

Poli Cas9-CKO Strategy

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Project Overview

Project Name

Poli

Project type

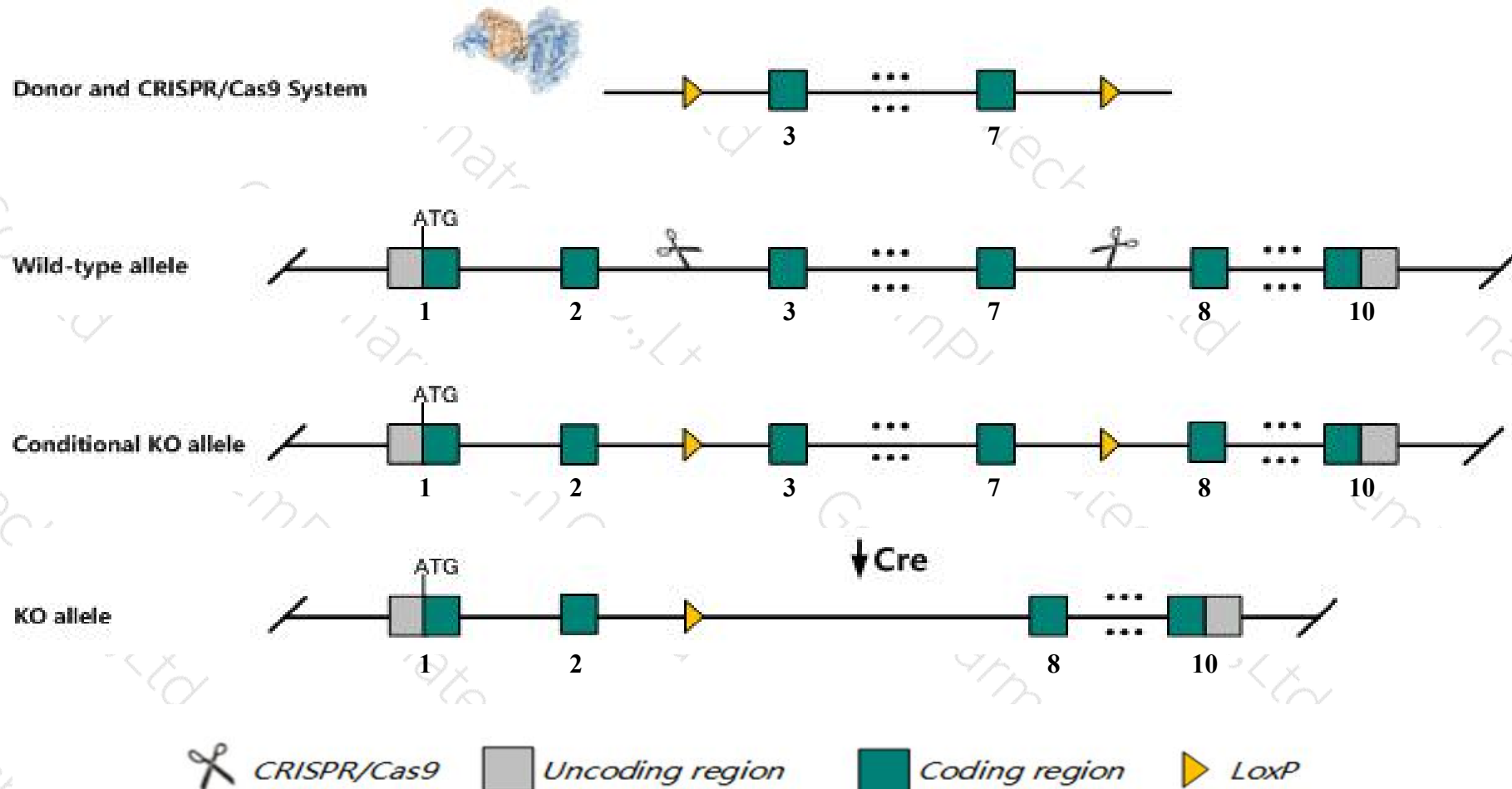
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Poli* gene has 6 transcripts. According to the structure of *Poli* gene, exon3-exon7 of *Poli*-202 (ENSMUST00000121674.8) transcript is recommended as the knockout region. The region contains 826bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Poli* 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.

- According to the existing MGI data, Mice homozygous for a spontaneous mutation show normal somatic hypermutation of immunoglobulin variable genes and no significant increase in UV-induced epithelial skin tumor formation relative to controls; in contrast, formation of mesenchymal tumors by chronic UV irradiation is enhanced.
- The effect on transcript *Poli-206* is unknown.
- The *Poli* gene is located on the Chr18. 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)

Poli polymerase (DNA directed), iota [*Mus musculus* (house mouse)]

Gene ID: 26447, updated on 12-Aug-2019

Summary

- Official Symbol** Poli provided by [MGI](#)
- Official Full Name** polymerase (DNA directed), iota provided by [MGI](#)
- Primary source** [MGI:MGI:1347081](#)
- See related** [Ensembl:ENSMUSG00000038425](#)
- 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** Rad30b
- Expression** Ubiquitous expression in testis adult (RPKM 4.0), CNS E18 (RPKM 2.2) and 26 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 18 44.48 cM; 18 E2

See Poli in [Genome Data Viewer](#)

Exon count: 11

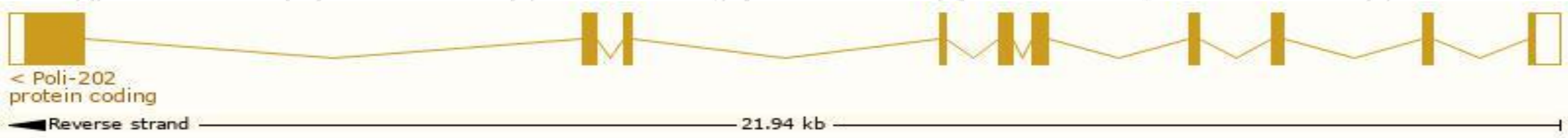
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (70508680..70534950, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (70668334..70689975, complement)

Transcript information (Ensembl)

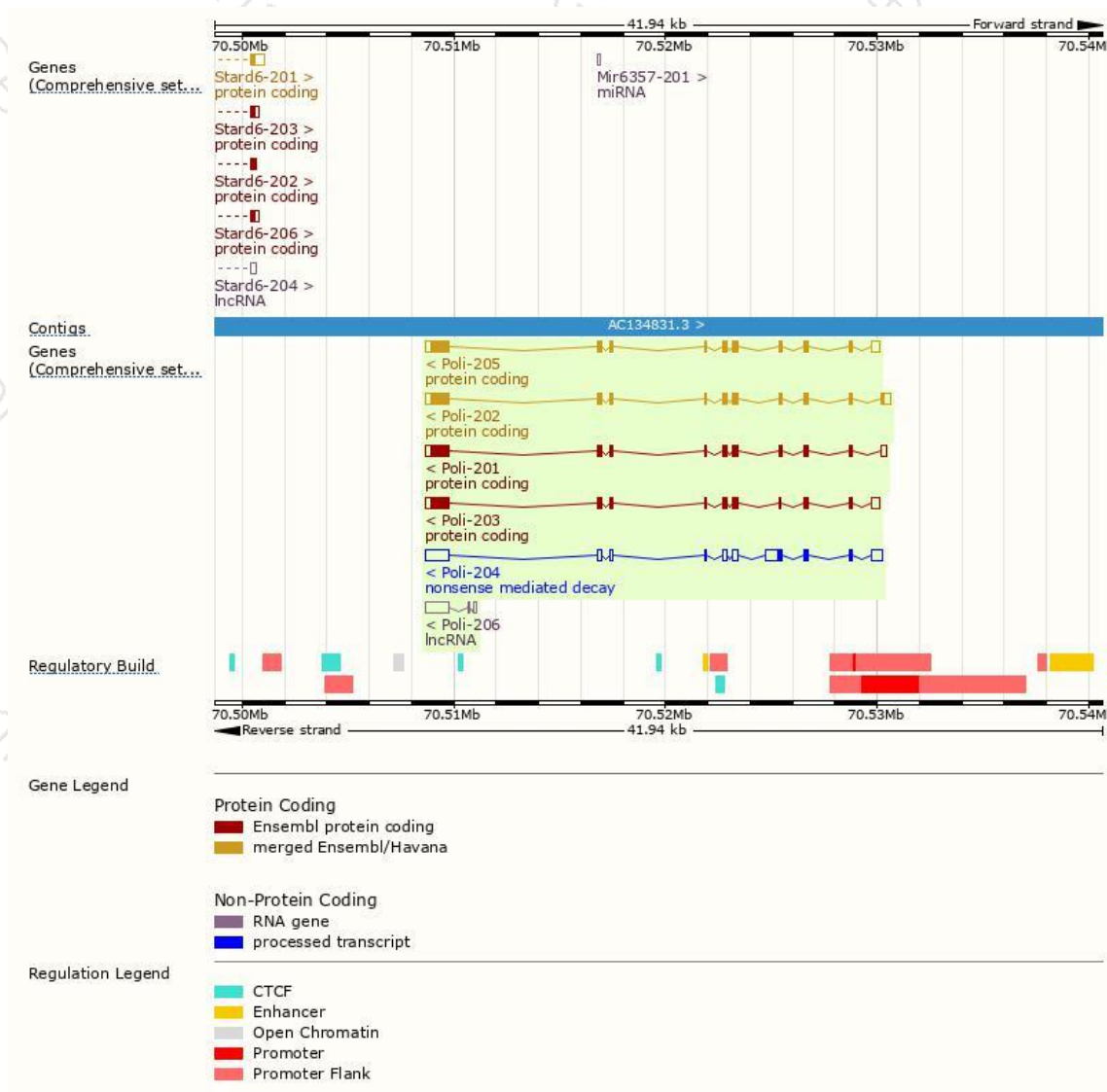
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Poli-202	ENSMUST00000121674.8	2778	737aa	Protein coding	CCDS29334	E9QJU6	TSL:1 GENCODE basic APPRIS P1
Poli-205	ENSMUST00000161542.7	2736	674aa	Protein coding	CCDS50317	A0A0R4J1Z5	TSL:1 GENCODE basic
Poli-203	ENSMUST00000159389.7	2662	651aa	Protein coding	CCDS79660	E9Q3H9	TSL:1 GENCODE basic
Poli-201	ENSMUST00000043286.14	2591	674aa	Protein coding	CCDS50317	A0A0R4J1Z5	TSL:1 GENCODE basic
Poli-204	ENSMUST00000160713.1	3504	135aa	Nonsense mediated decay	-	E0CZD6	TSL:1
Poli-206	ENSMUST00000235127.1	1229	No protein	lncRNA	-	-	

The strategy is based on the design of *Poli-202* transcript,The transcription is shown below



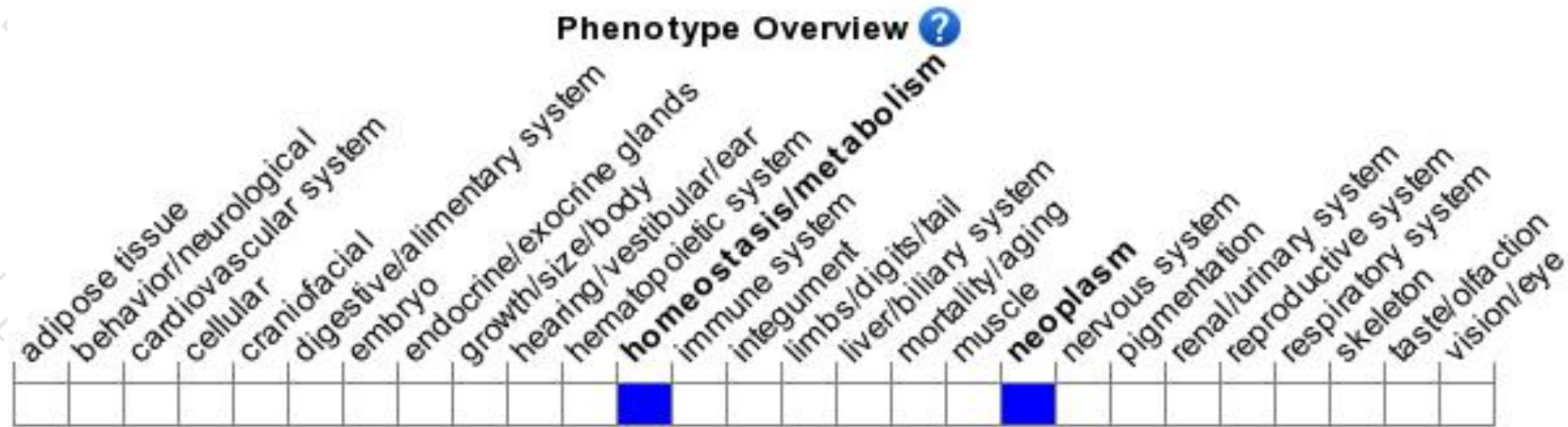
Genomic location distribution



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

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