

Lrrc4c Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Lrrc4c

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrrc4c* gene. The schematic diagram is as follows:



- The *Lrrc4c* gene has 4 transcripts. According to the structure of *Lrrc4c* gene, exon7 of *Lrrc4c-202* (ENSMUST00000135431.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrrc4c* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice exhibited an increased mean serum IL-6 response to LPS challenge when compared with controls. No other notable phenotype was detected in a high-throughput screen.
- The *Lrrc4c* gene is located on the Chr2. 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)

Lrrc4c leucine rich repeat containing 4C [Mus musculus (house mouse)]

Gene ID: 241568, updated on 31-Jan-2019

Summary



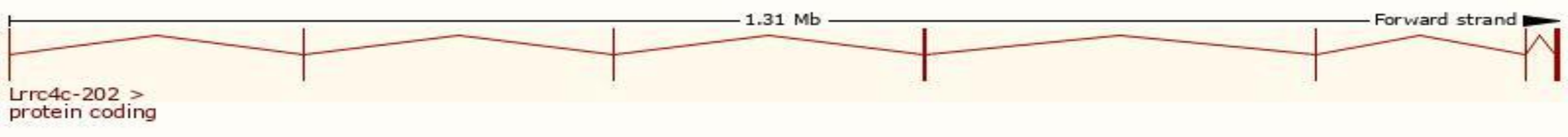
Official Symbol	Lrrc4c provided by MGI
Official Full Name	leucine rich repeat containing 4C provided by MGI
Primary source	MGI:MGI:2442636
See related	Ensembl:ENSMUSG00000050587
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6430556C10Rik, NGL-1
Expression	Biased expression in cortex adult (RPKM 4.7), frontal lobe adult (RPKM 3.8) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

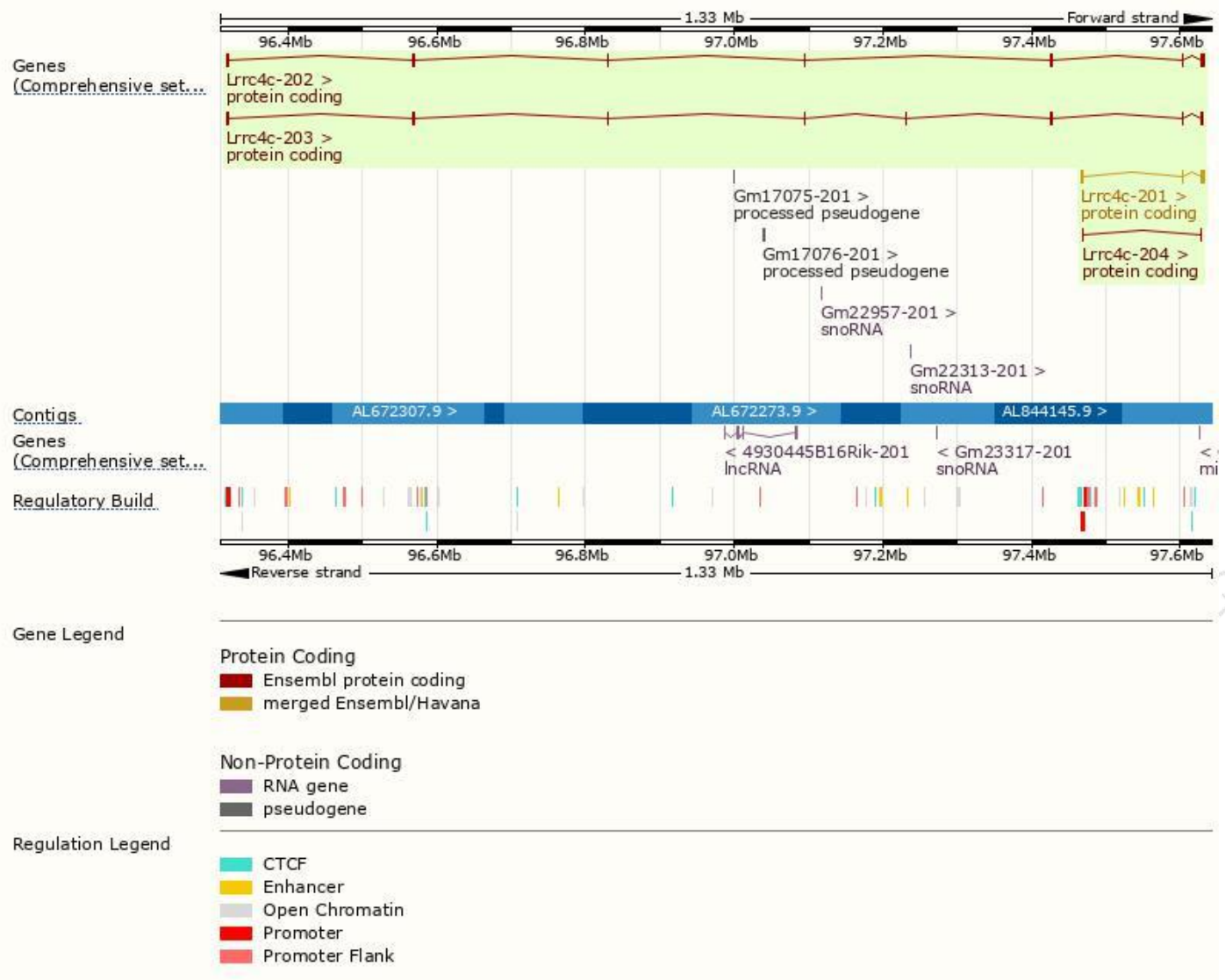
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrrc4c-202	ENSMUST00000135431.7	3646	640aa	Protein coding	CCDS16460	Q8C031	TSL:1 GENCODE basic APPRIS P1
Lrrc4c-201	ENSMUST00000059049.7	3492	640aa	Protein coding	CCDS16460	Q8C031	TSL:1 GENCODE basic APPRIS P1
Lrrc4c-203	ENSMUST00000162807.8	3132	640aa	Protein coding	CCDS16460	Q8C031	TSL:1 GENCODE basic APPRIS P1
Lrrc4c-204	ENSMUST00000170144.1	407	11aa	Protein coding	-	E9QA73	CDS 3' incomplete TSL:3

The strategy is based on the design of *Lrrc4c-202* transcript,The transcription is shown below



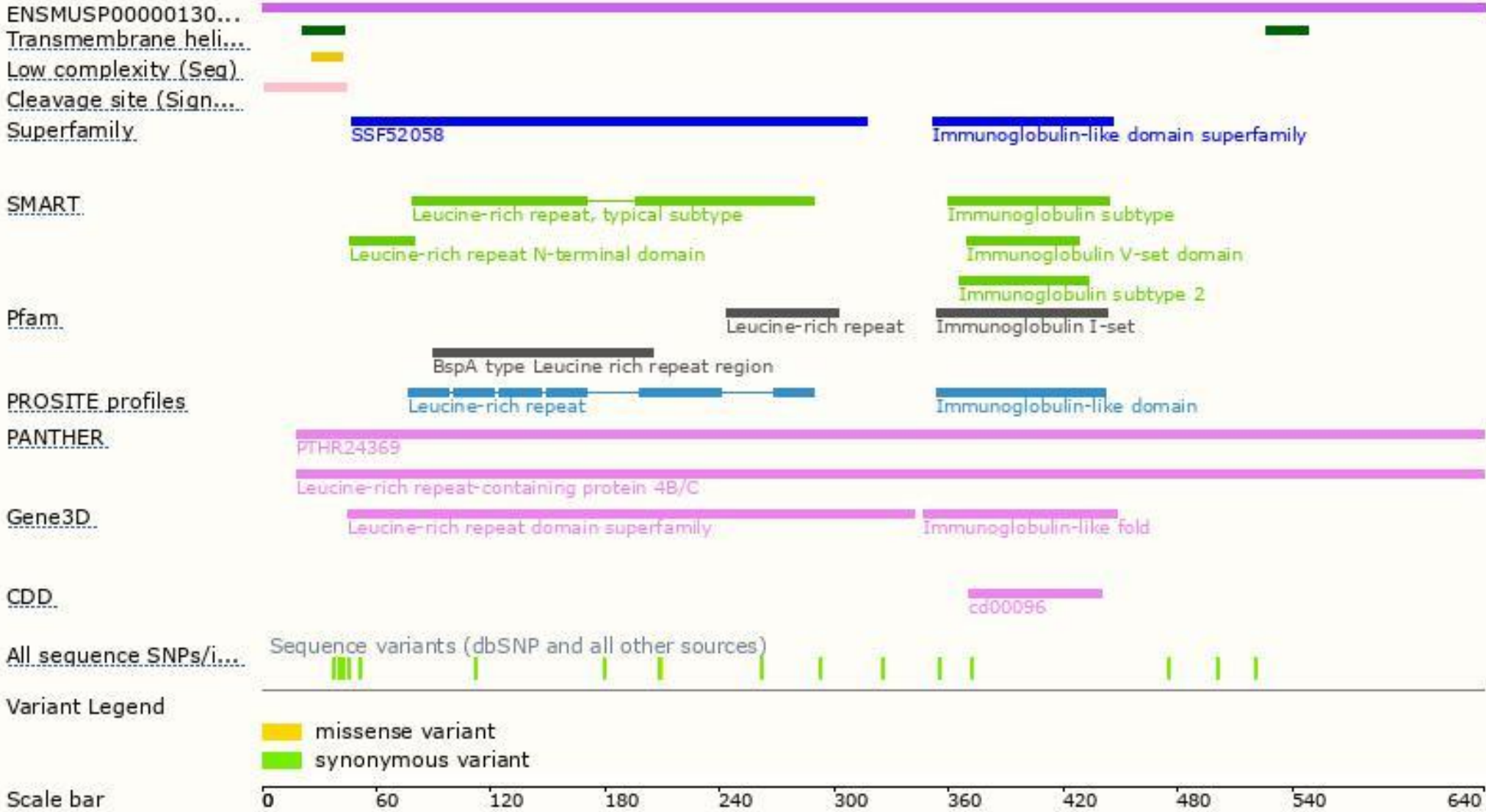
Genomic location distribution



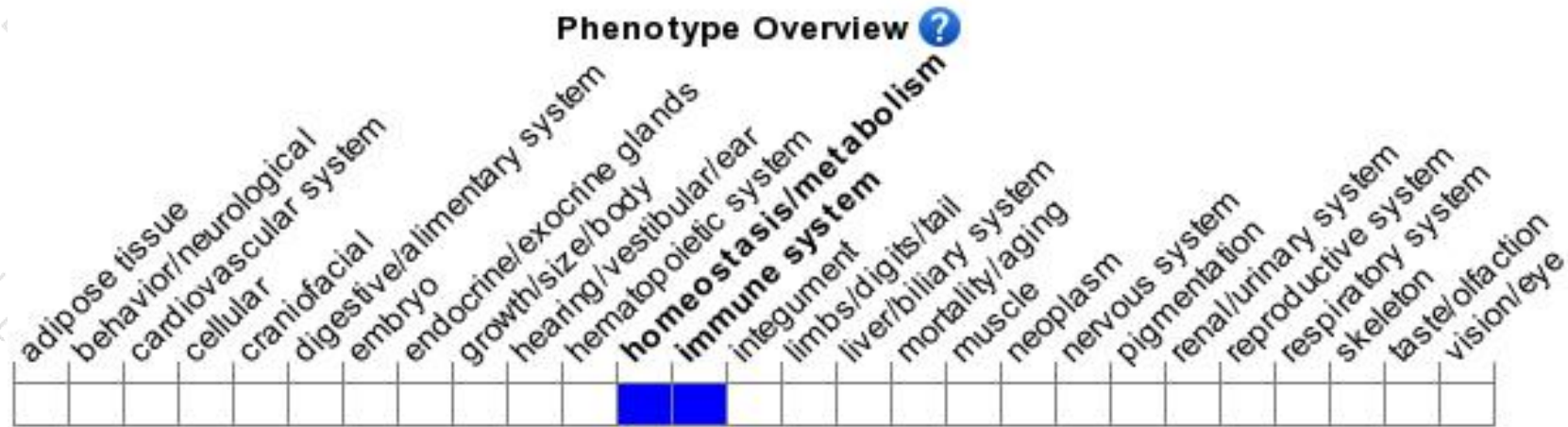
Protein domain



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/>).

According to the existing MGI data, Homozygous mutant mice exhibited an increased mean serum IL-6 response to LPS challenge when compared with controls. No other notable phenotype was detected in a high-throughput screen.

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

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