

Ccnh Cas9-KO Strategy

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Design Date:

2020-1-22

Project Overview



Project Name Ccnh

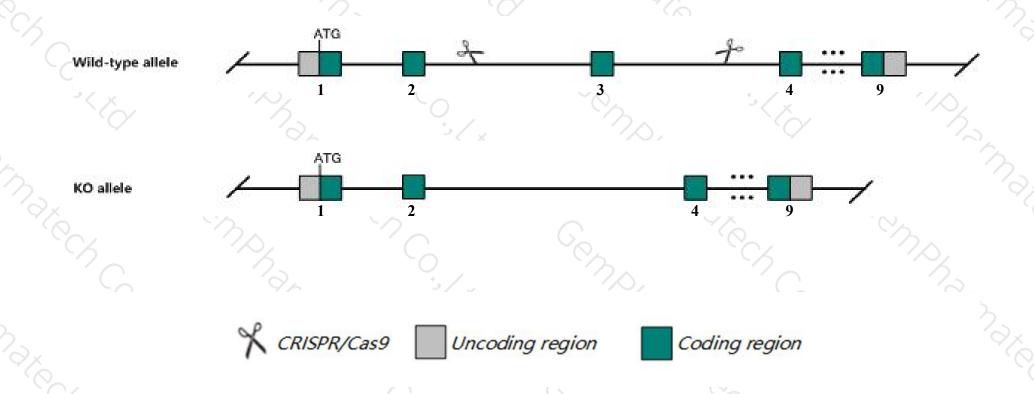
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Ccnh* gene has 7 transcripts. According to the structure of *Ccnh* gene, exon3 of *Ccnh-201*(ENSMUST00000022030.10) transcript is recommended as the knockout region. The region contains 74bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ccnh* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > The *Ccnh* gene is located on the Chr13. 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.
- > Transcript *Ccnh*-203 may not be affected.
- 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)



Ccnh cyclin H [Mus musculus (house mouse)]

Gene ID: 66671, updated on 10-Oct-2019

Summary

☆ ?

Official Symbol Ccnh provided by MGI

Official Full Name cyclin H provided by MGI

Primary source MGI:MGI:1913921

See related Ensembl: ENSMUSG00000021548

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 Al661354; AV102684; AW538719; 6330408H09Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 14.7), CNS E18 (RPKM 11.2) and 26 other tissues See more

Orthologs human all

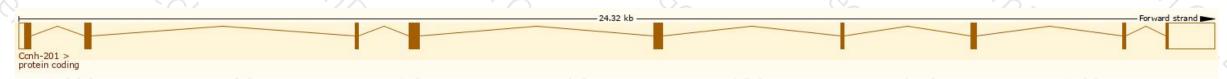
Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

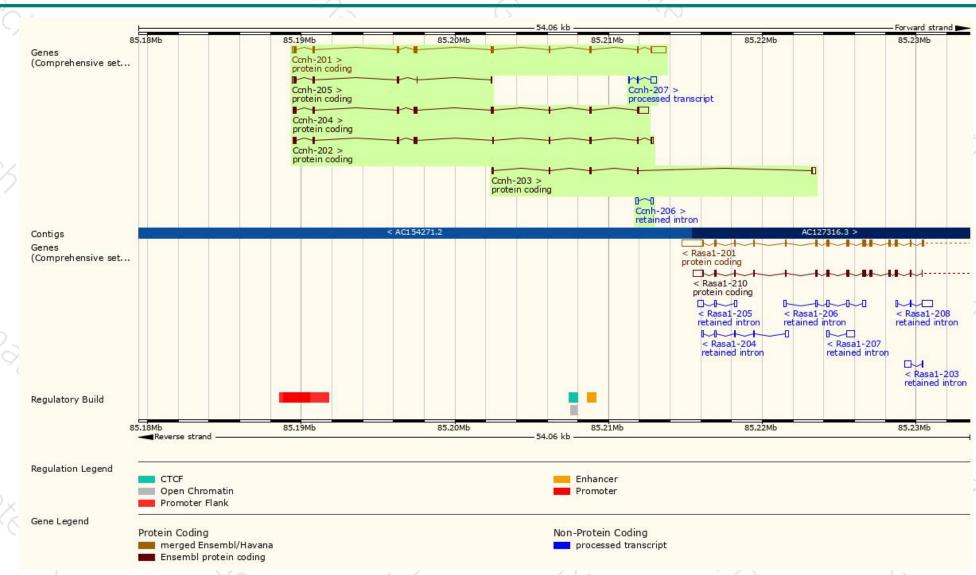
Name	Transcript ID	bp 🍦	Protein	Biotype	CCDS	UniProt	Flags
Ccnh-201	ENSMUST00000022030.10	2045	<u>323aa</u>	Protein coding	CCDS26666 ₽	Q61458₽	TSL:1 GENCODE basic APPRIS P1
Ccnh-202	ENSMUST00000163600.7	1055	287aa	Protein coding	CCDS84047 ₺	E9PWD3@	TSL:5 GENCODE basic
Ccnh-204	ENSMUST00000164127.7	1718	<u>327aa</u>	Protein coding		Q3UUW5₽	TSL:1 GENCODE basic
Ccnh-203	ENSMUST00000163713.1	599	<u>121aa</u>	Protein coding		F7D1U6₽	CDS 5' incomplete TSL:2
Ccnh-205	ENSMUST00000165077.7	527	<u>142aa</u>	Protein coding	-	E9QA43 €	CDS 3' incomplete TSL:1
Ccnh-207	ENSMUST00000172029.1	465	No protein	Processed transcript	-	-	TSL:5
Ccnh-206	ENSMUST00000166932.1	297	No protein	Retained intron	42	-	TSL:2

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



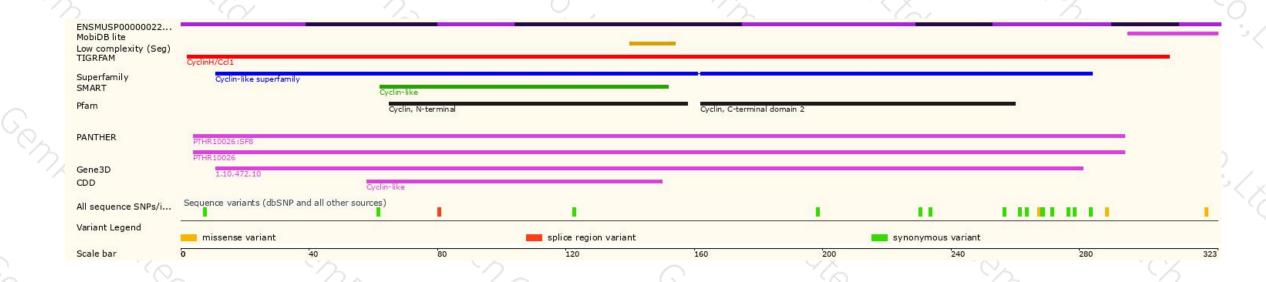
Genomic location distribution





Protein domain







If you have any questions, you are welcome to inquire. Tel: 400-9660890





