

# ***Lrrc8a* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Lrrc8a***

**Project type**

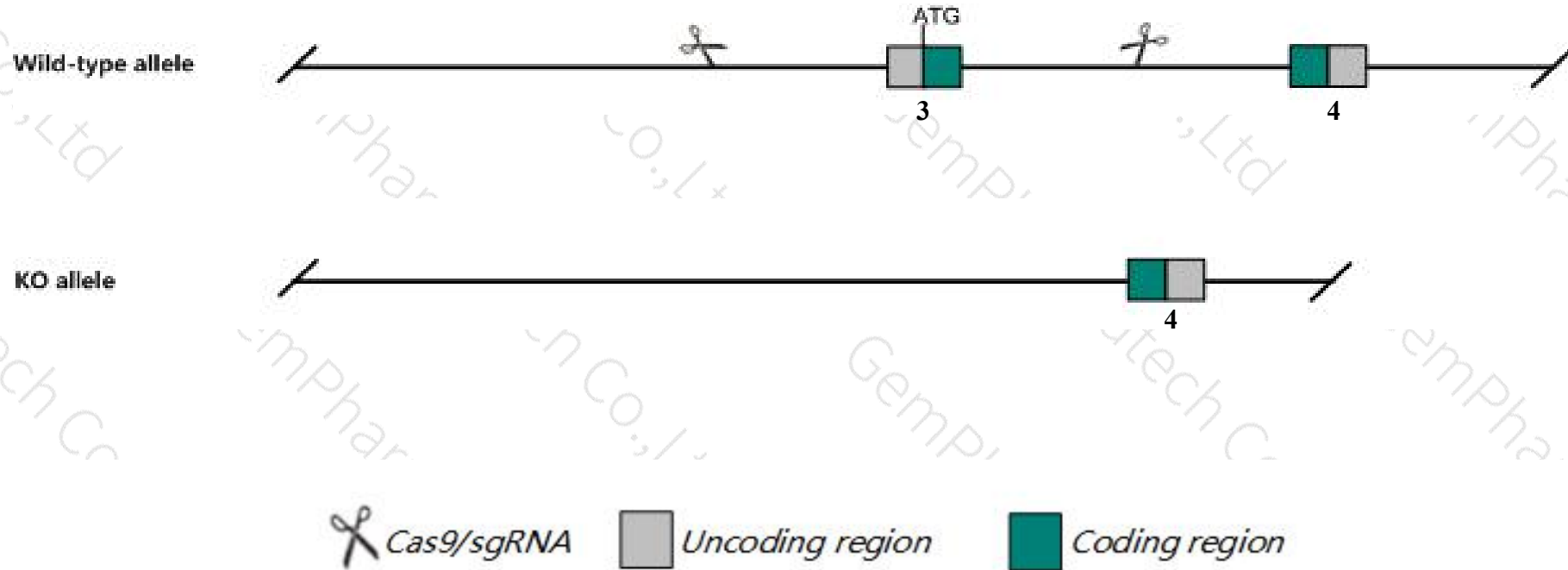
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrrc8a* gene. The schematic diagram is as follows:



# Technical routes

- The *Lrrc8a* gene has 2 transcripts. According to the structure of *Lrrc8a* gene, exon3 of *Lrrc8a-201* (ENSMUST00000095078.2) 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 *Lrrc8a* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

- According to the existing MGI data, Homozygous for a knock-out allele exhibit prenatal lethality and premature death, growth retardation, sterility, multiple tissue abnormalities, a severe block in early thymic development, and impaired peripheral T cell function. B cell development is modestly impaired but B cell function is normal.
- The *Lrrc8a* 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)

## Lrrc8a leucine rich repeat containing 8A [Mus musculus (house mouse)]

Gene ID: 241296, updated on 17-Feb-2019

### Summary



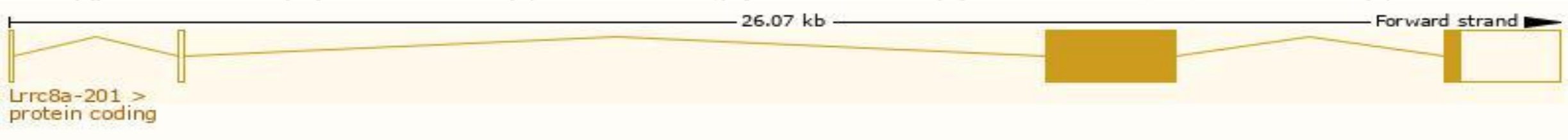
<b>Official Symbol</b>	Lrrc8a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	leucine rich repeat containing 8A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2652847</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000007476</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Lrrc8, ebo, mKIAA1437
<b>Expression</b>	Ubiquitous expression in lung adult (RPKM 34.6), ovary adult (RPKM 30.0) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

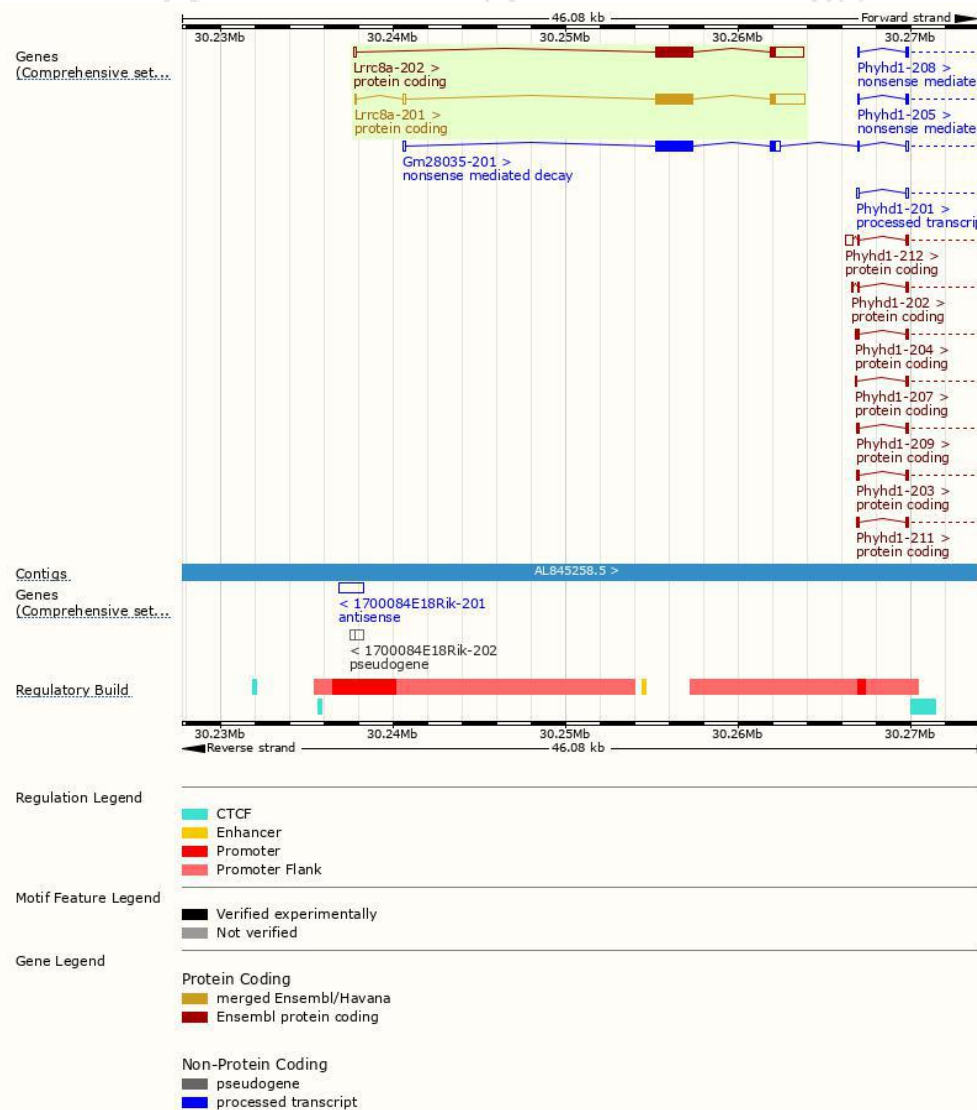
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrrc8a-201	<a href="#">ENSMUST00000095078.2</a>	4301	<a href="#">810aa</a>	Protein coding	<a href="#">CCDS15875</a>	<a href="#">Q80WG5</a>	TSL:5 GENCODE basic APPRIS P1
Lrrc8a-202	<a href="#">ENSMUST00000113654.7</a>	4194	<a href="#">810aa</a>	Protein coding	<a href="#">CCDS15875</a>	<a href="#">Q80WG5</a>	TSL:5 GENCODE basic APPRIS P1

The strategy is based on the design of *Lrrc8a-201* transcript,The transcription is shown below

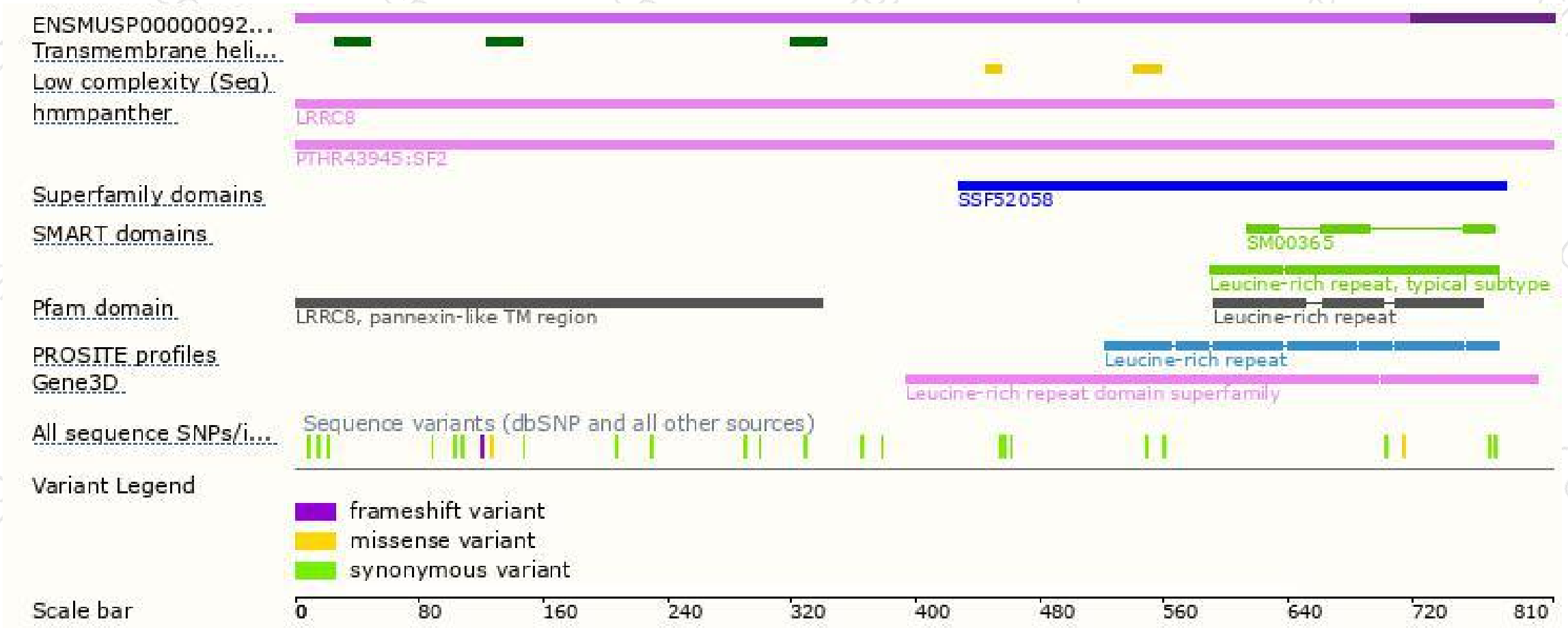


# Genomic location distribution

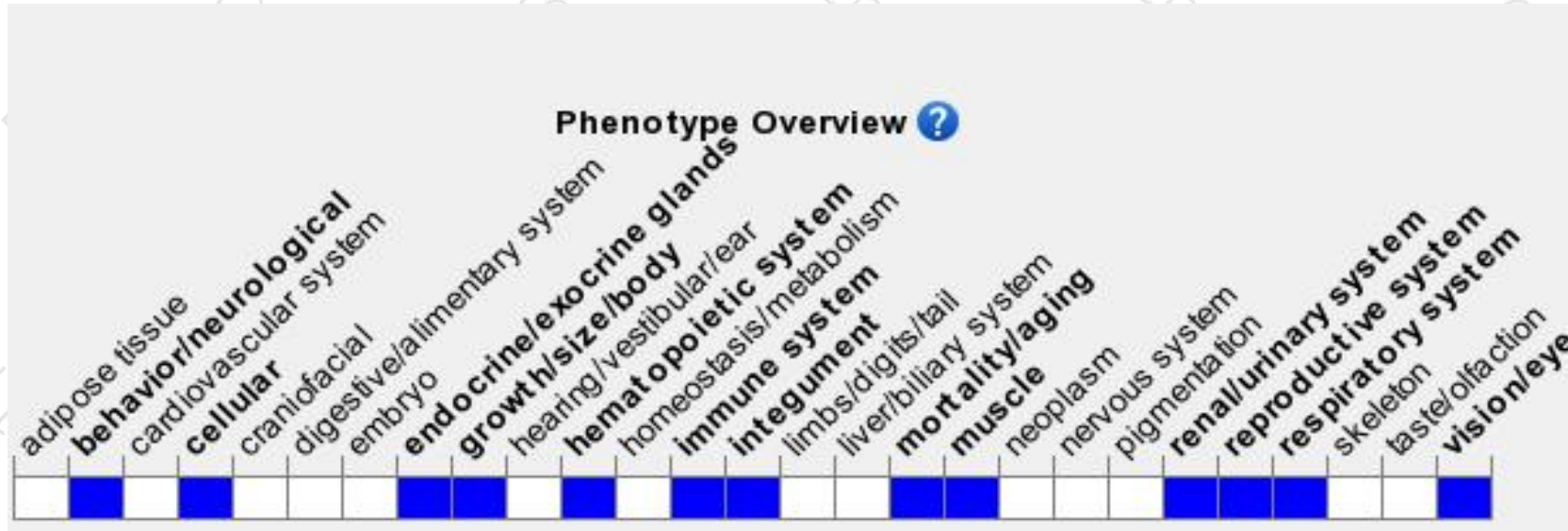




# Protein domain



# 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, Homozygous for a knock-out allele exhibit prenatal lethality and premature death, growth retardation, sterility, multiple tissue abnormalities, a severe block in early thymic development, and impaired peripheral T cell function. B cell development is modestly impaired but B cell function is normal.

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

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