

# Rbmx Cas9-KO Strategy

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## **Project Overview**



Project Name Rbmx

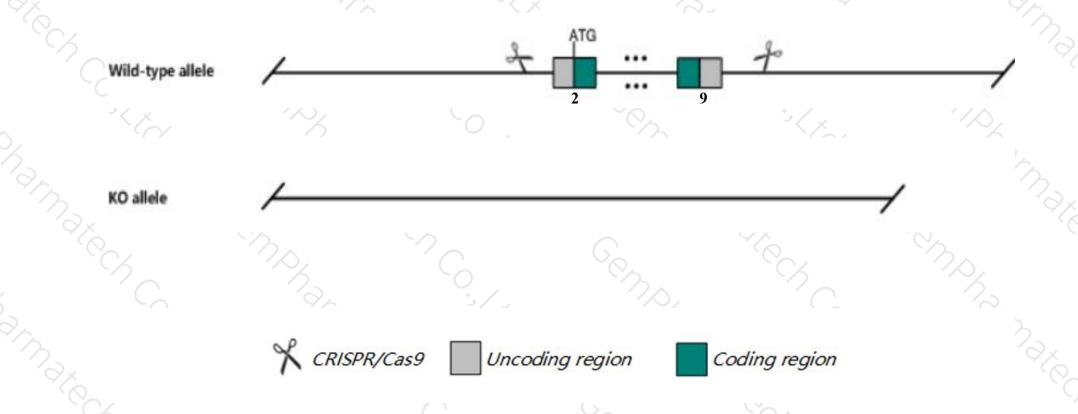
Project type Cas9-KO

Strain background C57BL/6JGpt

## **Knockout strategy**



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



### **Technical routes**



- The *Rbmx* gene has 6 transcripts. According to the structure of *Rbmx* gene, exon2-exon9 of *Rbmx-202* (ENSMUST00000114726.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rbmx* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > The *Rbmx* 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.
- ➤ The flox region contain the Snord61 gene, which may delet it after Cre.
- 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)



#### Rbmx RNA binding motif protein, X chromosome [Mus musculus (house mouse)]

Gene ID: 19655, updated on 7-Apr-2019

#### Summary

☆ ?

Official Symbol Rbmx provided by MGI

Official Full Name RNA binding motif protein, X chromosome provided by MGI

Primary source MGI:MGI:1343044

See related Ensembl: ENSMUSG00000031134

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 hnRNP G

Expression Broad expression in CNS E14 (RPKM 55.1), CNS E11.5 (RPKM 51.1) and 20 other tissuesSee more

Orthologs <u>human all</u>

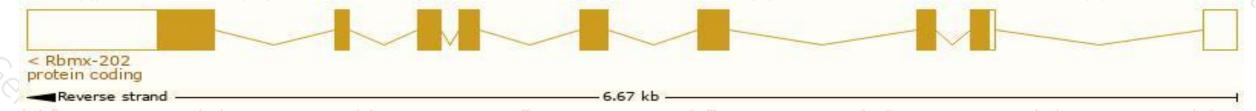
## Transcript information (Ensembl)



The gene has 6 transcripts, all transcripts are shown below:

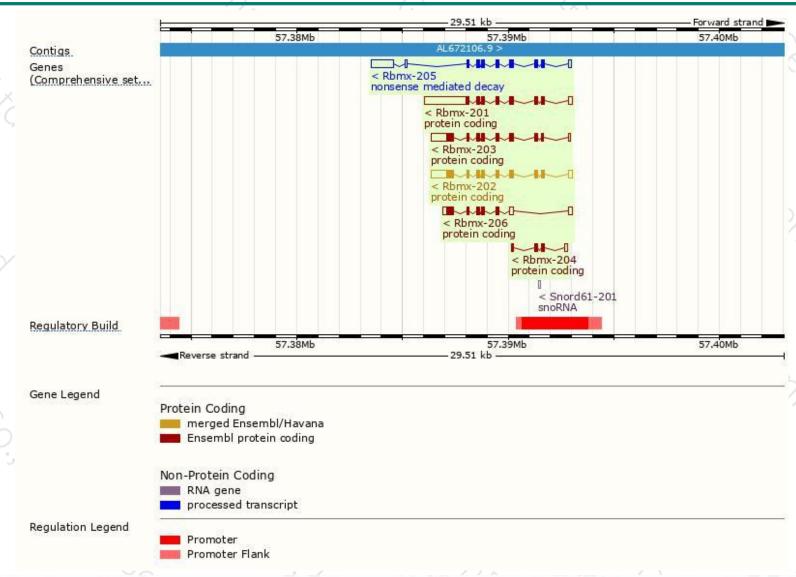
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rbmx-202	ENSMUST00000114726.7	2108	391aa	Protein coding	CCDS30153	Q9WV02	TSL:1 GENCODE basic APPRIS P1
Rbmx-203	ENSMUST00000114730.7	2019	<u>391aa</u>	Protein coding	CCDS30153	Q9WV02	TSL:5 GENCODE basic APPRIS P1
Rbmx-201	ENSMUST00000098470.8	3107	<u>301aa</u>	Protein coding		A2AFI3	TSL:5 GENCODE basic
Rbmx-206	ENSMUST00000143310.1	1296	<u>263aa</u>	Protein coding		S4R1F6	TSL:5 GENCODE basic
Rbmx-204	ENSMUST00000133346.1	434	<u>103aa</u>	Protein coding	5	A2AFI4	CDS 3' incomplete TSL:3
Rbmx-205	ENSMUST00000140384.7	2139	289aa	Nonsense mediated decay	-	Q9WV02	TSL:1

The strategy is based on the design of *Rbmx-202* transcript, The transcription is shown below



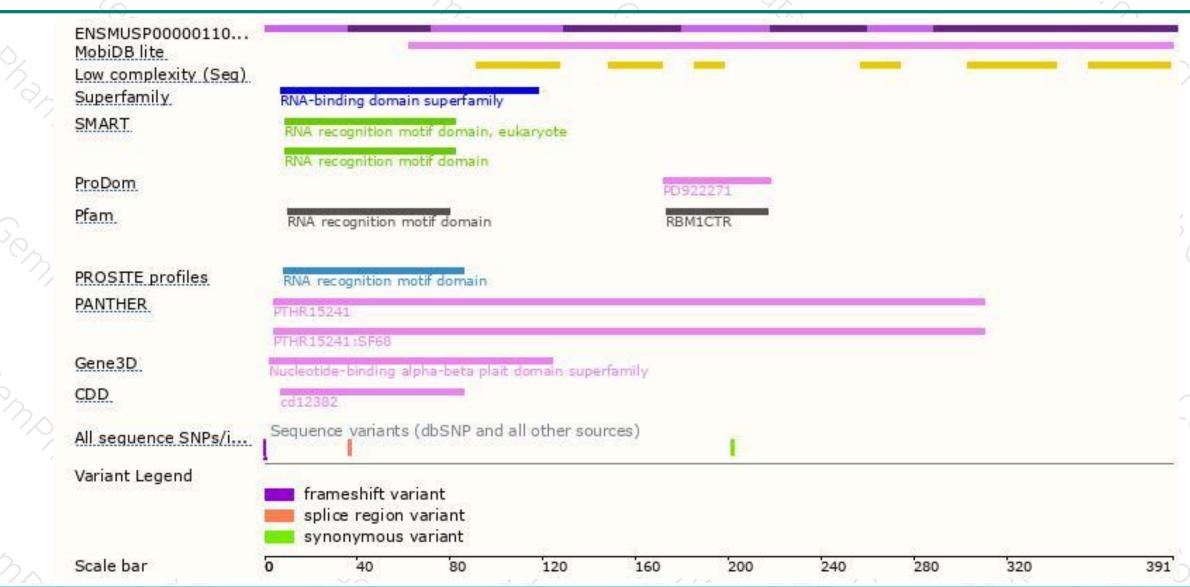
### Genomic location distribution





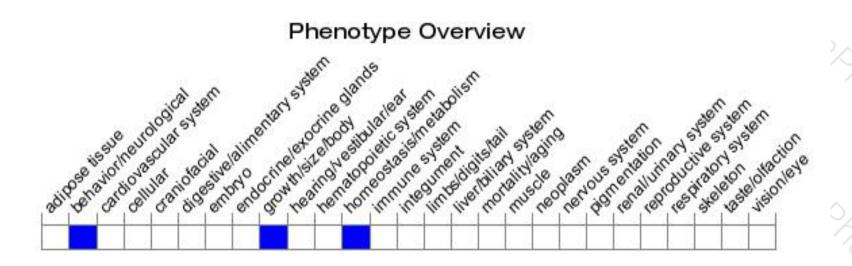
### Protein domain





## Mouse phenotype description(MGI)





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



If you have any questions, you are welcome to inquire. Tel: 400-9660890





