

Tnnt2 Cas9-KO Strategy

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Project Overview

Project Name

Tnnt2

Project type

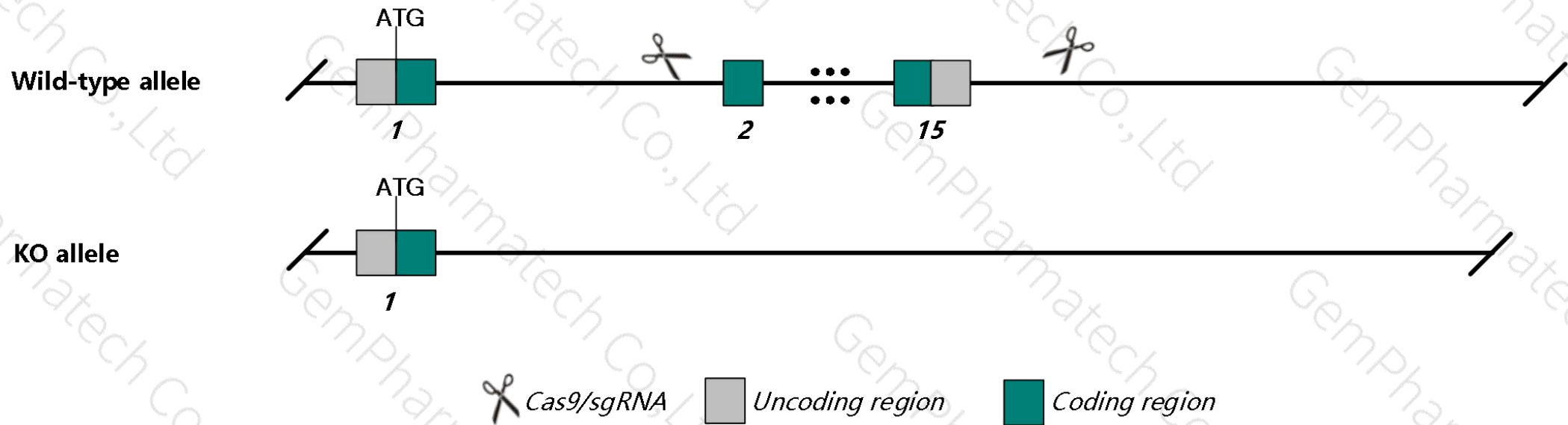
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tnnt2* gene. The schematic diagram is as follows:



- The *Tnnt2* gene has 15 transcripts. According to the structure of *Tnnt2* gene, exon2-exon15 of *Tnnt2*-204 (ENSMUST00000112087.8) transcript is recommended as the knockout region. The region contains most 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 *Tnnt2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit embryonic lethality during and prior to organogenesis and abnormal heart development. Mice homozygous for an allele that lacks the lysine residue at position 210 exhibit dilated cardiomyopathy.
- The *Tnnt2* 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)

Tnnt2 troponin T2, cardiac [Mus musculus (house mouse)]

Gene ID: 21956, updated on 9-Apr-2019

Summary



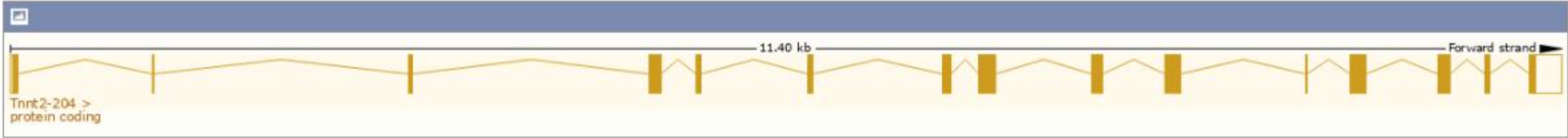
Official Symbol	Tnnt2 provided by MGI
Official Full Name	troponin T2, cardiac provided by MGI
Primary source	MGI:MGI:104597
See related	Ensembl:ENSMUSG00000026414
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Tnt, cTnT
Expression	Biased expression in heart adult (RPKM 846.5) and bladder adult (RPKM 77.4) See more
Orthologs	human all

Transcript information (Ensembl)

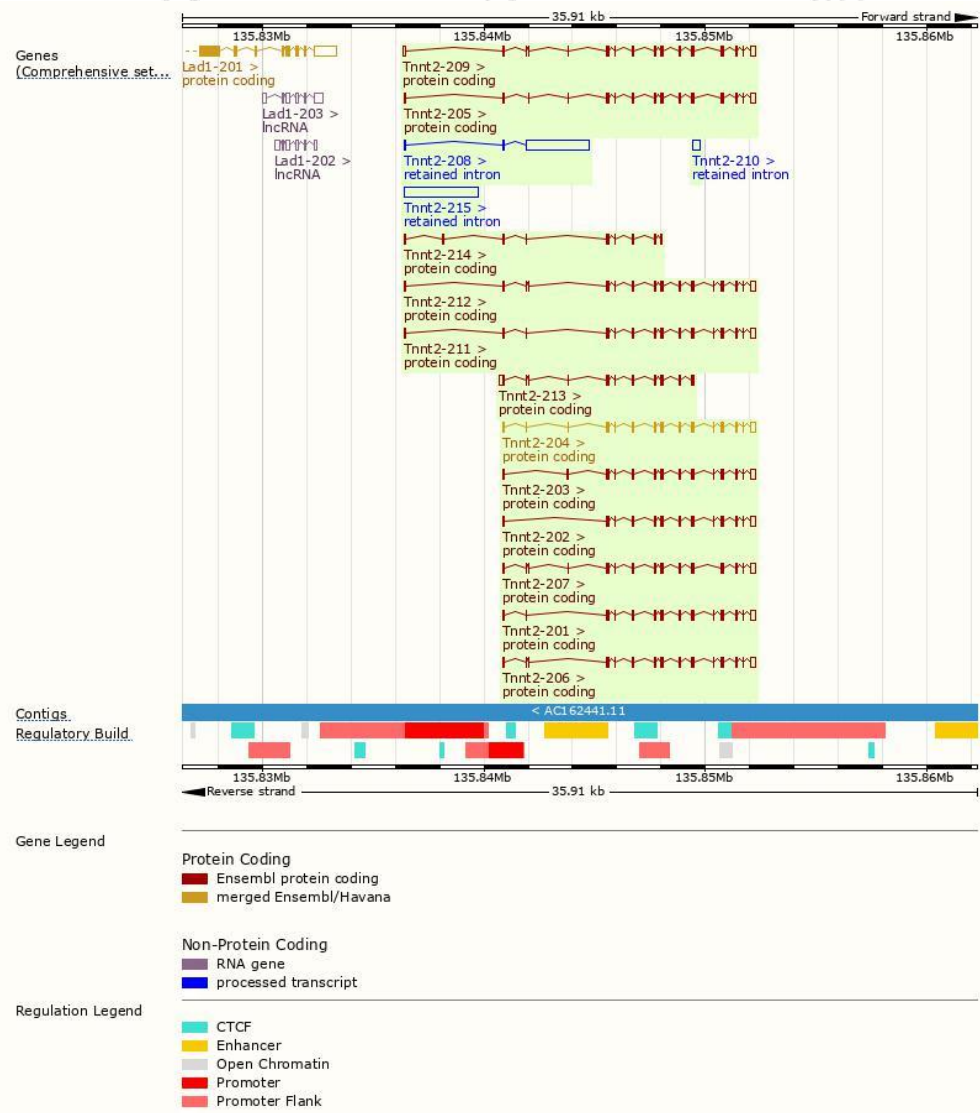
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnnt2-209	ENSMUST00000188028.6	1200	302aa	Protein coding	CCDS48375	Q6P3Z7	TSL:5 GENCODE basic APPRIS P4
Tnnt2-212	ENSMUST00000189732.6	1123	295aa	Protein coding	CCDS48376	P50752	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-204	ENSMUST00000112087.8	1112	301aa	Protein coding	CCDS48377	P50752 Q54AB6	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-211	ENSMUST00000189355.6	1112	291aa	Protein coding	CCDS48378	P50752	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-207	ENSMUST00000179863.7	1097	302aa	Protein coding	CCDS48375	Q6P3Z7	TSL:5 GENCODE basic APPRIS P4
Tnnt2-206	ENSMUST00000178854.7	1076	295aa	Protein coding	CCDS48376	P50752	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-201	ENSMUST00000027671.11	1064	291aa	Protein coding	CCDS48378	P50752	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-205	ENSMUST00000178204.7	1172	302aa	Protein coding	-	J3QQ13	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-203	ENSMUST00000112086.2	1094	301aa	Protein coding	-	K3W4R7	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-202	ENSMUST00000112085.8	1076	295aa	Protein coding	-	K3W4R6	TSL:5 GENCODE basic APPRIS ALT2
Tnnt2-213	ENSMUST00000189826.6	796	206aa	Protein coding	-	A0A087WRX3	CDS 3' incomplete TSL:5
Tnnt2-214	ENSMUST00000190451.6	433	114aa	Protein coding	-	A0A087WQP1	CDS 3' incomplete TSL:5
Tnnt2-215	ENSMUST00000191055.1	3330	No protein	Retained intron	-	-	TSL:NA
Tnnt2-208	ENSMUST00000186225.1	2961	No protein	Retained intron	-	-	TSL:2
Tnnt2-210	ENSMUST00000188098.1	292	No protein	Retained intron	-	-	TSL:NA

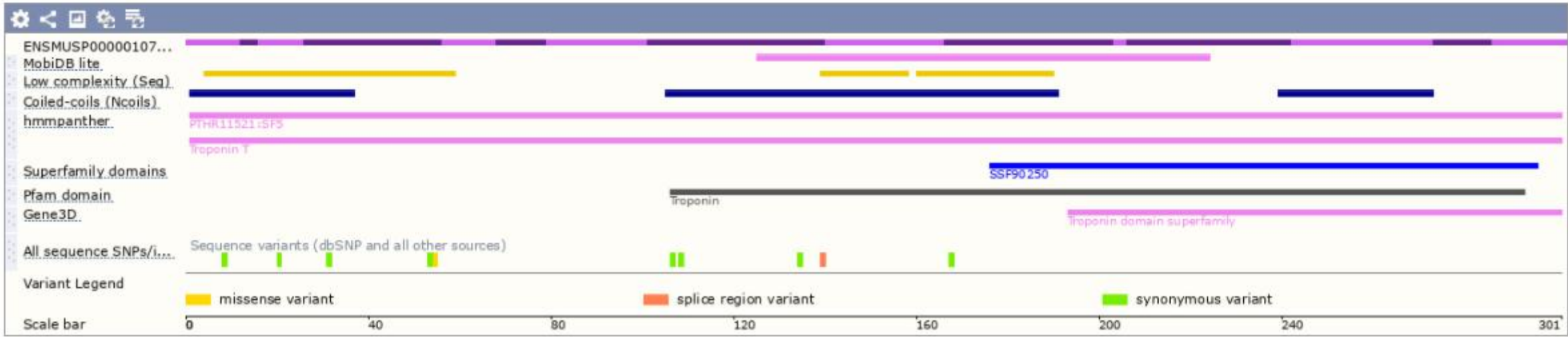
The strategy is based on the design of *Tnnt2-204* transcript,The transcription is shown below



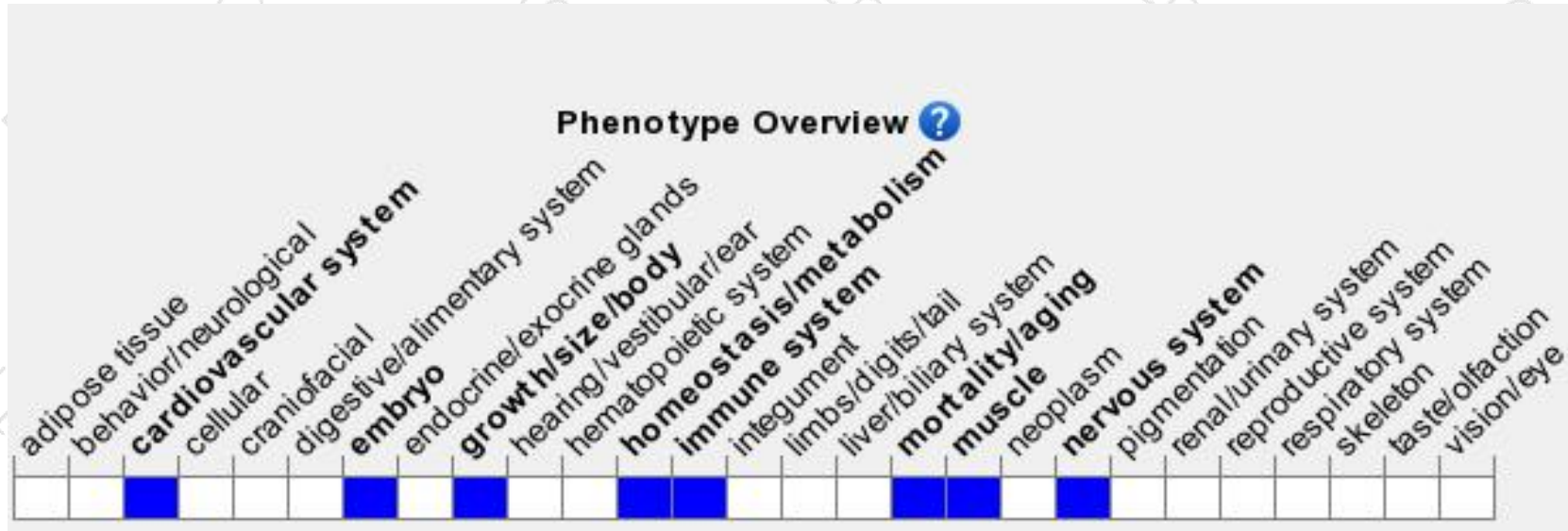
Genomic location distribution



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 embryonic lethality during and prior to organogenesis and abnormal heart development. Mice homozygous for an allele that lacks the lysine residue at position 210 exhibit dilated cardiomyopathy.

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

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