

Pml Cas9-KO Strategy

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Project Overview

Project Name

Pml

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Pml* gene has 12 transcripts. According to the structure of *Pml* gene, exon2 of *Pml*-201 (ENSMUST00000085673.10) transcript is recommended as the knockout region. The region contains 464bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pml* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, Mice homozygous for disruptions of this gene have an increased susceptibility to infection and to induction of tumors.
- Transcript *Pml*-203&208&209&210&212 may not be affected.
- The floxed region is near to the N-terminal of *Stoml1* gene, this strategy may influence the regulatory function of the N-terminal of *Stoml1* gene.
- The *Pml* 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.

Gene information (NCBI)

Pml promyelocytic leukemia [Mus musculus (house mouse)]

Gene ID: 18854, updated on 9-Feb-2019

Summary



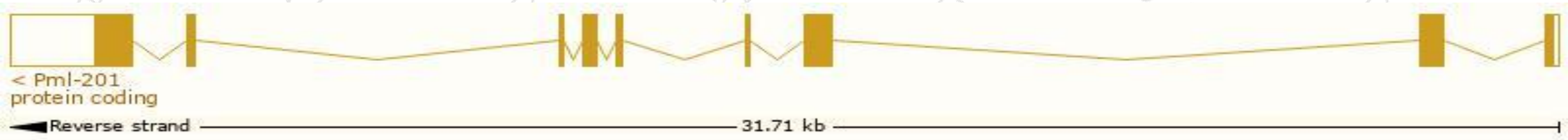
Official Symbol	Pml provided by MGI
Official Full Name	promyelocytic leukemia provided by MGI
Primary source	MGI:MGI:104662
See related	Ensembl:ENSMUSG00000036986
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200009E24Rik, A1661194, Trim19
Expression	Ubiquitous expression in spleen adult (RPKM 20.1), thymus adult (RPKM 9.8) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

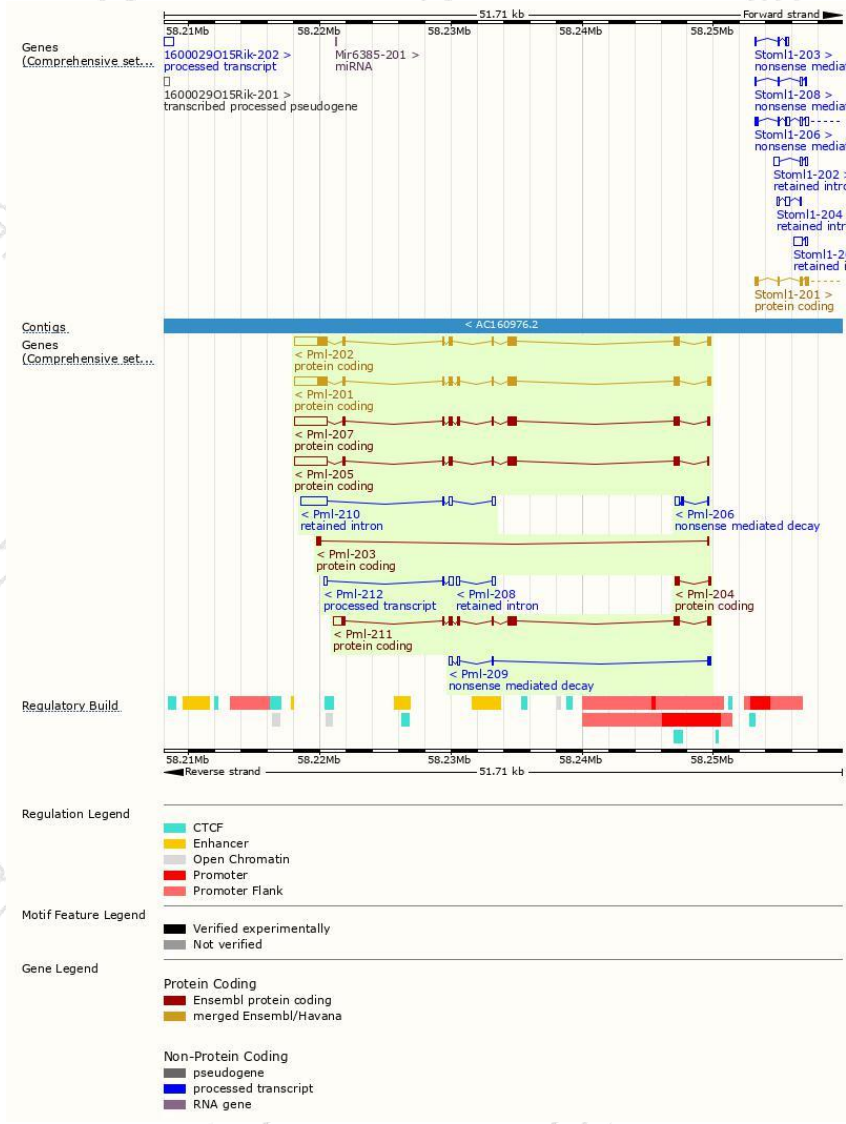
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pml-201	ENSMUST00000085673.10	4481	885aa	Protein coding	CCDS23239	A0A068EW80 Q60953	TSL:1 GENCODE basic APPRIS P4
Pml-207	ENSMUST00000135310.7	4413	632aa	Protein coding	CCDS81007	D3Z3A6	TSL:1 GENCODE basic APPRIS ALT2
Pml-202	ENSMUST00000114136.8	4343	839aa	Protein coding	CCDS23240	Q60953	TSL:1 GENCODE basic APPRIS ALT2
Pml-205	ENSMUST00000126690.7	4206	578aa	Protein coding	-	F7BTZ2	CDS 5' incomplete TSL:5
Pml-211	ENSMUST00000153820.7	2652	641aa	Protein coding	-	D3YXR5	TSL:1 GENCODE basic APPRIS ALT2
Pml-204	ENSMUST00000124982.1	452	118aa	Protein coding	-	D3Z2V0	CDS 3' incomplete TSL:3
Pml-203	ENSMUST00000124063.1	427	124aa	Protein coding	-	F6XUT1	CDS 5' incomplete TSL:5
Pml-209	ENSMUST00000148301.1	718	53aa	Nonsense mediated decay	-	D6RII9	TSL:3
Pml-206	ENSMUST00000130459.1	590	54aa	Nonsense mediated decay	-	F6RQM1	CDS 5' incomplete TSL:2
Pml-212	ENSMUST00000154572.1	655	No protein	Processed transcript	-	-	TSL:3
Pml-210	ENSMUST00000148628.7	2573	No protein	Retained intron	-	-	TSL:3
Pml-208	ENSMUST00000138775.1	481	No protein	Retained intron	-	-	TSL:2

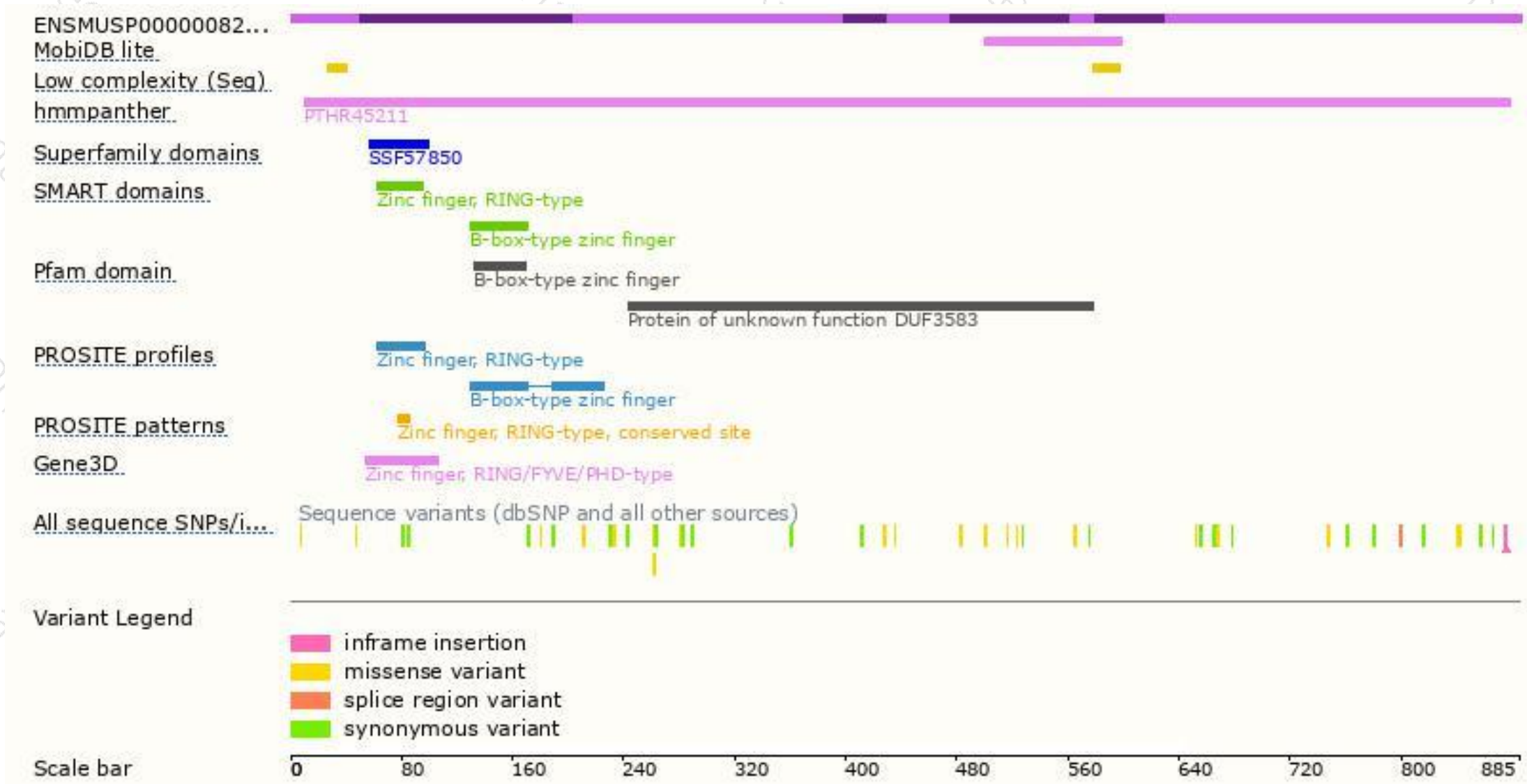
The strategy is based on the design of *Pml-201* transcript,The transcription is shown below



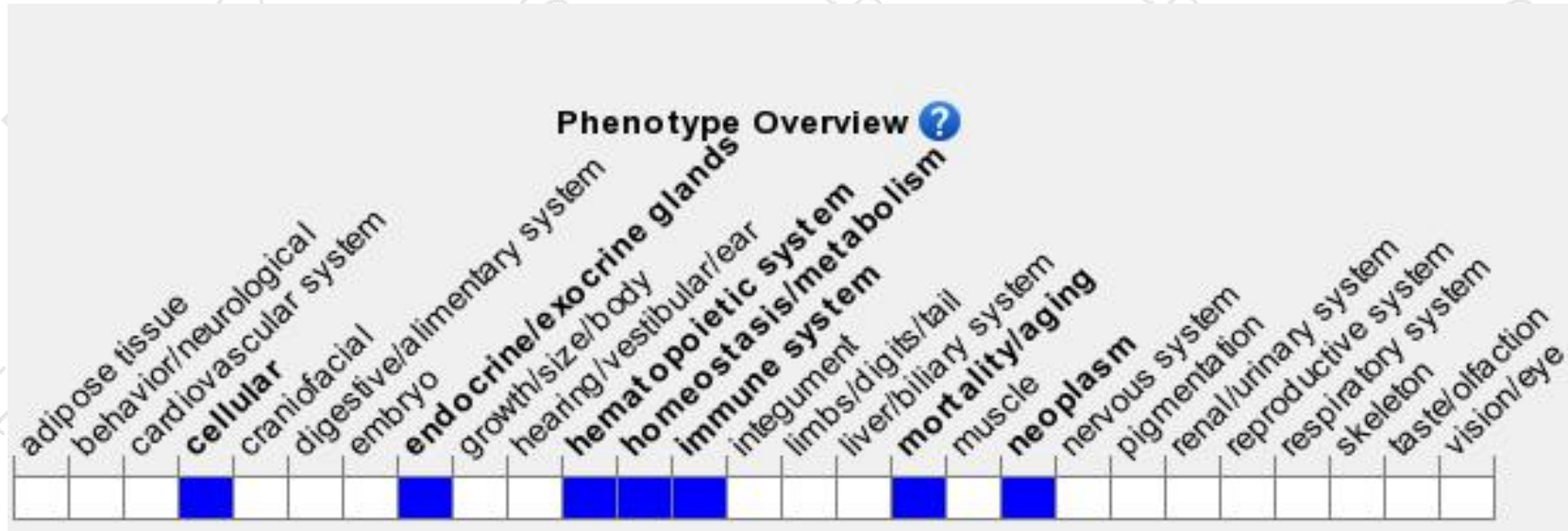
Genomic location distribution



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 disruptions of this gene have an increased susceptibility to infection and to induction of tumors.

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

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