Mbnl3 Cas9-KO Strategy

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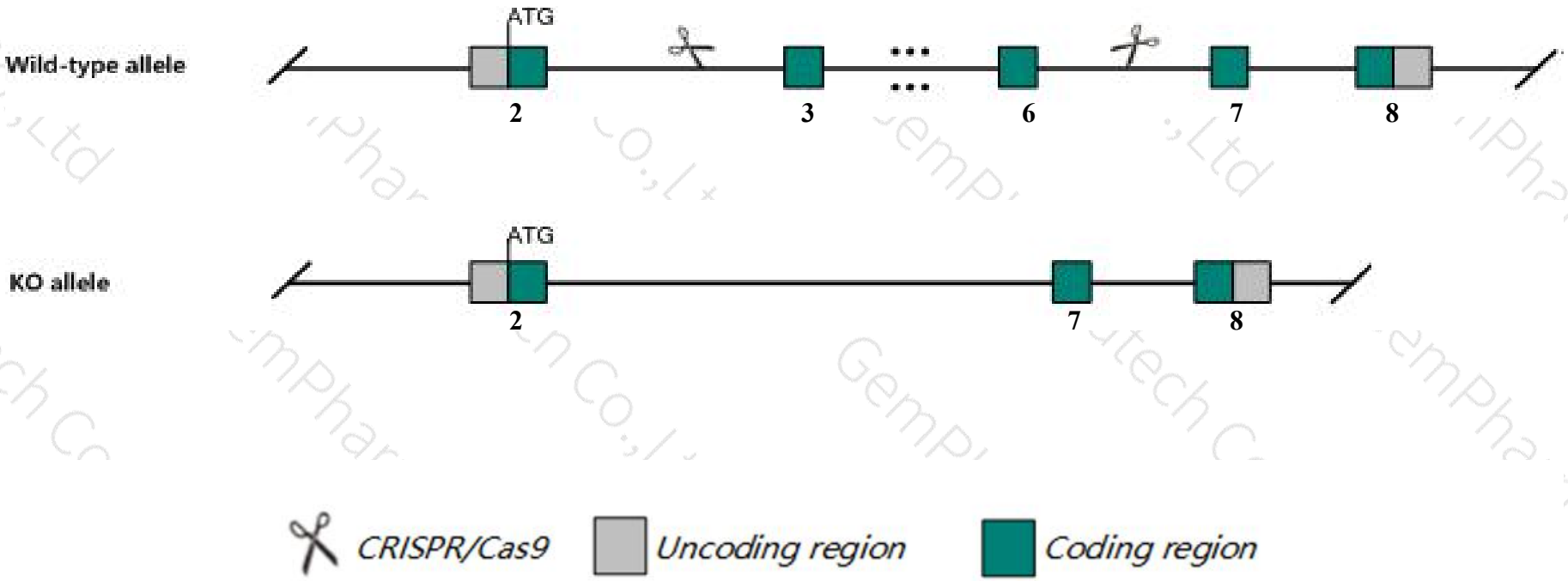
Project Overview

Project Name	***Mbnl3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mbnl3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mbnl3* gene has 7 transcripts. According to the structure of *Mbnl3* gene, exon3-exon6 of *Mbnl3-203* (ENSMUST00000114876.8) transcript is recommended as the knockout region.The region contains 745bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mbnl3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for an allele lacking exon 2 exhibit impaired muscle regeneration.

- The *Mbnl3* gene is located on the ChrX. 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）

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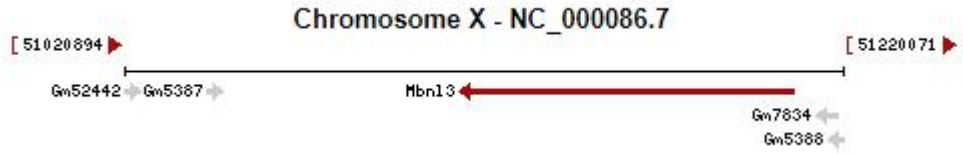
Mbnl3 muscleblind like splicing factor 3 [*Mus musculus* (house mouse)]

Gene ID: 171170, updated on 12-Aug-2019

Summary

Official Symbol	Mbnl3 provided by MGI
Official Full Name	muscleblind like splicing factor 3 provided by MGI
Primary source	MGI:MGI:2444912
See related	Ensembl:ENSMUSG00000036109
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CHCR; MBLX; MBXL; MBLX39; AI661274; A530038J18Rik; E430034C16Rik
Expression	Biased expression in placenta adult (RPKM 12.8), genital fat pad adult (RPKM 8.0) and 9 other tissues See more
Orthologs	human all

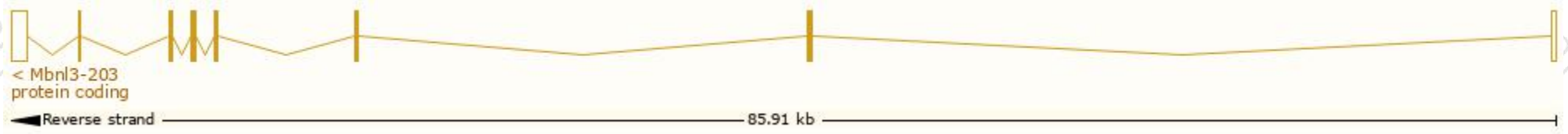


Transcript information（Ensembl）

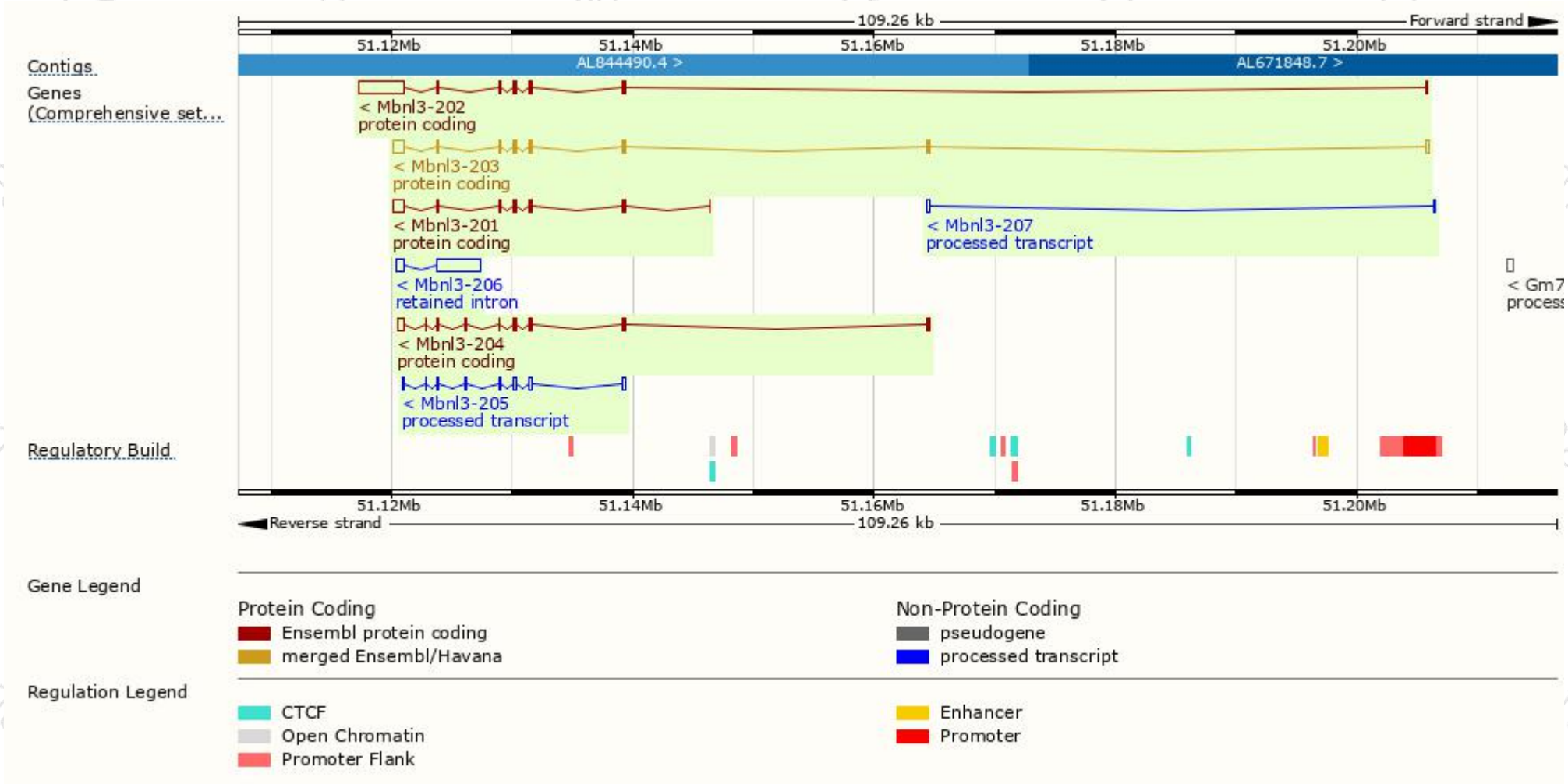
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mbnl3-202	ENSMUST00000114875.7	4649	246aa	Protein coding	CCDS81126	Q3TJQ3	TSL:1 GENCODE basic
Mbnl3-203	ENSMUST00000114876.8	2243	342aa	Protein coding	CCDS40969	Q542D8 Q8R003	TSL:1 GENCODE basic APPRIS P1
Mbnl3-201	ENSMUST00000041495.13	1803	246aa	Protein coding	CCDS81126	Q3TJQ3	TSL:1 GENCODE basic
Mbnl3-204	ENSMUST00000136404.2	1632	332aa	Protein coding	-	S4R267	TSL:5 GENCODE basic
Mbnl3-205	ENSMUST00000148116.1	1082	No protein	Processed transcript	-	-	TSL:5
Mbnl3-207	ENSMUST00000156028.1	356	No protein	Processed transcript	-	-	TSL:3
Mbnl3-206	ENSMUST00000150014.1	4121	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Mbnl3-203* transcript,The transcription is shown below

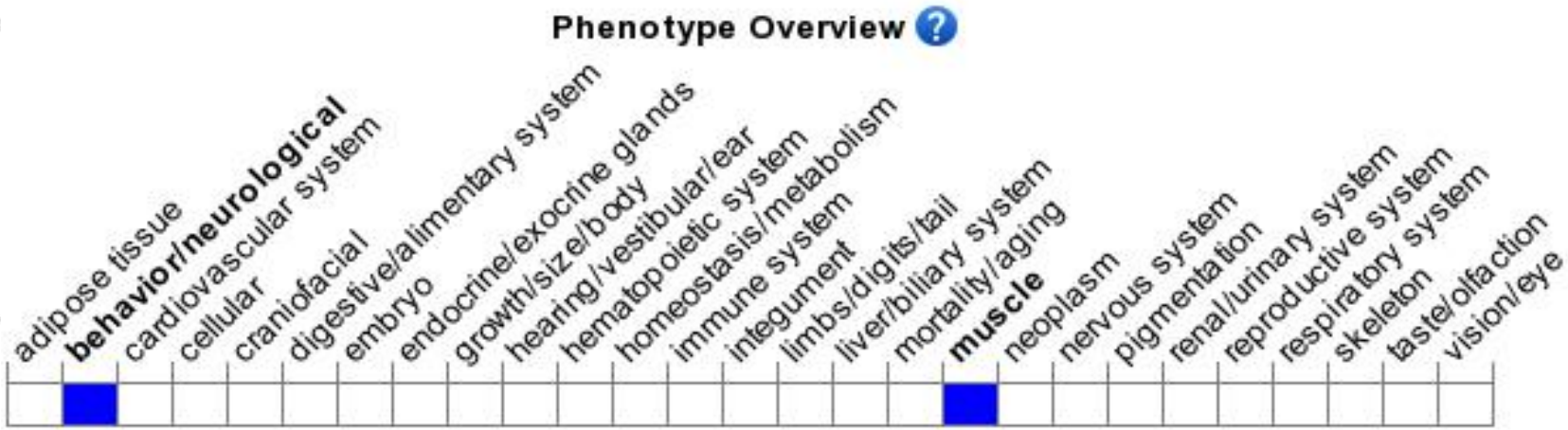


Genomic location distribution



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 an allele lacking exon 2 exhibit impaired muscle regeneration.

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

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