

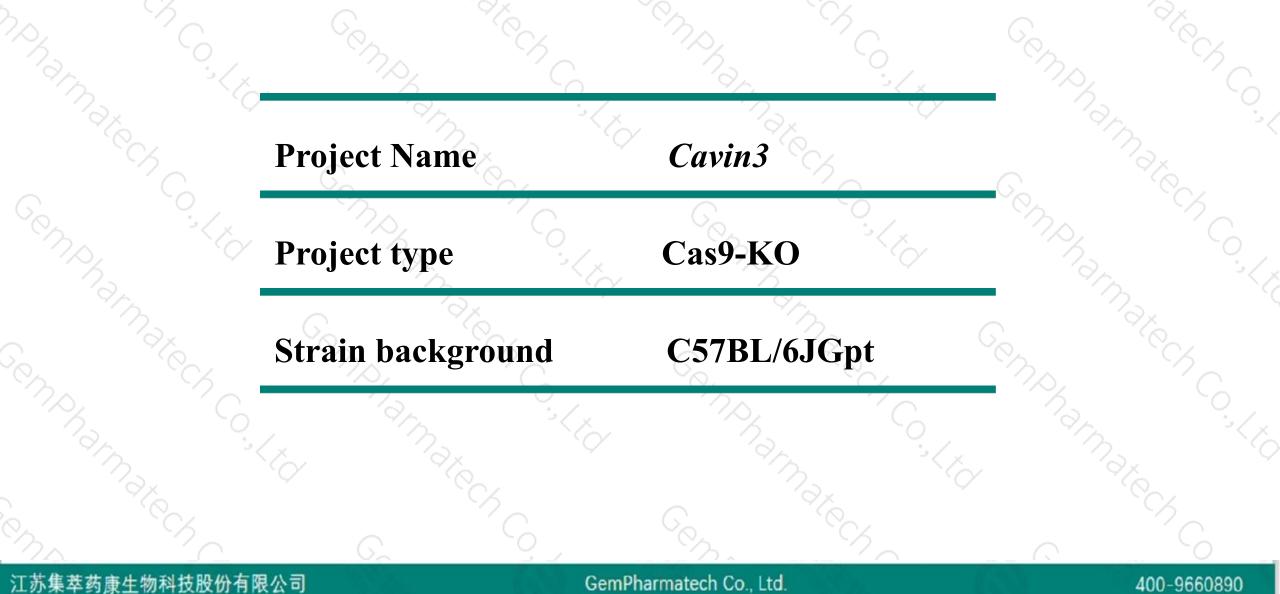
# Cavin3 Cas9-KO Strategy Romphamater Control

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# **Project Overview**

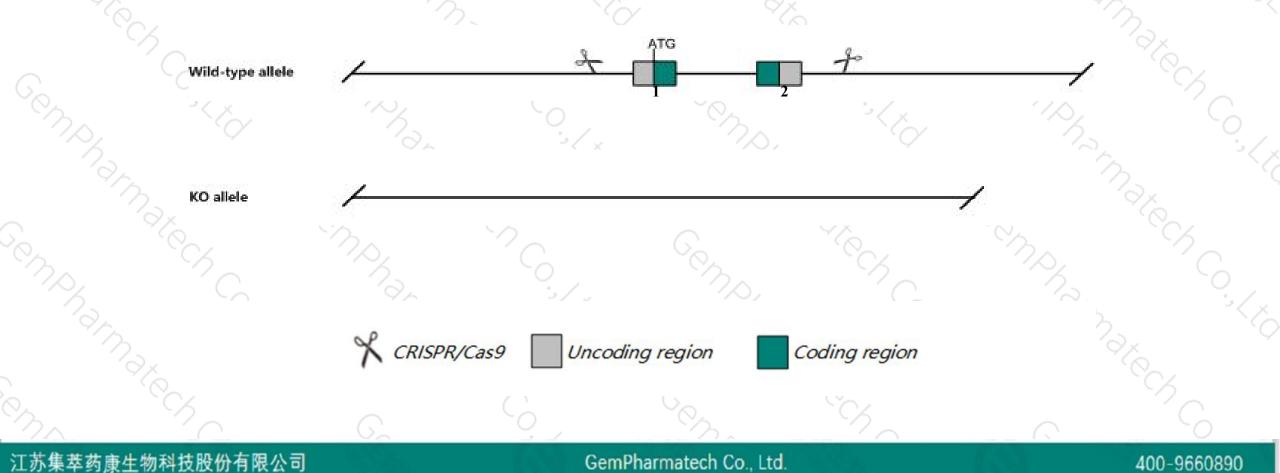




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the Cavin3 gene. The schematic diagram is as follows:





- The Cavin3 gene has 1 transcript. According to the structure of Cavin3 gene, exon1-exon2 of Cavin3-201 (ENSMUST00000047040.3) 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 Cavin3 gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased body weight, severe lipodystrophy, hepatic steatosis, increased fermentative glycolysis in lung tissue, and premature death as a result of cachexia.
- > The KO region contains the *Gm45667* gene. Knockout the region may affect the function of the *Gm45667* gene.
- The Cavin3 gene is located on the Chr7. 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.

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# **Gene information (NCBI)**



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### Cavin3 caveolae associated 3 [Mus musculus (house mouse)]

Gene ID: 109042, updated on 31-Jan-2019

### Summary

Official SymbolCavin3 provided by MGIOfficial Full Namecaveolae associated 3 provided by MGIPrimary soureMGI:MGI:1923422See relateEnsembl:ENSMUSG0000037060Gene typeprotein codingprotein codingPROVISIONALOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;<br/>Muroidea; Murinae; Mus; MusAlso knownas3110015B12Rik, 6330514M23Rik, Prkcdbp, SRBCExpressionBroad expression in ovary adult (RPKM 228.1), subcutaneous fat pad adult (RPKM 214.5) and 18 other tissuesSee more<br/>human all

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# **Transcript information (Ensembl)**



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

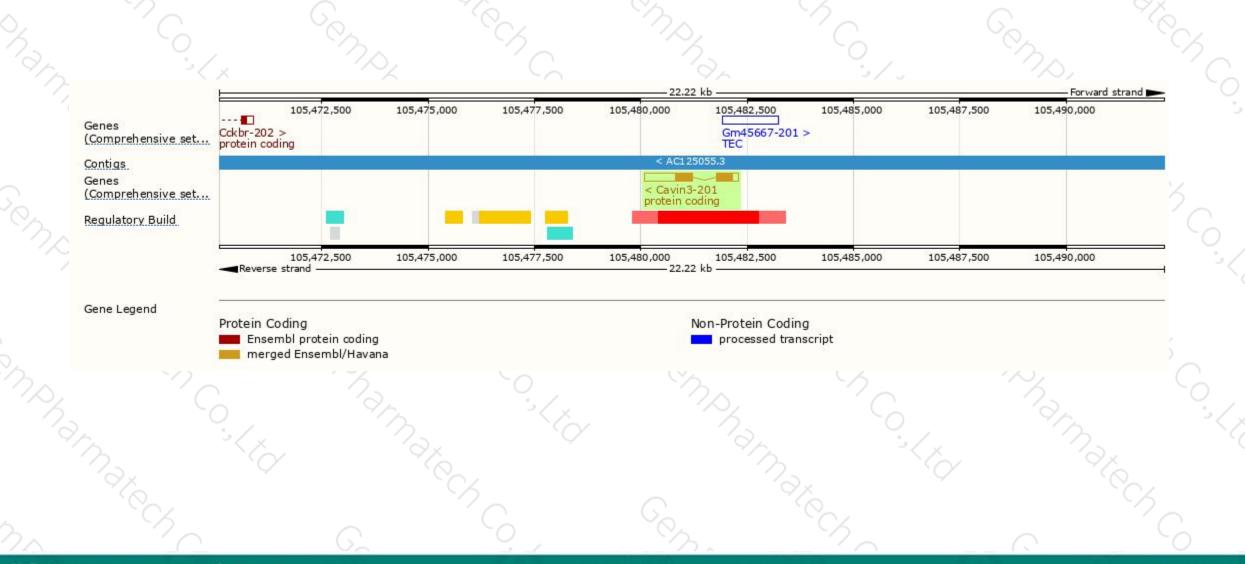
Name		Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
	Cavin3-201	ENSMUST0000047040.3	1662	<u>260aa</u>	Protein coding	CCDS21652	Q91VJ2	TSL:1 GENCODE basic APPRIS P1	Ŀ

The strategy is based on the design of *Cavin3-201* transcript, The transcription is shown below

< Cavin3-201 protein coding						
Reverse strand		2.22	2 kb			
Eng, arech	CUC	Nor Co	Ceno.	Note Ch	Const.	C C
narmax	orten orten	ALC A	- A	ma co	, <sup>19</sup> 17) X	
ma ch			Con .			S C

# **Genomic location distribution**





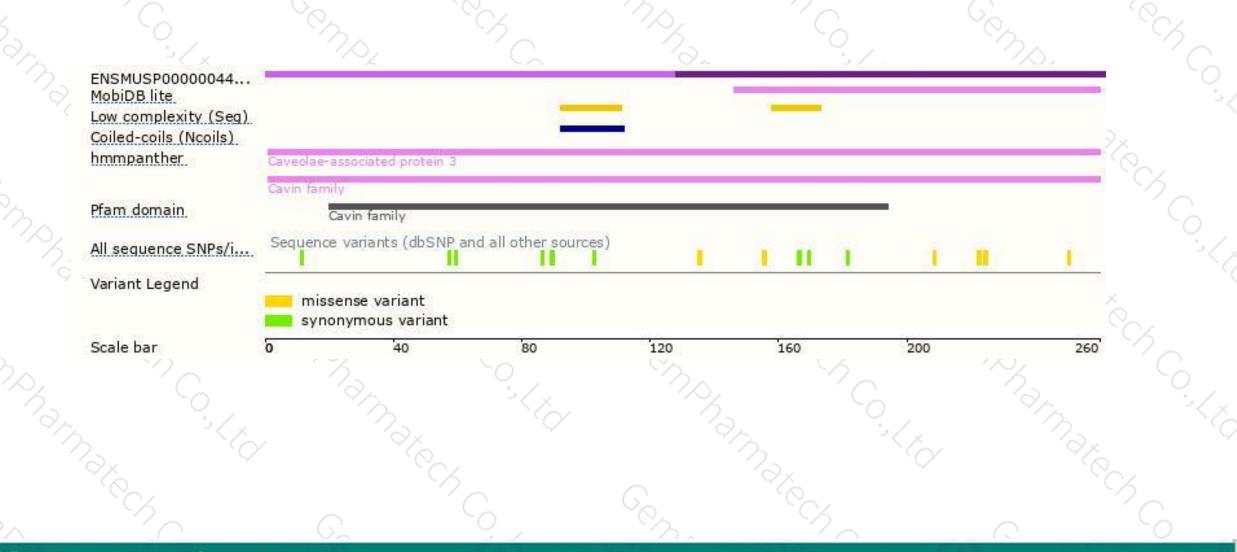
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# **Protein domain**



400-9660890

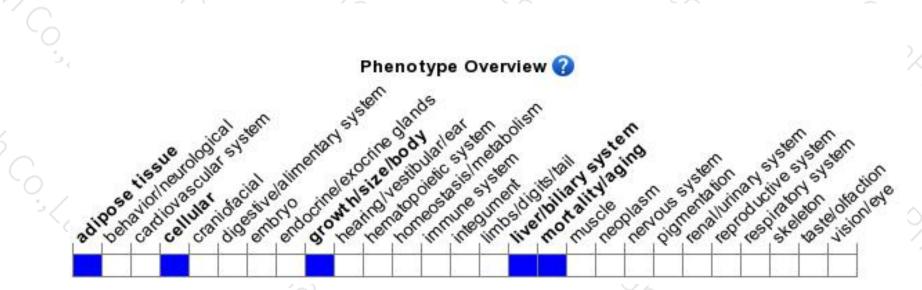


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## Mouse phenotype description(MGI)





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 decreased body weight, severe lipodystrophy, hepatic steatosis, increased fermentative glycolysis in lung tissue, and premature death as a result of cachexia.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



