

Col6a3 Cas9-KO Strategy

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Project Overview

Project Name

Col6a3

Project type

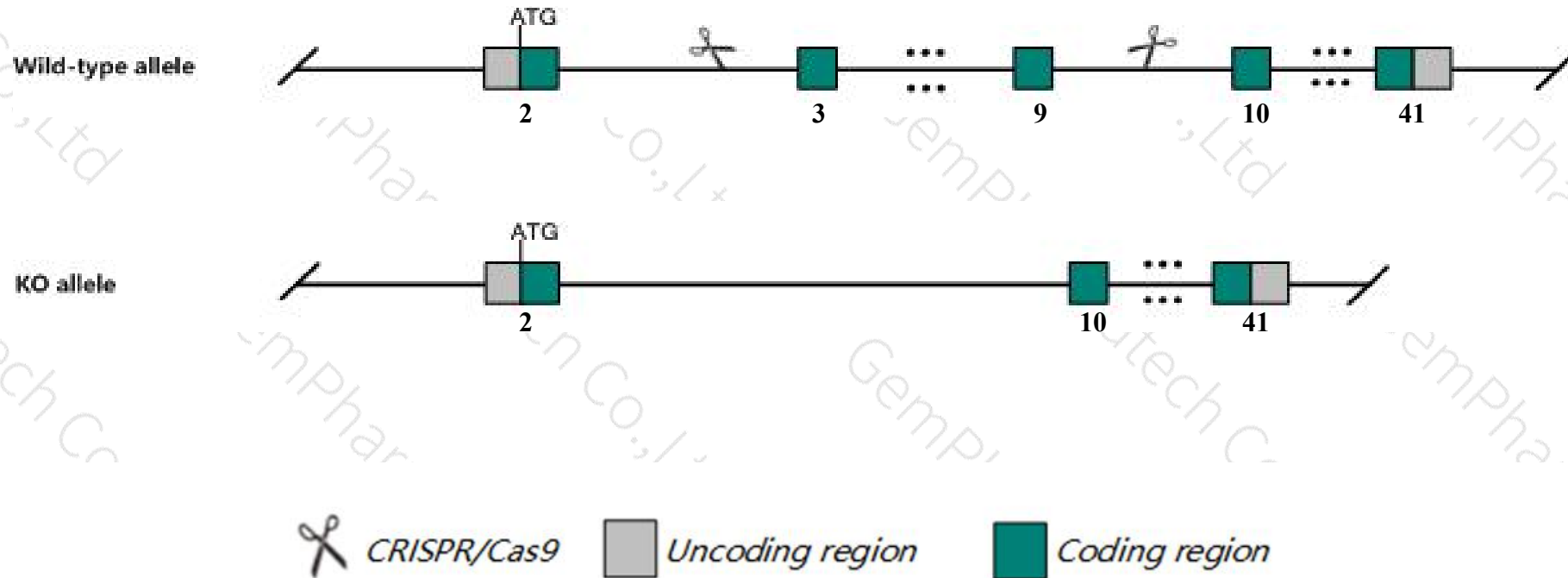
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Col6a3* gene. The schematic diagram is as follows:



- The *Col6a3* gene has 8 transcripts. According to the structure of *Col6a3* gene, exon3-exon9 of *Col6a3-202* (ENSMUST00000097653.10) transcript is recommended as the knockout region. The region contains 3920bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Col6a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a hypomorphic allele exhibit mild myopathy, decreased skeletal muscle weight, increased collagen deposition in muscles, skeletal muscle interstitial fibrosis and abnormal tendon collagen fibril morphology.
- The *Col6a3* gene is located on the Chr1. 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)

Col6a3 collagen, type VI, alpha 3 [Mus musculus (house mouse)]

Gene ID: 12835, updated on 3-Feb-2019

Summary



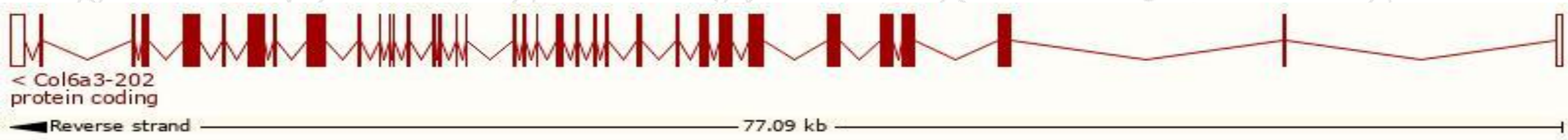
Official Symbol	Col6a3 provided by MGI
Official Full Name	collagen, type VI, alpha 3 provided by MGI
Primary source	MGI:MGI:88461
See related	Ensembl:ENSMUSG00000048126
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI507288, Col6a-3
Expression	Broad expression in limb E14.5 (RPKM 62.3), subcutaneous fat pad adult (RPKM 60.9) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

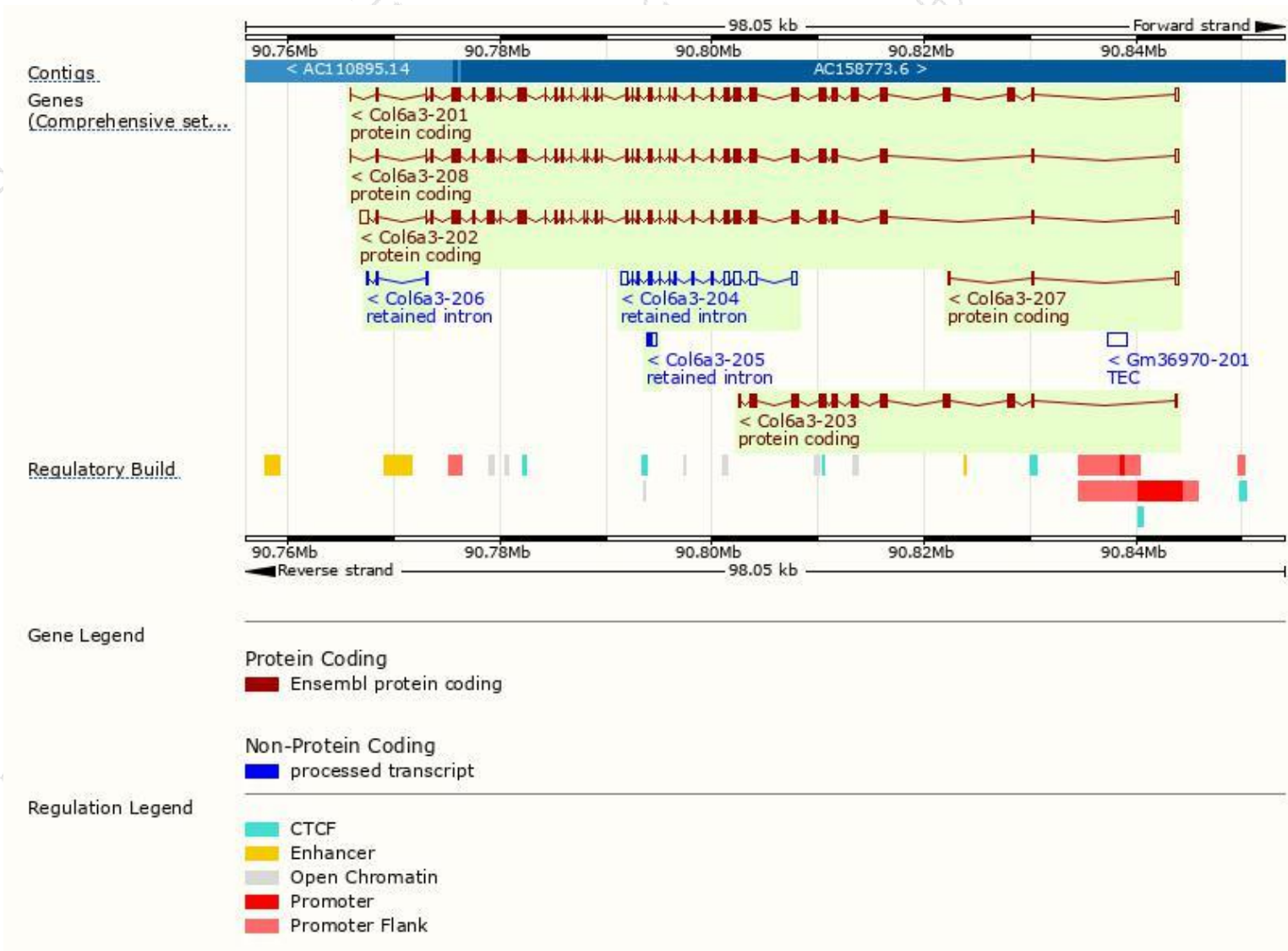
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Col6a3-202	ENSMUST00000097653.10	9001	2677aa	Protein coding	CCDS56640	J3QQ16	TSL:5 GENCODE basic APPRIS P1
Col6a3-201	ENSMUST00000056925.15	10106	3284aa	Protein coding	-	E9PWQ3	TSL:5 GENCODE basic
Col6a3-208	ENSMUST00000188587.6	8285	2677aa	Protein coding	-	A0A087WS16	TSL:5 GENCODE basic
Col6a3-203	ENSMUST00000130846.8	5321	1703aa	Protein coding	-	D3YWD1	CDS 3' incomplete TSL:1
Col6a3-207	ENSMUST00000187753.1	476	74aa	Protein coding	-	A0A087WQN9	CDS 3' incomplete TSL:2
Col6a3-204	ENSMUST00000136916.7	3275	No protein	Retained intron	-	-	TSL:1
Col6a3-206	ENSMUST00000150769.1	646	No protein	Retained intron	-	-	TSL:2
Col6a3-205	ENSMUST00000145750.1	615	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Col6a3-202* transcript,The transcription is shown below



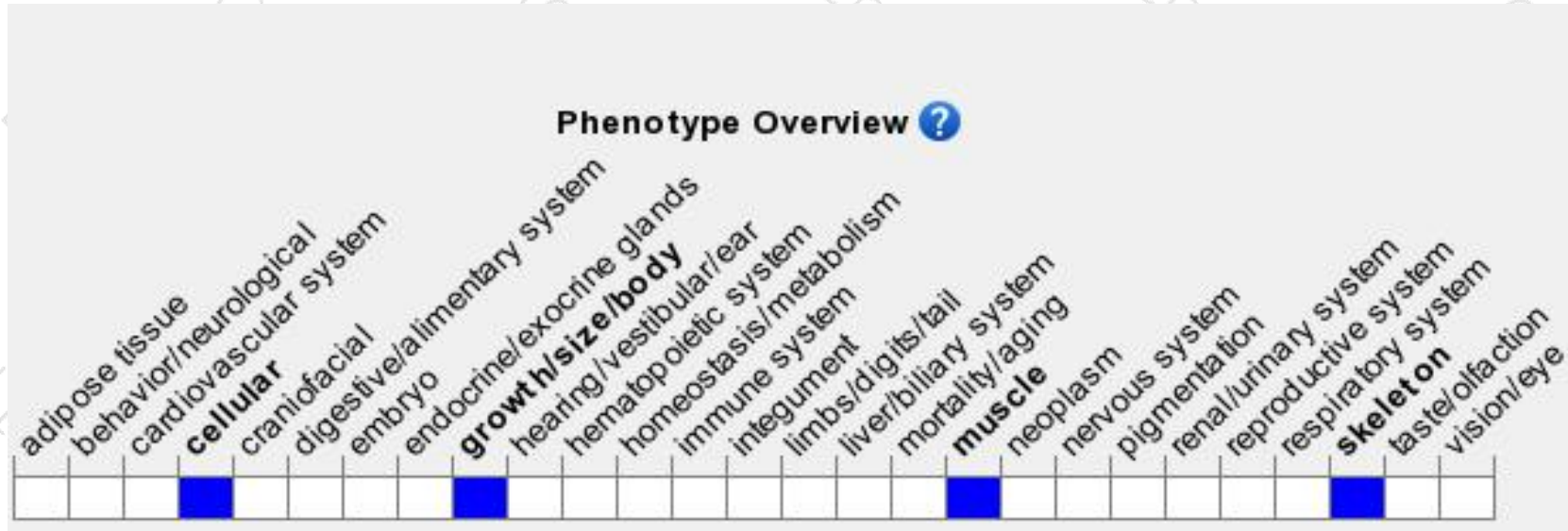
Genomic location distribution



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 a hypomorphic allele exhibit mild myopathy, decreased skeletal muscle weight, increased collagen deposition in muscles, skeletal muscle interstitial fibrosis and abnormal tendon collagen fibril morphology.

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

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