

Xpnpep1 Cas9-KO Strategy

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Reviewer:

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Design Date:

2020-8-4

Project Overview

Project Name

Xpnpep1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Xpnpep1* gene. The schematic diagram is as follows:



- The *Xpnpep1* gene has 17 transcripts. According to the structure of *Xpnpep1* gene, exon3 of *Xpnpep1-209* (ENSMUST00000183108.7) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Xpnpep1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit pre and postnatal lethality, reduced male survival, growth retardation with decreased body weight, size and length, microcephaly and peptiduria.
- The *Xpnpep1* 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)

Xpnpep1 X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Mus musculus (house mouse)]

Gene ID: 170750, updated on 20-Mar-2020

Summary



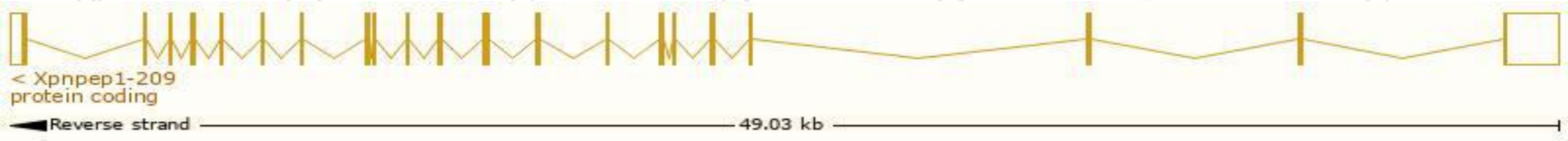
Official Symbol	Xpnpep1 provided by MGI
Official Full Name	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble provided by MGI
Primary source	MGI:MGI:2180003
See related	Ensembl:ENSMUSG00000025027
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D230045I08Rik, sAMP
Expression	Ubiquitous expression in large intestine adult (RPKM 157.6), small intestine adult (RPKM 86.1) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

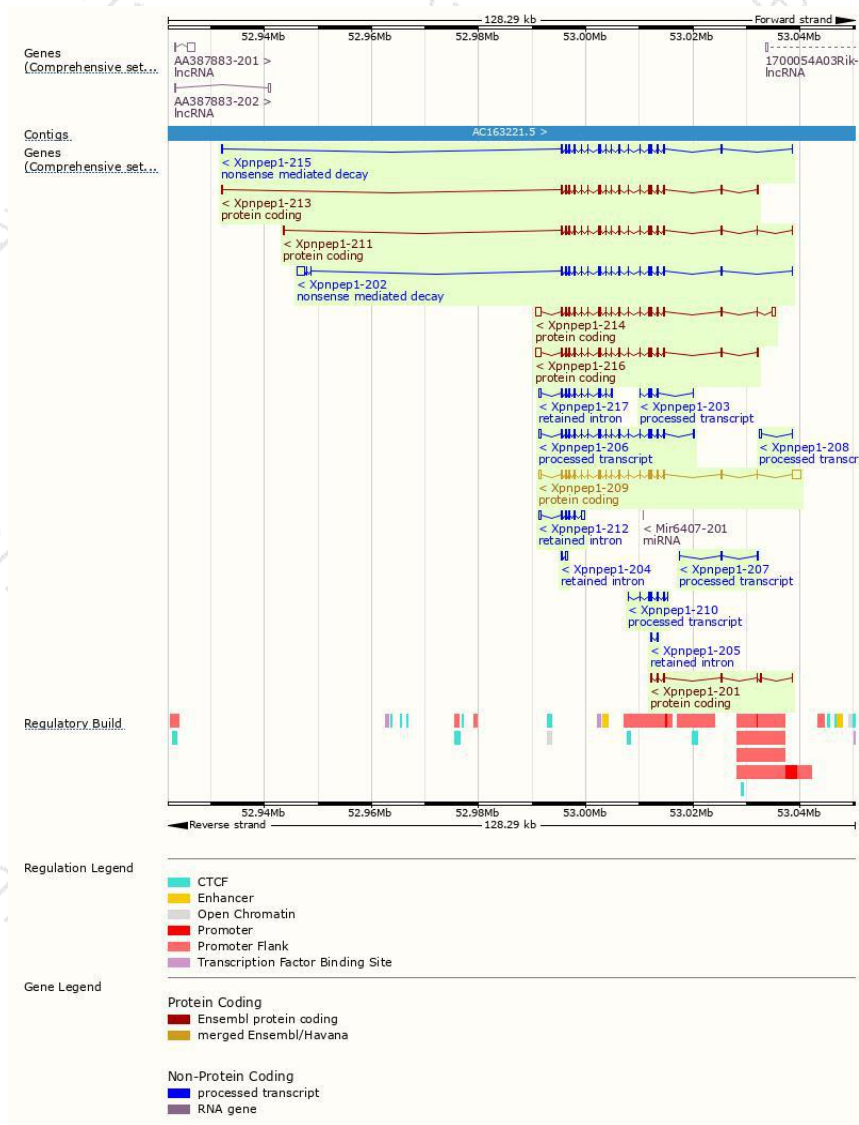
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Xpnp1-209	ENSMUST00000183108.7	4078	666aa	Protein coding	CCDS29899	Q3UE92	TSL:1 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
Xpnp1-214	ENSMUST00000236058.1	3442	623aa	Protein coding	-	Q3UKF5 Q6P1B1	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 ALT 1
Xpnp1-216	ENSMUST00000237294.1	2956	623aa	Protein coding	-	Q3UKF5 Q6P1B1	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 ALT 1
Xpnp1-213	ENSMUST00000236008.1	2221	587aa	Protein coding	-	A0A494BBG8	GENCODE basic
Xpnp1-211	ENSMUST00000183274.7	2120	635aa	Protein coding	-	S4R113	TSL:1 GENCODE basic
Xpnp1-201	ENSMUST00000182097.1	698	119aa	Protein coding	-	S4R228	CDS 3' incomplete TSL:3
Xpnp1-202	ENSMUST00000182500.7	3307	59aa	Nonsense mediated decay	-	S4R167	TSL:1
Xpnp1-215	ENSMUST00000236456.1	2216	59aa	Nonsense mediated decay	-	S4R167	
Xpnp1-206	ENSMUST00000182877.7	2475	No protein	Processed transcript	-	-	TSL:1
Xpnp1-210	ENSMUST00000183188.7	689	No protein	Processed transcript	-	-	TSL:5
Xpnp1-203	ENSMUST00000182534.1	585	No protein	Processed transcript	-	-	TSL:3
Xpnp1-208	ENSMUST00000182939.1	378	No protein	Processed transcript	-	-	TSL:3
Xpnp1-207	ENSMUST00000182887.1	350	No protein	Processed transcript	-	-	TSL:5
Xpnp1-212	ENSMUST00000235453.1	1679	No protein	Retained intron	-	-	
Xpnp1-217	ENSMUST00000238001.1	1422	No protein	Retained intron	-	-	
Xpnp1-204	ENSMUST00000182728.1	541	No protein	Retained intron	-	-	TSL:3
Xpnp1-205	ENSMUST00000182844.1	306	No protein	Retained intron	-	-	TSL:5

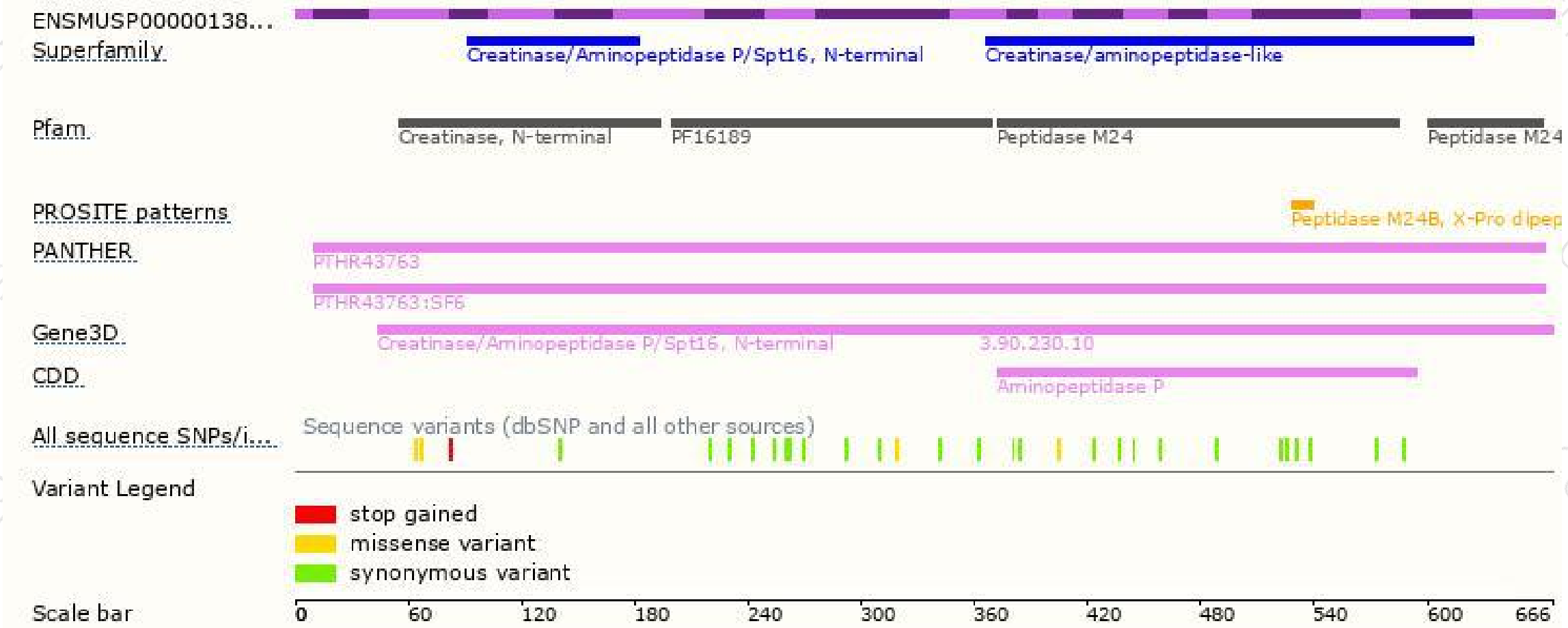
The strategy is based on the design of *Xpnp1-209* transcript,the transcription is shown below



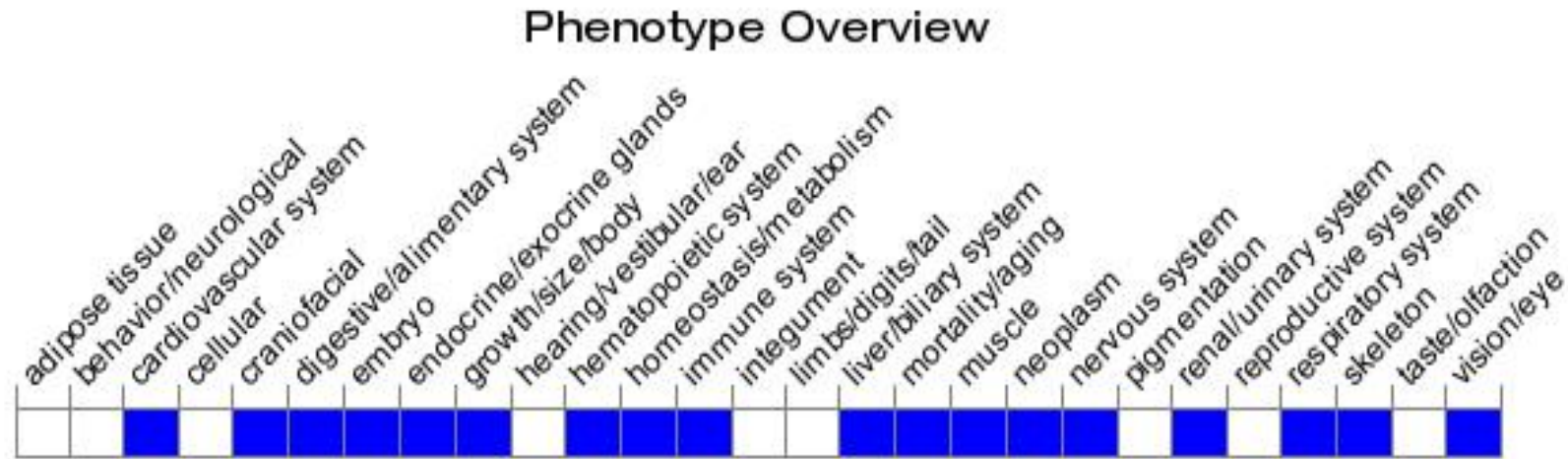
Genomic location distribution



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 a gene trap allele exhibit pre and postnatal lethality, reduced male survival, growth retardation with decreased body weight, size and length, microcephaly and peptiduria.

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

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