Prdm4 Cas9-CKO Strategy

Designer:Xueting Zhang
Reviewer：Yanhua Shen
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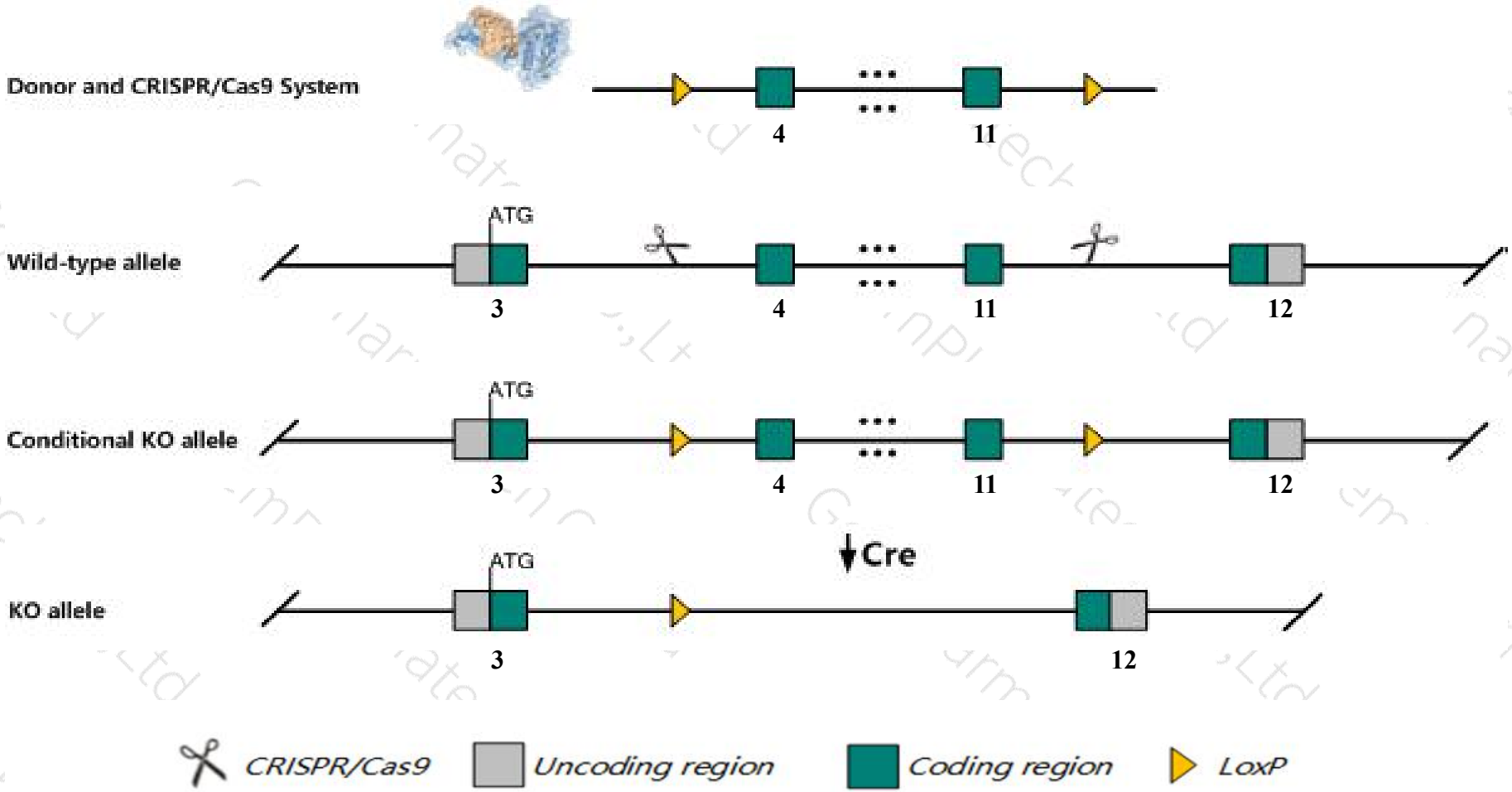
Project Overview

Project Name	***Prdm4***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prdm4* gene. The schematic diagram is as follows:



Technical routes

- The *Prdm4* gene has 7 transcripts. According to the structure of *Prdm4* gene, exon4-exon11 of *Prdm4-207* (ENSMUST00000220032.1) transcript is recommended as the knockout region.The region contains 1969bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Prdm4* 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.

Notice

- According to the existing MGI data,Mice homozygous for alleles lacking the zinc finger domain or PR/SET domain exhibit no abnormal phenotype.
- The effect on transcript *Prdm4*-204 is unknown.
- The *Prdm4* gene is located on the Chr10. 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）

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Prdm4 PR domain containing 4 [*Mus musculus* (house mouse)]

Gene ID: 72843, updated on 12-Aug-2019

Summary

Official Symbol	Prdm4 provided by MGI
Official Full Name	PR domain containing 4 provided by MGI
Primary source	MGI:MGI:1920093
See related	Ensembl:ENSMUSG00000035529
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SC1; SC-1; AW552272; 1700031E19Rik; 2810470D21Rik
Summary	This gene encodes a member of the PR/SET family of zinc finger proteins. This protein has been shown to bind DNA in a sequence-specific manner and has been implicated in neural stem cell proliferation and differentiation. Pseudogenes have been identified on chromosomes 14 and X. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2014]
Expression	Ubiquitous expression in testis adult (RPKM 15.6), whole brain E14.5 (RPKM 14.9) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 10; 10 C1

See Prdm4 in Genome Data Viewer

Exon count: 14

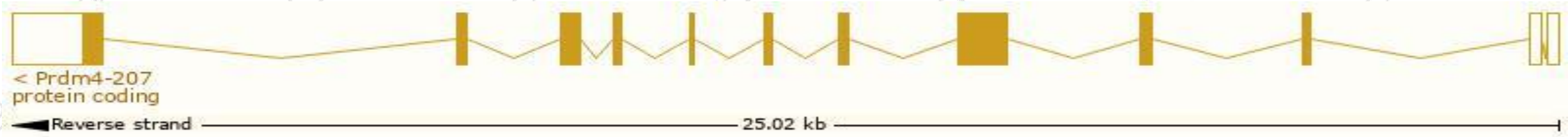
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (85891964..85917152, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (85354711..85379690, complement)

Transcript information（Ensembl）

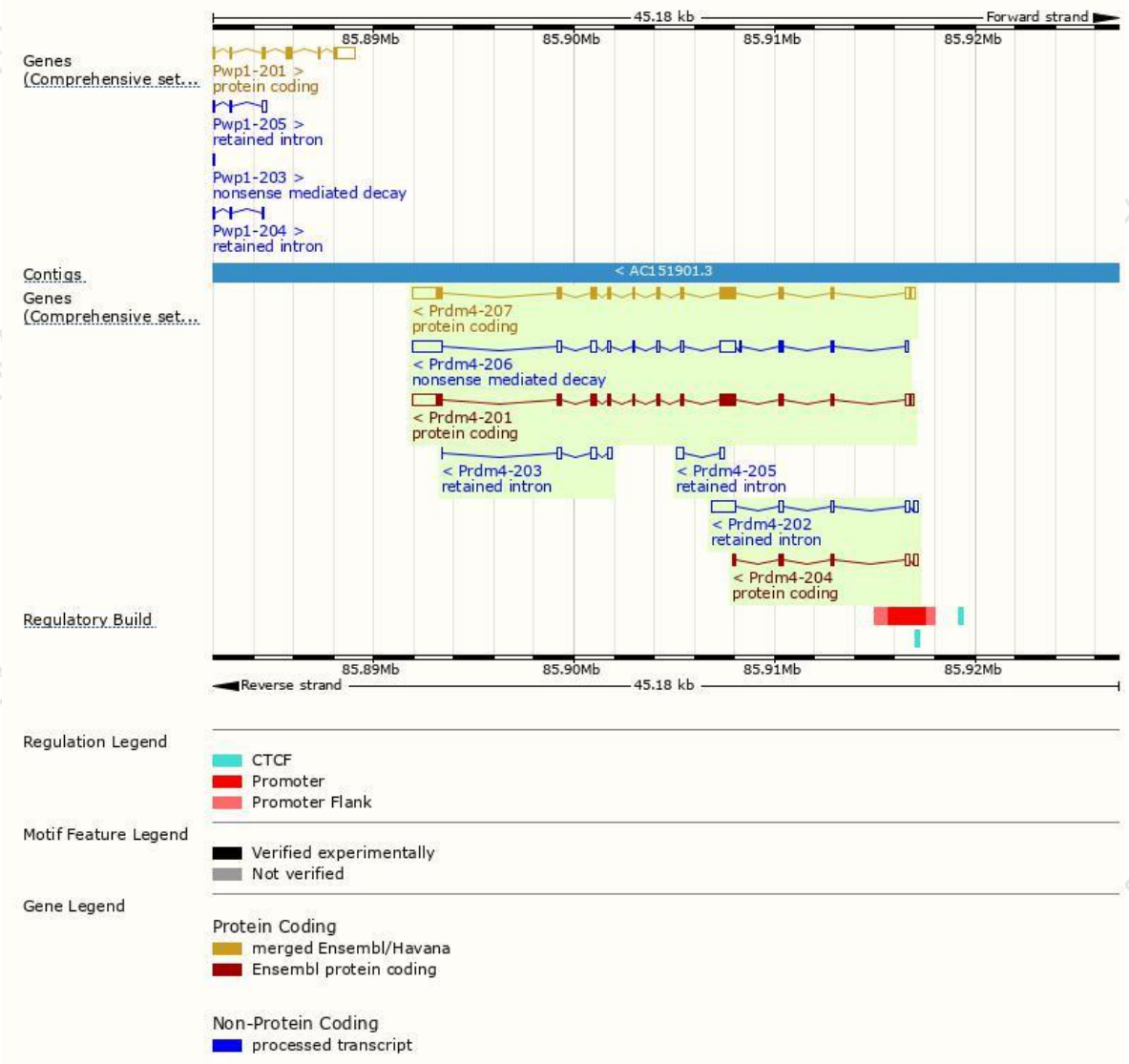
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prdm4-207	ENSMUST00000220032.1	3962	803aa	Protein coding	CCDS24093	Q80V63	TSL:5 GENCODE basic APPRIS P2
Prdm4-201	ENSMUST00000037646.8	3877	796aa	Protein coding	-	A0A1X7SB67	TSL:1 GENCODE basic APPRIS ALT2
Prdm4-204	ENSMUST00000218969.1	831	153aa	Protein coding	-	A0A1W2P7C2	CDS 3' incomplete TSL:2
Prdm4-206	ENSMUST00000219370.1	3772	120aa	Nonsense mediated decay	-	A0A1W2P779	TSL:1
Prdm4-202	ENSMUST00000218289.1	1918	No protein	Retained intron	-	-	TSL:2
Prdm4-203	ENSMUST00000218743.1	729	No protein	Retained intron	-	-	TSL:2
Prdm4-205	ENSMUST00000219112.1	592	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Prdm4-207* transcript,The transcription is shown below

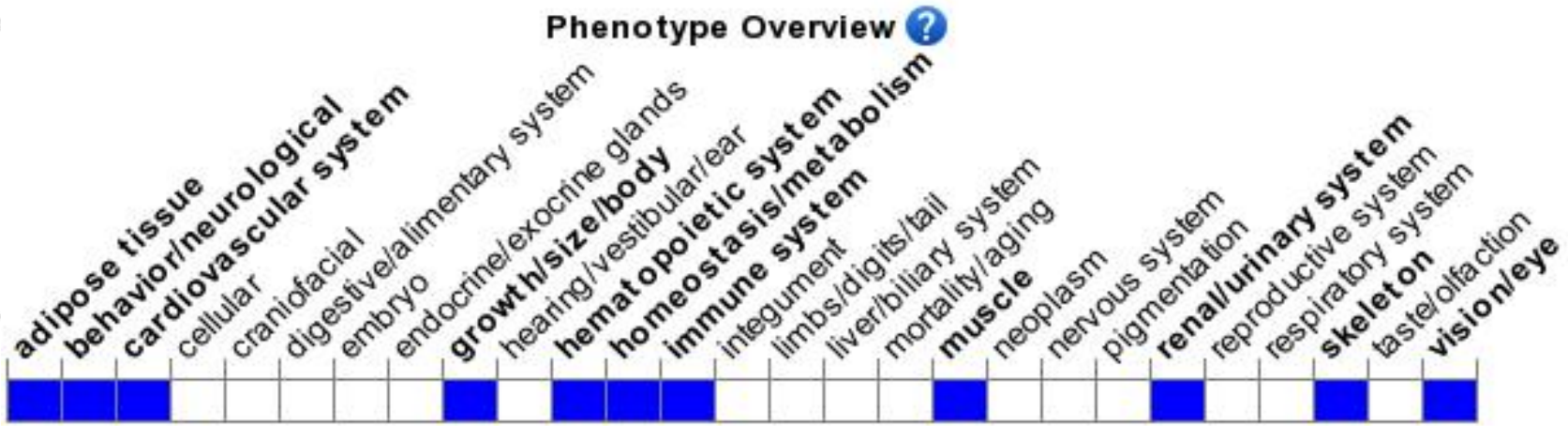


Genomic location distribution



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 alleles lacking the zinc finger domain or PR/SET domain exhibit no abnormal phenotype.

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GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd