

# Thap11 Cas9-CKO Strategy

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Design Date: 2024-04-10

# Overview

## Target Gene Name

- Thap11

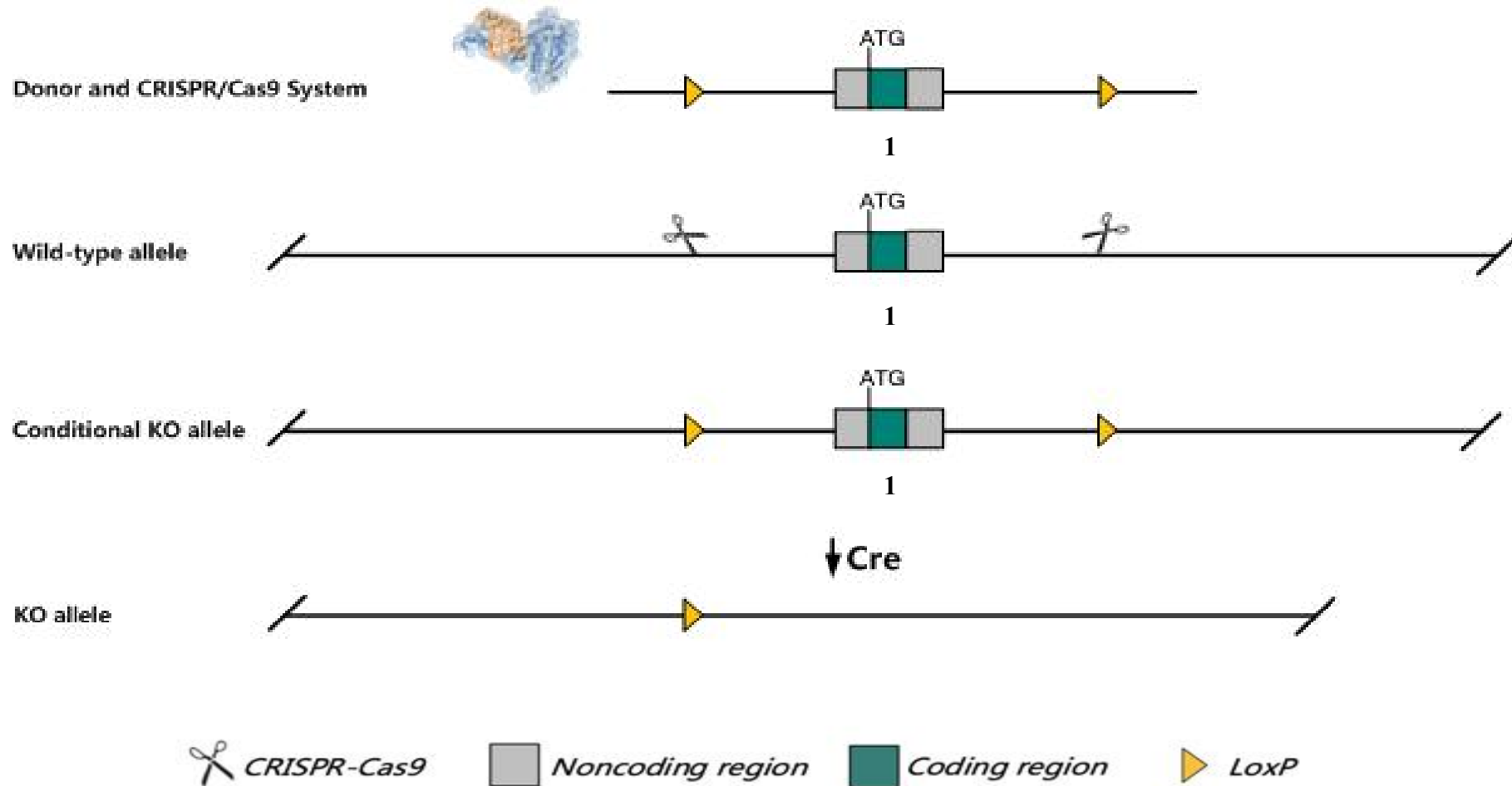
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Thap11* gene.

# Technical Information

- The *Thap11* gene has 1 transcript. According to the structure of *Thap11* gene, exon1 of *Thap11*-201 (ENSMUST00000040445.9) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Thap11* 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

## Thap11 THAP domain containing 11 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 59016, updated on 5-Mar-2024

### Summary

Official Symbol	Thap11 provided by <a href="#">MGI</a>
Official Full Name	THAP domain containing 11 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1930964</a>
See related	<a href="#">Ensembl:ENSMUSG00000036442</a> <a href="#">AllianceGenome:MGI:1930964</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ronin; CTG-B43a; CTG-B45d; 2810036E22Rik
Summary	Predicted to enable DNA-binding transcription repressor activity, RNA polymerase II-specific; RNA polymerase II cis-regulatory region sequence-specific DNA binding activity; and zinc ion binding activity. Predicted to be involved in negative regulation of transcription by RNA polymerase II. Predicted to be located in cytosol. Predicted to be active in nucleoplasm. Is expressed in 1-cell stage embryo; brain ventricular layer; forelimb bud; inferior colliculus; and oocyte. Orthologous to human THAP11 (THAP domain containing 11). [provided by Alliance of Genome Resources, Apr 2022]
Orthologs	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

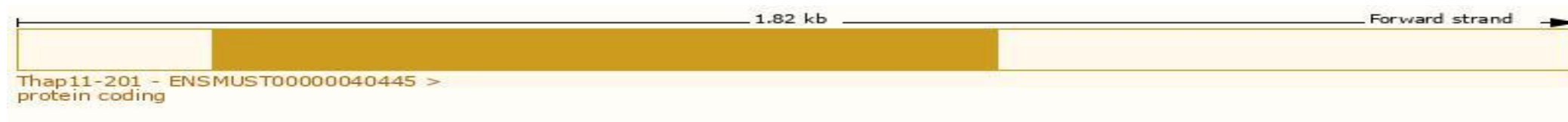
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

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

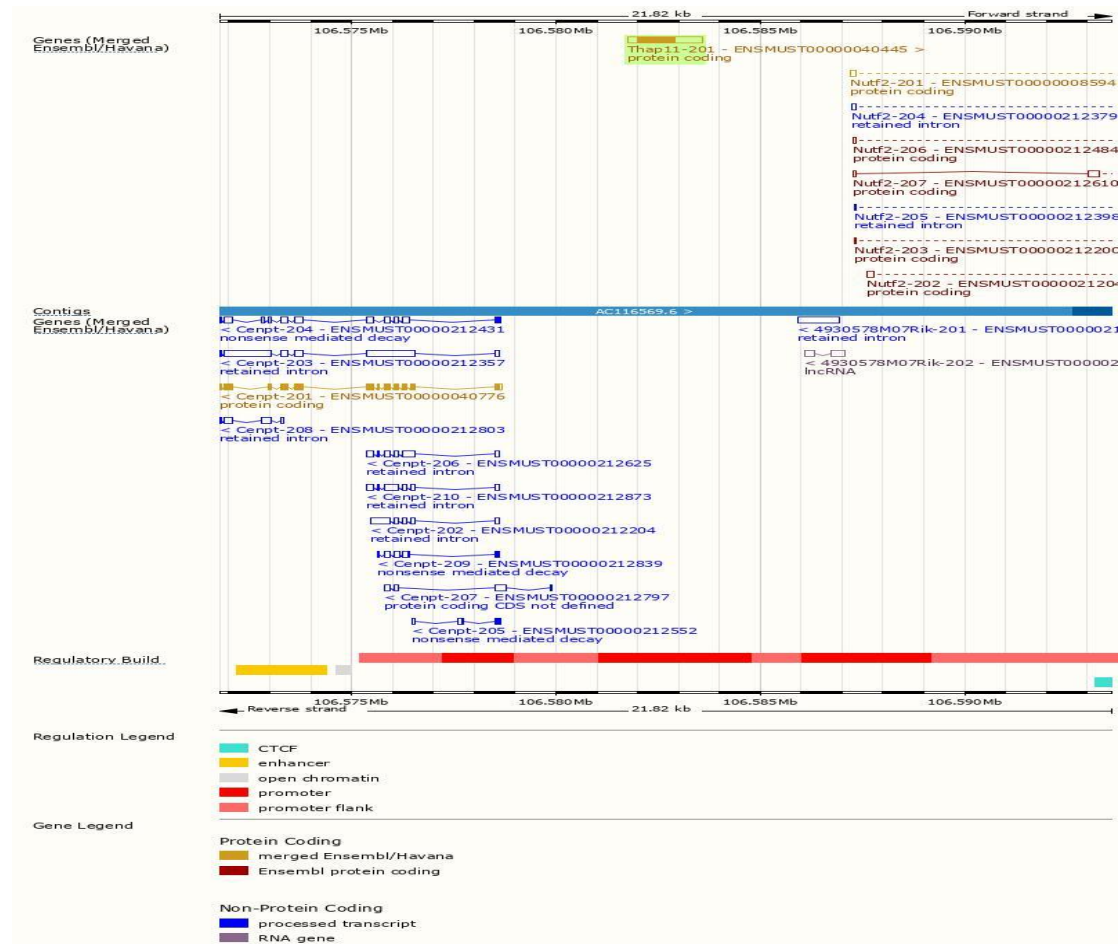
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
<a href="#">ENSMUST00000040445.9</a>	Thap11-201	1819	<a href="#">305aa</a>	Protein coding	<a href="#">CCDS22616</a>	<a href="#">Q9JJD0</a>	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:NA

The strategy is based on the design of *Thap11*-201 transcript, the transcription is shown below:



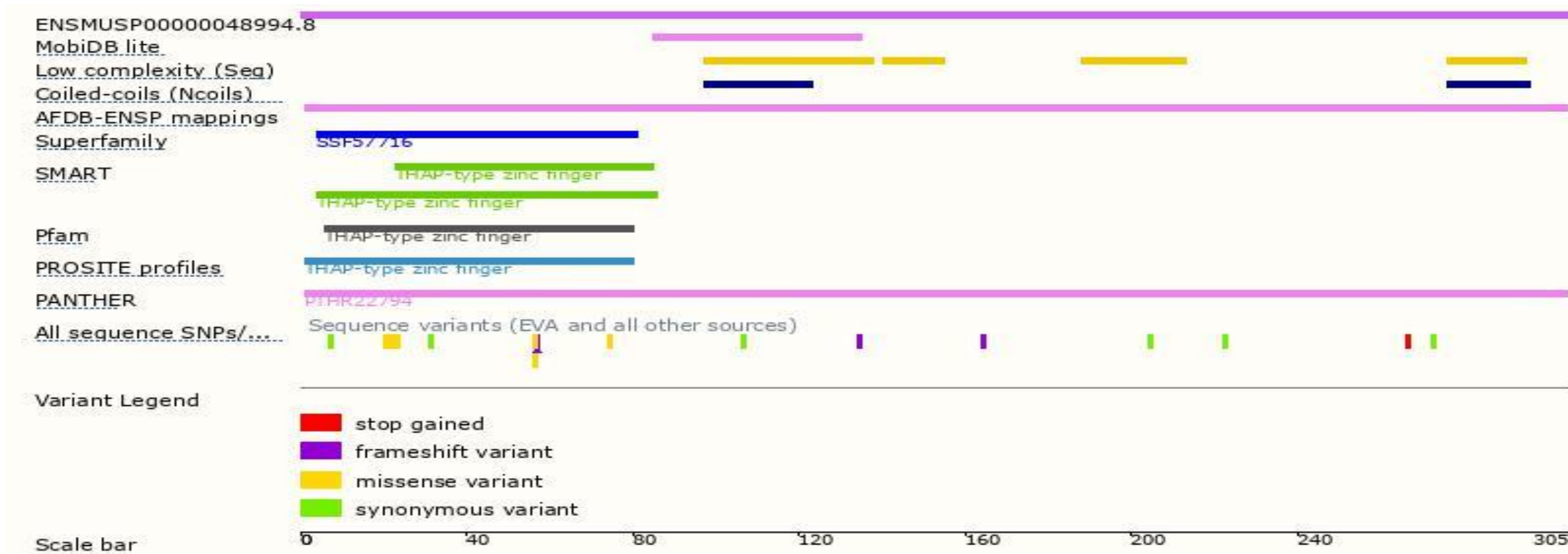
Source: <https://www.ensembl.org>

# Genomic Information





# Protein Information





# Mouse Phenotype Information (MGI)

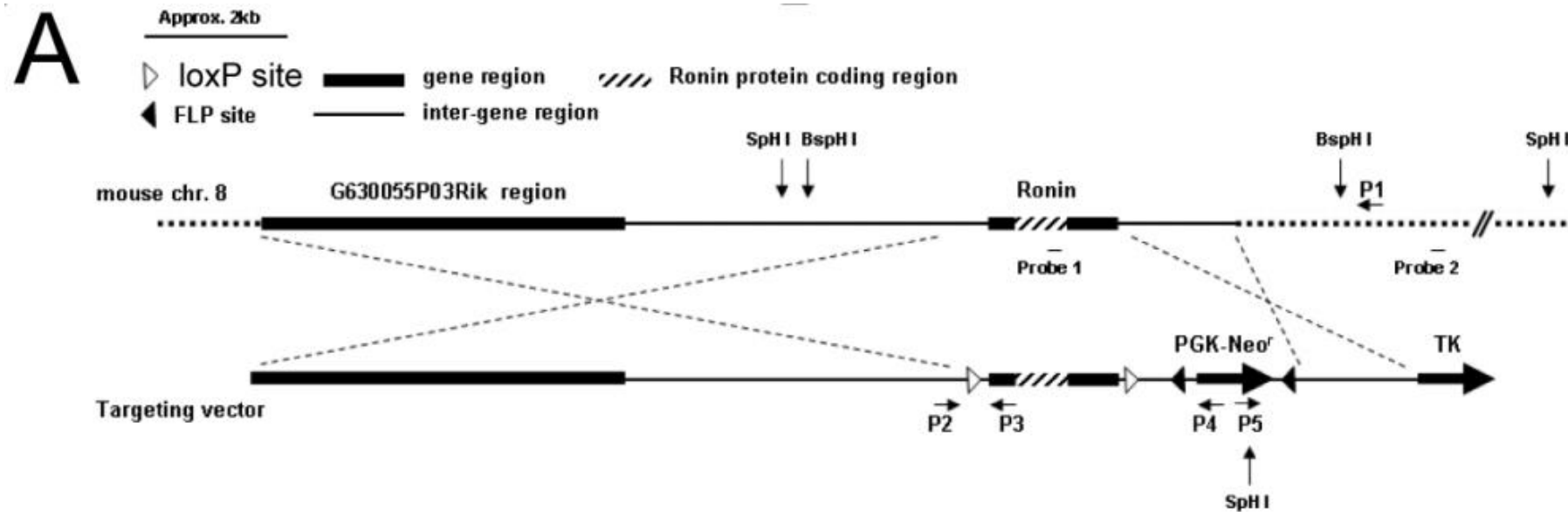


- Homozygous inactivation of this gene leads to peri-implantation lethality and defects in the inner cell mass. Homozygous null ES cells are not viable.

# Important Information

- According to the existing MGI data, homozygous inactivation of this gene leads to peri-implantation lethality and defects in the inner cell mass. Homozygous null ES cells are not viable.
- The *Thap11* gene is about 1.8 kb away from the N-terminus of the *Cenpt* gene, this strategy may influence the regulatory function of the N-terminal of *Cenpt* gene.
- The *Thap11* gene is about 3.5 kb away from the N-terminus of the *Nutf2* gene, this strategy may influence the regulatory function of the N-terminal of *Nutf2* gene.
- Both loxp are located in the promoter region of the *Thap11* gene, this strategy may influence the regulatory function of the *Thap11* gene.
- *Thap11* is located on Chr8. 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.

# References



(A) Illustration of the gene targeting strategy to create a conditional knockout mouse model. loxP flanked Ronin is located between two regions of low homology.

Dejosez M, Krumenacker JS, Ziturs LJ, Passeri M, Chu LF, Songyang Z, Thomson JA, Zwaka TP. Ronin is essential for embryogenesis and the pluripotency of mouse embryonic stem cells. *Cell*. 2008 Jun 27;133(7):1162-74. doi: 10.1016/j.cell.2008.05.047. Erratum in: *Cell*. 2008 Aug 22;134(4):692. PMID: 18585351; PMCID: PMC2495776.