

Ptcd3 Cas9-KO Strategy

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Reviewer :

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Design Date:

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Project Overview

Project Name

Ptcd3

Project type

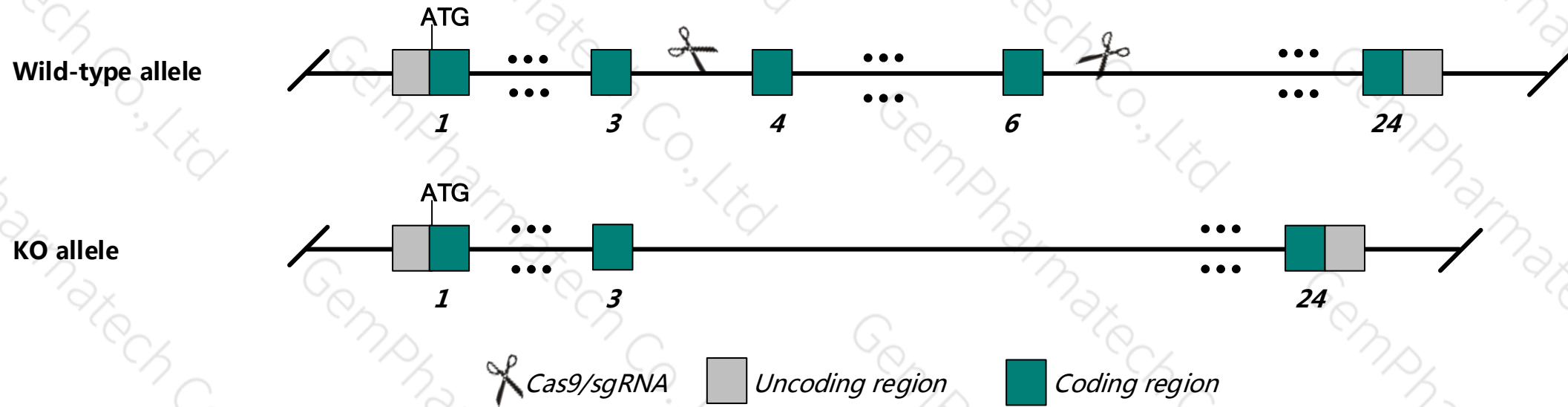
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptcd3* gene. The schematic diagram is as follows:



Technical routes

- The *Ptcd3* gene has 11 transcript. According to the structure of *Ptcd3* gene, exon4-6 of *Ptcd3*-201 (ENSMUST00000082094.4) transcript is recommended as the knockout region. The region contains 220bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptcd3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating Positive F0 generation mice with C57BL/6JGpt mice.

- The *Ptcd3* gene is located on the Chr6. 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)

Ptcd3 pentatricopeptide repeat domain 3 [*Mus musculus* (house mouse)]

Gene ID: 69956, updated on 12-Aug-2019

Summary



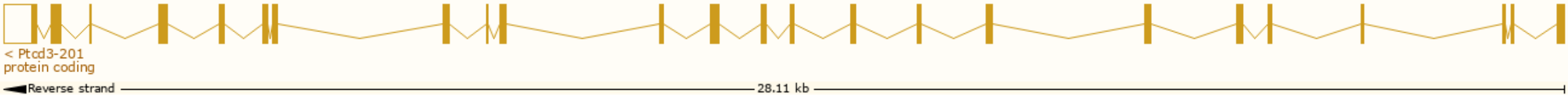
| | |
|--------------------|---|
| Official Symbol | Ptcd3 provided by MGI |
| Official Full Name | pentatricopeptide repeat domain 3 provided by MGI |
| Primary source | MGI:MGI:1917206 |
| See related | Ensembl:ENSMUSG00000063884 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | MRP-S39; AA589622; AU045708; 2610034F17Rik; 2810422B04Rik |
| Expression | Ubiquitous expression in CNS E11.5 (RPKM 15.2), liver E14 (RPKM 12.3) and 24 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

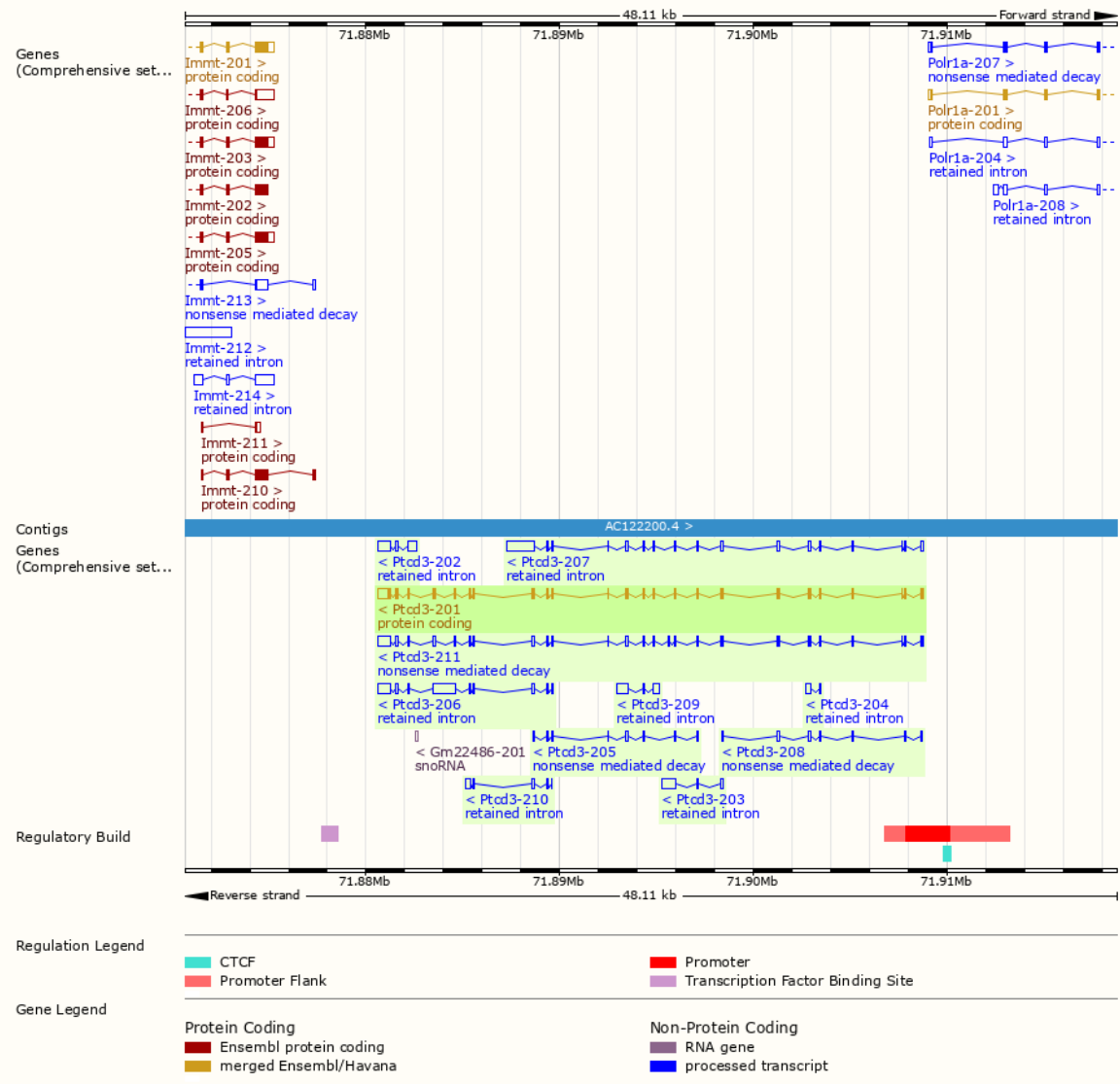
The gene has 11 transcripts, and all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|----------------------------|-------------------------------|
| Ptcd3-201 | ENSMUST00000082094.4 | 2581 | 685aa | Protein coding | CCDS20235 | Q14C51 | TSL:1 GENCODE basic APPRIS P1 |
| Ptcd3-211 | ENSMUST000000206879.1 | 2666 | 284aa | Nonsense mediated decay | - | A0A0U1RQ61 | TSL:1 |
| Ptcd3-205 | ENSMUST000000205556.1 | 588 | 51aa | Nonsense mediated decay | - | A0A0U1RP36 | CDS 5' incomplete TSL:5 |
| Ptcd3-208 | ENSMUST000000206284.1 | 545 | 59aa | Nonsense mediated decay | - | A0A0U1RNH5 | CDS 5' incomplete TSL:3 |
| Ptcd3-207 | ENSMUST000000205761.1 | 2680 | No protein | Retained intron | - | - | TSL:1 |
| Ptcd3-206 | ENSMUST000000205691.1 | 2364 | No protein | Retained intron | - | - | TSL:2 |
| Ptcd3-202 | ENSMUST000000205269.1 | 1161 | No protein | Retained intron | - | - | TSL:1 |
| Ptcd3-209 | ENSMUST000000206631.1 | 949 | No protein | Retained intron | - | - | TSL:2 |
| Ptcd3-203 | ENSMUST000000205293.1 | 853 | No protein | Retained intron | - | - | TSL:2 |
| Ptcd3-210 | ENSMUST000000206762.1 | 521 | No protein | Retained intron | - | - | TSL:5 |
| Ptcd3-204 | ENSMUST000000205420.1 | 320 | No protein | Retained intron | - | - | TSL:2 |

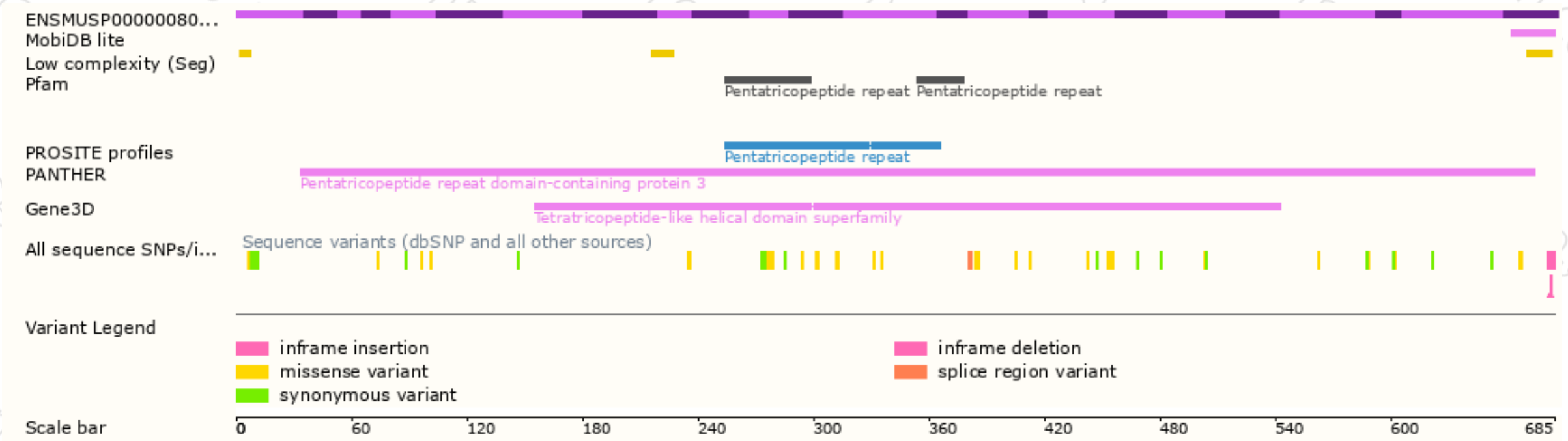
The strategy is based on the design of *Ptcd3-201* transcript, The transcription is shown below:



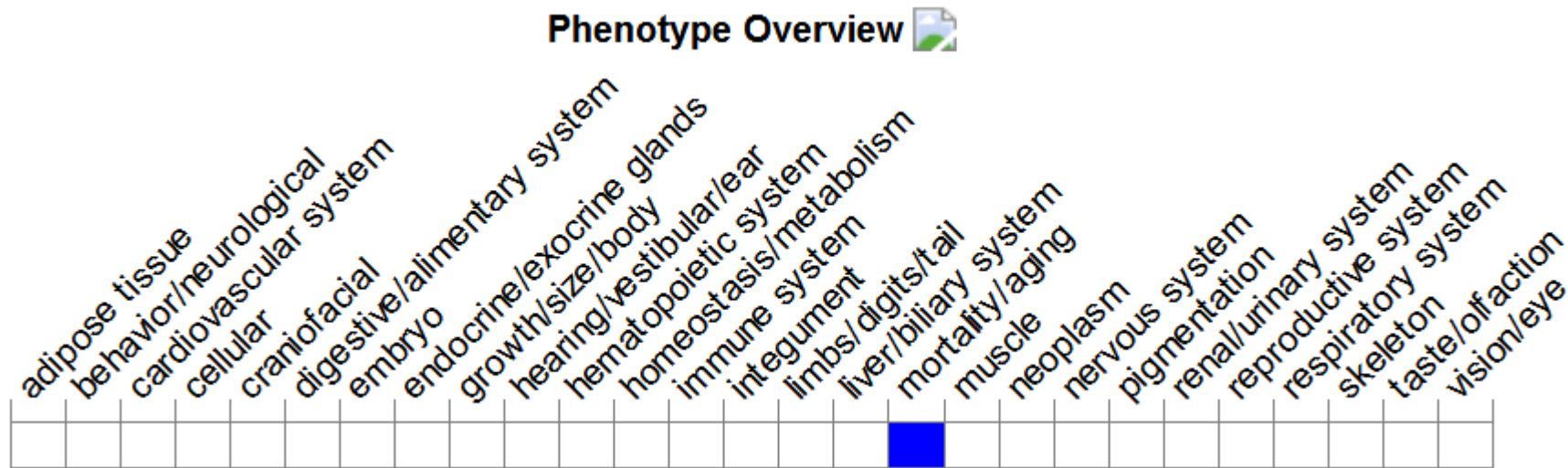
Genomic location (Ensembl)



Protein domain (Ensembl)



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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