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# *Ptk6* Cas9-CKO Strategy

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Design Date: 2023-10-18

# Overview

## Target Gene Name

- *Ptk6*

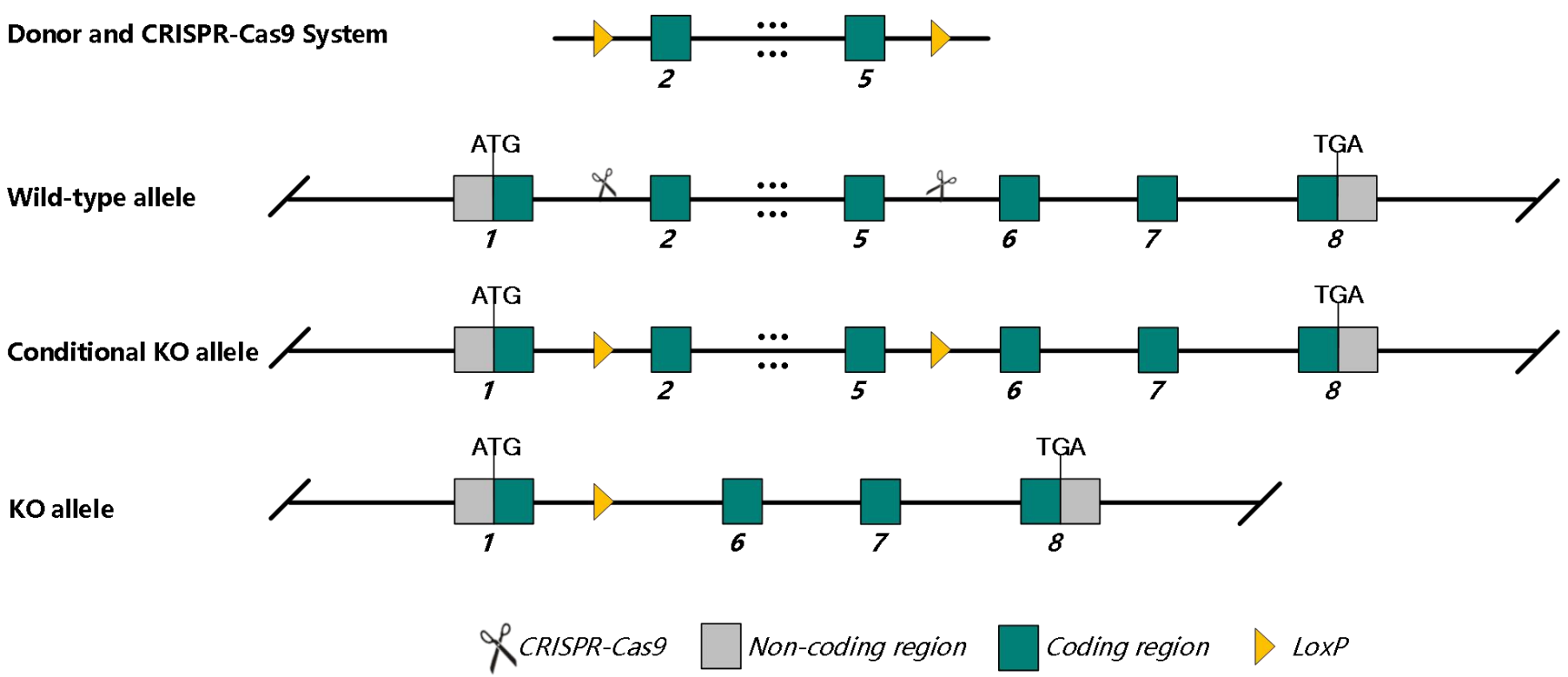
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy




Schematic representation of CRISPR-Cas9 engineering used to edit the *Ptk6* gene.

# Technical Information

- The *Ptk6* gene has 1 transcript. According to the structure of *Ptk6* gene, exon 2-5 of *Ptk6*-201 (ENSMUST00000016511.6) is recommended as the knockout region. The region contains 602 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Ptk6* gene. The brief process is as follows: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Gene Information

**Ptk6 PTK6 protein tyrosine kinase 6 [ *Mus musculus* (house mouse) ]**

Download Datasets

Gene ID: 20459, updated on 7-Sep-2023

**Summary**

| | |
|---|---|
| **Official Symbol** | Ptk6 provided by MGI |
| **Official Full Name** | PTK6 protein tyrosine kinase 6 provided by MGI |
| **Primary source** | MGI:MGI:99683 |
| **See related** | Ensembl:ENSMUSG00000038751 AllianceGenome:MGI:99683 |
| **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** | BRK; Sik; tks; Tksk |
| **Summary** | Predicted to enable identical protein binding activity; non-membrane spanning protein tyrosine kinase activity; and signaling receptor binding activity. Involved in intestinal epithelial cell differentiation and negative regulation of growth. Located in nucleus. Is expressed in several structures, including gut; liver; and skin. Orthologous to human PTK6 (protein tyrosine kinase 6). [provided by Alliance of Genome Resources, Apr 2022] |
| **Expression** | Biased expression in large intestine adult (RPKM 9.7), small intestine adult (RPKM 3.4) and 2 other tissues See more |
| **Orthologs** | human all |

NEW **Try the new Gene table**
**Try the new Transcript table**

**Genomic context**

**Location:** 2 H4; 2 103.62 cM — See Ptk6 in Genome Data Viewer

**Exon count:** 8

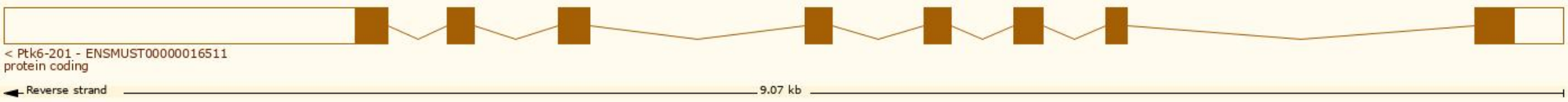
https://www.ncbi.nlm.nih.gov/gene/20459

# Transcript Information

The gene has 1 transcript, the transcript is shown below:

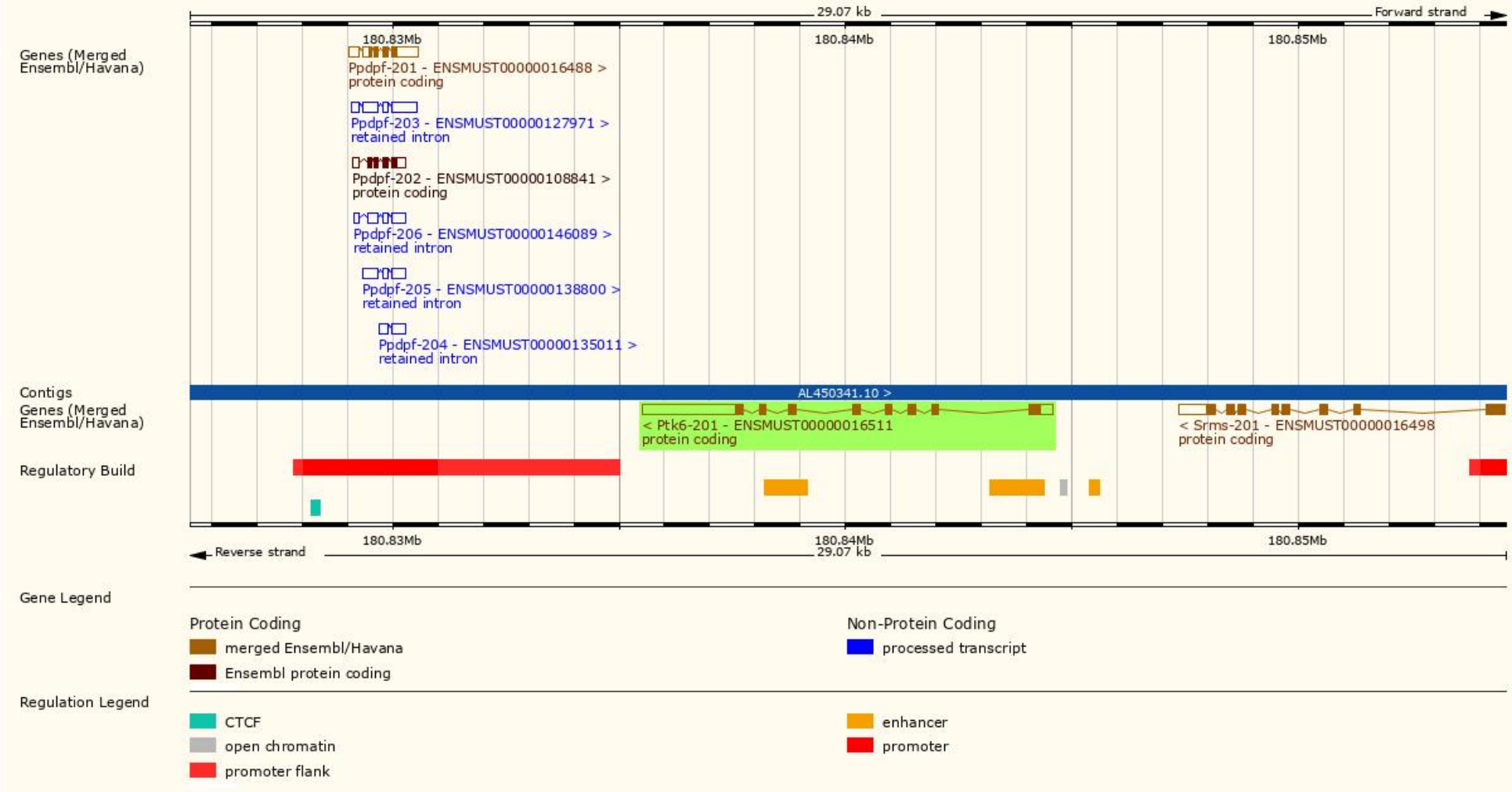
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|---|---|---|---|---|---|---|---|
| ENSMUST00000016511.6 | Ptk6-201 | 3689 | 451aa | Protein coding | CCDS17203 | Q05AA8 Q64434 | Ensembl Canonical GENCODE basic APPRIS P1 TSL:1 |

The strategy is based on the design of *Ptk6*-201 transcript, the transcription is shown below:




Source: http://asia.ensembl.org/

# Genomic Information

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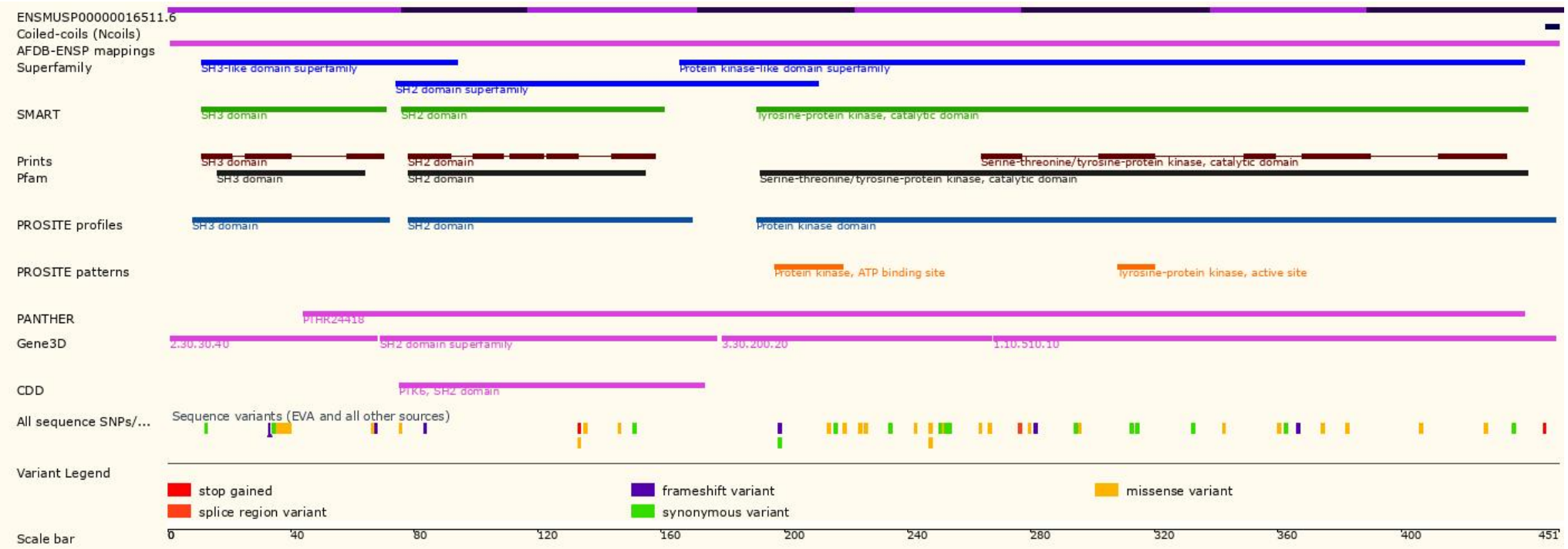
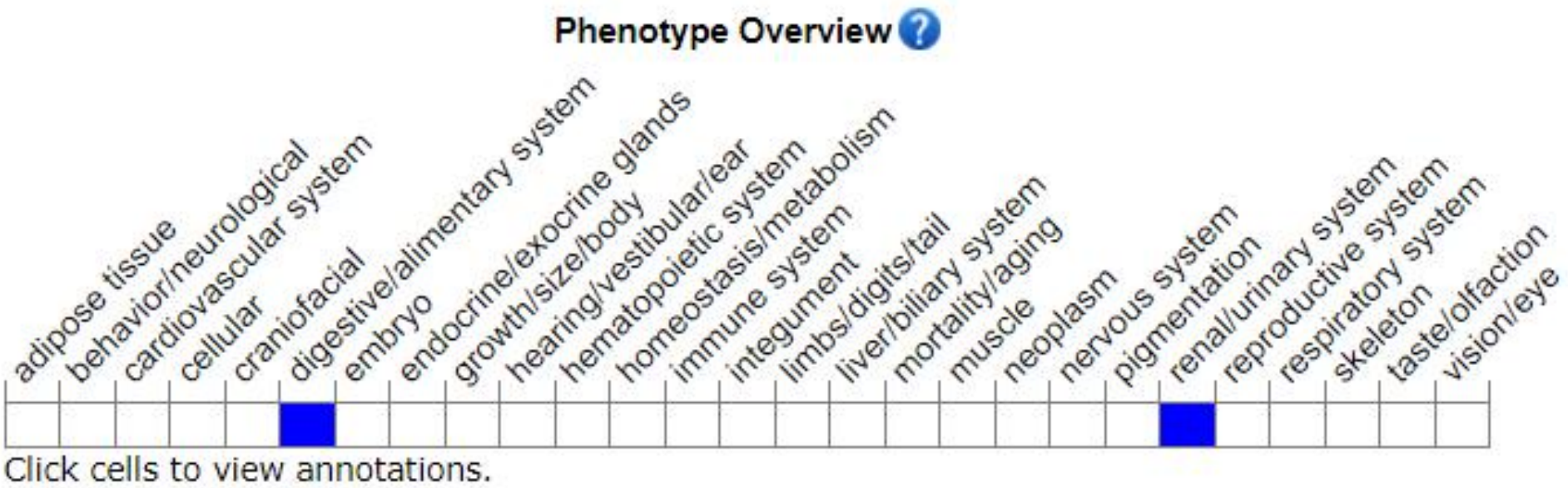
Source: http://asia.ensembl.org/

# Protein Information




Source: https://www.ensembl.org

# Mouse Phenotype Information (MGI)




Mice homozygous for a null allele display increased villus length in the jejunum and ileum and increased villus epithelial cell proliferation.



Source: https://www.informatics.jax.org

# Important Information

- A part of amino acid sequence (76 aa) will still remain at the N-terminal of *Ptk6* gene.
- *Ptk6* is located on Chr 2. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.