# *Mcm9* Cas9-KO Strategy

**Designer: Lingyan Wu**

**Reviewer: Miaomiao Cui**

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# Project Overview

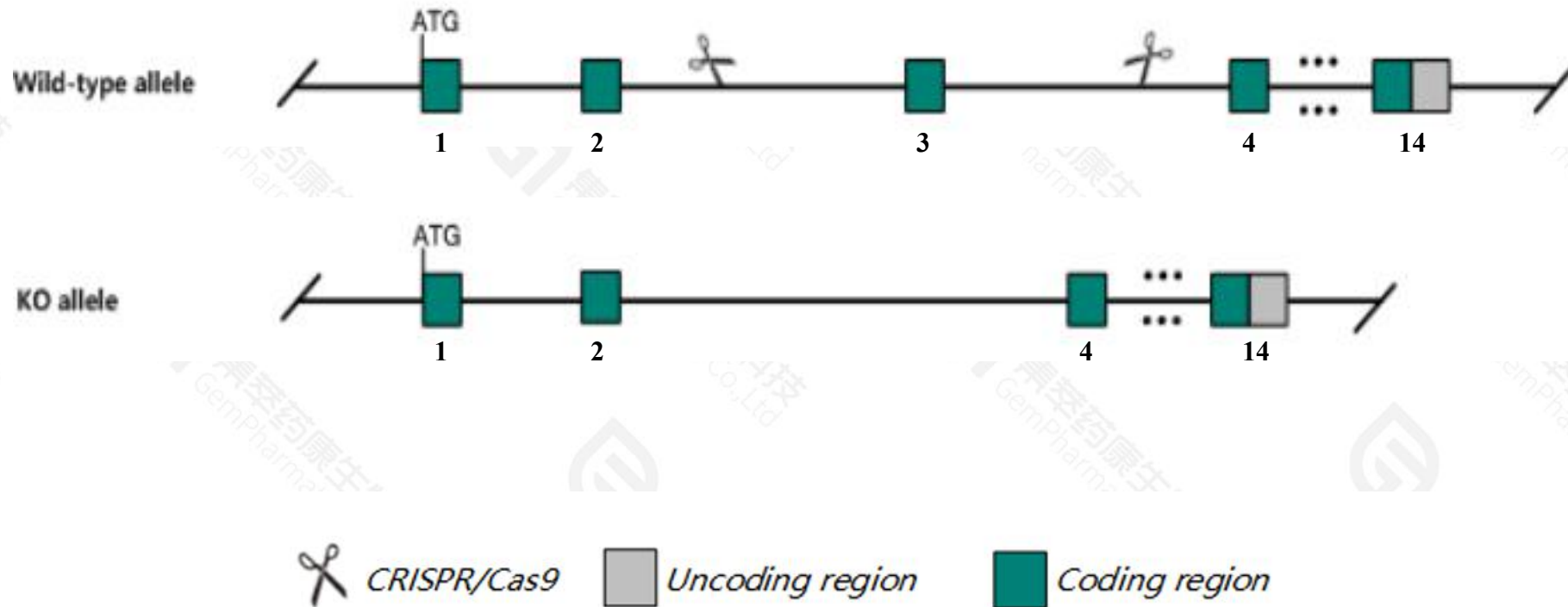| | |
|---|---|
| **Project Name** | *Mcm9* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcm9* gene. The schematic diagram is as follows:

➤ The *Mcm9* gene has 8 transcripts. According to the structure of *Mcm9* gene, exon3 of *Mcm9-201*(ENSMUST00000075540.8) transcript is recommended as the knockout region.The region contains 319bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Mcm9* 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.

➢ According to the existing MGI data,mice homozygous for gene trap alleles display germ cell loss with reduced fertility or infertility and increased tumor incidence, particulary of hepatocellular carcinomas.

➢ Transcript *Mcm9*-203&205&206 may not be affected.

➢ The *Mcm9* gene is located on the Chr10. 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）

**Mcm9 minichromosome maintenance 9 homologous recombination repair factor [Mus musculus (house mouse)]**

Gene ID: 71567, updated on 17-Feb-2021

## ▲Summary

| | |
|---|---|
| **Official Symbol** | Mcm9 provided by MGI |
| **Official Full Name** | minichromosome maintenance 9 homologous recombination repair factor provided byMGI |
| **Primary source** | MGI:MGI:1918817 |
| **See related** | Ensembl:ENSMUSG00000058298 |
| **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** | 9030408O17Rik, Gm235, Mcmdc1 |
| **Expression** | Ubiquitous expression in CNS E11.5 (RPKM 3.4), liver E14 (RPKM 2.7) and 28 other tissuesSee 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 |
|------|---------------|-----|---------|---------|------|---------|-------|
| Mcm9-201 | ENSMUST00000075540.8 | 4868 | 1290aa | Protein coding | CCDS23846 | | TSL:2 , GENCODE basic , APPRIS P2 , |
| Mcm9-208 | ENSMUST0000237608.2 | 4882 | 1134aa | Protein coding | - | | GENCODE basic , APPRIS ALT2 , |
| Mcm9-204 | ENSMUST00000219838.3 | 4132 | 386aa | Protein coding | - | | TSL:5 , GENCODE basic , |
| Mcm9-206 | ENSMUST00000220007.2 | 3513 | 552aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Mcm9-203 | ENSMUST00000219547.2 | 3168 | 552aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Mcm9-202 | ENSMUST00000218549.3 | 2421 | 414aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Mcm9-205 | ENSMUST00000219841.3 | 307 | 98aa | Protein coding | - | | CDS 5' incomplete , TSL:5 , |
| Mcm9-207 | ENSMUST00000220260.2 | 464 | No protein | Processed transcript | - | | TSL:5 , |

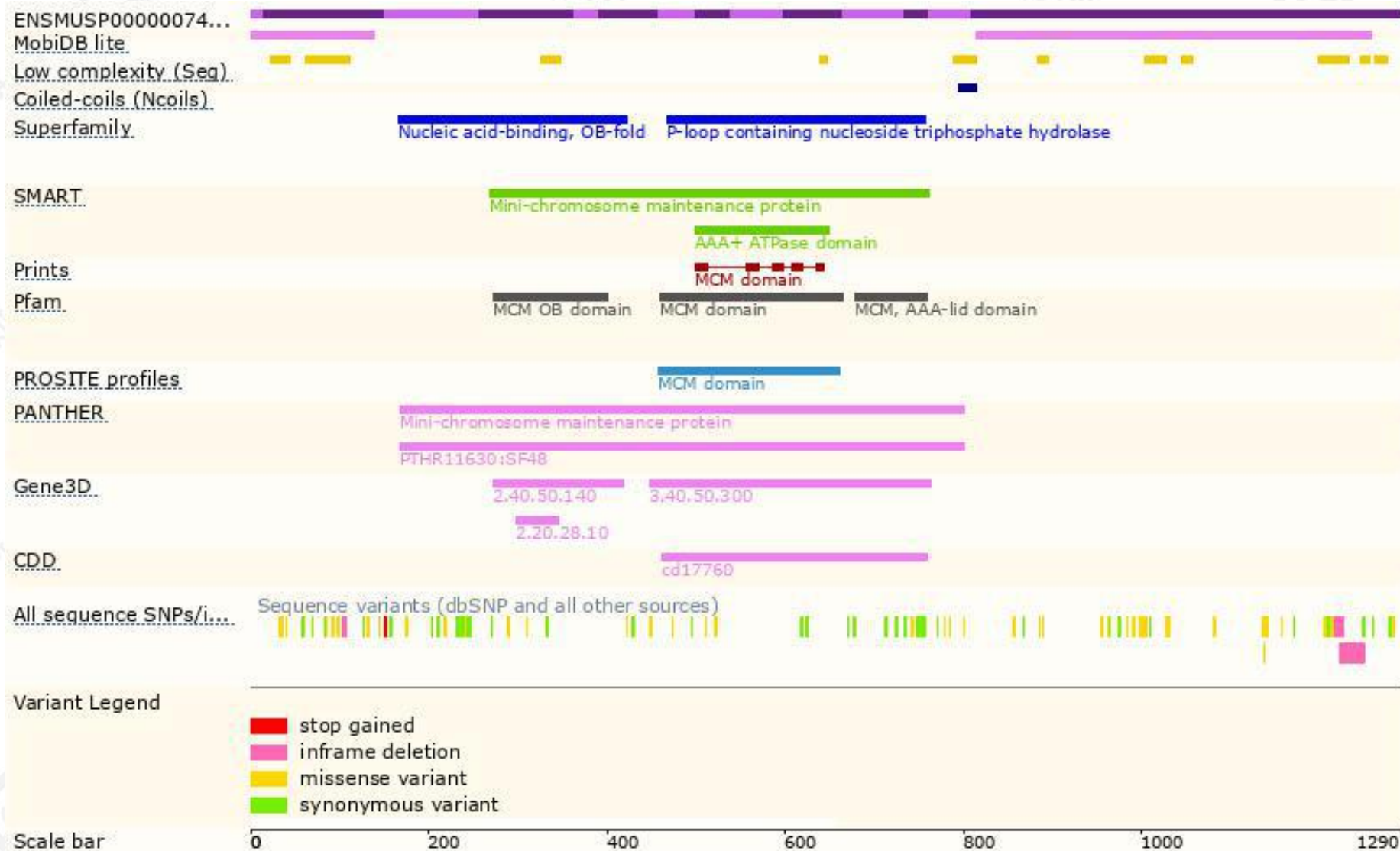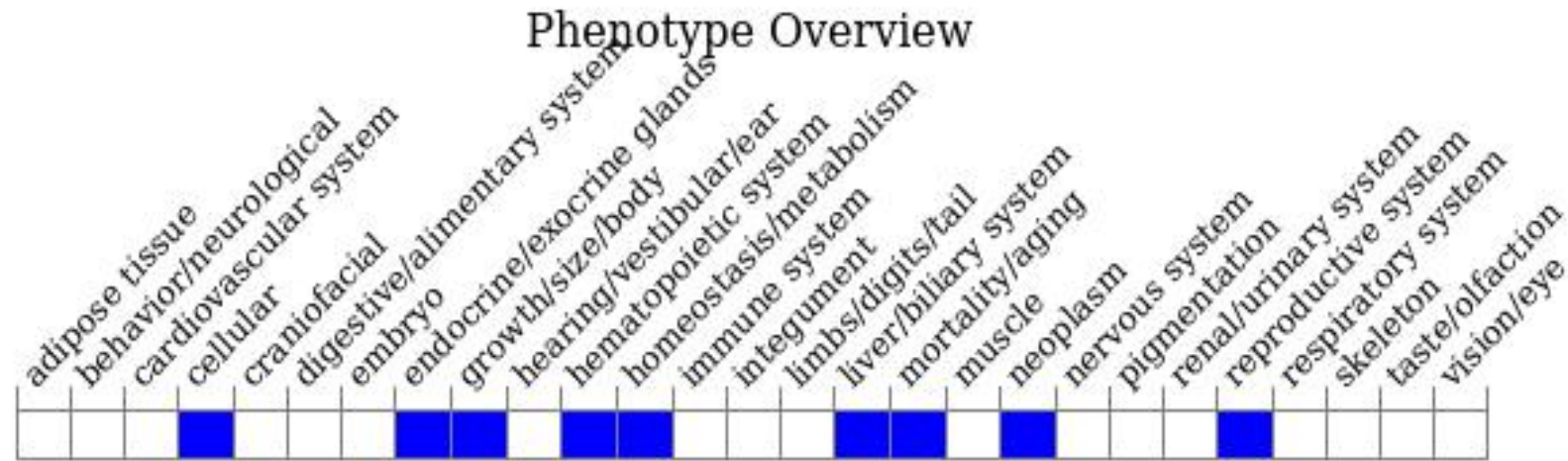The strategy is based on the design of *Mcm9-201* transcript,the transcription is shown below:



< Mcm9-201
protein coding

◄— Reverse strand

————— 94.11 kb —————
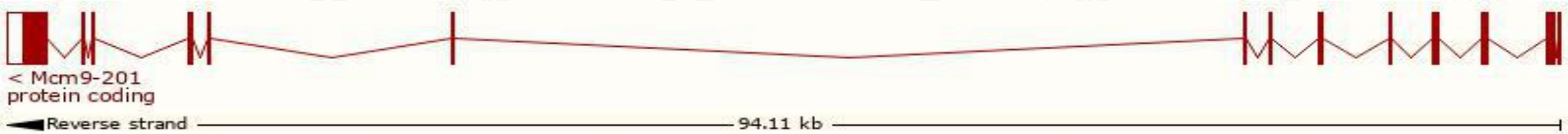
# Genomic location distribution
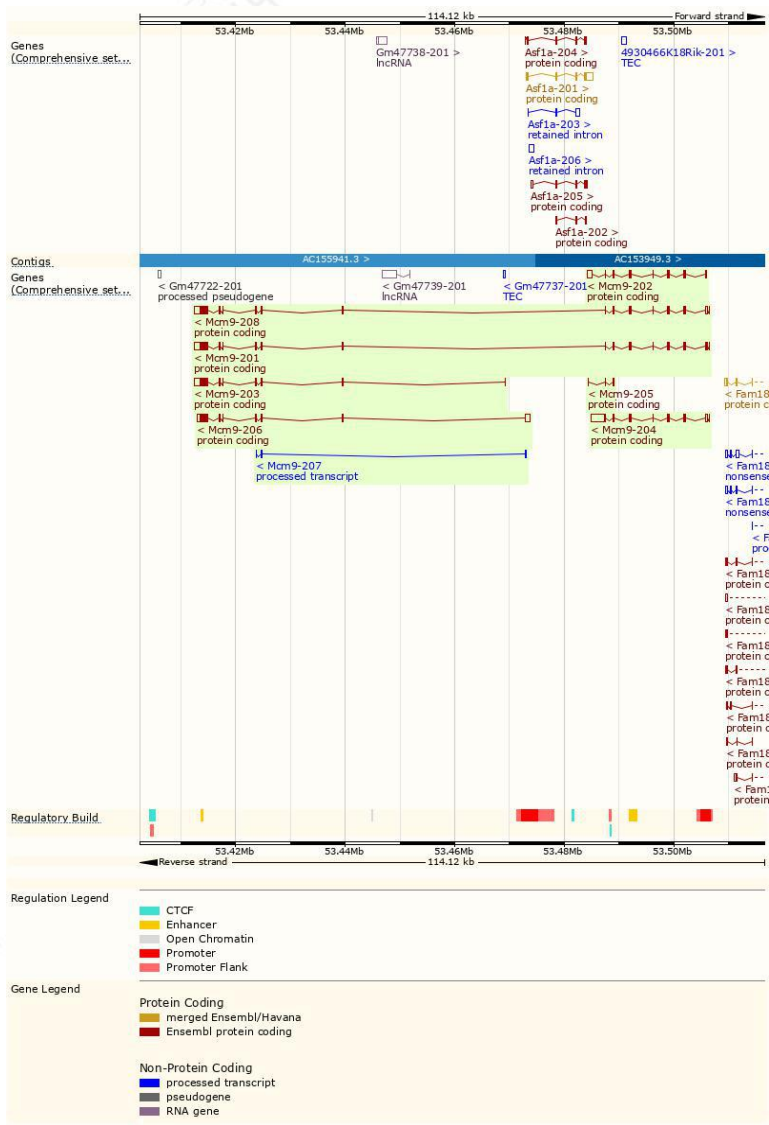
# Protein domain

# Mouse phenotype description(MGI )



## Phenotype Overview

*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 gene trap alleles display germ cell loss with reduced fertility or infertility and increased tumor incidence, particulary of hepatocellular carcinomas.

集萃药康
GemPharmatech

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd