

Cd200r1 Cas9-KO Strategy

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Project Overview

Project Name

Cd200r1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd200r1* gene. The schematic diagram is as follows:



- The *Cd200r1* gene has 3 transcripts. According to the structure of *Cd200r1* gene, exon2-exon6 of *Cd200r1-201* (ENSMUST00000057488.14) transcript is recommended as the knockout region. The region contains 776bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd200r1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a disruption of this gene display abnormal sleep patterns including fragmented vigilance states and diminished duration of wakefulness. Mice homozygous for a different knock-out allele exhibit protection from HSV-1 encephalitis.
- The *Cd200r1* gene is located on the Chr16. 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)

Cd200r1 CD200 receptor 1 [Mus musculus (house mouse)]

Gene ID: 57781, updated on 31-Jan-2019

Summary



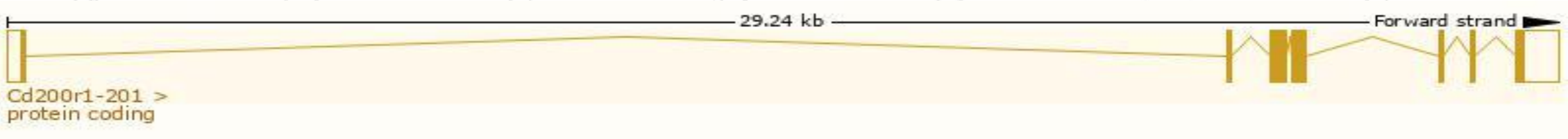
Official Symbol	Cd200r1 provided by MGI
Official Full Name	CD200 receptor 1 provided by MGI
Primary source	MGI:MGI:1889024
See related	Ensembl:ENSMUSG00000022667
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CD200R, Mox2r, OX2R
Expression	Broad expression in liver E18 (RPKM 1.8), liver E14 (RPKM 1.3) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

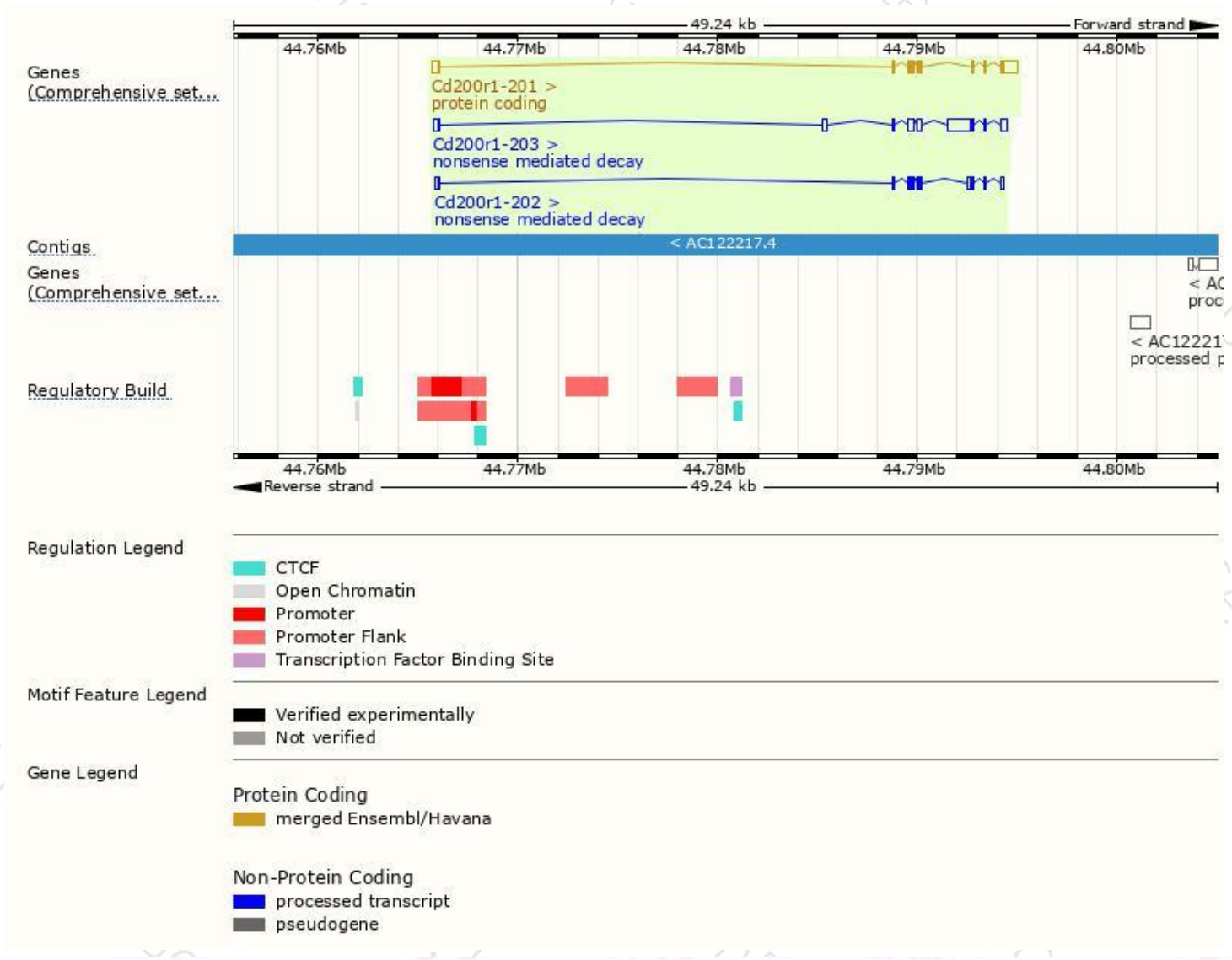
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd200r1-201	ENSMUST00000057488.14	1892	326aa	Protein coding	CCDS28189	Q9ES57	TSL:1 GENCODE basic APPRIS P1
Cd200r1-203	ENSMUST00000231633.1	2768	40aa	Nonsense mediated decay	-	A0A338P6B8	
Cd200r1-202	ENSMUST00000134625.1	1310	245aa	Nonsense mediated decay	-	M0QWY6	TSL:1

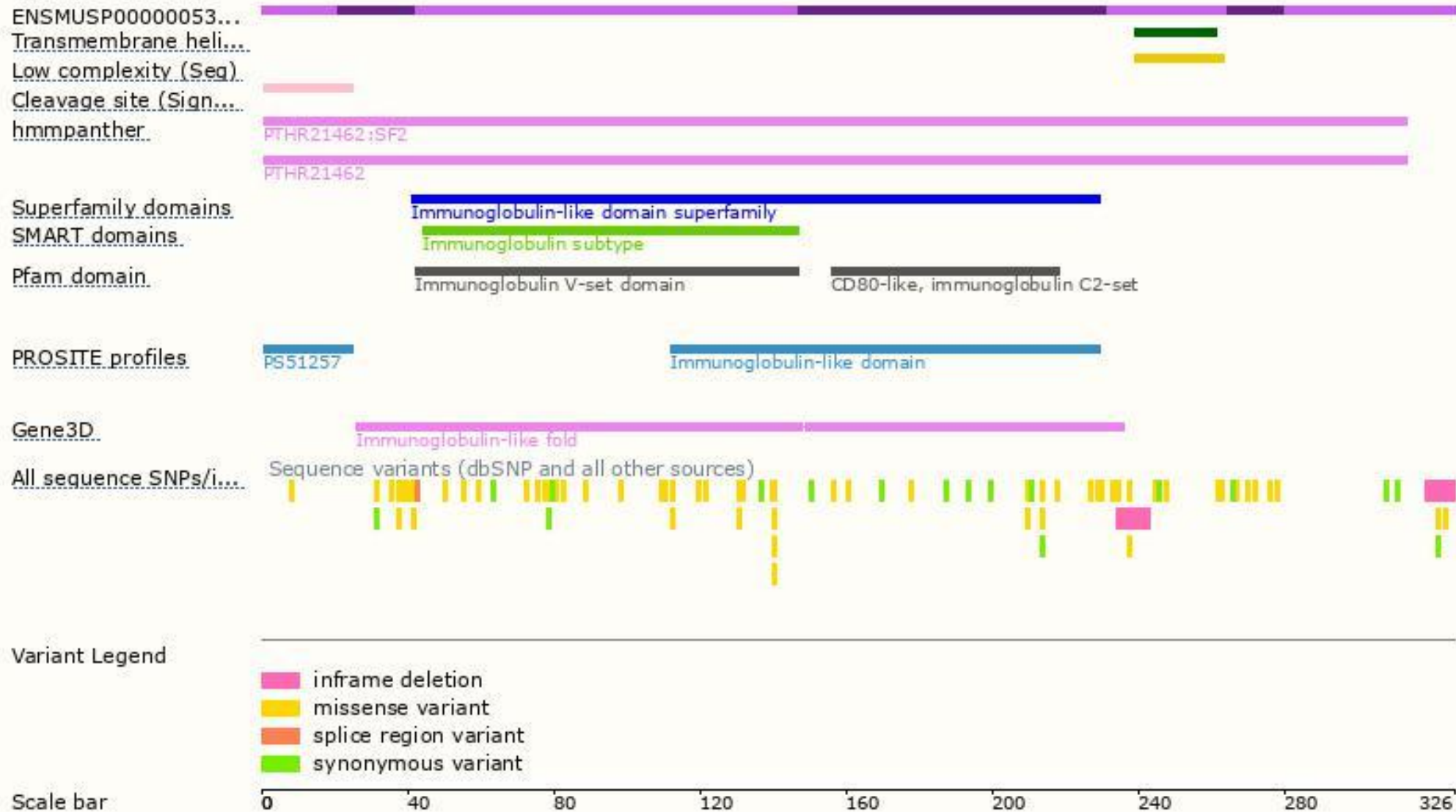
The strategy is based on the design of *Cd200r1-201* transcript,The transcription is shown below



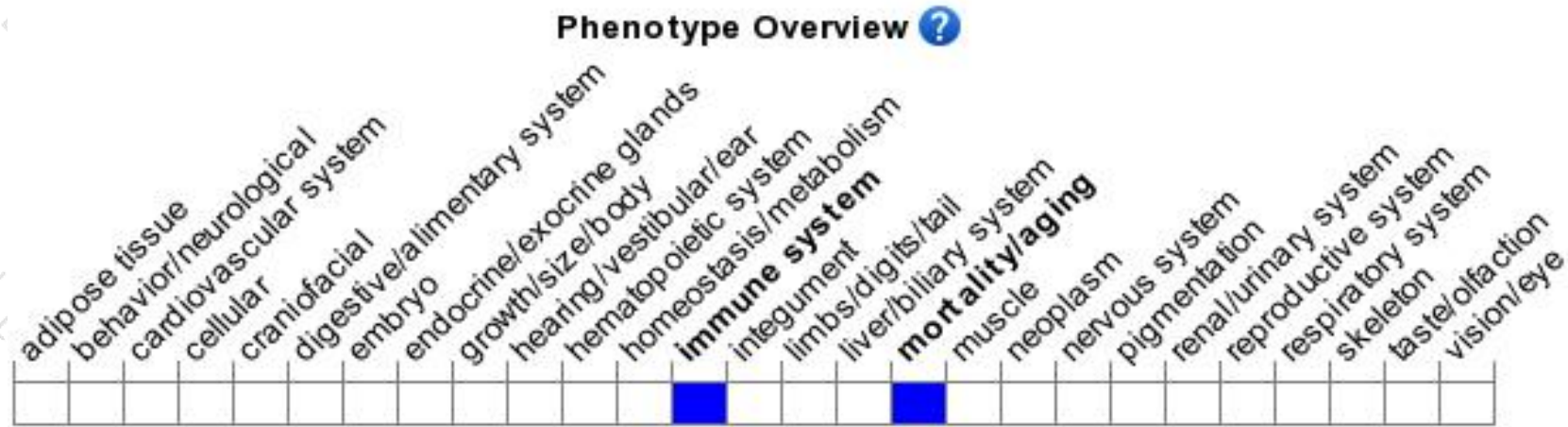
Genomic location distribution



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 a disruption of this gene display abnormal sleep patterns including fragmented vigilance states and diminished duration of wakefulness. Mice homozygous for a different knock-out allele exhibit protection from HSV-1 encephalitis.

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

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