

Myl3 Cas9-KO Strategy

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Project Overview

Project Name

Myl3

Project type

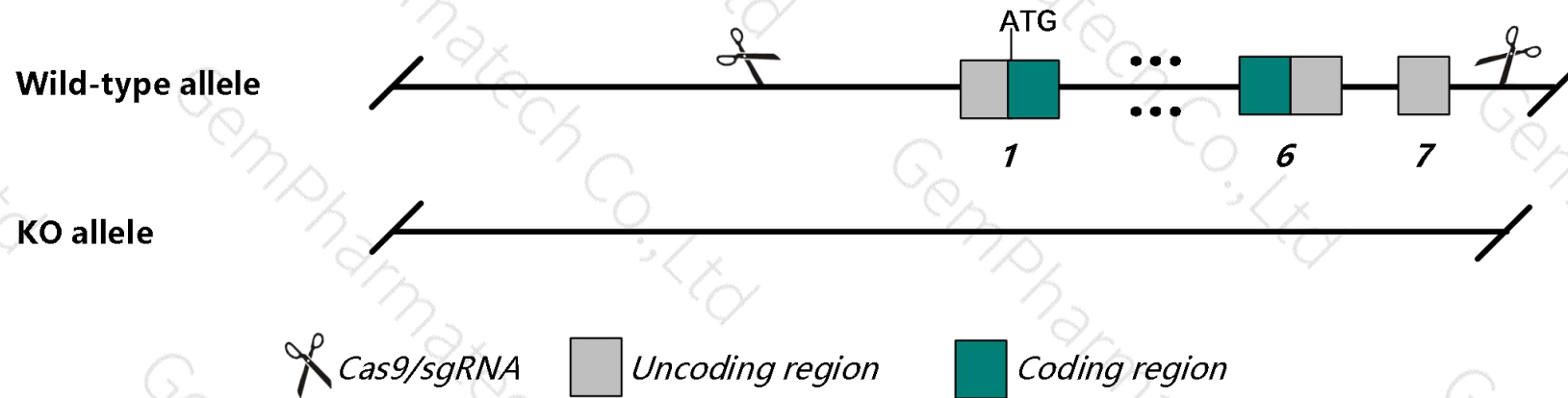
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myf3* gene. The schematic diagram is as follows:



- The *Myl3* gene has 5 transcripts. According to the structure of *Myl3* gene, exon1-exon7 of *Myl3-201* (ENSMUST00000079784.11) 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 *Myl3* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Myl3* gene is located on the Chr9. 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)

Myl3 myosin, light polypeptide 3 [*Mus musculus* (house mouse)]

Gene ID: 17897, updated on 24-Oct-2019

Summary

- Official Symbol** Myl3 provided by [MGI](#)
- Official Full Name** myosin, light polypeptide 3 provided by [MGI](#)
- Primary source** [MGI:MGI:97268](#)
- See related** [Ensembl:ENSMUSG00000059741](#)
- 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** Mylc; VLC1; MLC1s; MLC1v; MLC1SB
- Expression** Restricted expression toward heart adult (RPKM 3314.7) [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 9 F2; 9 60.69 cM See Myl3 in [Genome Data Viewer](#)

Exon count: 7

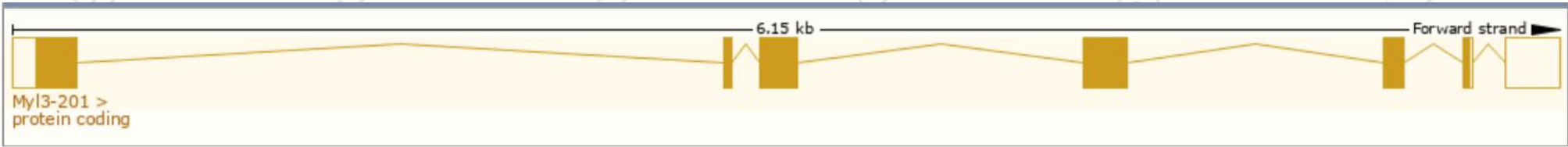
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (110763678..110769802)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (110666185..110672298)

Transcript information (Ensembl)

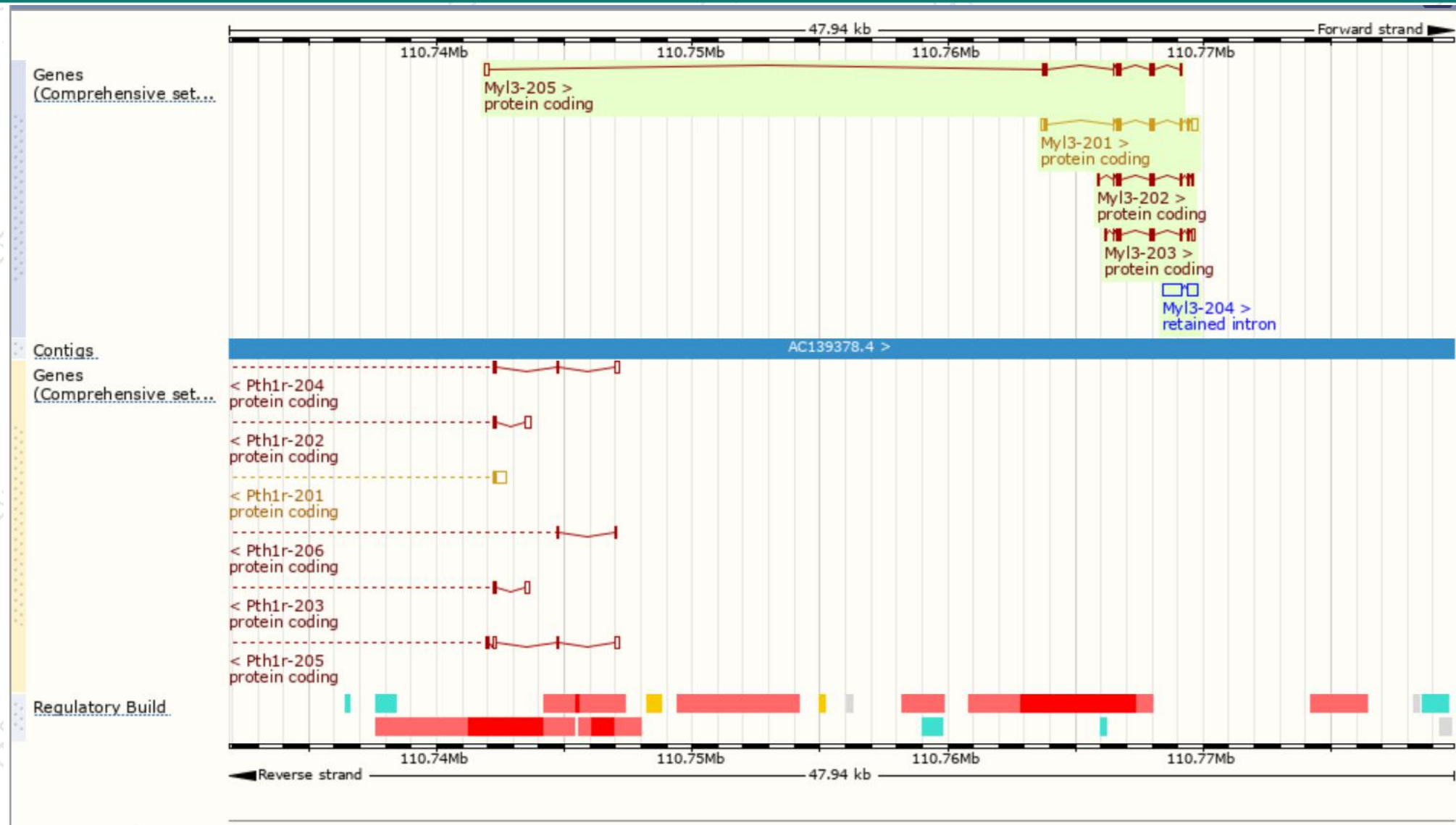
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
MyI3-201	ENSMUST00000079784.11	937	204aa	Protein coding	CCDS23571	P09542	TSL:1 GENCODE basic APPRIS P2
MyI3-205	ENSMUST00000200011.4	737	184aa	Protein coding	-	A0A0G2JDW2	CDS 3' incomplete TSL:5
MyI3-203	ENSMUST00000136695.2	614	127aa	Protein coding	-	A0A0G2JDM3	TSL:3 GENCODE basic APPRIS ALT2
MyI3-202	ENSMUST00000124267.7	575	127aa	Protein coding	-	A0A0G2JDM3	TSL:5 GENCODE basic APPRIS ALT2
MyI3-204	ENSMUST00000153142.2	1125	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *MyI3-201* transcript,The transcription is shown below



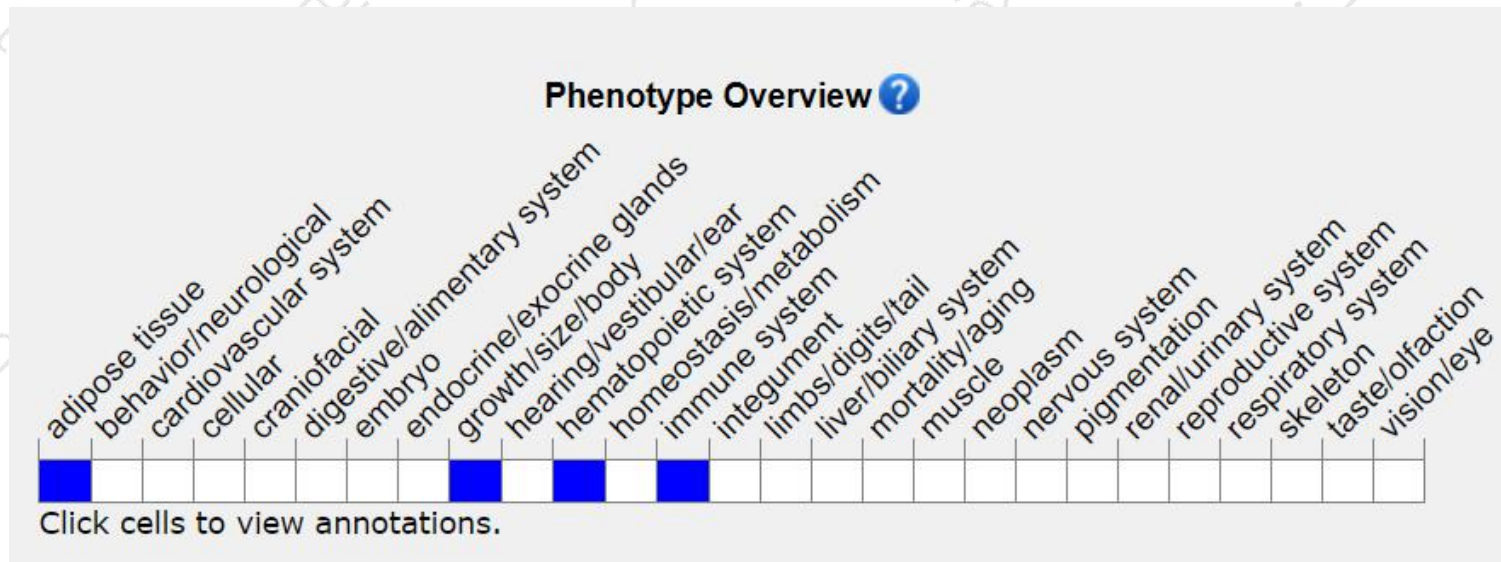
Genomic location distribution



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/>).

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

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