

Rpl26 Cas9-KO Strategy

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Project Overview

Project Name

Rpl26

Project type

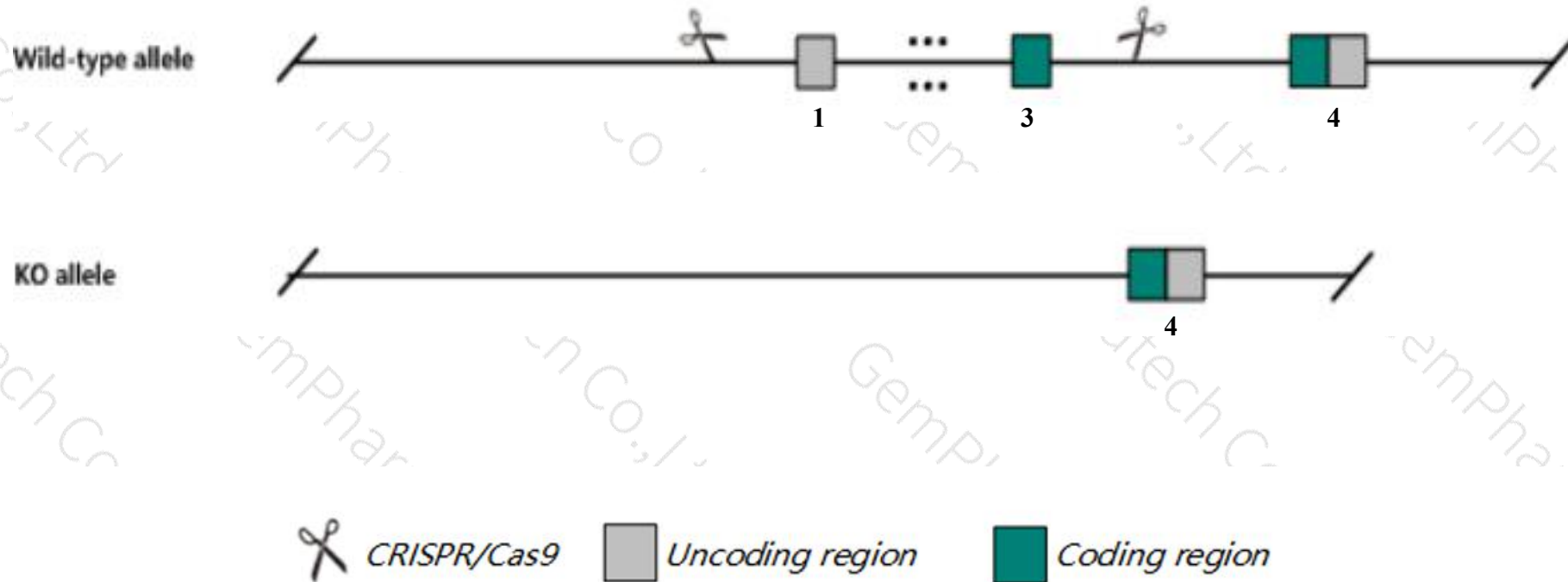
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rpl26* gene. The schematic diagram is as follows:



- The *Rpl26* gene has 6 transcripts. According to the structure of *Rpl26* gene, exon1-exon3 of *Rpl26-206* (ENSMUST00000167436.2) 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 *Rpl26* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Rpl26* gene is located on the Chr11. 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)

Rpl26 ribosomal protein L26 [Mus musculus (house mouse)]

Gene ID: 19941, updated on 13-Mar-2020

Summary



Official Symbol Rpl26 provided by [MGI](#)

Official Full Name ribosomal protein L26 provided by [MGI](#)

Primary source [MGI:MGI:106022](#)

See related [Ensembl:ENSMUSG00000060938](#)

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 SIG-20

Expression Ubiquitous expression in bladder adult (RPKM 768.2), liver E14 (RPKM 703.5) and 28 other tissues [See more](#)

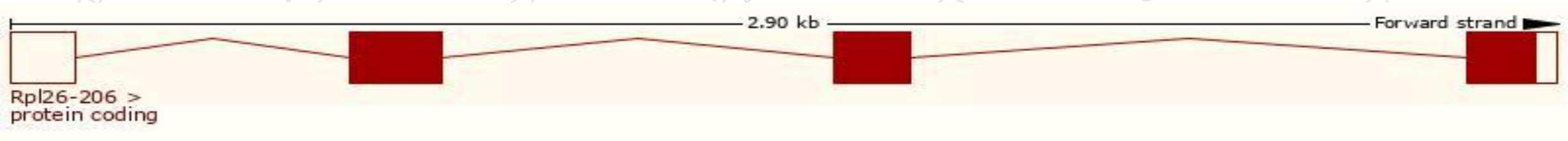
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

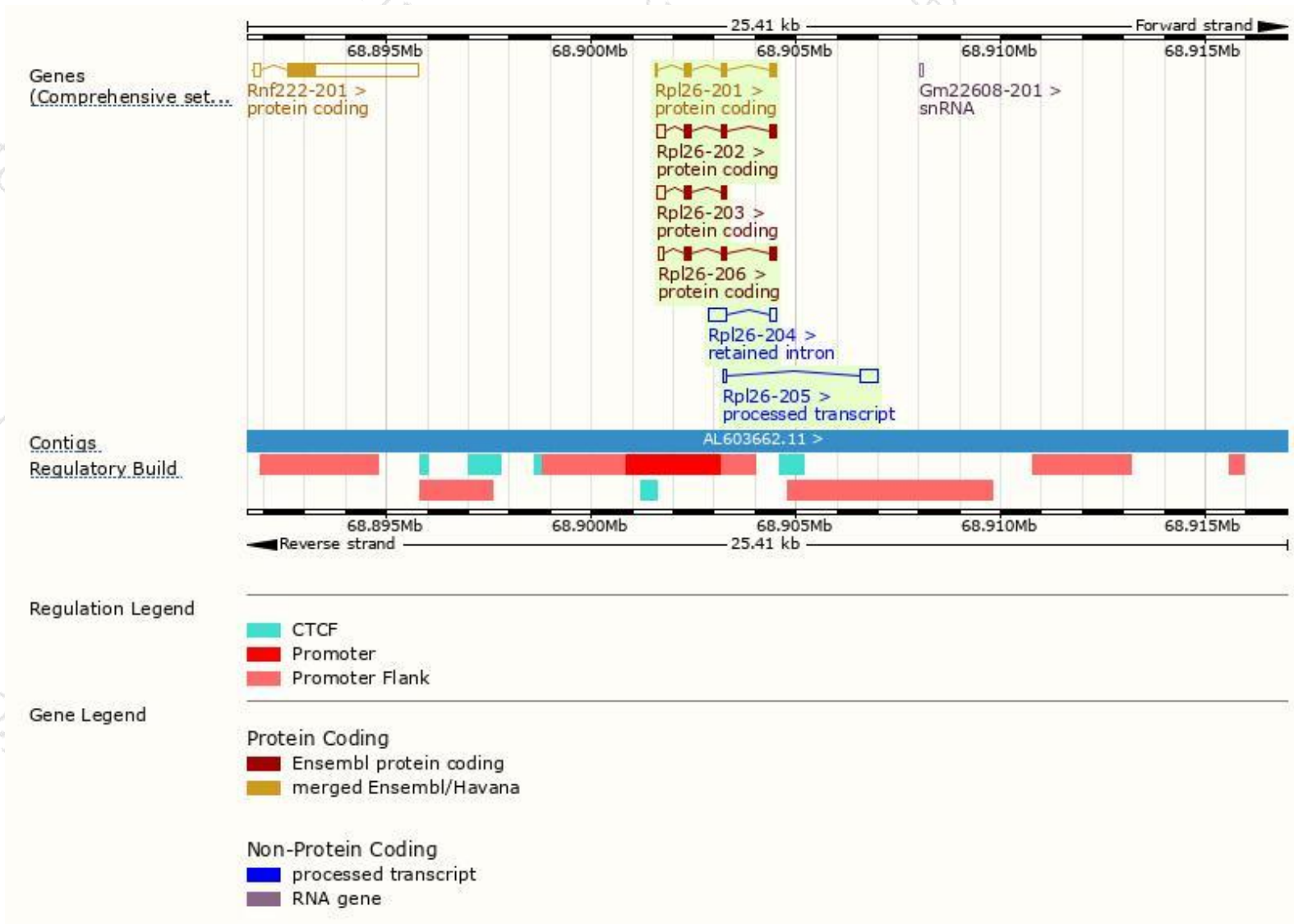
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rpl26-206	ENSMUST00000167436.2	606	145aa	Protein coding	CCDS36187	P61255 Q4FZH2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Rpl26-201	ENSMUST00000073471.12	526	145aa	Protein coding	CCDS36187	P61255 Q4FZH2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Rpl26-202	ENSMUST00000101014.8	657	143aa	Protein coding	-	B1ARA5	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Rpl26-203	ENSMUST00000128952.7	500	103aa	Protein coding	-	B1ARA3	CDS 3' incomplete TSL:2
Rpl26-205	ENSMUST00000138973.1	490	No protein	Processed transcript	-	-	TSL:2
Rpl26-204	ENSMUST00000134403.1	636	No protein	Retained intron	-	-	TSL:2

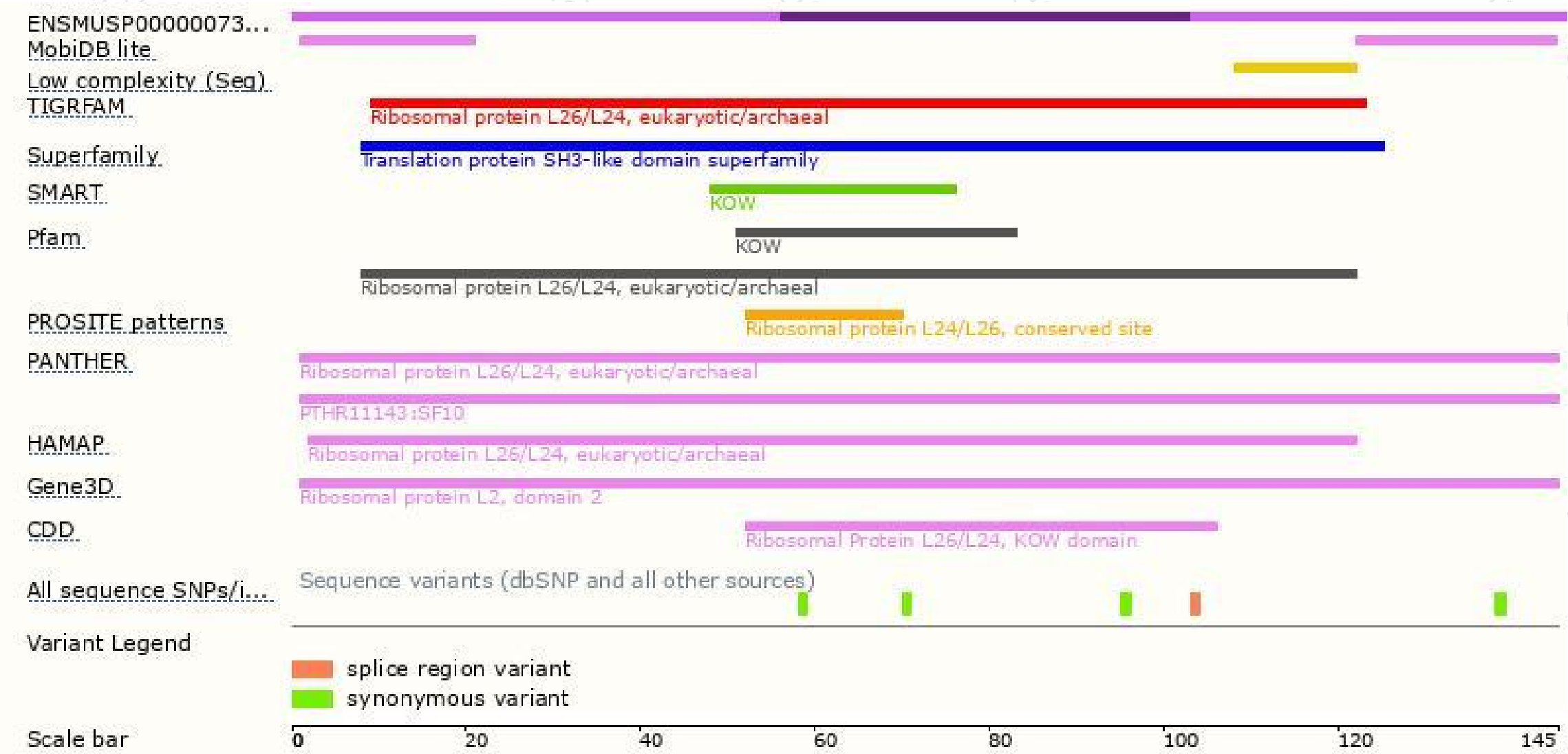
The strategy is based on the design of *Rpl26-206* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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