

Phospho2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Phospho2

Project type

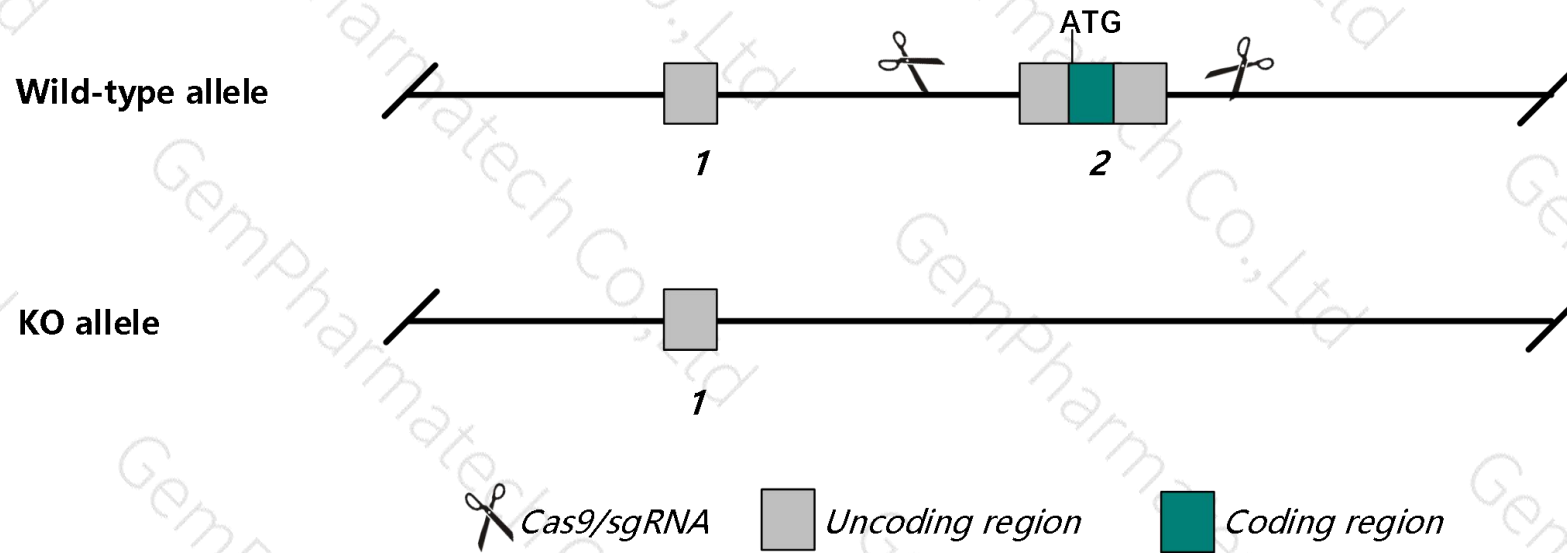
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phospho2* gene. The schematic diagram is as follows:



- The *Phospho2* gene has 6 transcripts. According to the structure of *Phospho2* gene, exon2 of *Phospho2*-206 (ENSMUST00000180290.1) 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 *Phospho2* gene. The brief process is as follows: CRISPR/Cas9 sys

- Transcript 204 may not be affected. The effect of transcripts 203,205 is unknown.
- The *Phospho2* gene is located on the Chr2. 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)

Phospho2 phosphatase, orphan 2 [Mus musculus (house mouse)]

Gene ID: 73373, updated on 13-Mar-2020

Summary



Official Symbol	Phospho2 provided by MGI
Official Full Name	phosphatase, orphan 2 provided by MGI
Primary source	MGI:MGI:1920623
See related	Ensembl:ENSMUSG000000027088
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700048E23Rik, A1661517, AU021728, AV006103, Phos2
Expression	Broad expression in testis adult (RPKM 58.1), adrenal adult (RPKM 8.9) and 25 other tissues See more
Orthologs	human all

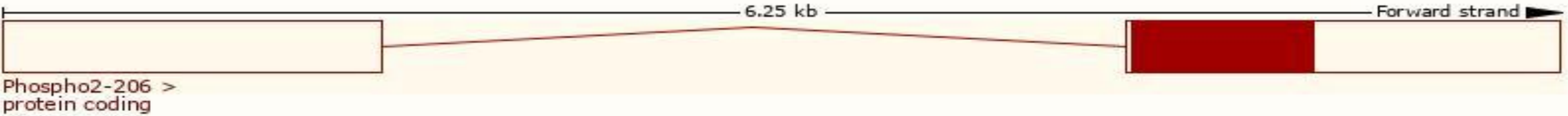
Transcript information（Ensembl）



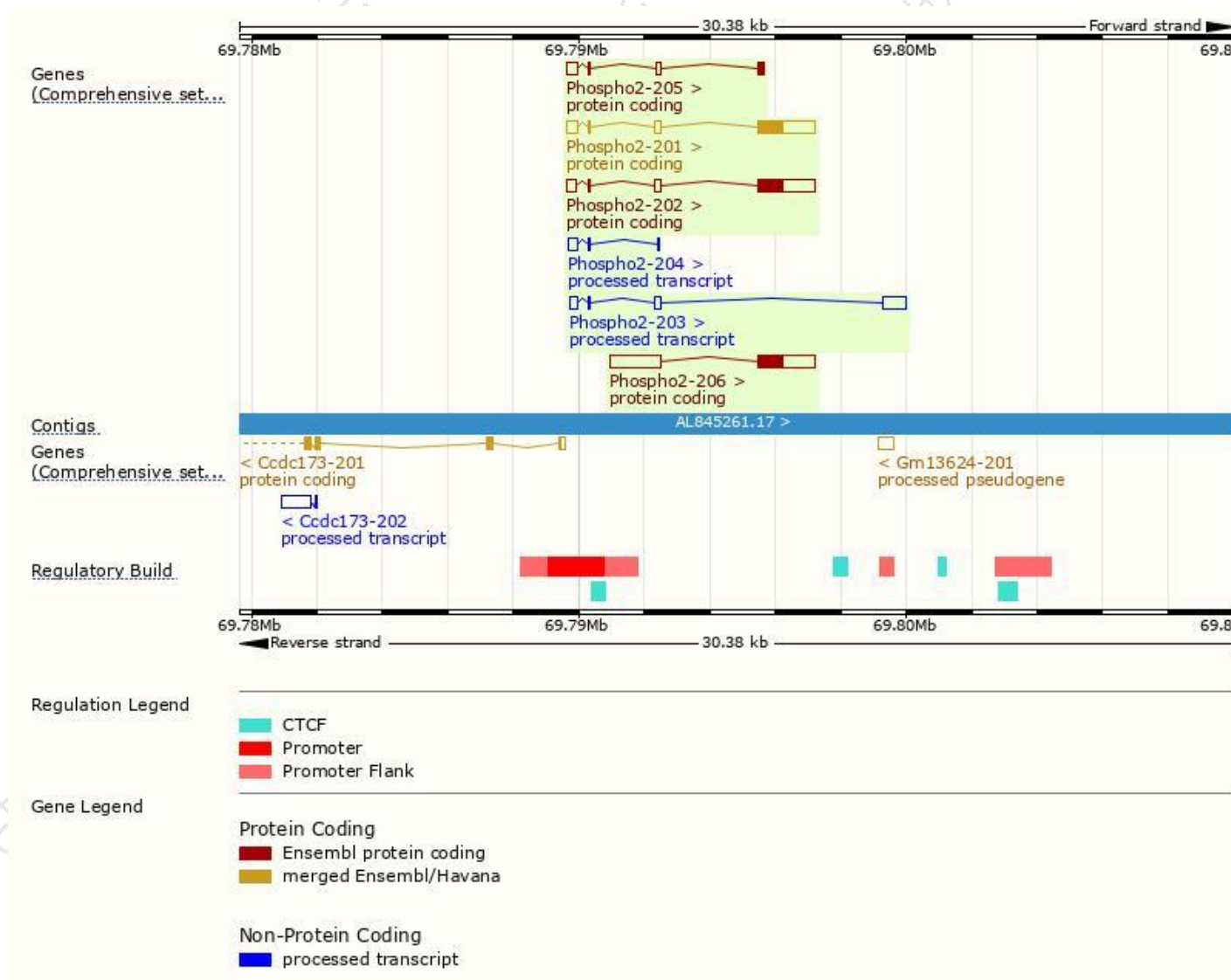
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phospho2-206	ENSMUST00000180290.1	3267	241aa	Protein coding	CCDS16099	Q9D9M5	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
Phospho2-201	ENSMUST00000028494.8	2260	241aa	Protein coding	CCDS16099	Q9D9M5	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
Phospho2-202	ENSMUST00000112266.7	2194	241aa	Protein coding	CCDS16099	Q9D9M5	TSL:3 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
Phospho2-205	ENSMUST00000151298.7	667	50aa	Protein coding	-	B0R0D2	CDS 3' incomplete TSL:2
Phospho2-203	ENSMUST00000128765.1	1133	No protein	Processed transcript	-	-	TSL:1
Phospho2-204	ENSMUST00000131100.7	415	No protein	Processed transcript	-	-	TSL:2

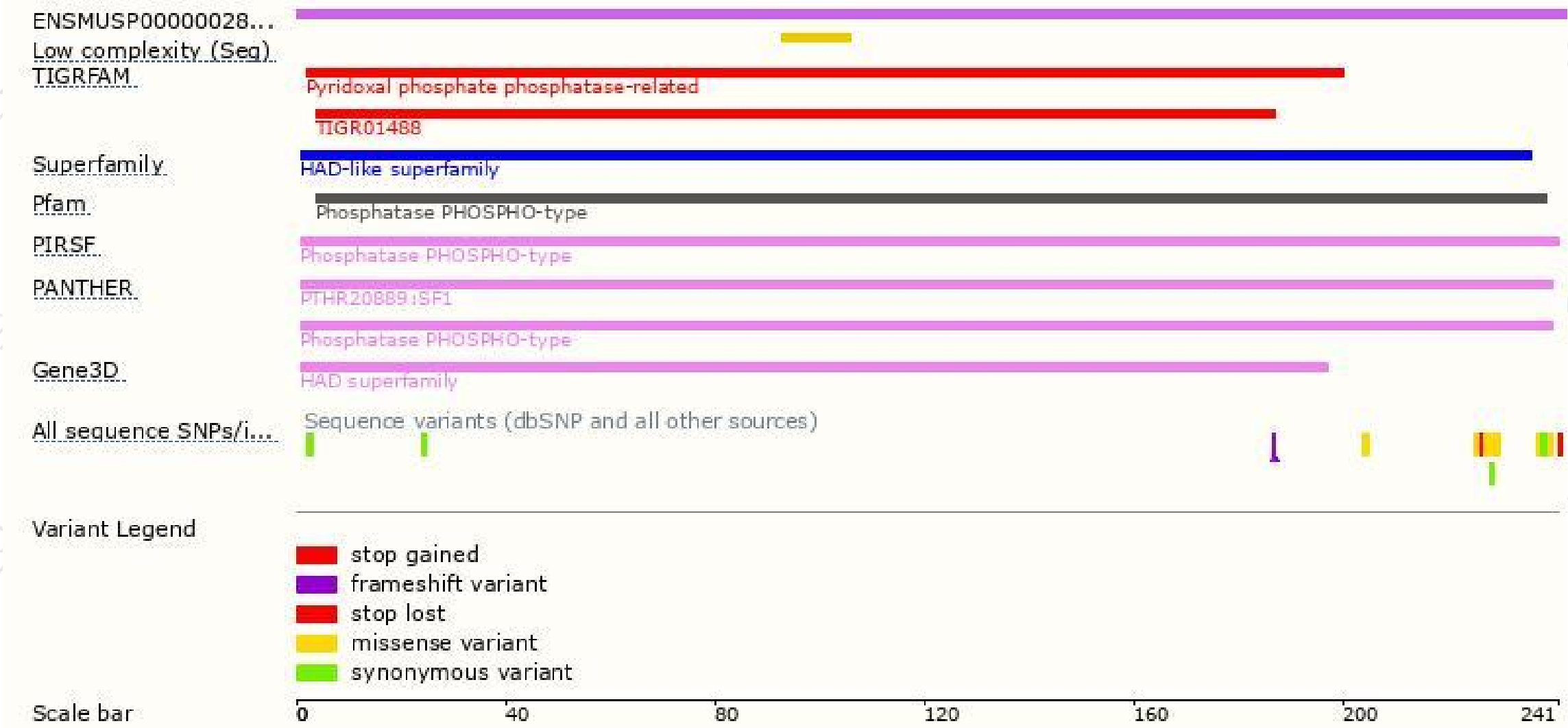
The strategy is based on the design of *Phospho2-206* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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