

Myh7 Cas9-KO Strategy

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Project Overview

Project Name

Myh7

Project type

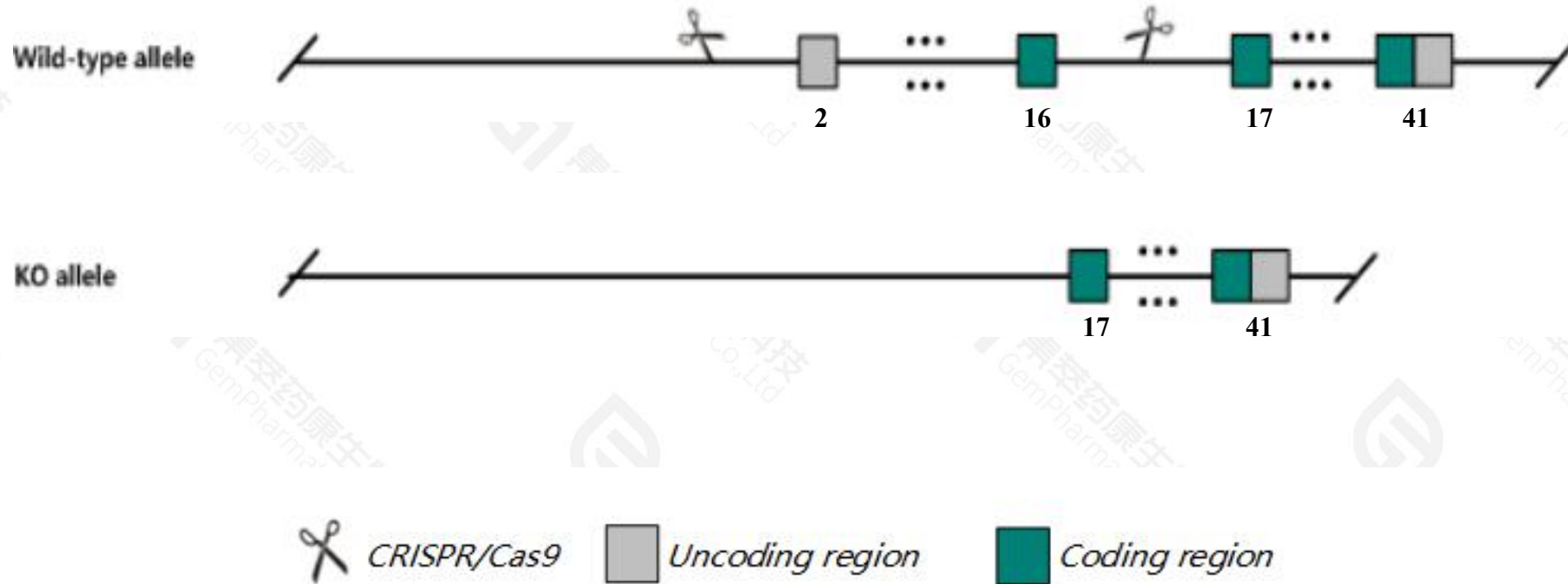
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myh7* gene. The schematic diagram is as follows:



- The *Myh7* gene has 8 transcripts. According to the structure of *Myh7* gene, exon2-exon16 of *Myh7*-201(ENSMUST00000102803.11) 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 *Myh7* 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 an endonuclease-mediated allele exhibit complete embryonic lethality during organogenesis with evidence of heart failure.
- The KO region overlaps with *Gm31251* gene. Knockout the region may affect the function of *Gm31251* gene.
- *Myh7-202* and *Myh7-206* may not be affected.
- The *Myh7* gene is located on the Chr14. 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.

Myh7 myosin, heavy polypeptide 7, cardiac muscle, beta [Mus musculus (house mouse)]

Gene ID: 140781, updated on 9-Mar-2021

Summary



Official Symbol Myh7 provided by [MGI](#)

Official Full Name myosin, heavy polypeptide 7, cardiac muscle, beta provided by [MGI](#)

Primary source [MGI:MGI:2155600](#)

See related [Ensembl:ENSMUSG00000053093](#)

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 B-MHC, MYH-beta/slow, MyHC-, MyHC-I, Myhc-b, Myhcb, beta-MH, beta-MHC, betaMH, betaMHC, myHC-beta, myHC-slow

Expression Restricted expression toward heart adult (RPKM 264.5) [See more](#)

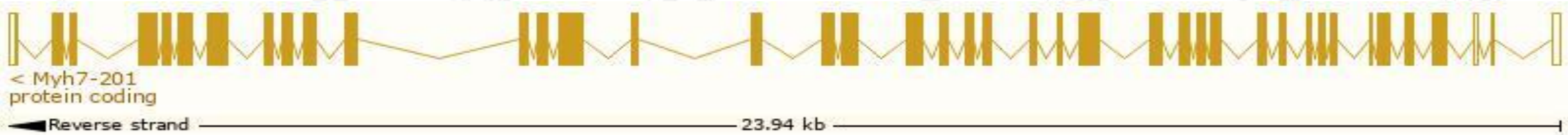
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

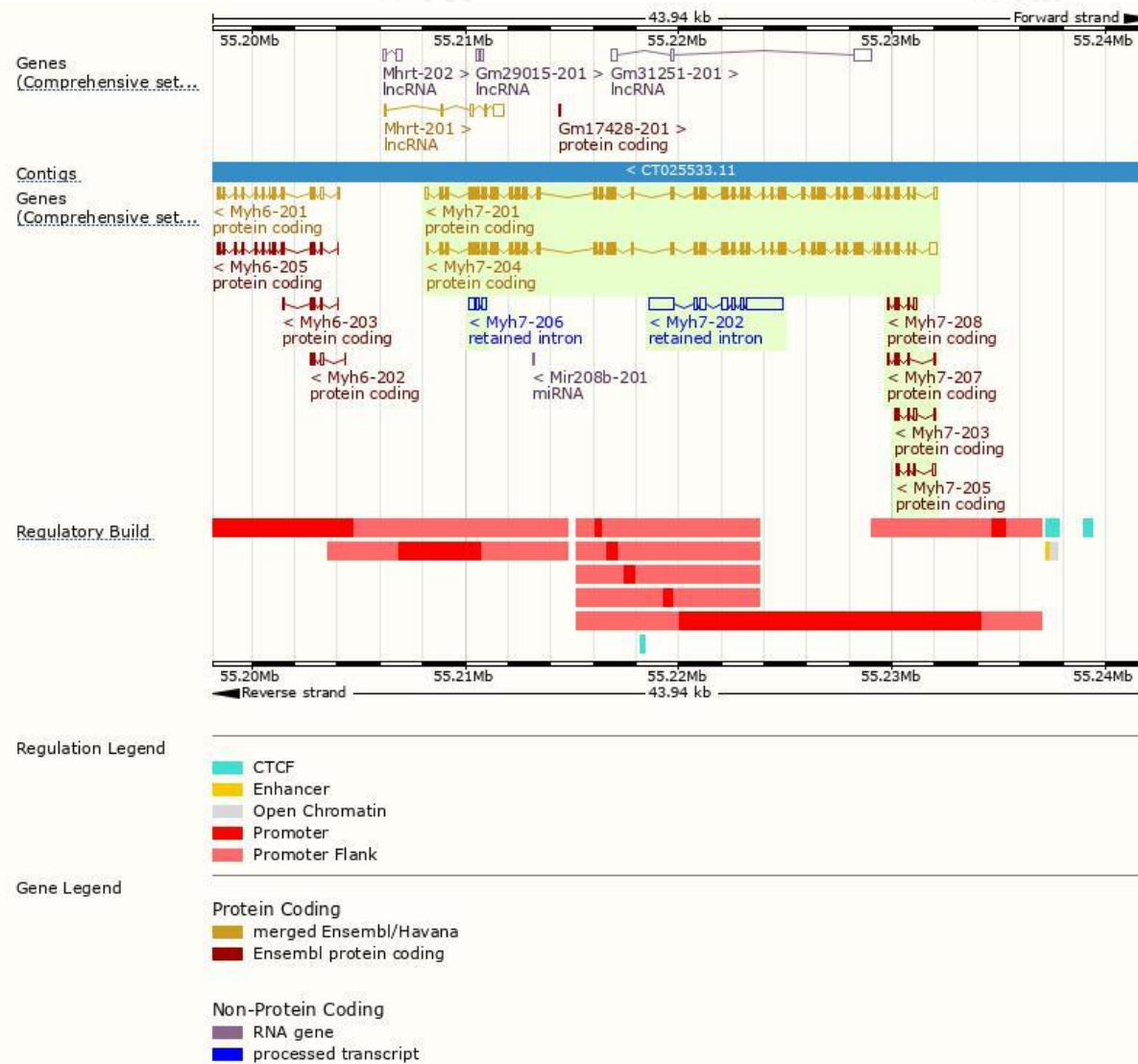
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myh7-204	ENSMUST00000168485.8	6230	1935aa	Protein coding	CCDS27106		TSL:1 , GENCODE basic , APPRIS P1 ,
Myh7-201	ENSMUST00000102803.11	6135	1935aa	Protein coding	CCDS27106		TSL:1 , GENCODE basic , APPRIS P1 ,
Myh7-208	ENSMUST00000228837.2	451	94aa	Protein coding	-		CDS 3' incomplete ,
Myh7-203	ENSMUST00000153783.2	377	60aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Myh7-207	ENSMUST00000227518.2	360	87aa	Protein coding	-		CDS 3' incomplete ,
Myh7-205	ENSMUST00000226424.2	345	36aa	Protein coding	-		CDS 3' incomplete ,
Myh7-202	ENSMUST00000149852.2	3769	No protein	Retained intron	-		TSL:1 ,
Myh7-206	ENSMUST00000227401.2	595	No protein	Retained intron	-		

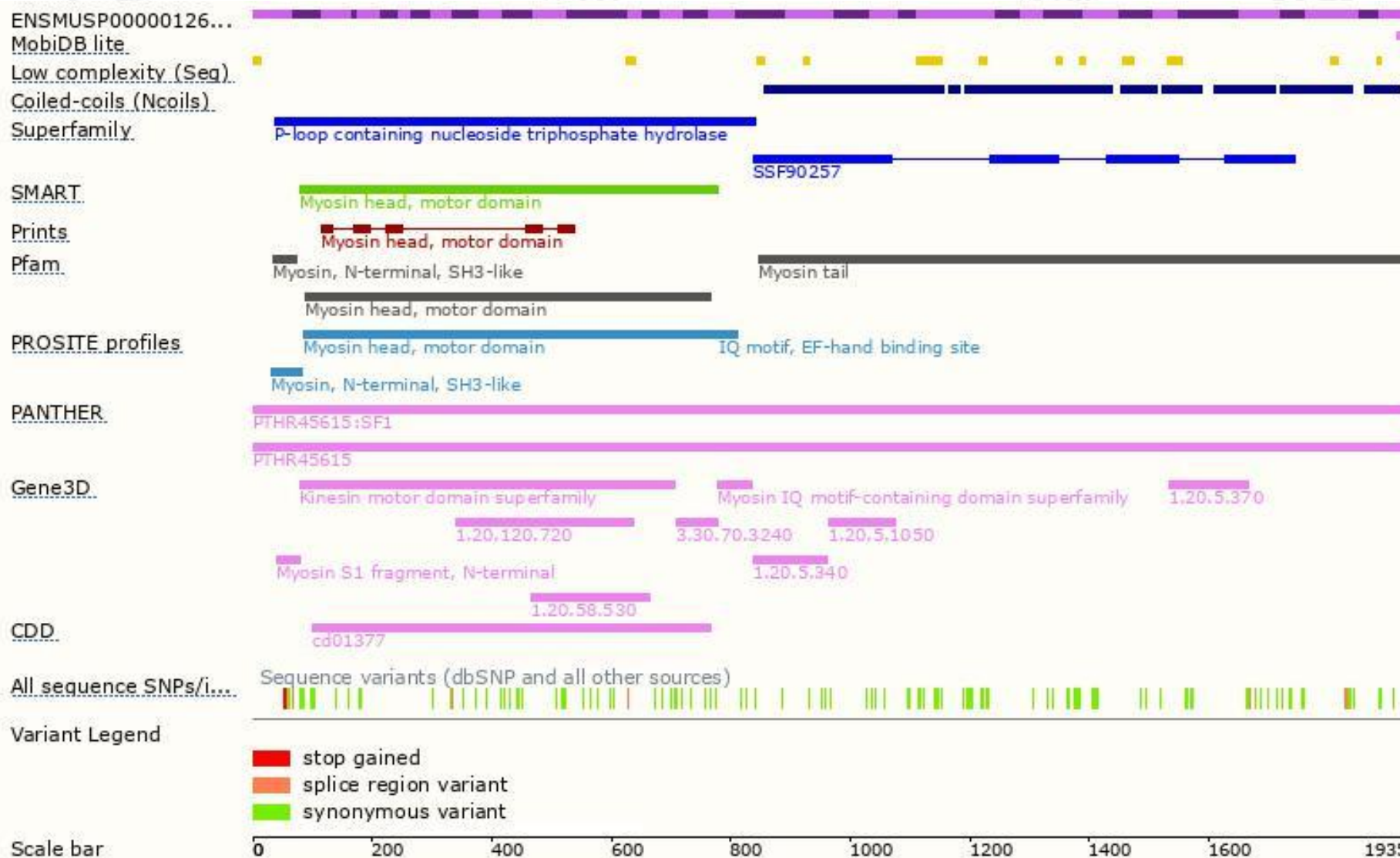
The strategy is based on the design of *Myh7-201* transcript,the transcription is shown below:



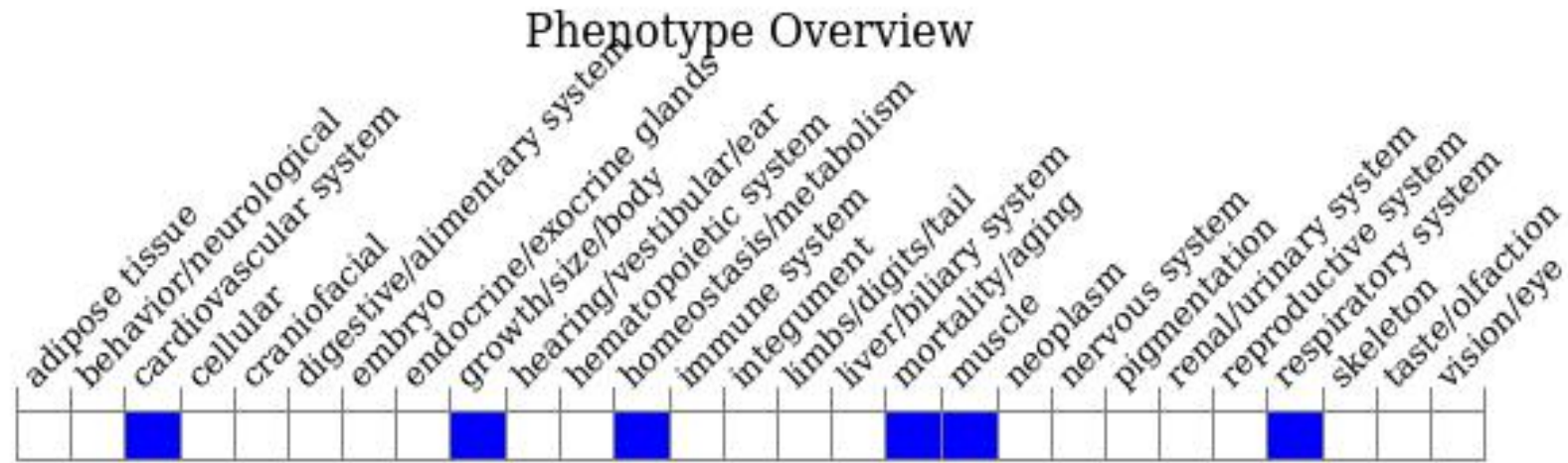
Genomic location distribution



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 an endonuclease-mediated allele exhibit complete embryonic lethality during organogenesis with evidence of heart failure.

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