

Cnksr2 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

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Project Overview

Project Name

Cnksr2

Project type

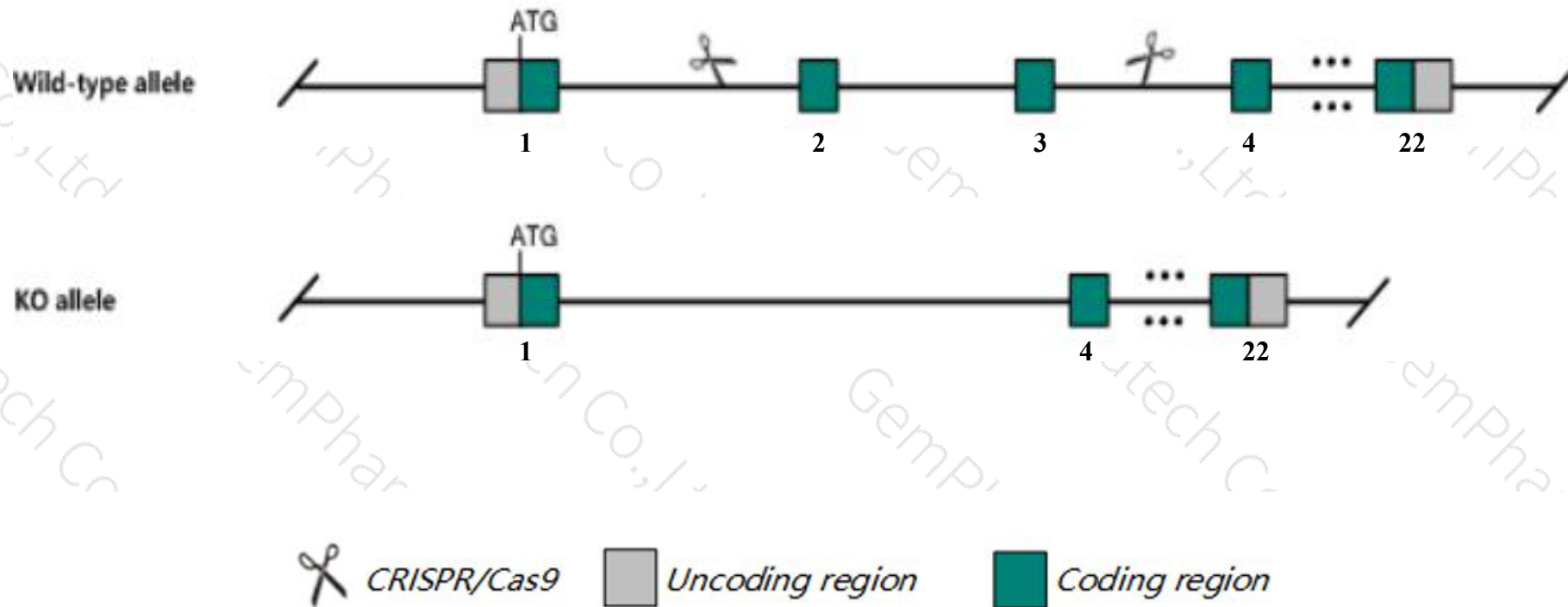
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cnksr2* gene. The schematic diagram is as follows:



- The *Cnksr2* gene has 3 transcripts. According to the structure of *Cnksr2* gene, exon2-exon3 of *Cnksr2-201* (ENSMUST00000026750.14) transcript is recommended as the knockout region. The region contains 367bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cnksr2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Cnksr2*-203 may not be affected.
- The *Cnksr2* 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)

Cnksr2 connector enhancer of kinase suppressor of Ras 2 [Mus musculus (house mouse)]

Gene ID: 245684, updated on 13-Mar-2020

Summary



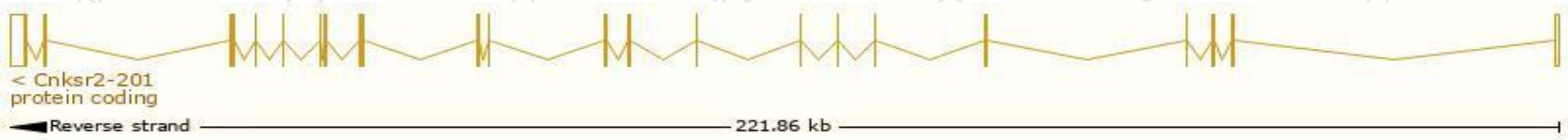
Official Symbol	Cnksr2 provided by MGI
Official Full Name	connector enhancer of kinase suppressor of Ras 2 provided by MGI
Primary source	MGI:MGI:2661175
See related	Ensembl:ENSMUSG000000025658
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cnk2, Ksr2
Expression	Biased expression in cortex adult (RPKM 15.3), frontal lobe adult (RPKM 12.0) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

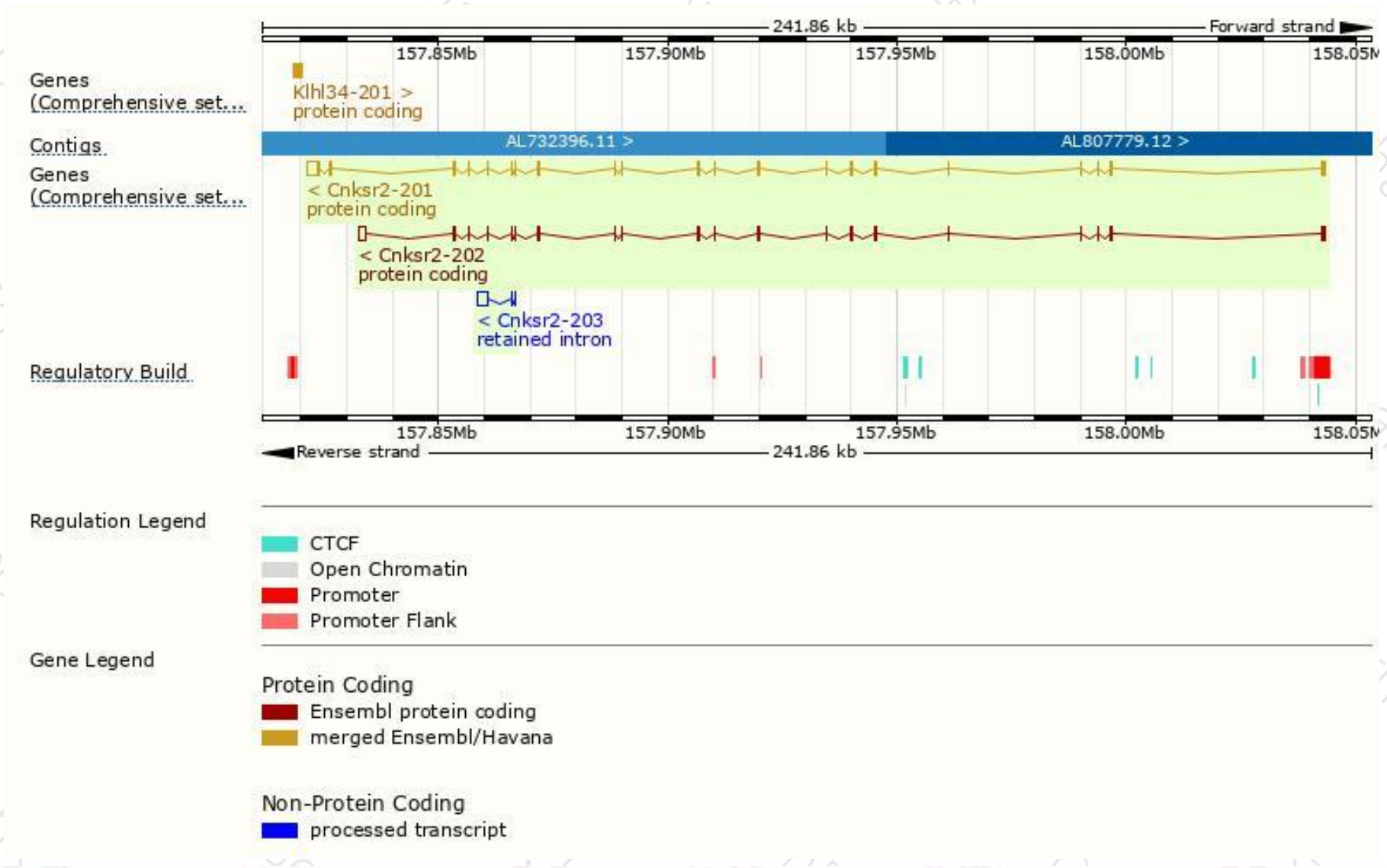
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnksr2-201	ENSMUST00000026750.14	5738	1032aa	Protein coding	CCDS30501	Q80YA9	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
Cnksr2-202	ENSMUST00000112513.1	4471	896aa	Protein coding	-	A2AI78	TSL:5 GENCODE basic
Cnksr2-203	ENSMUST00000139664.1	2412	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Cnksr2-201* transcript,the transcription is shown below:



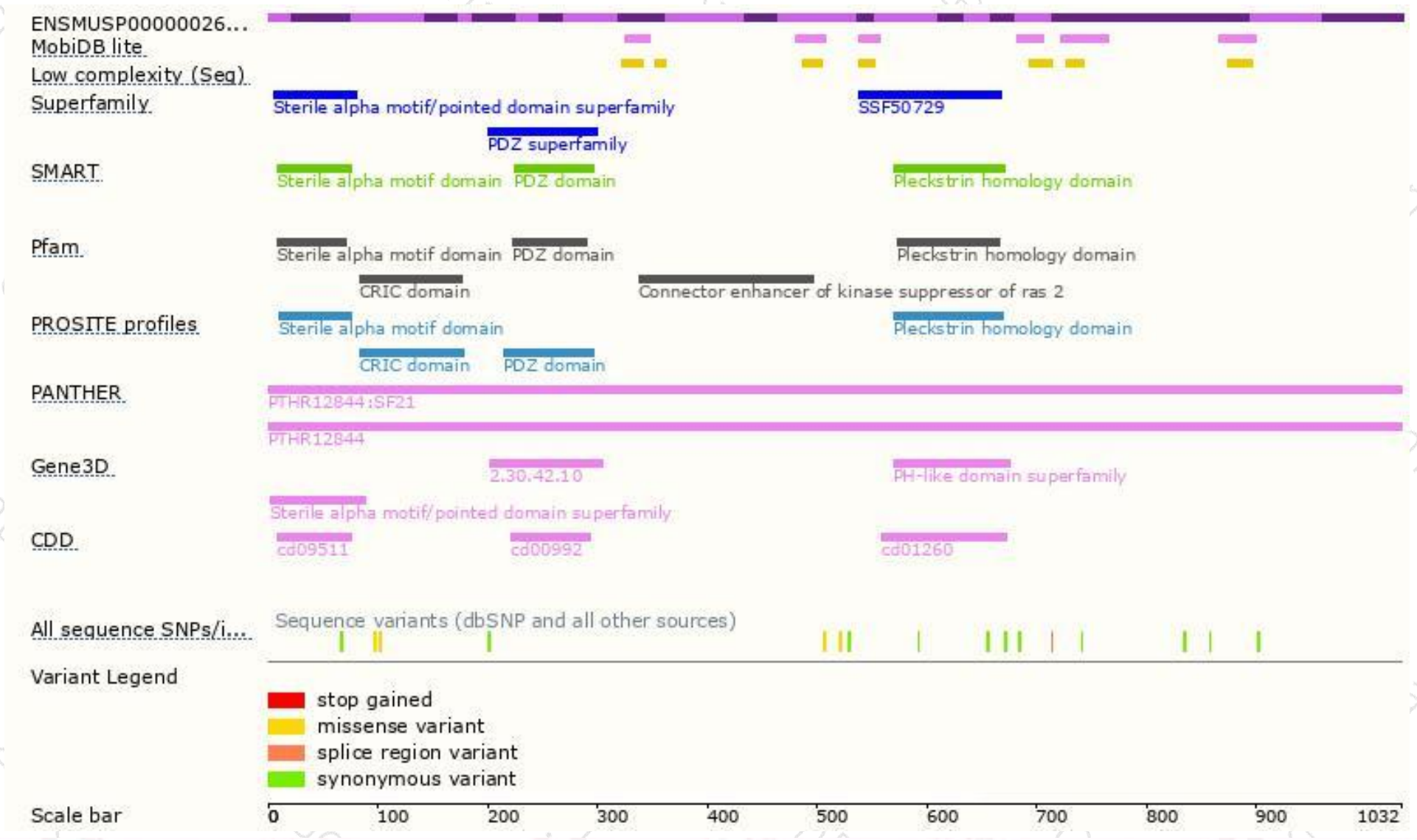
Genomic location distribution



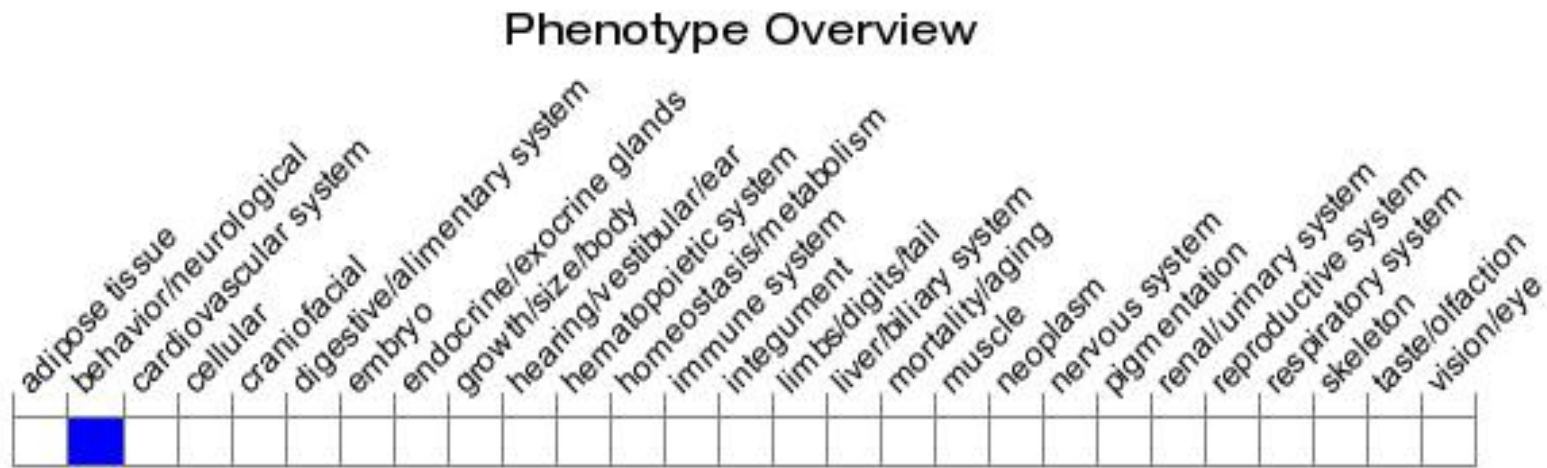
Protein domain



集萃药康
GemPharmatech



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

