

Myf5 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-4-16

Project Overview

Project Name

Myf5

Project type

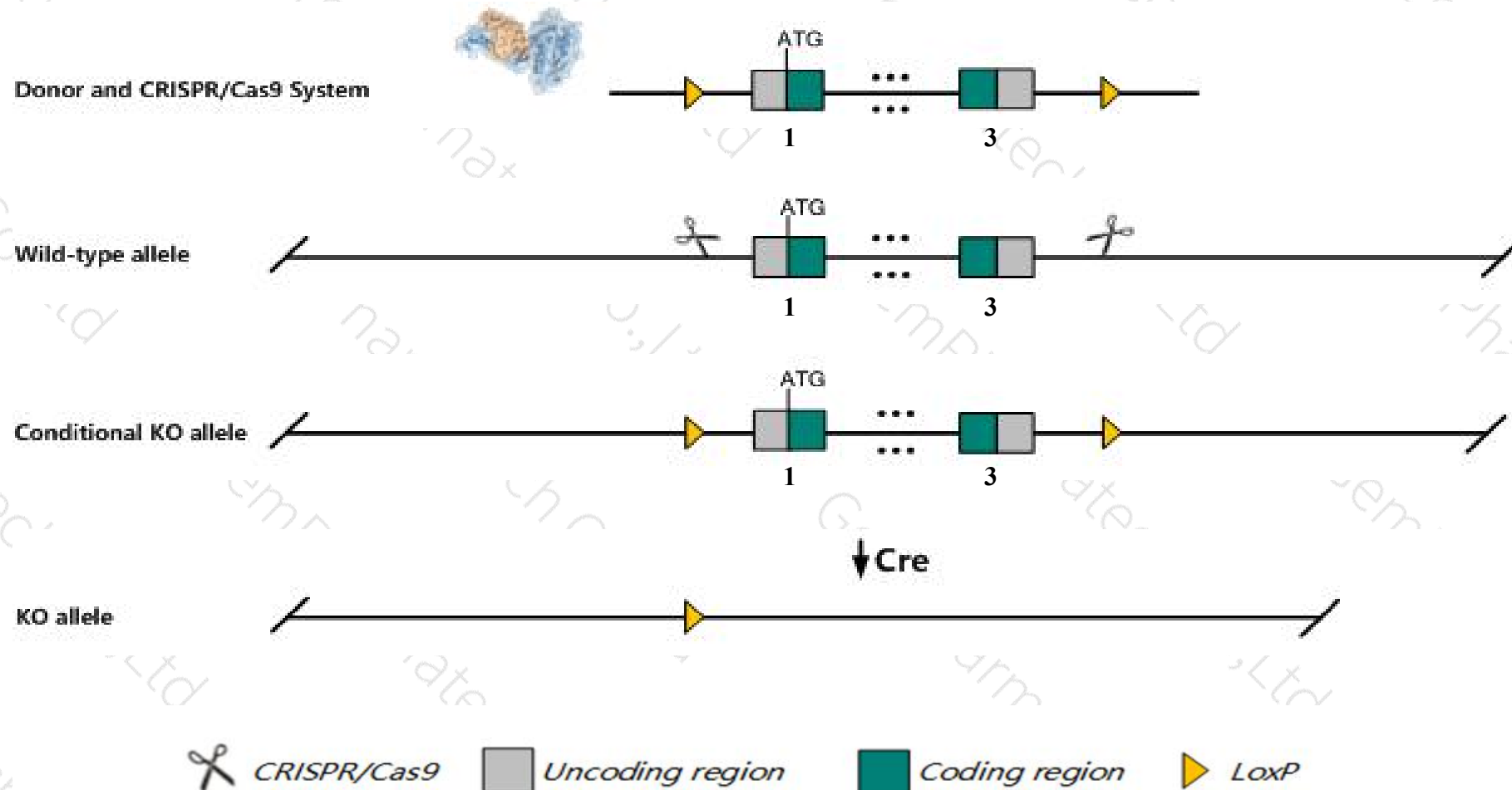
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myf5* gene. The schematic diagram is as follows:



- The *Myf5* gene has 1 transcript. According to the structure of *Myf5* gene, exon1-exon3 of *Myf5-201* (ENSMUST00000000445.1) 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 *Myf5* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, homozygotes for targeted null mutations exhibit delayed appearance of myotomal cells in somites, and lack the distal portion of ribs resulting in inability to breathe and lethality at birth. other mutants lack the rib phenotype.
- The *Myf5* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Myf5 myogenic factor 5 [Mus musculus (house mouse)]

Gene ID: 17877, updated on 13-Mar-2020

Summary



Official Symbol Myf5 provided by [MGI](#)

Official Full Name myogenic factor 5 provided by [MGI](#)

Primary source [MGI:MGI:97252](#)

See related [Ensembl:ENSMUSG000000000435](#)

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 B130010J22Rik, Myf-5, bHLHc2

Expression Biased expression in limb E14.5 (RPKM 2.7), ovary adult (RPKM 0.6) and 1 other tissue [See more](#)

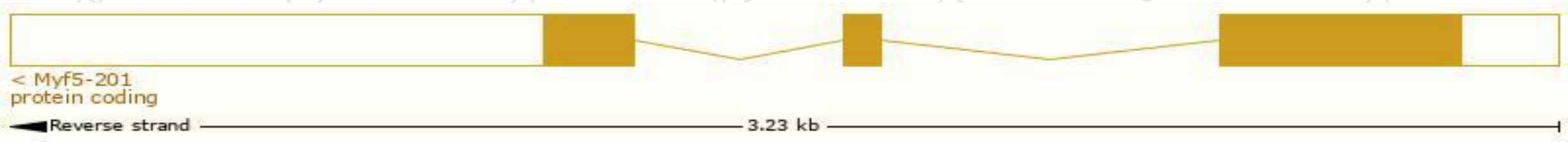
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

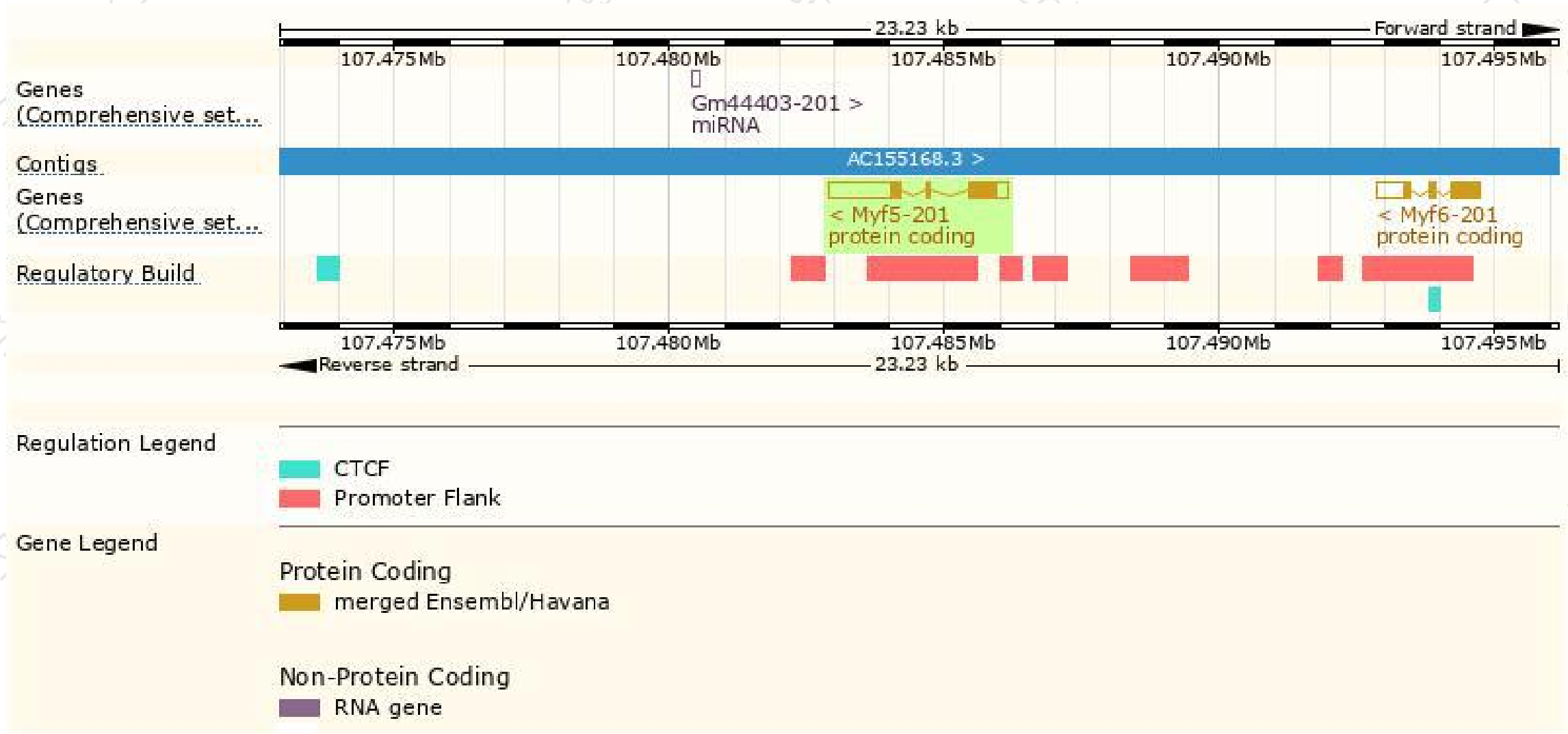
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myf5-201	ENSMUST00000000445.1	2083	255aa	Protein coding	CCDS24161	A2RSK4 P24699	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Myf5-201* transcript, the transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP000000000...

[MobiDB lite](#)

[Low complexity \(Seq\)](#)

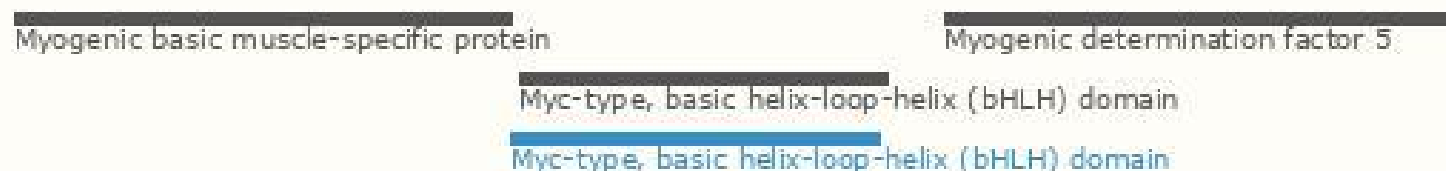
[Coiled-coils \(Ncoils\)](#)

[Superfamily](#)

[SMART](#)



[Pfam](#)



[PROSITE profiles](#)

[PANTHER](#)



[Gene3D](#)

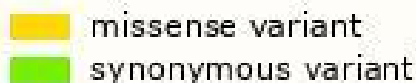
[CDD](#)



[All sequence SNPs/i...](#)



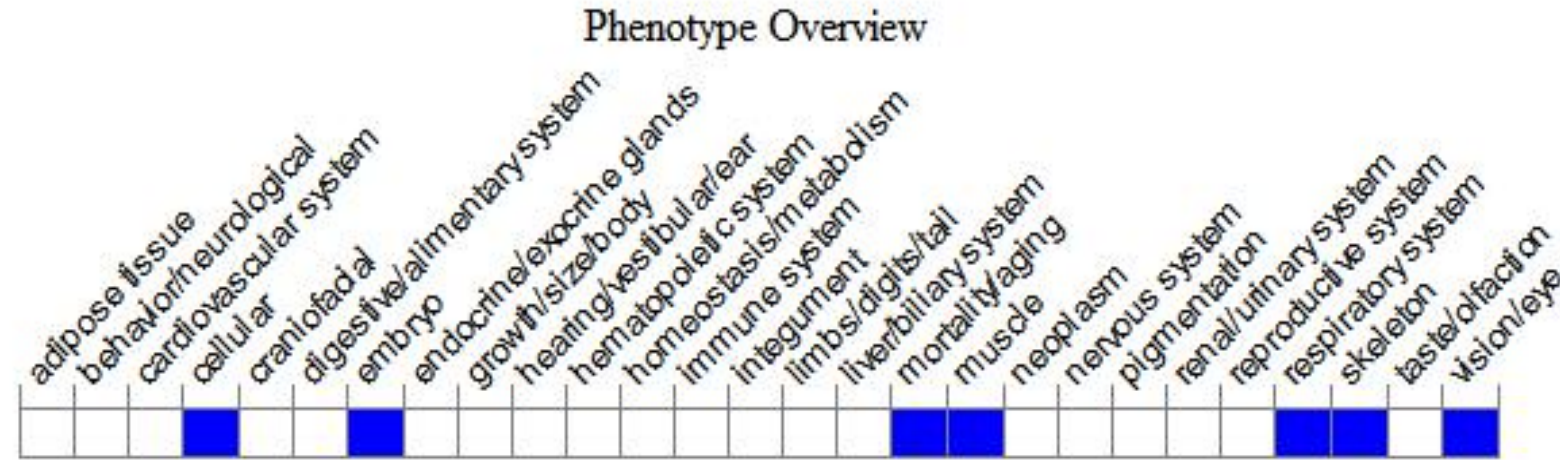
[Variant Legend](#)



[Scale bar](#)



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, homozygotes for targeted null mutations exhibit delayed appearance of myotomal cells in somites, and lack the distal portion of ribs resulting in inability to breathe and lethality at birth. Other mutants lack the rib phenotype.

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

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