

Enpp7 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Enpp7

Project type

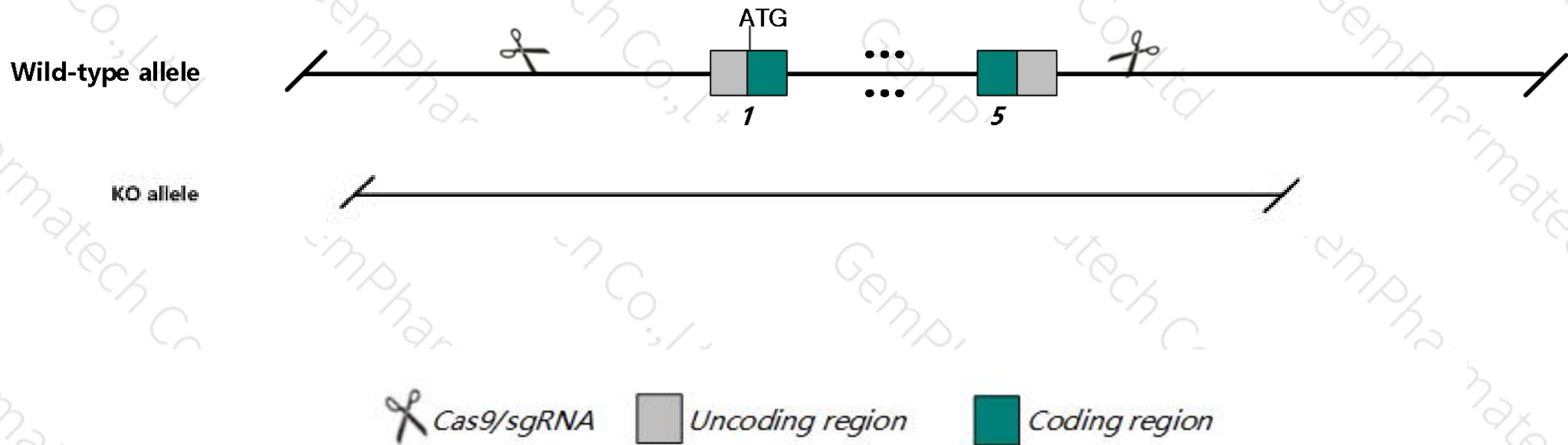
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Enpp7* gene. The schematic diagram is as follows:



- The *Enpp7* gene has 2 transcripts. According to the structure of *Enpp7* gene, exon1-exon5 of *Enpp7*-202 (ENSMUST00000106273.2) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Enpp7* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit intestinal epithelium hypertrophy, decreased crypt and villi width, and impaired sphingomyelin digestion.
- The *Enpp7* gene is located on the Chr11. 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)

Enpp7 ectonucleotide pyrophosphatase/phosphodiesterase 7 [*Mus musculus* (house mouse)]

Gene ID: 238011, updated on 13-Mar-2020

Summary

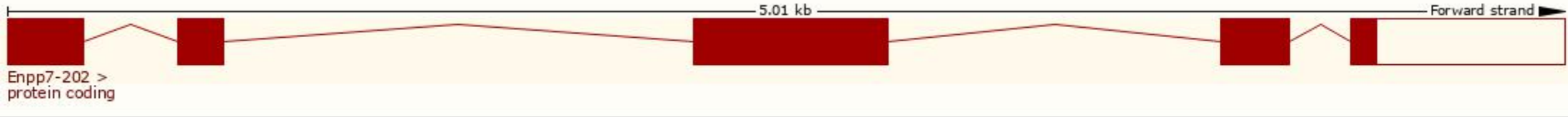
Official Symbol	Enpp7 provided by MGI
Official Full Name	ectonucleotide pyrophosphatase/phosphodiesterase 7 provided by MGI
Primary source	MGI:MGI:3027917
See related	Ensembl:ENSMUSG00000046697
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm254; Alk-SMase
Expression	Biased expression in small intestine adult (RPKM 379.6), large intestine adult (RPKM 371.9) and 1 other tissue See more
Orthologs	human all

Transcript information (Ensembl)

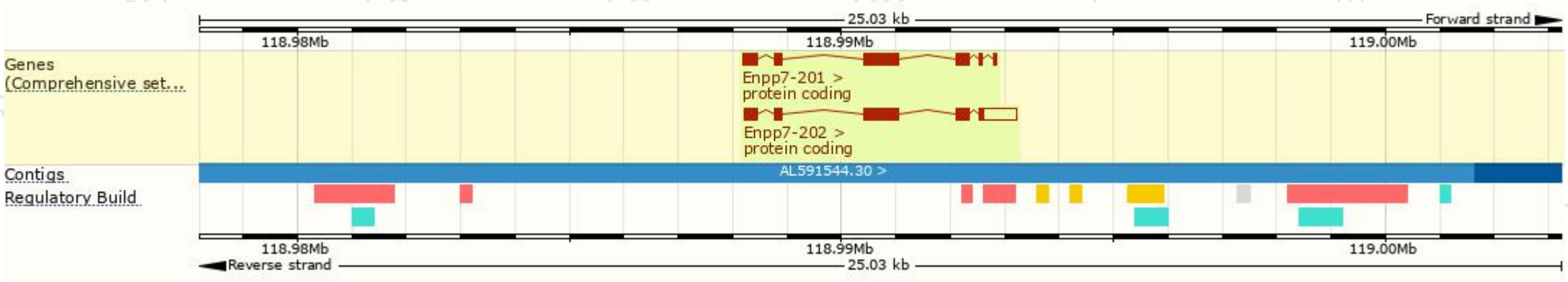
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Enpp7-202	ENSMUST00000106273.2	1923	439aa	Protein coding	-	Q3TIW9	TSL:5 GENCODE basic APPRIS ALT2
Enpp7-201	ENSMUST00000092373.12	1370	446aa	Protein coding	-	D3Z6V6	TSL:2 GENCODE basic APPRIS P5

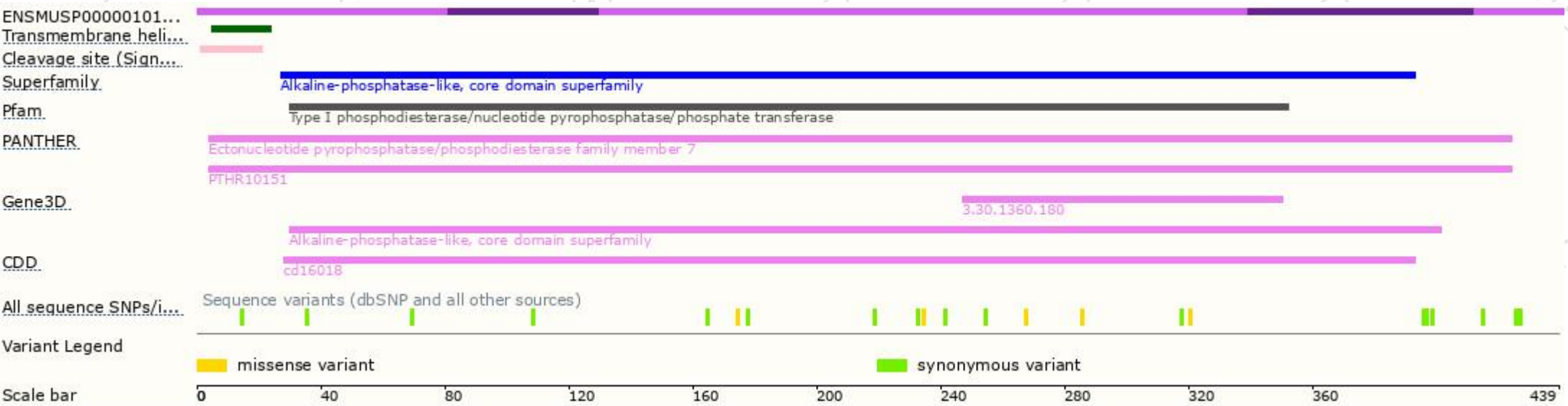
The strategy is based on the design of *Enpp7-202* transcript,The transcription is shown below



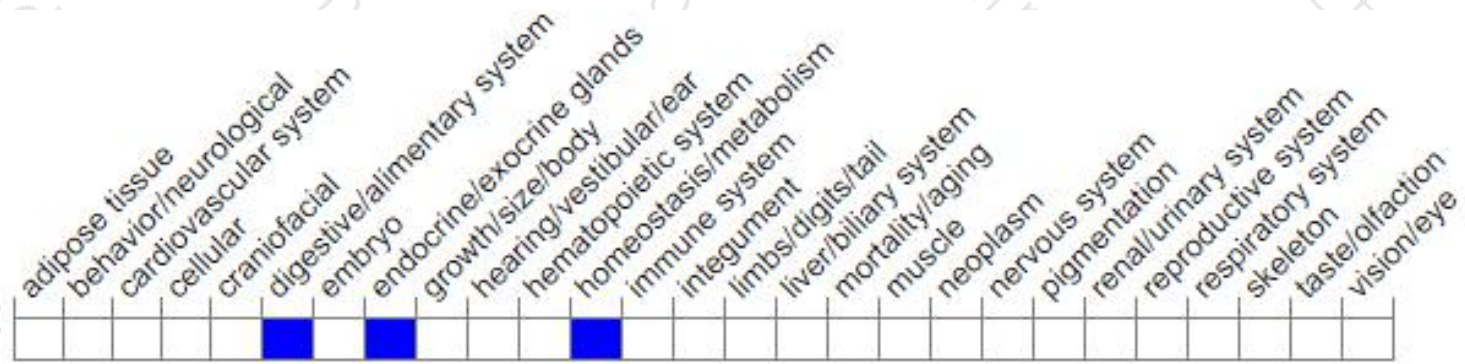
Genomic location distribution



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 a knock-out allele exhibit intestinal epithelium hypertrophy, decreased crypt and villi width, and impaired sphingomyelin digestion.

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

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