

Polm Cas9-KO Strategy

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Date: 2020-1-21

Project Overview

Project Name

Polm

Project type

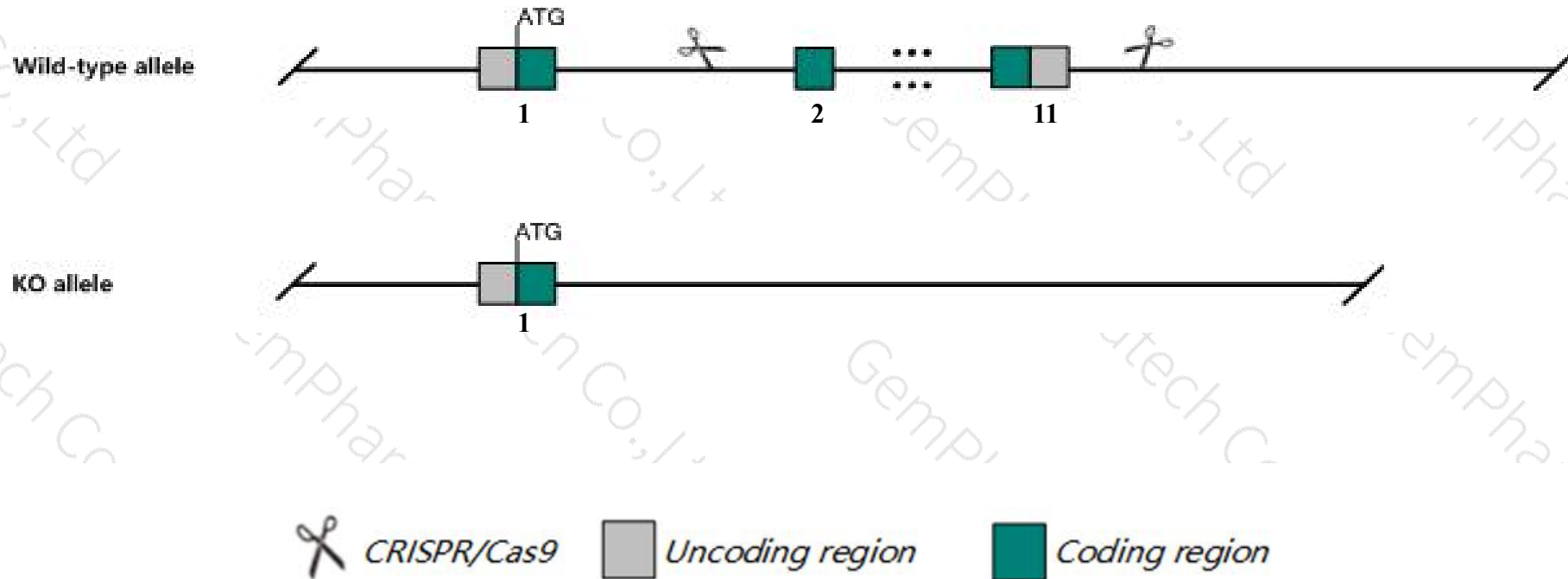
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Polm* gene has 6 transcripts. According to the structure of *Polm* gene, exon2-exon11 of *Polm-201* (ENSMUST00000020767.3) transcript is recommended as the knockout region. The region contains most 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 *Polm* gene. The brief process is as follows: CRISPR/Cas9 system were

- According to the existing MGI data, Mice homozygous for disruptions in this gene display an apparently normal phenotype. However, B cell maturation and proliferation is abnormal.
- The *Polm* 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)

Polm polymerase (DNA directed), mu [*Mus musculus* (house mouse)]

Gene ID: 54125, updated on 10-Oct-2019

Summary

- Official Symbol** Polm provided by MGI
- Official Full Name** polymerase (DNA directed), mu provided by MGI
- Primary source** MGI:MGI:1860191
- See related** Ensembl:ENSMUSG00000020474
- 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** Tdt-N; AI462166; B230309I03Rik
- Expression** Ubiquitous expression in spleen adult (RPKM 19.9), ovary adult (RPKM 12.7) and 27 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 11; 11 A1 See Polm in [Genome Data Viewer](#)

Exon count: 11

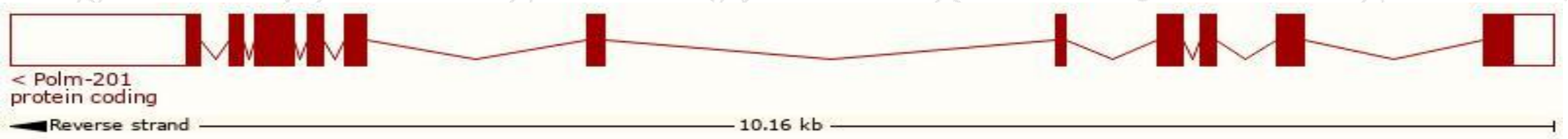
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (5827860..5838832, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (5727863..5738019, complement)

Transcript information (Ensembl)

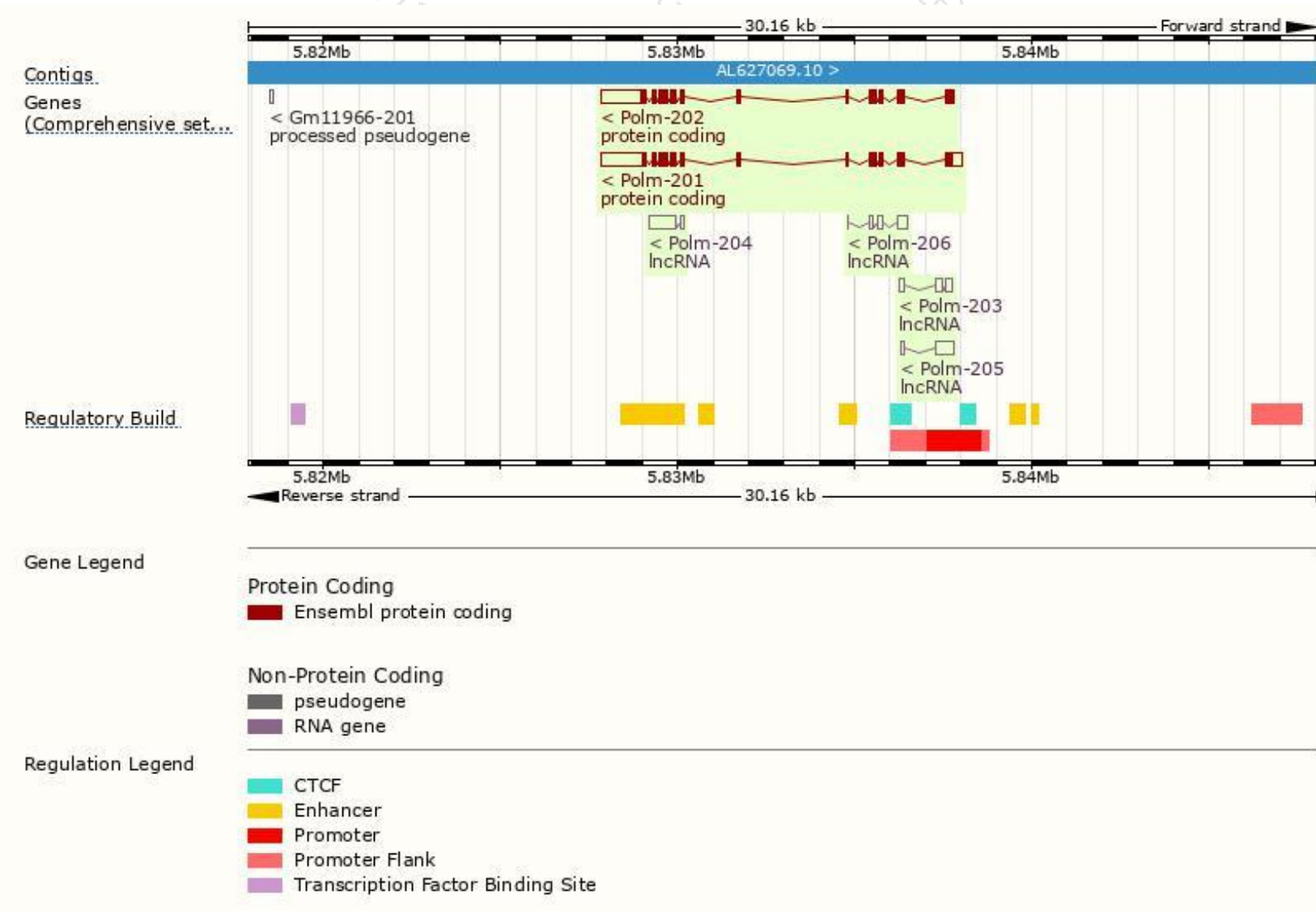
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Polm-201	ENSMUST00000020767.3	2924	496aa	Protein coding	CCDS24405	Q9JIW4	TSL:1 GENCODE basic APPRIS P1
Polm-202	ENSMUST00000109837.7	2697	511aa	Protein coding	-	Q5NCI3	TSL:5 GENCODE basic
Polm-204	ENSMUST00000143478.1	847	No protein	lncRNA	-	-	TSL:3
Polm-205	ENSMUST00000153987.1	579	No protein	lncRNA	-	-	TSL:1
Polm-206	ENSMUST00000156913.1	577	No protein	lncRNA	-	-	TSL:5
Polm-203	ENSMUST00000124564.1	479	No protein	lncRNA	-	-	TSL:5

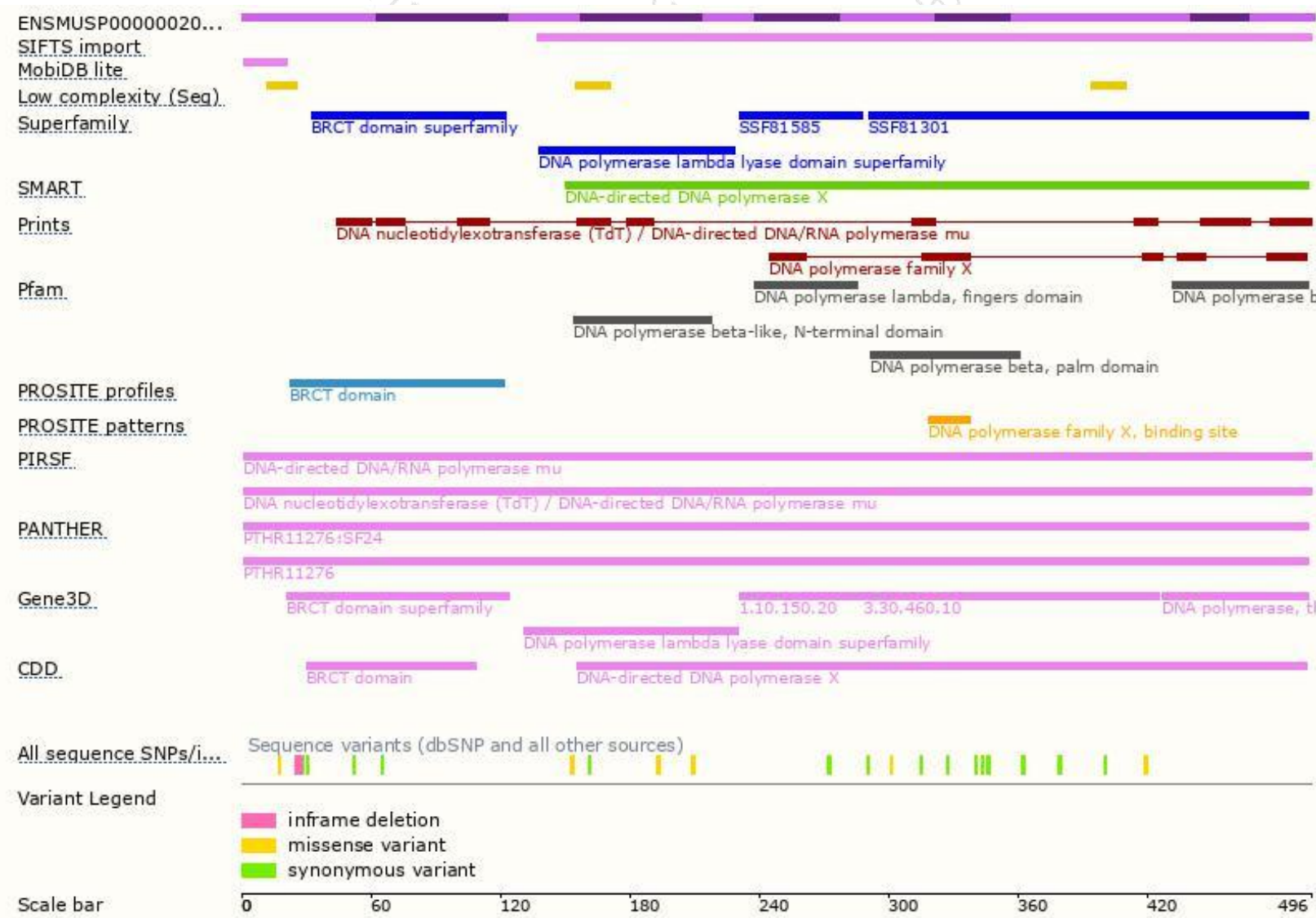
The strategy is based on the design of *Polm-201* transcript,The transcription is shown below



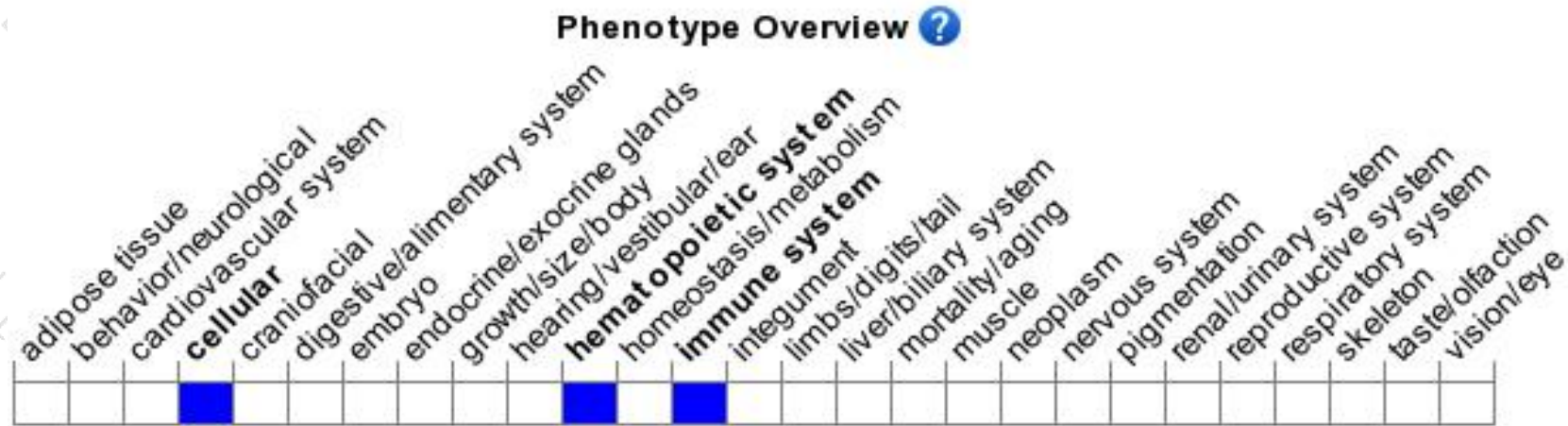
Genomic location distribution



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/>).

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However, B cell maturation and proliferation is abnormal.

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

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