GemPharmatech™

Dnajc15 Cas9-CKO Strategy

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Reviewer: Jiaojiao Yan

Design Date: 2024-3-7

Overview

Target Gene Name

- *Dnajc15*

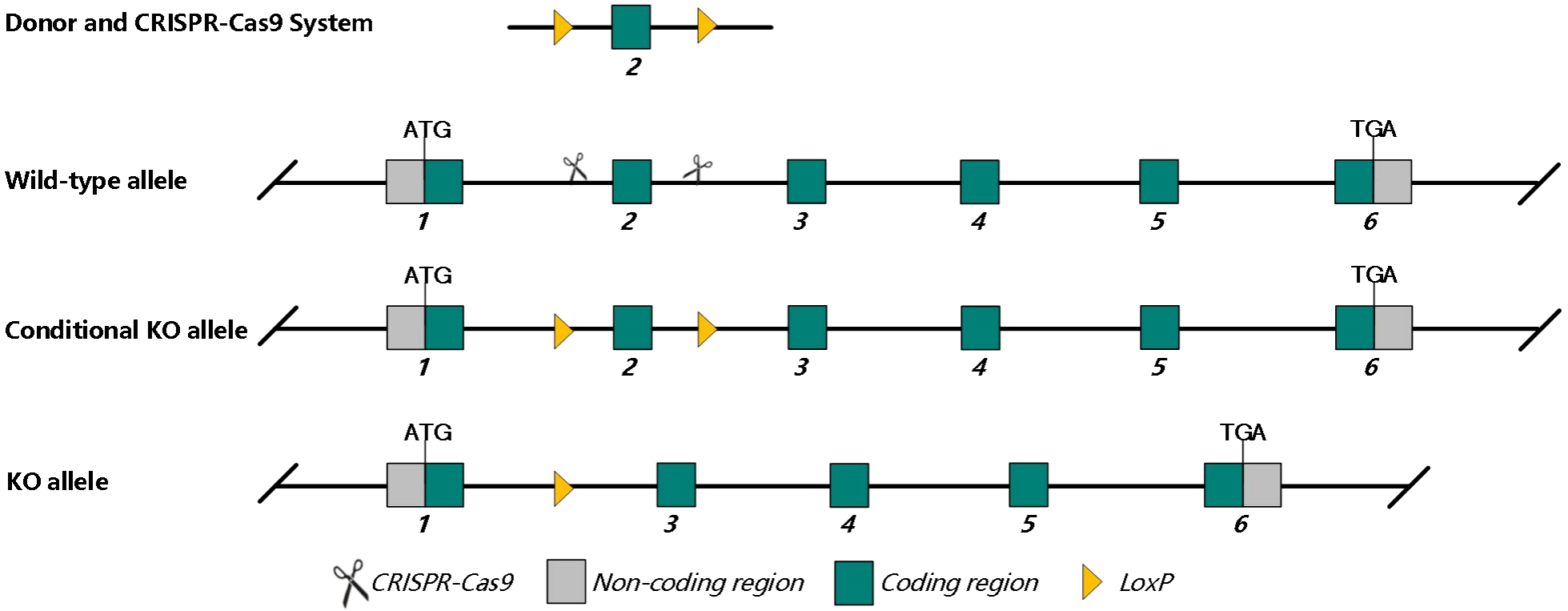
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Dnajc15* gene.

Technical Information

- The *Dnajc15* gene has 3 transcripts. According to the structure of *Dnajc15* gene, exon 2 of *Dnajc15*-202 (ENSMUST00000226459.2) is recommended as the knockout region. The region contains 52 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Dnajc15* 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

Dnajc15 DnaJ heat shock protein family (Hsp40) member C15 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 66148, updated on 5-Mar-2024

Summary

Official Symbol	Dnajc15 provided by MGI
Official Full Name	DnaJ heat shock protein family (Hsp40) member C15 provided by MGI
Primary source	MGI:MGI:1913398
See related	Ensembl:ENSMUSG00000022013 AllianceGenome:MGI:1913398
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MCJ; Dnajd1; 1110003P16Rik
Summary	Predicted to enable ATPase activator activity. Acts upstream of or within several processes, including cellular response to starvation; negative regulation of mitochondrial electron transport, NADH to ubiquinone; and negative regulation of protein-containing complex assembly. Located in mitochondrial inner membrane. Is expressed in endocrine gland; genitourinary system; heart; and nervous system. Orthologous to human DNAJC15 (DnaJ heat shock protein family (Hsp40) member C15). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in testis adult (RPKM 177.3), ovary adult (RPKM 65.1) and 27 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Genomic context

Location: 14 D3; 14 41.04 cM

See Dnajc15 in Genome Data Viewer

Exon count: 6

https://www.ncbi.nlm.nih.gov/gene/66148

Transcript Information

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

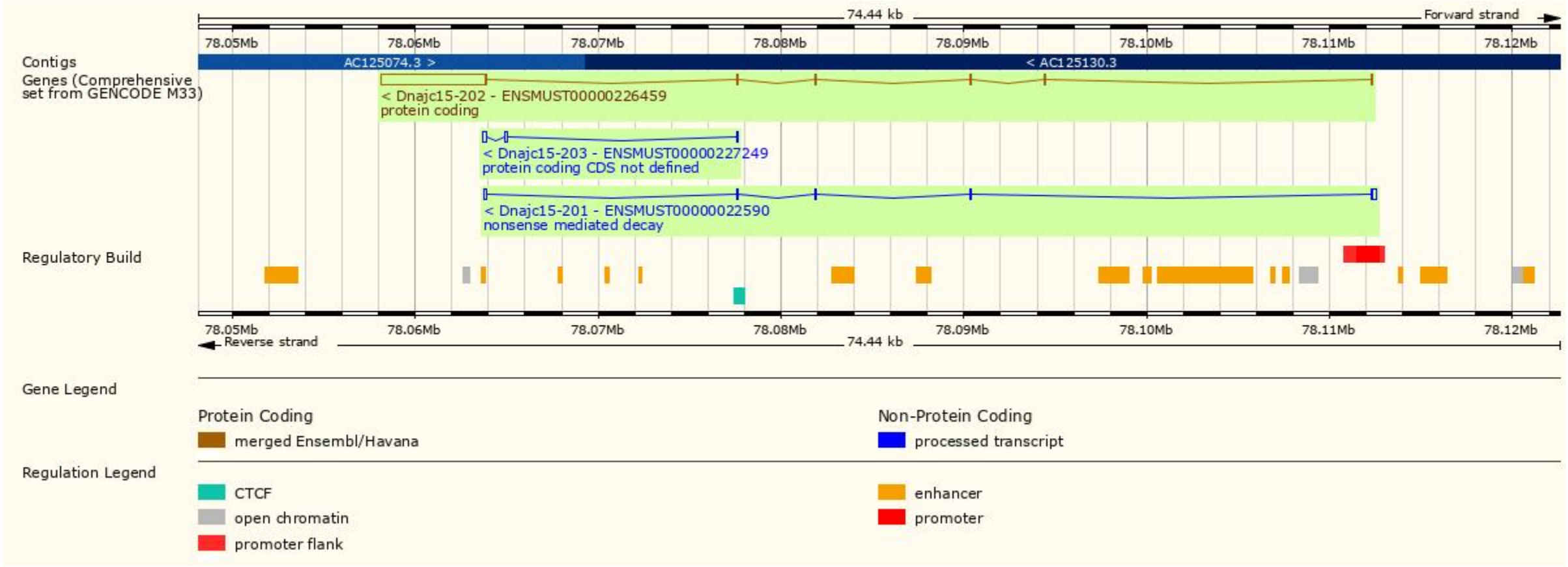
Show/hide columns (1 hidden) Filter

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000226459.2	Dnajc15-202	6193	149aa	Protein coding	CCDS27292	Q78YY6	Ensembl Canonical GENCODE basic APPRIS P1
ENSMUST00000022590.5	Dnajc15-201	674	44aa	Nonsense mediated decay		A0A2K6EDK0	TSL:1
ENSMUST00000227249.2	Dnajc15-203	419	No protein	Protein coding CDS not defined		-	-

The strategy is based on the design of *Dnajc15*-202 transcript, the transcription is shown below:

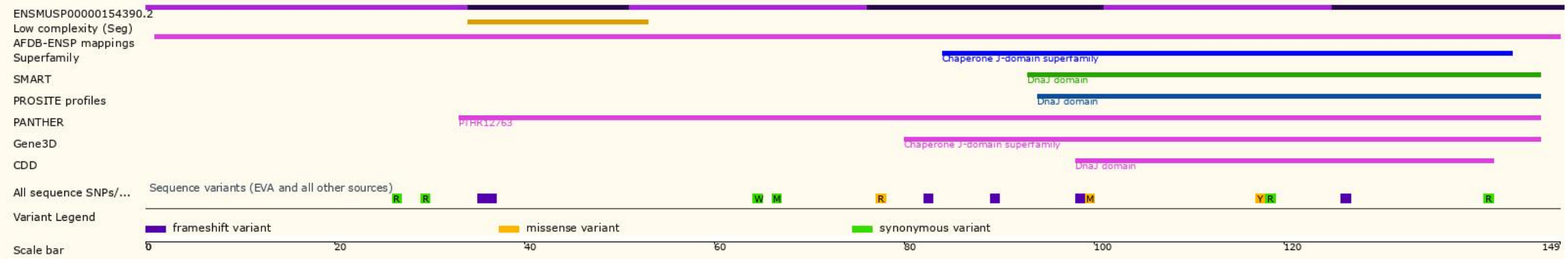
Source: http://asia.ensembl.org/

Genomic Information



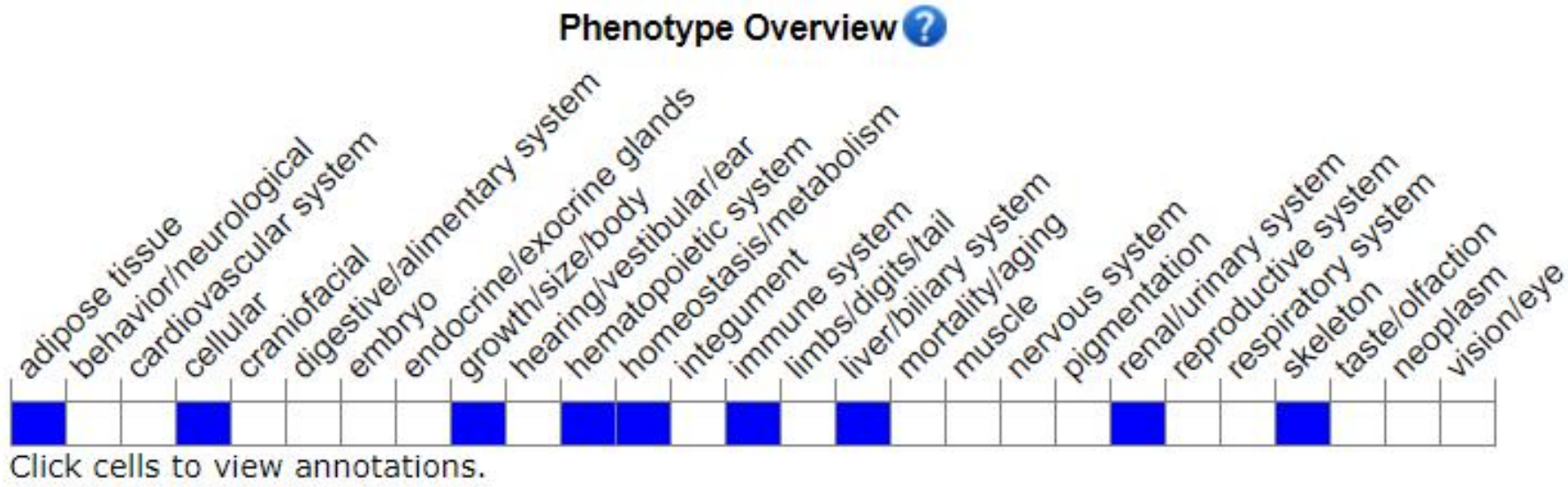
Source: http://asia.ensembl.org/

Protein Information



Source: https://www.ensembl.org

Mouse Phenotype Information (MGI)



Mice homozygous for a knock-out allele exhibit increased mitochondrial activity that results in rapid metabolism in fasted mice or mice fed a high fat diet.

Source: https://www.informatics.jax.org

Important Information

- This stratergy may not affect *Dnajc15*-203 transcript.
- *Dnajc15* is located on Chr 14. 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.