

Pxylp1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Pxylp1

Project type

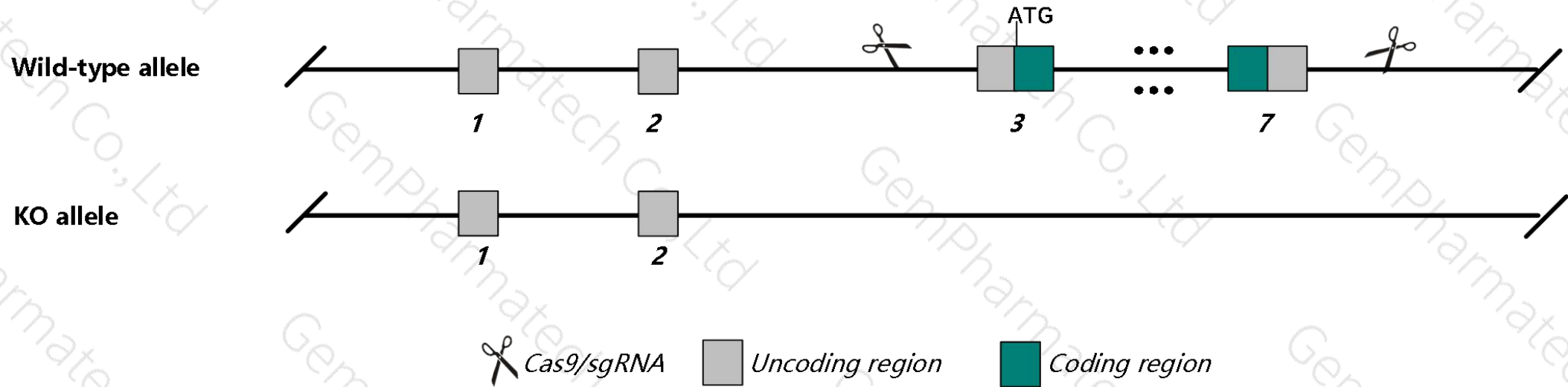
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pxylp1* gene. The schematic diagram is as follows:



- The *Pxylp1* gene has 13 transcripts. According to the structure of *Pxylp1* gene, exon3-exon7 of *Pxylp1*-204 (ENSMUST00000120101.7) 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 *Pxylp1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Pxylp1* gene is located on the Chr9. 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)

Pxylp1 2-phosphoxylose phosphatase 1 [Mus musculus (house mouse)]

Gene ID: 235534, updated on 13-Mar-2020

Summary



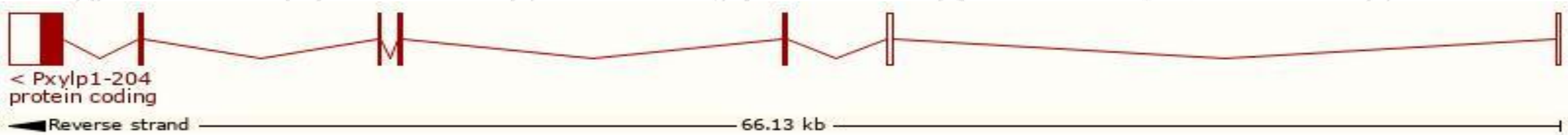
Official Symbol	Pxylp1 provided by MGI
Official Full Name	2-phosphoxylose phosphatase 1 provided by MGI
Primary source	MGI:MGI:2442444
See related	Ensembl:ENSMUSG00000043587
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9430094M07Rik, Acpl2, BB177120, C130099A20Rik
Expression	Ubiquitous expression in colon adult (RPKM 9.1), CNS E14 (RPKM 7.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

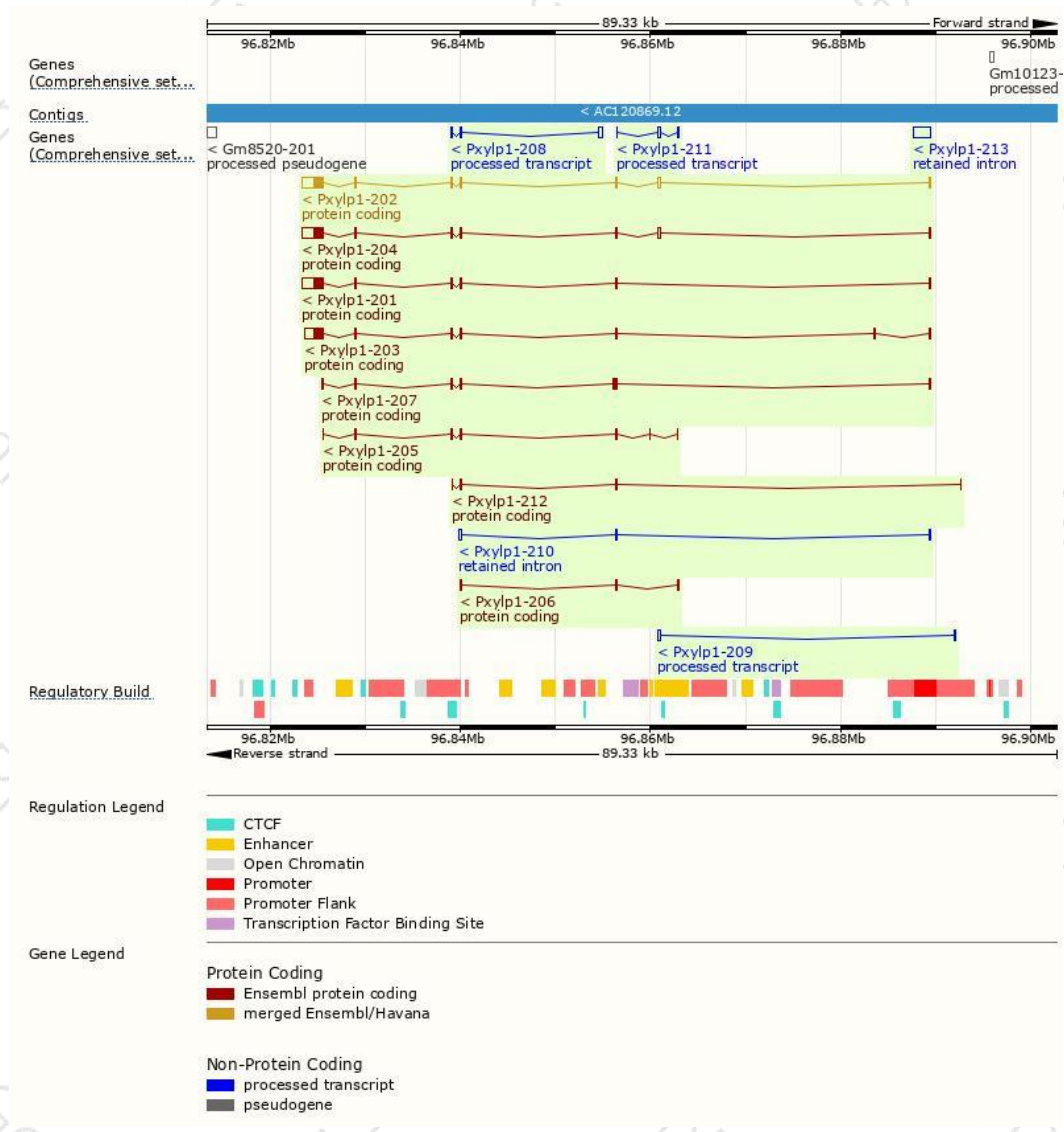
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pxylp1-204	ENSMUST00000120101.7	3189	480aa	Protein coding	CCDS23418	Q8BHA9	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 P1
Pxylp1-202	ENSMUST00000112951.8	3118	480aa	Protein coding	CCDS23418	Q8BHA9	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 P1
Pxylp1-201	ENSMUST00000078478.7	2908	480aa	Protein coding	CCDS23418	Q8BHA9	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 P1
Pxylp1-203	ENSMUST00000119141.7	2768	480aa	Protein coding	CCDS23418	Q8BHA9	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 P1
Pxylp1-207	ENSMUST00000126411.7	996	190aa	Protein coding	-	D3Z2N0	CDS 3' incomplete TSL:5
Pxylp1-205	ENSMUST00000121077.7	731	180aa	Protein coding	-	D3Z7C3	CDS 3' incomplete TSL:3
Pxylp1-206	ENSMUST00000124923.1	393	65aa	Protein coding	-	D3YZM5	CDS 3' incomplete TSL:3
Pxylp1-212	ENSMUST00000154146.7	372	85aa	Protein coding	-	D3YUT4	CDS 3' incomplete TSL:5
Pxylp1-208	ENSMUST00000135834.2	709	No protein	Processed transcript	-	-	TSL:2
Pxylp1-211	ENSMUST00000141127.1	395	No protein	Processed transcript	-	-	TSL:3
Pxylp1-209	ENSMUST00000136987.1	393	No protein	Processed transcript	-	-	TSL:2
Pxylp1-213	ENSMUST00000185561.1	1803	No protein	Retained intron	-	-	TSL:NA
Pxylp1-210	ENSMUST00000137770.1	427	No protein	Retained intron	-	-	TSL:2

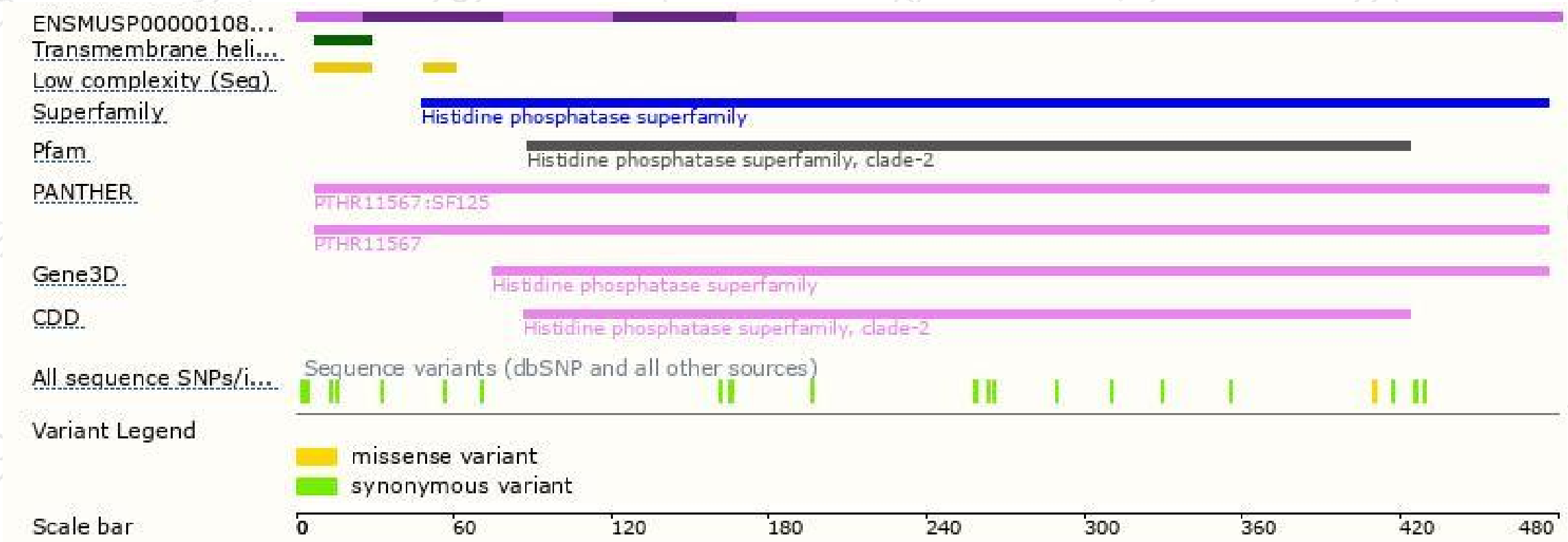
The strategy is based on the design of *Pxylp1-204* transcript,The transcription is shown below



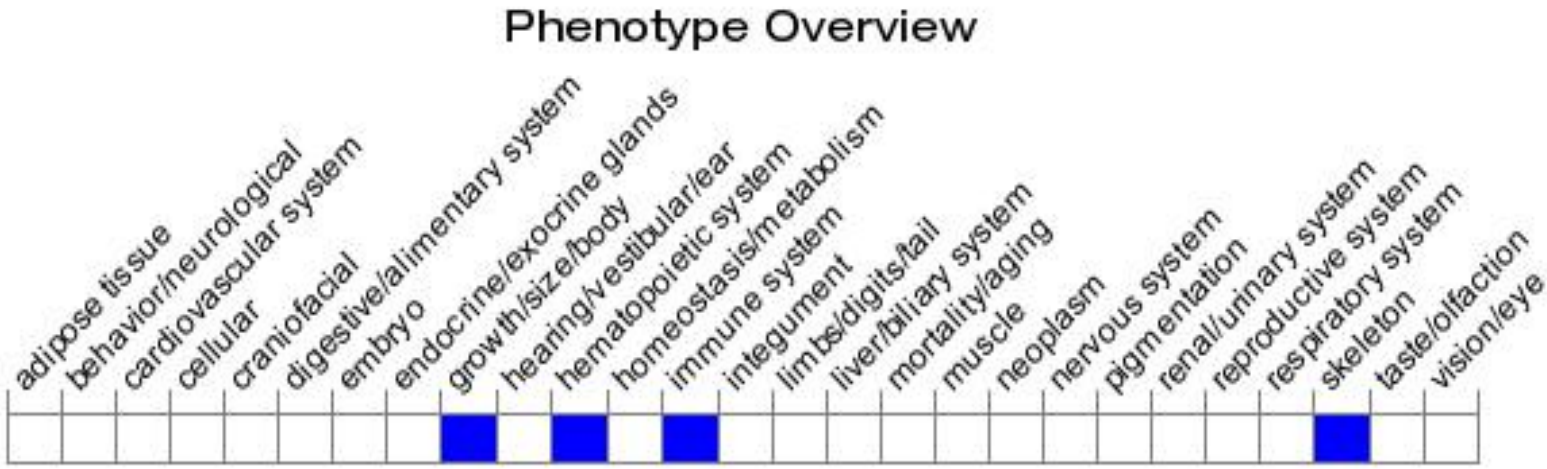
Genomic location distribution



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/>).

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

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