GemPharmatech™

Rpl31 Cas9-KO Strategy

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Overview

Target Gene Name

- Rpl31

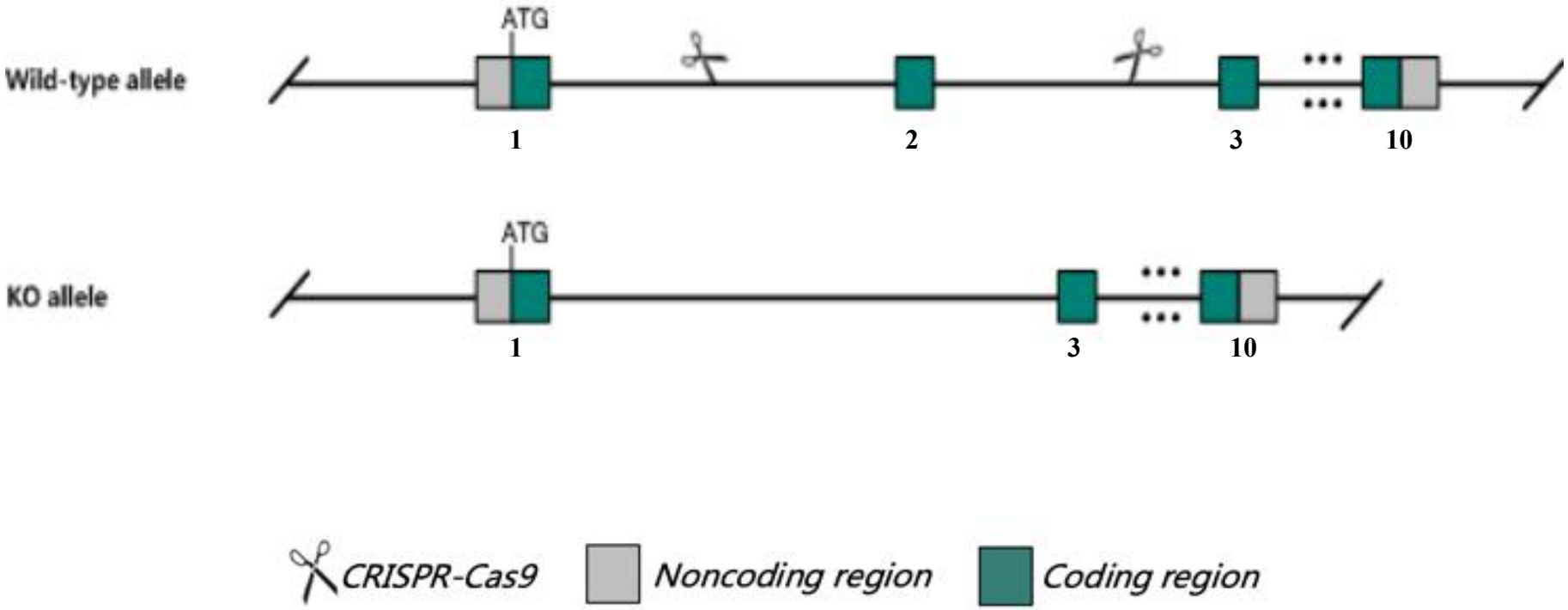
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Rpl3l* gene has 3 transcripts. According to the structure of *Rpl3l* gene, exon2 of *Rpl3l*-202 (ENSMUST00000170239.9) transcript is recommended as the knockout region. The region contains 193bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rpl3l* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Rpl3l ribosomal protein L3-like [Mus musculus (house mouse)]

Gene ID: 66211, updated on 30-May-2023

Summary

Official Symbol	Rpl3l provided by MGI
Official Full Name	ribosomal protein L3-like provided byMGI
Primary source	MGI:MGI:1913461
See related	Ensembl:ENSMUSG00000002500
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	1110057H16Rik
Summary	Predicted to enable RNA binding activity. Predicted to be a structural constituent of ribosome. Predicted to be involved in ribosomal large subunit assembly. Predicted to be part of cytosolic large ribosomal subunit. Human ortholog(s) of this gene implicated in dilated cardiomyopathy. Orthologous to human RPL3L (ribosomal protein L3 like). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in heart adult (RPKM 33.5), mammary gland adult (RPKM 7.6) and 1 other tissueSee more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

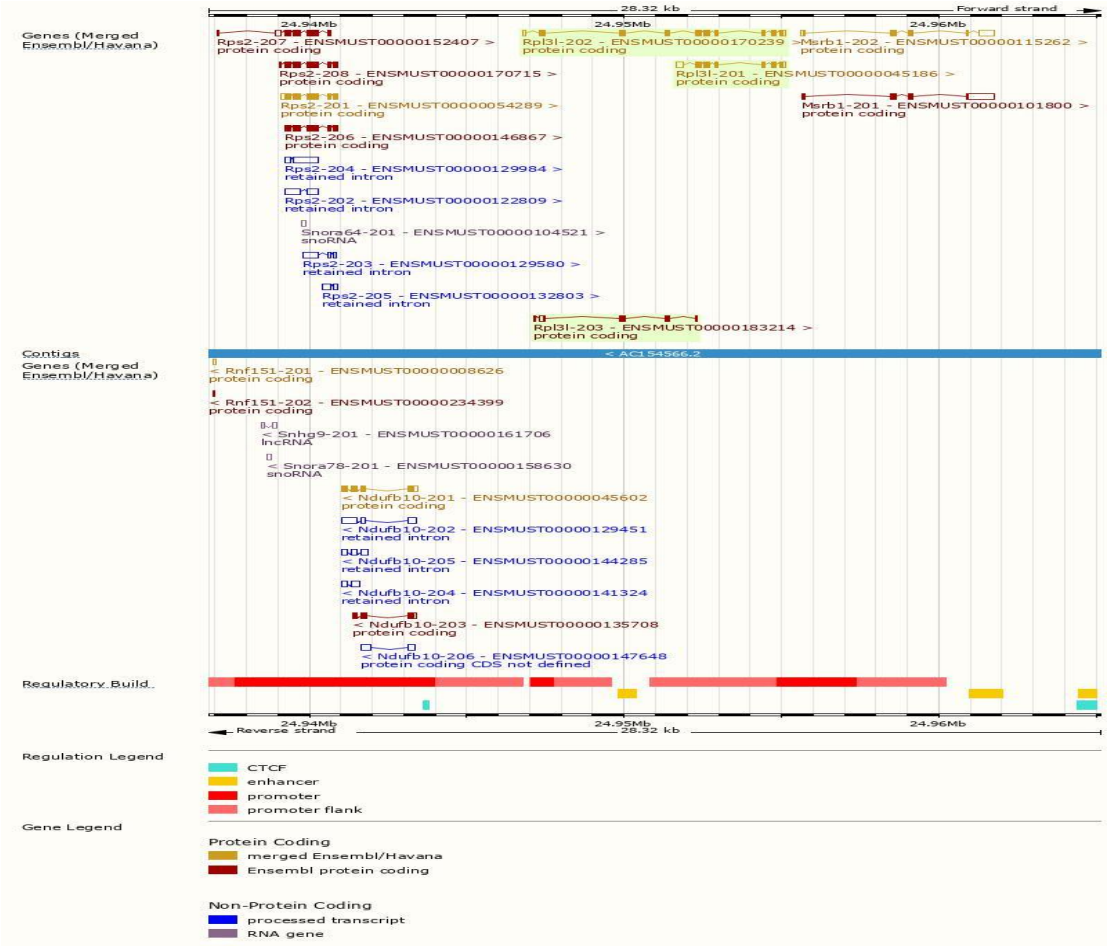
Show/hide columns (1 hidden) Filter

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000170239.9	Rpl3l-202	1375	407aa	Protein coding	CCDS50019	E9PWZ3	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000045186.11	Rpl3l-201	1033	240aa	Protein coding	CCDS37494	Q9CQ09	GENCODE basic TSL:1
ENSMUST00000183214.2	Rpl3l-203	599	133aa	Protein coding		S4R242	TSL:3 CDS 3' incomplete

The strategy is based on the design of *Rpl3l*-202 transcript, the transcription is shown below:

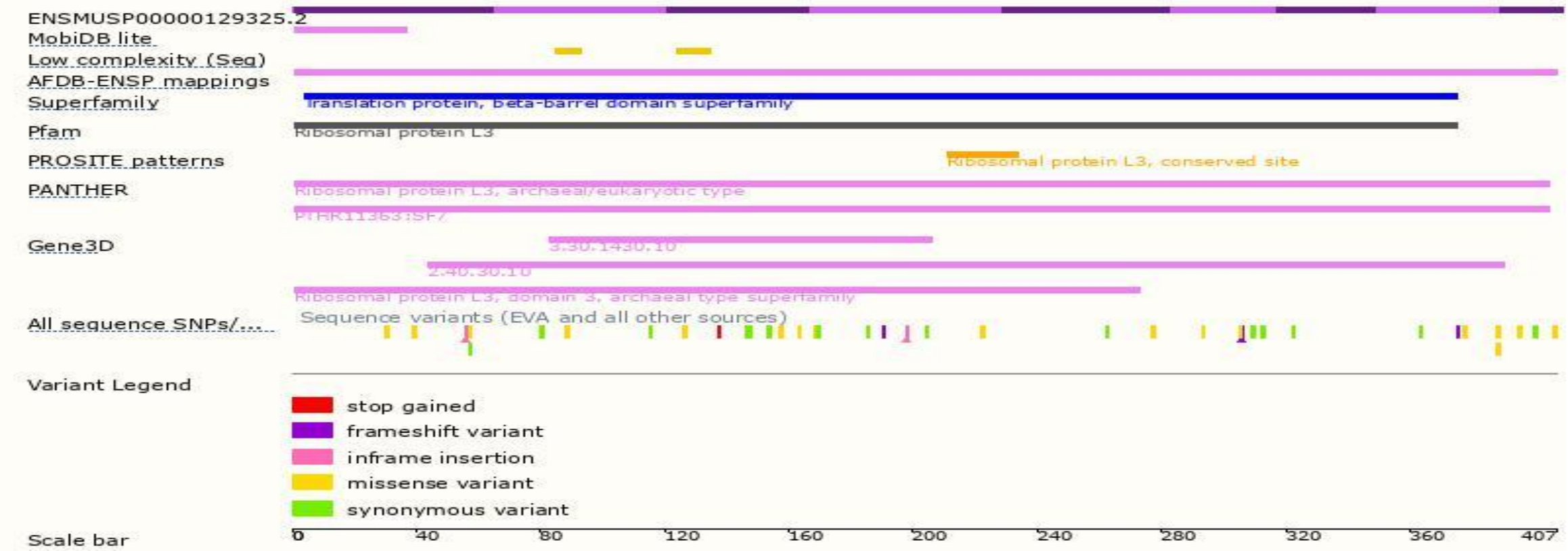
Source: https://www.ensembl.org

Genomic Information



Source: : https://www.ensembl.org

Protein Information



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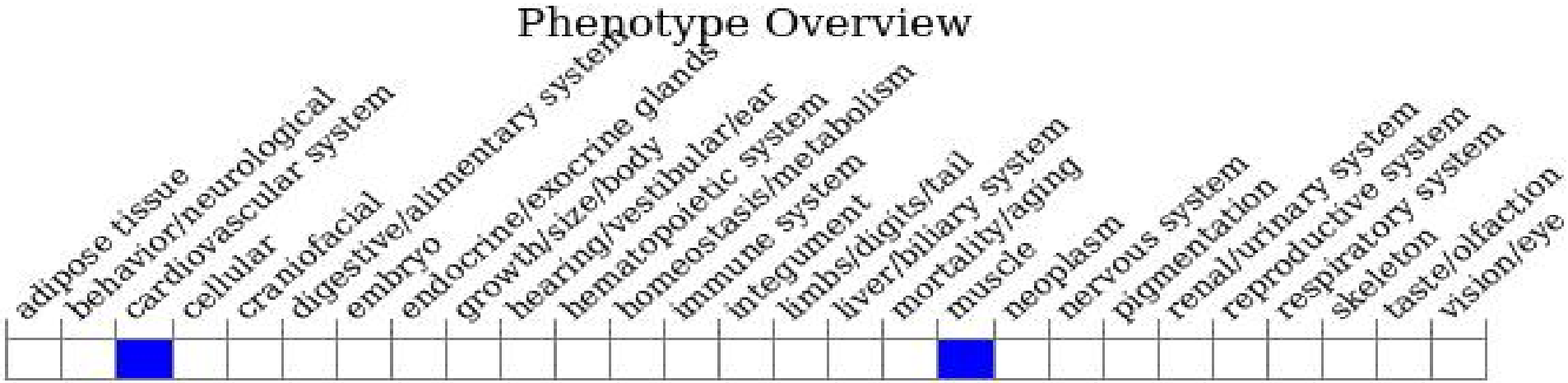
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Mice homozygous for a knock-out allele exhibit a reduction in heart weight with age. Another null allele shows reduced cardiac muscle contractility.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data,mice homozygous for a knock-out allele exhibit a reduction in heart weight with age. Another null allele shows reduced cardiac muscle contractility.
- The knockout region is about 4.0 kb away from the 5' end of the *Ndufb10* and is about 8.3 kb away from the 5' end of the *Msrb1*, which may affect the regulation of these genes.
- The effect of transcript *Rpl3l-203* is unknown.
- *Rpl3l* is located on Chr17. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.