

# *Phf10* Cas9-KO Strategy

|                     |                   |
|---------------------|-------------------|
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| <b>Reviewer</b>     | <b>Huan Wang</b>  |
| <b>Design Date:</b> | <b>2019-12-16</b> |

# Project Overview

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**Project Name**

***Phf10***

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**Project type**

**Cas9-KO**

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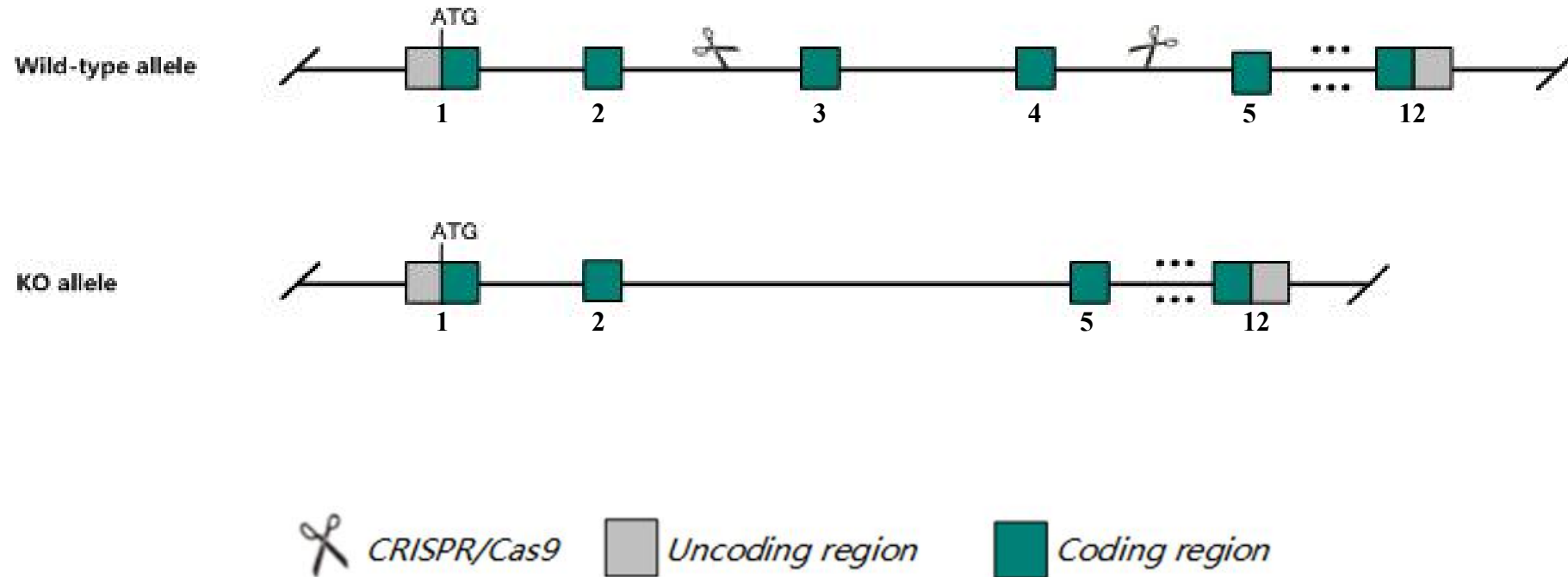
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phf10* gene. The schematic diagram is as follows:



The *Phf10* gene has 5 transcripts. According to the structure of *Phf10* gene, exon3-exon4 of *Phf10-201* (ENSMUST00000024657.11) transcript is recommended as the knockout region. The region contains 215bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Phf10* gene. The brief process is as follows: CRISPR/Cas9 system

According to the existing MGI data, Mice homozygous for a floxed allele are viable and fertile.

The KO region contains functional region of the *1600012H06Rik* gene. Knockout the region may affect the function of *1600012H06Rik* gene.

The *Phf10* gene is located on the Chr17. 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.

## Phf10 PHD finger protein 10 [Mus musculus (house mouse)]

Gene ID: 72057, updated on 19-Feb-2019

### Summary



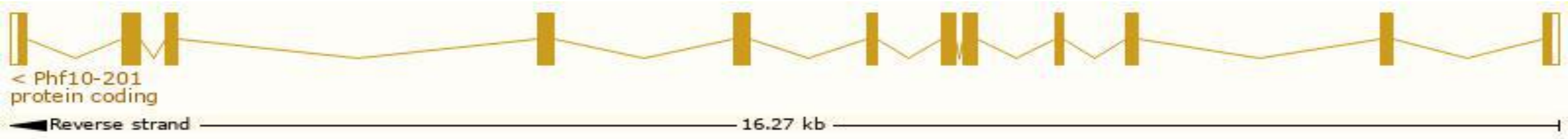
|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Phf10 provided by <a href="#">MGI</a>   |
| <b>Official Full Name</b> | PHD finger protein 10 provided by <a href="#">MGI</a>   |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1919307</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000023883</a>  |
| <b>Gene type</b>          | protein coding  |
| <b>RefSeq status</b>      | VALIDATED   |
| <b>Organism</b>           | <a href="#">Mus musculus</a>  |
| <b>Lineage</b>            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| <b>Also known as</b>      | 1810055P05Rik, AV024533   |
| <b>Expression</b>         | Ubiquitous expression in liver E14 (RPKM 29.8), liver E14.5 (RPKM 23.5) and 25 other tissues <a href="#">See more</a>   |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>   |

# Transcript information      Ensembl

The gene has 5 transcripts,all transcripts are shown below:

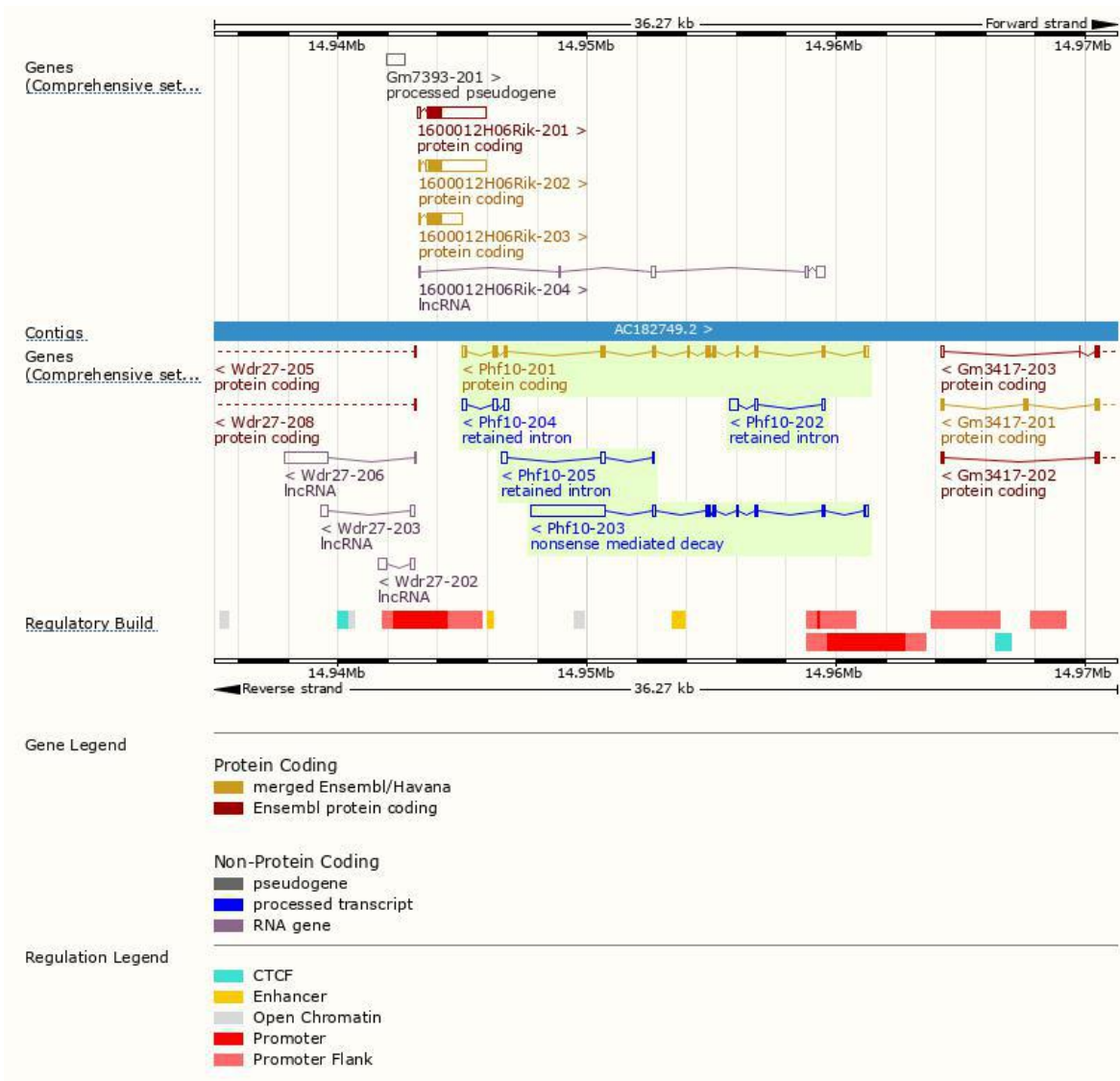
| Name      | Transcript ID                         | bp   | Protein               | Biotype                 | CCDS                      | UniProt                | Flags                         |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|-------------------------------|
| Phf10-201 | <a href="#">ENSMUST00000024657.11</a> | 1663 | <a href="#">497aa</a> | Protein coding          | <a href="#">CCDS28407</a> | <a href="#">K4DI61</a> | TSL:1 GENCODE basic APPRIS P1 |
| Phf10-203 | <a href="#">ENSMUST00000168938.2</a>  | 3901 | <a href="#">234aa</a> | Nonsense mediated decay | -                         | <a href="#">E9Q5L7</a> | TSL:5                         |
| Phf10-202 | <a href="#">ENSMUST00000167805.1</a>  | 597  | No protein            | Retained intron         | -                         | -                      | TSL:5                         |
| Phf10-204 | <a href="#">ENSMUST00000171526.1</a>  | 534  | No protein            | Retained intron         | -                         | -                      | TSL:2                         |
| Phf10-205 | <a href="#">ENSMUST00000172054.1</a>  | 441  | No protein            | Retained intron         | -                         | -                      | TSL:3                         |

The strategy is based on the design of *Phf10-201* 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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