

Zc3hav1 Cas9-KO Strategy

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Project Overview

Project Name

Zc3hav1

Project type

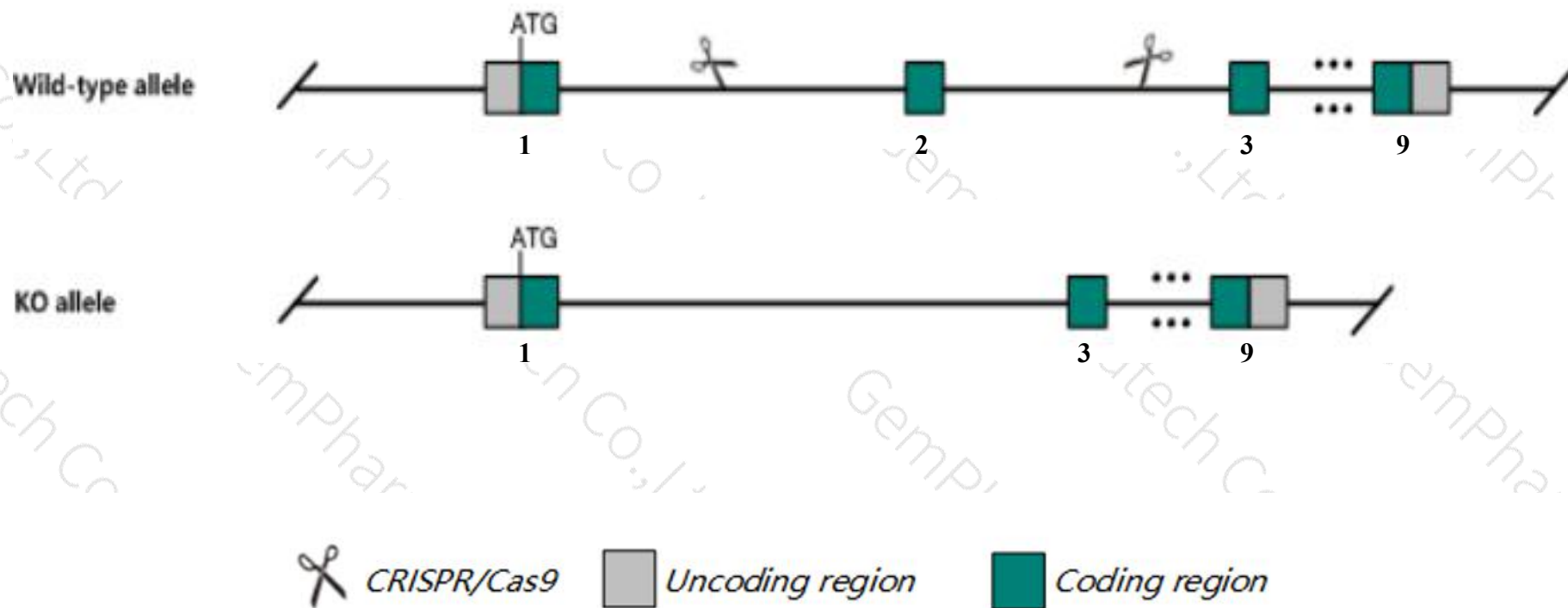
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zc3hav1* gene. The schematic diagram is as follows:



- The *Zc3hav1* gene has 4 transcripts. According to the structure of *Zc3hav1* gene, exon2 of *Zc3hav1*-201(ENSMUST00000031850.9) transcript is recommended as the knockout region. The region contains 136bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zc3hav1* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit reduced murine leukemia virus replication efficiency in mouse embryonic fibroblasts.
- The *Zc3hav1* gene is located on the Chr6. 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)

Zc3hav1 zinc finger CCCH type, antiviral 1 [Mus musculus (house mouse)]

Gene ID: 78781, updated on 13-Mar-2020

Summary



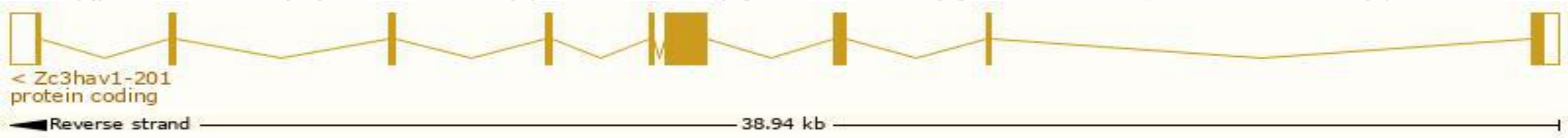
Official Symbol	Zc3hav1 provided by MGI
Official Full Name	zinc finger CCCH type, antiviral 1 provided by MGI
Primary source	MGI:MGI:1926031
See related	Ensembl:ENSMUSG00000029826
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200014N16Rik, 2900058M19Rik, 9130009D18Rik, 9830115L13Rik, ARTD13, D6Bwg1452e, PARP13, ZAP
Expression	Ubiquitous expression in thymus adult (RPKM 12.8), spleen adult (RPKM 10.0) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

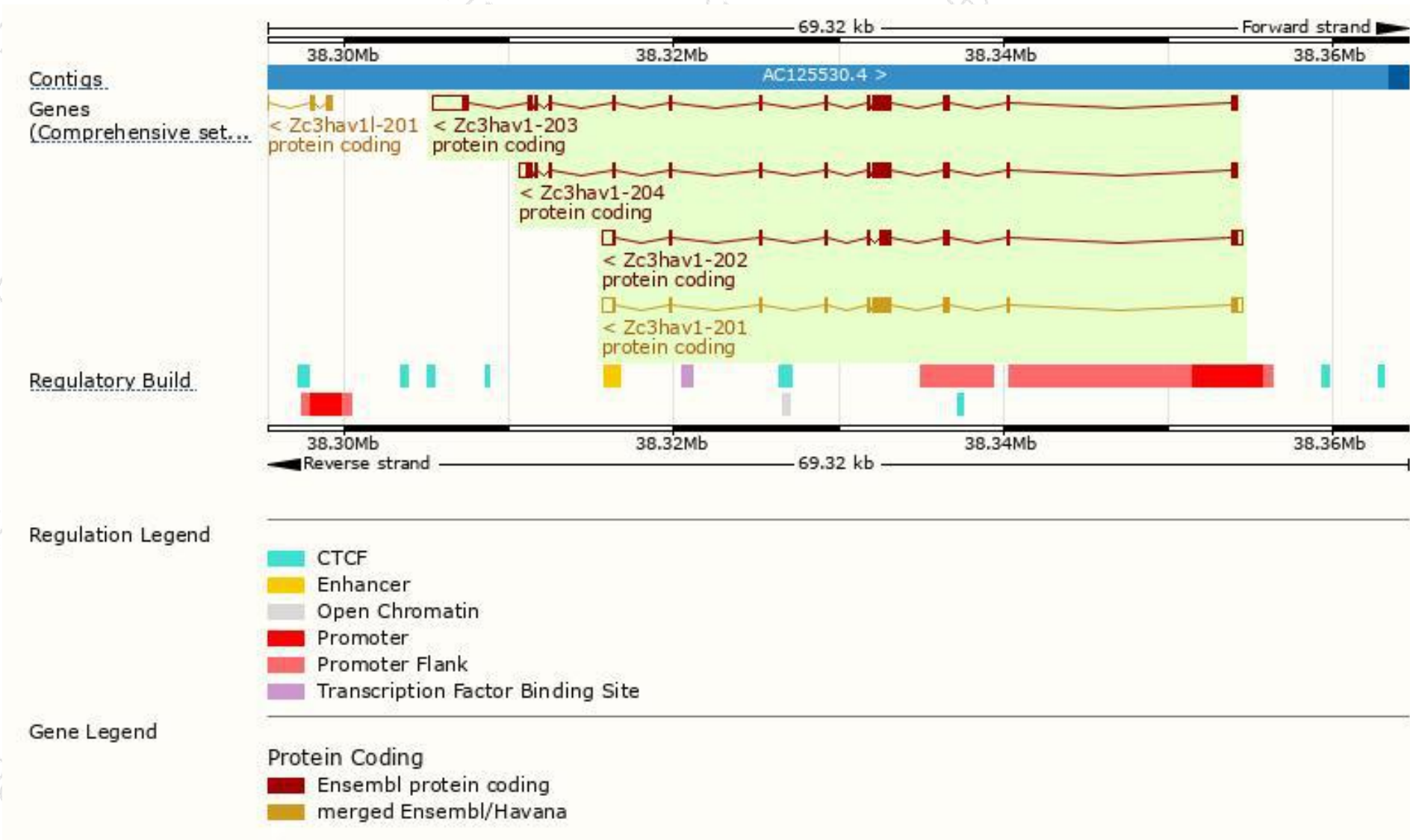
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zc3hav1-203	ENSMUST00000114900.7	4944	996aa	Protein coding	CCDS85033	D3Z5I1	TSL:5 GENCODE basic APPRIS P1
Zc3hav1-201	ENSMUST00000031850.9	3400	789aa	Protein coding	CCDS20012	Q3UPF5	TSL:1 GENCODE basic
Zc3hav1-204	ENSMUST00000143702.4	3364	946aa	Protein coding	CCDS80522	Q3UPF5	TSL:1 GENCODE basic
Zc3hav1-202	ENSMUST00000114898.2	3052	673aa	Protein coding	-	G3X9X5	TSL:1 GENCODE basic

The strategy is based on the design of *Zc3hav1-201* transcript,the transcription is shown below:



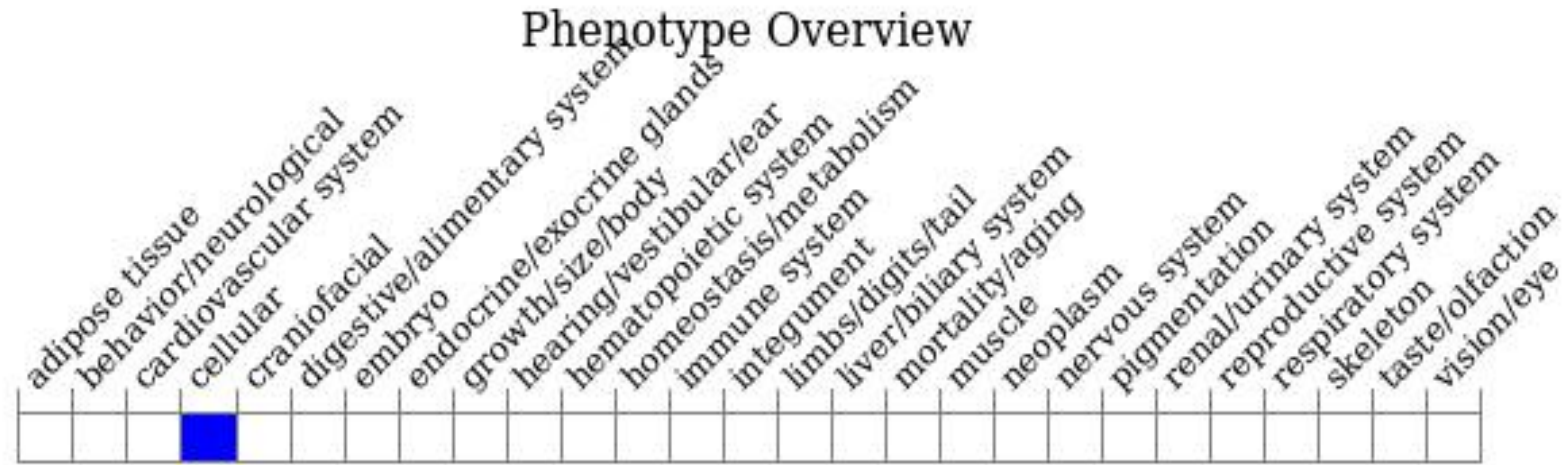
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, mice homozygous for a knock-out allele exhibit reduced murine leukemia virus replication efficiency in mouse embryonic fibroblasts.

If you have any questions, you are welcome to inquire.

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