

Myl4 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Myl4

Project type

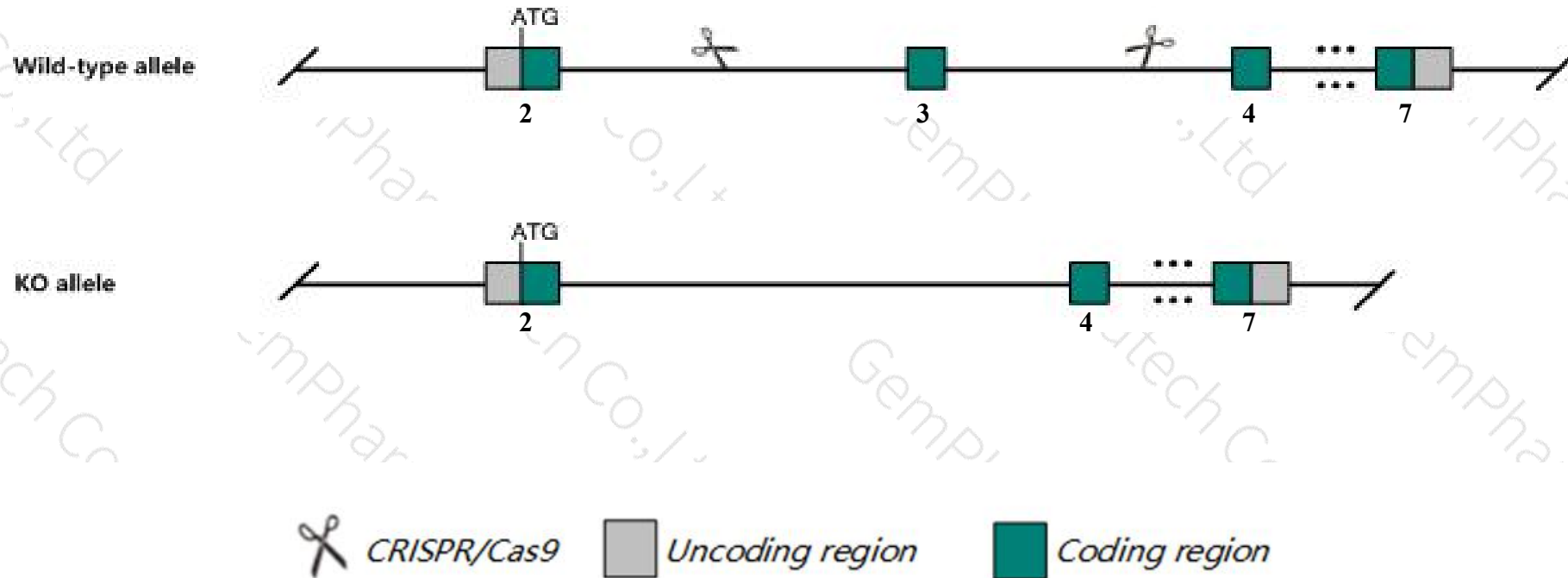
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myl4* gene. The schematic diagram is as follows:



- The *Myl4* gene has 8 transcripts. According to the structure of *Myl4* gene, exon3 of *Myl4-203* (ENSMUST00000106957.7) transcript is recommended as the knockout region. The region contains 28bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Myl4* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Myl4* 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.
- Transcript *Myl4-206* may not be affected.
- 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)

Myl4 myosin, light polypeptide 4 [Mus musculus (house mouse)]

Gene ID: 17896, updated on 31-Jan-2019

Summary



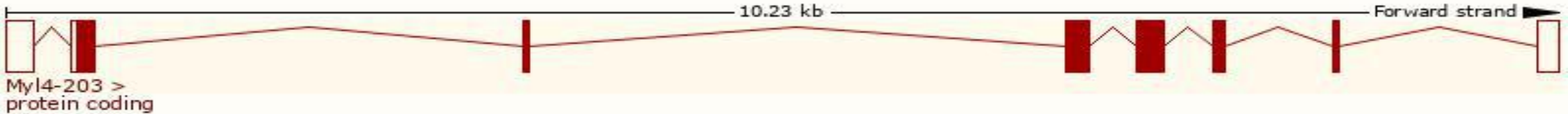
Official Symbol	Myl4 provided by MGI
Official Full Name	myosin, light polypeptide 4 provided by MGI
Primary source	MGI:MGI:97267
See related	Ensembl:ENSMUSG00000061086
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ALC1, AMLC, ELC, ELC1a, GT1, MLC1EMB, MLC1a, Myla
Expression	Biased expression in heart adult (RPKM 169.8), limb E14.5 (RPKM 32.0) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

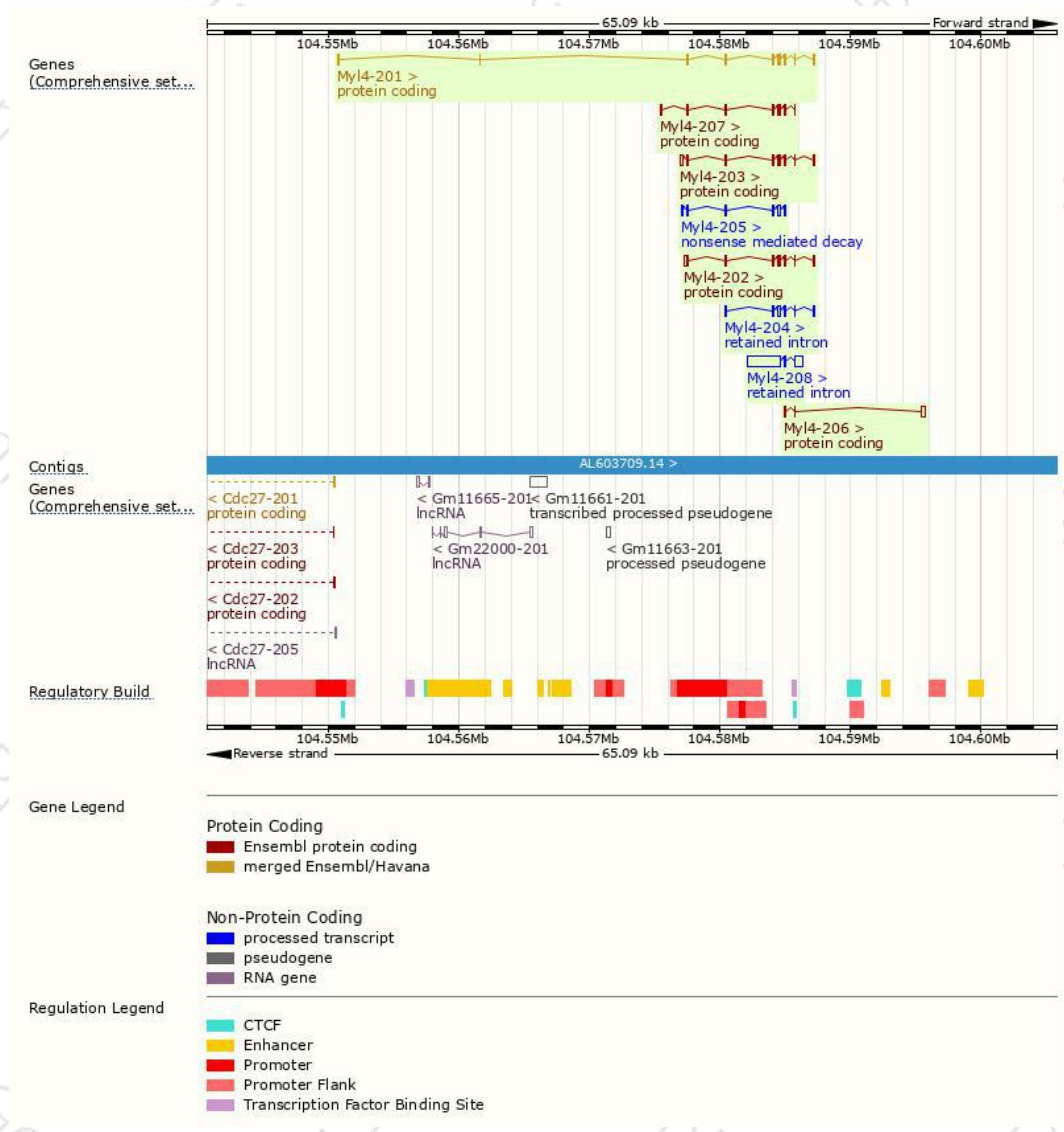
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myl4-203	ENSMUST00000106957.7	943	193aa	Protein coding	CCDS25535	Q9CZ19	TSL:3 GENCODE basic APPRIS P1
Myl4-202	ENSMUST00000106956.9	900	193aa	Protein coding	CCDS25535	Q9CZ19	TSL:1 GENCODE basic APPRIS P1
Myl4-201	ENSMUST00000018800.8	879	193aa	Protein coding	CCDS25535	Q9CZ19	TSL:1 GENCODE basic APPRIS P1
Myl4-207	ENSMUST00000153761.7	702	191aa	Protein coding	-	A2A6Q8	CDS 3' incomplete TSL:5
Myl4-206	ENSMUST00000136244.1	486	26aa	Protein coding	-	F6XL79	CDS 5' incomplete TSL:3
Myl4-205	ENSMUST00000130588.7	781	74aa	Nonsense mediated decay	-	D6RFU4	TSL:3
Myl4-208	ENSMUST00000155271.1	3273	No protein	Retained intron	-	-	TSL:1
Myl4-204	ENSMUST00000123074.7	677	No protein	Retained intron	-	-	TSL:3

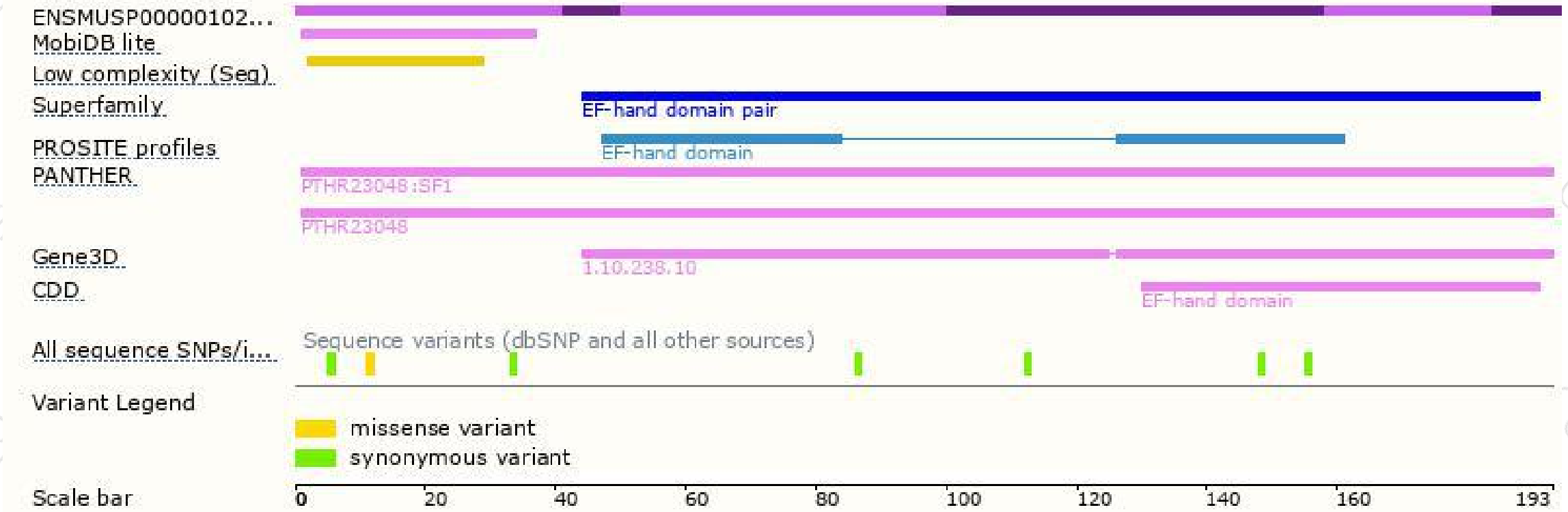
The strategy is based on the design of *Myl4-203* transcript,The transcription is shown below



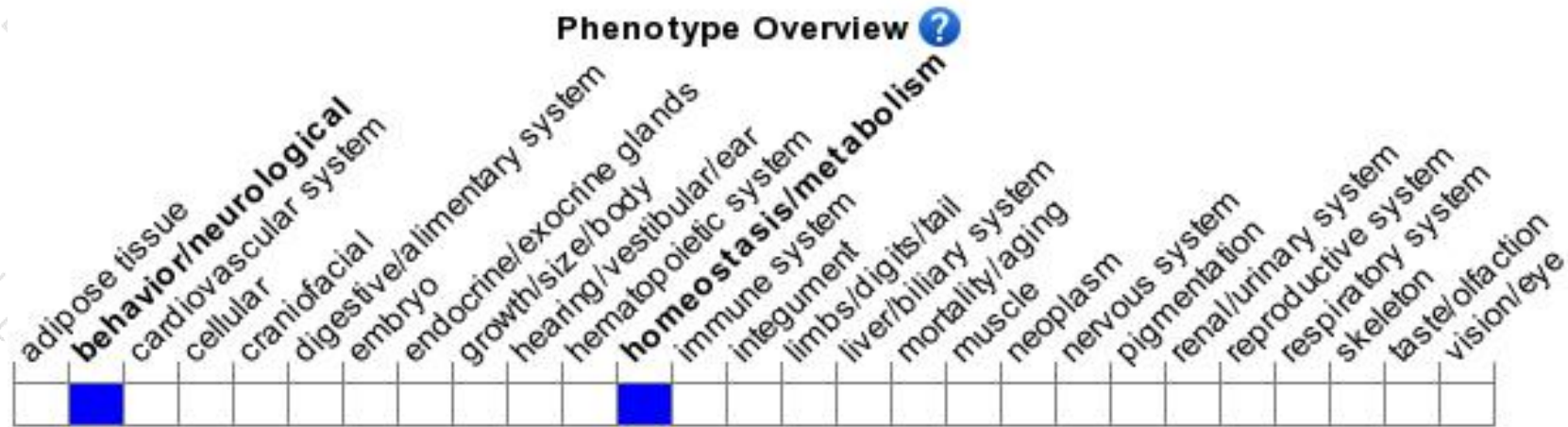
Genomic location distribution



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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