

Ctnna3 Cas9-KO Strategy

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Project Overview

Project Name

Ctnna3

Project type

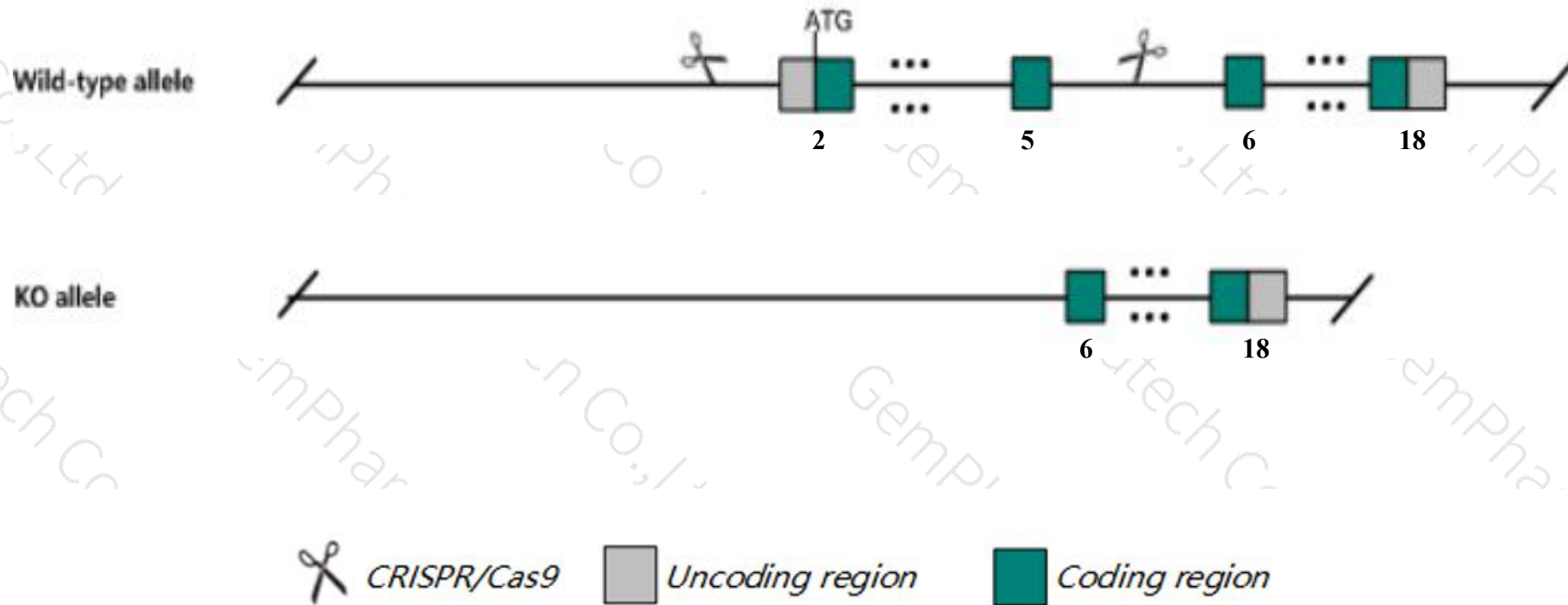
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ctnna3* gene. The schematic diagram is as follows:



- The *Ctnna3* gene has 5 transcripts. According to the structure of *Ctnna3* gene, exon2-exon5 of *Ctnna3*-202(ENSMUST00000105440.7) 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 *Ctnna3* 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 increased heart weight, increased ventricle size, dilated cardiomyopathy and increased susceptibility to ischemia-induced arrhythmias and mortality.
- The *Ctnna3* gene is located on the Chr10. 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)

Ctnna3 catenin (cadherin associated protein), alpha 3 [Mus musculus (house mouse)]

Gene ID: 216033, updated on 13-Mar-2020

Summary



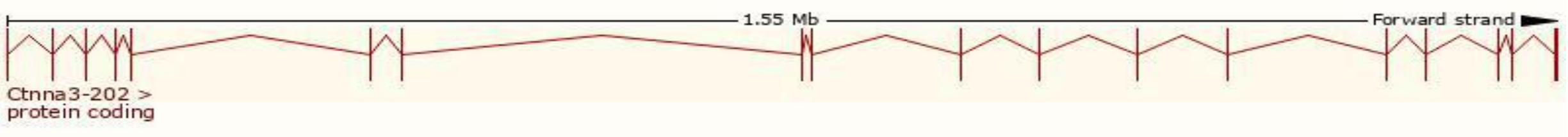
Official Symbol	Ctnna3 provided by MGI
Official Full Name	catenin (cadherin associated protein), alpha 3 provided by MGI
Primary source	MGI:MGI:2661445
See related	Ensembl:ENSMUSG00000060843
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930429L08Rik, 4933408A16, Catna3, Vr22
Expression	Biased expression in testis adult (RPKM 9.1), heart adult (RPKM 3.0) and 1 other tissue See more
Orthologs	human all

Transcript information (Ensembl)

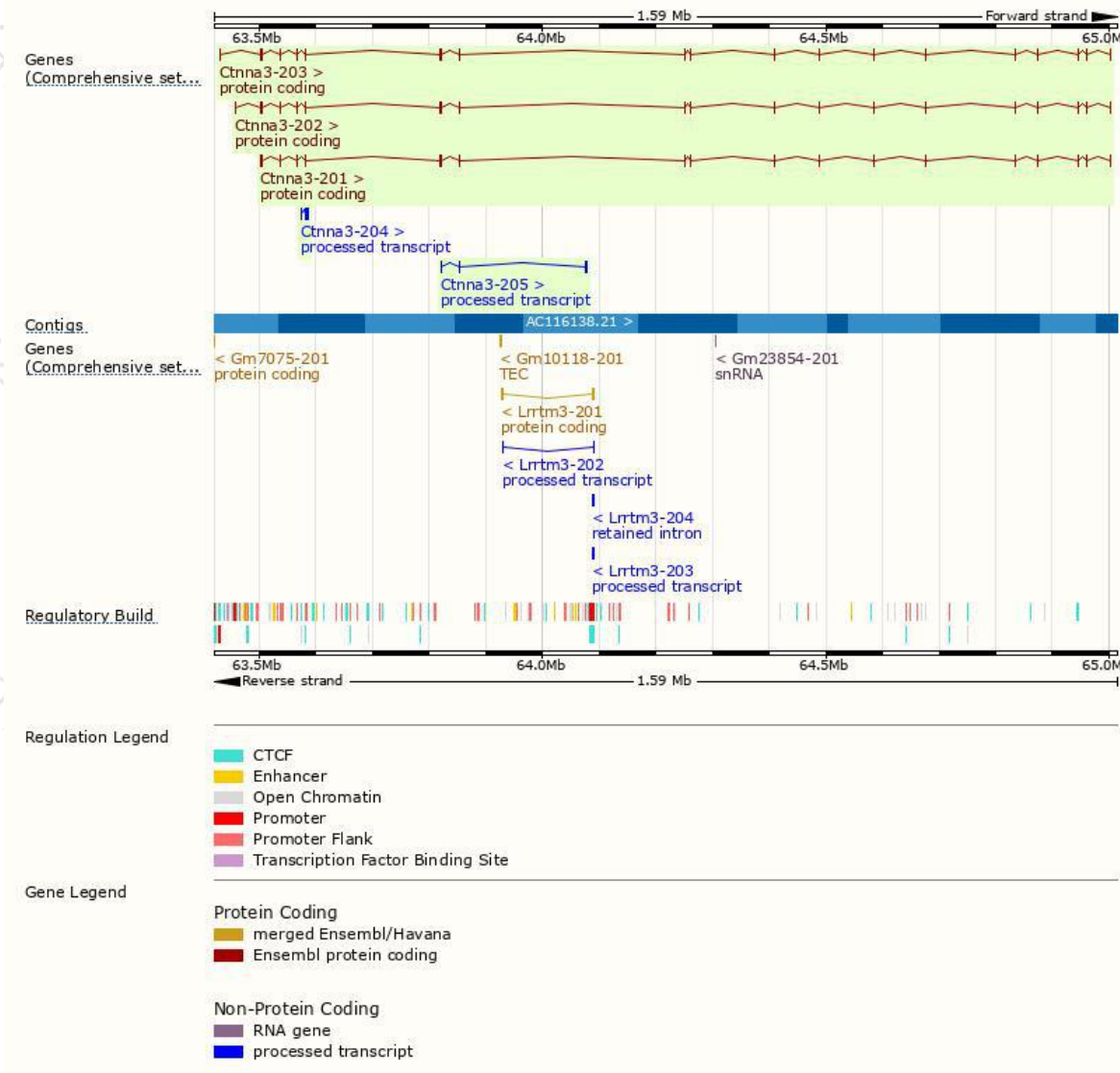
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ctnna3-202	ENSMUST00000105440.7	3682	895aa	Protein coding	CCDS23901	Q65CL1	TSL:1 GENCODE basic APPRIS P1
Ctnna3-203	ENSMUST00000105441.7	2907	895aa	Protein coding	CCDS23901	Q65CL1	TSL:1 GENCODE basic APPRIS P1
Ctnna3-201	ENSMUST00000075099.4	2688	895aa	Protein coding	CCDS23901	Q65CL1	TSL:5 GENCODE basic APPRIS P1
Ctnna3-204	ENSMUST00000133190.1	2795	No protein	Processed transcript	-	-	TSL:1
Ctnna3-205	ENSMUST00000135474.1	992	No protein	Processed transcript	-	-	TSL:1

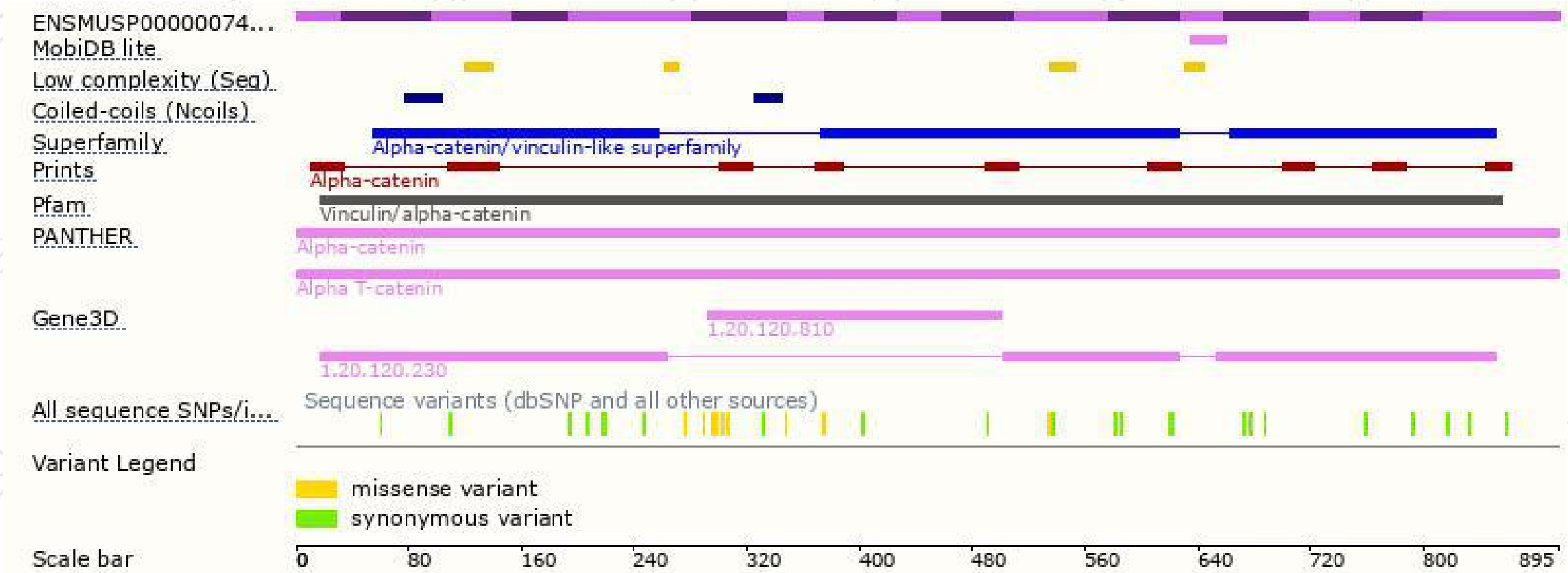
The strategy is based on the design of *Ctnna3-202* transcript,the transcription is shown below:



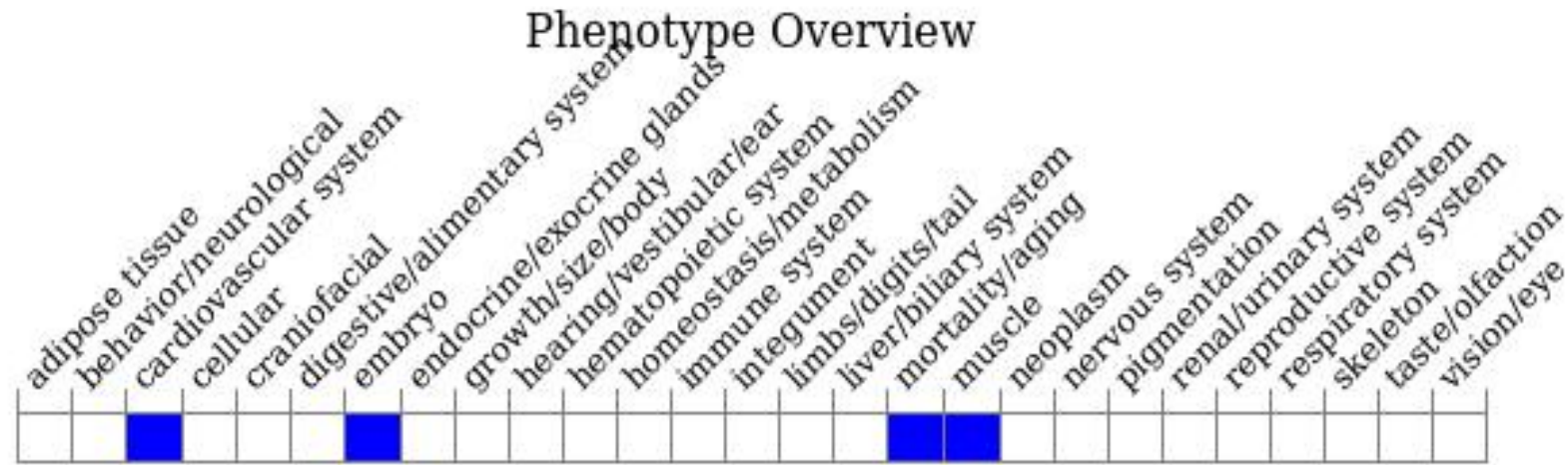
Genomic location distribution



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 increased heart weight, increased ventricle size, dilated cardiomyopathy and increased susceptibility to ischemia-induced arrhythmias and mortality.

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

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