

Prdm5 Cas9-CKO Strategy

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Project Overview

Project Name

Prdm5

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

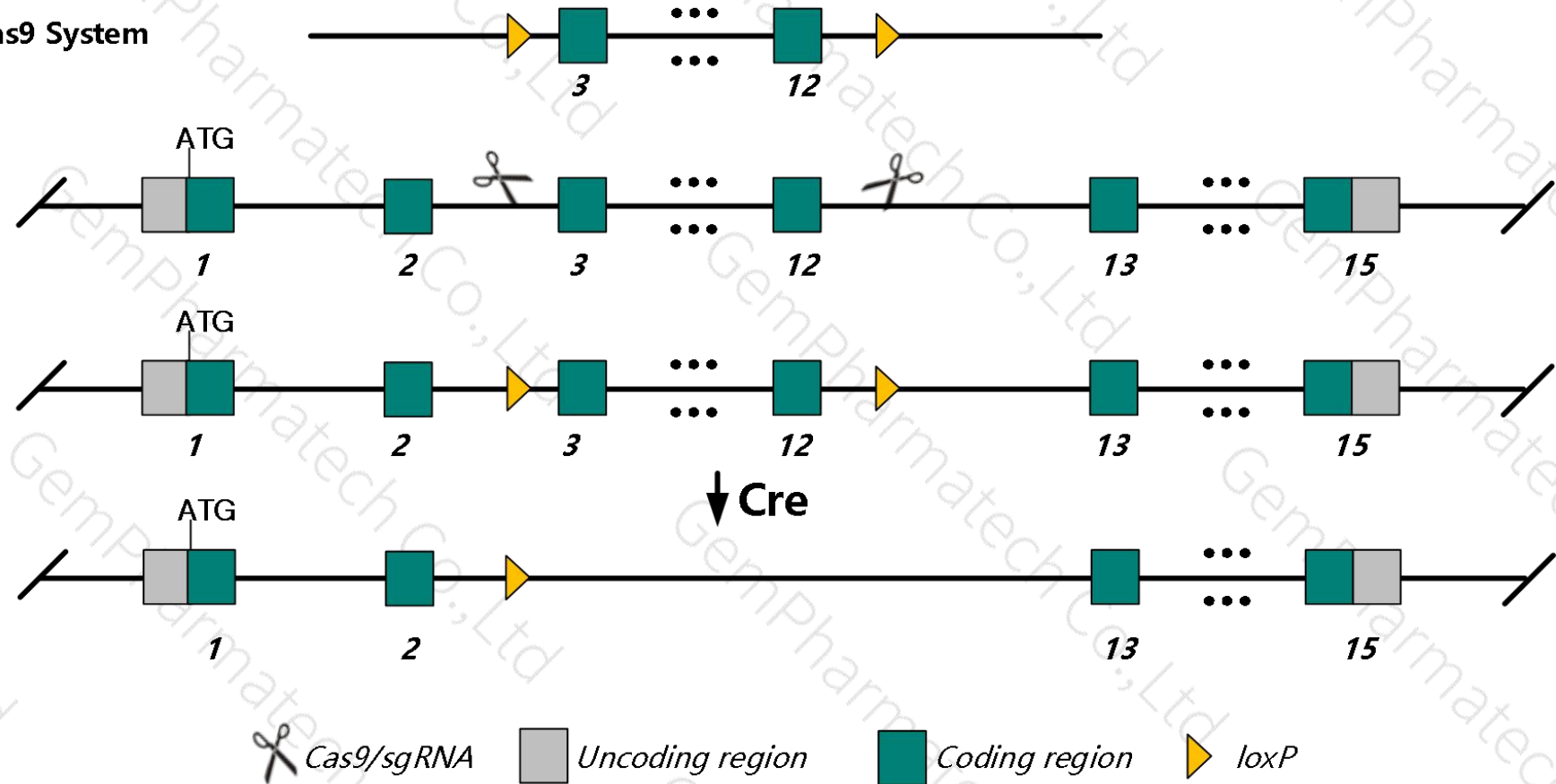
This model will use CRISPR/Cas9 technology to edit the *Prdm5* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Floxed allele

KO allele



- The *Prdm5* gene has 7 transcripts. According to the structure of *Prdm5* gene, exon3-exon12 of *Prdm5*-202 (ENSMUST00000031976.13) transcript is recommended as the knockout region. The region contains 1267bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prdm5* 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 hypomorphic allele display delayed bone ossification with reduced collagen fibril formation, total bone area, bone mineral content and bone mineral density.
- The flox region contain the Gm20445 and Gm23543 gene, which may delete it after Cre.
- The *Prdm5* gene is located on the Chr6. 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)

Prdm5 PR domain containing 5 [*Mus musculus* (house mouse)]

Gene ID: 70779, updated on 13-Mar-2020

Summary

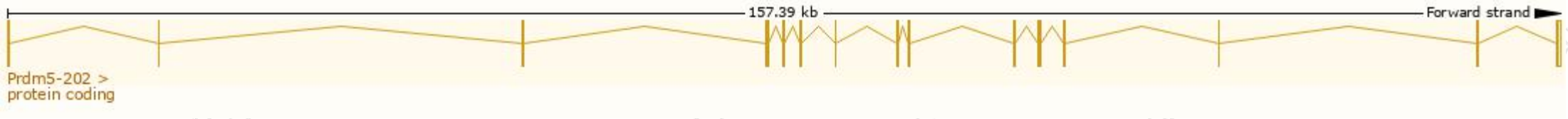
Official Symbol	Prdm5 provided by MGI
Official Full Name	PR domain containing 5 provided by MGI
Primary source	MGI:MGI:1918029
See related	Ensembl:ENSMUSG00000029913
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PFM2; AI197291; 4432417F03Rik; 6530401I24Rik; E130112L17Rik
Expression	Broad expression in limb E14.5 (RPKM 2.9), CNS E11.5 (RPKM 1.9) and 20 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

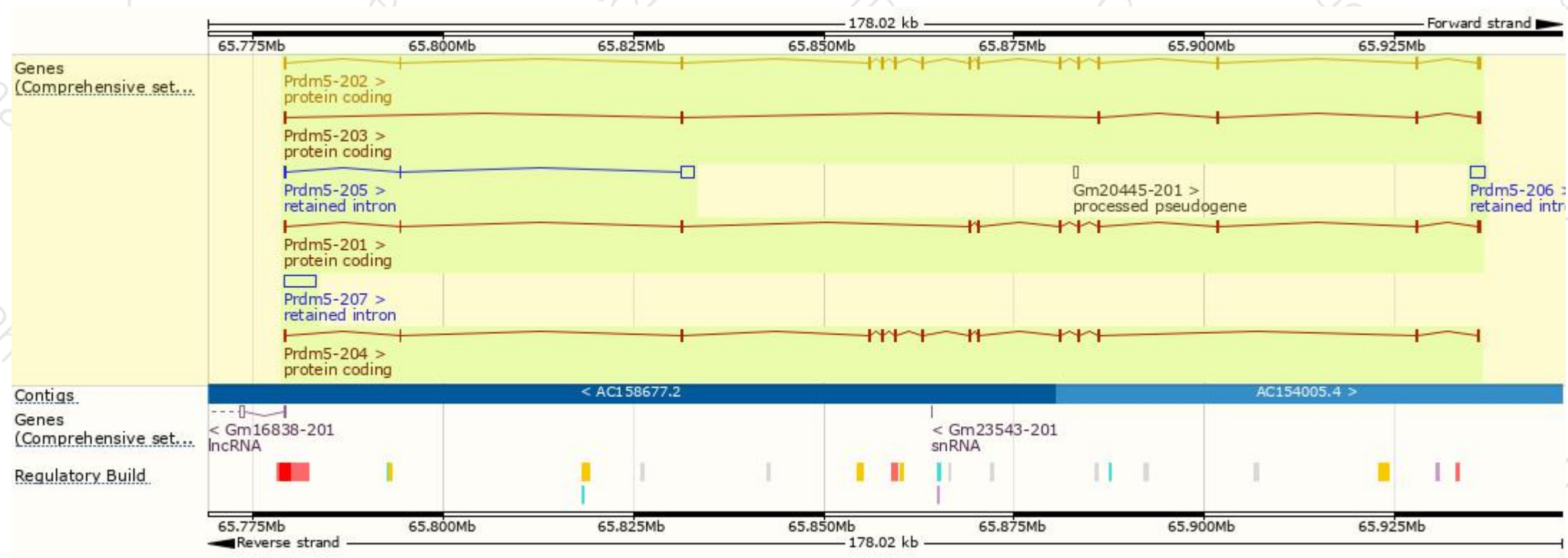
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prdm5-202	ENSMUST000000031976.13	2155	599aa	Protein coding	CCDS20208	Q9CXEQ	TSL:1 GENCODE basic APPRIS P1
Prdm5-201	ENSMUST000000031973.12	1488	415aa	Protein coding	CCDS85059	E9Q707	TSL:1 GENCODE basic
Prdm5-204	ENSMUST00000172638.1	1714	501aa	Protein coding	-	G3UWU3	TSL:5 GENCODE basic
Prdm5-203	ENSMUST000000081219.13	984	221aa	Protein coding	-	Q9D1T8	TSL:1 GENCODE basic
Prdm5-207	ENSMUST00000205168.1	4168	No protein	Retained intron	-	-	TSL:NA
Prdm5-205	ENSMUST00000173538.1	1938	No protein	Retained intron	-	-	TSL:1
Prdm5-206	ENSMUST00000205155.1	1920	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Prdm5-202* transcript,The transcription is shown below



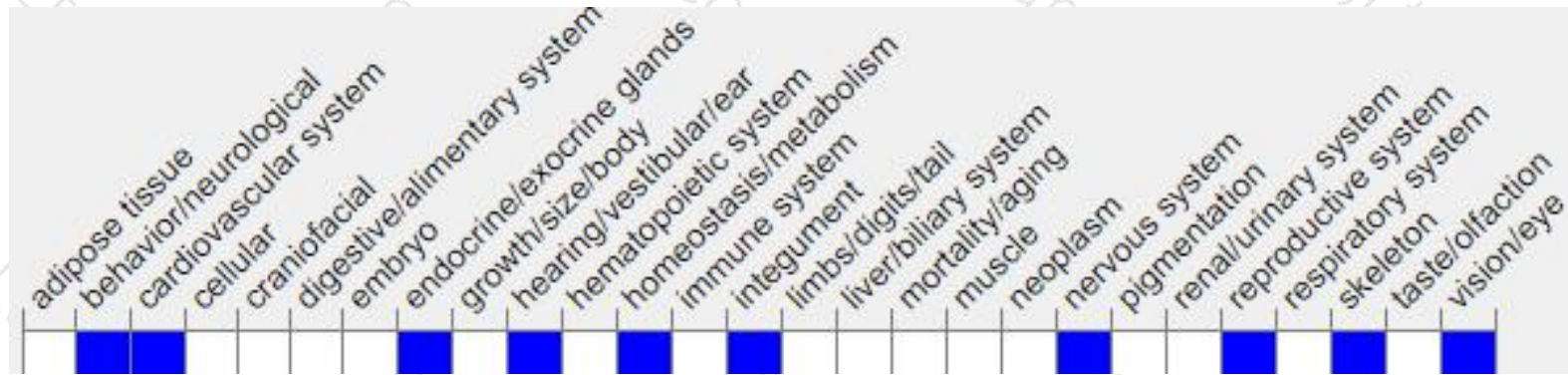
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a hypomorphic allele display delayed bone ossification with reduced collagen fibril formation, total bone area, bone mineral content and bone mineral density.

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

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