

Prdx6 Cas9-KO Strategy

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Design Date:	2020-5-12

Project Overview

Project Name

Prdx6

Project type

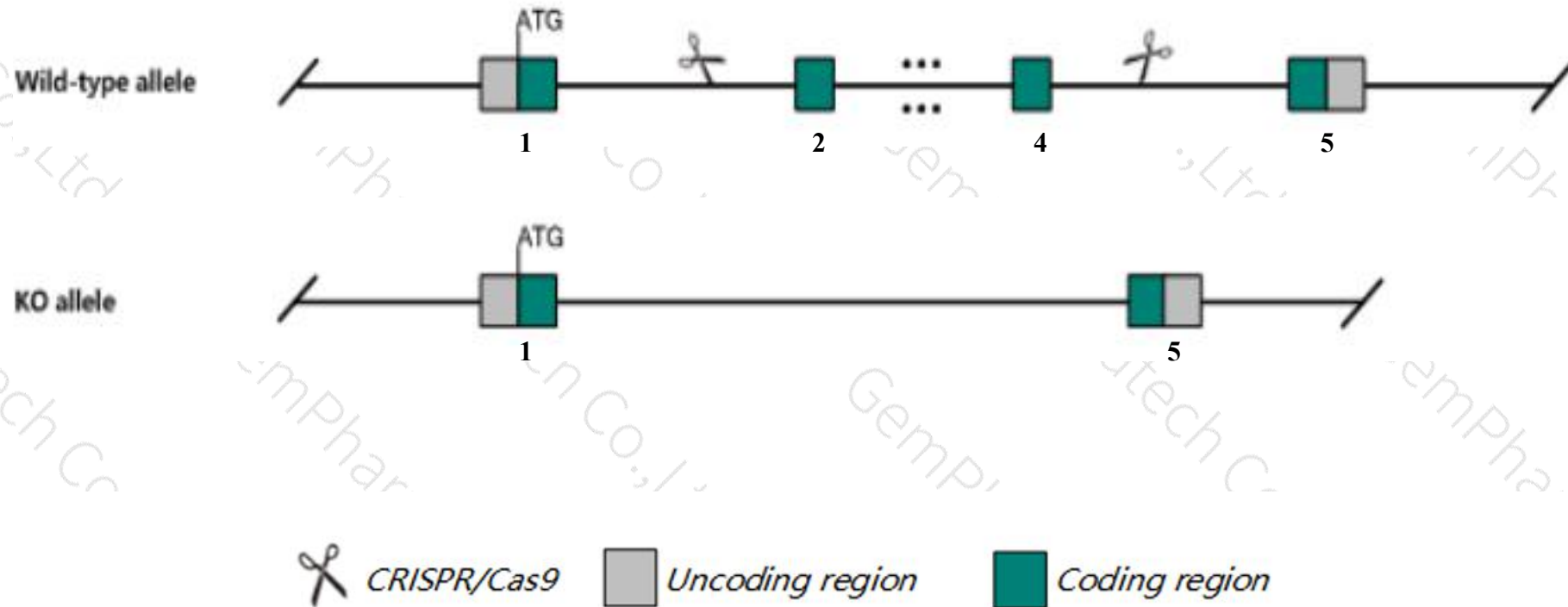
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prdx6* gene. The schematic diagram is as follows:



- The *Prdx6* gene has 9 transcripts. According to the structure of *Prdx6* gene, exon2-exon4 of *Prdx6*-202 (ENSMUST00000071718.11) transcript is recommended as the knockout region. The region contains 451bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prdx6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for disruptions of this gene show no macroscopic or microscopic abnormalities. however, they have an increased susceptibility to oxidative stress.
- The *Prdx6* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Prdx6 peroxiredoxin 6 [Mus musculus (house mouse)]

Gene ID: 11758, updated on 13-Mar-2020

Summary

Official Symbol Prdx6 provided by [MGI](#)

Official Full Name peroxiredoxin 6 provided by [MGI](#)

Primary source [MGI:MGI:894320](#)

See related [Ensembl:ENSMUSG00000026701](#)

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 1-Cys Prx, 1-cysPrx, 9430088D19Rik, AA690119, Aop2, Brp-12, CP-3, GPx, Ltw-4, Ltw4, Ltw-4, NSGPx, ORF06, Prdx5, aiPLA2

Summary This gene encodes a member of the peroxiredoxin family of peroxidases. The encoded protein is a bifunctional enzyme that has glutathione peroxidase and phospholipase activities. This protein is an antioxidant that reduces peroxidized membrane phospholipids and plays an important role in phospholipid homeostasis based on its ability to generate lysophospholipid substrate for the remodeling pathway of phospholipid synthesis. Mice lacking this gene are sensitive to oxidant stress, have altered lung phospholipid metabolism and susceptible to skin tumorigenesis. Alternate splicing of this gene results in multiple transcript variants. A pseudogene of this gene is found on chromosome 4. [provided by RefSeq, Dec 2014]

Expression Ubiquitous expression in colon adult (RPKM 178.6), lung adult (RPKM 85.0) and 27 other tissues [See more](#)

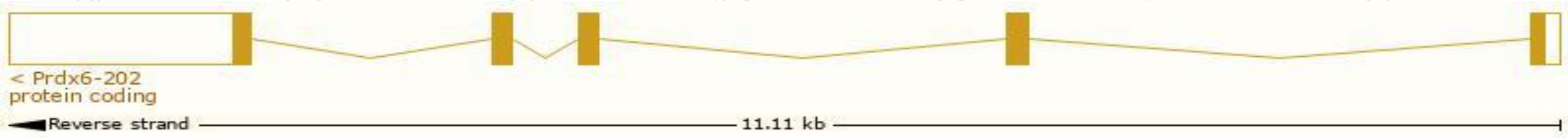
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

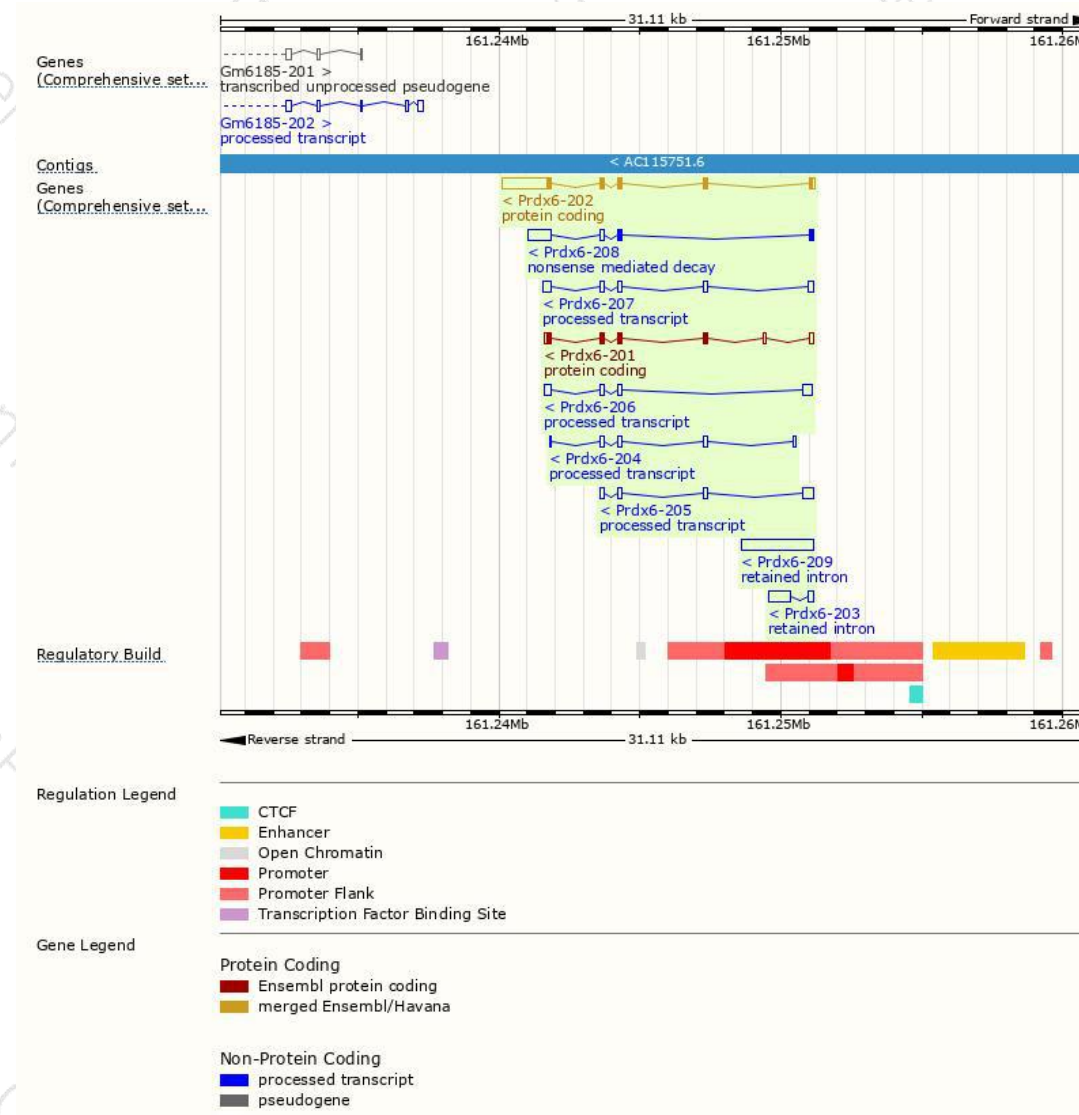
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prdx6-202	ENSMUST00000071718.11	2387	224aa	Protein coding	CCDS15415	Q6GT24	TSL:1 GENCODE basic APPRIS P1
Prdx6-201	ENSMUST000000051925.4	959	200aa	Protein coding	CCDS78724	D3Z0Y2	TSL:2 GENCODE basic
Prdx6-208	ENSMUST00000192639.5	1294	76aa	Nonsense mediated decay	-	A0A0A6YXQ7	TSL:1
Prdx6-207	ENSMUST00000156678.7	913	No protein	Processed transcript	-	-	TSL:2
Prdx6-206	ENSMUST00000156318.7	874	No protein	Processed transcript	-	-	TSL:3
Prdx6-205	ENSMUST00000155135.1	825	No protein	Processed transcript	-	-	TSL:5
Prdx6-204	ENSMUST00000139387.7	603	No protein	Processed transcript	-	-	TSL:3
Prdx6-209	ENSMUST00000194613.1	2558	No protein	Retained intron	-	-	TSL:NA
Prdx6-203	ENSMUST00000130867.1	967	No protein	Retained intron	-	-	TSL:2

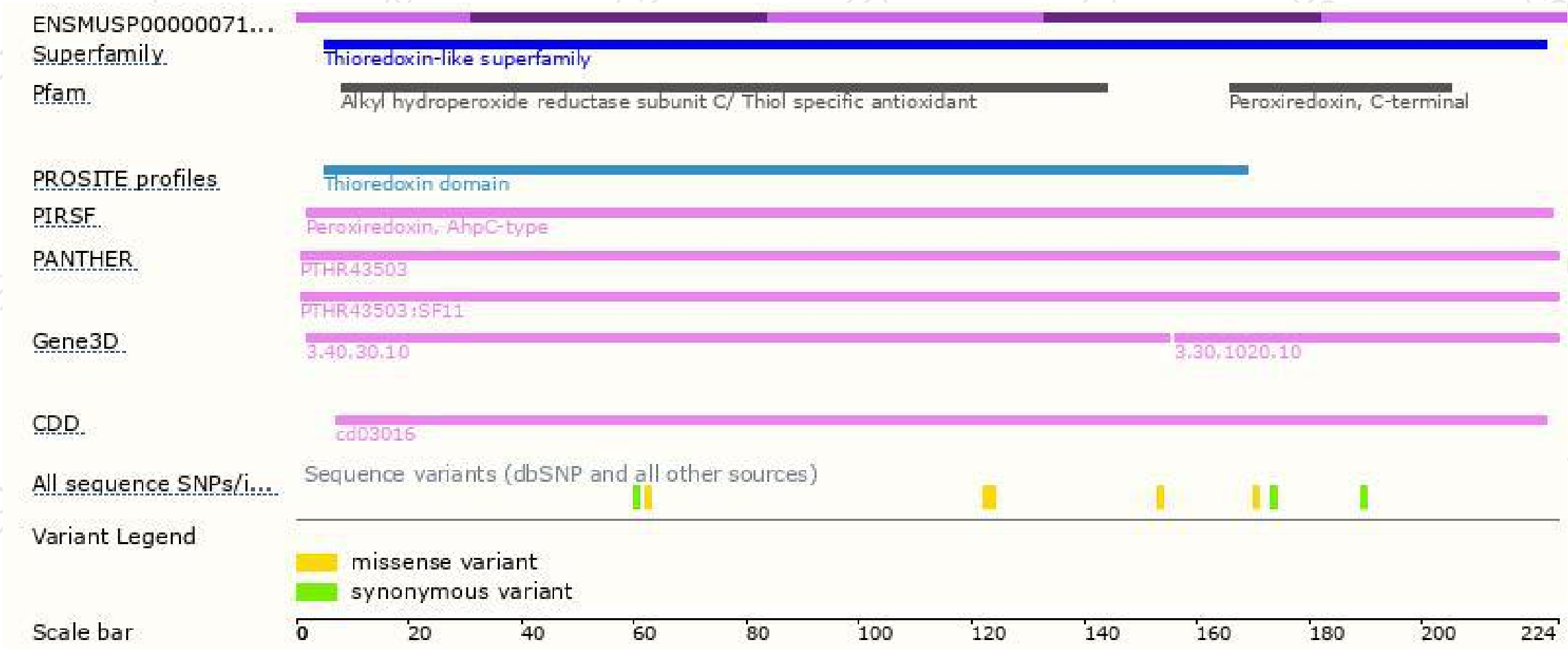
The strategy is based on the design of *Prdx6-202* transcript,the transcription is shown below



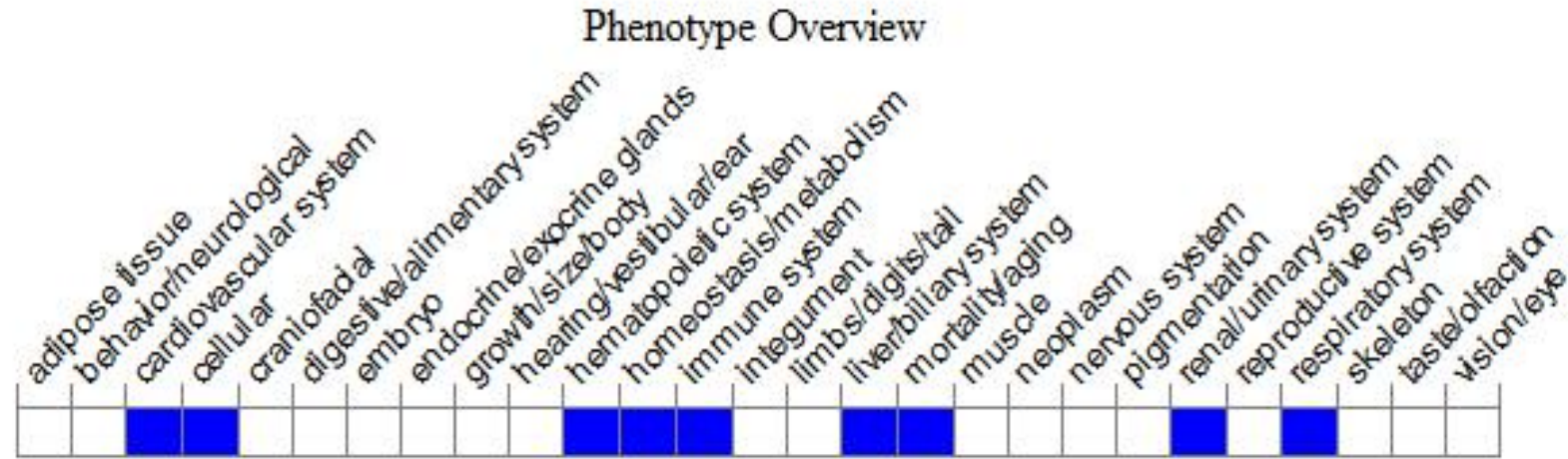
Genomic location distribution



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 disruptions of this gene show no macroscopic or microscopic abnormalities. However, they have an increased susceptibility to oxidative stress.

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

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