

Peli3 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Jiayuan Yao

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Project Overview

Project Name

Peli3

Project type

Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Peli3* gene. The schematic diagram is as follows:



- The *Peli3* gene has 7 transcripts. According to the structure of *Peli3* gene, exon3 of *Peli3-201* (ENSMUST00000025834.14) transcript is recommended as the knockout region. The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Peli3* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a null mutation display decreased susceptibility to viral infection.
- The *Peli3* gene is located on the Chr19. 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)

Peli3 pellino 3 [Mus musculus (house mouse)]

Gene ID: 240518, updated on 13-Mar-2020

Summary



Official Symbol	Peli3 provided by MGI
Official Full Name	pellino 3 provided by MGI
Primary source	MGI:MGI:1924963
See related	Ensembl:ENSMUSG00000024901
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	6030441F14Rik, A930011L17, BC028931
Expression	Broad expression in adrenal adult (RPKM 5.8), cerebellum adult (RPKM 4.8) and 22 other tissues See more
Orthologs	human all

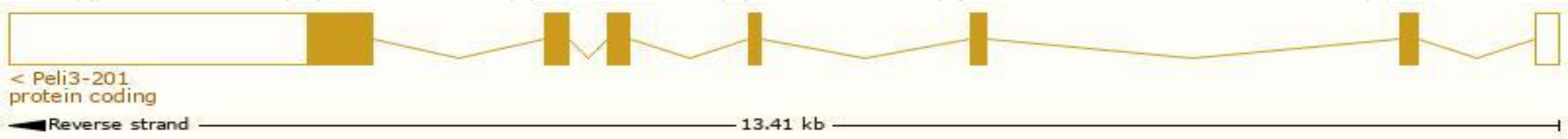
Transcript information（Ensembl）



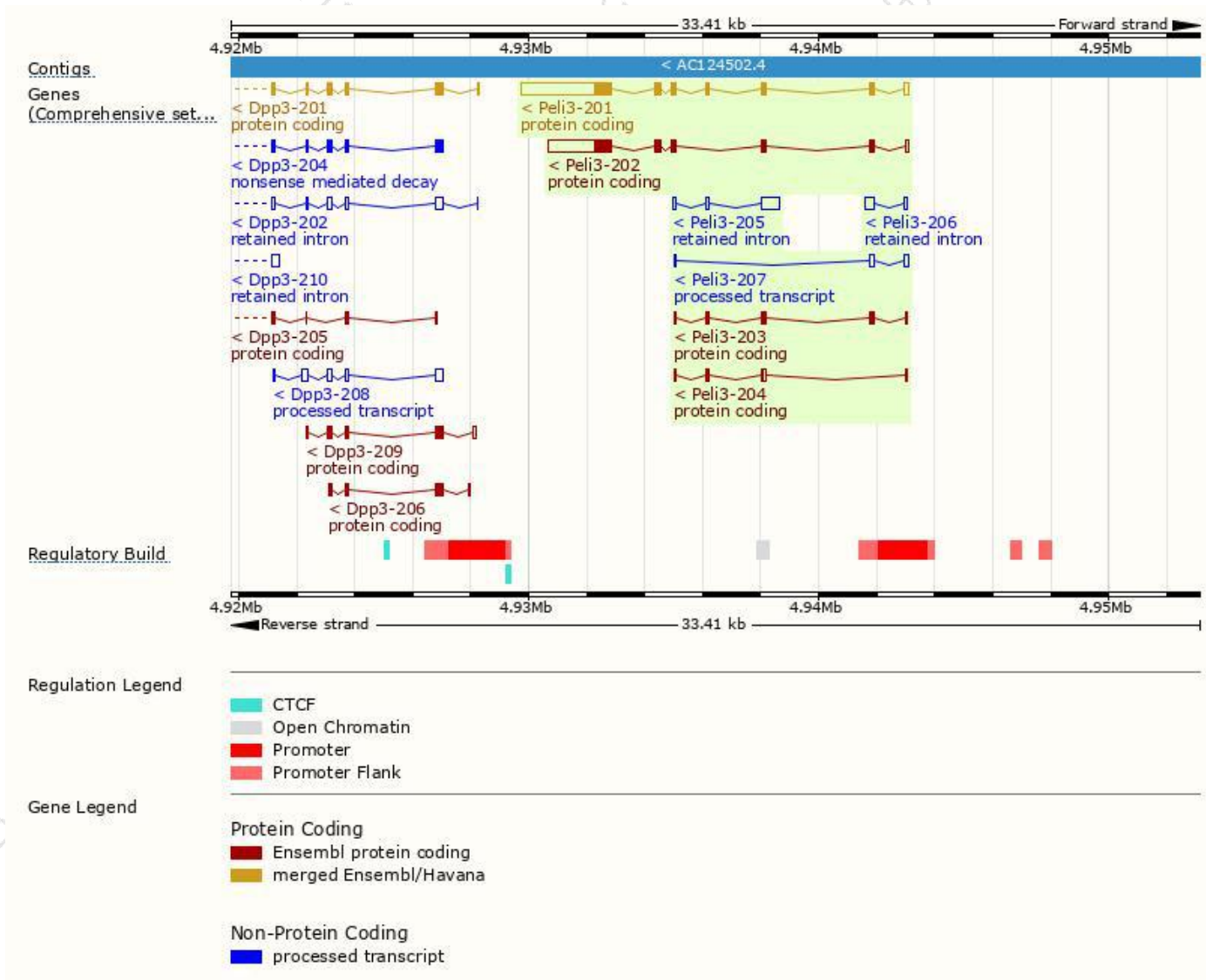
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Peli3-201	ENSMUST00000025834.14	4110	445aa	Protein coding	CCDS37888	A0A0R4J057	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 P1
Peli3-202	ENSMUST00000120475.7	2988	411aa	Protein coding	CCDS84408	D3Z6V8	TSL:1 GENCODE basic
Peli3-203	ENSMUST00000133254.1	552	155aa	Protein coding	-	D3YYQ7	CDS 3' incomplete TSL:2
Peli3-204	ENSMUST00000133504.1	386	70aa	Protein coding	-	A0A494B9W5	CDS 3' incomplete TSL:3
Peli3-207	ENSMUST00000146289.1	400	No protein	Processed transcript	-	-	TSL:3
Peli3-205	ENSMUST00000139436.7	794	No protein	Retained intron	-	-	TSL:3
Peli3-206	ENSMUST00000143930.1	422	No protein	Retained intron	-	-	TSL:2

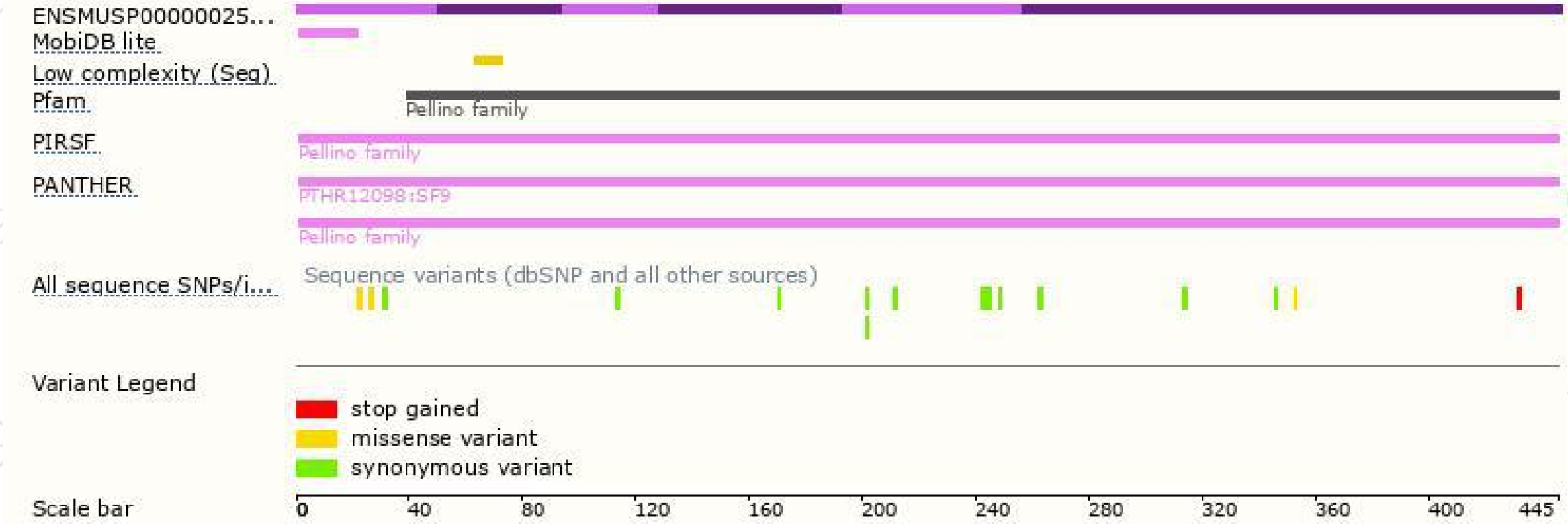
The strategy is based on the design of *Peli3-201* transcript,the transcription is shown below:



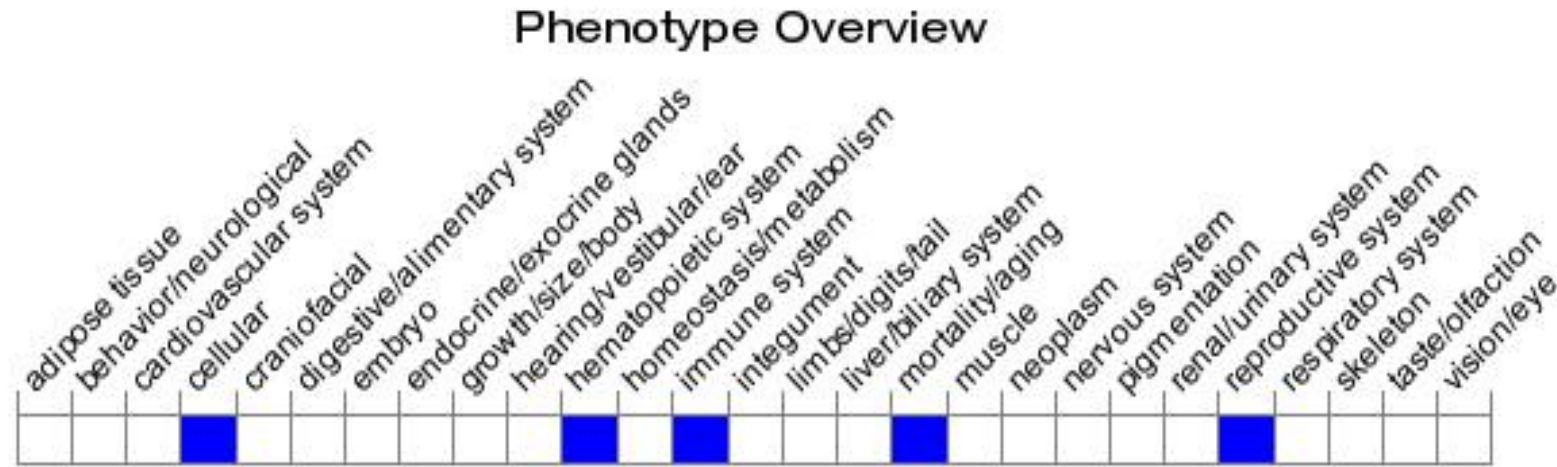
Genomic location distribution



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 null mutation display decreased susceptibility to viral infection.

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

Tel: 400-9660890

