

Pard3b Cas9-CKO Strategy

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Project Overview

Project Name

Pard3b

Project type

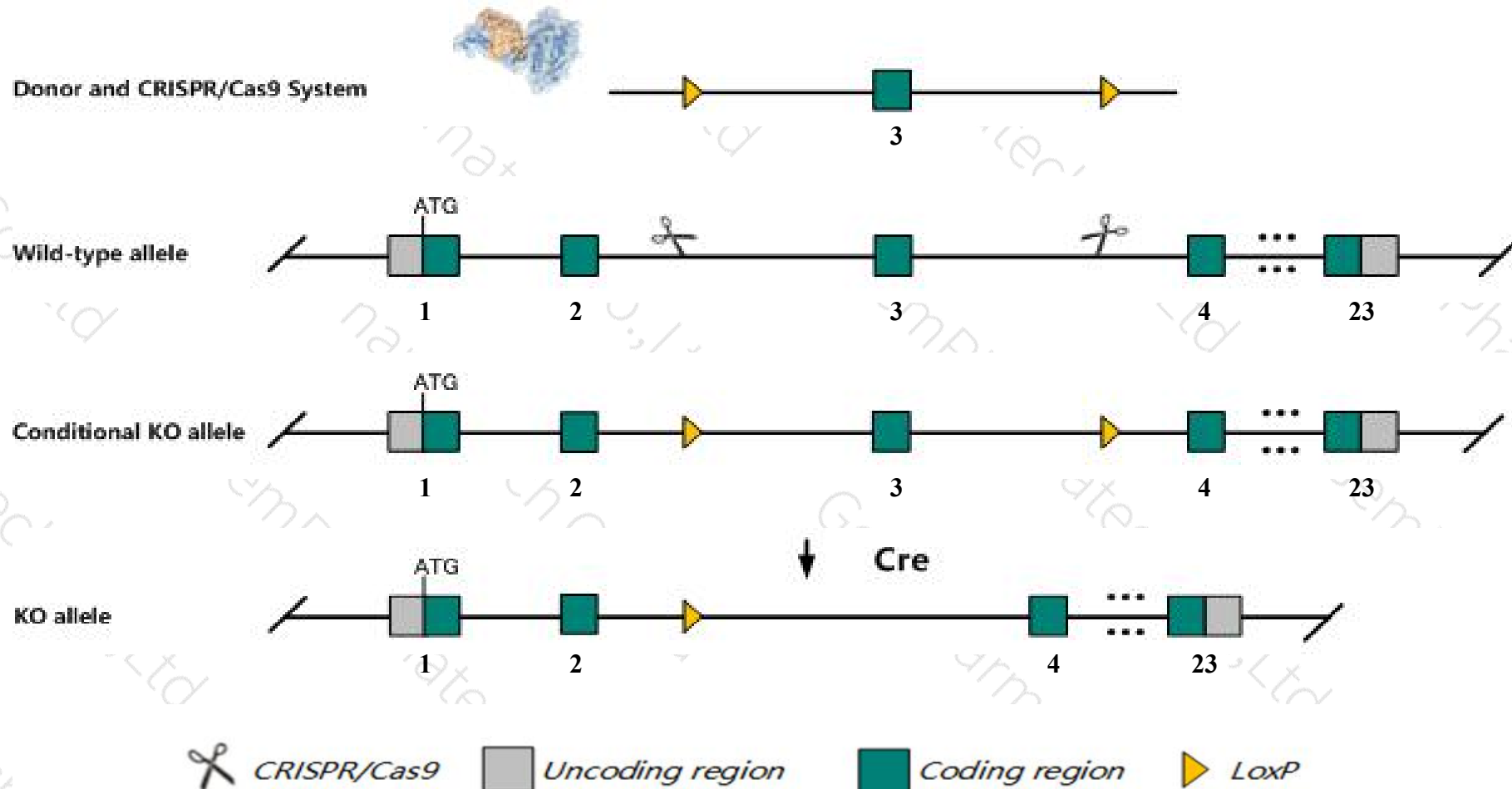
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pard3b* gene. The schematic diagram is as follows:



Technical routes

- The *Pard3b* gene has 6 transcripts. According to the structure of *Pard3b* gene, exon3 of *Pard3b*-202(ENSMUST00000075374.9) transcript is recommended as the knockout region. The region contains 172bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pard3b* 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

- The *Pard3b* gene is located on the Chr1. 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)

Pard3b par-3 family cell polarity regulator beta [Mus musculus (house mouse)]

Gene ID: 72823, updated on 13-Mar-2020

Summary



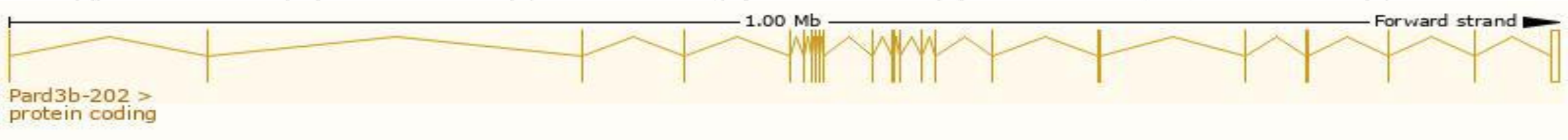
Official Symbol	Pard3b provided by MGI
Official Full Name	par-3 family cell polarity regulator beta provided by MGI
Primary source	MGI:MGI:1919301
See related	Ensembl:ENSMUSG00000052062
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810008K04Rik, 2010002N16Rik, 2810455B10Rik, Als2cr19, PAR3B, PAR3L, PAR3beta
Expression	Ubiquitous expression in bladder adult (RPKM 4.0), colon adult (RPKM 2.1) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

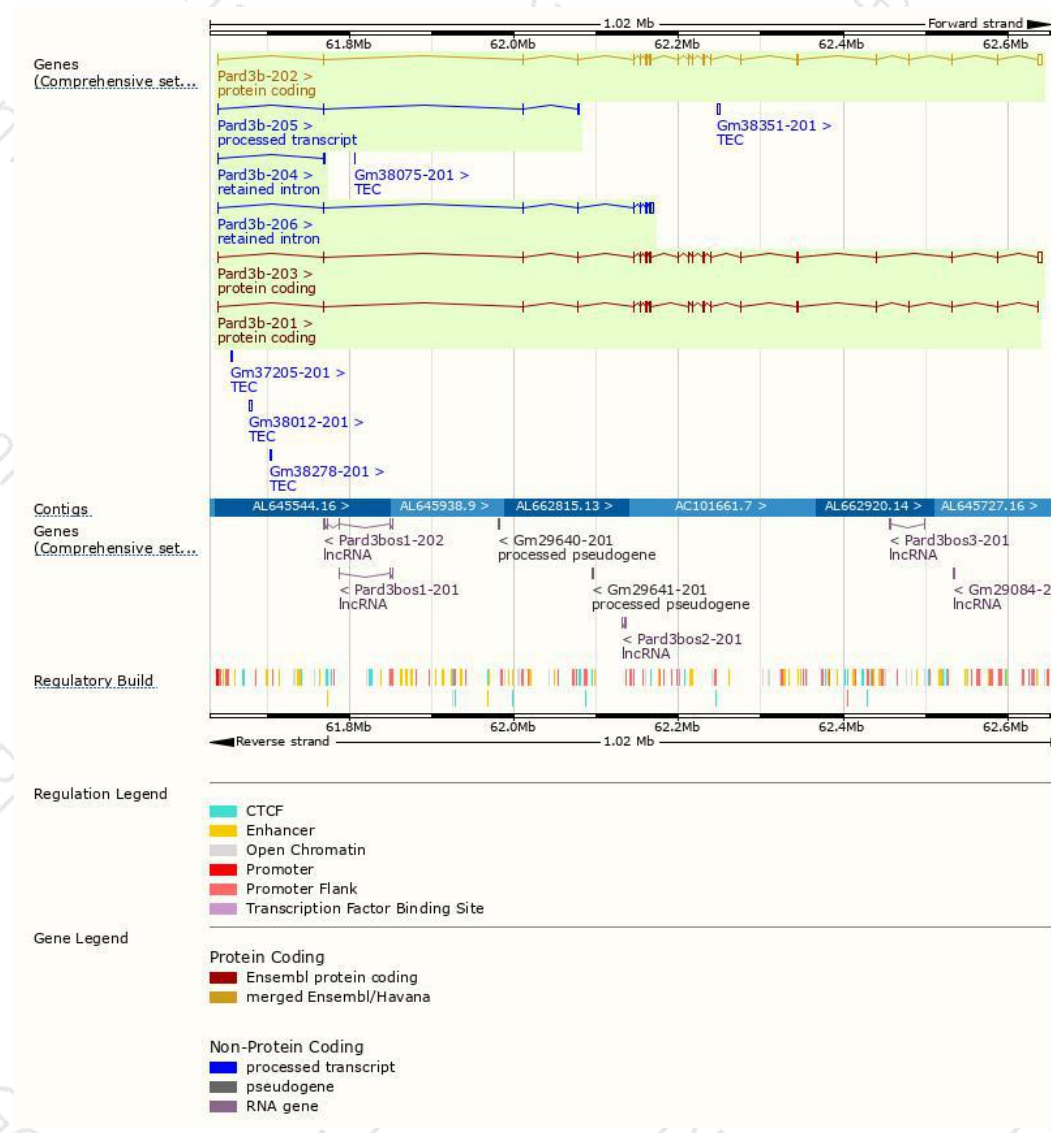
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pard3b-202	ENSMUST00000075374.9	8392	1203aa	Protein coding	CCDS48276	Q9CSB4	TSL:5 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 P2
Pard3b-203	ENSMUST00000094906.3	7676	1104aa	Protein coding	-	Q5SV54	TSL:5 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 ALT2
Pard3b-201	ENSMUST00000046673.10	3426	1141aa	Protein coding	-	Q5SV55	TSL:5 GENCODE basic
Pard3b-205	ENSMUST00000136768.7	1057	No protein	Processed transcript	-	-	TSL:1
Pard3b-206	ENSMUST00000188325.1	4608	No protein	Retained intron	-	-	TSL:1
Pard3b-204	ENSMUST00000129030.1	2400	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Pard3b-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain

ENSMUSP00000074...

PDB-ENSP mappings

MobiDB lite

Low complexity (Seg)

Coiled-coils (Ncoils)

Superfamily

SMART

Pfam

PROSITE profiles

PANTHER

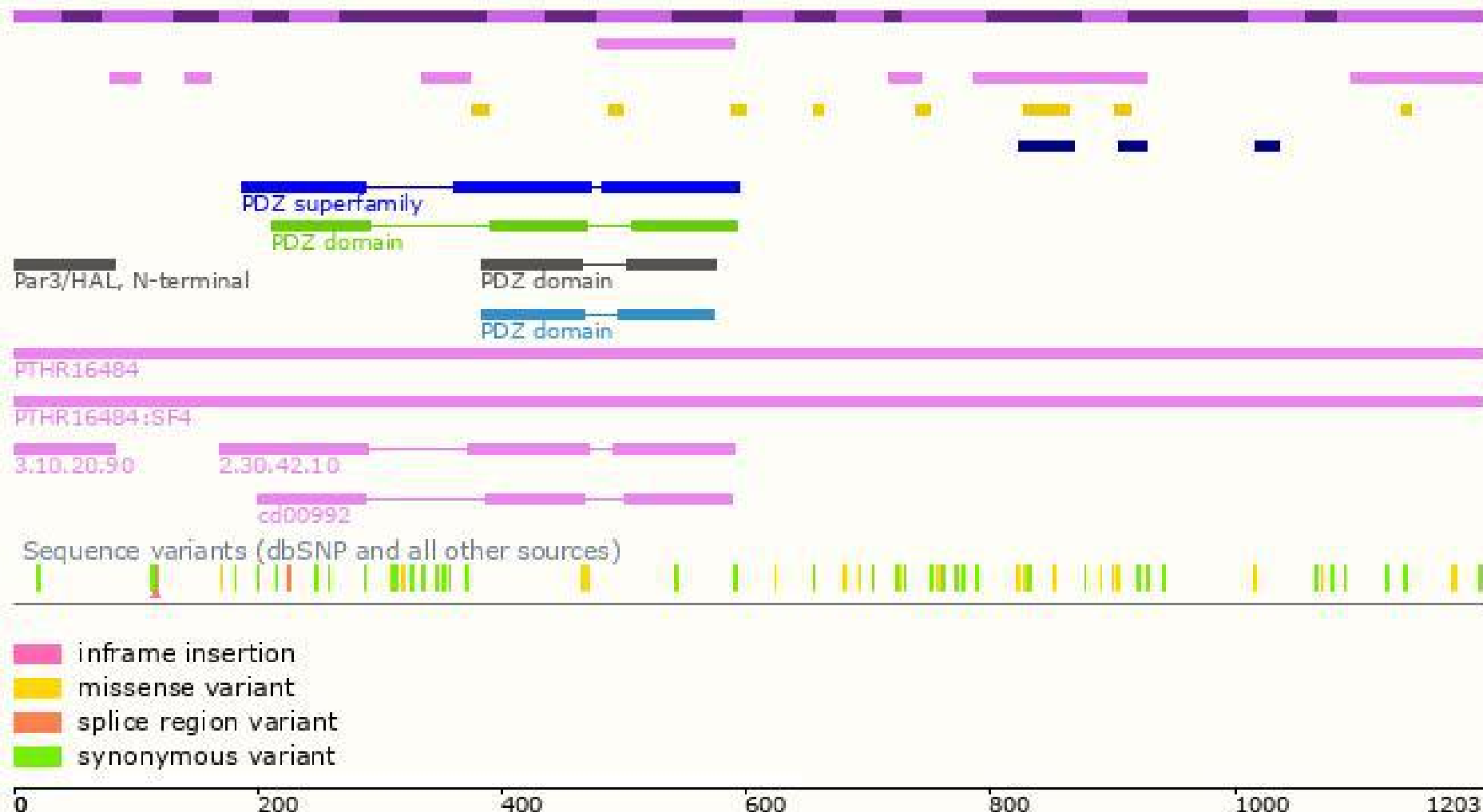
Gene3D

CDD

All sequence SNPs/i....

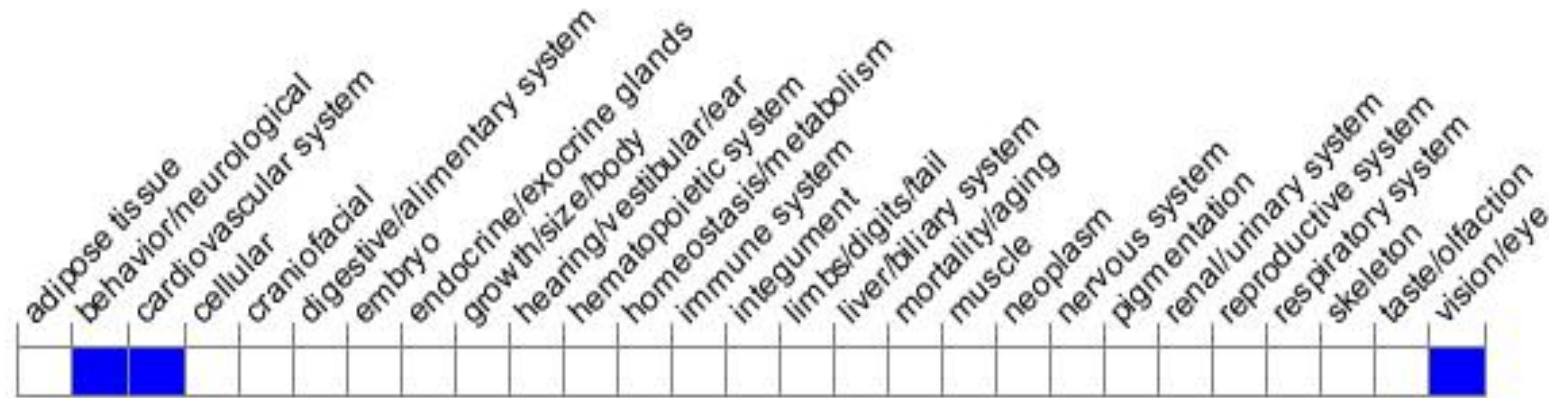
Variant Legend

Scale bar



Mouse phenotype description(MGI)

Phenotype Overview



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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