

Jmy Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Imy

Project type

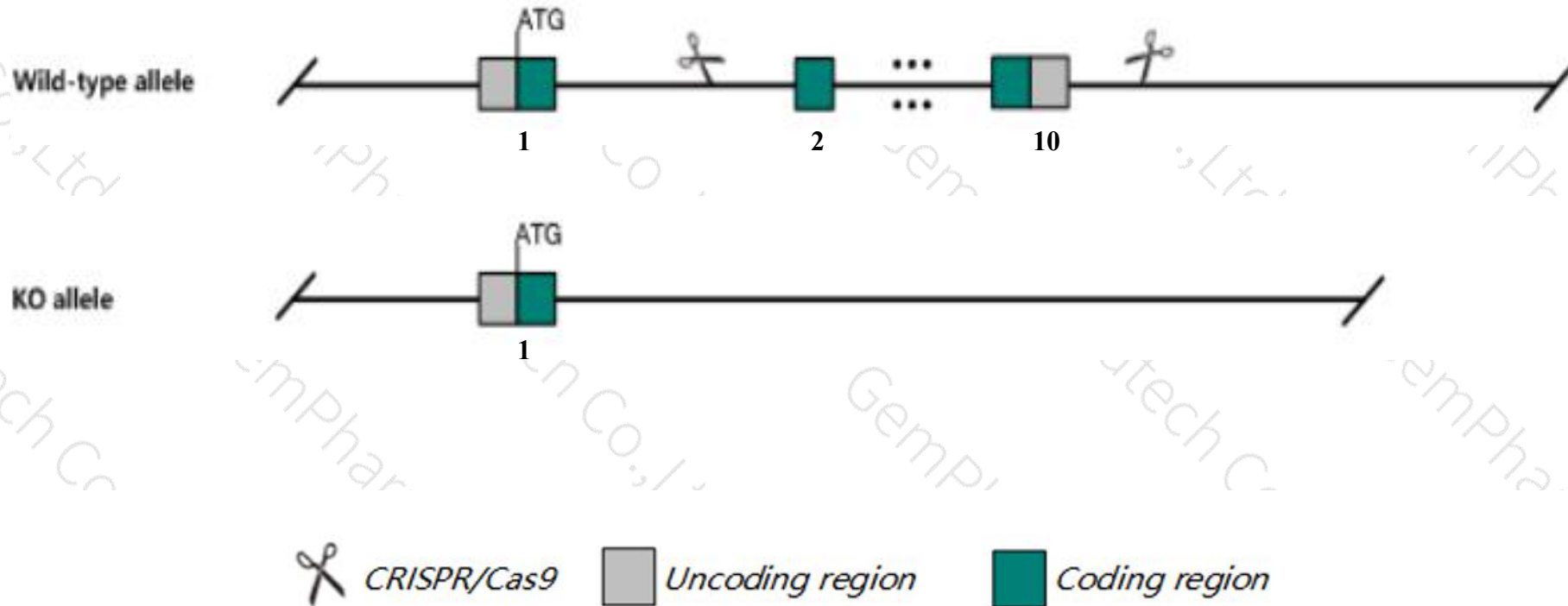
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Jmy* gene has 2 transcripts. According to the structure of *Jmy* gene, exon2-exon10 of *Jmy*-201 (ENSMUST00000065537.8) transcript is recommended as the knockout region. The region contains 1947bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Jmy* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Jmy* gene is located on the Chr13. 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)

Jmy junction-mediating and regulatory protein [Mus musculus (house mouse)]

Gene ID: 57748, updated on 13-Mar-2020

Summary



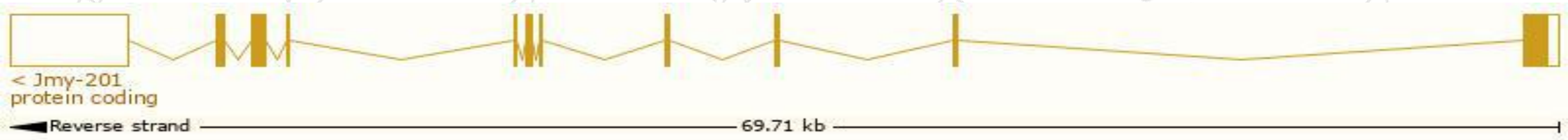
Official Symbol	Jmy provided by MGI
Official Full Name	junction-mediating and regulatory protein provided by MGI
Primary source	MGI:MGI:1913096
See related	Ensembl:ENSMUSG000000021690
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in bladder adult (RPKM 9.3), ovary adult (RPKM 8.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

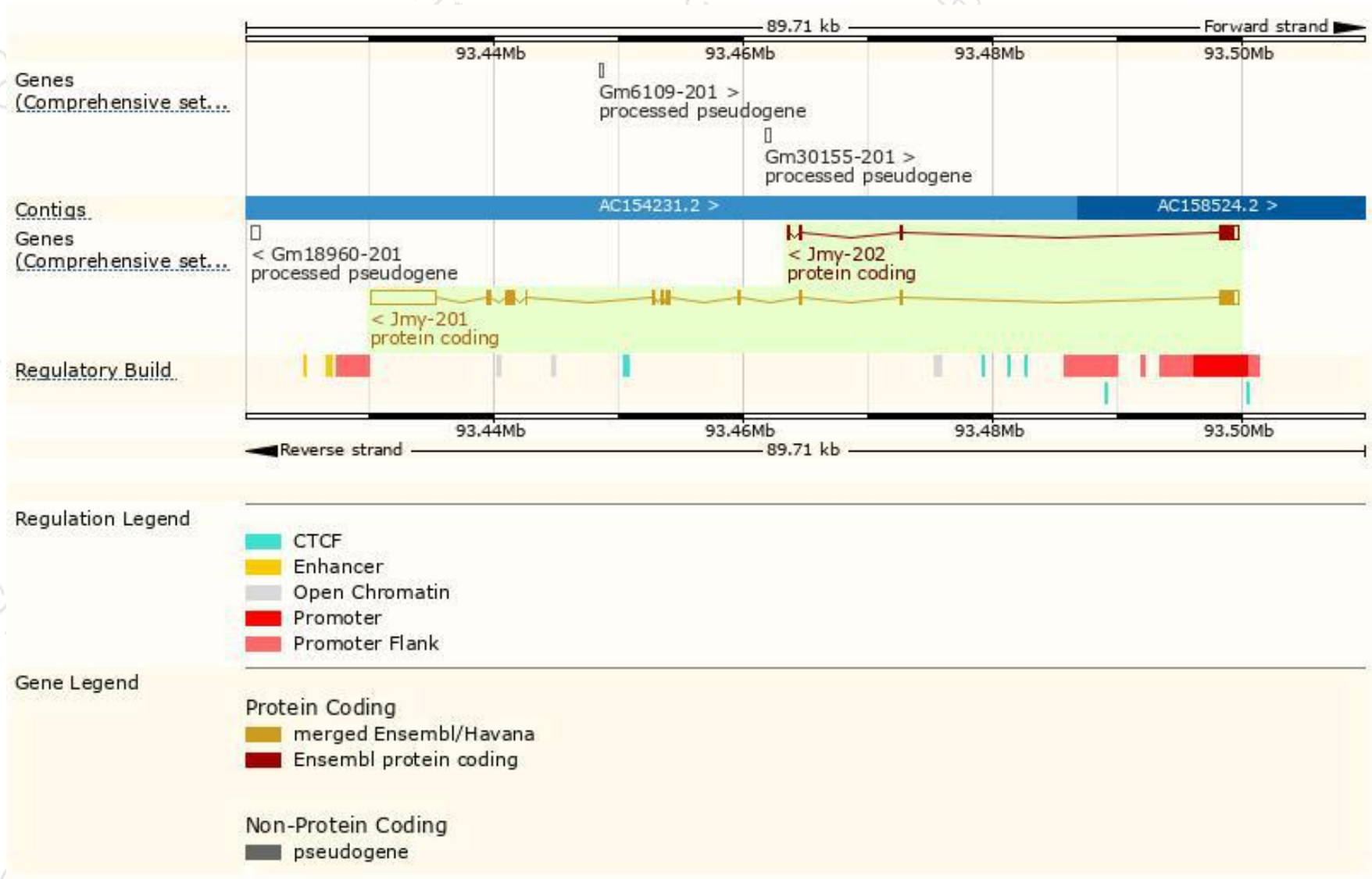
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jmy-201	ENSMUST00000065537.8	8776	983aa	Protein coding	CCDS26688	A0A0R4J0V4	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
Jmy-202	ENSMUST00000220513.1	1843	446aa	Protein coding	-	A0A1Y7VLC3	TSL:1 GENCODE basic

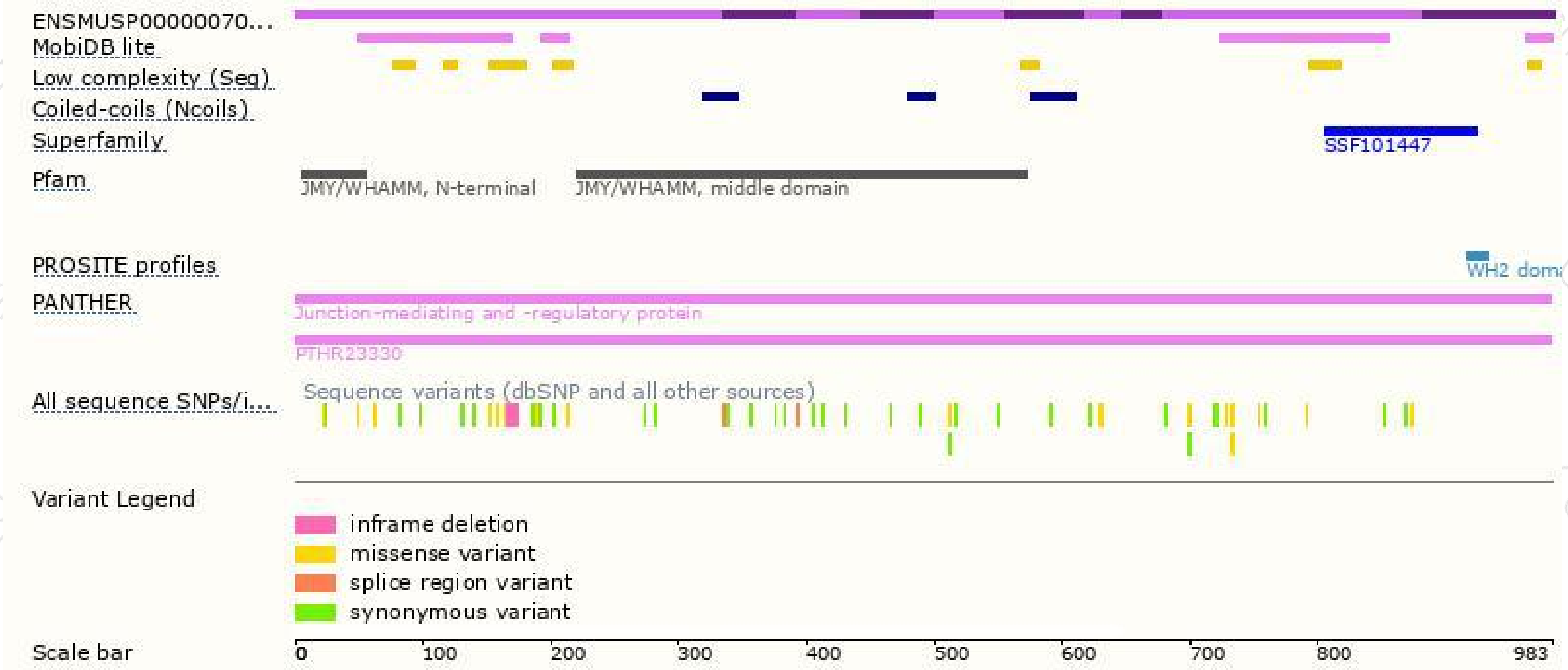
The strategy is based on the design of *Jmy-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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