

# ***Mov10l1*** Cas9-KO Strategy

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Design Date: 2020-4-20

# Project Overview

**Project Name**

*Mov10l1*

**Project type**

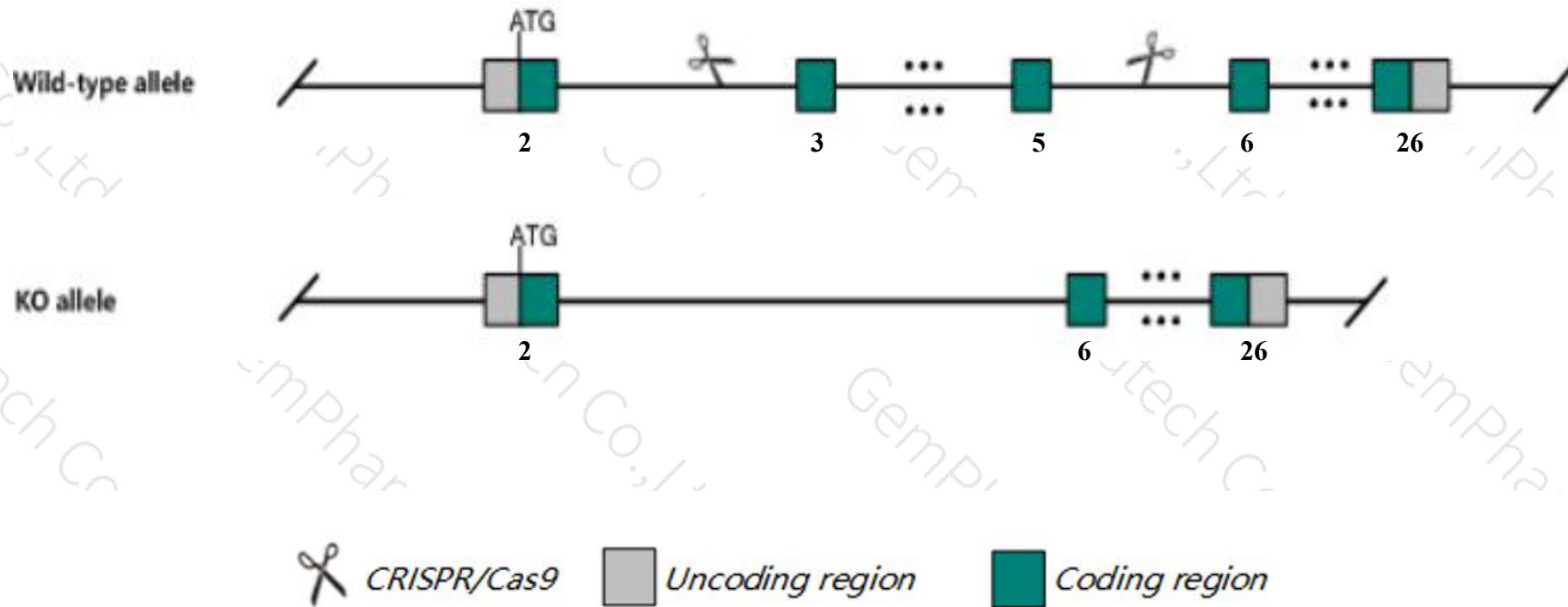
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mov10l1* gene. The schematic diagram is as follows:



- The *Mov10l1* gene has 5 transcripts. According to the structure of *Mov10l1* gene, exon3-exon5 of *Mov10l1-201* (ENSMUST00000015509.10) transcript is recommended as the knockout region. The region contains 461bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mov10l1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a targeted allele lacking the helicase domain exhibit male infertility due to meiotic arrest, apoptosis, and derepression of retrotransposons in male germ cells.
- The *Mov10l1* gene is located on the Chr15. 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)

## Mov10l1 Mov10 like RISC complex RNA helicase 1 [Mus musculus (house mouse)]

Gene ID: 83456, updated on 22-Mar-2020

### Summary



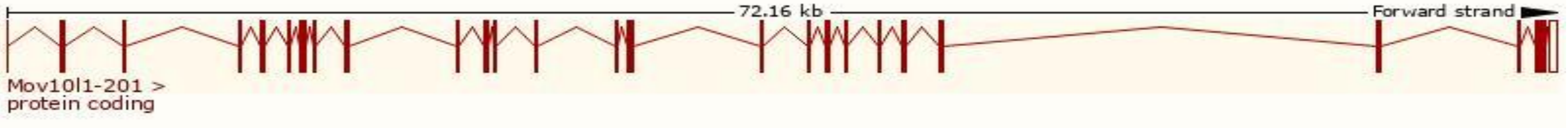
<b>Official Symbol</b>	Mov10l1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Mov10 like RISC complex RNA helicase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1891384</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000015365</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	CHAMP, Csm
<b>Expression</b>	Biased expression in testis adult (RPKM 12.7) and heart adult (RPKM 9.4) <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

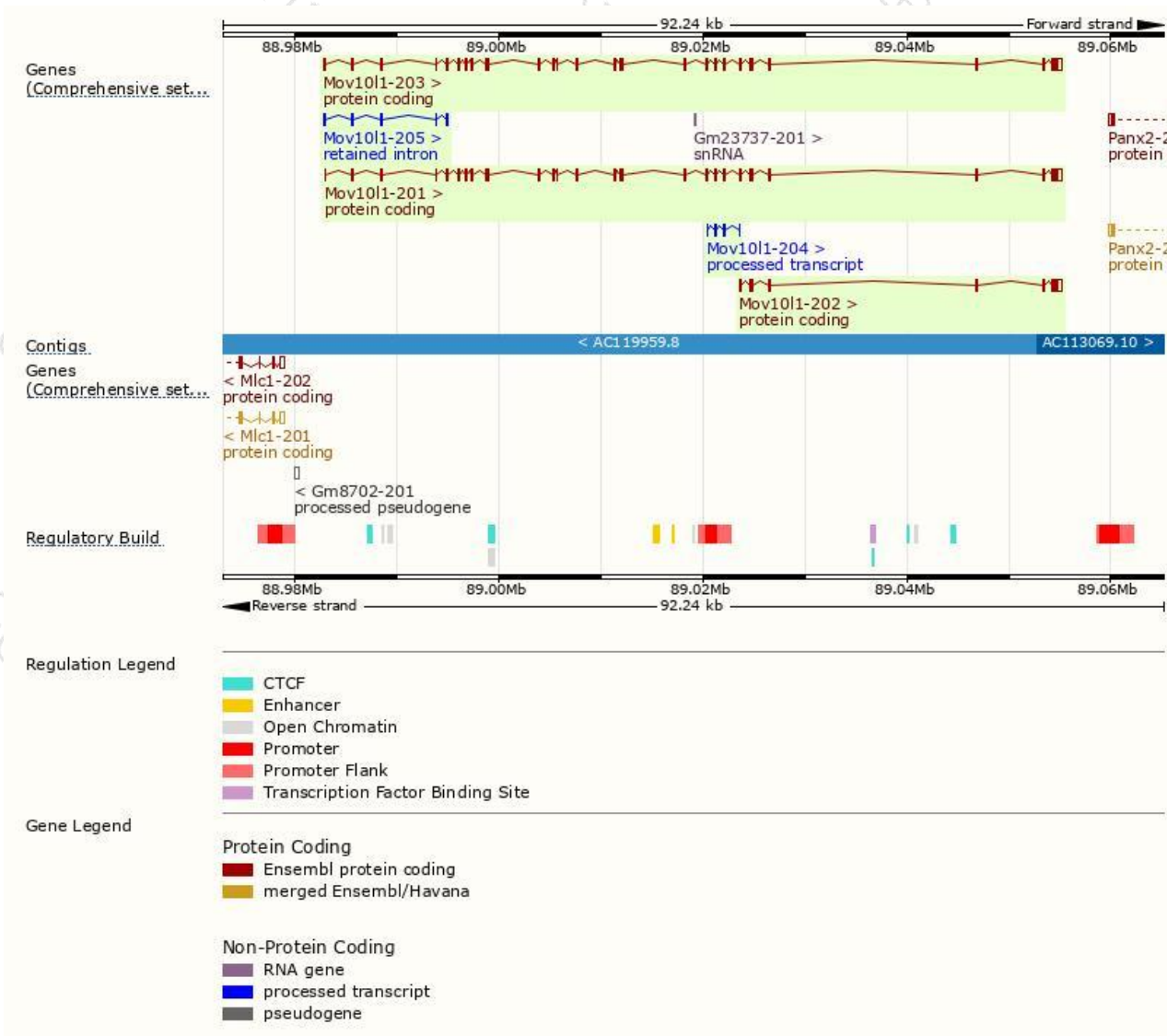
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mov10l1-201	<a href="#">ENSMUST00000015509.10</a>	4052	<a href="#">1187aa</a>	Protein coding	<a href="#">CCDS27737</a>	<a href="#">G3X8T0</a>	TSL:5 GENCODE basic APPRIS P2
Mov10l1-203	<a href="#">ENSMUST00000146993.7</a>	4133	<a href="#">1239aa</a>	Protein coding	-	<a href="#">D3YWG8</a>	TSL:5 GENCODE basic APPRIS ALT2
Mov10l1-202	<a href="#">ENSMUST00000143030.2</a>	1260	<a href="#">310aa</a>	Protein coding	-	<a href="#">G3UYS5</a>	CDS 5' incomplete TSL:5
Mov10l1-204	<a href="#">ENSMUST00000148198.2</a>	265	No protein	Processed transcript	-	-	TSL:5
Mov10l1-205	<a href="#">ENSMUST00000156949.1</a>	845	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Mov10l1-201* transcript,The transcription is shown below

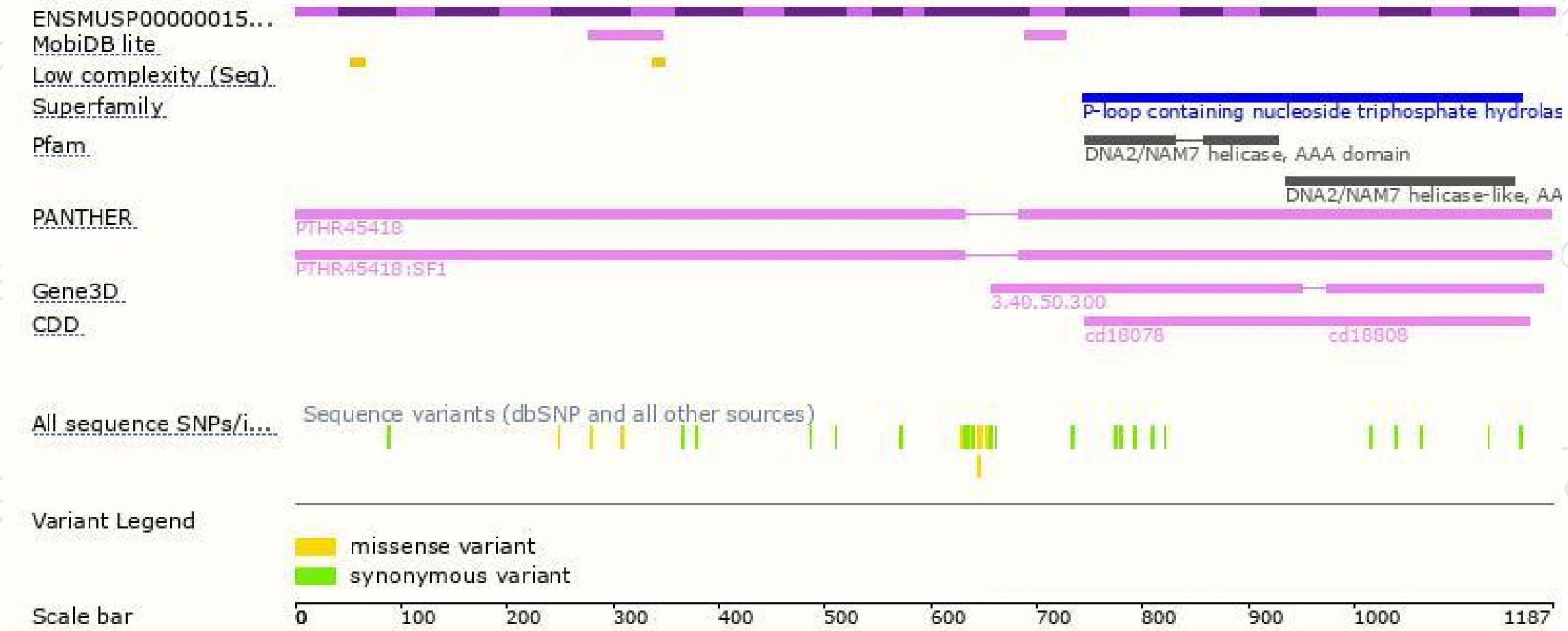


# Genomic location distribution

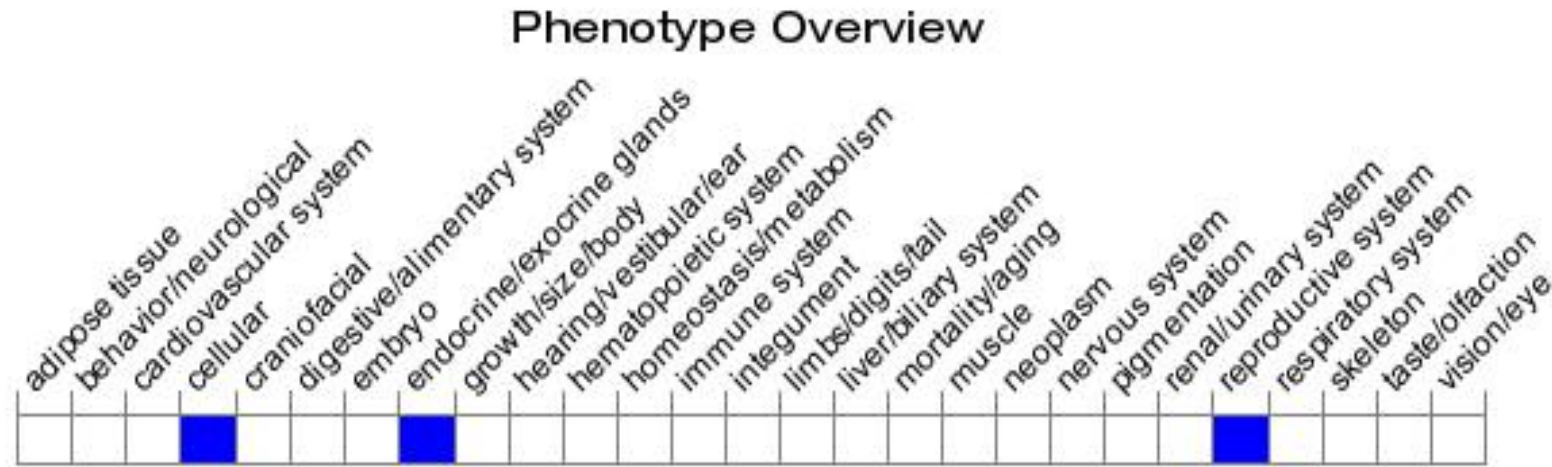




# Protein domain



# 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 targeted allele lacking the helicase domain exhibit male infertility due to meiotic arrest, apoptosis, and derepression of retrotransposons in male germ cells.

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

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