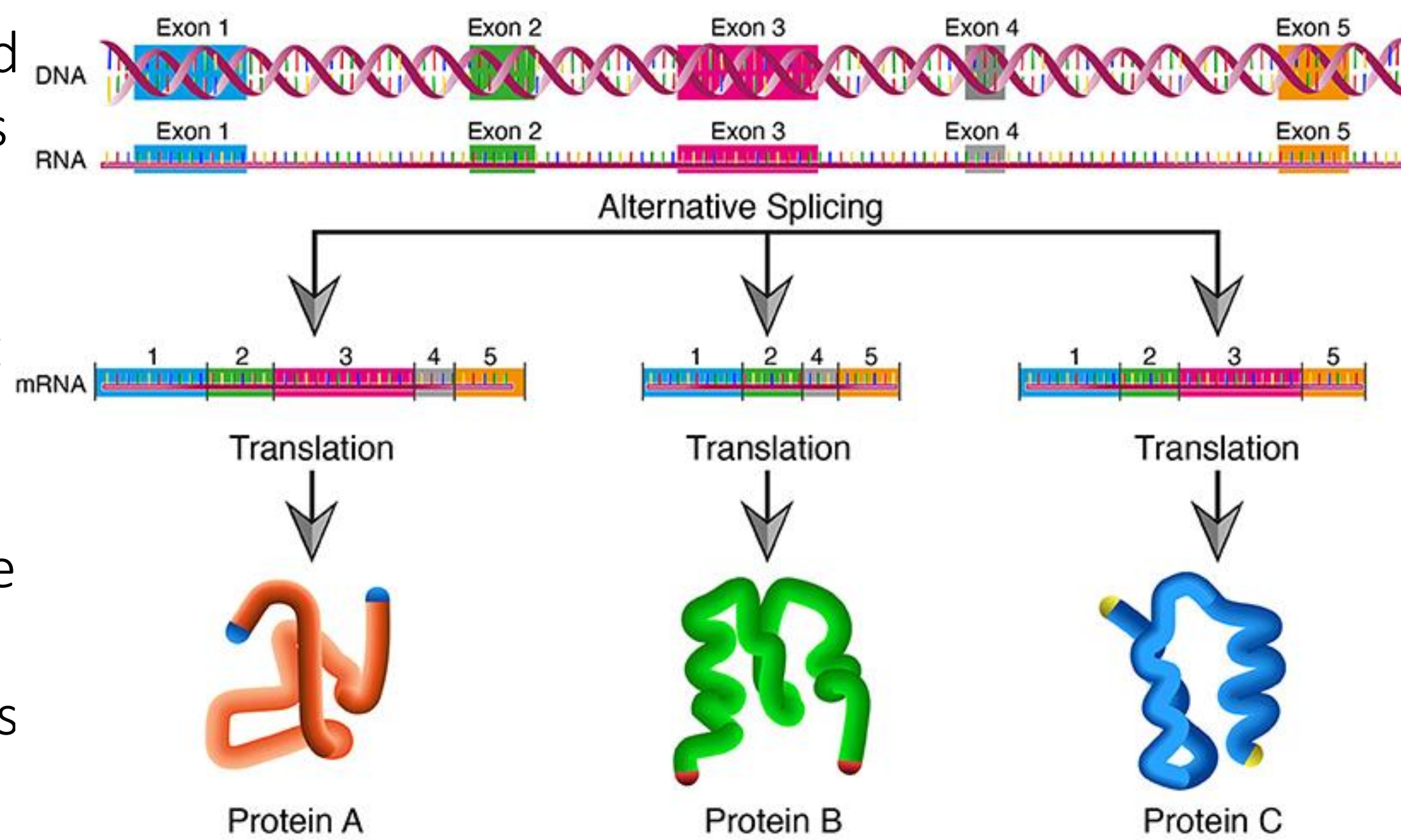


# Investigating the Effect of the Nab2 RNA-Binding Protein on CircMbl Biogenesis in *Drosophila melanogaster*

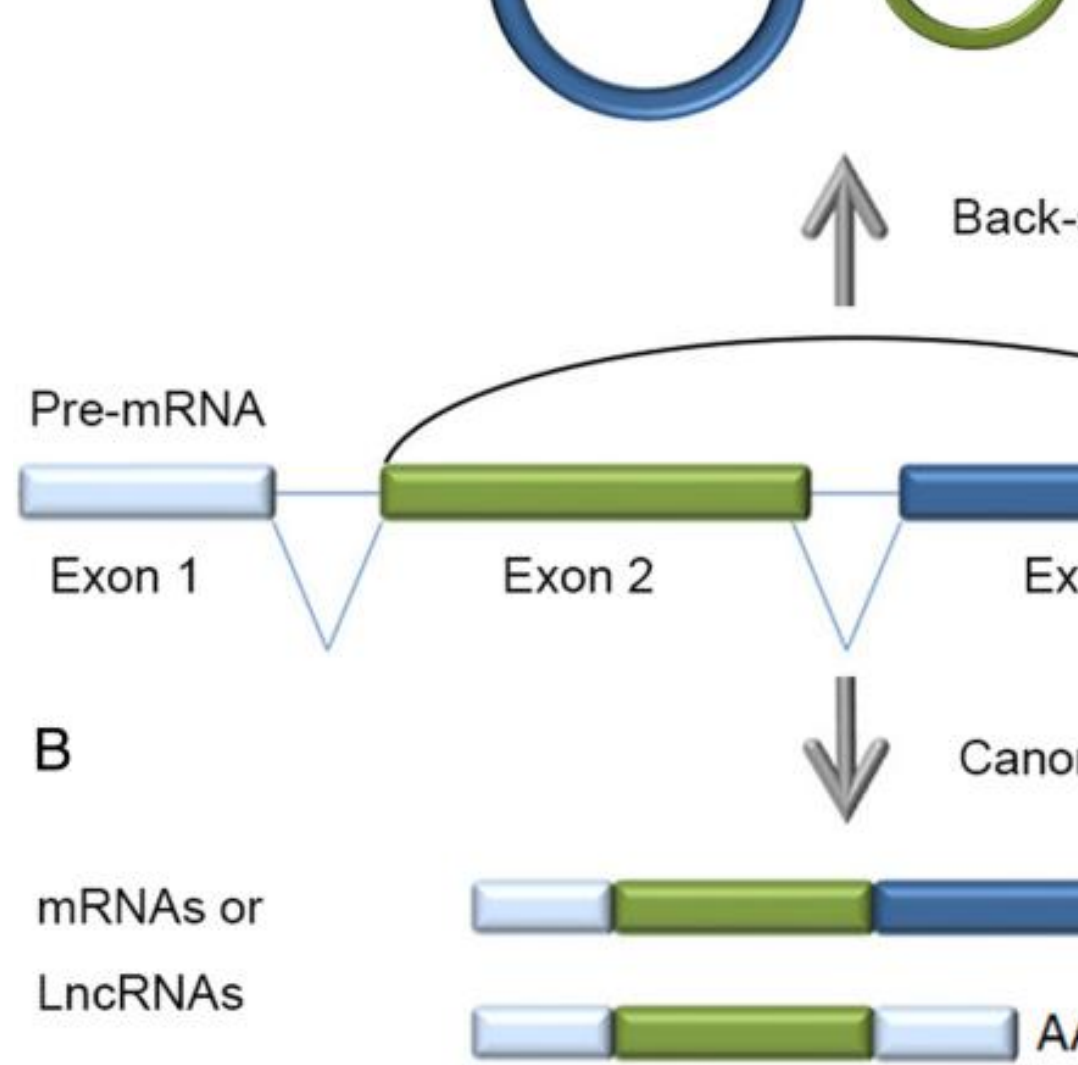
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## Introduction

- DNA is transcribed into RNA, which is translated into protein.
- Proteins carry out functions in cells.
- Within genes, coding regions are exons, and noncoding regions are introns.
- Exons are spliced together to generate proper transcripts, but alternative splicing can lead to non-canonical transcripts.



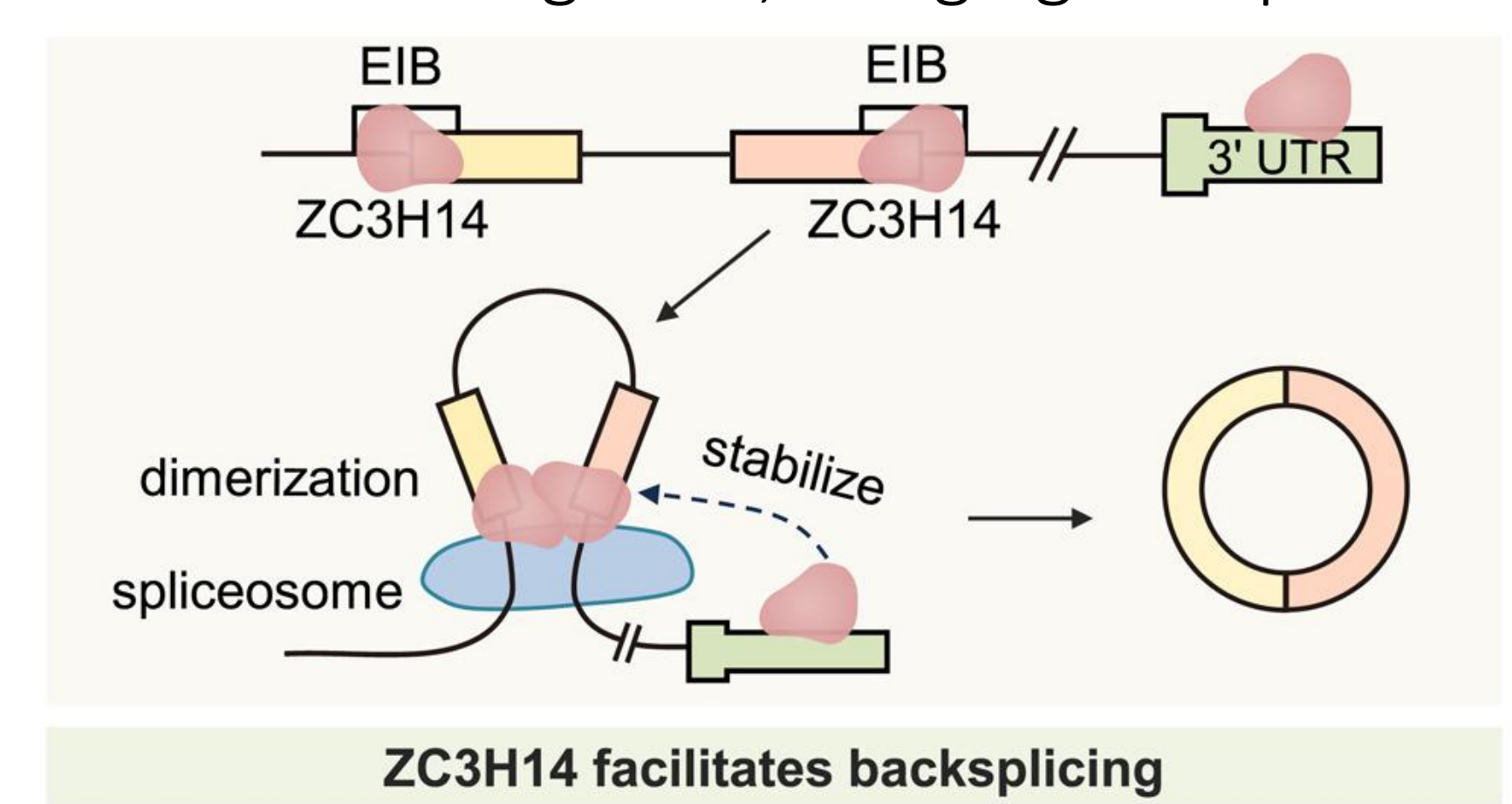
### A circRNAs



- One type of alternative splicing forms circRNAs via back-splicing.
- CircRNAs rarely encode any protein and are resilient to degradation.
- Other functional roles have remained unclear since their discovery.
- Several mechanisms can lead to back-splicing.

### B mRNAs or lncRNAs

- One common mechanism is assisted by the formation of temporary base-pairs in introns adjacent to a circularizing exon, bringing the splice sites into close proximity.
- The RNA-binding protein Nab2/ZC3H14 can facilitate back-splicing by binding to intron-exon boundaries and bring them into proximity for splicing.



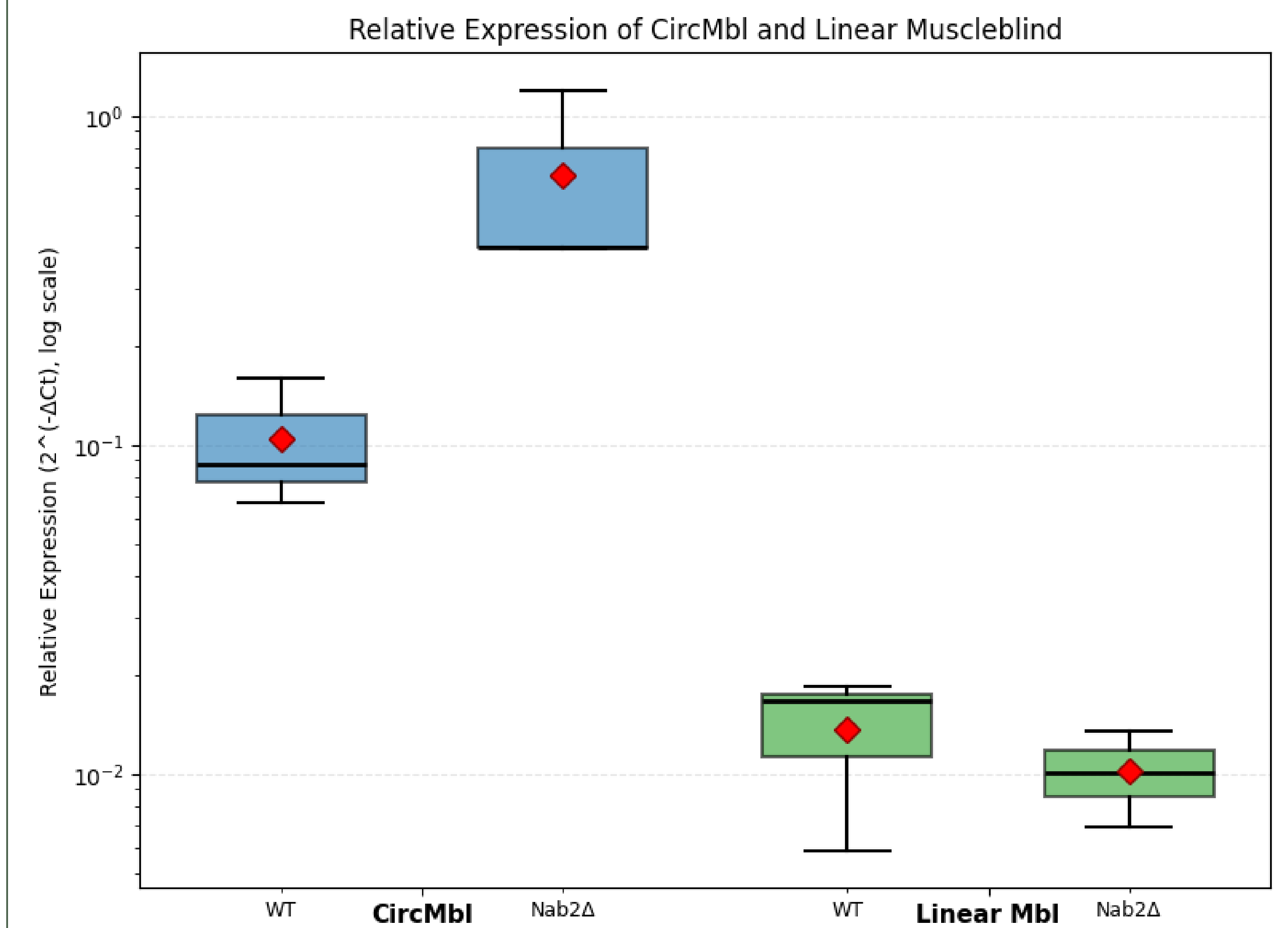
## Research Question

Does the presence of the Nab2 RNA-binding protein affect the biosynthesis and abundance of circMbl from *Muscleblind* transcripts?

- Aims:**
- Compare circMbl abundance levels in Nab2-knockout and wild-type *Drosophila* brain tissue
  - Analyze sequence conservation of the back-spliced region of circMbl

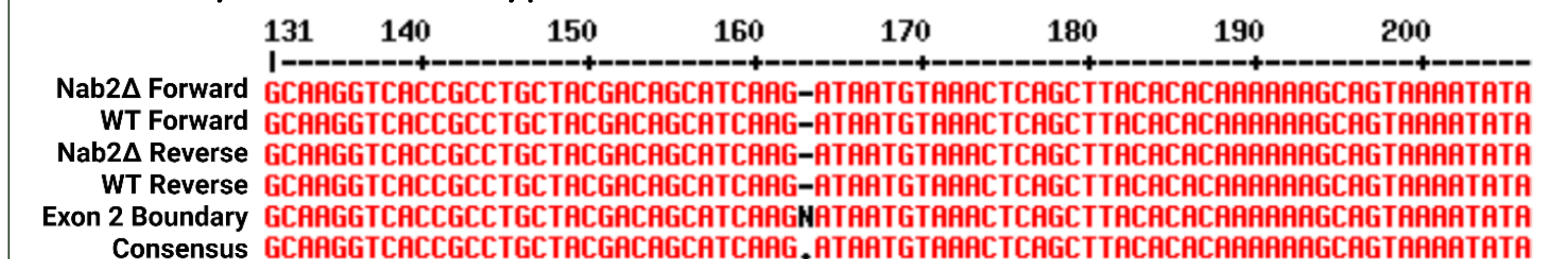
## Results

CircMbl expression was ~9-fold greater in larval brain tissue of Nab2-knockout mutants compared to wild type, a substantial difference which demonstrates practical significance ( $p = 0.1038$ ,  $d = 1.7$ ,  $n=3$ ).



- RNA was isolated from ~60 larval fly brains per biological replicate and used to generate cDNA libraries.
- QPCR data was collected from three biological replicates using three primer pairs, targeting circMbl, linear Muscleblind, and RP49.
- Data was normalized using RP49, followed by a fold change calculation to find relative expression.
- Statistical analysis included a two-tailed t-test and effect size calculation.

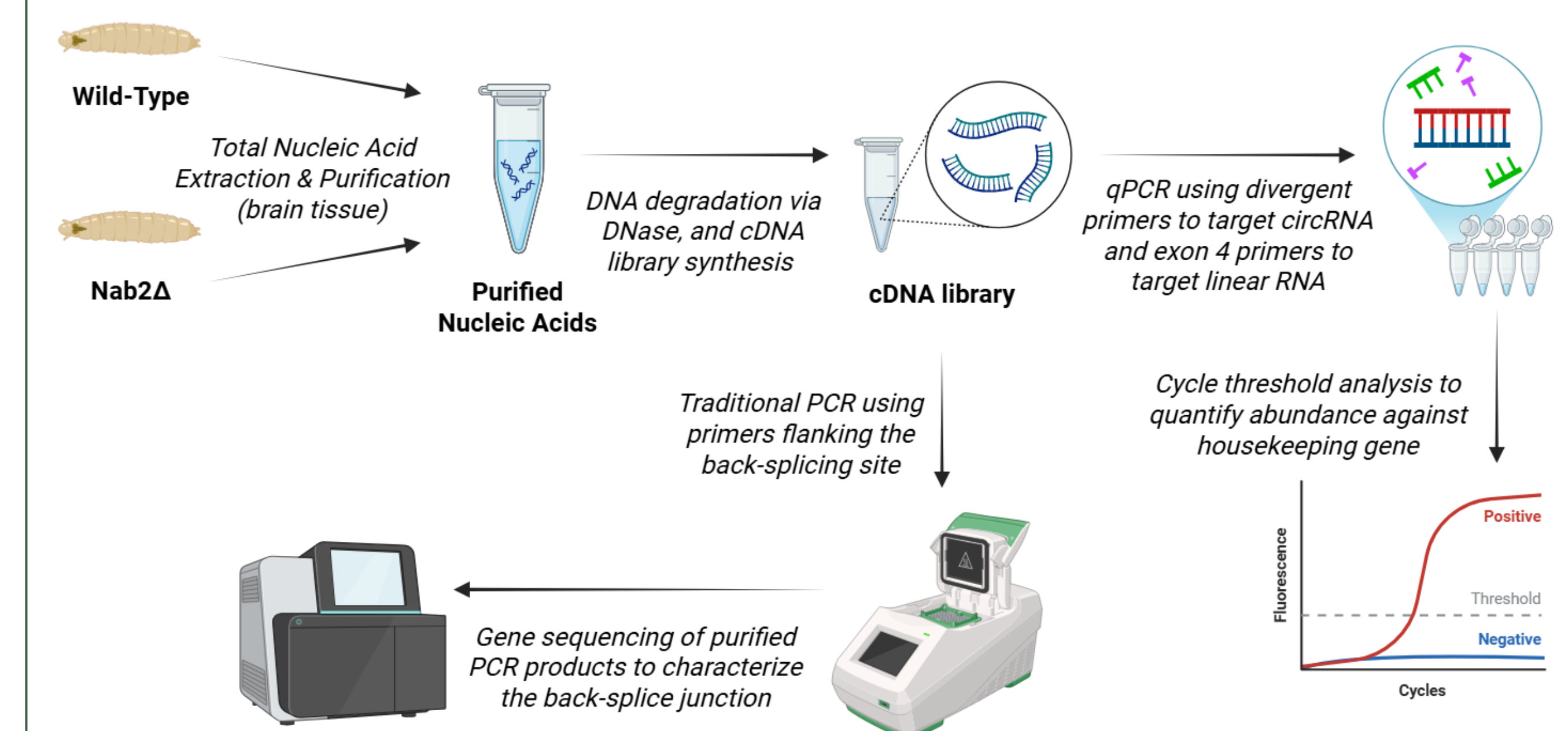
Synthesis of circMbl via back-splicing occurs at the canonical intron-exon boundary in both wild type and Nab2-knockout



- The back-spliced region of circMbl was amplified using divergent primers, generating PCR amplicons of this site.
- These amplicons were sequenced and aligned, demonstrating complete conservation as shown above.
- The sequenced PCR product was consistent with canonical exon 2 boundaries.

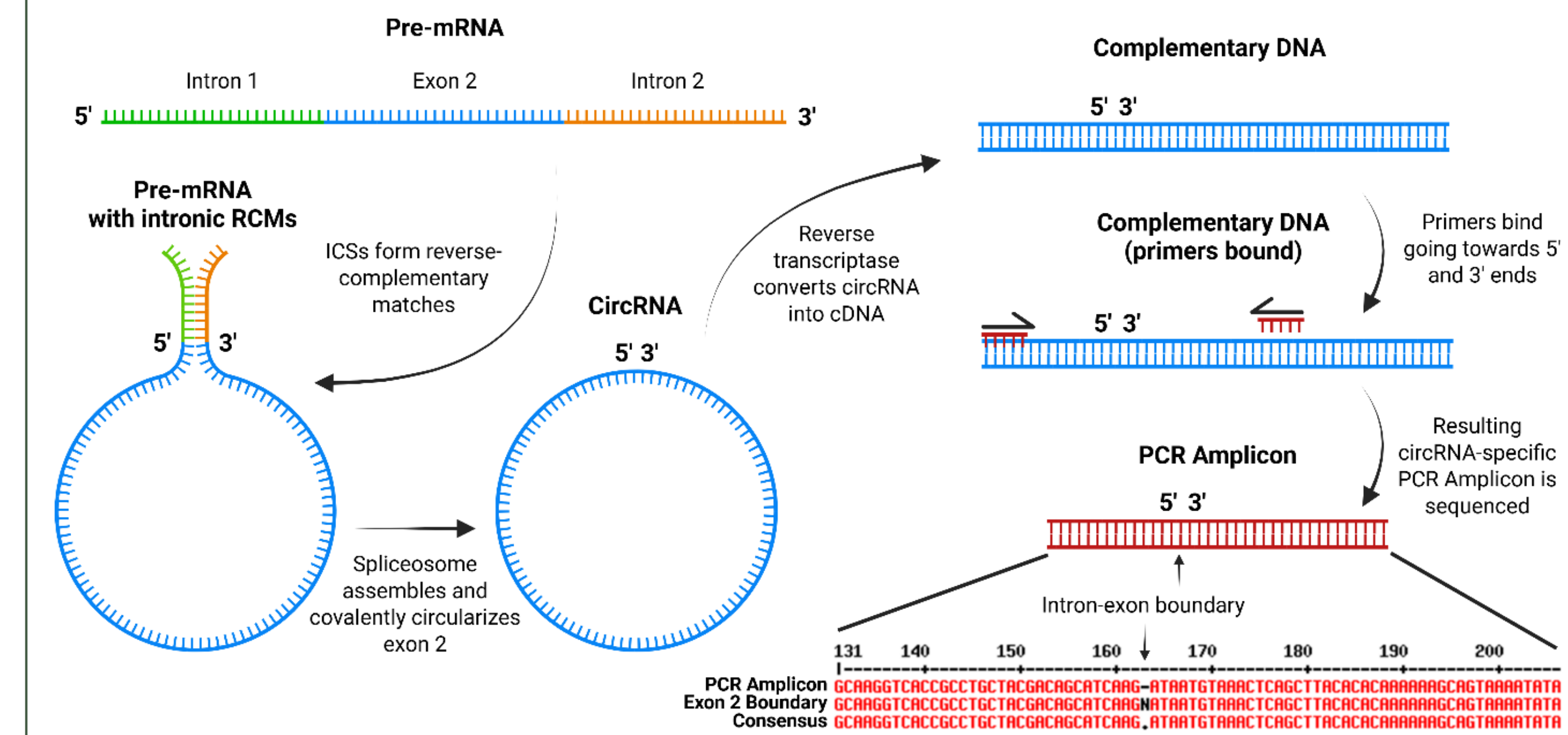
## Methodology

Hypothesis: The presence of Nab2 affects the frequency of circMbl biogenesis, and therefore circMbl abundance.



- Dissected and extracted DNA & RNA from fly larvae brain tissue
- Purified RNA and synthesized a complementary cDNA library
- Tested abundances of linear and circMbl using quantitative PCR
- Amplified and sequenced the back-spliced region of circMbl

Divergent Primers, Circularization, and Reverse Transcriptase:



- Reverse transcriptase makes a DNA copy of RNA sequences
- Divergent primers bind to the DNA copy but only amplify if the RNA was circularized

## Conclusions and Future Work

**Conclusion:** CircMbl biosynthesis in *Drosophila* is upregulated when Nab2 is absent, which is the opposite of Nab2's typical effect on circularization.

- Future aims:**
- Testing the binding specificity of the Nab2 protein
  - Determining localization and potential sequestration of Nab2 and Muscleblind by excess circMbl