

Cavin2 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

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Project Overview

Project Name

Cavin2

Project type

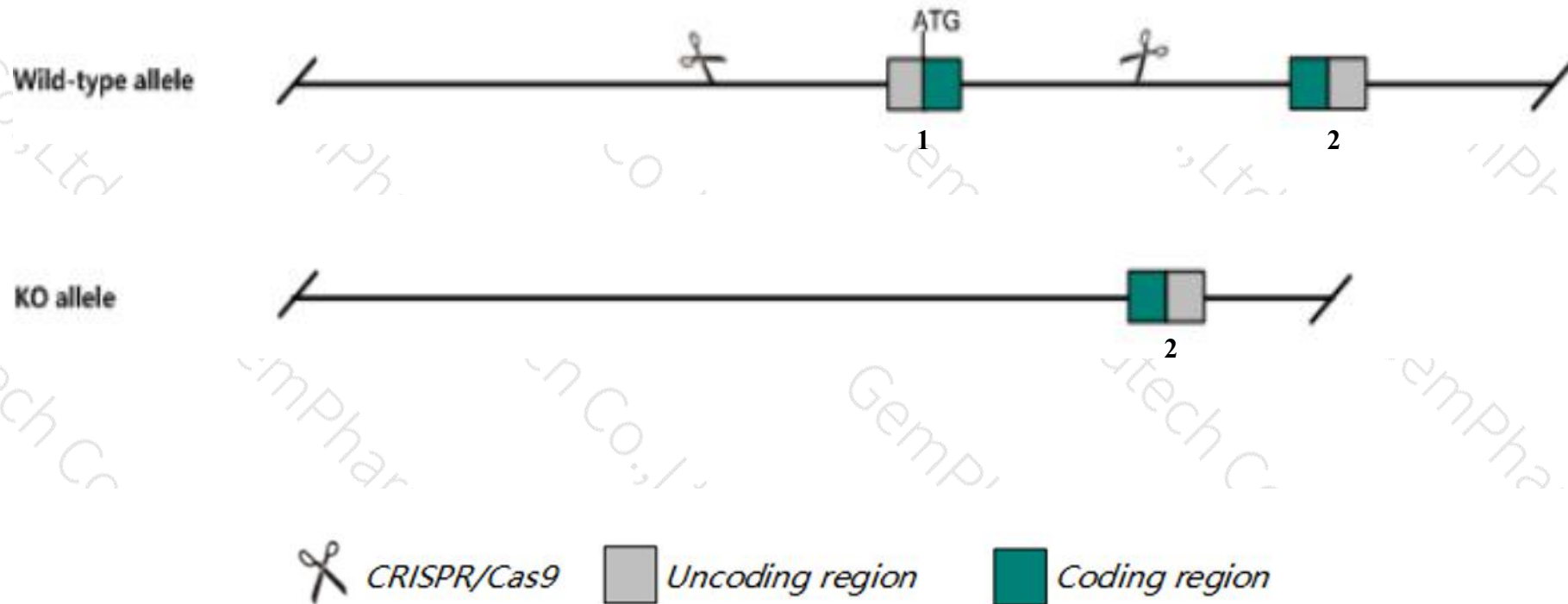
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cavin2* gene. The schematic diagram is as follows:



- The *Cavin2* gene has 1 transcript. According to the structure of *Cavin2* gene, exon1 of *Cavin2-201* (ENSMUST00000051572.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cavin2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit abnormal caveolae formation in lung and adipose endothelia and adipocytes with gaps in the lung capillaries.
- The KO region contains partial intron of the *9330175M20Rik* gene. Knockout the region may affect the function of *9330175M20Rik* gene.
- The *Cavin2* gene is located on the Chr1. 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)

Cavin2 caveolae associated 2 [Mus musculus (house mouse)]

Gene ID: 20324, updated on 13-Mar-2020

Summary



Official Symbol Cavin2 provided by [MGI](#)

Official Full Name caveolae associated 2 provided by [MGI](#)

Primary source [MGI:MGI:99513](#)

See related [Ensembl:ENSMUSG00000045954](#)

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 Sdpr

Expression Broad expression in lung adult (RPKM 123.4), subcutaneous fat pad adult (RPKM 70.9) and 16 other tissues [See more](#)

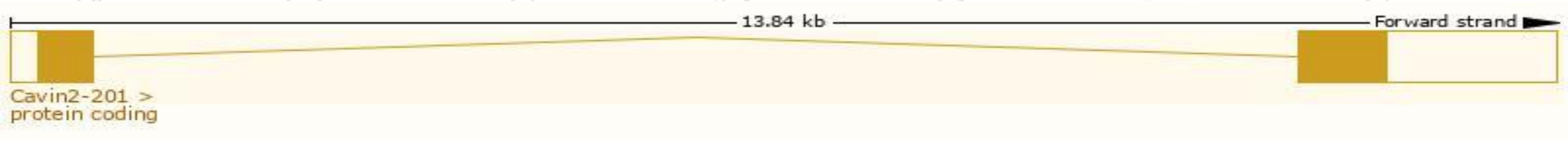
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cavin2-201	ENSMUST00000051572.7	3055	418aa	Protein coding	CCDS14940	Q63918	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

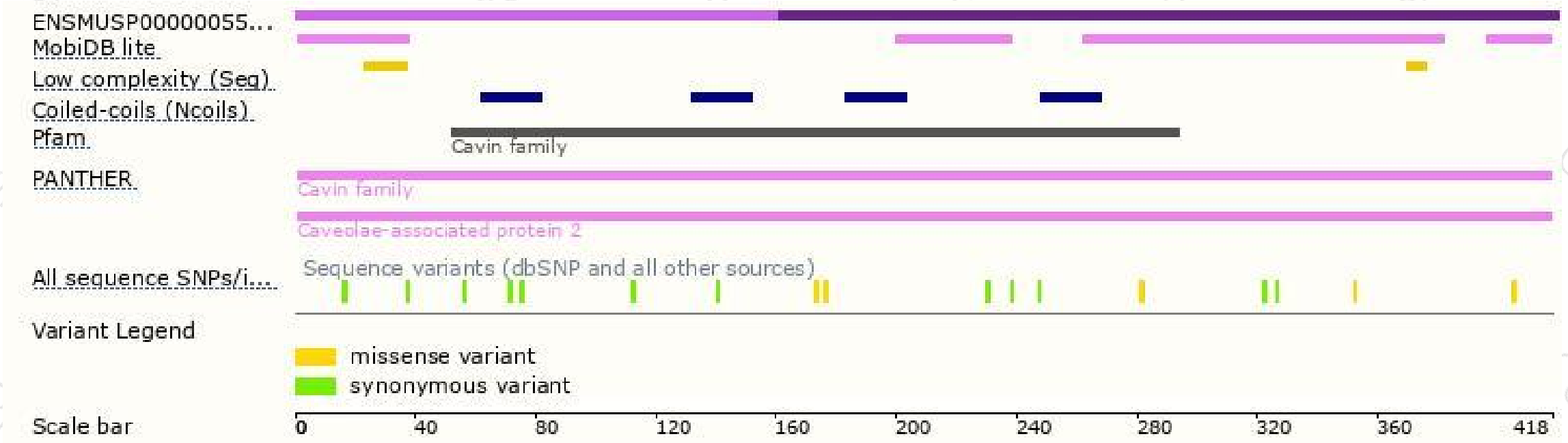
The strategy is based on the design of *Cavin2-201* transcript, the transcription is shown below:



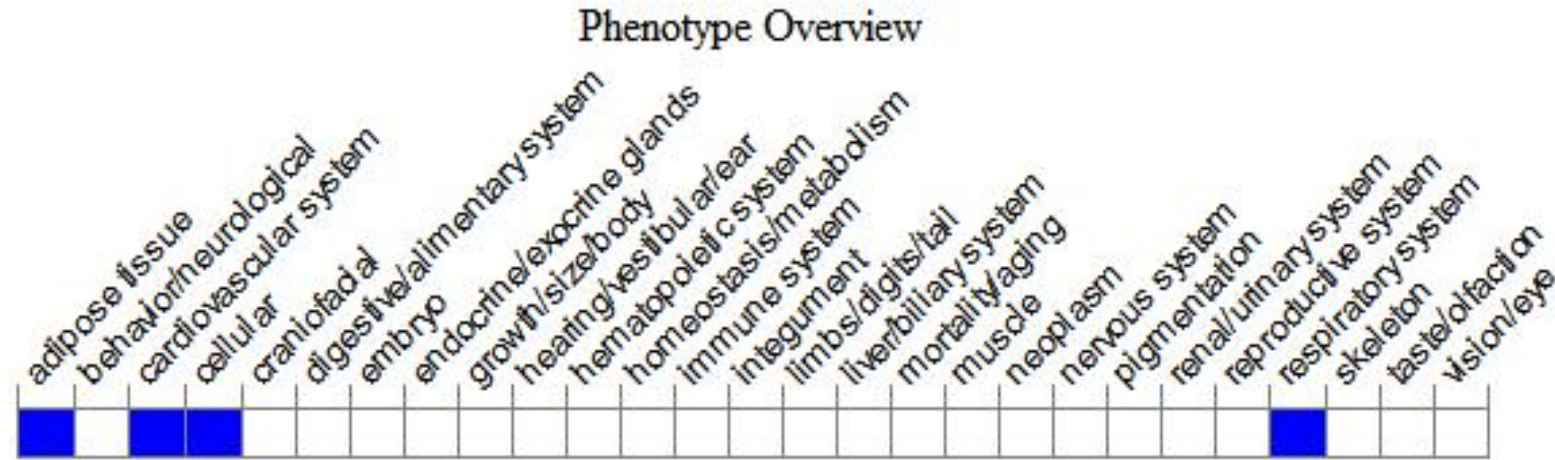
Genomic location distribution



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 abnormal caveolae formation in lung and adipose endothelia and adipocytes with gaps in the lung capillaries.

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

Tel: 400-9660890

