

Larp7 Cas9-KO Strategy

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Project Overview

Project Name

Larp7

Project type

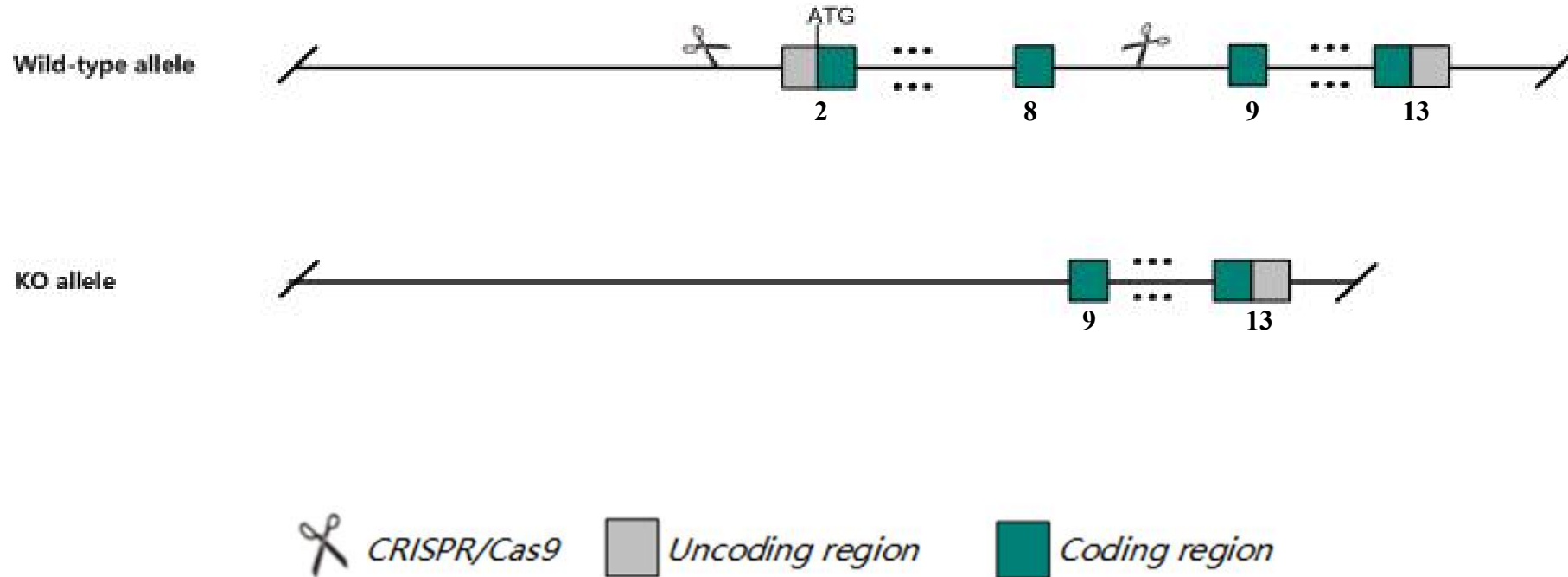
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Larp7* gene. The schematic diagram is as follows:



The *Larp7* gene has 4 transcripts. According to the structure of *Larp7* gene, exon2-exon8 of *Larp7-201* (ENSMUST00000029588.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Larp7* gene. The brief process is as follows: CRISPR/Cas9 system

According to the existing MGI data, Mice homozygous for a null mutation display complete perinatal lethality and a decrease in primordial germ cell number and proliferation.

Mir302a, Mir302b, Mir302c, Mir302d, Mir367 will be deleted.

The *Larp7* gene is located on the Chr3. 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.

Larp7 La ribonucleoprotein domain family, member 7 [Mus musculus (house mouse)]

Gene ID: 28036, updated on 31-Jan-2019

Summary



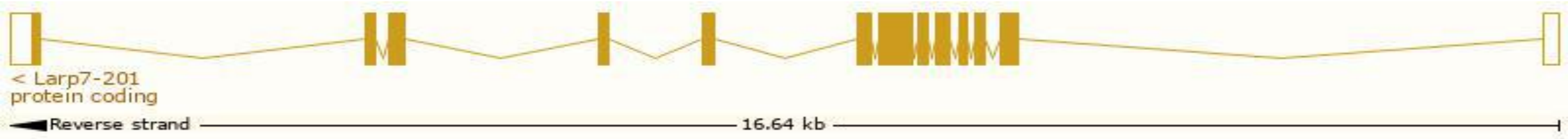
Official Symbol	Larp7 provided by MGI
Official Full Name	La ribonucleoprotein domain family, member 7 provided by MGI
Primary source	MGI:MGI:107634
See related	Ensembl:ENSMUSG000000027968
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C330027G06Rik, D3Wsu161e
Expression	Biased expression in CNS E11.5 (RPKM 27.9), testis adult (RPKM 22.9) and 12 other tissues See more
Orthologs	human all

Transcript information Ensembl

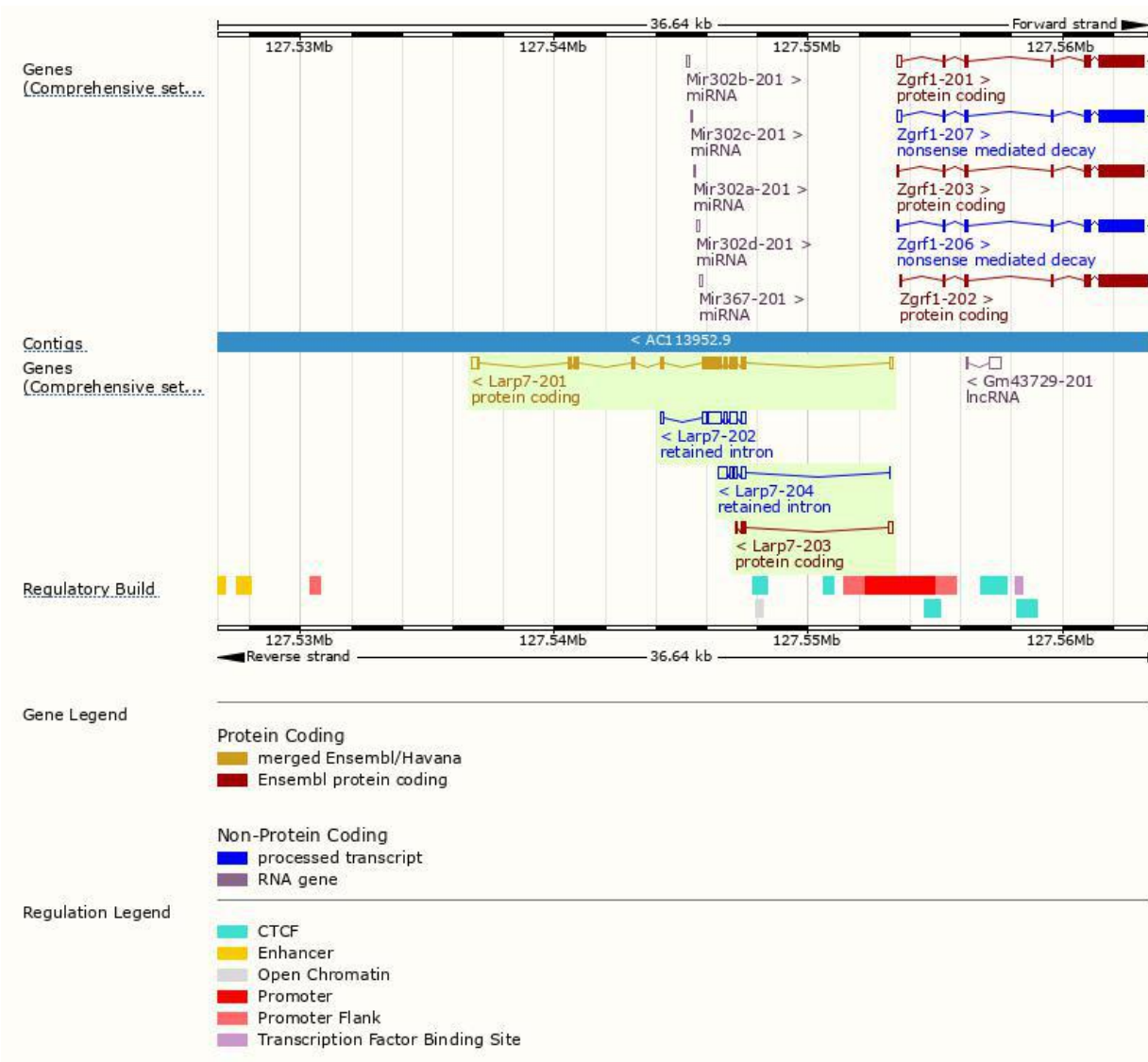
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Larp7-201	ENSMUST00000029588.9	2121	570aa	Protein coding	CCDS38626	Q05CL8	TSL:5 GENCODE basic APPRIS P1
Larp7-203	ENSMUST00000197668.1	411	80aa	Protein coding	-	A0A0G2JFW4	CDS 3' incomplete TSL:3
Larp7-202	ENSMUST00000195976.1	1391	No protein	Retained intron	-	-	TSL:5
Larp7-204	ENSMUST00000197698.1	733	No protein	Retained intron	-	-	TSL:1

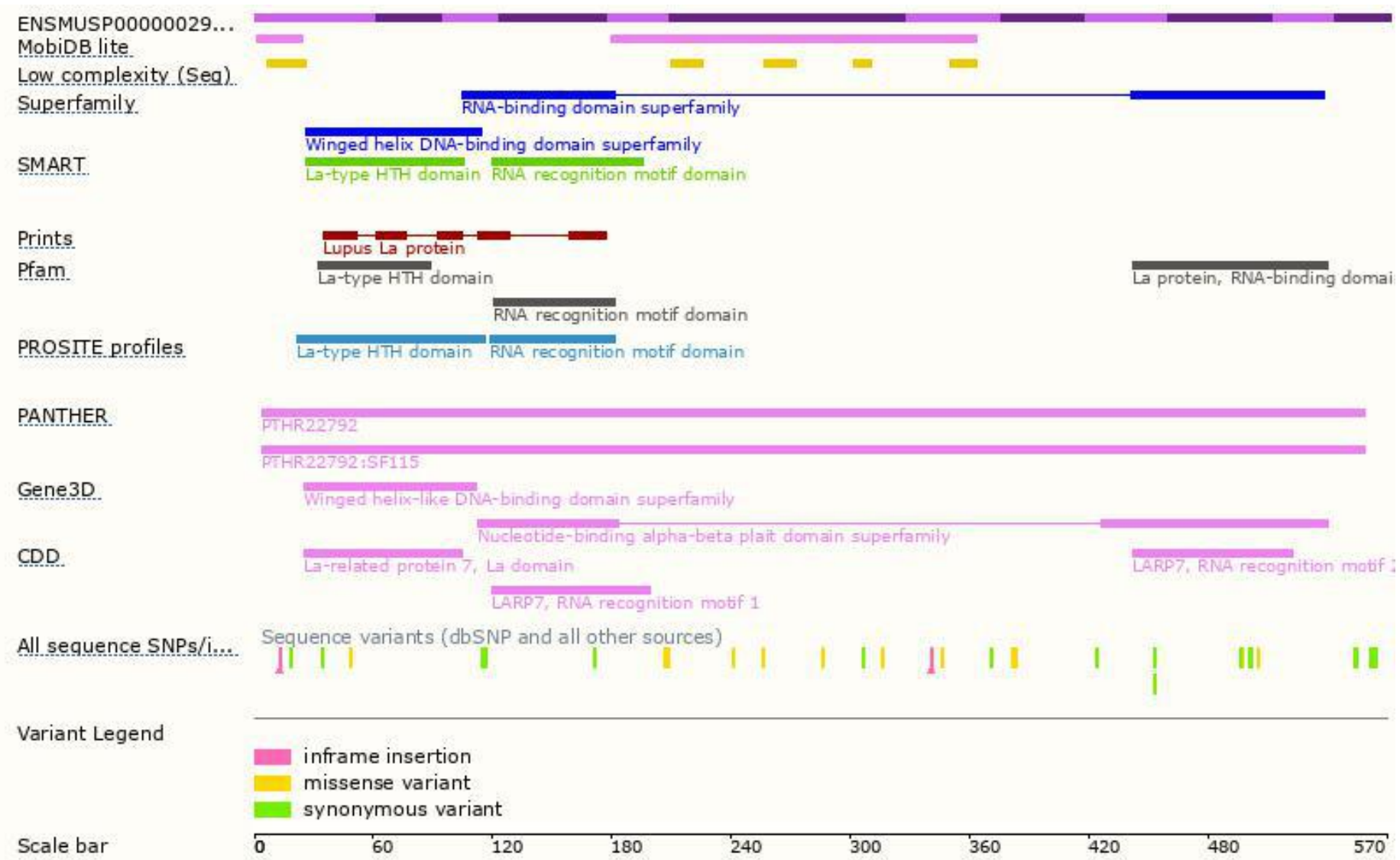
The strategy is based on the design of *Larp7-201* transcript,The transcription is shown below



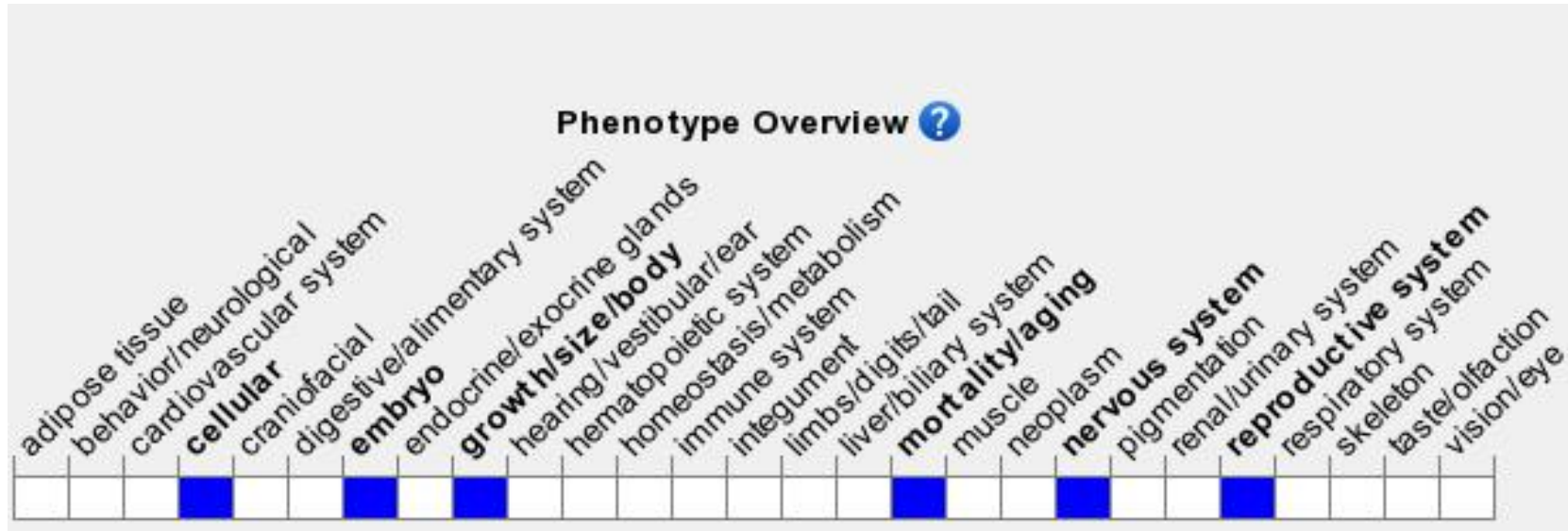
Genomic location distribution



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/>).

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