

Entpd5 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Entpd5

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Entpd5* gene. The schematic diagram is as follows:



- The *Entpd5* gene has 8 transcripts. According to the structure of *Entpd5* gene, exon5-exon6 of *Entpd5-203* (ENSMUST00000110272.8) transcript is recommended as the knockout region. The region contains 224bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Entpd5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele develop progressive hepatopathy, hepatocellular tumors, and spermatogenic arrest.
- The *Entpd5* gene is located on the Chr12. 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)

Entpd5 ectonucleoside triphosphate diphosphohydrolase 5 [Mus musculus (house mouse)]

Gene ID: 12499, updated on 3-Feb-2019

Summary



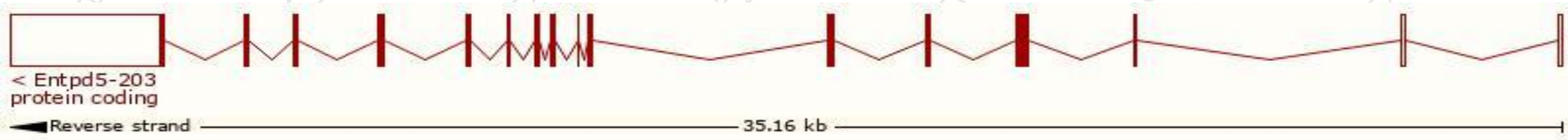
Official Symbol	Entpd5 provided by MGI
Official Full Name	ectonucleoside triphosphate diphosphohydrolase 5 provided by MGI
Primary source	MGI:MGI:1321385
See related	Ensembl:ENSMUSG000000021236
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI196558, AI987697, Cd39I4, ER-UDPase, NTPDase-5, NTPDase5, Pcph, mNTPase
Expression	Broad expression in kidney adult (RPKM 30.8), bladder adult (RPKM 19.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

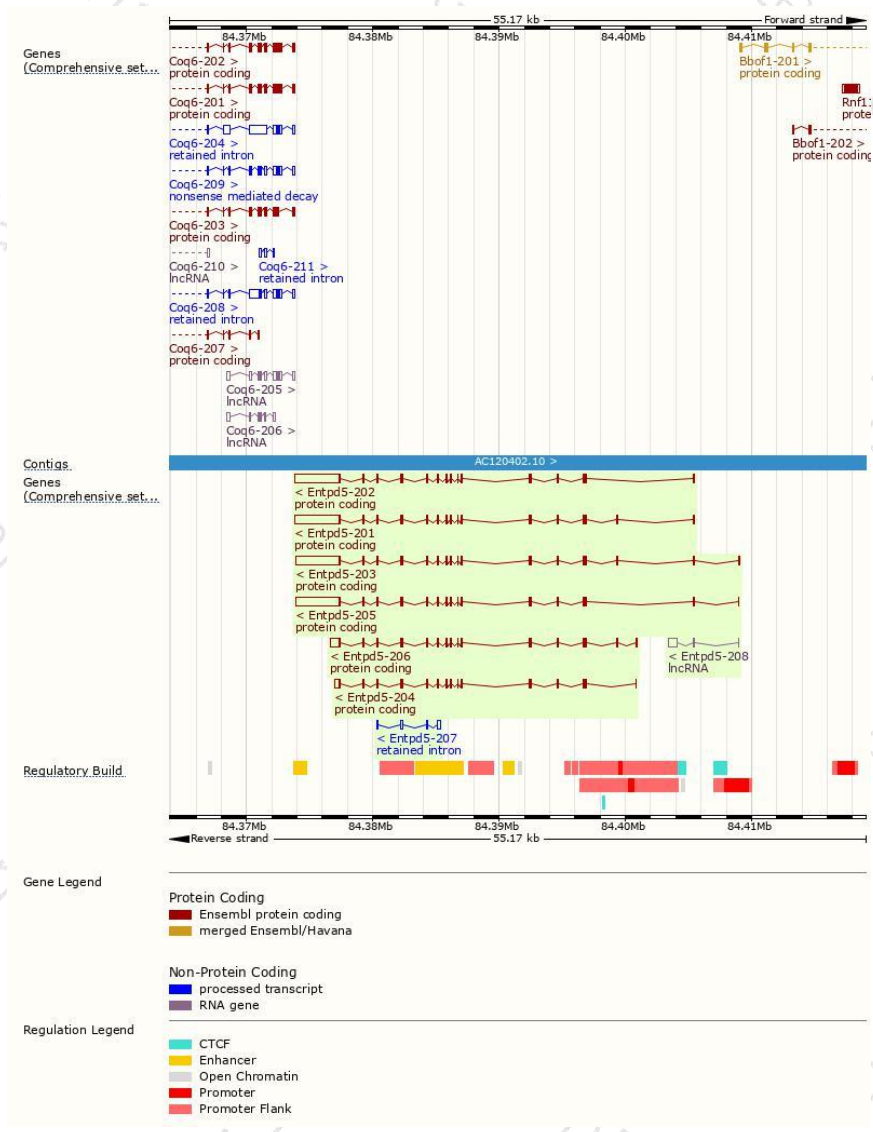
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Entpd5-203	ENSMUST00000110272.8	4972	427aa	Protein coding	CCDS26045	Q9WUZ9	TSL:1 GENCODE basic APPRIS P1
Entpd5-201	ENSMUST00000021662.11	4931	427aa	Protein coding	CCDS26045	Q9WUZ9	TSL:1 GENCODE basic APPRIS P1
Entpd5-205	ENSMUST00000120942.7	4881	427aa	Protein coding	CCDS26045	Q9WUZ9	TSL:1 GENCODE basic APPRIS P1
Entpd5-202	ENSMUST00000072061.11	4858	452aa	Protein coding	CCDS36491	Q3TQC7	TSL:5 GENCODE basic
Entpd5-206	ENSMUST00000122194.7	2145	427aa	Protein coding	CCDS26045	Q9WUZ9	TSL:1 GENCODE basic APPRIS P1
Entpd5-204	ENSMUST00000117286.1	1691	427aa	Protein coding	CCDS26045	Q9WUZ9	TSL:1 GENCODE basic APPRIS P1
Entpd5-207	ENSMUST00000135061.1	526	No protein	Retained intron	-	-	TSL:5
Entpd5-208	ENSMUST00000136511.1	827	No protein	lncRNA	-	-	TSL:1

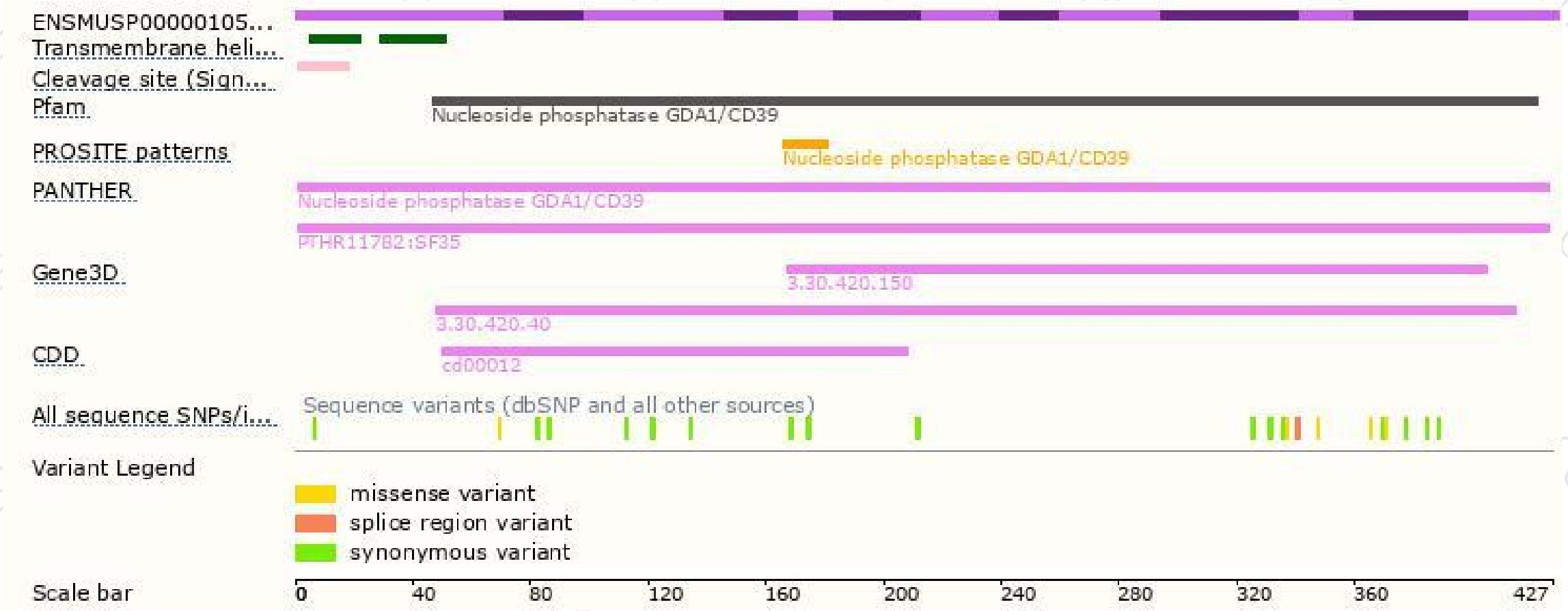
The strategy is based on the design of *Entpd5-203* transcript,The transcription is shown below



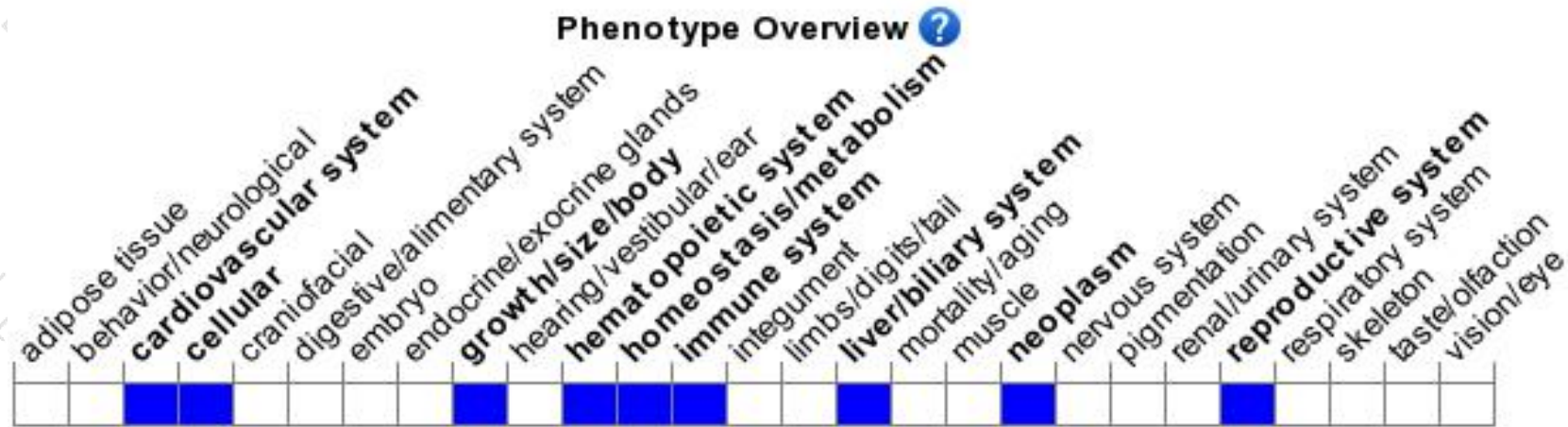
Genomic location distribution



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 null allele develop progressive hepatopathy, hepatocellular tumors, and spermatogenic arrest.

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

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