

***Msl3* Cas9-CKO Strategy**

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Project Overview

Project Name

Msl3

Project type

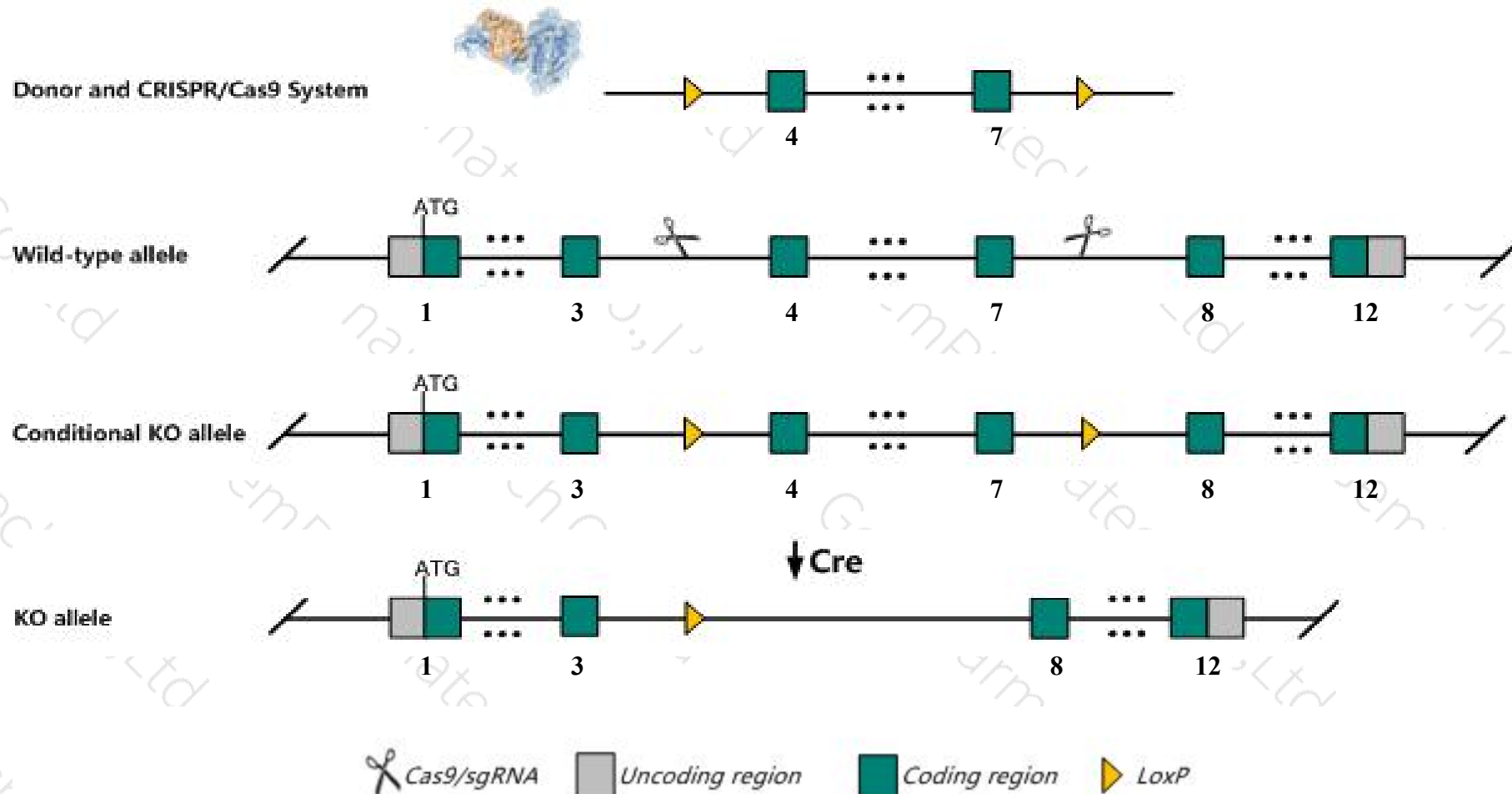
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ms13* gene. The schematic diagram is as follows:



- The *Msl3* gene has 4 transcripts. According to the structure of *Msl3* gene, exon4-exon7 of *Msl3*-202(ENSMUST00000112137.1) transcript is recommended as the knockout region. The region contains 538bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Msl3* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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.

- The *Ms13* gene is located on the ChrX. 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)

Msl3 MSL complex subunit 3 [Mus musculus (house mouse)]

Gene ID: 17692, updated on 13-Mar-2020

Summary

Official Symbol Msl3 provided by [MGI](#)

Official Full Name MSL complex subunit 3 provided by [MGI](#)

Primary source [MGI:MGI:1341851](#)

See related [Ensembl:ENSMUSG000000031358](#)

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 AU018931, Msl31, Msl3l1

Expression Ubiquitous expression in bladder adult (RPKM 7.1), placenta adult (RPKM 6.4) and 28 other tissues [See more](#)

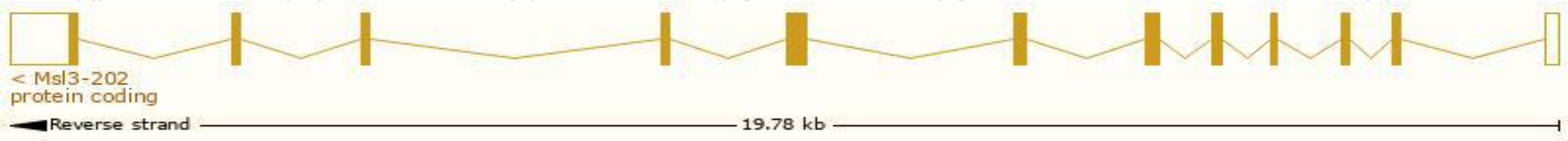
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

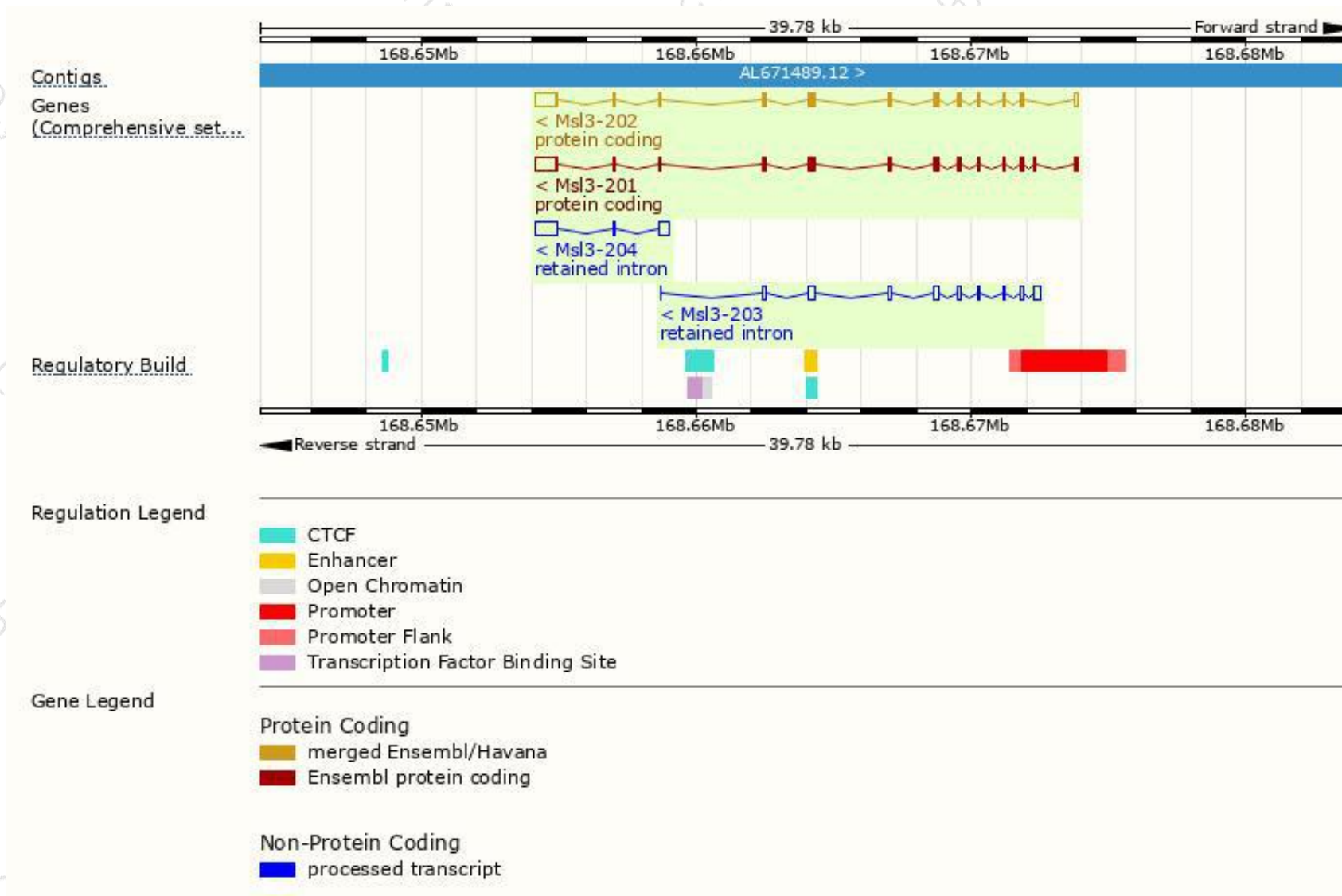
The gene has 4 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Msl3-202 | ENSMUST00000112137.1 | 2316 | 466aa | Protein coding | CCDS41211 | Q9WVG9 | TSL:1 GENCODE basic |
| Msl3-201 | ENSMUST00000033725.15 | 2399 | 525aa | Protein coding | - | Q9WVG9 | TSL:5 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 |
| Msl3-203 | ENSMUST00000129860.1 | 1390 | No protein | Retained intron | - | - | TSL:1 |
| Msl3-204 | ENSMUST00000145564.1 | 1336 | No protein | Retained intron | - | - | TSL:2 |

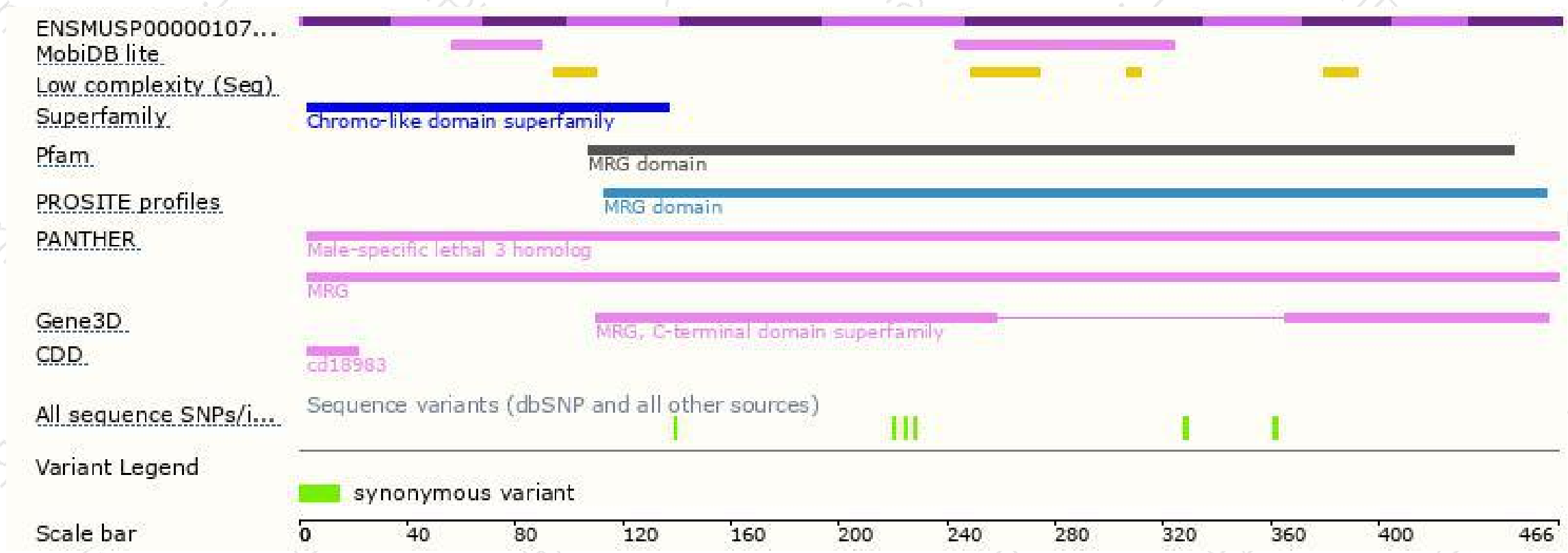
The strategy is based on the design of *Msl3-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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