

# Dnajc17 Cas9-KO Strategy

Designer: Mingzhu Xu

Reviewer: Xioajing Li

Design Date: 2023-12-5

# Overview

## Target Gene Name

- Dnajc17

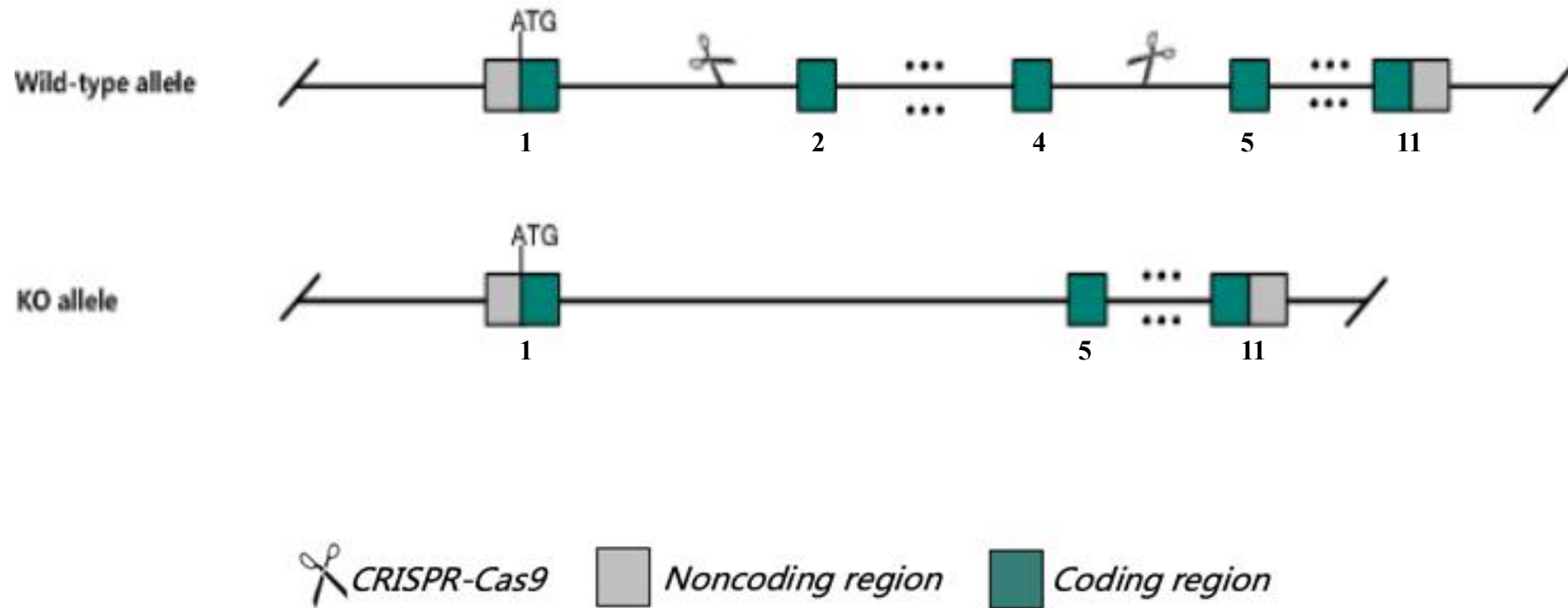
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



# Technical Information

- The *Dnajc17* gene has 3 transcripts. According to the structure of *Dnajc17* gene, exon2-exon4 of *Dnajc17*-201 (ENSMUST00000038439.4) transcript is recommended as the knockout region. The region contains 217bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Dnajc17* 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 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.

# Gene Information

## Dnajc17 DnaJ heat shock protein family (Hsp40) member C17 [Mus musculus (house mouse)]

Gene ID: 69408, updated on 12-Apr-2023

### Summary

<b>Official Symbol</b>	Dnajc17 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	DnaJ heat shock protein family (Hsp40) member C17 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1916658</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000034278</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>	1700025B16Rik, D9Bwg1371e
<b>Summary</b>	Predicted to enable RNA binding activity. Acts upstream of or within negative regulation of transcription by RNA polymerase II and toxin transport. Predicted to be located in cytoplasm and nucleus. Is expressed in brain; thyroid gland; and thyroid primordium. Orthologous to human DNAJC17 (DnaJ heat shock protein family (Hsp40) member C17). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 9.6), CNS E14 (RPKM 7.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

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

# Transcript Information

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

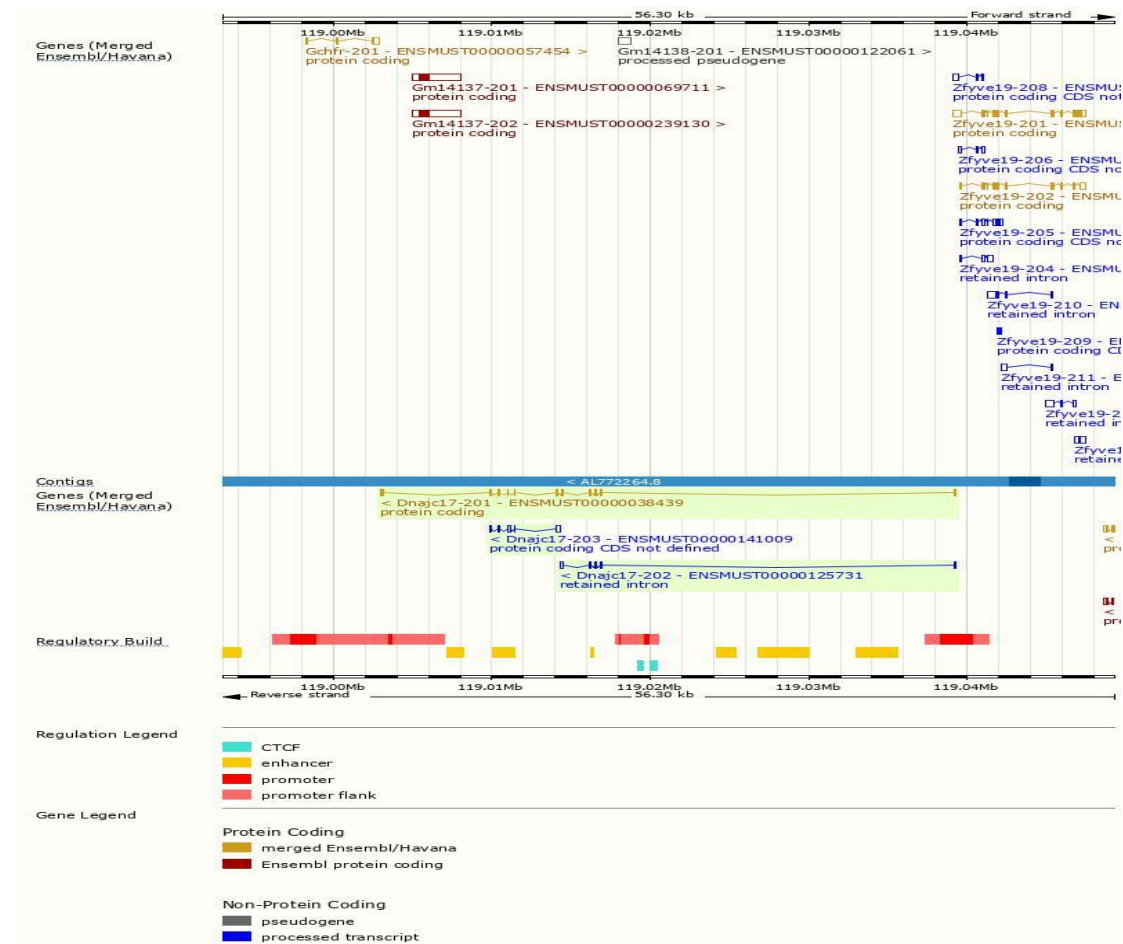
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
<a href="#">ENSMUST00000038439.4</a>	Dnajc17-201	1008	<a href="#">303aa</a>	Protein coding	<a href="#">CCDS16593</a>	<a href="#">Q91WT4</a>	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000141009.2</a>	Dnajc17-203	616	No protein	Protein coding CDS not defined		-	TSL:3	
<a href="#">ENSMUST00000125731.2</a>	Dnajc17-202	450	No protein	Retained intron		-	TSL:2	

The strategy is based on the design of *Dnajc17-201* transcript, the transcription is shown below:



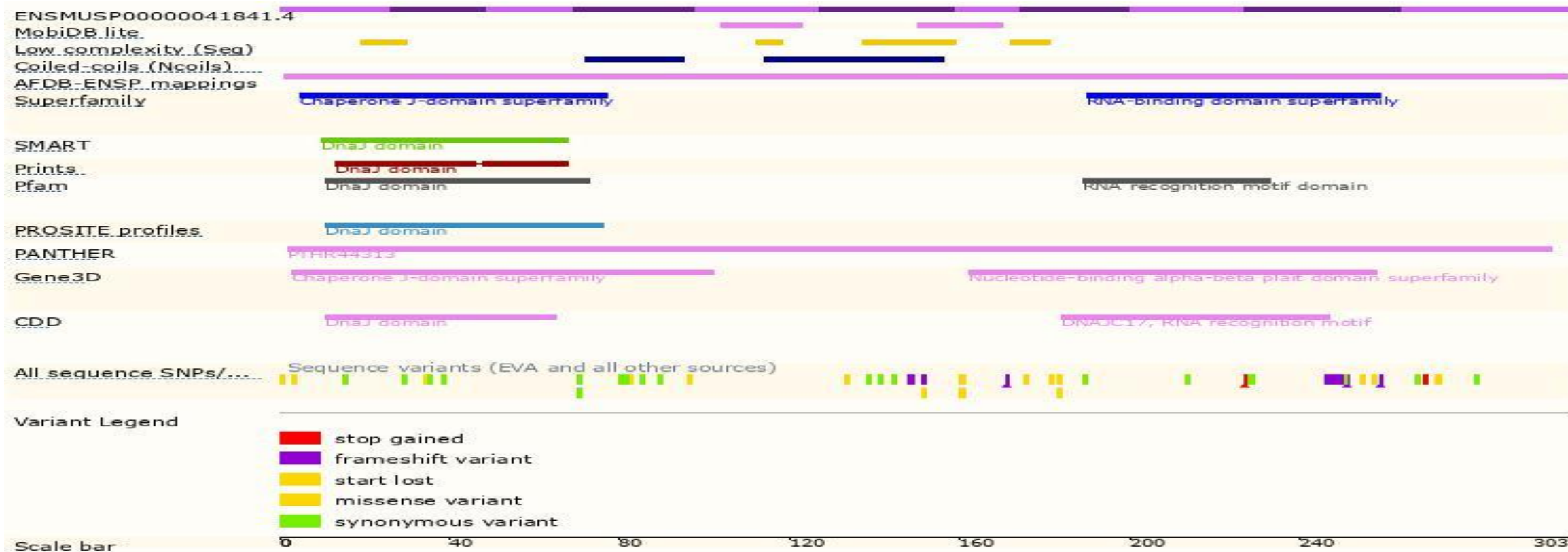
Source: <https://www.ensembl.org>

# Genomic Information



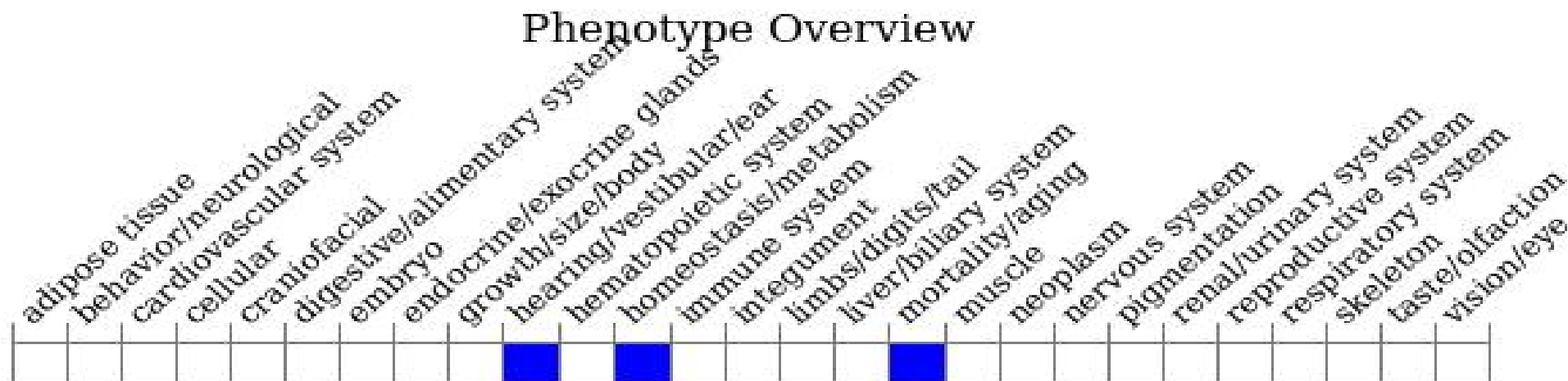


# Protein Information





# Mouse Phenotype Information (MGI)



- Mice homozygous for a gene trapped allele die before implantation.

# Important Information

- According to the existing MGI data, mice homozygous for a gene trapped allele die before implantation.
- The strategy may destroy the 5-terminal regulation function of *Gm14138*.
- *Dnajc17* is located on Chr2. 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.