Rps27l Cas9-KO Strategy

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Project Overview

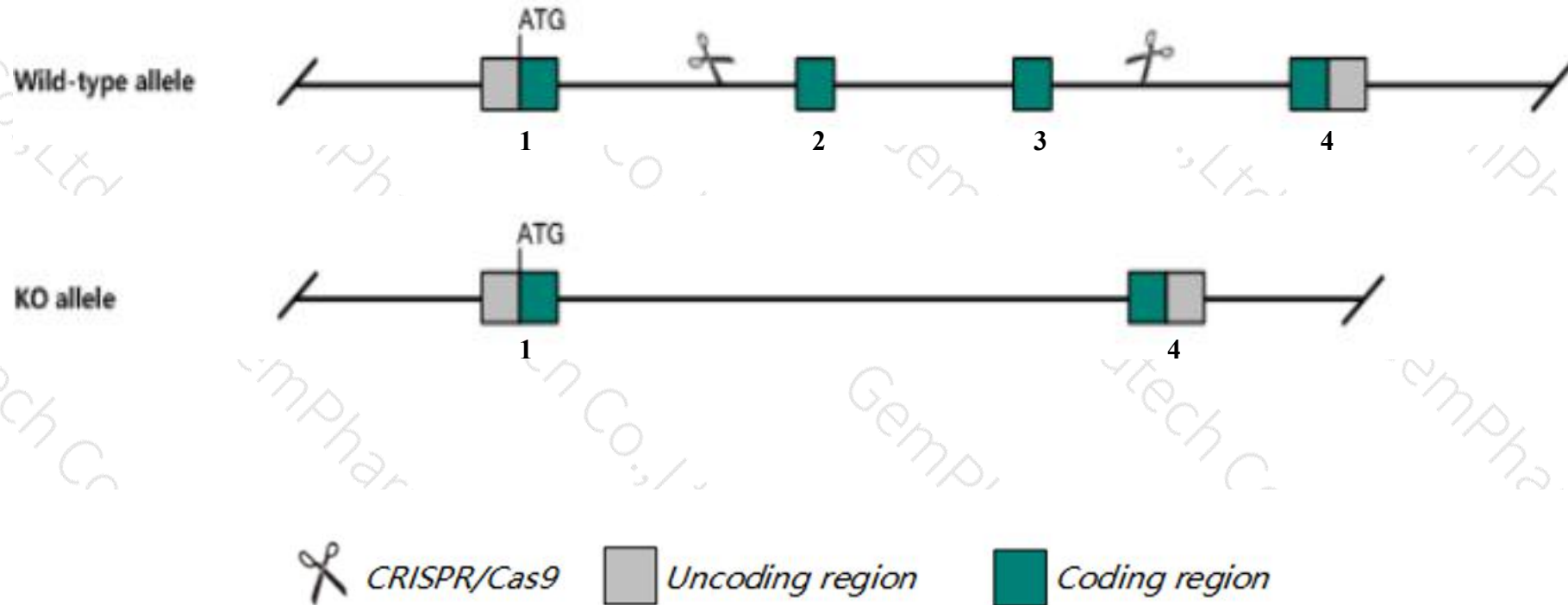|	
Project Name	*Rps27l*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rps27l* gene. The schematic diagram is as follows:

Technical routes

➢ The *Rps27l* gene has 6 transcripts. According to the structure of *Rps27l* gene, exon2-exon3 of *Rps27l-201* (ENSMUST00000040917.13) transcript is recommended as the knockout region.The region contains 220bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rps27l* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit complete postnatal lethality, decreased body weight, hypoplasia of the thymus cortex and liver, and decreased hsc numbers and function.

➢ The transcript of *Rps27l*-202 may not be affected.

➢ The *Rps27l* gene is located on the Chr9. 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.

Rps27l ribosomal protein S27-like [Mus musculus (house mouse)]

Gene ID: 67941, updated on 20-Mar-2020

▲ Summary

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Official Symbol	Rps27l provided by MGI
Official Full Name	ribosomal protein S27-like provided by MGI
Primary source	MGI:MGI:1915191
See related	Ensembl:ENSMUSG00000036781
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	1810034D23Rik
Expression	Broad expression in placenta adult (RPKM 58.6), liver E14 (RPKM 50.1) and 22 other tissuesSee 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
Rps27l-203	ENSMUST00000127896.7	575	105aa	Protein coding	CCDS81028	D3YYB0	TSL:5 GENCODE basic
Rps27l-201	ENSMUST00000040917.13	499	84aa	Protein coding	CCDS40673	Q6ZWY3	TSL:1 GENCODE basic APPRIS P1
Rps27l-205	ENSMUST00000146573.1	271	33aa	Protein coding	-	F6S6Q3	CDS 5' incomplete TSL:3
Rps27l-206	ENSMUST00000147394.7	452	77aa	Nonsense mediated decay	-	D6RH49	TSL:5
Rps27l-204	ENSMUST00000143044.1	566	No protein	Processed transcript	-	-	TSL:2
Rps27l-202	ENSMUST00000123931.1	338	No protein	Retained intron	-	-	TSL:2

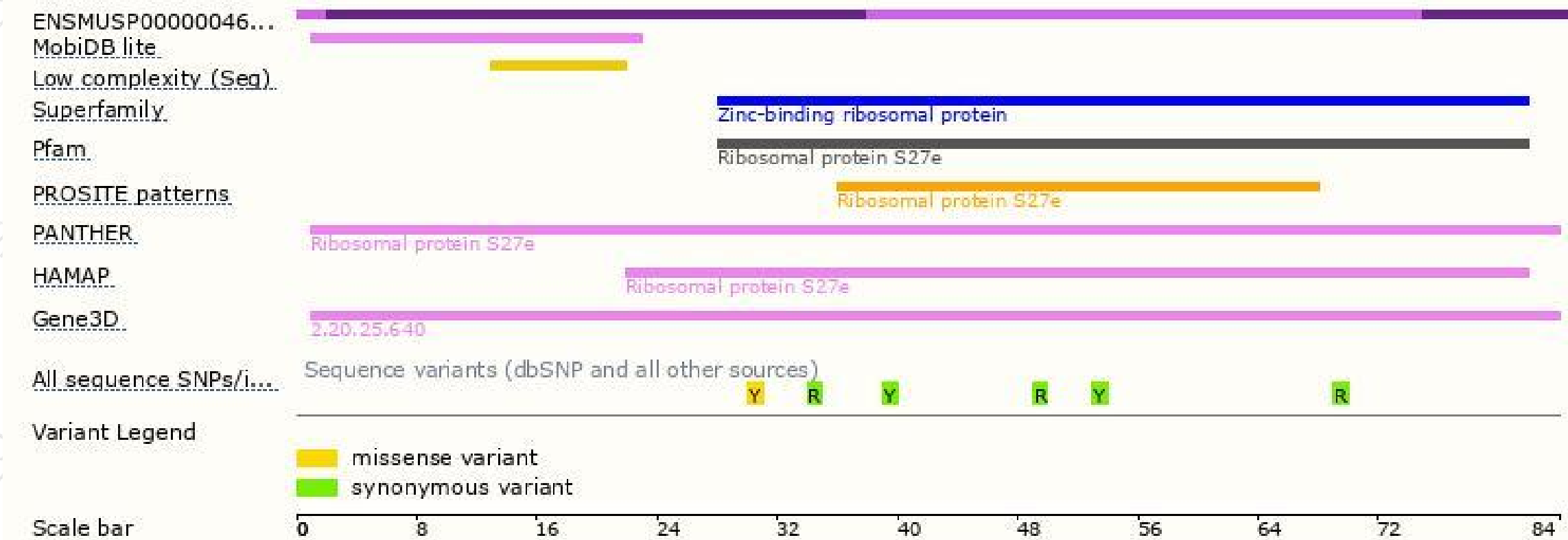The strategy is based on the design of *Rps27l-201* transcript,the transcription is shown below:
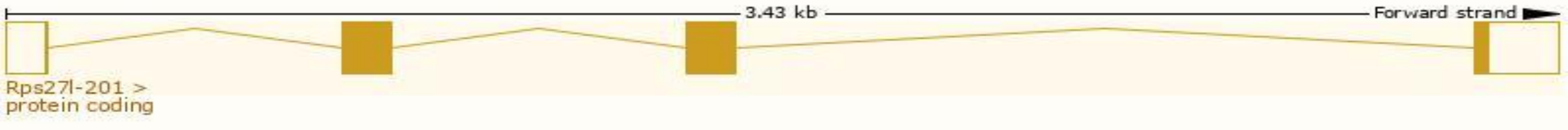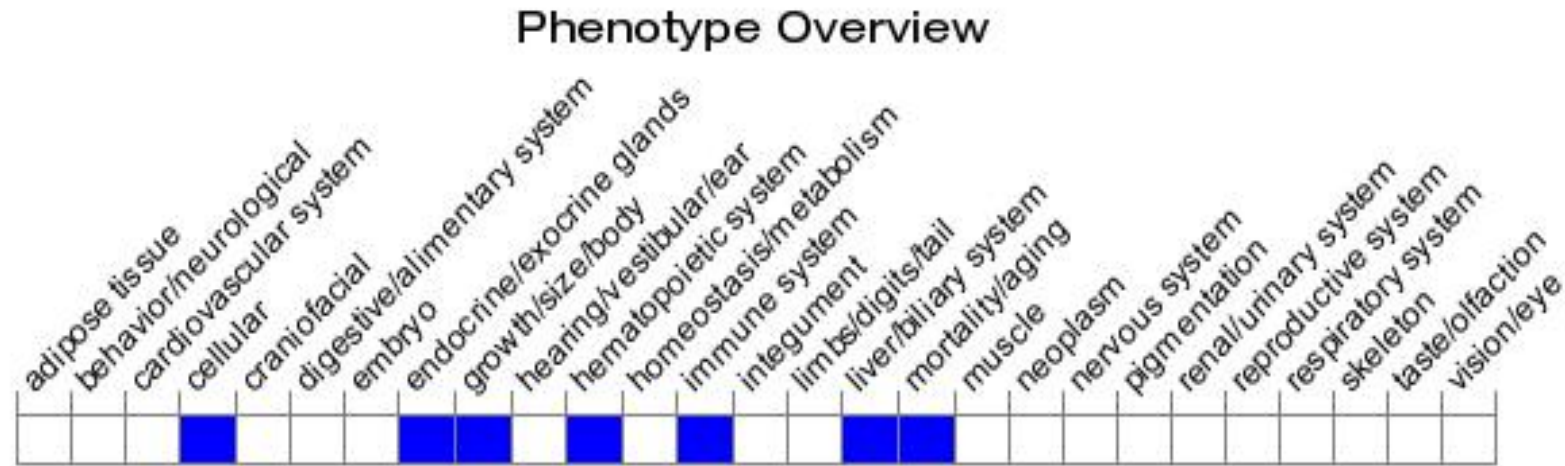
Genomic location distribution

Protein domain

| | Scale bar | 0 | 8 | 16 | 24 | 32 | 40 | 48 | 56 | 64 | 72 | 84 |
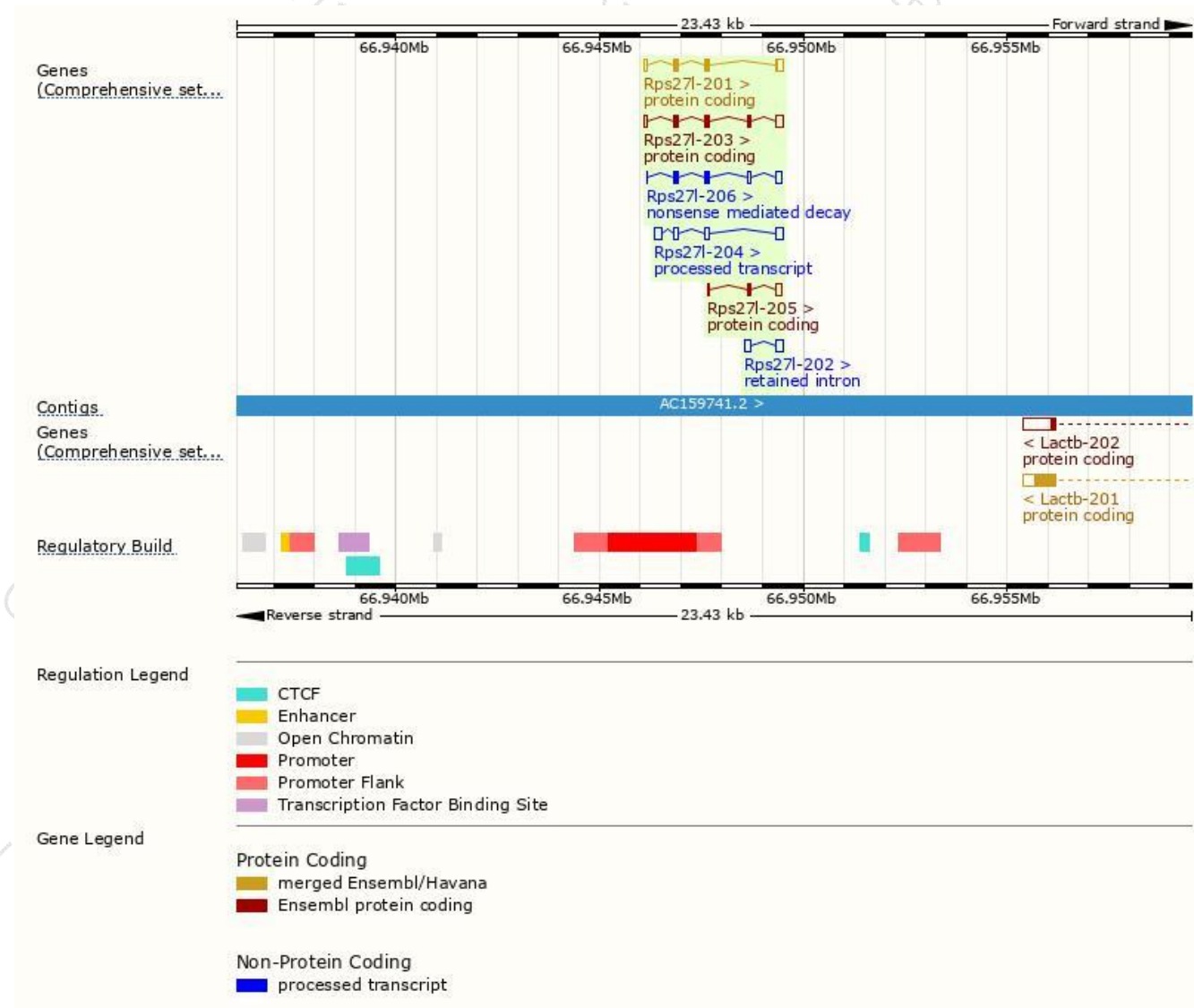
Mouse phenotype description(MGI)

Phenotype Overview

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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