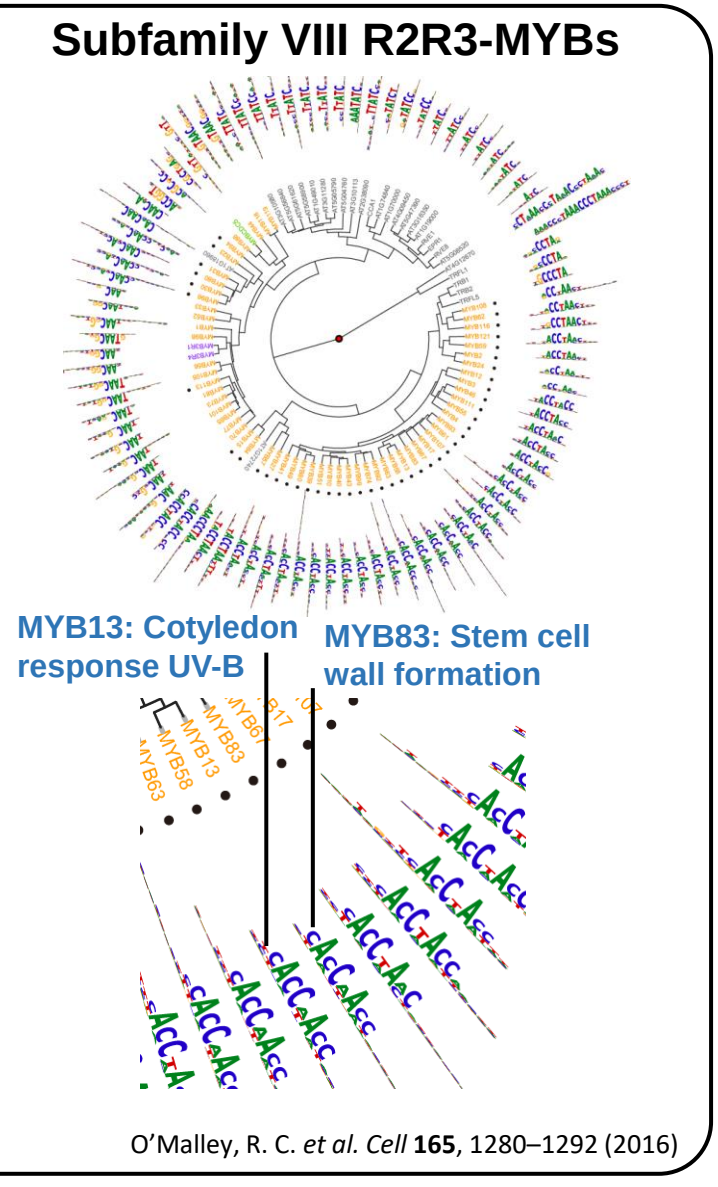
Tian Li, Hao Chen, Nana Ma, Dingkun Jiang, Jiacheng Wu, Xinfeng Zhang, et al. 2025. Specificity landscapes of 40 R2R3-MYBs reveal how paralogs target different cis-elements by homodimeric binding. ***iMeta*** **4: e70009.**
https://doi.org/10.1002/imt2.70009

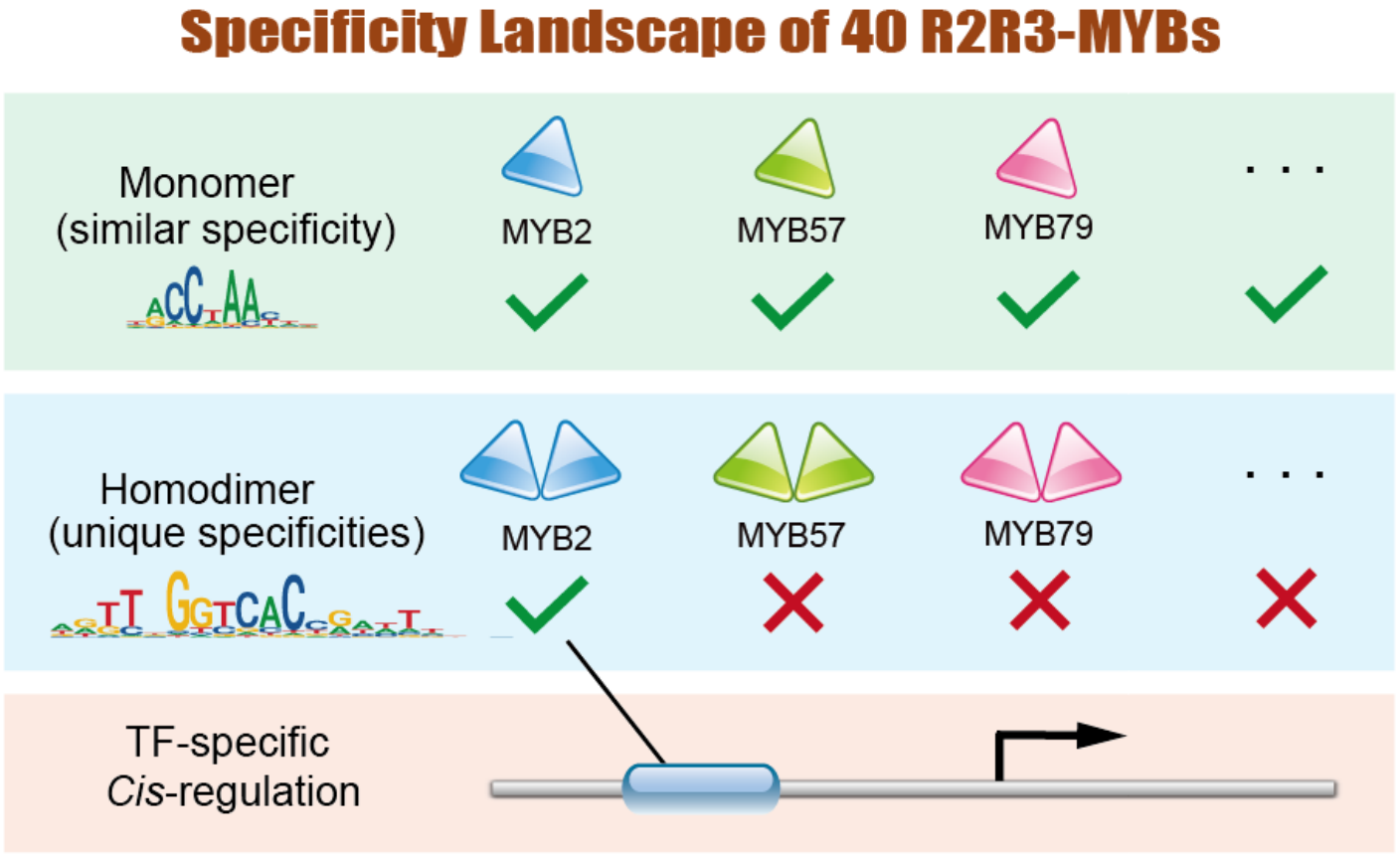
Introduction

- Specificity paradox of paralogous transcription factors





Highlights



- A homodimerization-based mechanism enables eukaryotes to distinguish paralogous TFs.
- The largest plant SELEX dataset illustrates the sequence preferences of 40 VIII R2R3-MYBs.
- The high specificity AtMYBs were discovered and named CCWAA-box.

Specificity landscapes reveal a high selectivity of CCWAA-box MYBs

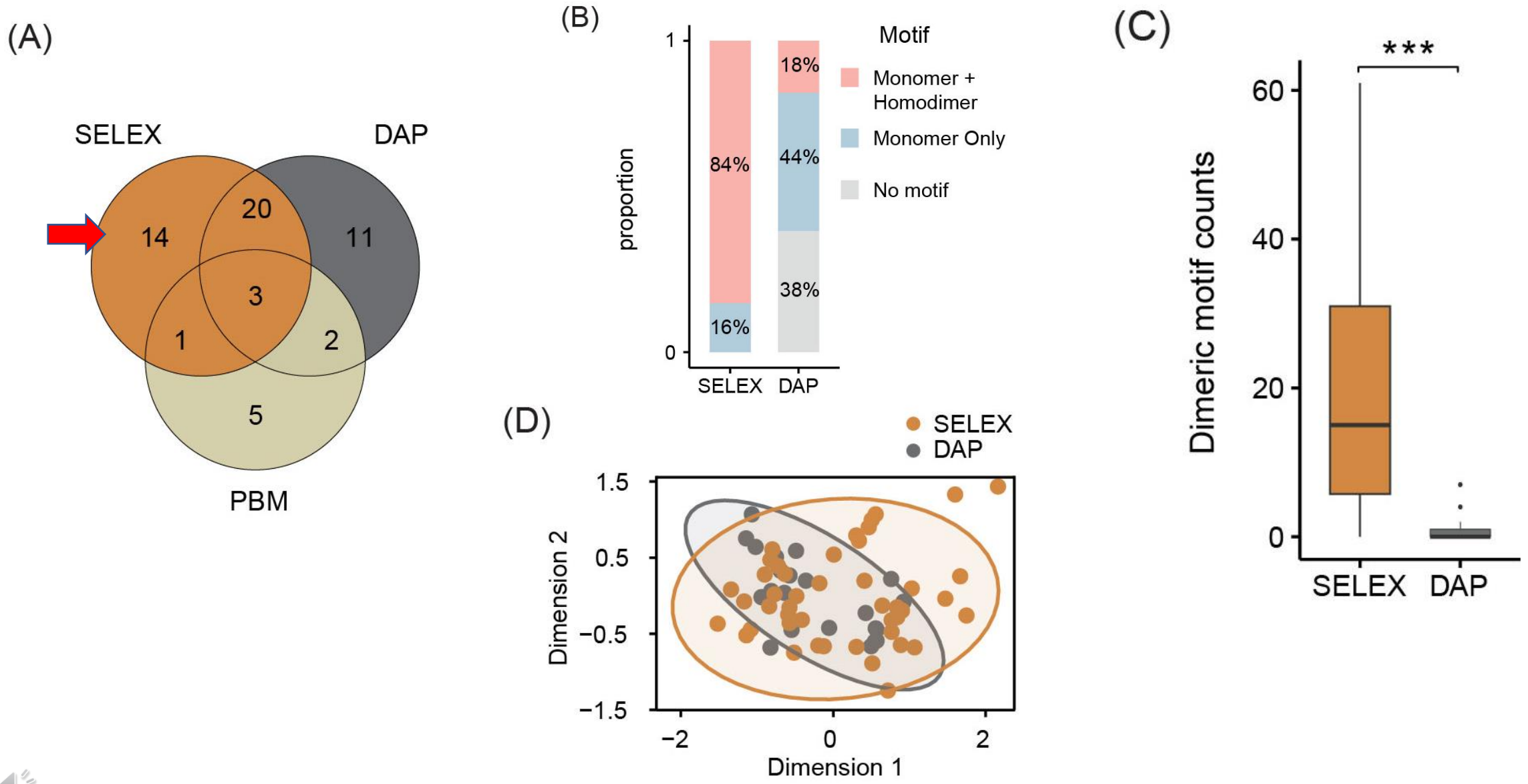
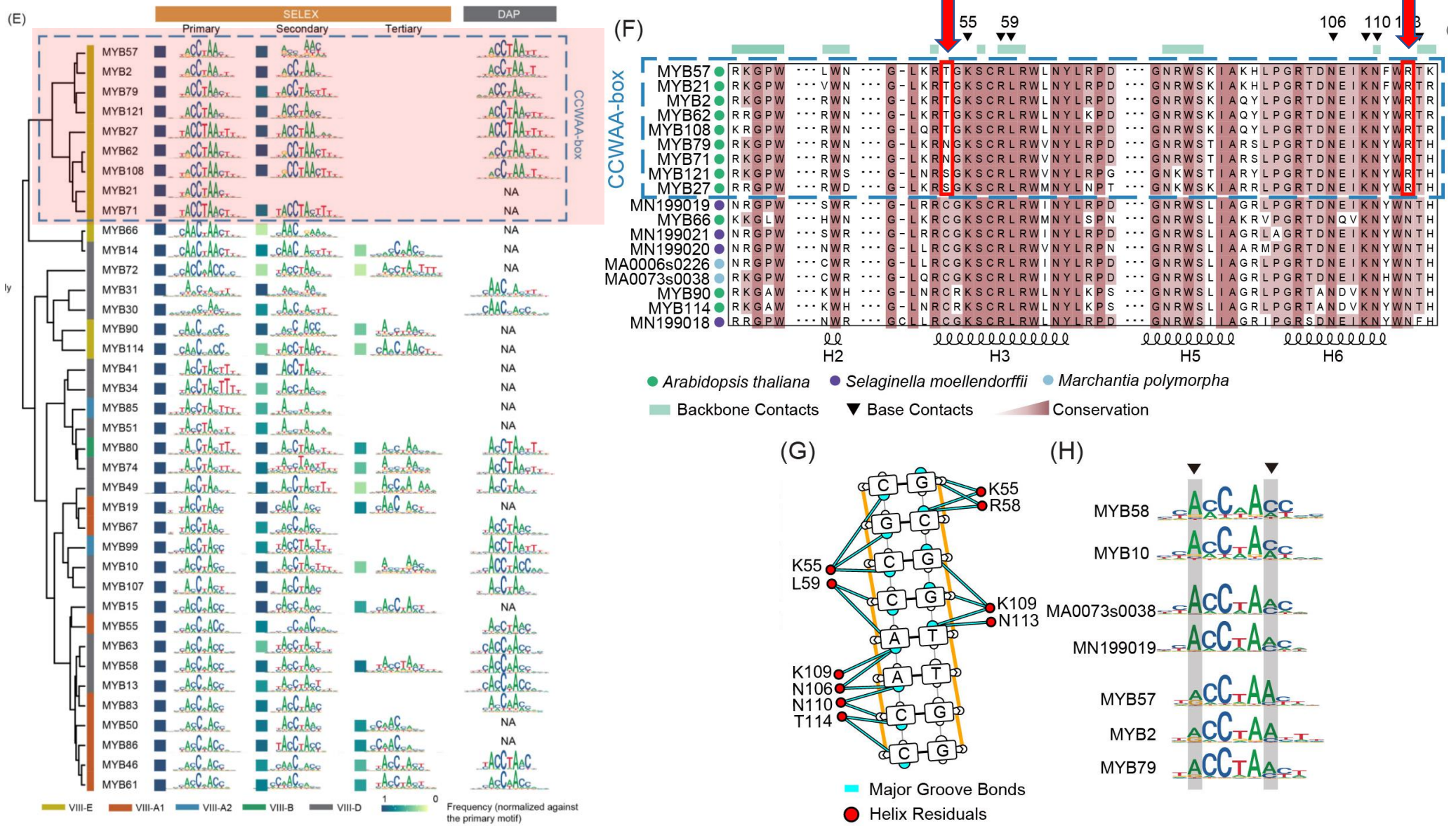


Figure 1. The landscape of binding specificity of VIII R2R3-MYBs

Specificity landscapes reveal a high selectivity of CCWAA-box MYBs



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Modified specificity of closely spaced AtMYB2 homodimers

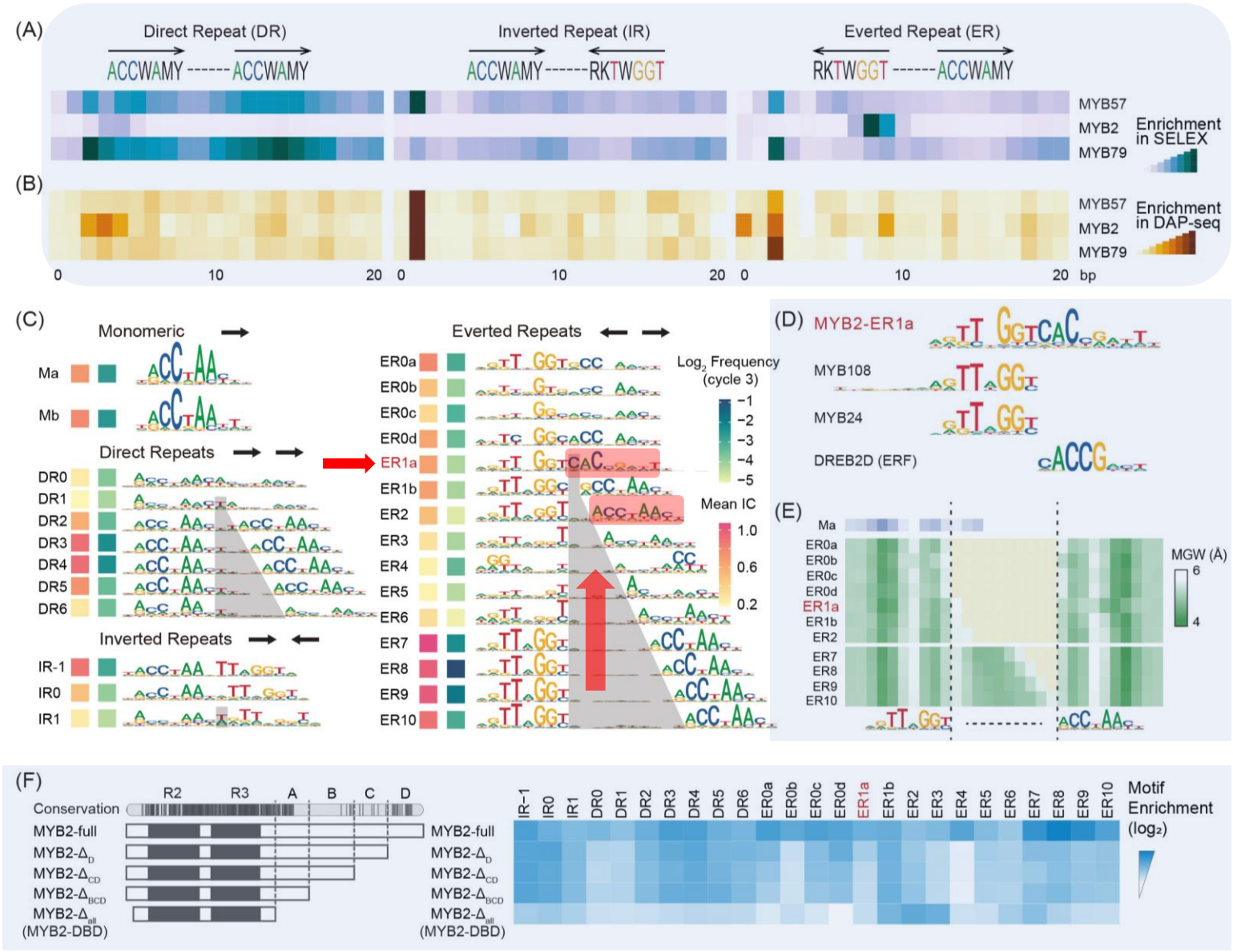

Figure 2. Modified specificities of closely spaced AtMYB2 homodimers

The modified specificities are unique to AtMYB2

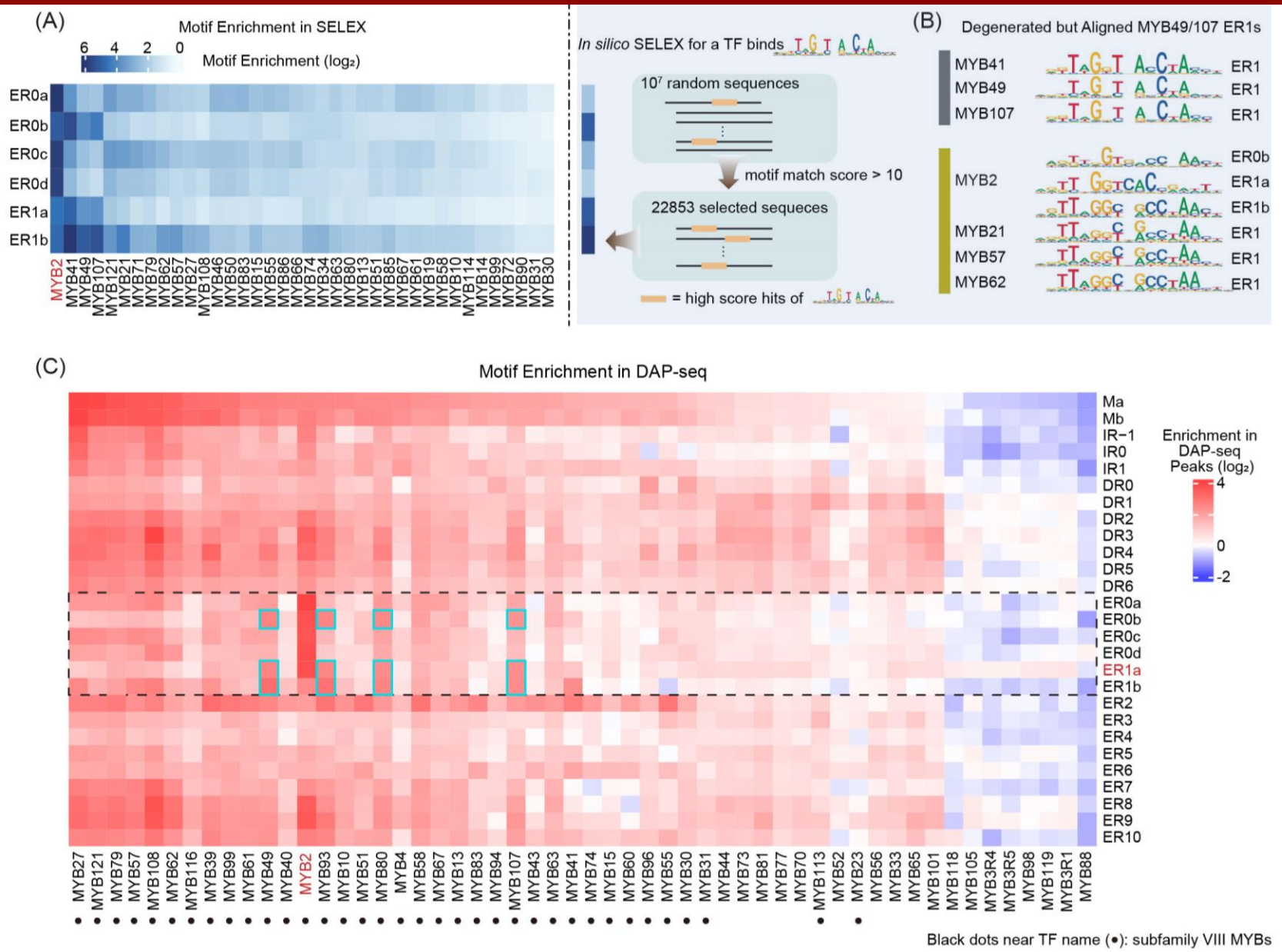

Figure 3. The modified specificities are unique to AtMYB2

The modified specificities allow AtMYB2 to recognize additional genomic sites

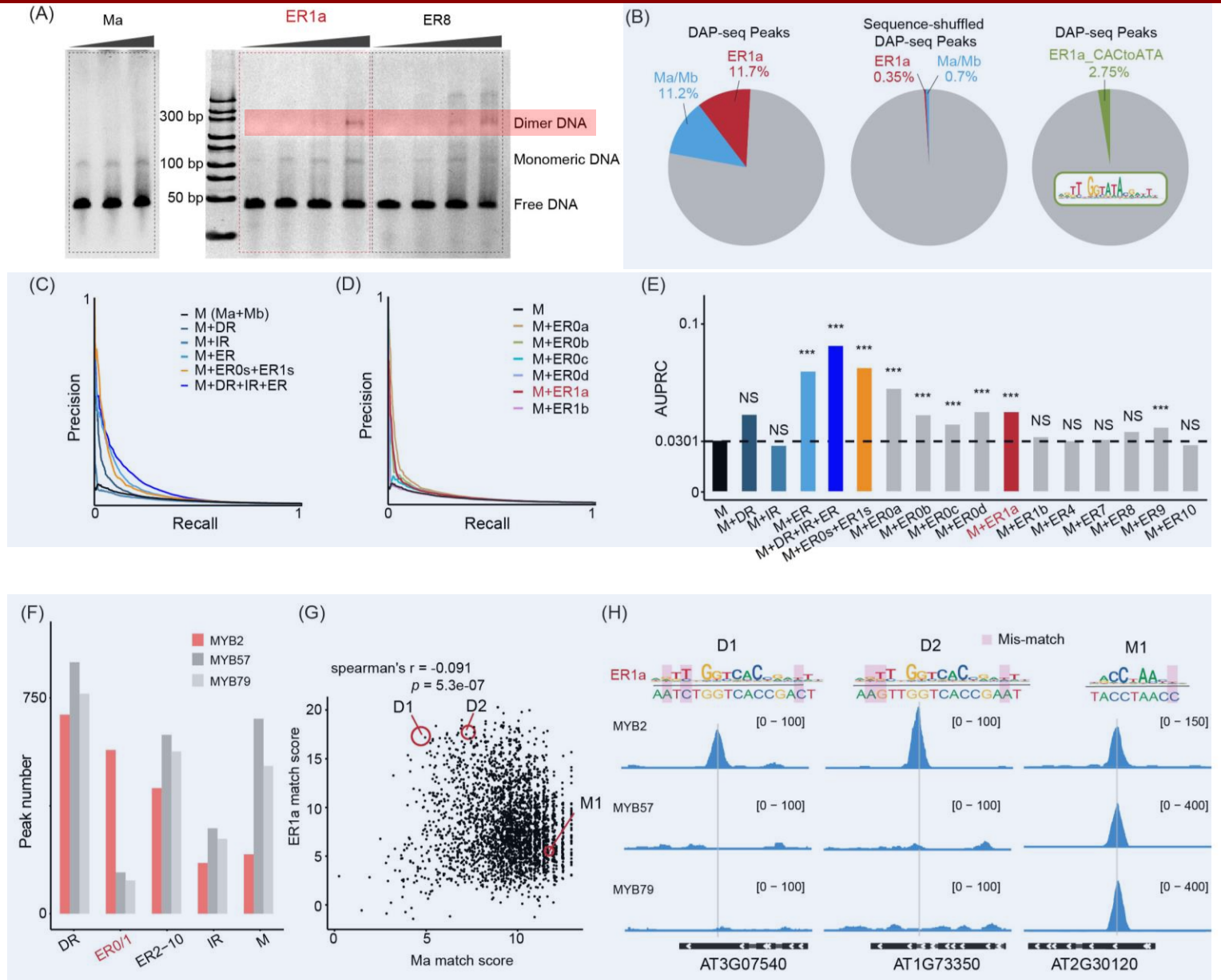

Figure 4. The modified specificities allow AtMYB2 to recognize additional genomic sites

The modified specificities of AtMYB2 are functional to activate transcription

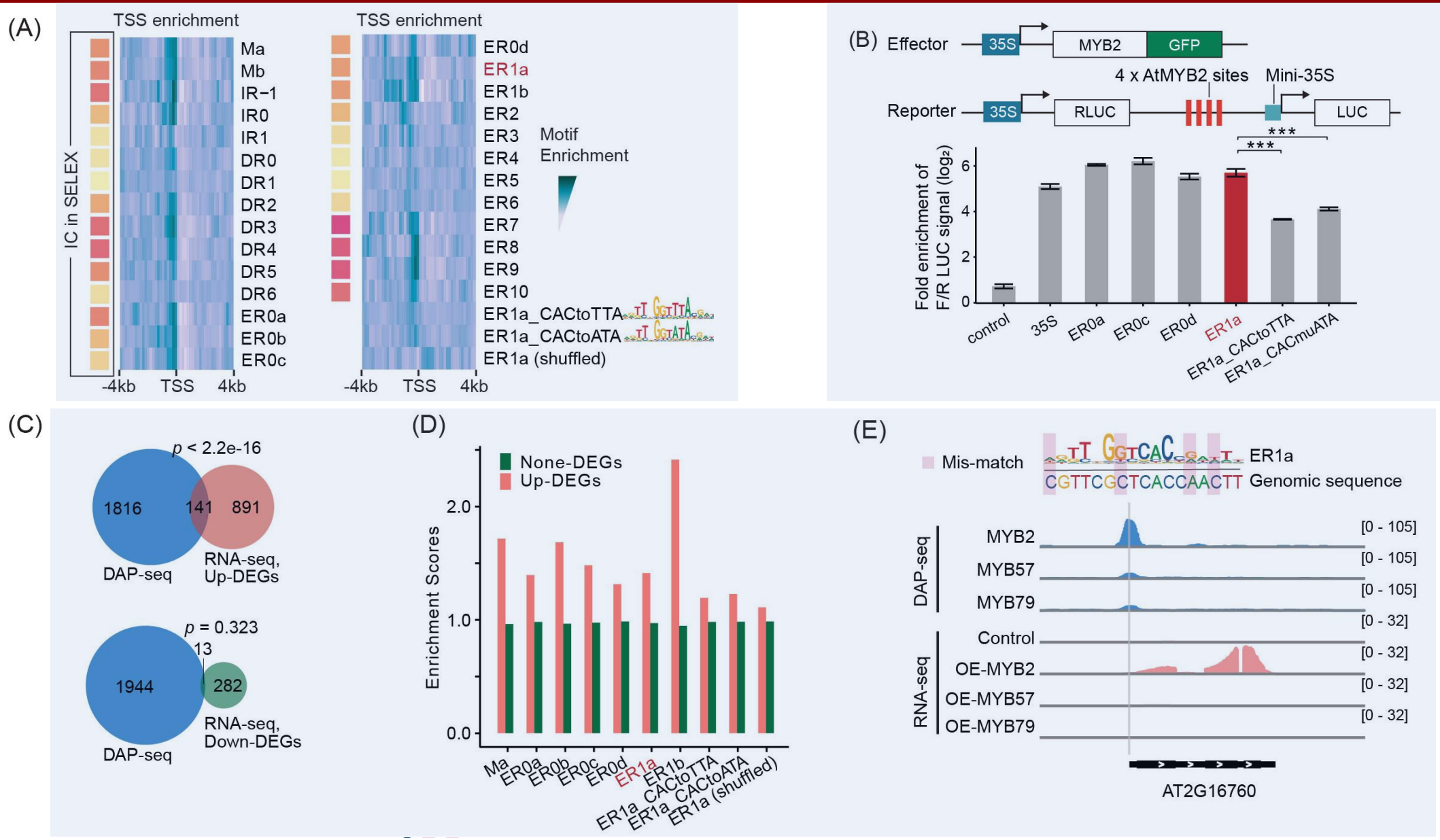

Figure 5. The modified specificities of AtMYB2 are functional to activate transcription

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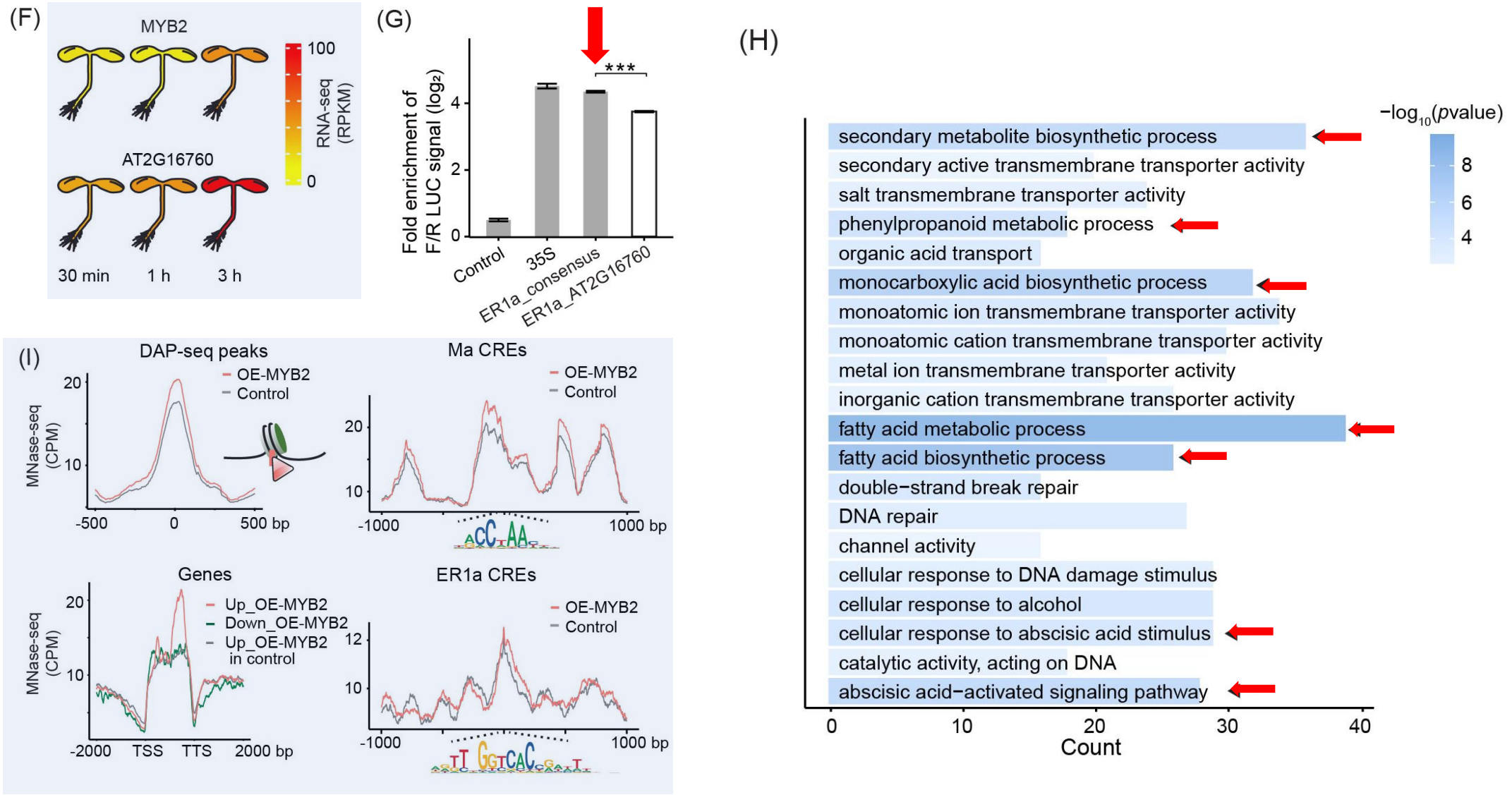


Figure 5. The modified specificities of AtMYB2 are functional to activate transcription

The modified specificities of AtMYB2 are conserved in evolution

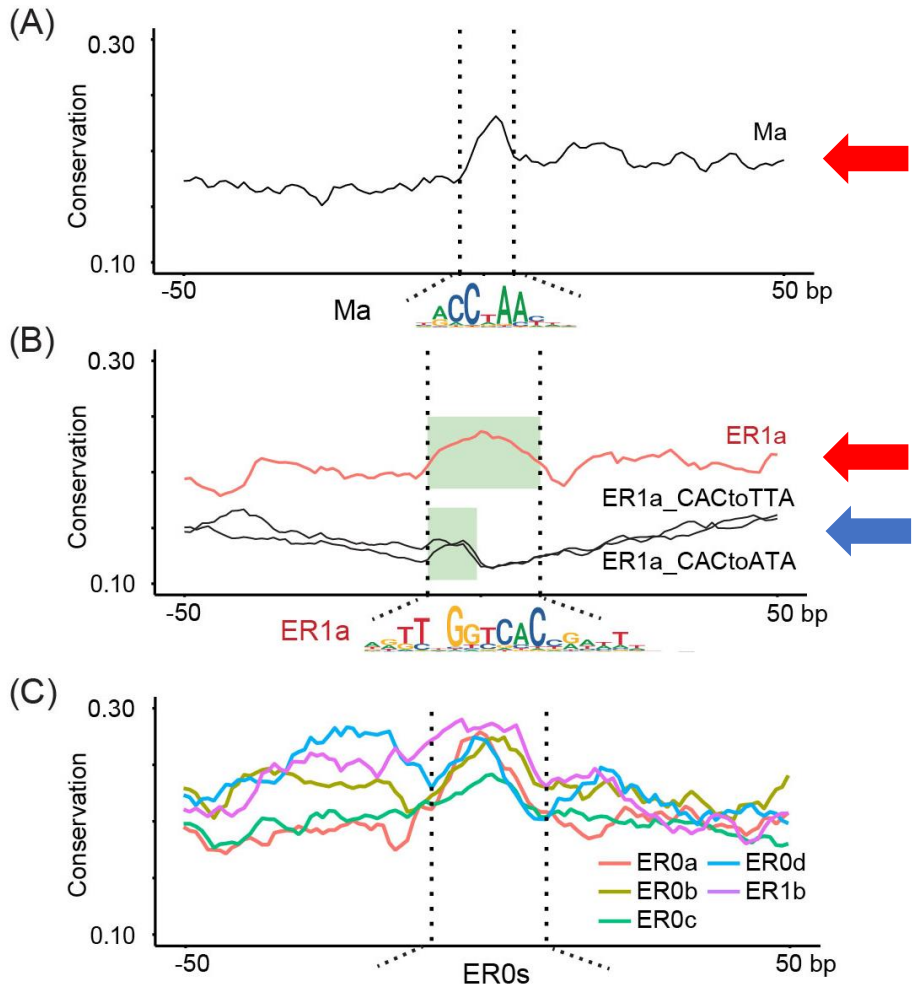
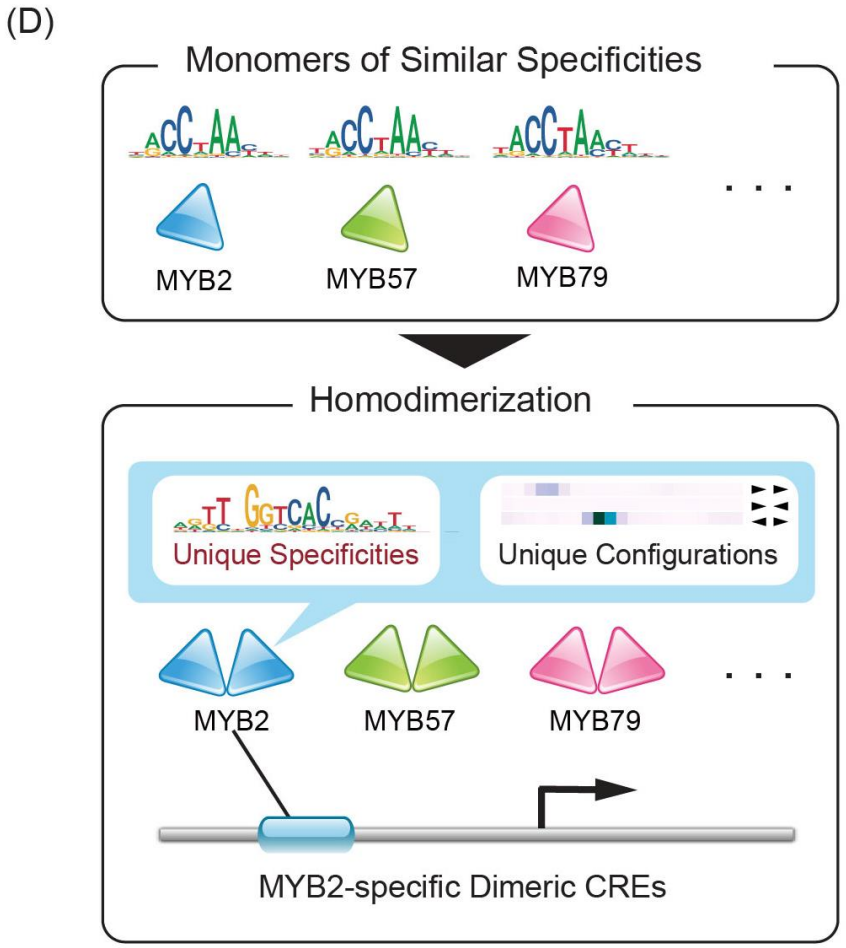


Figure 6. The modified specificities of AtMYB2 are conserved in evolution

Summary



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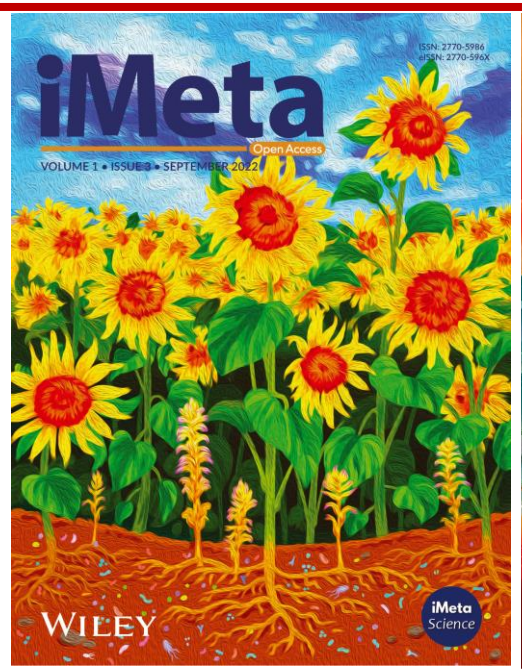

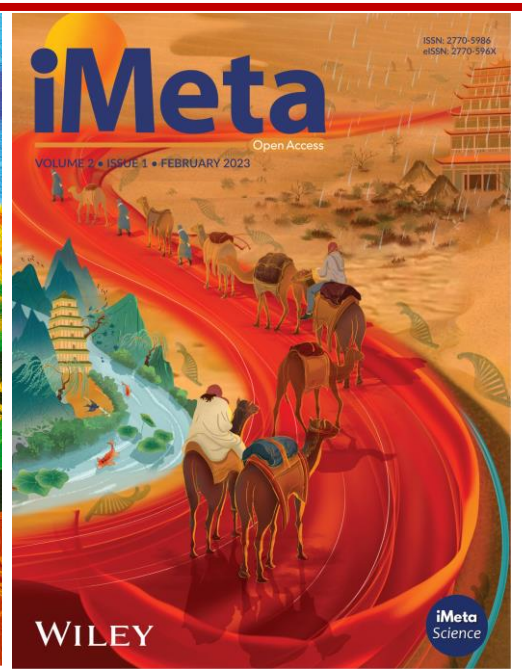

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