

# *Calhm4* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Calhm4*

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**Project type**

**Cas9-KO**

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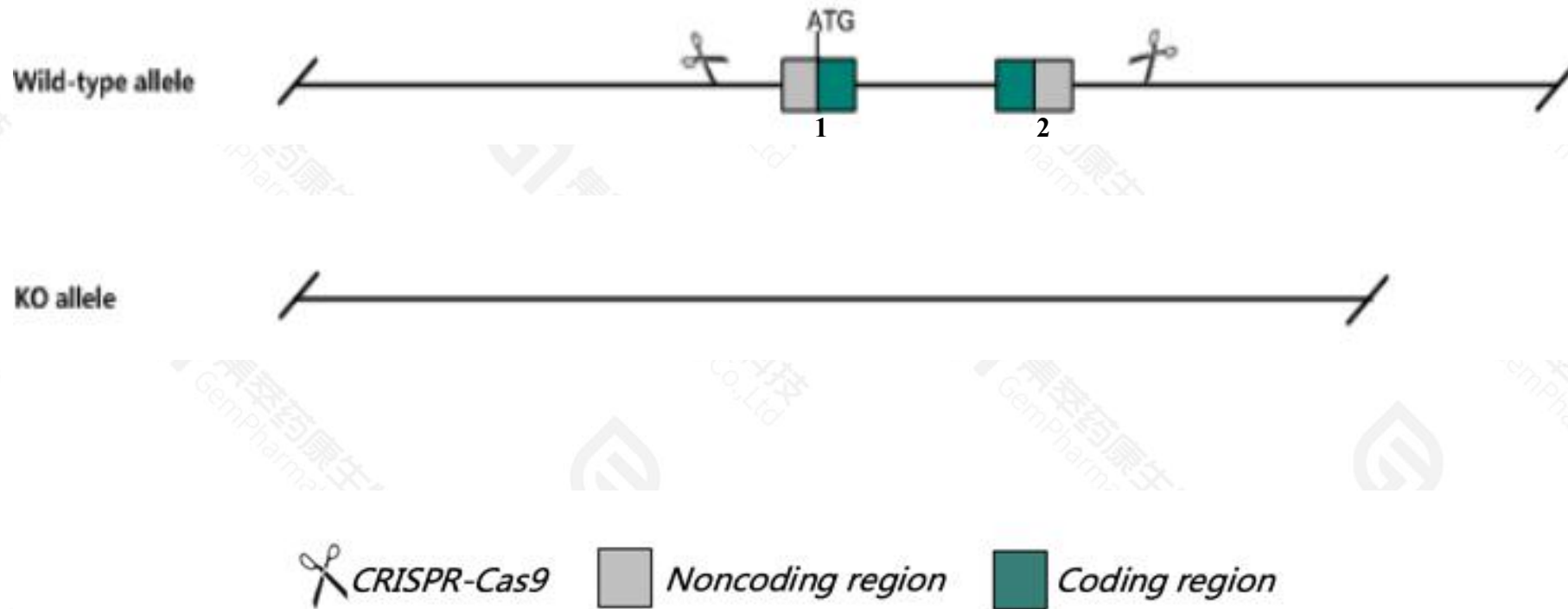
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Calhm4* gene. The schematic diagram is as follows:



- The *Calhm4* gene has 2 transcripts. According to the structure of *Calhm4* gene, exon1-exon2 of *Calhm4*-201(ENSMUST00000048052.7) 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 *Calhm4* gene. The brief process is as follows: CRISPR-Cas9 system 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 KO region contains partial intron of the *Trappc3l* gene. Knockout the region may affect the function of *Trappc3l* gene.
- The *Calhm4* gene is located on the Chr10. 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)

## Calhm4 calcium homeostasis modulator family member 4 [ *Mus musculus* (house mouse) ]

Gene ID: 270711, updated on 24-Apr-2022

[Download Datasets](#)

### Summary

Official Symbol	Calhm4 provided by <a href="#">MGI</a>
Official Full Name	calcium homeostasis modulator family member 4 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:2685489</a>
See related	<a href="#">Ensembl:ENSMUSG00000039508</a> <a href="#">AllianceGenome:MGI:2685489</a>
Gene type	protein coding
RefSeq status	PROVISIONAL
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	Gm643; Fam26d; AI586164; 4732454E20Rik
Summary	Predicted to enable cation channel activity. Predicted to act upstream of or within ion transport. Predicted to be located in membrane. Predicted to be integral component of membrane. Predicted to be integral component of plasma membrane. Orthologous to human CALHM4 (calcium homeostasis modulator family member 4). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Low expression observed in reference dataset <a href="#">See more</a>
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>

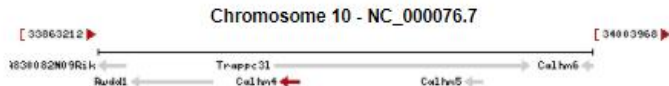
### Genomic context

Location: 10; 10 B1

See Calhm4 in [Genome Data Viewer](#)

Exon count: 2

Annotation release	Status	Assembly	Chr	Location
<a href="#">109</a>	current	GRCm39 ( <a href="#">GCF_000001635.27</a> )	10	NC_000076.7 (33914780..33920309, complement)
108.20200622	previous assembly	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	10	NC_000076.6 (34038784..34044313, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	10	NC_000076.5 (33758590..33764119, complement)

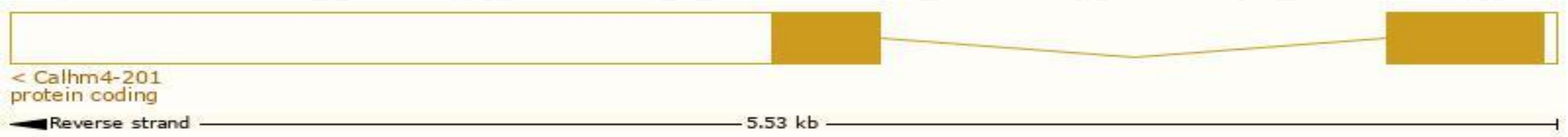


# Transcript information (Ensembl)

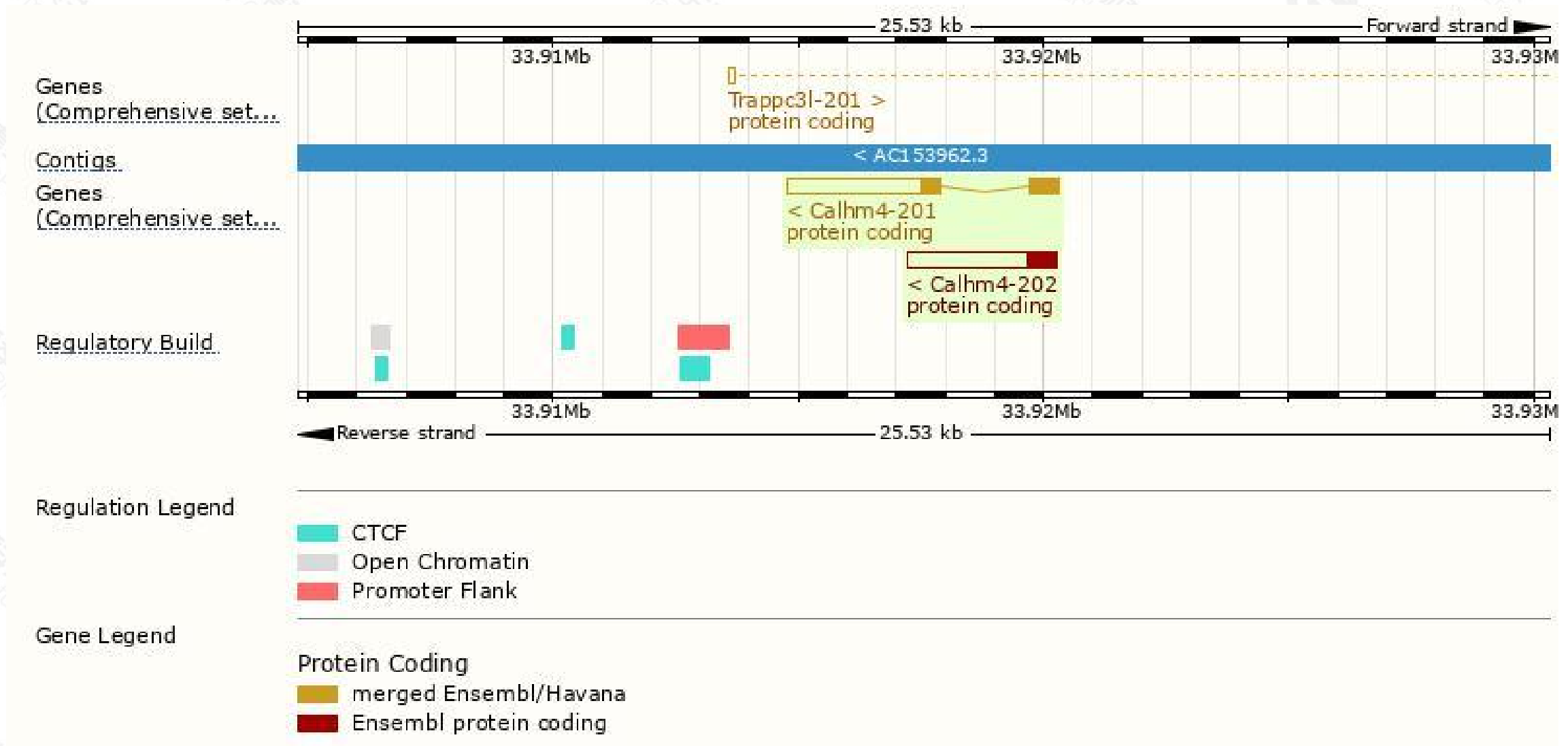
The gene has 2 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000048052.7</a>	Calhm4-201	3711	<a href="#">315aa</a>	Protein coding	<a href="#">CCDS35878</a>	<a href="#">Q8CE93</a>	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000218239.2</a>	Calhm4-202	3075	<a href="#">190aa</a>	Protein coding		<a href="#">A0A1W2P6Z6</a>	GENCODE basic TSL:NA

The strategy is based on the design of *Calhm4-201* 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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