# *Mamstr* Cas9-KO Strategy

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**Design Date: 2020-9-9**

# Project Overview

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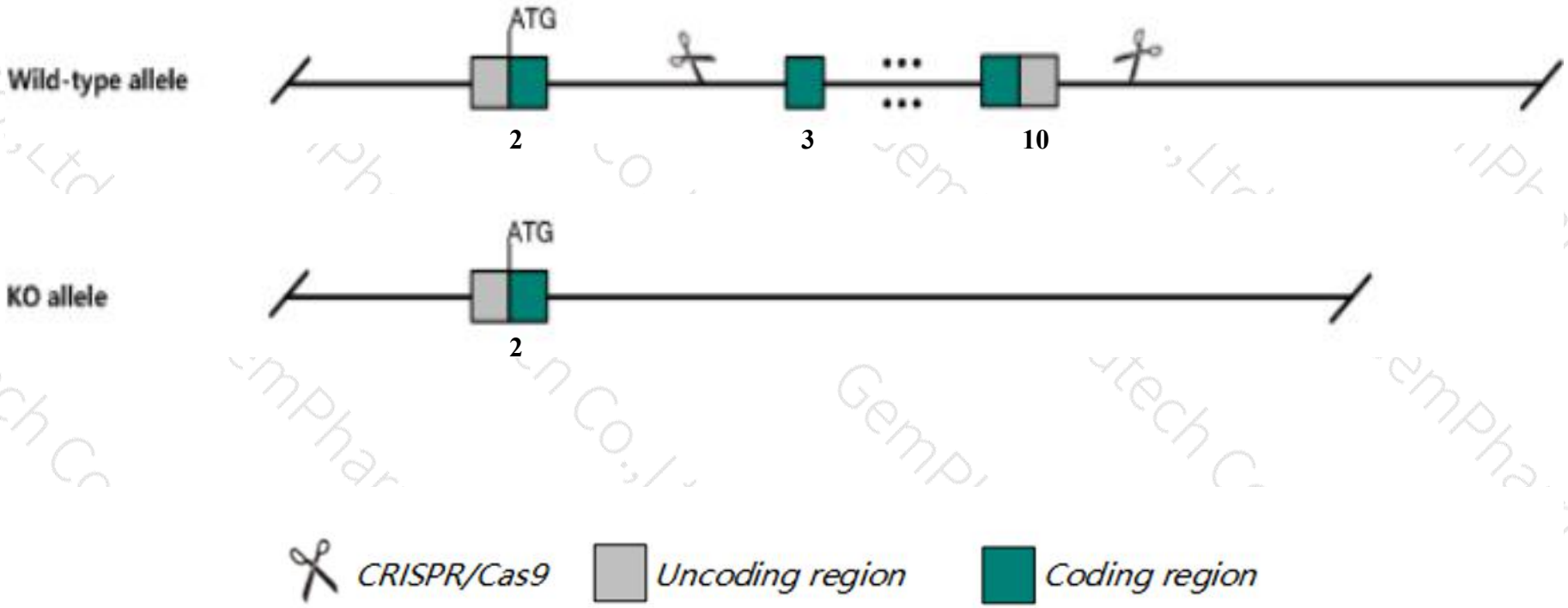
|---|---|
| **Project Name** | ***Mamstr*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

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



# Technical routes

➢ The *Mamstr* gene has 6 transcripts. According to the structure of *Mamstr* gene, exon3-exon10 of *Mamstr-201*(ENSMUST00000148532.3) transcript is recommended as the knockout region.The region contains most 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 *Mamstr* gene. The brief process is as follows: CRISPR/Cas9 system 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.

# Notice

➢ According to the existing MGI data,mice homozygous for a null mutation display impaired muscle regeneration.

➢ The knockout region is near to the N-terminal of *A030001D20Rik* gene and C-terminal of *Fut2* gene,this strategy may influence the regulatory function of the N-terminal of *A030001D20Rik* gene and C-terminal of *Fut2* gene.

➢ The *Mamstr* gene is located on the Chr7. 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）

集萃药康 GemPharmatech

## Mamstr MEF2 activating motif and SAP domain containing transcriptional regulator [Mus musculus (house mouse)]

Gene ID: 74490, updated on 13-Mar-2020

### Summary

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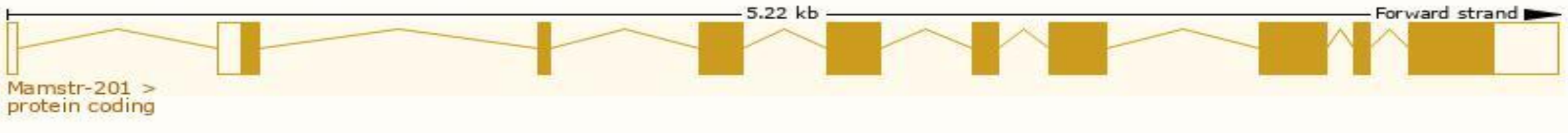
|---|---|
| **Official Symbol** | Mamstr provided by MGI |
| **Official Full Name** | MEF2 activating motif and SAP domain containing transcriptional regulator provided by MGI |
| **Primary source** | MGI:MGI:1921740 |
| **See related** | Ensembl:ENSMUSG00000042918 |
| **Gene type** | protein coding |
| **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** | 2810022D01Rik, 5430432N15Rik, AW743872, Mastr |
| **Expression** | Broad expression in limb E14.5 (RPKM 3.5), mammary gland adult (RPKM 1.7) and 19 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

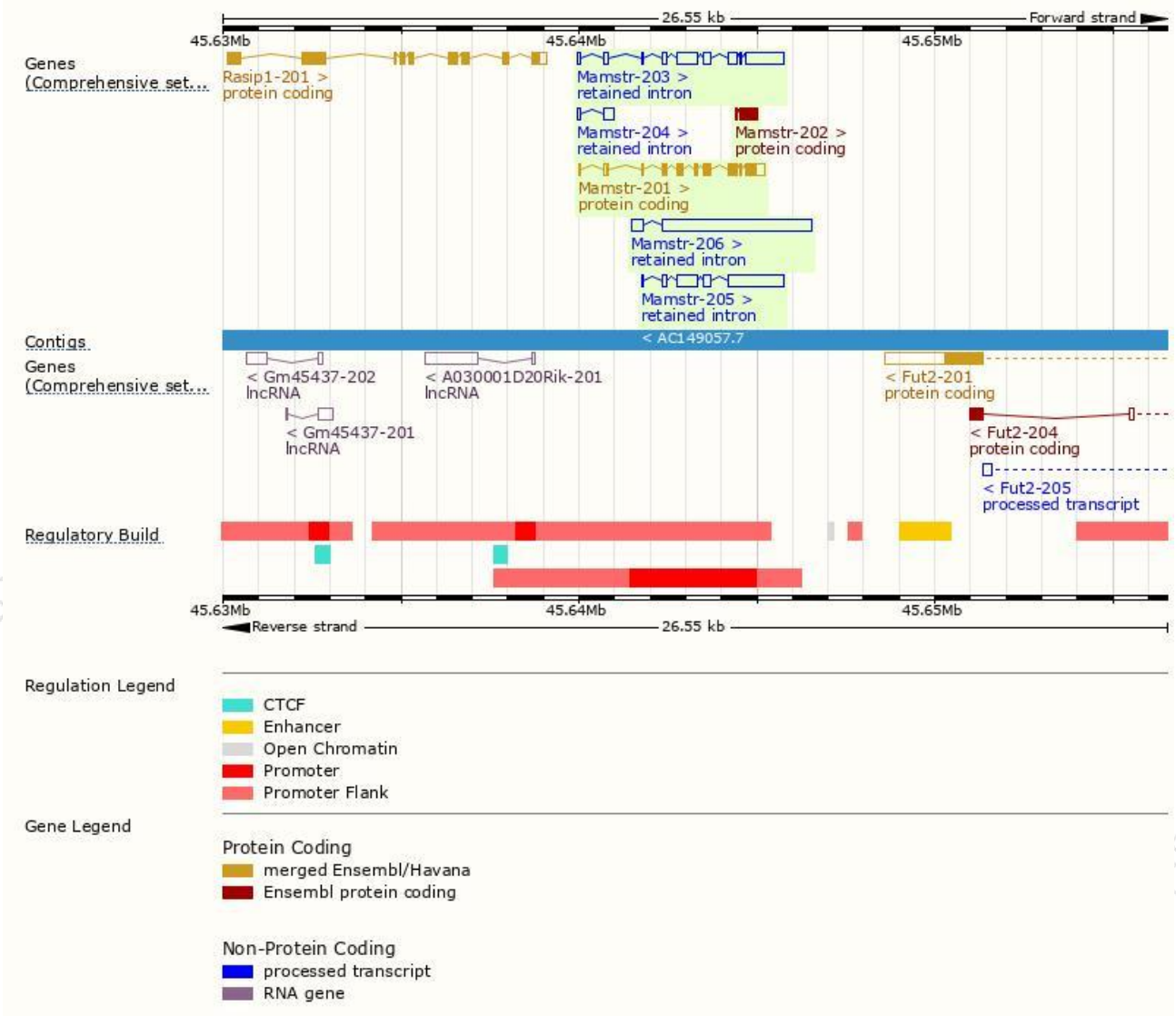
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| **Mamstr-201** | ENSMUST00000148532.3 | 1606 | 421aa | Protein coding | CCDS21257 | Q0ZCJ7 | TSL:1 GENCODE basic APPRIS P1 |
| **Mamstr-202** | ENSMUST00000210169.1 | 536 | 171aa | Protein coding | - | A0A1B0GQV8 | CDS 5' incomplete TSL:2 |
| **Mamstr-206** | ENSMUST00000210988.1 | 4534 | No protein | Retained intron | - | - | TSL:1 |
| **Mamstr-205** | ENSMUST00000210957.1 | 2491 | No protein | Retained intron | - | - | TSL:1 |
| **Mamstr-203** | ENSMUST00000210213.1 | 2486 | No protein | Retained intron | - | - | TSL:2 |
| **Mamstr-204** | ENSMUST00000210648.1 | 343 | No protein | Retained intron | - | - | TSL:3 |

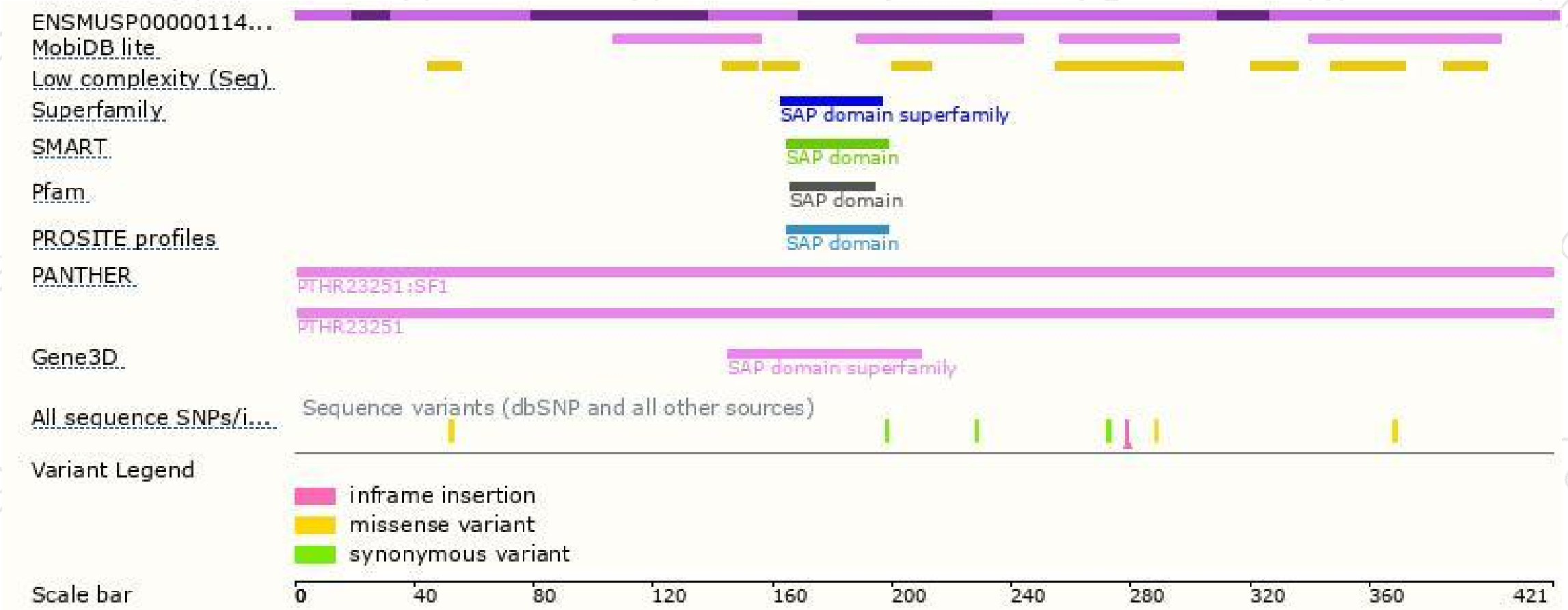
The strategy is based on the design of *Mamstr-201* transcript,the transcription is shown below:



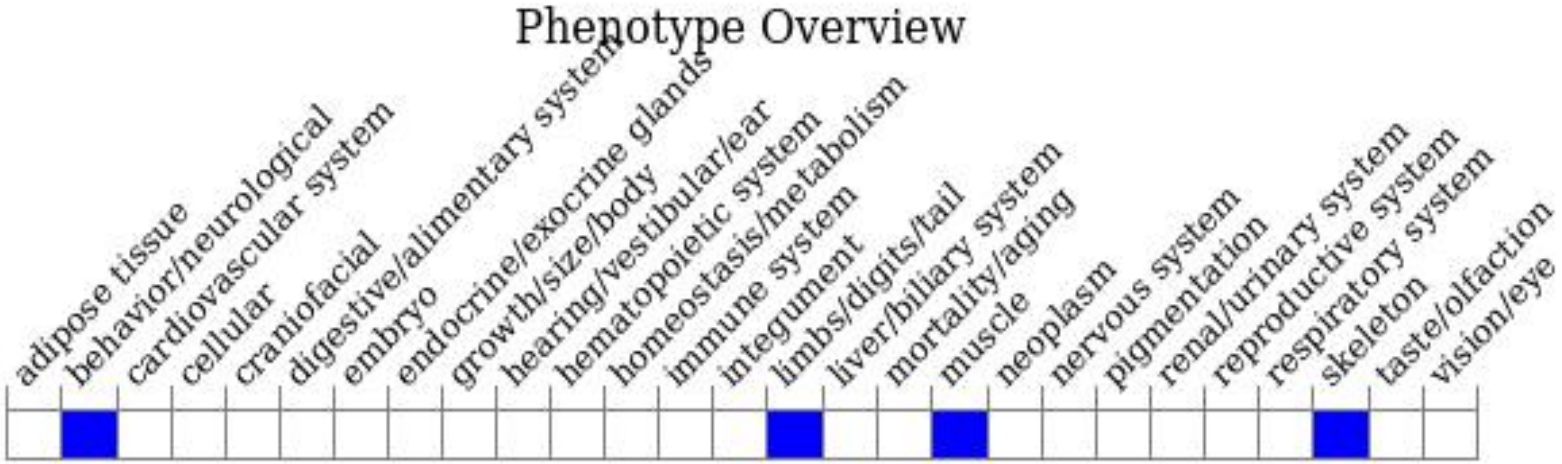
# Genomic location distribution



# 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/).*

According to the existing MGI data,mice homozygous for a null mutation display impaired muscle regeneration.

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

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