

Lyar Cas9-KO Strategy

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Project Overview

Project Name

Lyar

Project type

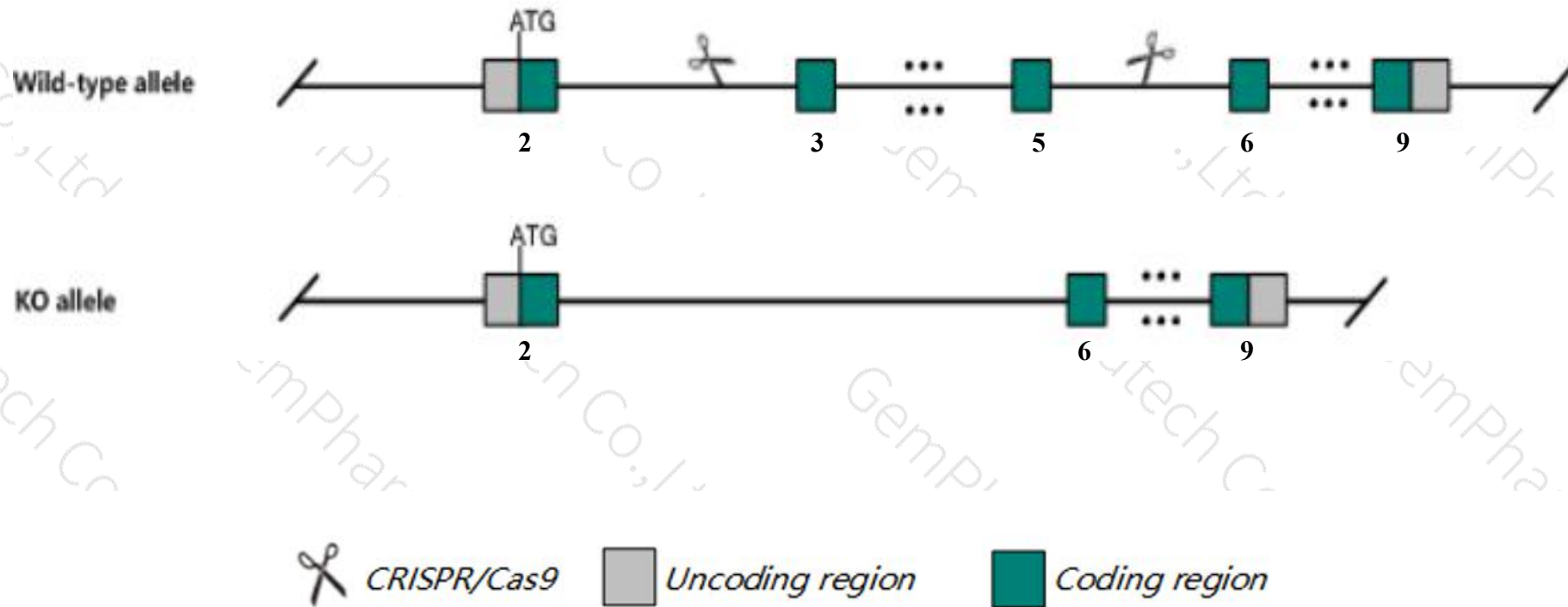
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Lyar* gene has 11 transcripts. According to the structure of *Lyar* gene, exon3-exon5 of *Lyar*-201(ENSMUST00000087514.8) transcript is recommended as the knockout region. The region contains 307bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lyar* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit reduced proliferation of mouse embryonic fibroblasts and results in female prenatal lethality when present with a Trp53 null allele.
- The *Lyar* gene is located on the Chr5. 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)

Lyar Ly1 antibody reactive clone [Mus musculus (house mouse)]

Gene ID: 17089, updated on 13-Mar-2020

Summary



Official Symbol	Lyar provided by MGI
Official Full Name	Ly1 antibody reactive clone provided by MGI
Primary source	MGI:MGI:107470
See related	Ensembl:ENSMUSG00000067367
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	MLZ-264
Expression	Biased expression in testis adult (RPKM 89.4), liver E14 (RPKM 24.9) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

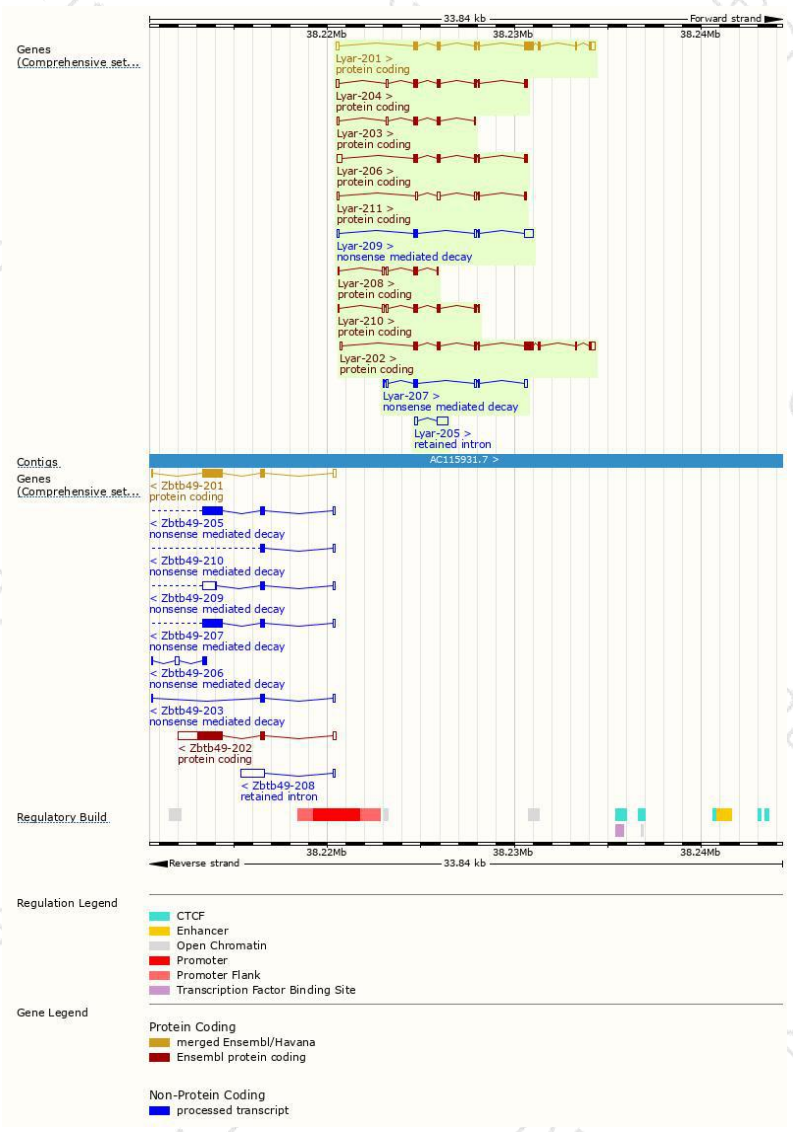
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lyar-201	ENSMUST00000087514.8	1563	388aa	Protein coding	CCDS19253	Q08288	TSL:1 GENCODE basic APPRIS P1
Lyar-202	ENSMUST00000114106.7	1504	388aa	Protein coding	CCDS19253	Q08288	TSL:5 GENCODE basic APPRIS P1
Lyar-206	ENSMUST00000132190.7	885	191aa	Protein coding	-	D3Z345	CDS 3' incomplete TSL:1
Lyar-204	ENSMUST00000130721.7	873	190aa	Protein coding	-	D3Z7N3	CDS 3' incomplete TSL:5
Lyar-210	ENSMUST00000155300.7	744	131aa	Protein coding	-	D3Z5X8	CDS 3' incomplete TSL:5
Lyar-203	ENSMUST00000123207.7	557	99aa	Protein coding	-	D3YU83	CDS 3' incomplete TSL:3
Lyar-211	ENSMUST00000202506.1	554	45aa	Protein coding	-	A0A0J9YVD4	CDS 3' incomplete TSL:3
Lyar-208	ENSMUST00000152066.7	504	49aa	Protein coding	-	D3Z009	CDS 3' incomplete TSL:3
Lyar-209	ENSMUST00000154975.7	898	40aa	Nonsense mediated decay	-	D6RDT2	TSL:2
Lyar-207	ENSMUST00000146401.1	674	40aa	Nonsense mediated decay	-	D6RDT2	TSL:2
Lyar-205	ENSMUST00000131492.1	722	No protein	Retained intron	-	-	TSL:2

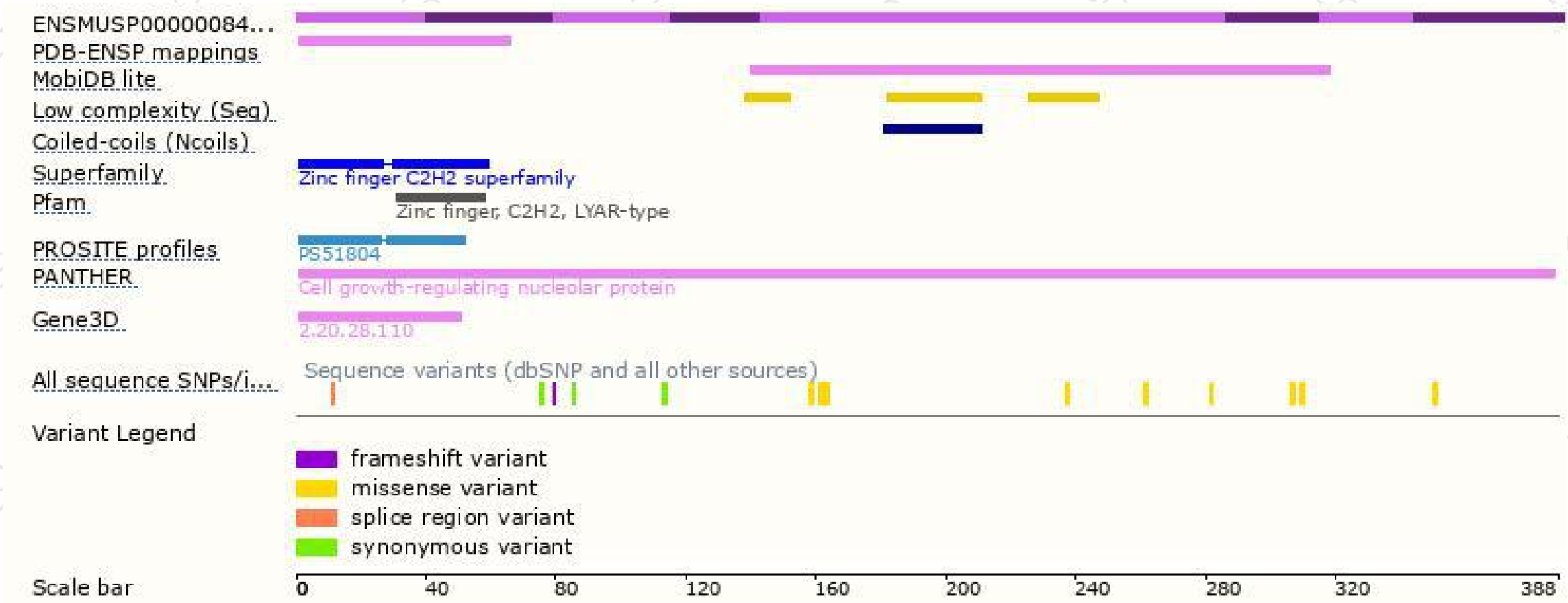
The strategy is based on the design of *Lyar-201* transcript,the transcription is shown below:



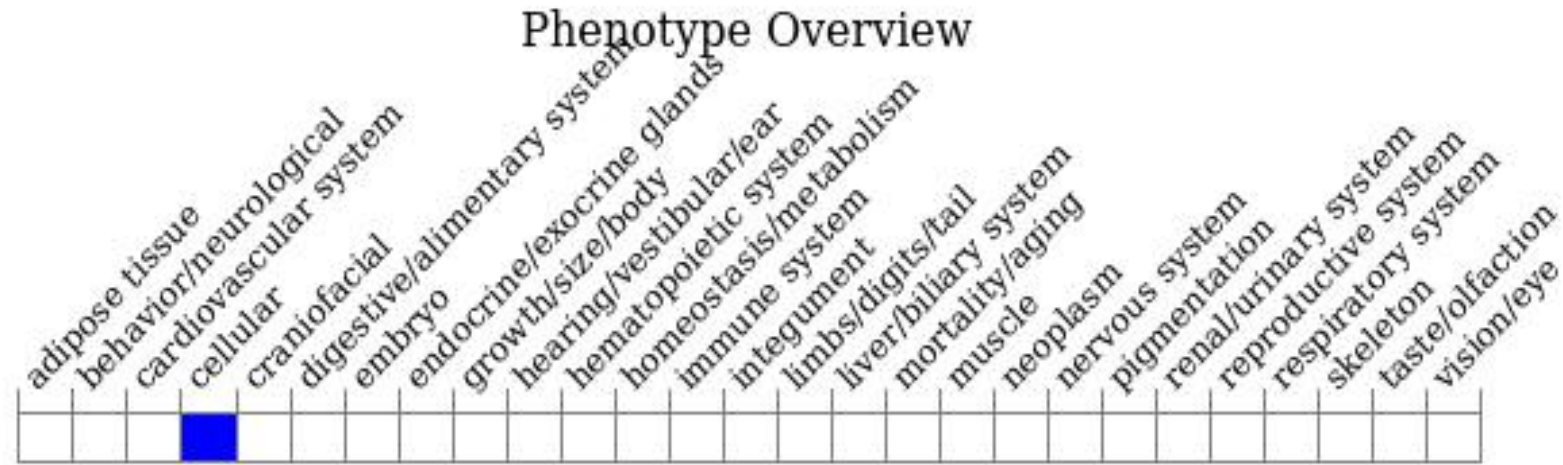
Genomic location distribution



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 knock-out allele exhibit reduced proliferation of mouse embryonic fibroblasts and results in female prenatal lethality when present with a Trp53 null allele.

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

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