

Rpl22 Cas9-KO Strategy

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Project Overview

Project Name

Rpl22

Project type

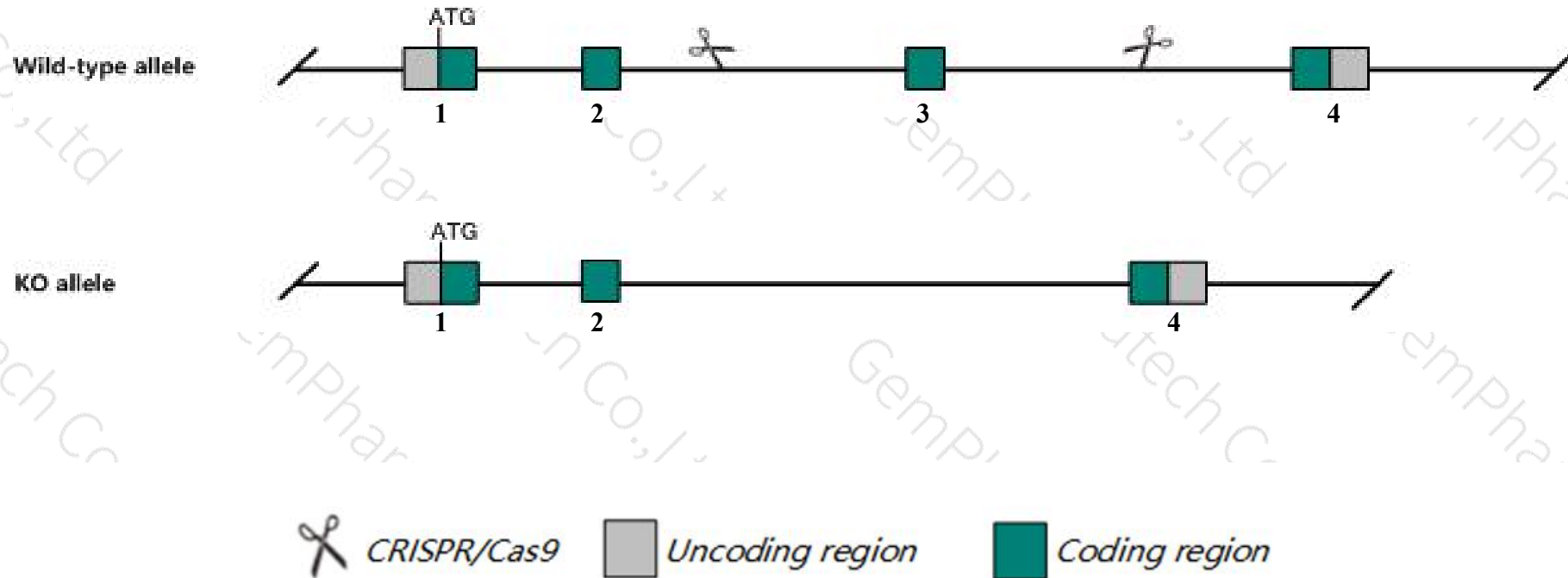
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rpl22* gene. The schematic diagram is as follows:



- The *Rpl22* gene has 8 transcripts. According to the structure of *Rpl22* gene, exon3 of *Rpl22-204* (ENSMUST00000139685.7) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rpl22* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit arrested alpha beta lineage T cell differentiation at the beta selection stage.
- The *Rpl22* gene is located on the Chr4. 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)

Rpl22 ribosomal protein L22 [*Mus musculus* (house mouse)]

Gene ID: 19934, updated on 5-Nov-2019

Summary

- Official Symbol

Rpl22 provided by [MGI](#)
- Official Full Name

ribosomal protein L22 provided by [MGI](#)
- Primary source

[MGI:MGI:99262](#)
- See related

[Ensembl:ENSMUSG00000028936](#)
- 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

2700038K18Rik
- Expression

Broad expression in CNS E11.5 (RPKM 82.1), bladder adult (RPKM 62.7) and 25 other tissues [See more](#)
- Orthologs

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

Genomic context

Location: 4: 4 E2

Exon count: 6

See Rpl22 in [Genome Data Viewer](#)

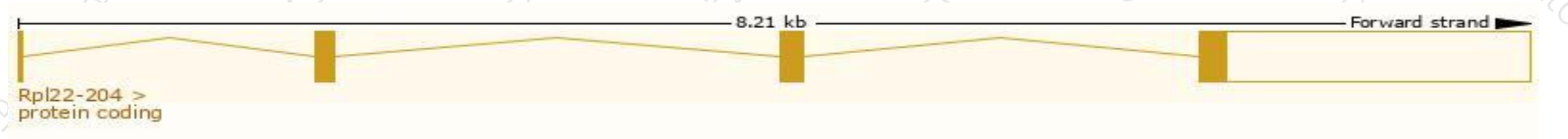
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (152324436..152334082)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (151699987..151708180)

Transcript information (Ensembl)

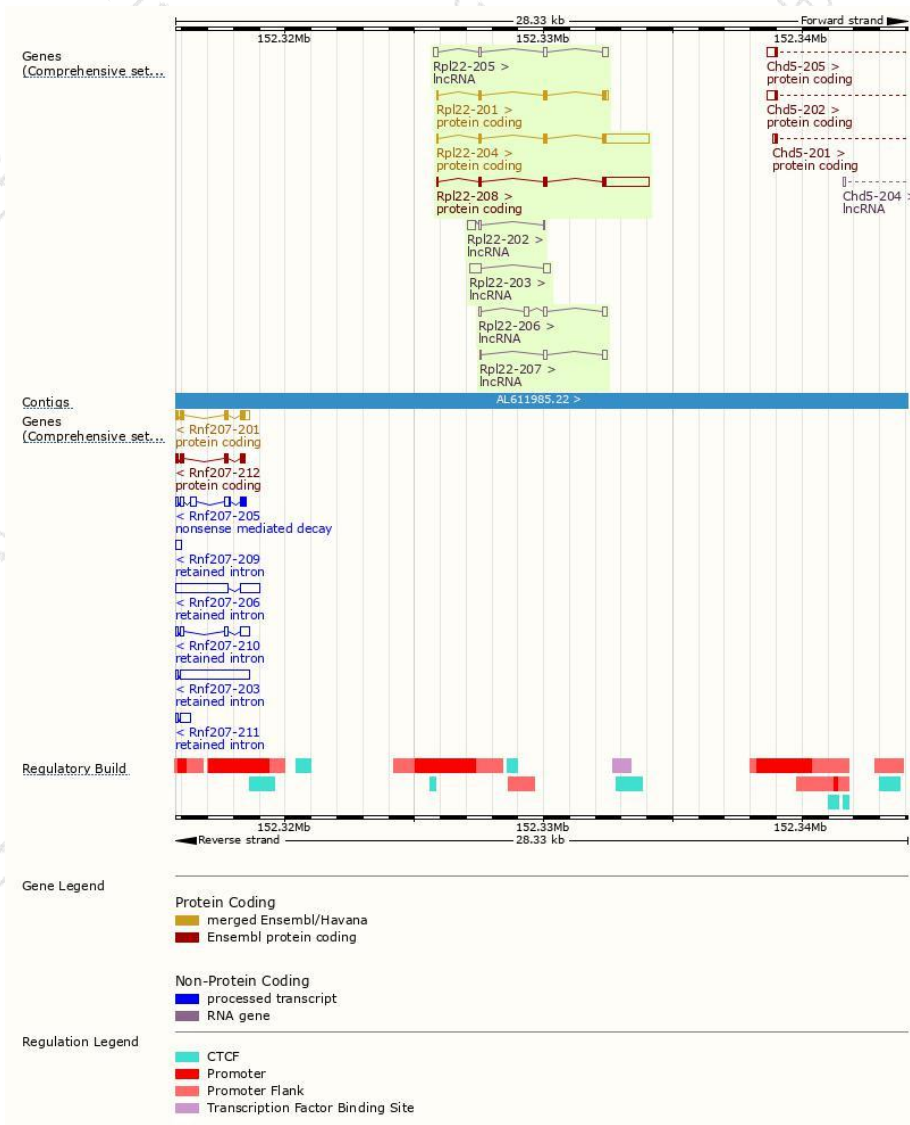
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rpl22-204	ENSMUST00000139685.7	2051	128aa	Protein coding	CCDS18999	P67984 Q4VAG4	TSL:1 GENCODE basic APPRIS P1
Rpl22-208	ENSMUST00000188151.1	2048	128aa	Protein coding	CCDS18999	P67984 Q4VAG4	TSL:1 GENCODE basic APPRIS P1
Rpl22-201	ENSMUST00000103191.10	474	128aa	Protein coding	CCDS18999	P67984 Q4VAG4	TSL:1 GENCODE basic APPRIS P1
Rpl22-203	ENSMUST00000127659.1	732	No protein	lncRNA	-	-	TSL:2
Rpl22-205	ENSMUST00000142735.7	581	No protein	lncRNA	-	-	TSL:1
Rpl22-206	ENSMUST00000150485.1	576	No protein	lncRNA	-	-	TSL:5
Rpl22-202	ENSMUST00000126519.1	441	No protein	lncRNA	-	-	TSL:3
Rpl22-207	ENSMUST00000156445.1	369	No protein	lncRNA	-	-	TSL:5

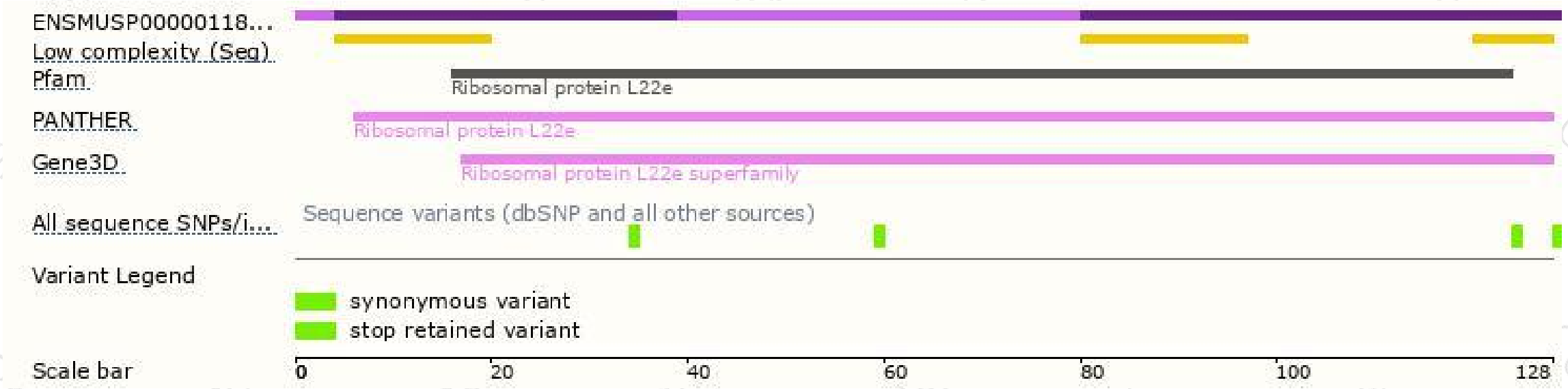
The strategy is based on the design of *Rpl22-204* transcript,The transcription is shown below



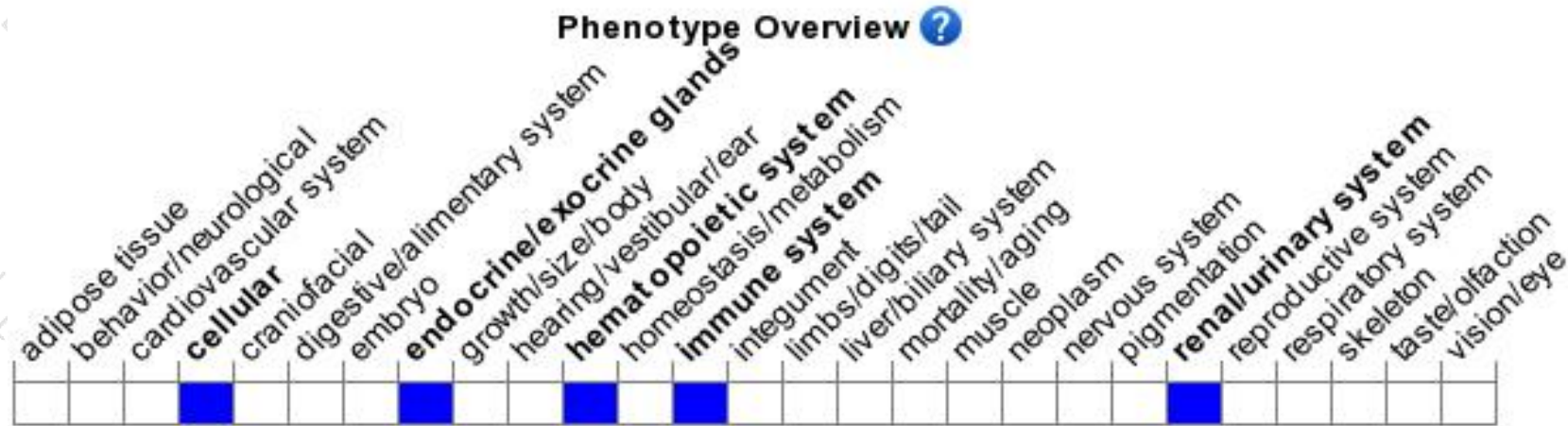
Genomic location distribution



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 null allele exhibit arrested alpha beta lineage T cell differentiation at the beta selection stage.

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

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