

***Pus10* Cas9-CKO Strategy**

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Design Date: 2020-5-14

Project Overview

Project Name

Pus10

Project type

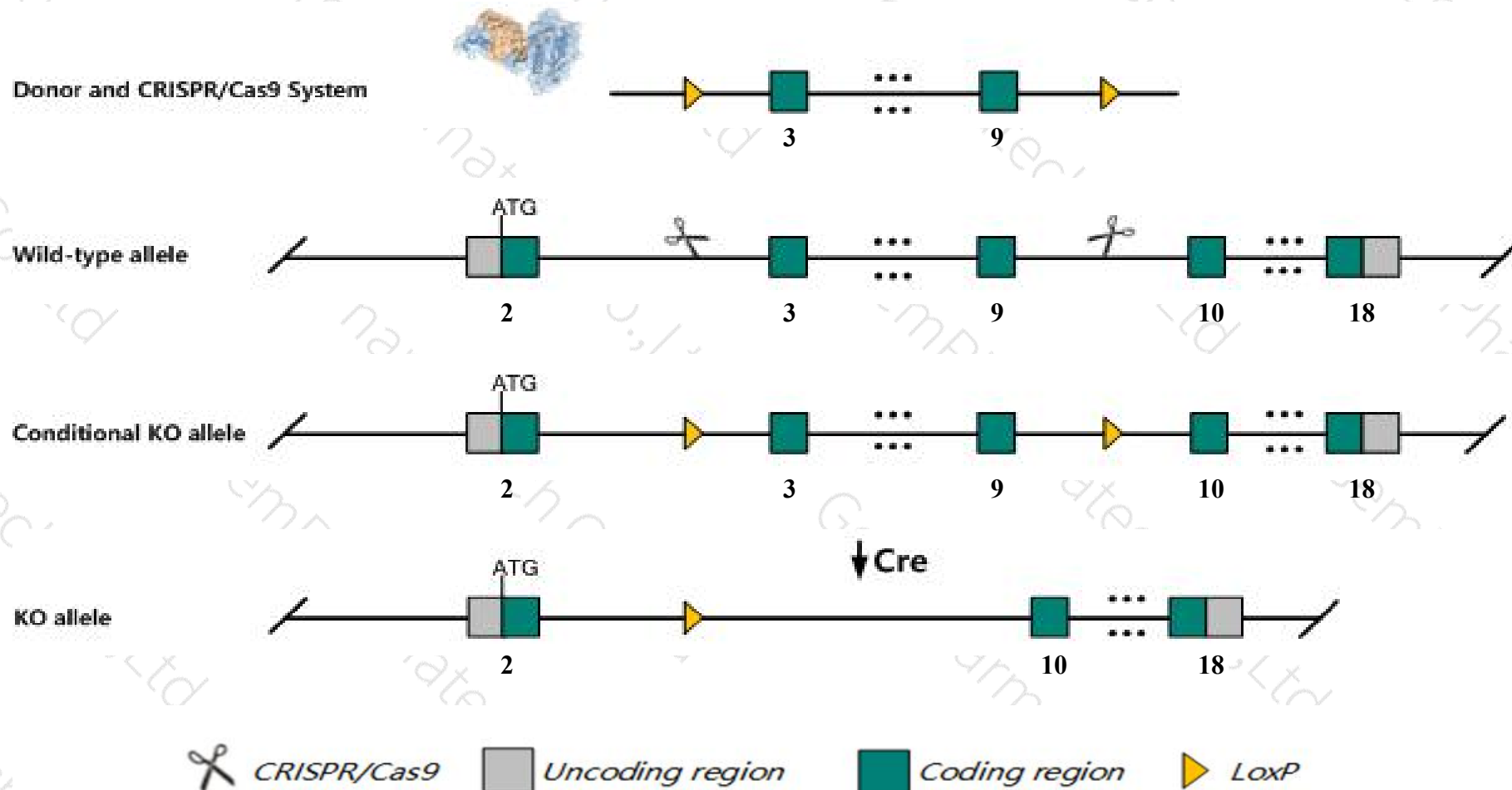
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pus10* gene. The schematic diagram is as follows:



Technical routes

- The *Pus10* gene has 7 transcripts. According to the structure of *Pus10* gene, exon3-exon9 of *Pus10*-202 (ENSMUST00000058163.10) transcript is recommended as the knockout region. The region contains 656bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pus10* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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.

Notice

- The *Pus10* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Pus10 pseudouridylate synthase 10 [Mus musculus (house mouse)]

Gene ID: 74467, updated on 13-Mar-2020

Summary



Official Symbol Pus10 provided by [MGI](#)

Official Full Name pseudouridylate synthase 10 provided by [MGI](#)

Primary source [MGI:MGI:1921717](#)

See related [Ensembl:ENSMUSG00000020280](#)

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 2810013G11Rik, 4933435A13Rik, AU014648, C77560, Ccdc139

Expression Ubiquitous expression in CNS E11.5 (RPKM 5.9), placenta adult (RPKM 5.2) and 26 other tissues [See more](#)

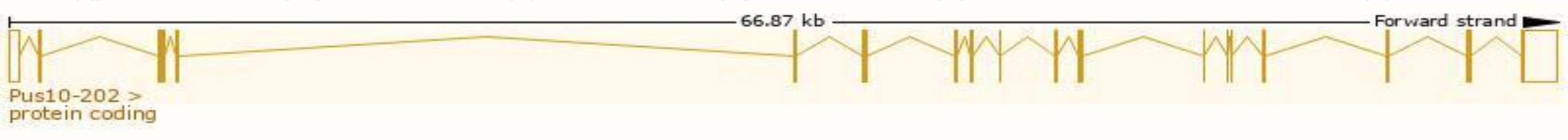
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

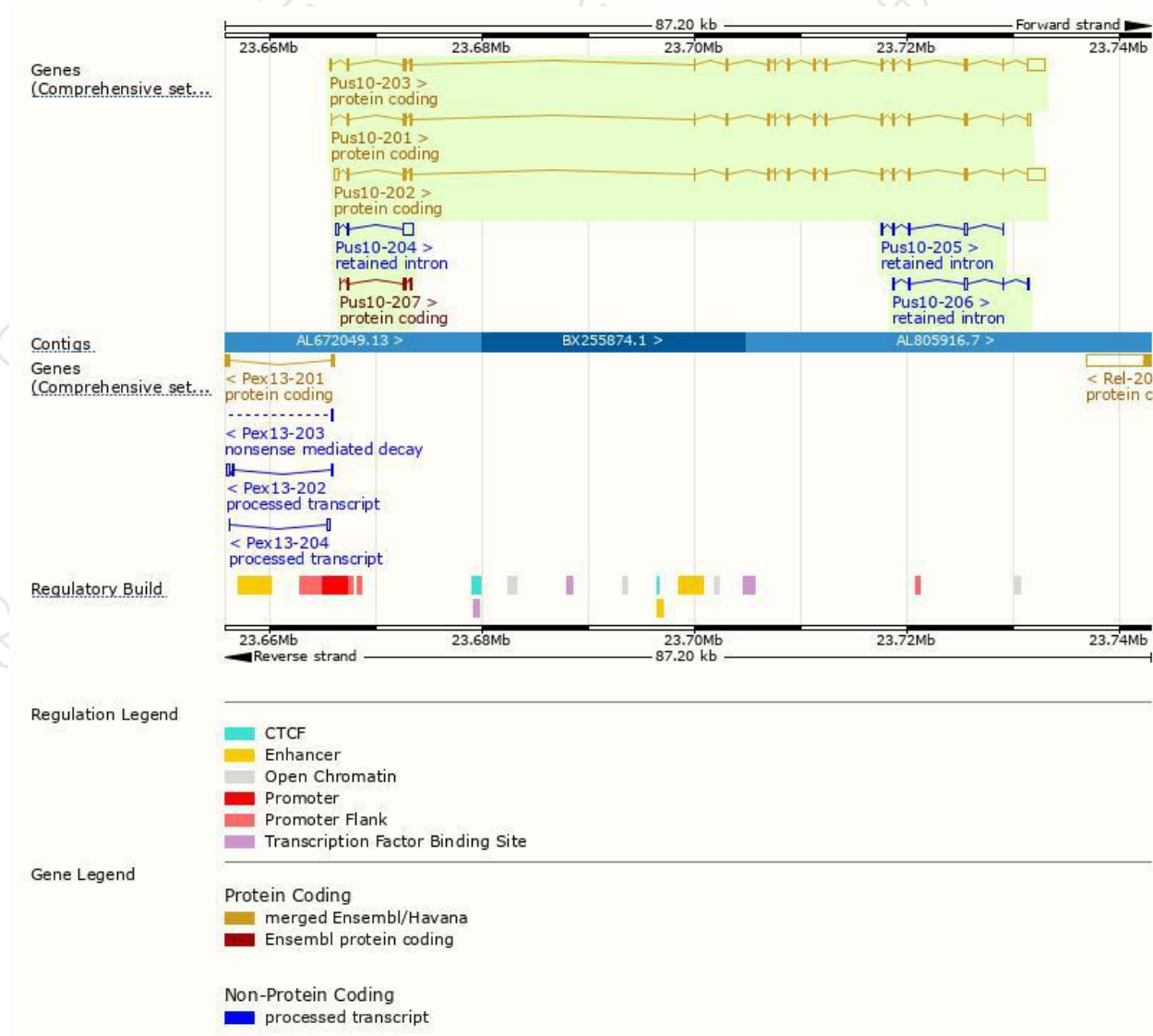
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pus10-202	ENSMUST00000058163.10	3559	527aa	Protein coding	CCDS24479	Q9D3U0	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
Pus10-203	ENSMUST00000109525.7	3177	527aa	Protein coding	CCDS24479	Q9D3U0	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
Pus10-201	ENSMUST00000020520.10	1813	527aa	Protein coding	CCDS24479	Q9D3U0	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
Pus10-207	ENSMUST00000143117.1	469	139aa	Protein coding	-	B0QZU5	CDS 3' incomplete TSL:3
Pus10-204	ENSMUST00000136365.1	1281	No protein	Retained intron	-	-	TSL:1
Pus10-205	ENSMUST00000139646.7	628	No protein	Retained intron	-	-	TSL:3
Pus10-206	ENSMUST00000142287.1	592	No protein	Retained intron	-	-	TSL:2

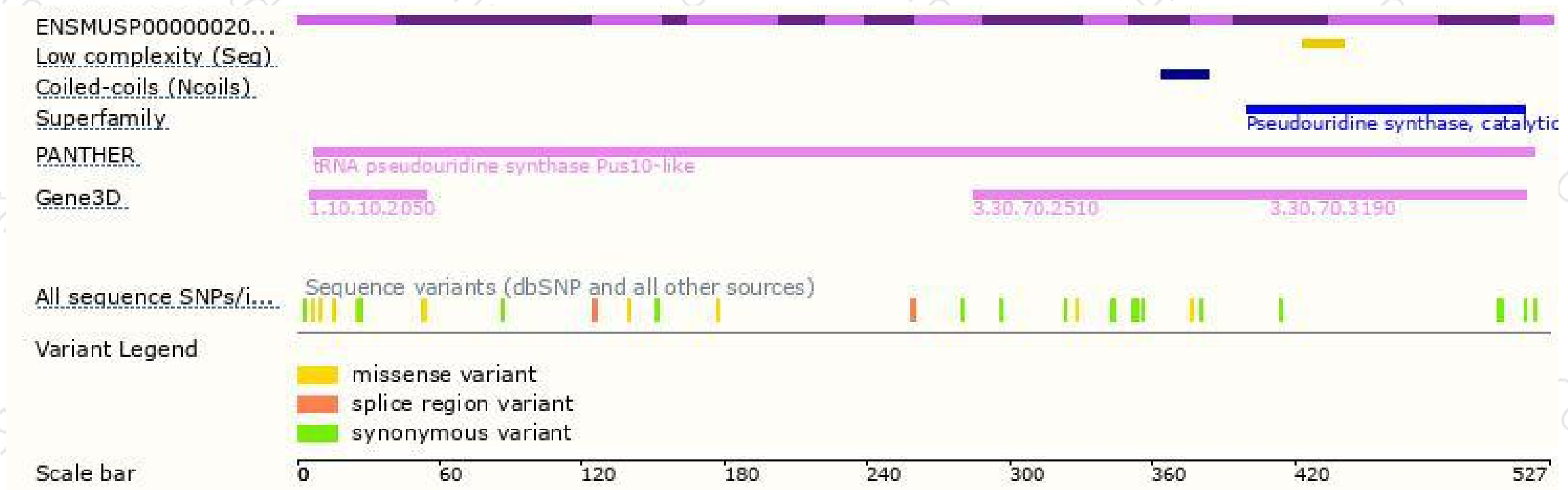
The strategy is based on the design of *Pus10-202* transcript,the transcription is shown below:



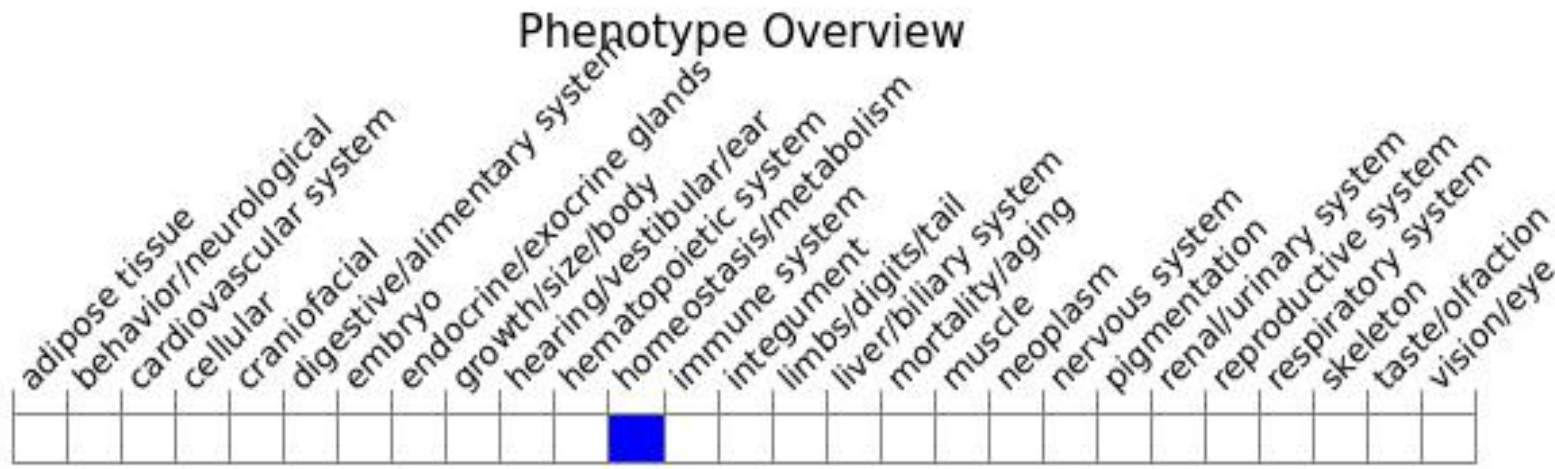
Genomic location distribution



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/>).

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

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