Csrnp2 Cas9-KO Strategy

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Project Overview

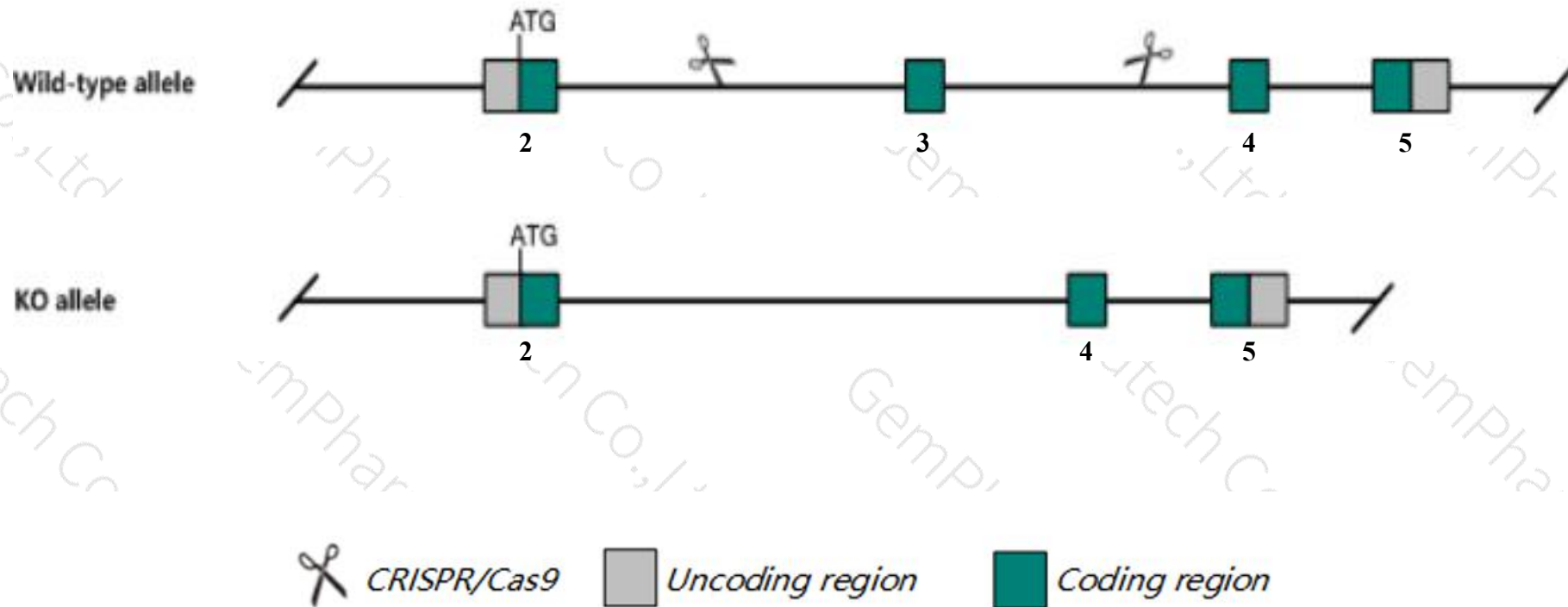|	
Project Name	*Csrnp2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Csrnp2* gene. The schematic diagram is as follows:

Technical routes

➢ The *Csrnp2* gene has 1 transcript. According to the structure of *Csrnp2* gene, exon3 of *Csrnp2-201* (ENSMUST00000061457.6) transcript is recommended as the knockout region.The region contains 260bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Csrnp2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele are viable, fertile and healthy and display normal development, hematopoiesis and T cell function.

➢ The *Csrnp2* gene is located on the Chr15. 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）

Csrnp2 cysteine-serine-rich nuclear protein 2 [Mus musculus (house mouse)]
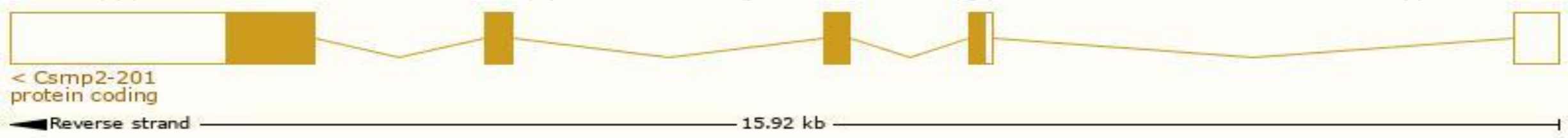
Gene ID: 207785, updated on 13-Mar-2020

▲Summary

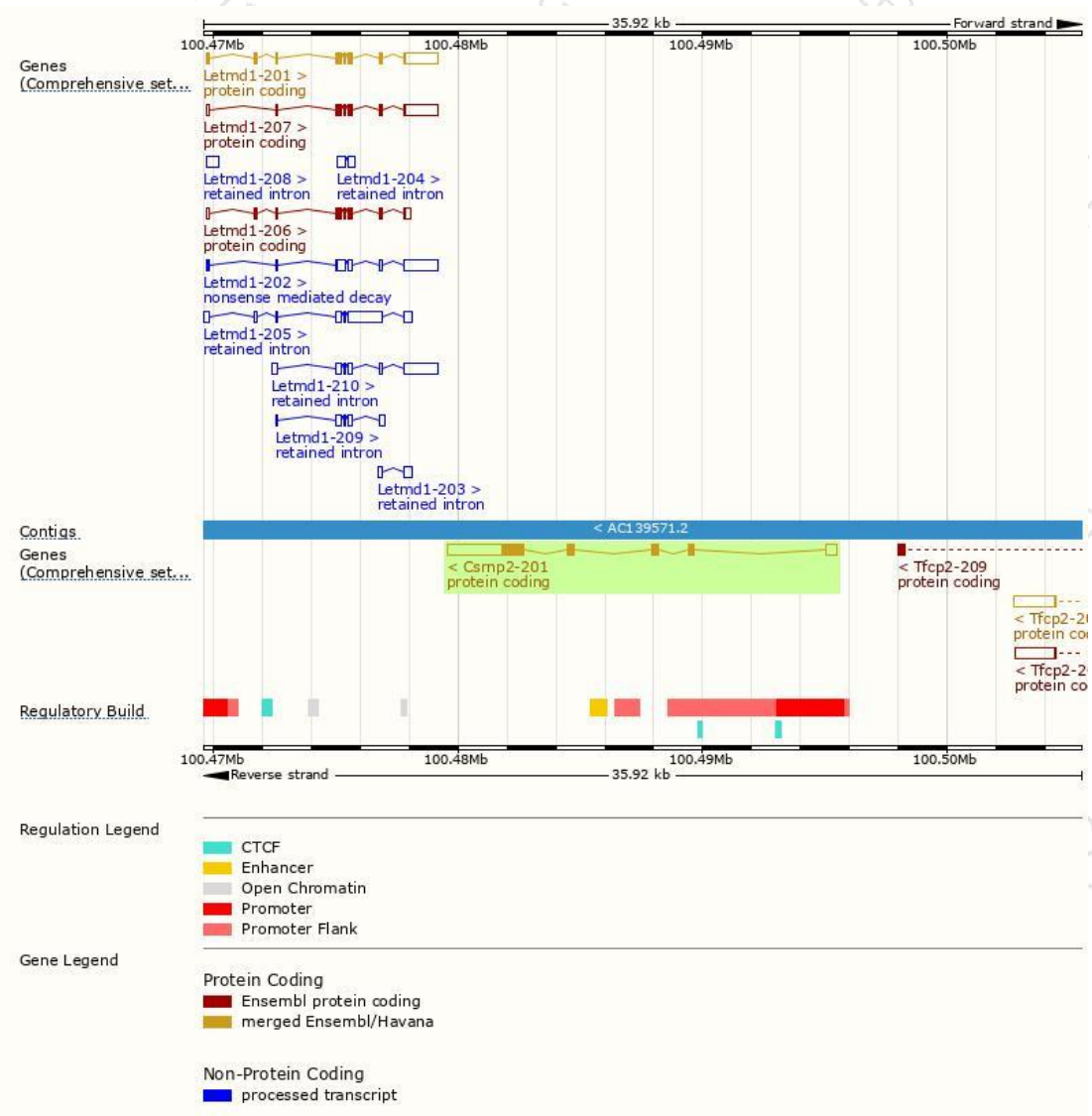|	
Official Symbol	Csrnp2 provided by MGI
Official Full Name	cysteine-serine-rich nuclear protein 2 provided by MGI
Primary source	MGI:MGI:2386852
See related	Ensembl:ENSMUSG00000044636
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CSRNP-2, Csnrp2, taip-12
Expression	Broad expression in whole brain E14.5 (RPKM 9.8), CNS E18 (RPKM 9.3) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 1 transcript,and the transcript is shown below:

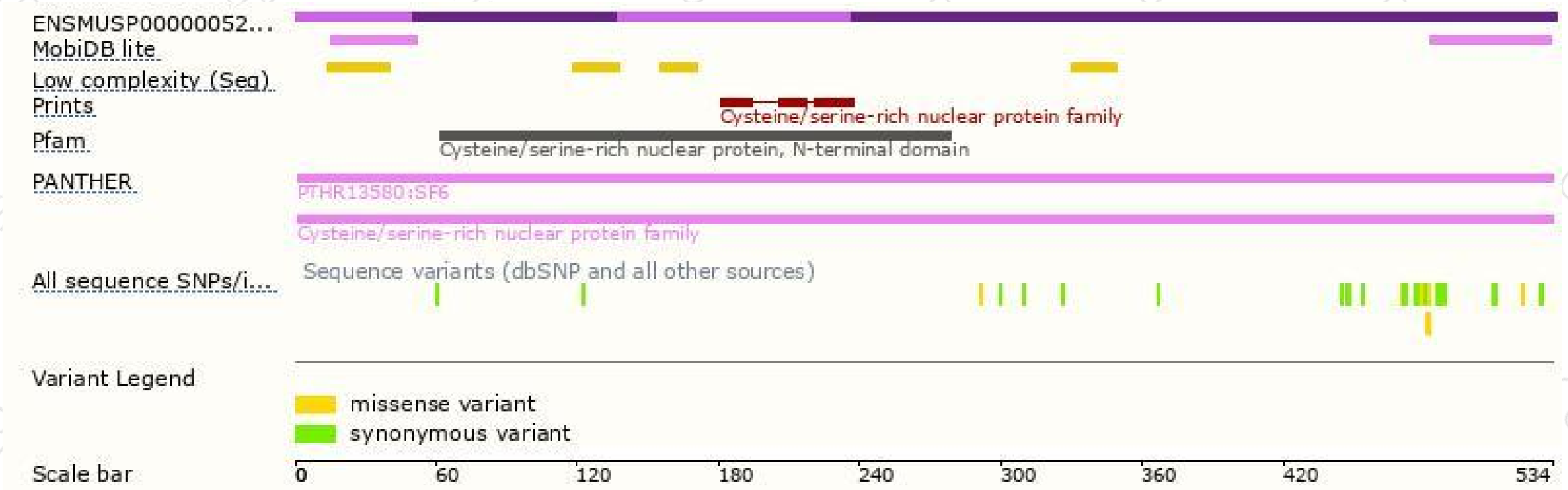| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Csrnp2-201	ENSMUST00000061457.6	4375	534aa	Protein coding	CCDS27839	Q8BGQ2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Csrnp2-201* transcript,the transcription is shown below:

< Csmp2-201
protein coding

◀ Reverse strand ————————————— 15.92 kb —————————————

Genomic location distribution

Protein domain

ENSMUSP00000052...	
MobiDB lite	
Low complexity (Seg)	
Prints	Cysteine/serine-rich nuclear protein family
Pfam	Cysteine/serine-rich nuclear protein, N-terminal domain
PANTHER	PTHR13580:SF6
	Cysteine/serine-rich nuclear protein family
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- 🟨 missense variant
- 🟩 synonymous variant

Scale bar
0   60   120   180   240   300   360   420   534

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 are viable, fertile and healthy and display normal development, hematopoiesis and T cell function.

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