

Ptp4a2 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Ptp4a2

Project type

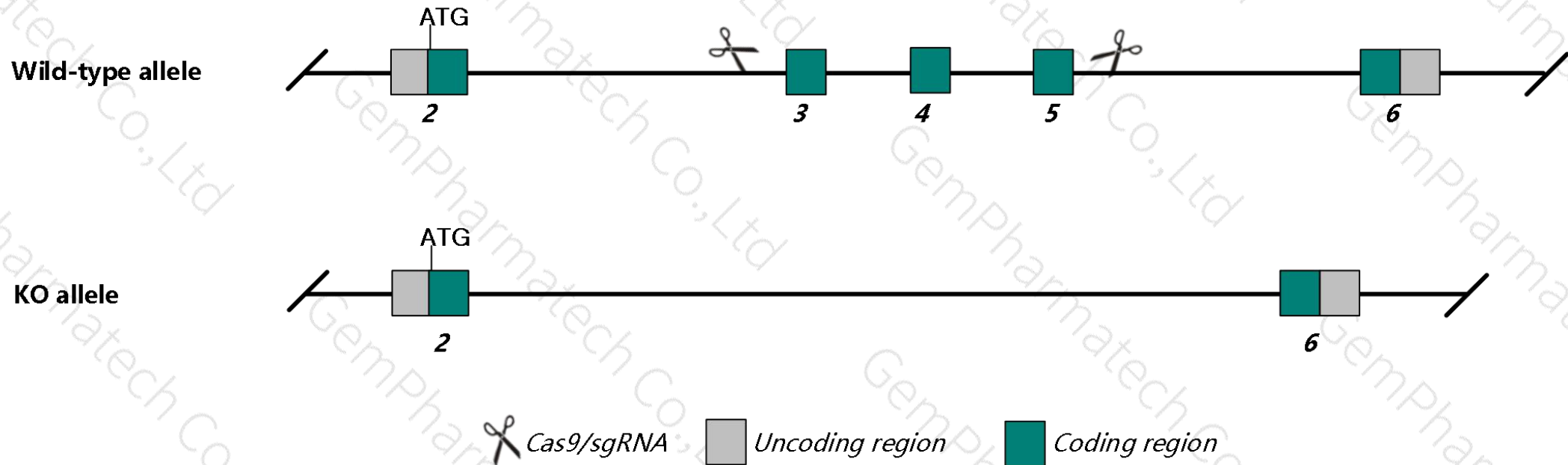
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptp4a2* gene. The schematic diagram is as follows:



- The *Ptp4a2* gene has 7 transcripts. According to the structure of *Ptp4a2* gene, exon3-exon5 of *Ptp4a2-201* (ENSMUST00000030578.13) transcript is recommended as the knockout region. The region contains 299bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptp4a2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit growth retardation associated with reduced decidual, spongiotrophoblast (due to reduced cell proliferation) and placental labyrinth.
- The *Ptp4a2* gene is located on the Chr4. 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)

Ptp4a2 protein tyrosine phosphatase 4a2 [*Mus musculus* (house mouse)]

Gene ID: 19244, updated on 13-Mar-2020

Summary

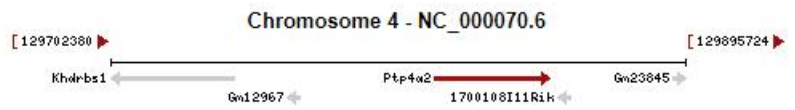
- Official Symbol Ptp4a2 provided by MGI
- Official Full Name protein tyrosine phosphatase 4a2 provided by MGI
- Primary source MGI:MGI:1277117
- See related Ensembl:ENSMUSG00000028788
- Gene type protein coding
- RefSeq status VALIDATED
- Organism *Mus musculus*
- Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as Prl-2
- Expression Ubiquitous expression in bladder adult (RPKM 35.0), CNS E11.5 (RPKM 30.5) and 28 other tissues [See more](#)
- Orthologs [human](#) [all](#)

Genomic context

Location: 4; 4 D2.2 [See Ptp4a2 in Genome Data Viewer](#)

Exon count: 11

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (129811165..129850003)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (129497723..129527247)



Transcript information (Ensembl)

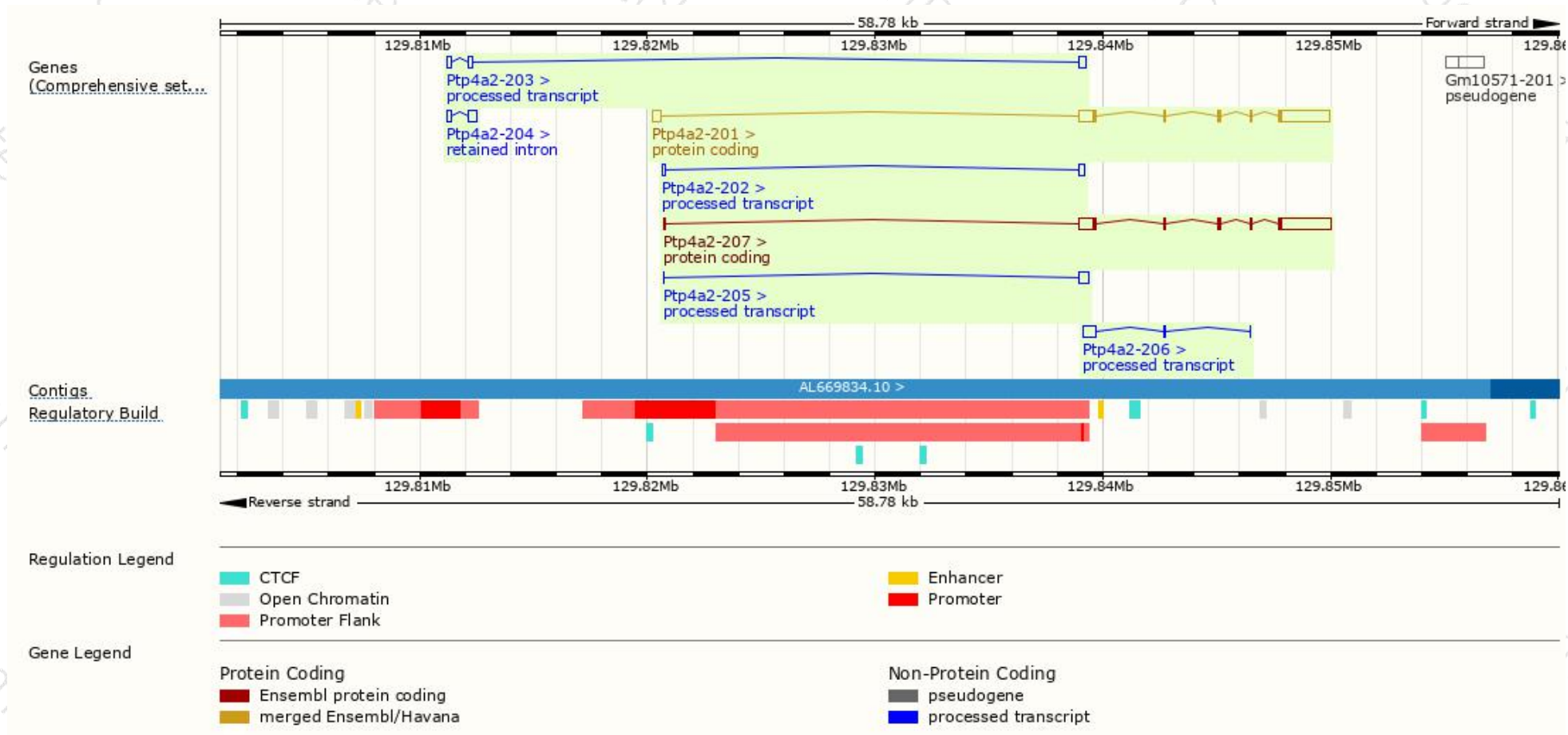
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptp4a2-201	ENSMUST00000030578.13	3646	167aa	Protein coding	CCDS18704	Q70274	TSL:5 GENCODE basic APPRIS P1
Ptp4a2-207	ENSMUST000000165853.1	3382	167aa	Protein coding	CCDS18704	Q70274	TSL:5 GENCODE basic APPRIS P1
Ptp4a2-206	ENSMUST000000141754.1	658	No protein	Processed transcript	-	-	TSL:2
Ptp4a2-203	ENSMUST000000132386.1	624	No protein	Processed transcript	-	-	TSL:5
Ptp4a2-205	ENSMUST000000133662.1	417	No protein	Processed transcript	-	-	TSL:2
Ptp4a2-202	ENSMUST000000127558.1	339	No protein	Processed transcript	-	-	TSL:2
Ptp4a2-204	ENSMUST000000132411.1	583	No protein	Retained intron	-	-	TSL:3

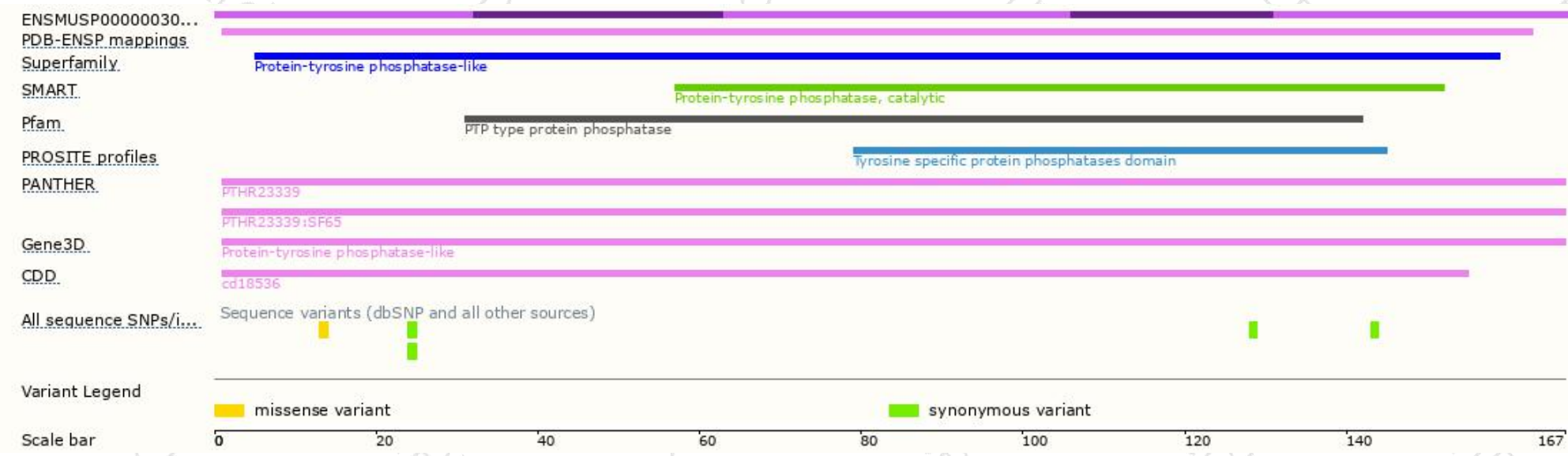
The strategy is based on the design of *Ptp4a2-201* transcript, the transcription is shown below:



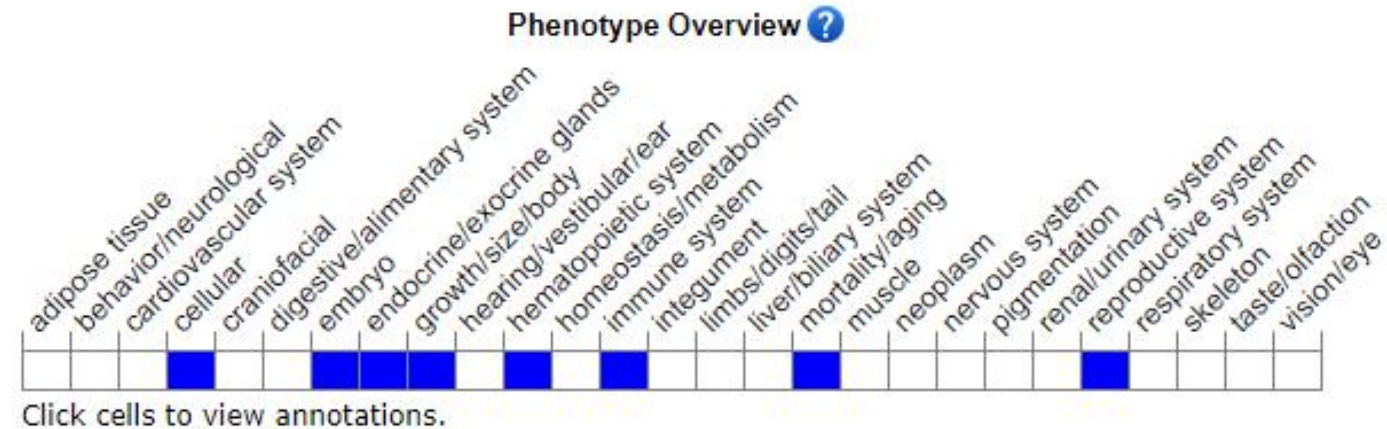
Genomic location distribution



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/>).

Mice homozygous for a gene trap allele exhibit growth retardation associated with reduced decidual, spongiotrophoblast (due to reduced cell proliferation) and placental labyrinth.

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

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