

Pole2 Cas9-CKO Strategy

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Project Overview

Project Name

Pole2

Project type

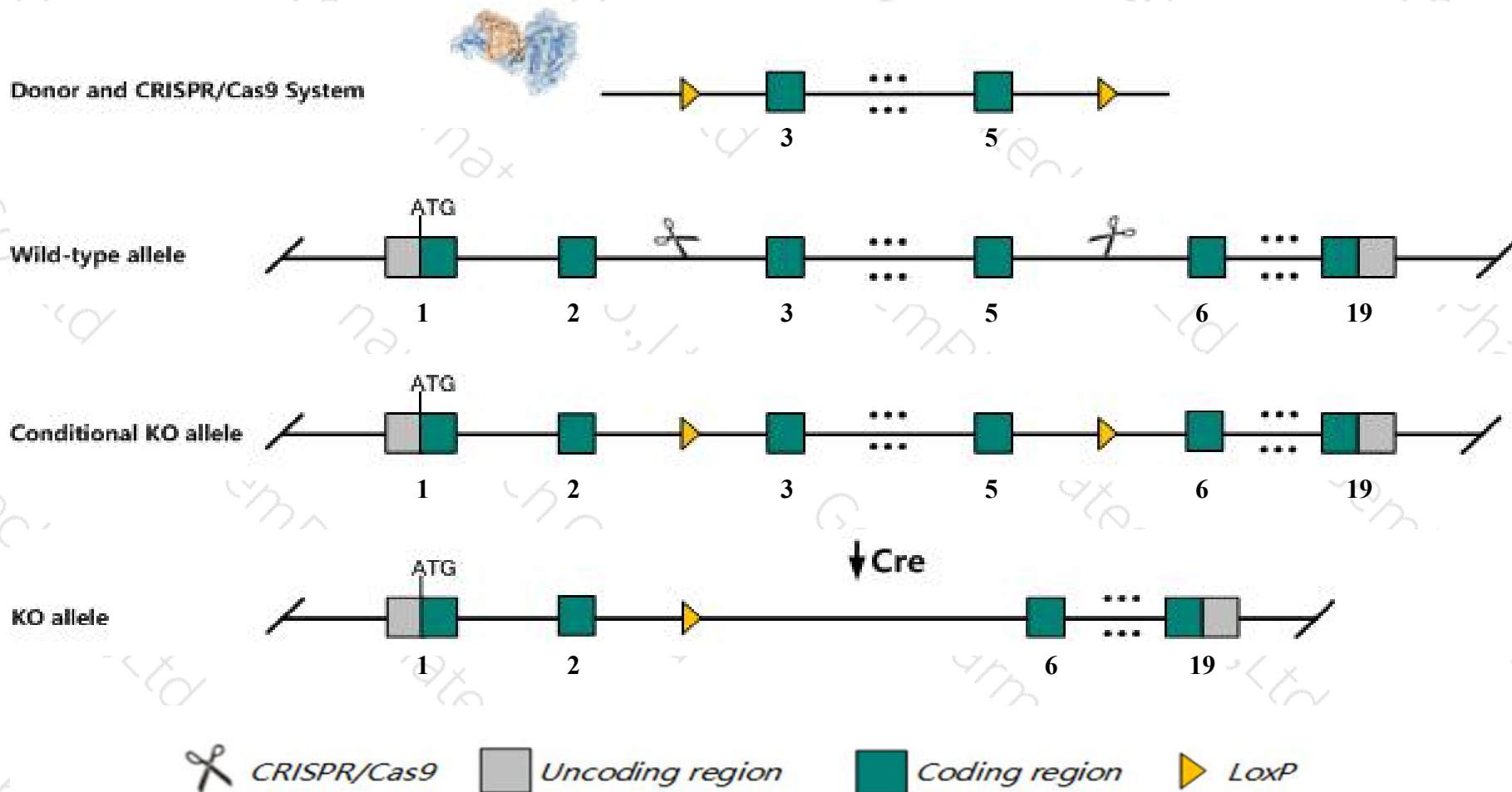
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pole2* gene. The schematic diagram is as follows:



Technical routes

- The *Pole2* gene has 4 transcripts. According to the structure of *Pole2* gene, exon3-exon5 of *Pole2*-201 (ENSMUST00000021359.6) transcript is recommended as the knockout region. The region contains 248bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pole2* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Pole2* gene is located on the Chr12. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Pole2 polymerase (DNA directed), epsilon 2 (p59 subunit) [Mus musculus (house mouse)]

Gene ID: 18974, updated on 13-Mar-2020

Summary



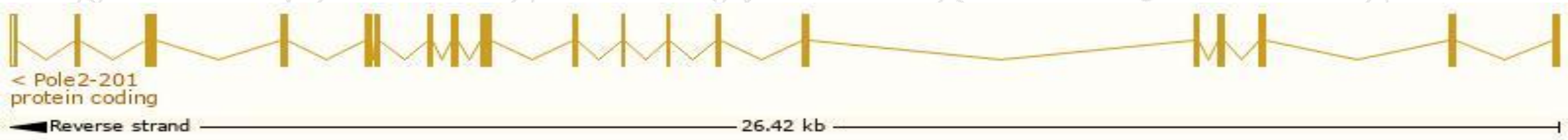
Official Symbol	Pole2 provided by MGI
Official Full Name	polymerase (DNA directed), epsilon 2 (p59 subunit) provided by MGI
Primary source	MGI:MGI:1197514
See related	Ensembl:ENSMUSG00000020974
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Broad expression in liver E14 (RPKM 11.5), liver E14.5 (RPKM 10.1) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

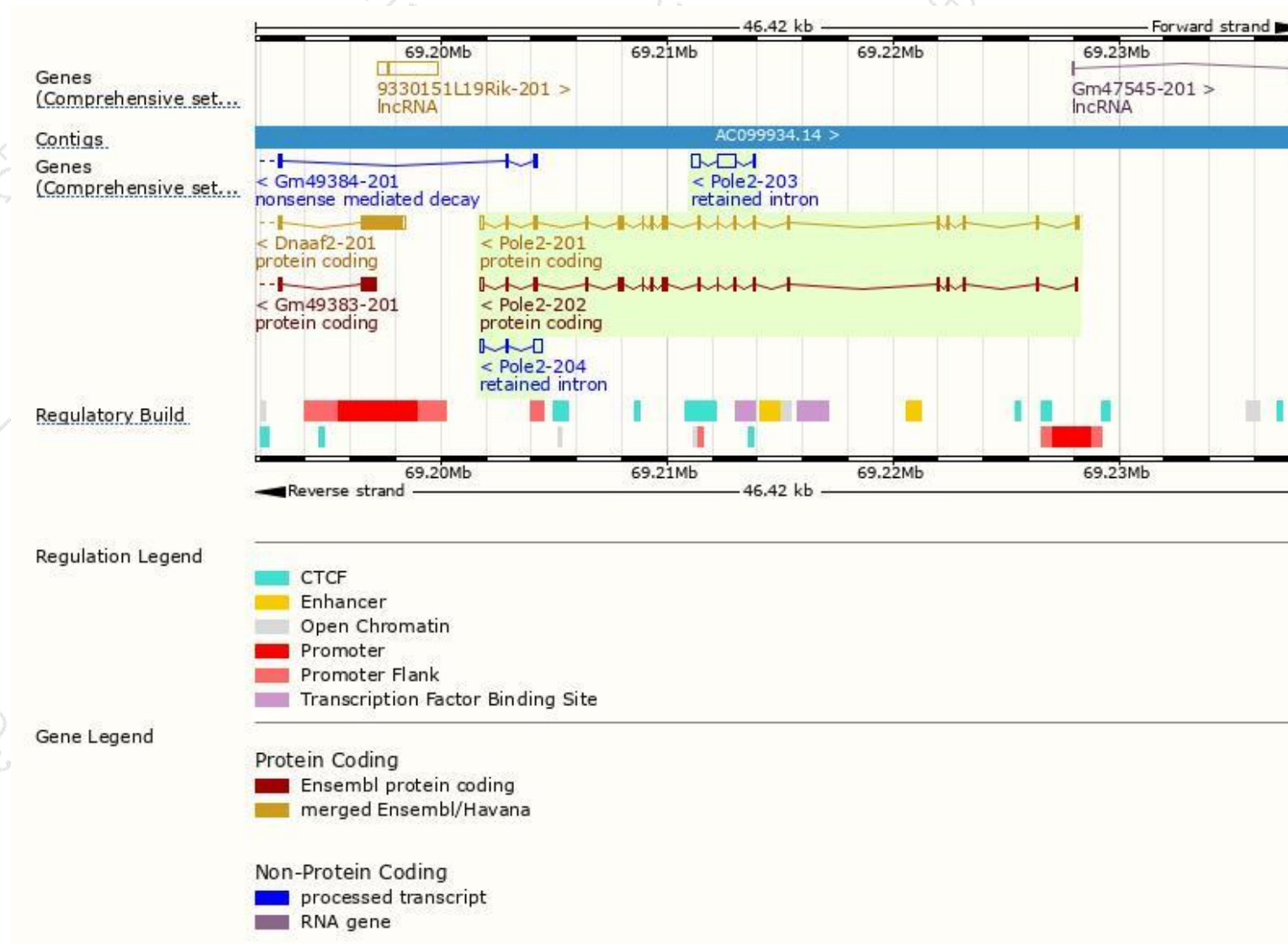
The gene has 4 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Pole2-201	ENSMUST00000021359.6	1706	527aa	Protein coding	CCDS36463	O54956	TSL:1 GENCODE basic APPRIS P1
Pole2-202	ENSMUST00000221411.1	1641	502aa	Protein coding	-	A0A1Y7VN66	TSL:1 GENCODE basic
Pole2-203	ENSMUST00000221806.1	1237	No protein	Retained intron	-	-	TSL:5
Pole2-204	ENSMUST00000221986.1	545	No protein	Retained intron	-	-	TSL:2

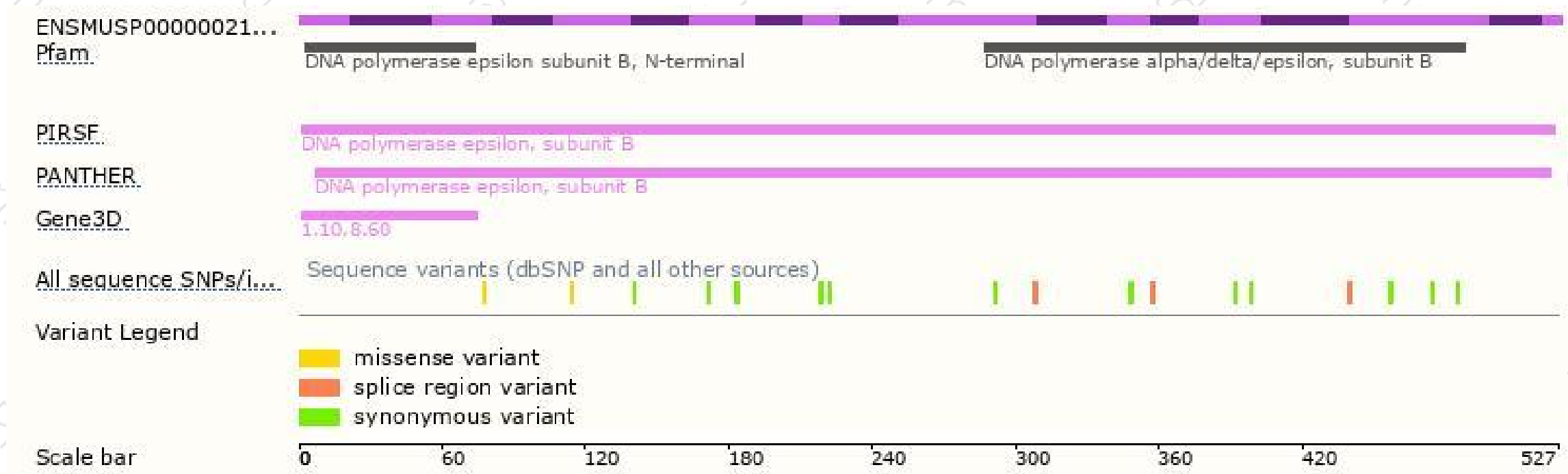
The strategy is based on the design of *Pole2-201* transcript,The transcription is shown below



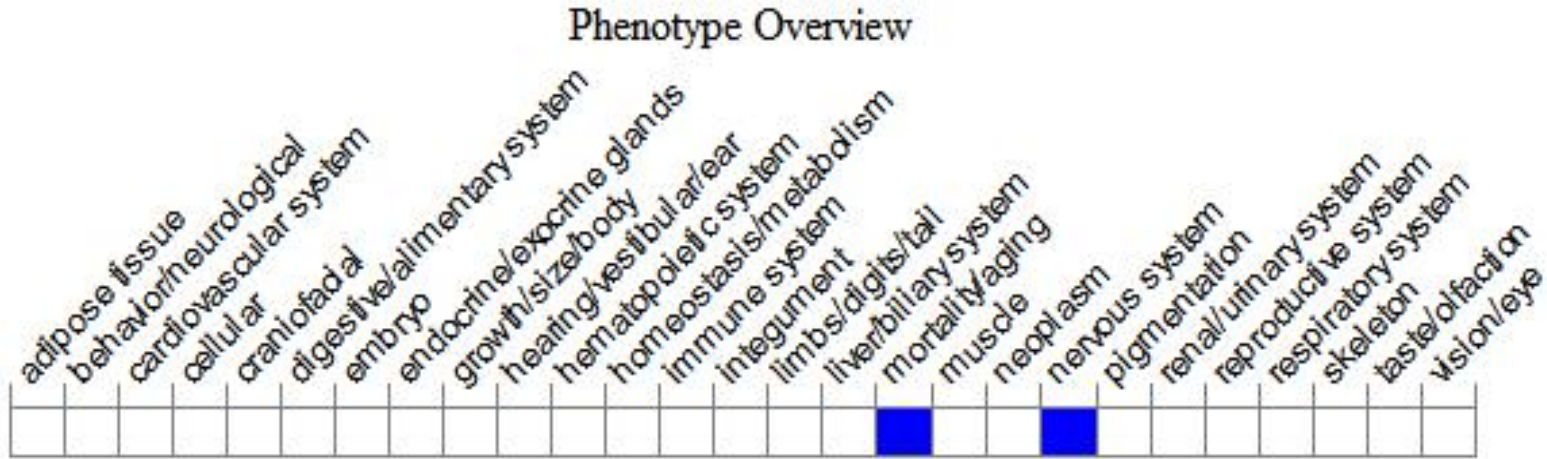
Genomic location distribution



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/>).

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

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