

# ***Mbnl2* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Mbnl2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mbnl2* gene. The schematic diagram is as follows:



- The *Mbnl2* gene has 10 transcripts. According to the structure of *Mbnl2* gene, exon3-exon7 of *Mbnl2-201* (ENSMUST00000088419.12) transcript is recommended as the knockout region. The region contains 838bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mbnl2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for one gene trap exhibit myotonia, lordosis and altered skeletal muscle fiber morphology.
- The KO region contains functional region of the *Gm26679* gene. Knockout the region will affect the function of *Gm26679* gene.
- The *Mbnl2* gene is located on the Chr14. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Mbnl2 muscleblind like splicing factor 2 [Mus musculus (house mouse)]

Gene ID: 105559, updated on 9-Apr-2019

### Summary



<b>Official Symbol</b>	Mbnl2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	muscleblind like splicing factor 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2145597</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022139</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1110002M11Rik, AI047808, AI837313, AI849185, AL118326, MBLL, R75232, mKIAA4072
<b>Expression</b>	Ubiquitous expression in bladder adult (RPKM 30.1), cerebellum adult (RPKM 20.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

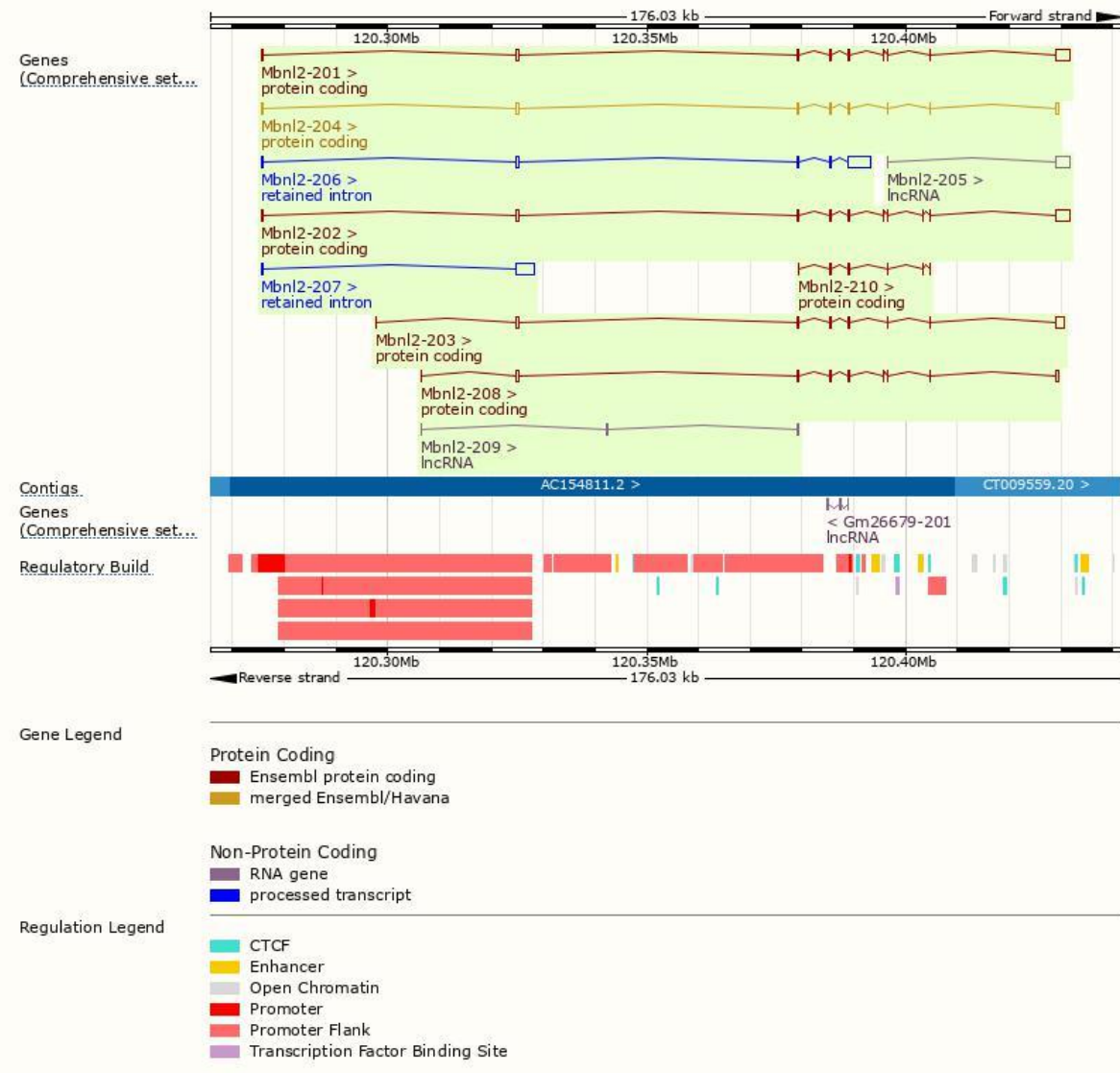
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mbnl2-201	<a href="#">ENSMUST00000088419.12</a>	4552	<a href="#">373aa</a>	Protein coding	<a href="#">CCDS49567</a>	<a href="#">Q8C181</a>	TSL:1 GENCODE basic APPRIS P4
Mbnl2-203	<a href="#">ENSMUST00000226800.1</a>	3328	<a href="#">355aa</a>	Protein coding	<a href="#">CCDS49568</a>	<a href="#">Q8C181</a>	GENCODE basic APPRIS ALT1
Mbnl2-204	<a href="#">ENSMUST00000227012.1</a>	2390	<a href="#">355aa</a>	Protein coding	<a href="#">CCDS49568</a>	<a href="#">Q8C181</a>	GENCODE basic APPRIS ALT1
Mbnl2-208	<a href="#">ENSMUST00000227594.1</a>	2334	<a href="#">373aa</a>	Protein coding	<a href="#">CCDS49567</a>	<a href="#">Q8C181</a>	GENCODE basic APPRIS P4
Mbnl2-202	<a href="#">ENSMUST00000167459.2</a>	4534	<a href="#">385aa</a>	Protein coding	-	<a href="#">A0A2K6EDM5</a>	TSL:1 GENCODE basic APPRIS ALT1
Mbnl2-210	<a href="#">ENSMUST00000228115.1</a>	758	<a href="#">253aa</a>	Protein coding	-	<a href="#">A0A2I3BRX8</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Mbnl2-206	<a href="#">ENSMUST00000227484.1</a>	5561	No protein	Retained intron	-	-	
Mbnl2-207	<a href="#">ENSMUST00000227508.1</a>	3789	No protein	Retained intron	-	-	
Mbnl2-205	<a href="#">ENSMUST00000227153.1</a>	2881	No protein	lncRNA	-	-	
Mbnl2-209	<a href="#">ENSMUST00000227644.1</a>	339	No protein	lncRNA	-	-	

The strategy is based on the design of *Mbnl2-201* transcript,The transcription is shown below

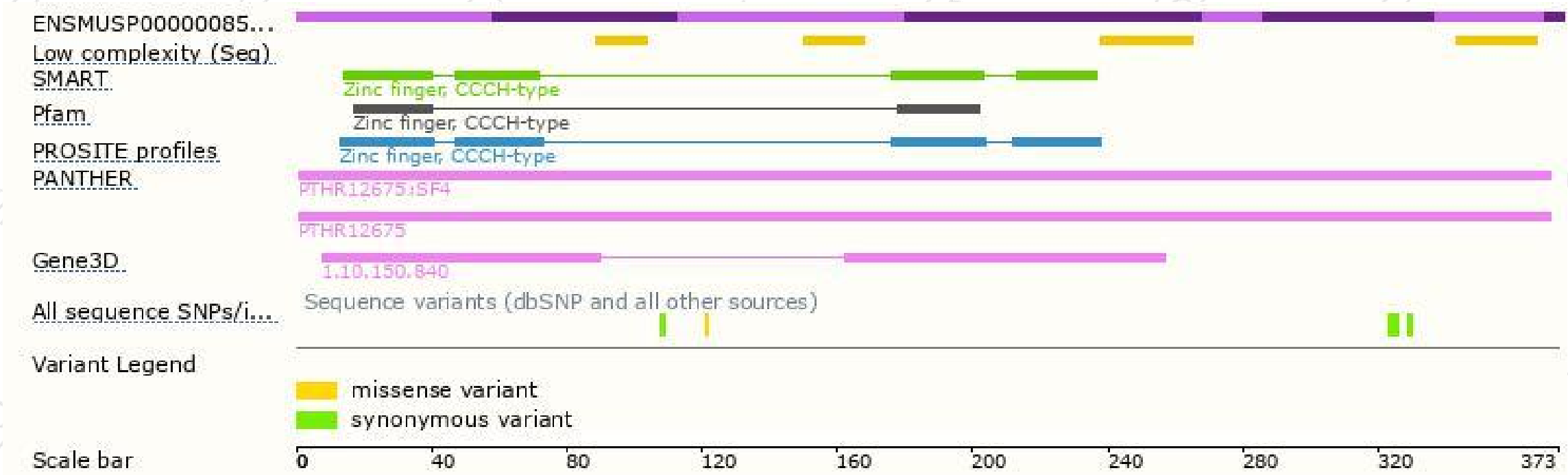


# Genomic location distribution

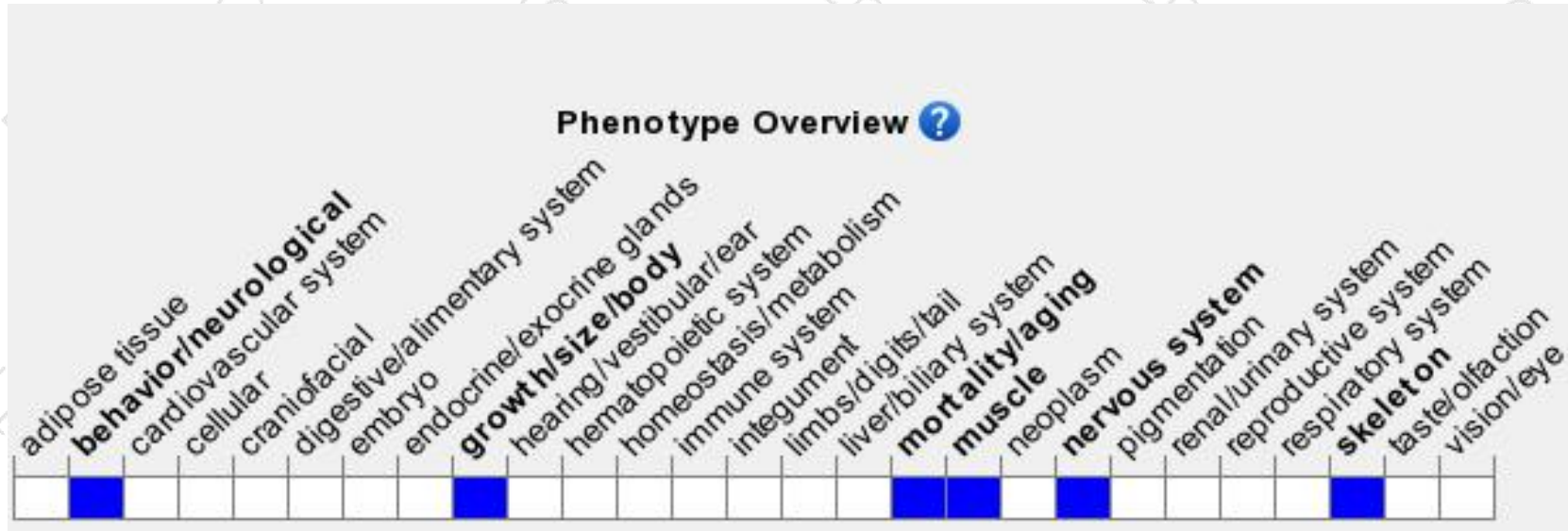




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Mice homozygous for one gene trap exhibit myotonia, lordosis and altered skeletal muscle fiber morphology.

If you have any questions, you are welcome to inquire.

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