

Myh1 Cas9-KO Strategy

Designer:

Yang Zeng

Reviewer:

Xiaojing Li

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Project Overview

Project Name

Myh1

Project type

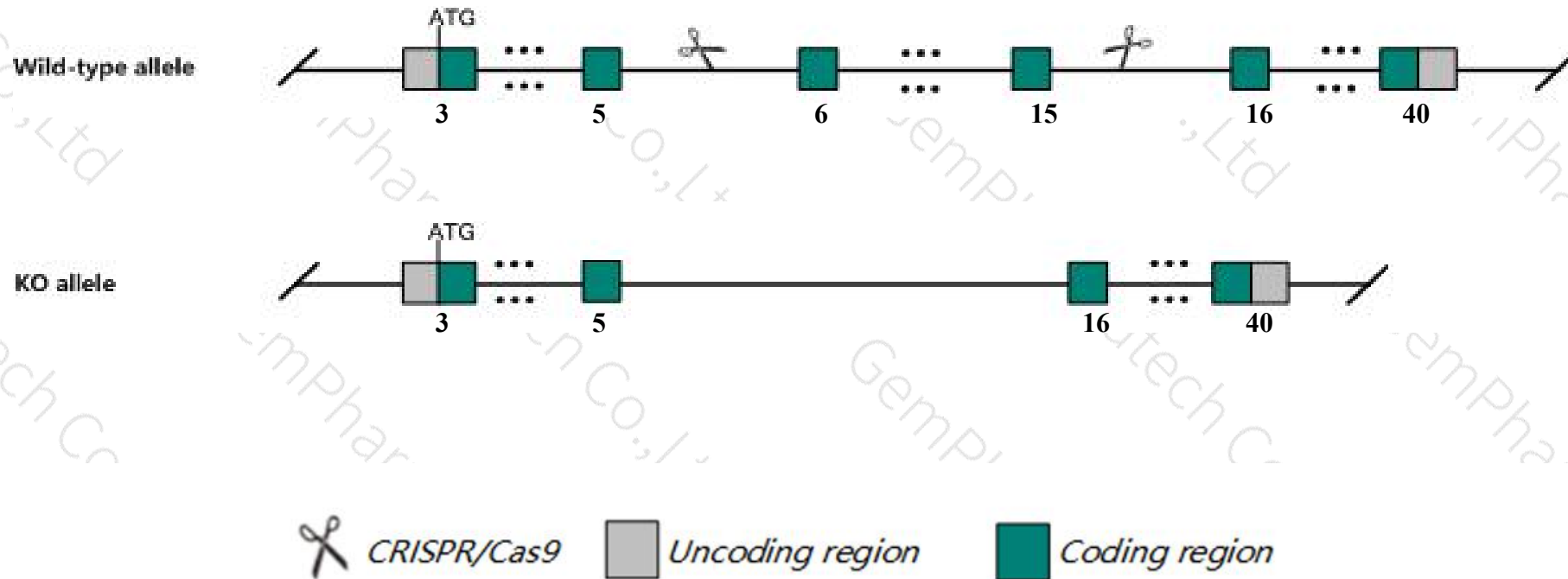
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myh1* gene. The schematic diagram is as follows:



- The *Myh1* gene has 4 transcripts. According to the structure of *Myh1* gene, exon6-exon15 of *Myh1*-203 (ENSMUST00000124516.7) transcript is recommended as the knockout region. The region contains 1082bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Myh1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for a targeted null mutation exhibit reduced growth, muscular weakness, kyphosis, and abnormal kinetics of muscle contraction and relaxation.
- Transcript *Myh1*-204 CDS 3' is incomplete, whether it will be affected is unknown.
- The *Myh1* 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.

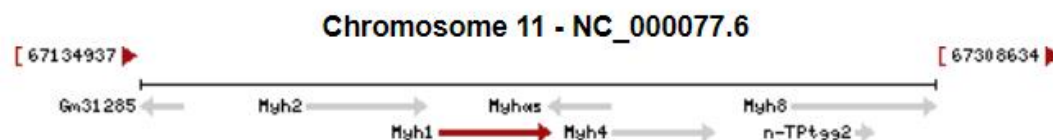
Gene information (NCBI)

Myh1 myosin, heavy polypeptide 1, skeletal muscle, adult [*Mus musculus* (house mouse)]

Gene ID: 17879, updated on 12-Aug-2019

Summary

Official Symbol	Myh1 provided by MGI
Official Full Name	myosin, heavy polypeptide 1, skeletal muscle, adult provided by MGI
Primary source	MGI:MGI:1339711
See related	Ensembl:ENSMUSG00000056328
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	Ild; MdMs; Ild/x; Myhs-f; Myhsf2; MHC2X/D; Myhs-f2; MHC-2X/D; MYHC-IIx; MyHC-Ild/x; MyHC-Ilx/d; A530084A17Rik
Expression	Biased expression in mammary gland adult (RPKM 25.2), lung adult (RPKM 11.6) and 2 other tissues See more
Orthologs	human all

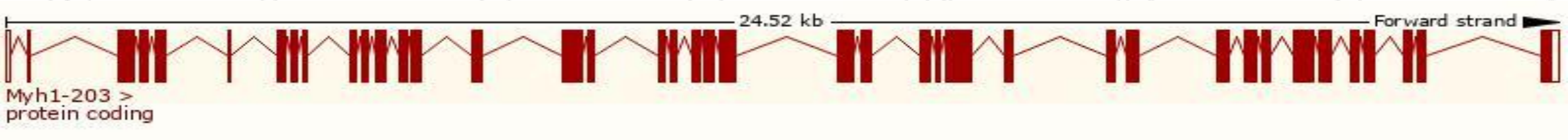


Transcript information (Ensembl)

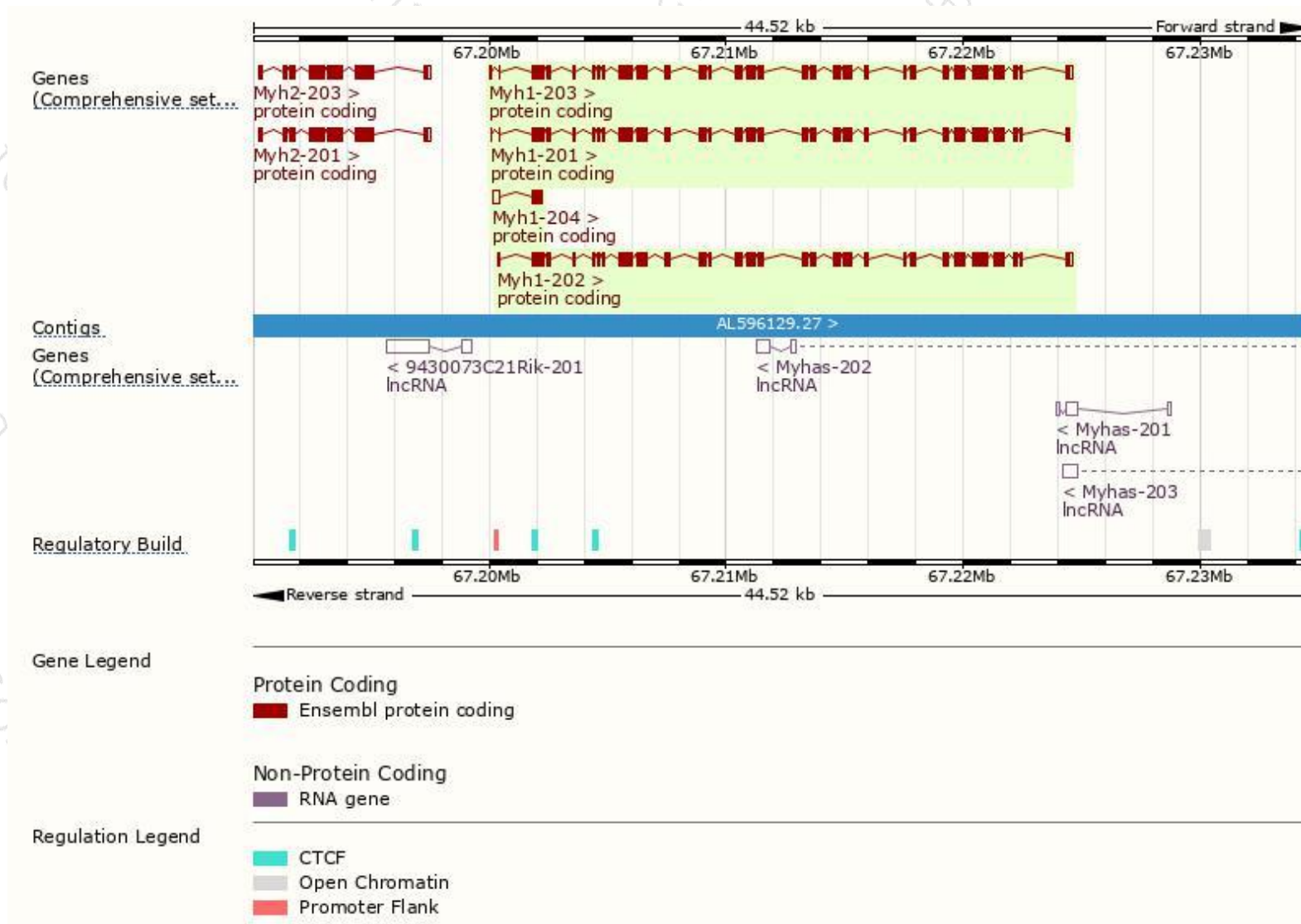
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Myh1-203	ENSMUST00000124516.7	6081	1942aa	ENSMUSP00000117569.1	Protein coding	CCDS24855	Q5SX40	TSL:1 GENCODE basic APPRIS P1
Myh1-202	ENSMUST00000075734.5	6012	1942aa	ENSMUSP00000075147.5	Protein coding	CCDS24855	Q5SX40	TSL:1 GENCODE basic APPRIS P1
Myh1-201	ENSMUST00000018637.14	5938	1942aa	ENSMUSP00000018637.8	Protein coding	CCDS24855	Q5SX40	TSL:5 GENCODE basic APPRIS P1
Myh1-204	ENSMUST00000129018.7	631	95aa	ENSMUSP00000115583.1	Protein coding	-	Q1WNQ6	CDS 3' incomplete TSL:1

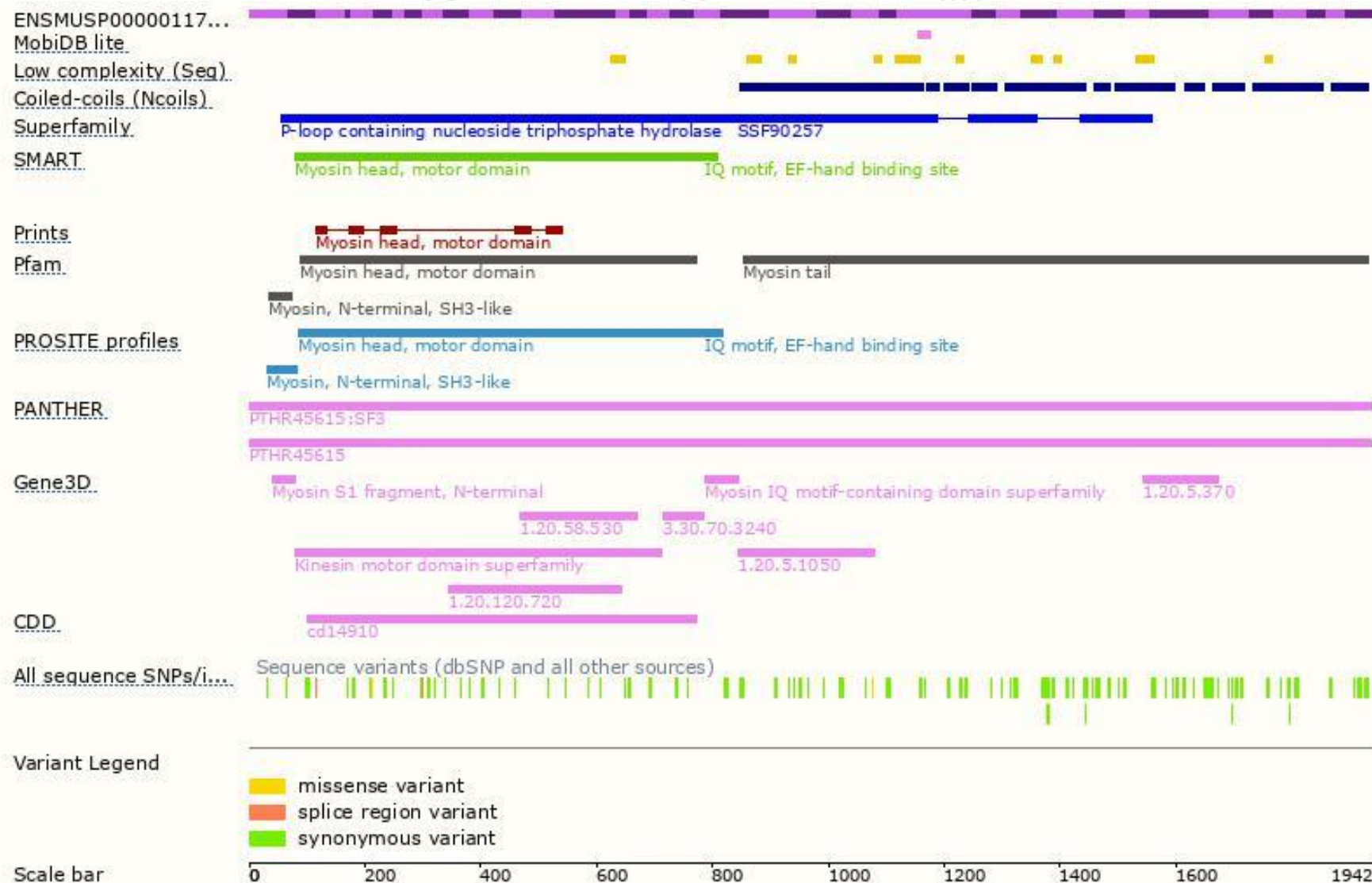
The strategy is based on the design of *Myh1-203* transcript,The transcription is shown below



Genomic location distribution

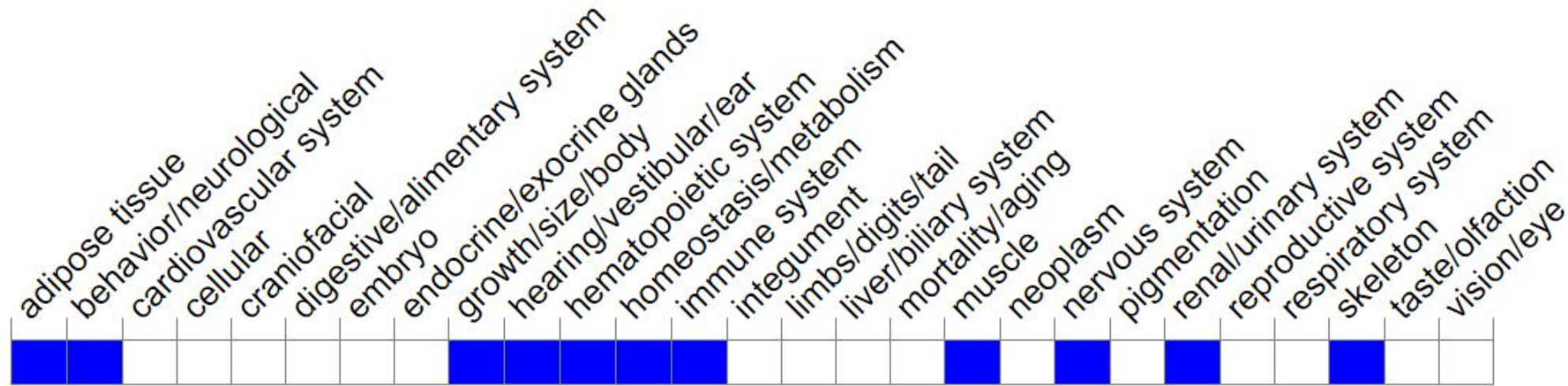


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

Tel: 400-9660890

