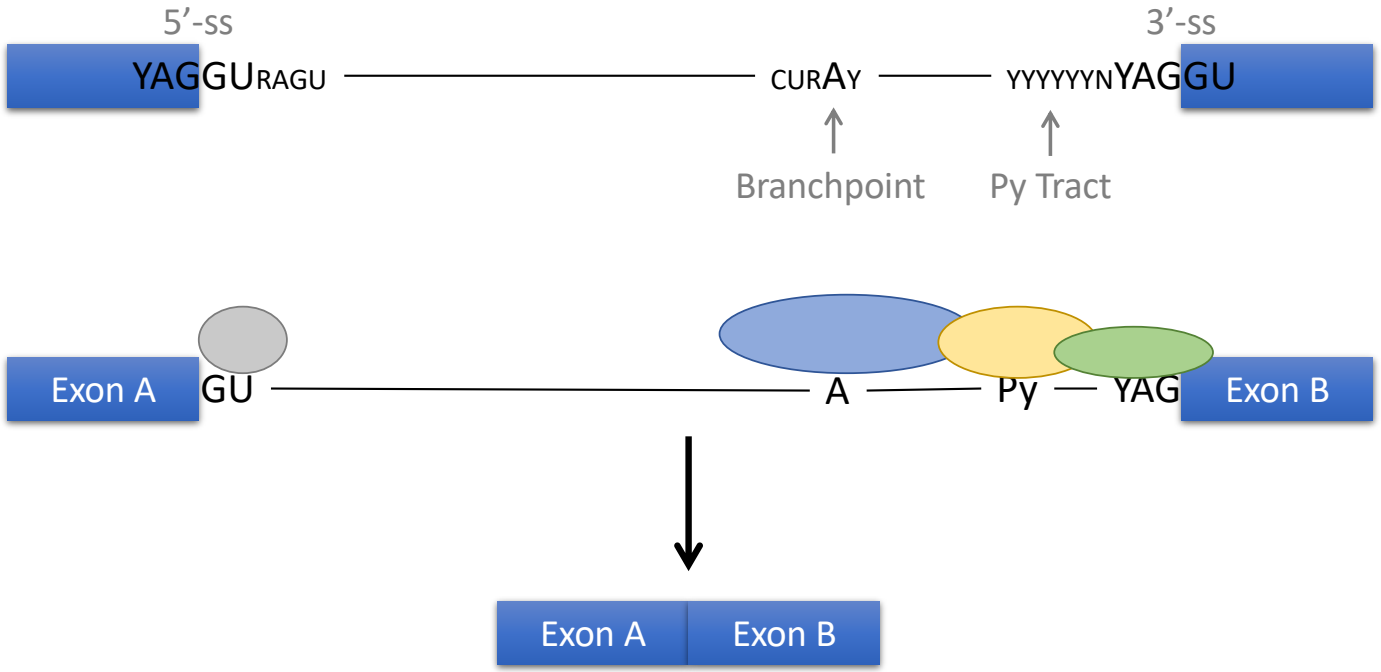
# Motif Mark

February 8, 2018

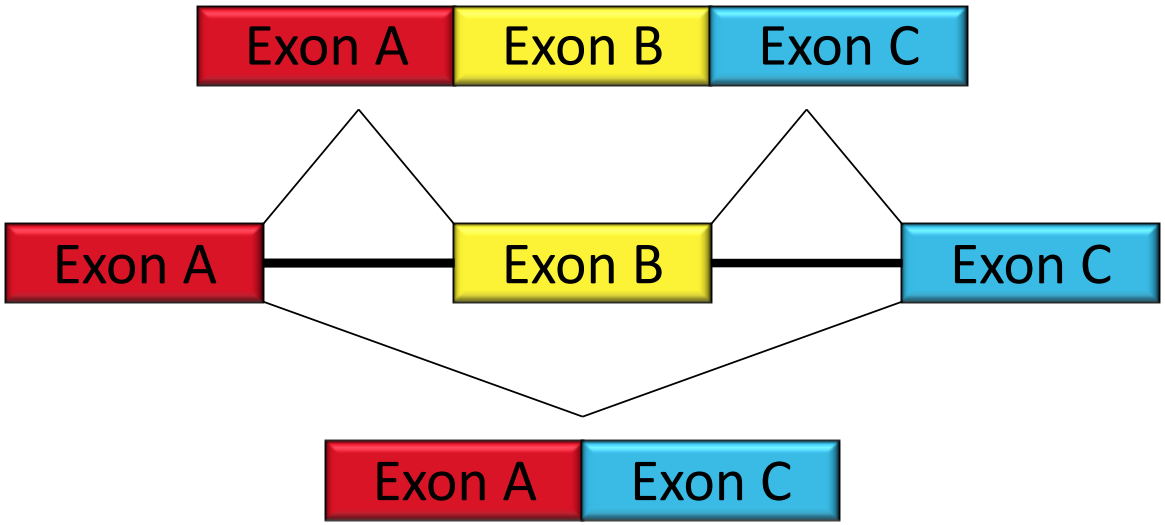
# Observations

- MBNL1 and RBFOX1 are both regulators of alternative splicing

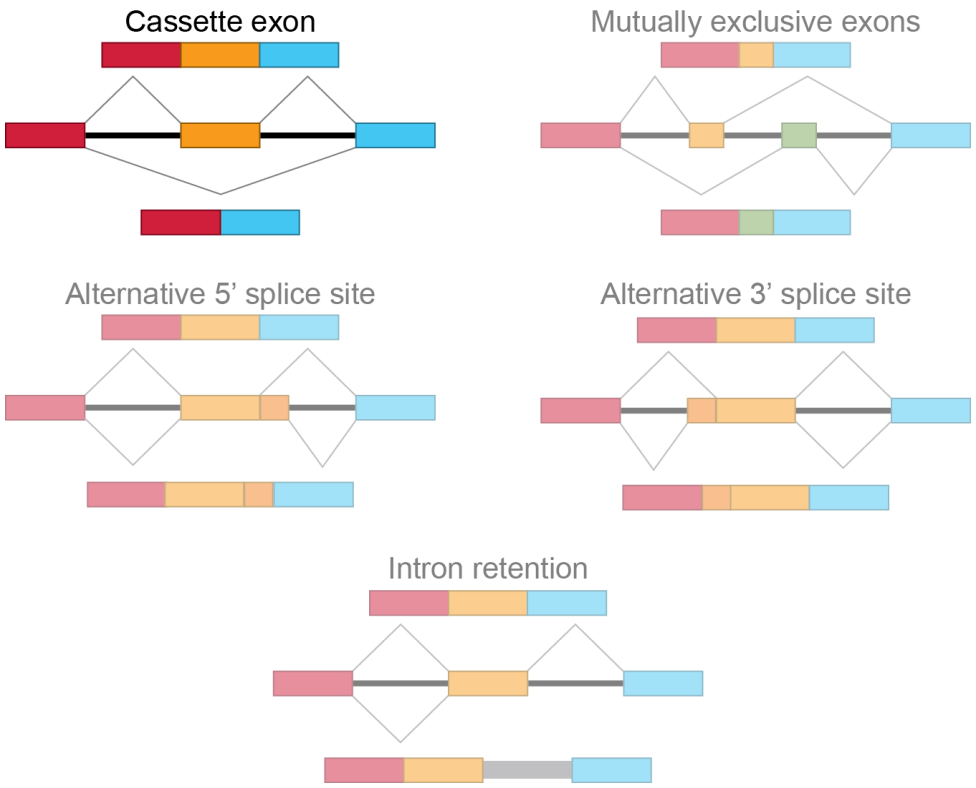
# What is splicing?



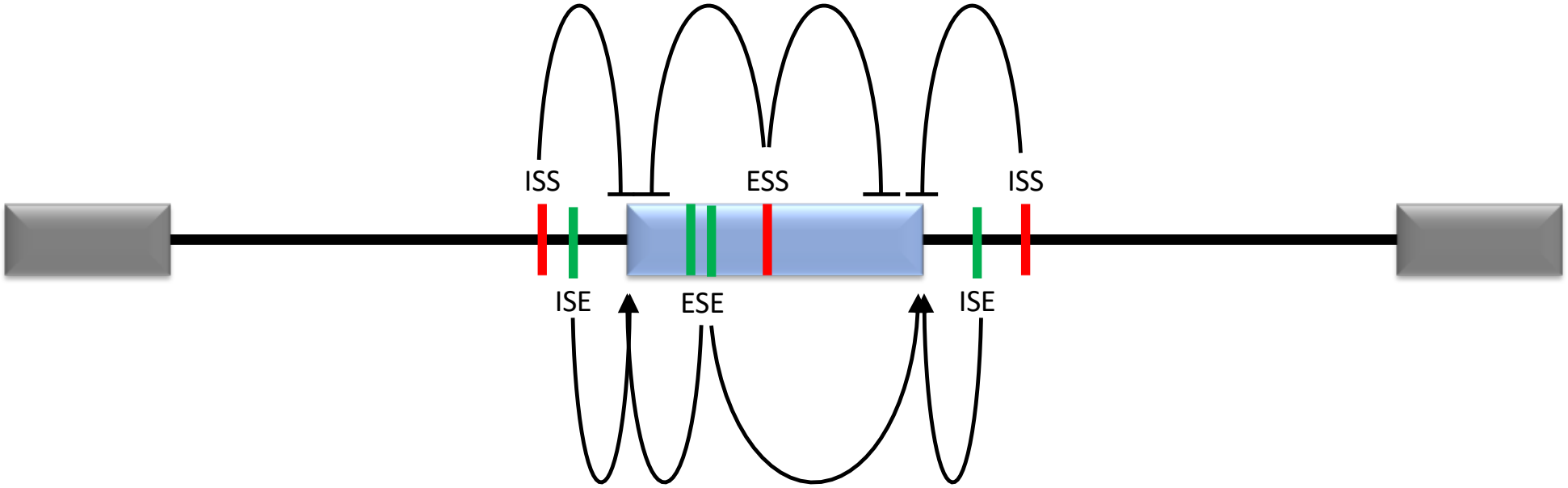
# What is alternative splicing?



# What is alternative splicing?

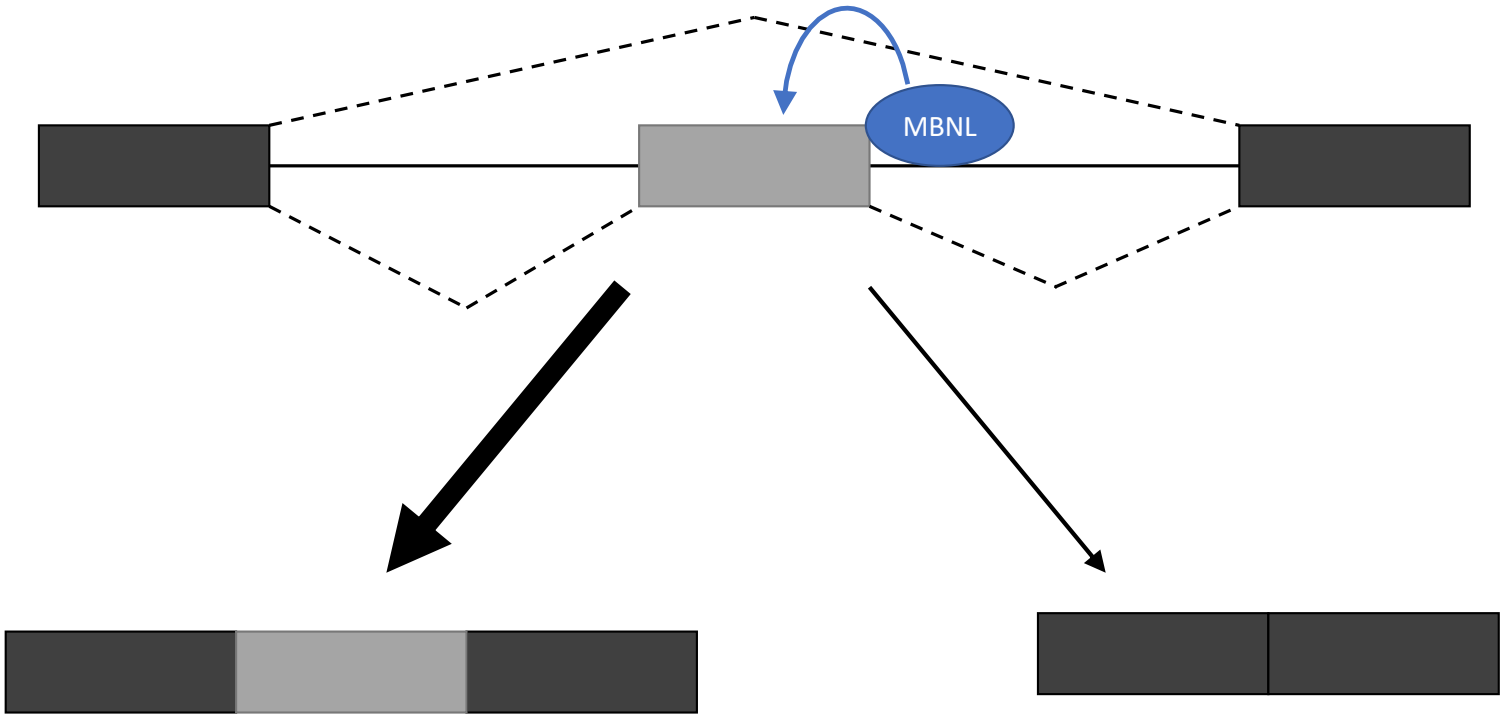


# How is the splicing decision made?

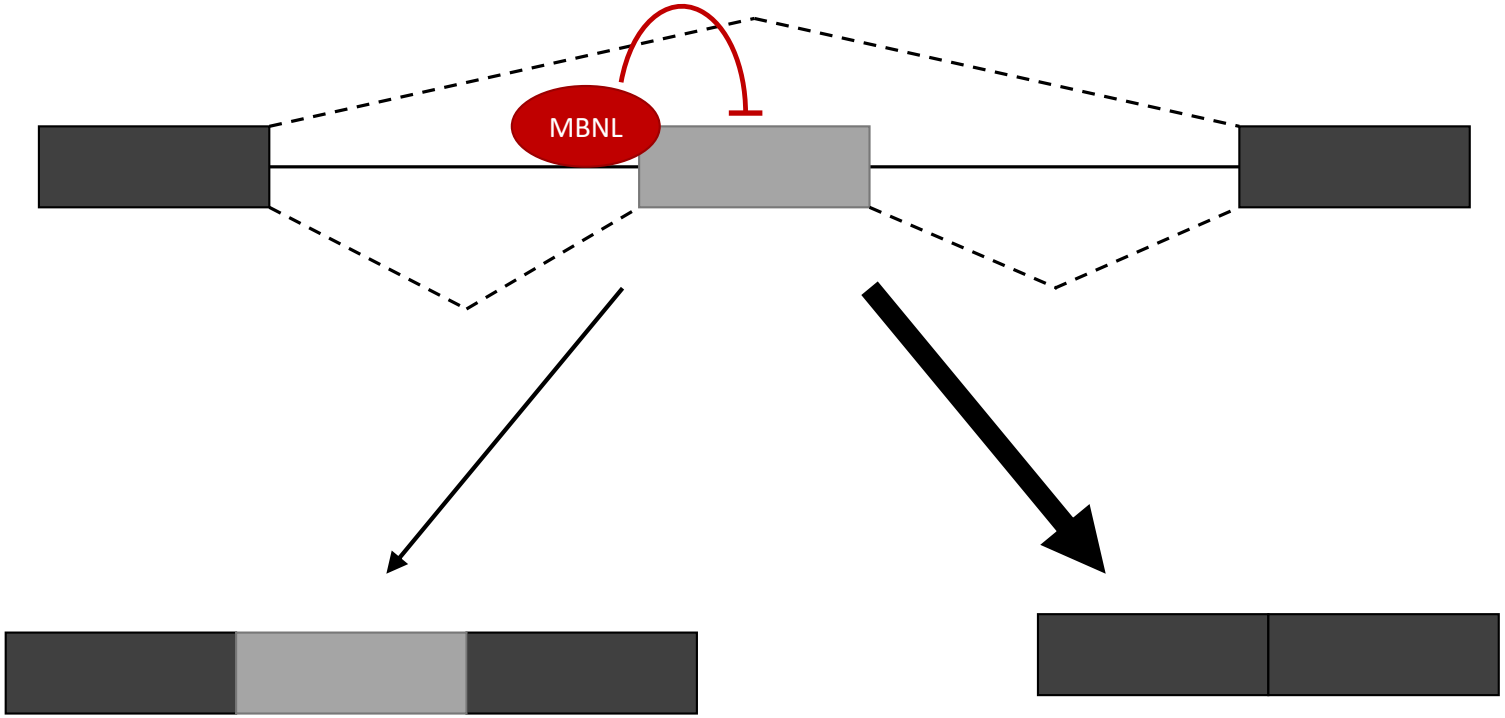



- ISS – intron splicing silencer
- ISE – intron splicing enhancer
- ESS – exon splicing silencer
- ESE – exon splicing enhancer

MBNL is a splicing factor that is both an activator and suppressor of exon inclusion for pre-mRNA splicing



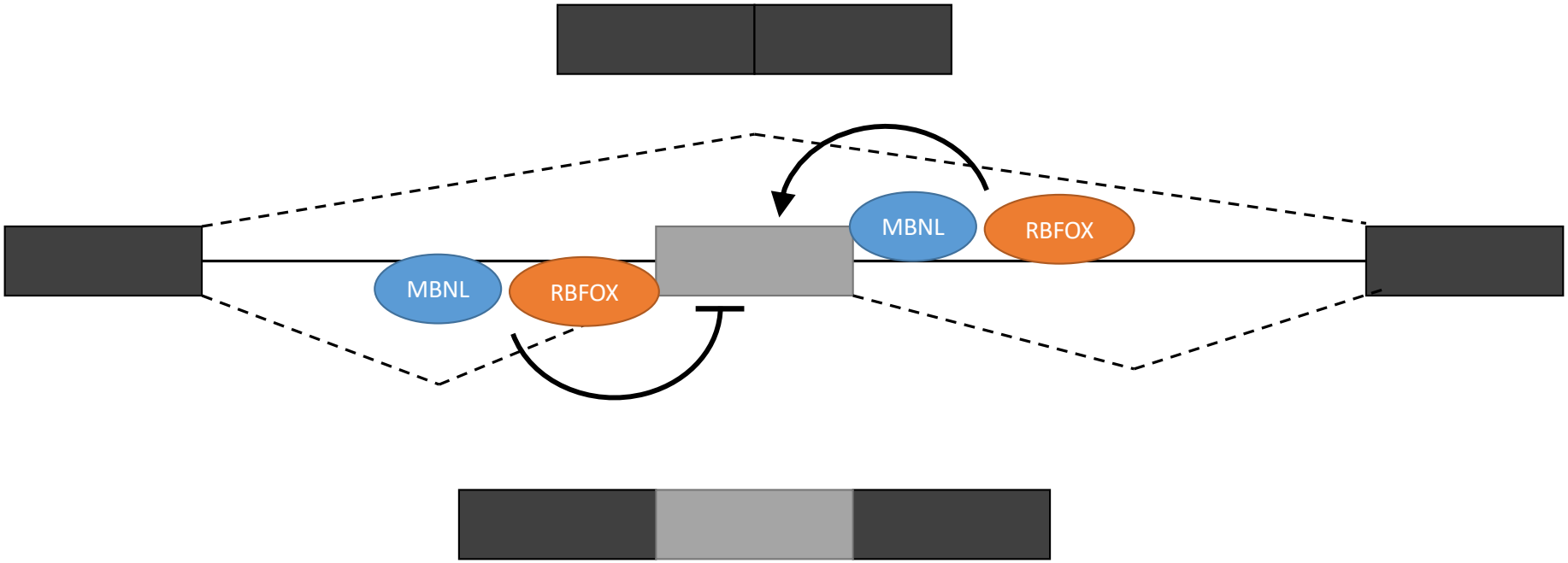
MBNL is a splicing factor that is both an **activator** and **suppressor** of exon inclusion for pre-mRNA splicing



# Observations

- MBNL1 and RBFOX1 are both regulators of alternative splicing
- MBNL1 and RBFOX1 regulate splicing in similar manners

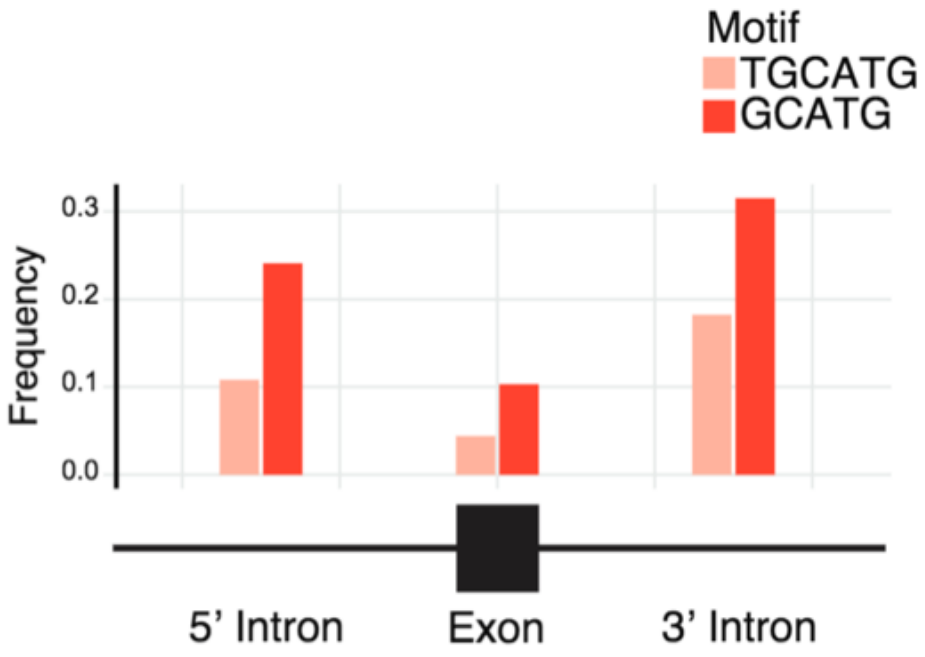
# RBFOX1 regulates alternative splicing in a similar manner to MBNL1



# Observations

- MBNL1 and RBFOX1 are both regulators of alternative splicing
- MBNL1 and RBFOX1 regulate splicing in similar manners
- MBNL1 and RBFOX1 have similar expression profiles
  - Both expressed in brain, heart, and skeletal muscle
  - Increased expression leads to alternative splicing changes critical for development
  - Depletions in expression have been associated with neurological disorders
- Some MBNL1 regulated splicing events have RBFOX1 binding sites

# Analysis of 203 MBNL-regulated exons in mouse revealed the presence of RBFOX binding motifs




66% contain a GCAUG and
33% contain a UGCAUG
RBFOX motif in the exon or within 250 nucleotides for the flanking exons

# Research question

- How do MBNL1 and RBFOX1 work together to regulate splicing events in transcripts that are regulated by both?

# Our goal

- Develop a Python script to plot protein binding motifs on an image of the an exon and flanking introns

>INSR chr19:7149896-7151209 (reverse complement)

agaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagagaaagaaagaaaggaaagagagaaagaaa
ggacagagaaaggaaggggggcaagggagggagagaggagggaaggaaggaaggaaaaaaggaaaagaaagaaaaga
aagagaaagaaaatgaaaaaaagaaggaaggaaagagaaagaaagcaaatgaaggaaggaaagagggaaaaagaga
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>INSR chr19:7149896-7151209 (reverse complement)

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# Activity

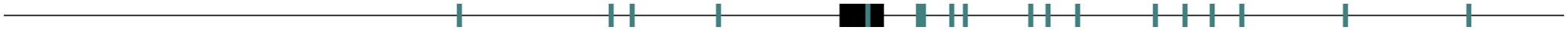
- Working in groups, discuss general strategy for the algorithm
  - What should the input look like?
  - What should the output look like?
  - What functions are you going to write?
  - How can you handle multiple motifs and multiple genes?
  - How are you going to identify motifs with ambiguity, i.e. YCGY?

# Input

- FASTA file
  - How denote introns vs exons?
- Coordinates
  - UCSC genome browser
  - Need assembly info
  - How interface with UCSC?
- Other?

# Output

- Vector based image
- To scale!
- Introns vs exons
- Denote multiple motifs
- Key?

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ggacagagaaaggaaggggcaagggagggagagaggagggaaggaaggaaggaaaaaaggaaaagaaagaaaaga
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# Functions

- Parse FASTA
- Parse file with motifs
- Drawing function?

# Activity

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# Drawing with 


```
conda install -c conda-forge pycairo
```

```
import pycairo
surface = cairo.SVGSurface("plot.svg", width, height)
context = cairo.Context(surface)
context.set_line_width(1)
context.move_to(50,25)
context.line_to(intron1+exon+intron2,25)
context.stroke()
```

https://pycairo.readthedocs.io

https://cairographics.org/documentation/pycairo/3/

# Your assignment: Motif Mark

- Create a repository in your Github profile called motif-mark
- Write a python script to visualize motifs on sequences
  - Minimum requirements:
    - Python3 compatible code
    - Use argparse
    - Input FASTA file and motifs file
    - Multiple sequences
    - Multiple motifs
    - Ambiguous motif handling
    - svg output
    - Key/labeling
  - Stretch:
    - Alternate inputs (coordinates)
    - Option of output
    - Offers user customizable colors
    - Color palate options