

# *Cavin1* Cas9-KO Strategy

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Design Date: 2020-5-26

# Project Overview

**Project Name**

*Cavin1*

**Project type**

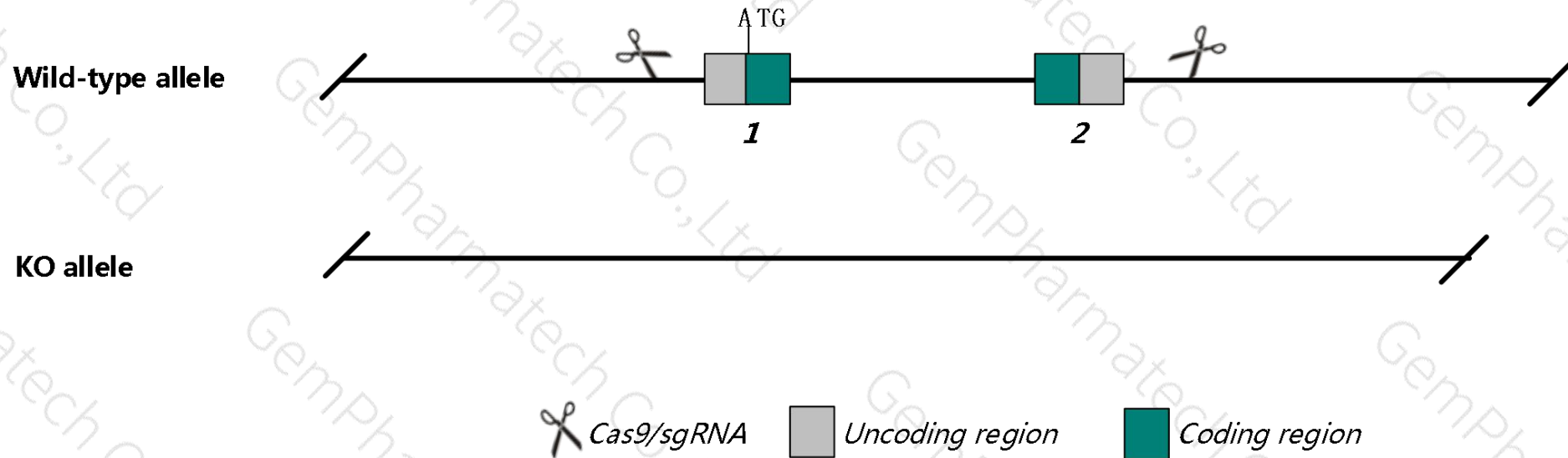
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cavin1* gene. The schematic diagram is as follows:



- The *Cavin1* gene has 2 transcripts. According to the structure of *Cavin1* gene, exon1-exon2 of *Cavin1-201* (ENSMUST00000060792.5) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cavin1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null allele exhibit the absence of calveolae, dyslipidemia, and glucose intolerance, pulmonary arterial hypertension, and urinary bladder abnormalities.
- The *Cavin1* gene is located on the Chr11. 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)

## Cavin1 caveolae associated 1 [Mus musculus (house mouse)]

Gene ID: 19285, updated on 15-Mar-2020

### Summary



**Official Symbol** Cavin1 provided by [MGI](#)

**Official Full Name** caveolae associated 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1277968](#)

**See related** [Ensembl:ENSMUSG00000004044](#)

**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** 2310075E07Rik, AW546441, Cav-p60, Cavin, Ptrf

**Expression** Broad expression in subcutaneous fat pad adult (RPKM 99.6), bladder adult (RPKM 84.6) and 18 other tissues [See more](#)

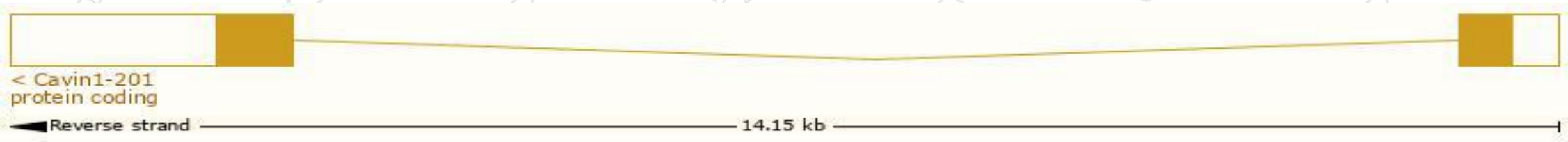
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

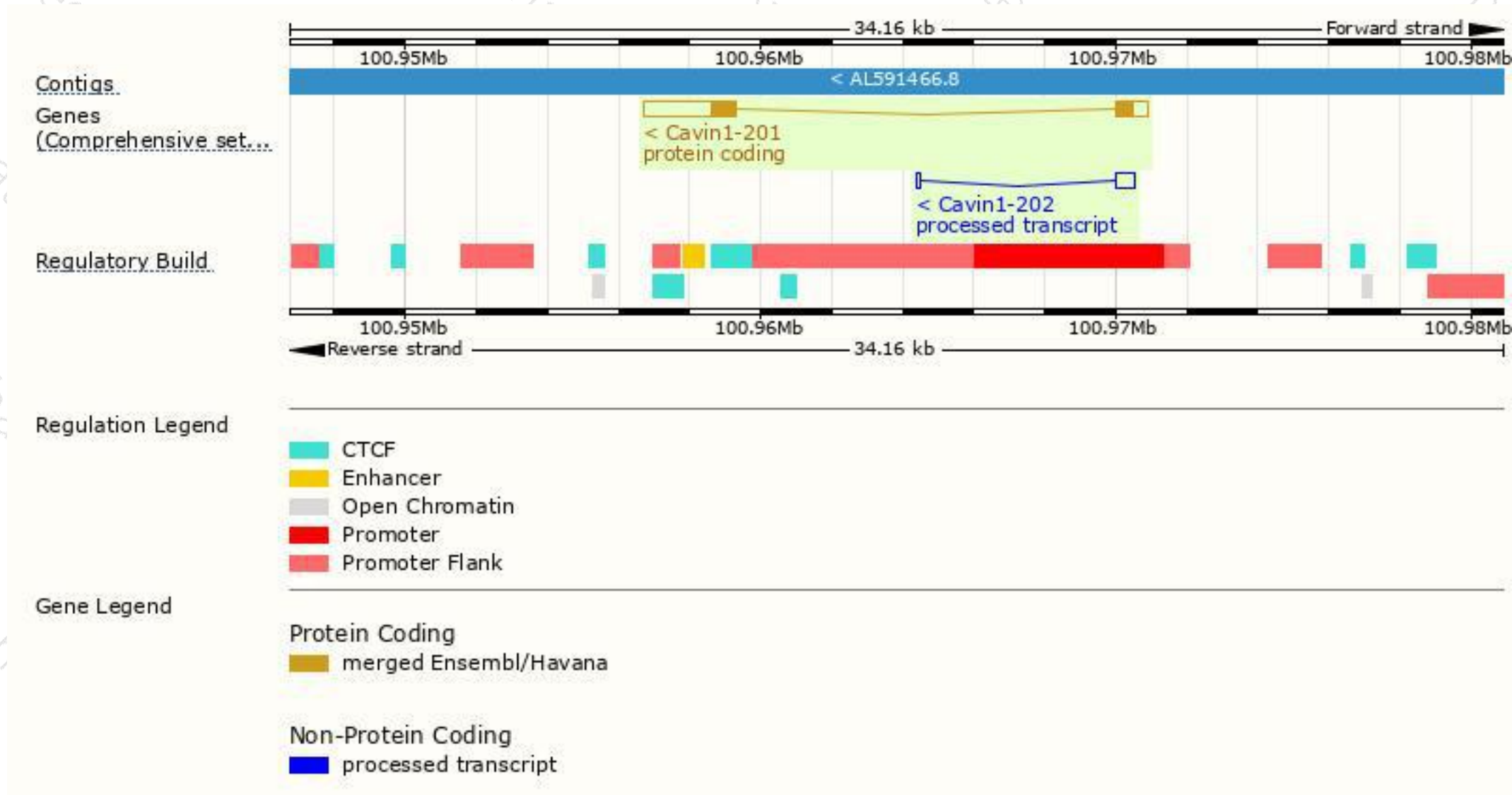
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cavin1-201	<a href="#">ENSMUST00000060792.5</a>	3491	<a href="#">392aa</a>	Protein coding	<a href="#">CCDS25442</a>	<a href="#">O54724</a>	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
Cavin1-202	<a href="#">ENSMUST00000132934.1</a>	658	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Cavin1-201* transcript,the transcription is shown below:

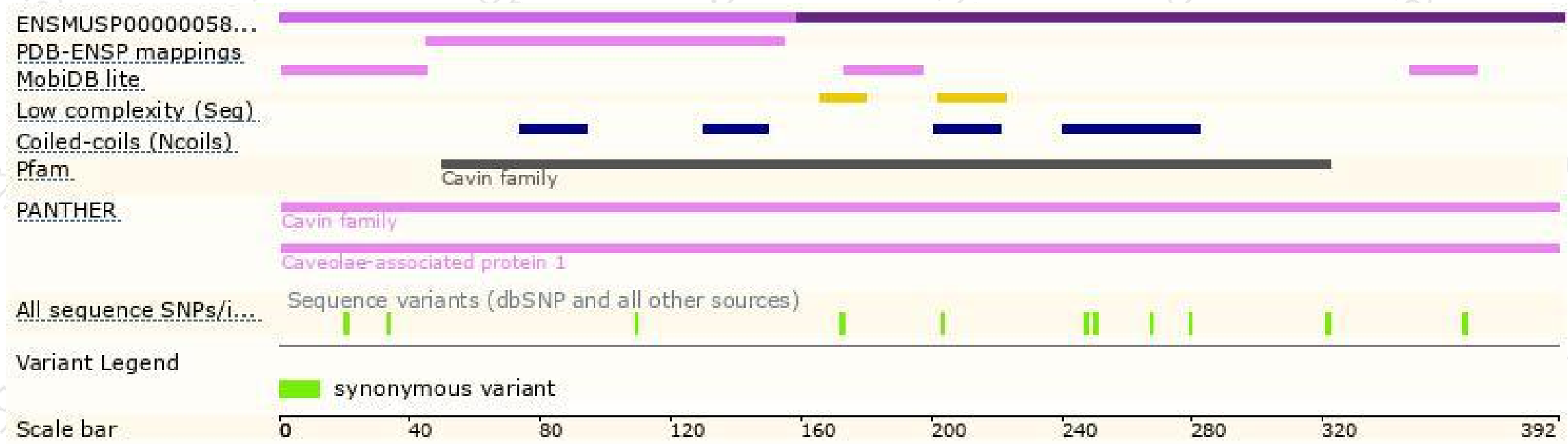


# Genomic location distribution

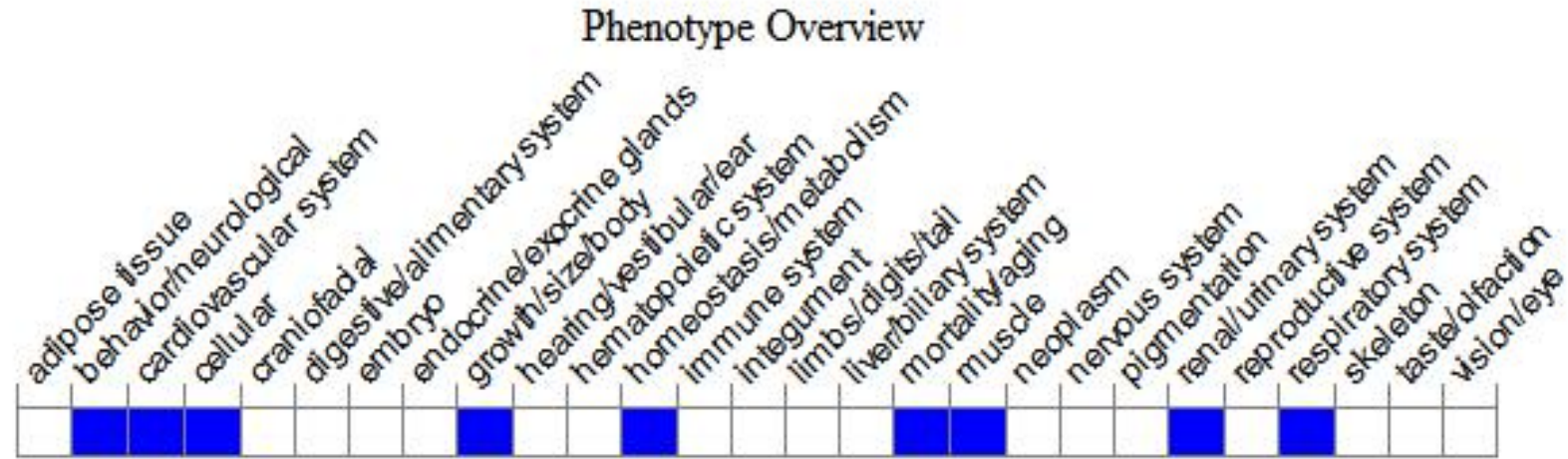




# Protein domain



# 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 null allele exhibit the absence of calveolae, dyslipidemia, and glucose intolerance, pulmonary arterial hypertension, and urinary bladder abnormalities.

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

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