

Rem2 Cas9-KO Strategy

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Project Overview



Project Name

Rem2

Project type

Cas9-KO

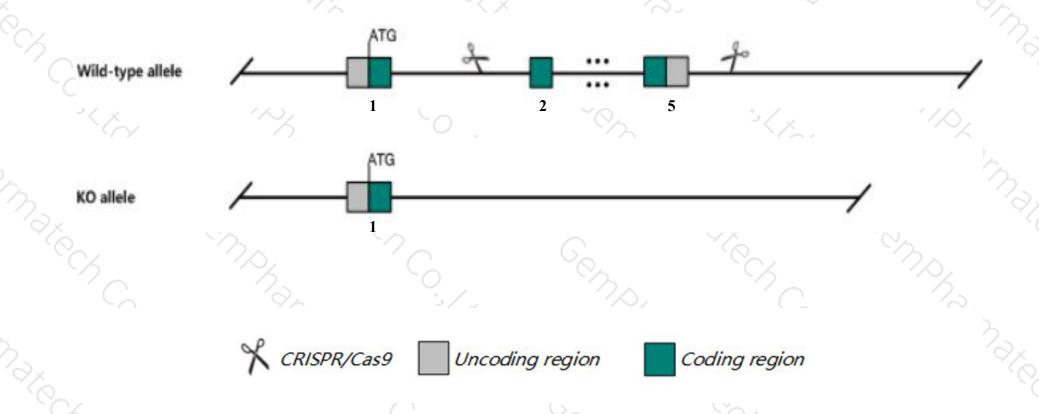
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Rem2 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Rem2* gene has 4 transcripts. According to the structure of *Rem2* gene, exon2-exon5 of *Rem2-202*(ENSMUST00000164766.7) transcript is recommended as the knockout region. The region contains 923bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rem2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for a knock-out allele exhibit strain-specific impaired viability and fertility as well as altered intrinsic excitability and spontaneous firing in visual circuits.
- The *Rem2* 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)



Rem2 rad and gem related GTP binding protein 2 [Mus musculus (house mouse)]

Gene ID: 140743, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Rem2 provided by MGI

Official Full Name rad and gem related GTP binding protein 2 provided by MGI

Primary source MGI:MGI:2155260

See related Ensembl: ENSMUSG00000022176

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 AW411893

Expression Biased expression in whole brain E14.5 (RPKM 7.7), CNS E14 (RPKM 6.4) and 9 other tissues See more

Orthologs human all

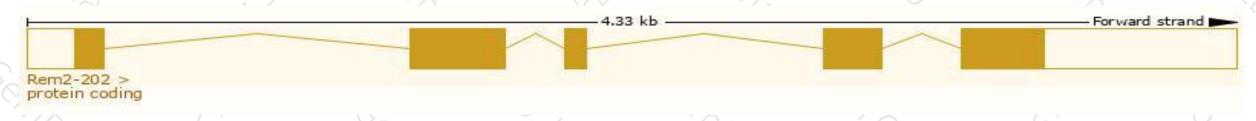
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

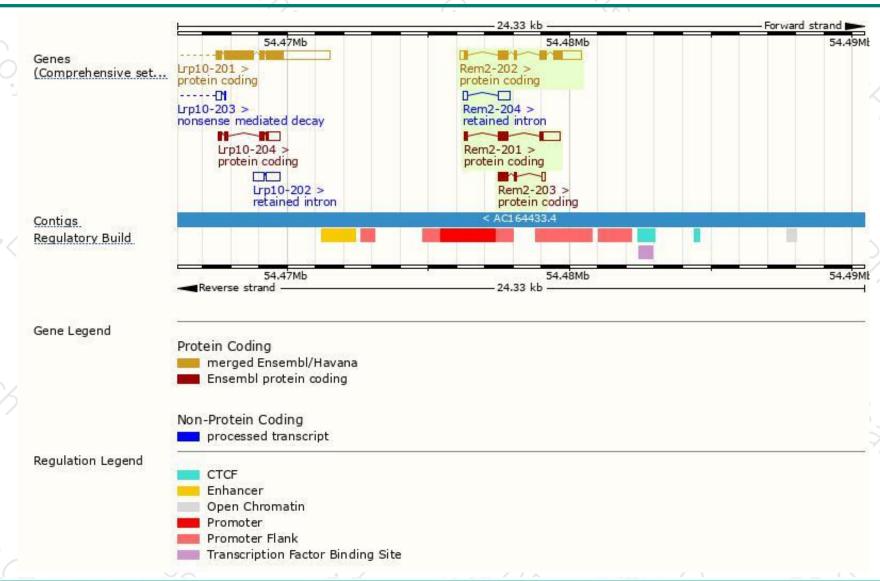
Name 🍦	Transcript ID 👙	bp 👙	Protein 4	Biotype 🍦	CCDS 🍦	UniProt 🌲	Flags
Rem2-202	ENSMUST00000164766.7	1884	<u>341aa</u>	Protein coding	CCDS27090@	E9Q4D5@	TSL:1 GENCODE basic APPRIS P1
Rem2-201	ENSMUST00000164697.7	1194	180aa	Protein coding	5	E9PVZ0₽	TSL:5 GENCODE basic
Rem2-203	ENSMUST00000168930.1	513	140aa	Protein coding	- 5	<u>F6Z0Z5</u> ₽	CDS 5' incomplete TSL:5
Rem2-204	ENSMUST00000170337.1	556	No protein	Retained intron	3	11 - 21	TSL:3

The strategy is based on the design of Rem2-202 transcript, The transcription is shown below



Genomic location distribution





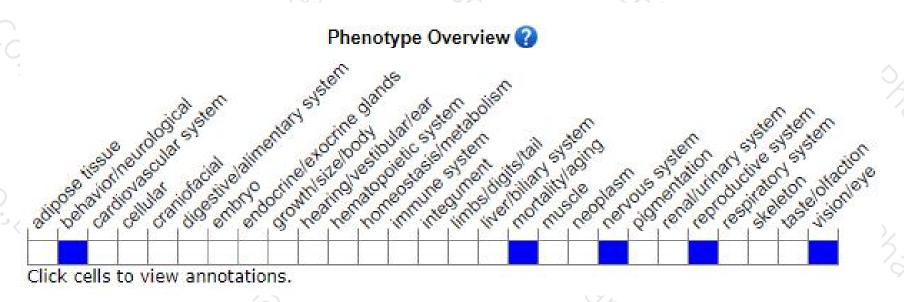
Protein domain





Mouse phenotype description(MGI)





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

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit strain-specific impaired viability and fertility as well as altered intrinsic excitability and spontaneous firing in visual circuits.



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





