Prdx3 Cas9-KO Strategy

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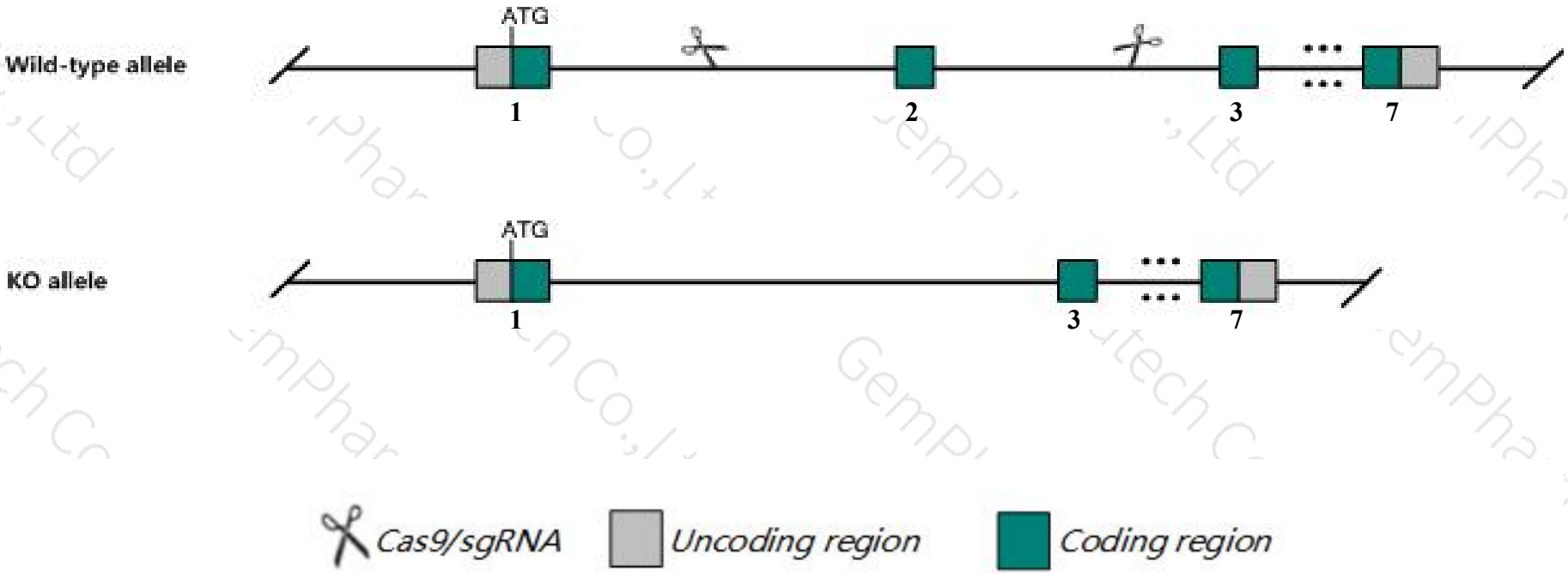
Project Overview

Project Name	***Prdx3***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prdx3* gene. The schematic diagram is as follows:



Technical routes

- The *Prdx3* gene has 1 transcript. According to the structure of *Prdx3* gene, exon2 of *Prdx3-201* (ENSMUST00000025961.6) transcript is recommended as the knockout region.The region contains 136bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Prdx3* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

- According to the existing MGI data,Homozygotes for a null allele show increased fat mass, adipocyte hypertrophy, mitochondrial dysfunction, oxidative stress, adipokine dysregulation and altered lipid and glucose metabolism. Homozygotes for a gene-trap allele show reduced weight and high susceptibility to LPS-induced oxidative stress.

- The *Prdx3* gene is located on the Chr19. 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）

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Prdx3 peroxiredoxin 3 [Mus musculus (house mouse)]

Gene ID: 11757, updated on 31-Jan-2019

Summary

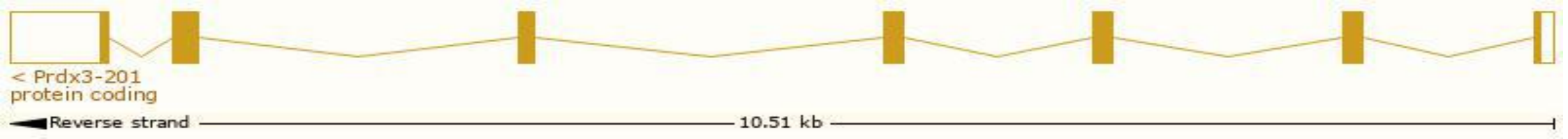
Official Symbol	Prdx3 provided by MGI
Official Full Name	peroxiredoxin 3 provided by MGI
Primary source	MGI:MGI:88034
See related	Ensembl:ENSMUSG00000024997
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW822249, Aop1, D0Tohi1, Ef2l, Mer5, Prx3, SP22, TDXM
Expression	Ubiquitous expression in adrenal adult (RPKM 248.6), heart adult (RPKM 175.6) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

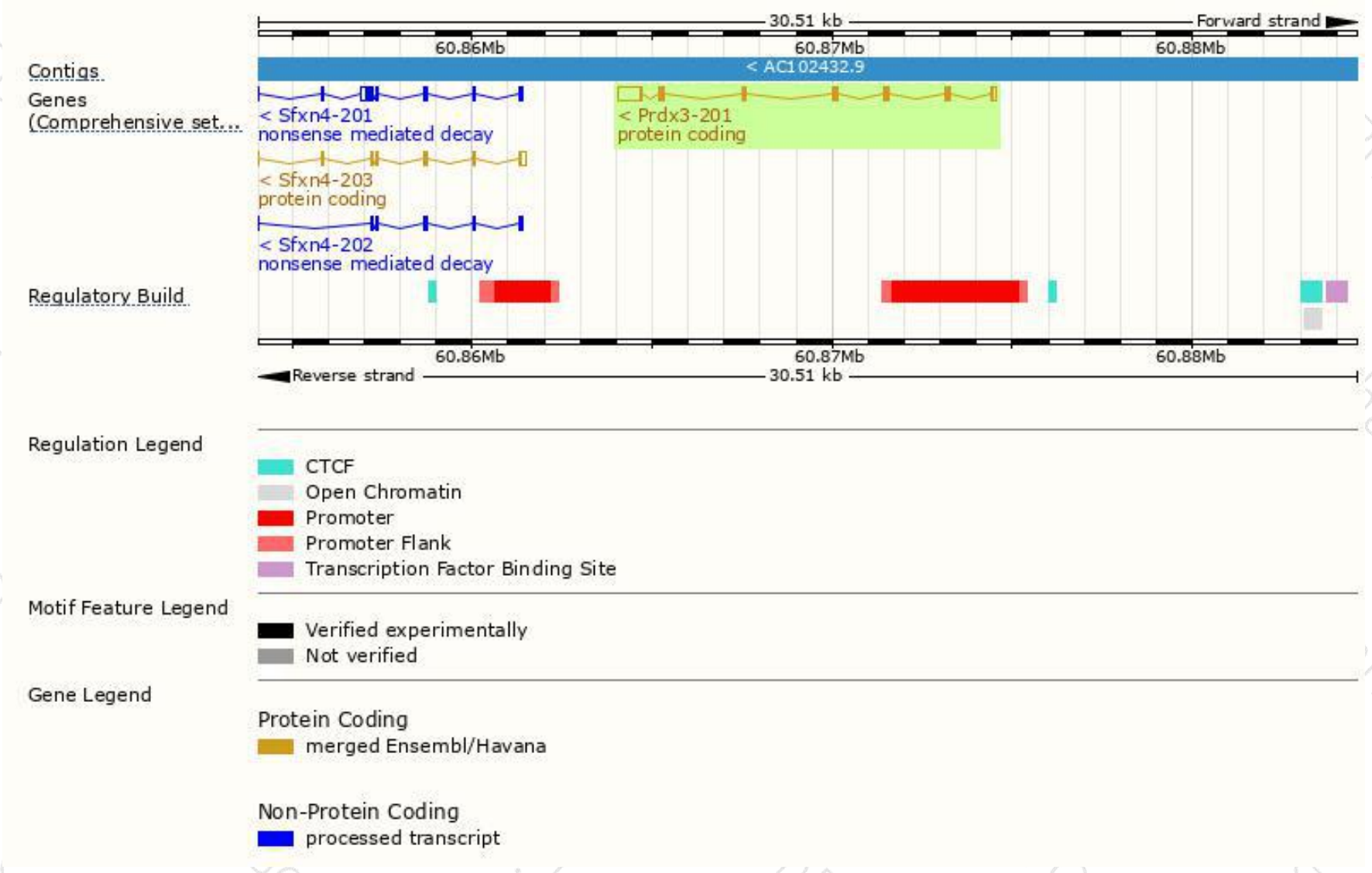
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prdx3-201	ENSMUST00000025961.6	1478	257aa	Protein coding	CCDS29944	P20108	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Prdx3-201* transcript,The transcription is shown below

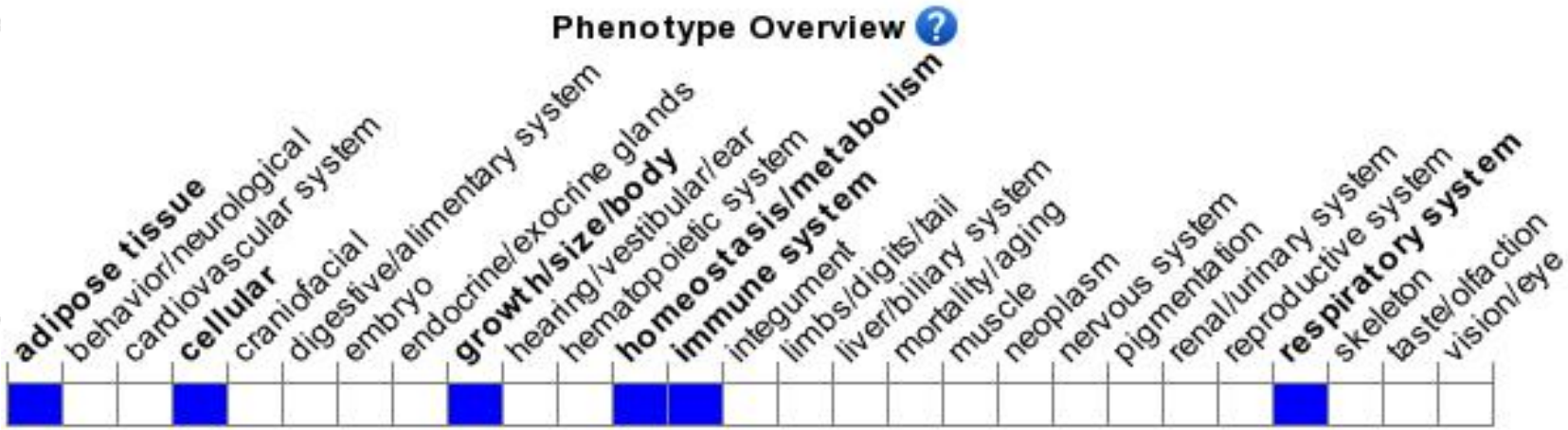


Genomic location distribution



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,Homozygotes for a null allele show increased fat mass, adipocyte hypertrophy, mitochondrial dysfunction, oxidative stress, adipokine dysregulation and altered lipid and glucose metabolism. Homozygotes for a gene-trap allele show reduced weight and high susceptibility to LPS-induced oxidative stress.

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

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