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Xpnpep3 Cas9-CKO Strategy

Designer: Yun Li

Reviewer: Longyun Hu

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Overview

Target Gene Name

- Xpnpep3

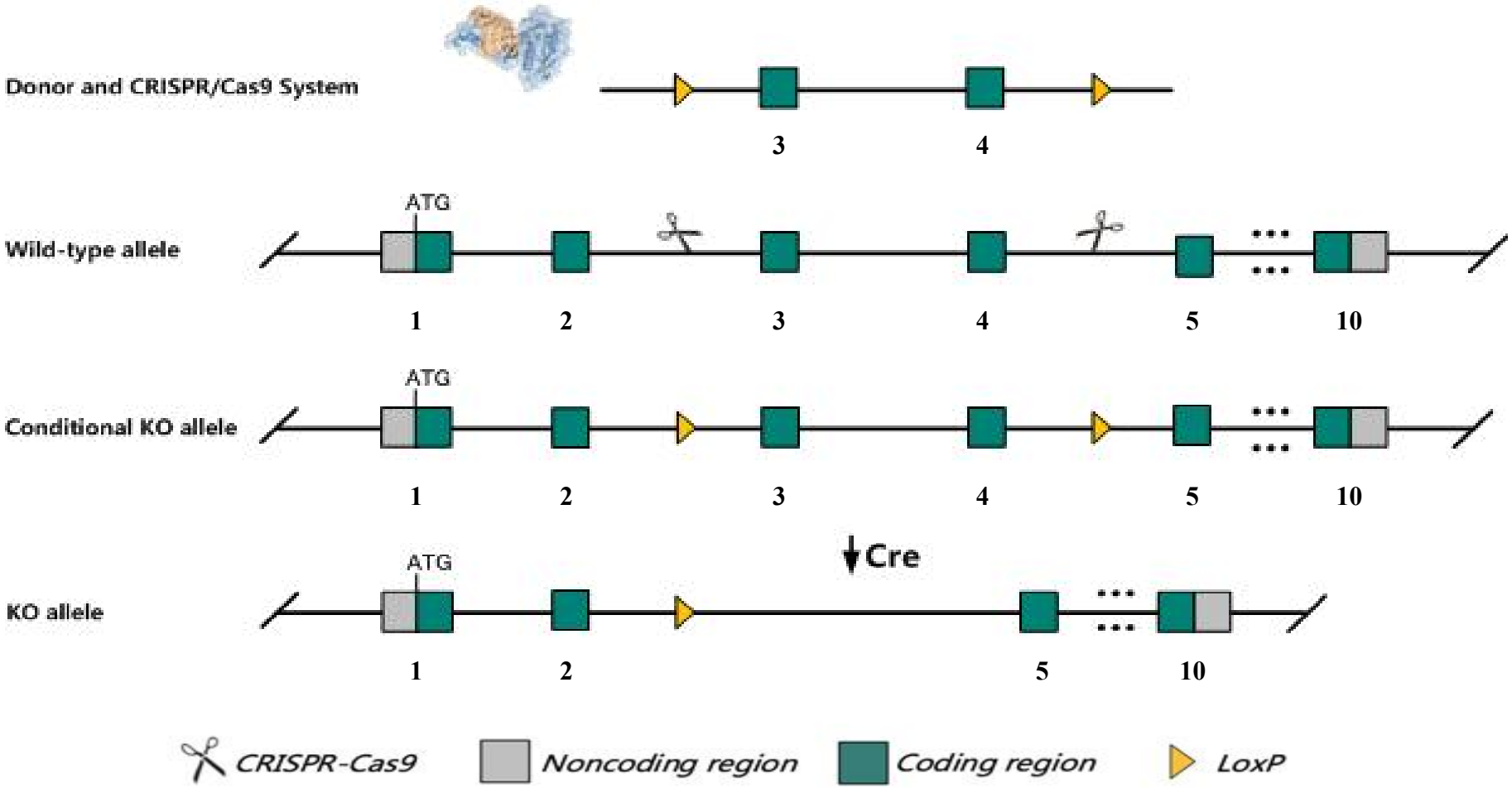
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Xpnpep3* gene.

Technical Information

- The *Xpnpep3* gene has 7 transcripts. According to the structure of *Xpnpep3* gene, exon3-exon4 of *Xpnpep3*-203 (ENSMUST00000163754.9) transcript is recommended as the knockout region. The region contains 611bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Xpnpep3* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Xpnpep3 X-prolyl aminopeptidase 3, mitochondrial [Mus musculus (house mouse)]

Gene ID: 321003, updated on 18-May-2023

Summary

Official Symbol	Xpnpep3 provided by MGI
Official Full Name	X-prolyl aminopeptidase 3, mitochondrial provided byMGI
Primary source	MGI:MGI:2445217
See related	Ensembl:ENSMUSG00000022401
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	APP3, E430012M05Rik
Summary	Predicted to enable manganese ion binding activity; metalloaminopeptidase activity; and protein homodimerization activity. Predicted to be involved in proteolysis. Predicted to act upstream of or within glomerular filtration and protein processing. Located in mitochondrion. Is expressed in several structures, including alimentary system; brain; cardiovascular system; genitourinary system; and immune system. Human ortholog(s) of this gene implicated in nephronophthisis-like nephropathy 1. Orthologous to human XPNPEP3 (X-prolyl aminopeptidase 3). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 3.3), placenta adult (RPKM 2.9) and 28 other tissuesSee more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

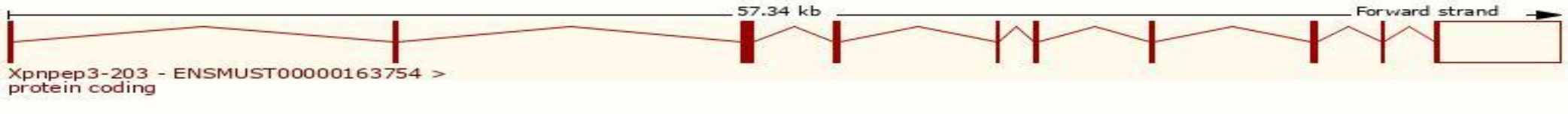
Transcript Information

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

Show/hide columns (1 hidden) Filter

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000041609.11	Xpnpep3-201	3236	386aa	Protein coding	CCDS27668	B7ZMP1-2	GENCODE basic TSL:1
ENSMUST00000163296.8	Xpnpep3-202	1082	No protein	Retained intron		-	TSL:1
ENSMUST00000163754.9	Xpnpep3-203	6058	506aa	Protein coding	CCDS84182	B7ZMP1-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000164144.3	Xpnpep3-204	666	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000165258.8	Xpnpep3-205	1641	69aa	Nonsense mediated decay		E9Q7I3	TSL:5
ENSMUST00000166831.9	Xpnpep3-206	1501	No protein	Retained intron		-	TSL:3
ENSMUST00000167799.2	Xpnpep3-207	771	No protein	Protein coding CDS not defined		-	TSL:3

The strategy is based on the design of *Xpnpep3*-203 transcript, the transcription is shown below:

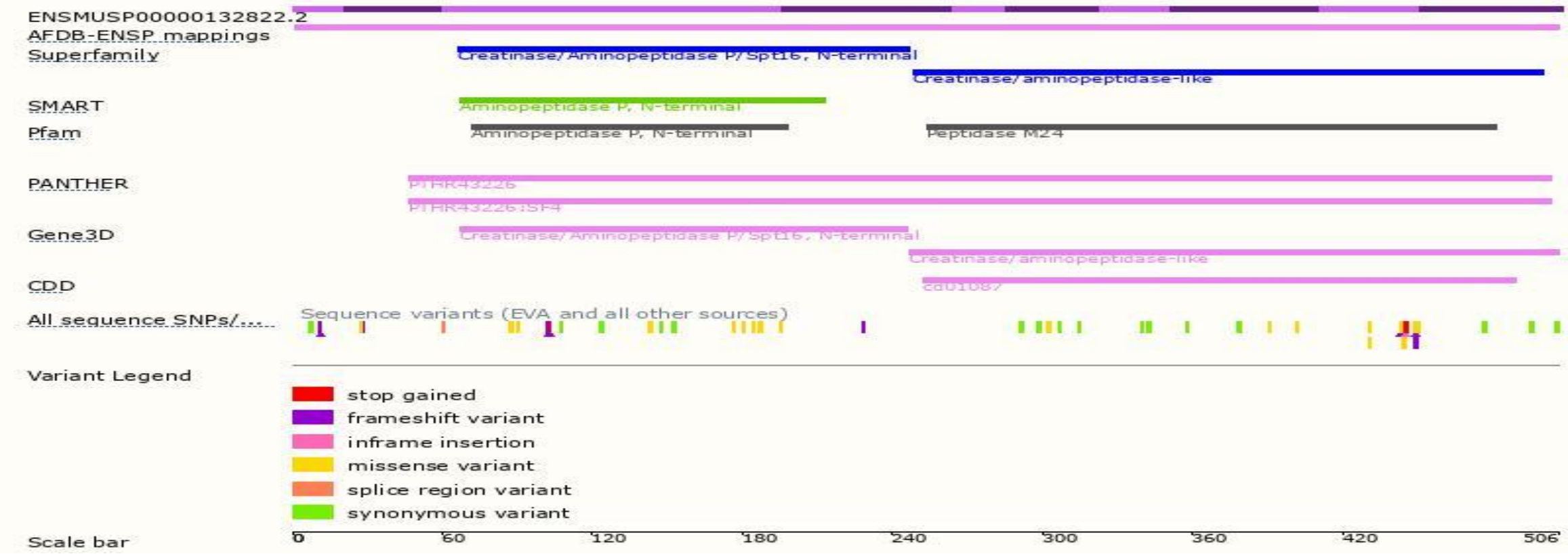


Source: https://www.ensembl.org

Genomic Information

Source: : https://www.ensembl.org

Protein Information



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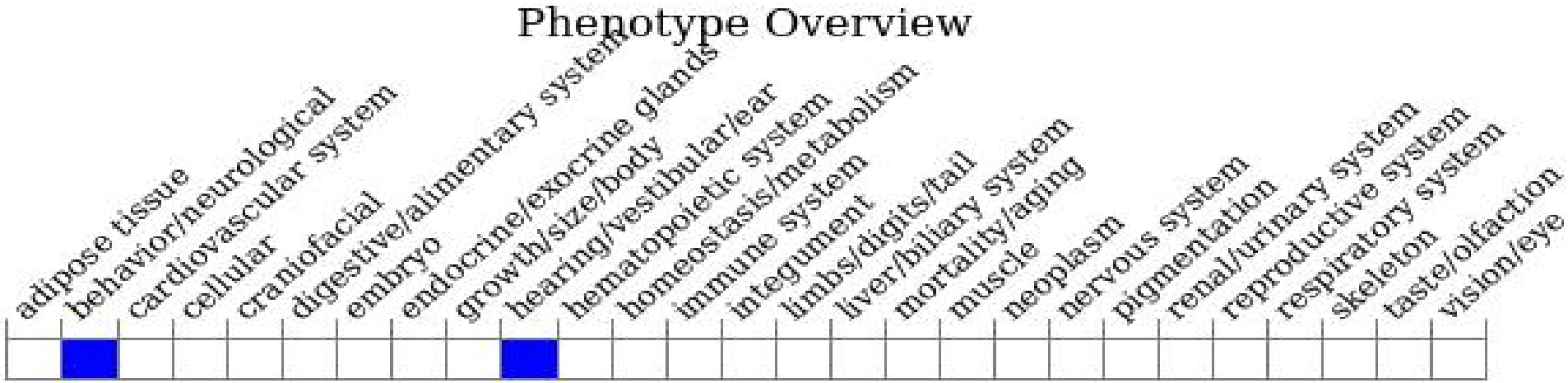
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



Source: https://www.informatics.jax.org

Important Information

- *Xpnpep3* is located on Chr15. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.