

Haus1 Cas9-KO Strategy

Designer: Yanhua Shen

Reviewer: Xueting Zhang

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Overview

Target Gene Name

• Haus1

Project Type

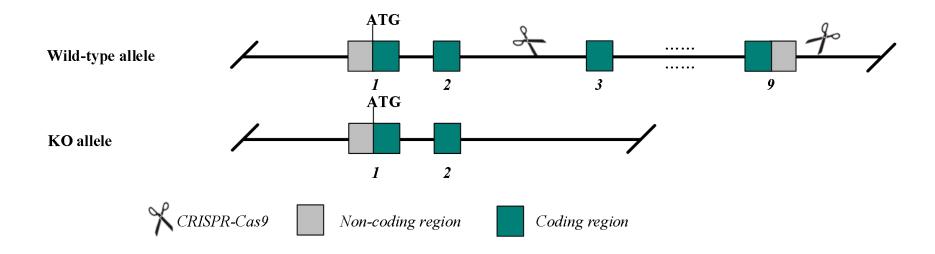
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy

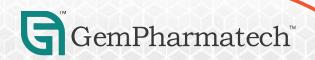


Schematic representation of CRISPR-Cas9 engineering used to edit the Haus1 gene.



Technical Information

- The *Haus1* gene has 3 transcripts. According to the structure of *Haus1* gene, exon3-9 of *Haus1*-201 (ENSMUST00000048192.9) transcript is recommended as the knockout region. The region contains most of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Haus1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 ontarget 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.



Gene Information

Haus1 HAUS augmin-like complex, subunit 1 [Mus musculus (house mouse)]

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Gene ID: 225745, updated on 5-Mar-2024

Summary



Official Symbol Haus1 provided by MGI
Official Full Name HAUS augmin-like complex, subunit 1 provided by MGI

Primary source MGI:MGI:2385076

See related Ensembl: ENSMUSG00000041840 AllianceGenome: MGI: 2385076

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 Ccdc5; HEI-C

Summary Predicted to be involved in centrosome cycle and spindle assembly. Predicted to act upstream of or within cell division. Predicted to be located in centrosome and mitotic

spindle microtubule. Predicted to be part of HAUS complex. Predicted to be active in cytosol. Is expressed in alimentary system; brain ventricular layer; chondrocranium;

liver lobe; and renal cortex. Orthologous to human HAUS1 (HAUS augmin like complex subunit 1). [provided by Alliance of Genome Resources, Apr 2022]

Expression Broad expression in CNS E11.5 (RPKM 6.2), testis adult (RPKM 5.4) and 19 other tissues See more

Orthologs human all

Try the new Gene table

Try the new Transcript table

≜ Genomic context

≈ ?

Location: 18 E3; 18 52.38 cM

See Haus1 in Genome Data Viewer

Exon count: 15

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

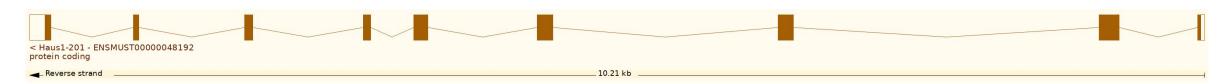


Transcript Information

The gene has 3 transcripts, all transcript are shown below:

Transcript ID	Name	bp 🛊	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000236234.2	Haus1-202	1226	293aa	Protein coding		A0A494BB26₺	Ensembl Canonical GENCODE basic
ENSMUST00000048192.9	Haus1-201	1003	278aa	Protein coding	CCDS29357₺	Q8BHX1 ₽	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000236575.2	Haus1-203	6882	No protein	Retained intron		2	2

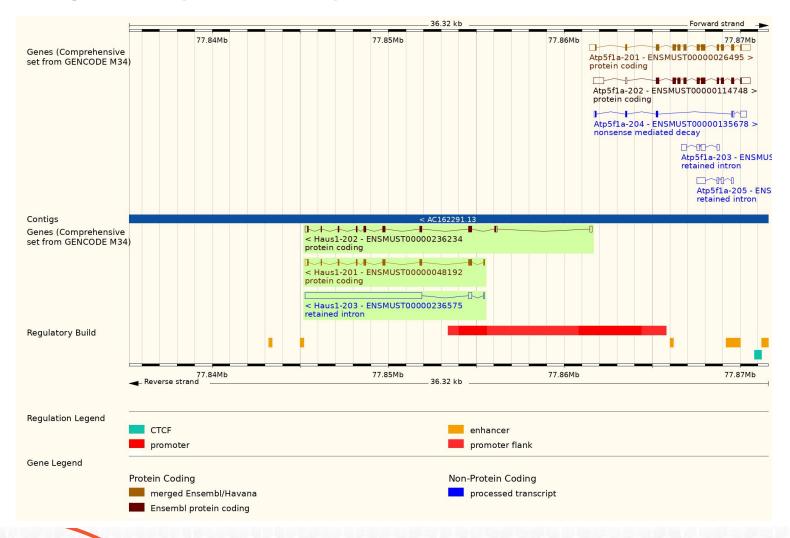
The strategy is based on the design of *Haus1-201* transcript, the transcription is shown below:



Source: https://www.ensembl.org



Genomic Information





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

Protein Information





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

Important Information

- Some amino acids will remain at the N-terminus and some functions may be retained.
- After breeding verification, the knockout homozygous mice has an embryonic lethal phenotype.
- *Haus1* is located on Chr18. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

