

# ***Mecom* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Mecom*

**Project type**

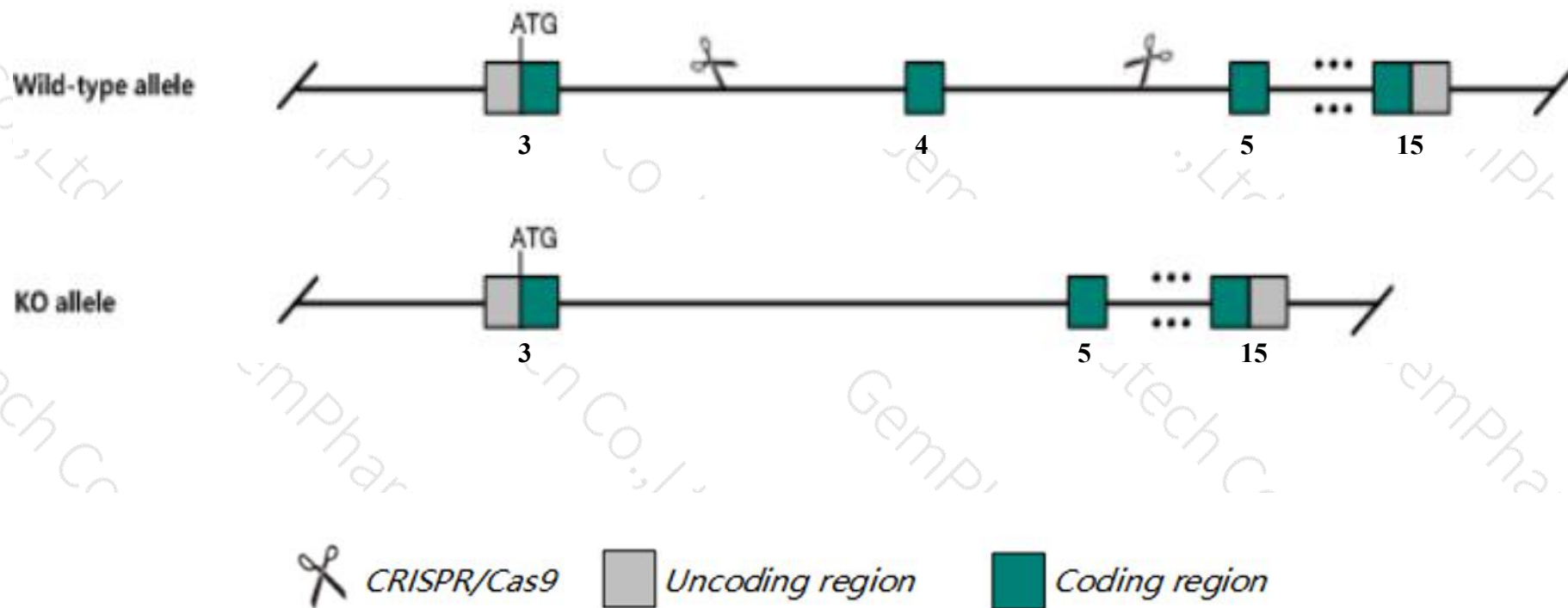
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Mecom* gene has 17 transcripts. According to the structure of *Mecom* gene, exon4 of *Mecom*-206 (ENSMUST00000172694.7) transcript is recommended as the knockout region. The region contains 217bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mecom* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, embryos homozygous for a targeted null mutation die at 10.5 dpc displaying widespread hypocellularity, hemorrhage, and disruption in the development of the heart, somites, and neural crest-derived cells.
- The *Mecom* gene is located on the Chr3. 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)

## Mecom MDS1 and EVI1 complex locus [Mus musculus (house mouse)]

Gene ID: 14013, updated on 20-Mar-2020

### Summary

**Official Symbol** Mecom provided by [MGI](#)

**Official Full Name** MDS1 and EVI1 complex locus provided by [MGI](#)

**Primary source** [MGI:MGI:95457](#)

**See related** [Ensembl:ENSMUSG00000027684](#)

**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** D630039M04Rik, Evi-1, Evi1, Jbo, Mds, Mds1, Mds1-Evi1, Prdm3, Znfpr1b1

**Expression** Broad expression in bladder adult (RPKM 7.5), limb E14.5 (RPKM 5.2) and 15 other tissues [See more](#)

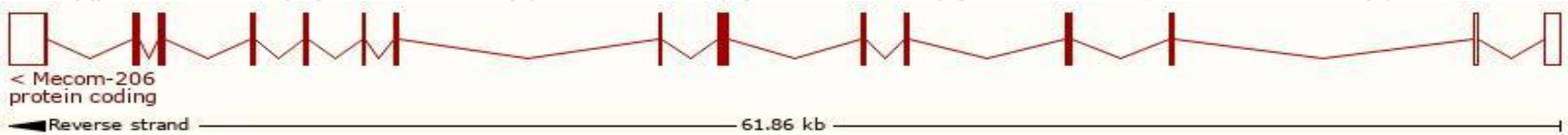
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

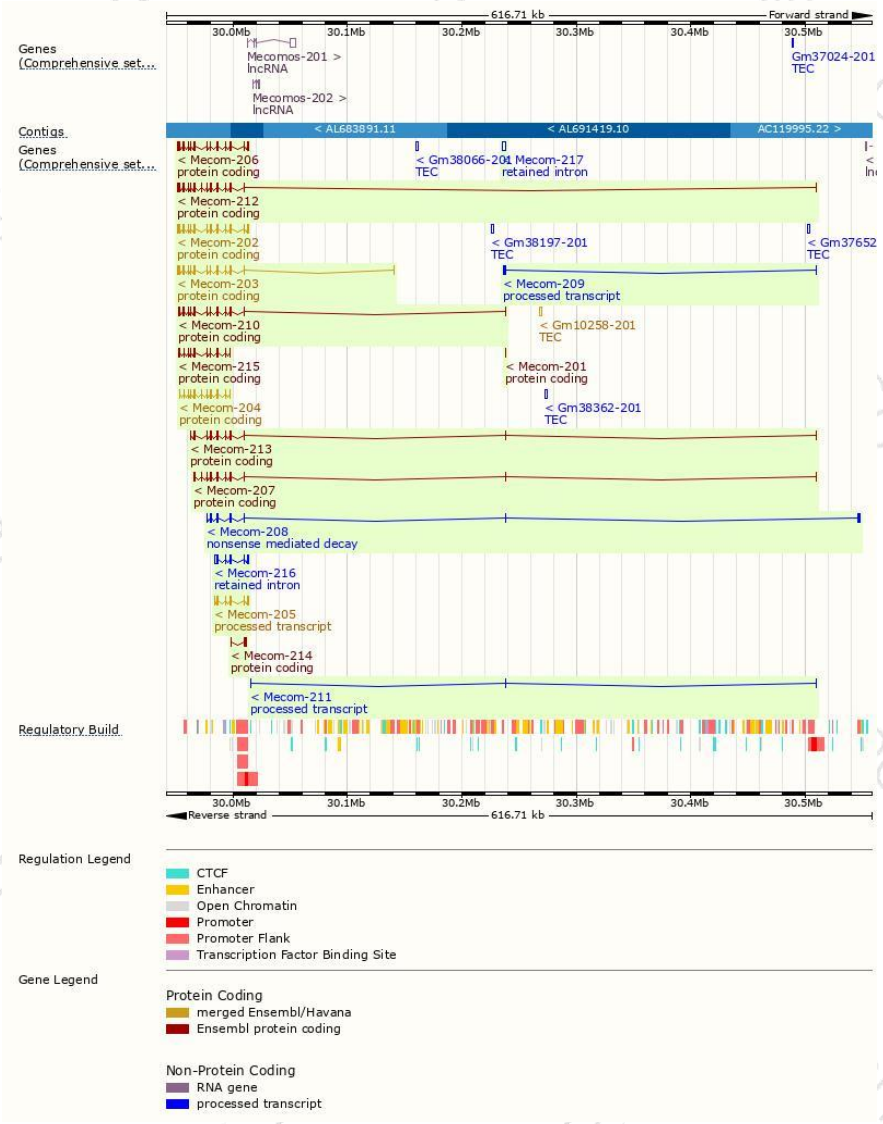
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mecom-206	<a href="#">ENSMUST00000172694.7</a>	4381	<a href="#">718aa</a>	Protein coding	<a href="#">CCDS17281</a>	<a href="#">G3UZ13</a>	TSL:1 GENCODE basic
Mecom-202	<a href="#">ENSMUST00000108270.9</a>	5692	<a href="#">1042aa</a>	Protein coding	-	<a href="#">H9T841 P14404</a>	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 ALT2
Mecom-212	<a href="#">ENSMUST00000173495.7</a>	5066	<a href="#">1051aa</a>	Protein coding	-	<a href="#">G3UZT5</a>	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 P5
Mecom-203	<a href="#">ENSMUST00000108271.9</a>	3851	<a href="#">795aa</a>	Protein coding	-	<a href="#">Q8CCA6</a>	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 ALT2
Mecom-207	<a href="#">ENSMUST00000172697.7</a>	3204	<a href="#">949aa</a>	Protein coding	-	<a href="#">G3UYK2</a>	CDS 3' incomplete TSL:5
Mecom-213	<a href="#">ENSMUST00000173899.7</a>	3031	<a href="#">994aa</a>	Protein coding	-	-	CDS 3' incomplete TSL:5
Mecom-204	<a href="#">ENSMUST00000166001.7</a>	2914	<a href="#">949aa</a>	Protein coding	-	<a href="#">Q35700</a>	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 ALT2
Mecom-210	<a href="#">ENSMUST00000173059.7</a>	2680	<a href="#">843aa</a>	Protein coding	-	<a href="#">G3UWJ0</a>	CDS 5' incomplete TSL:5
Mecom-215	<a href="#">ENSMUST00000174413.7</a>	1942	<a href="#">606aa</a>	Protein coding	-	<a href="#">G3UYY9</a>	CDS 5' incomplete TSL:1
Mecom-214	<a href="#">ENSMUST00000174406.1</a>	524	<a href="#">52aa</a>	Protein coding	-	<a href="#">G3UY46</a>	CDS 3' incomplete TSL:5
Mecom-201	<a href="#">ENSMUST00000061088.6</a>	348	<a href="#">116aa</a>	Protein coding	-	<a href="#">F6SZX1</a>	TSL:NA GENCODE basic
Mecom-208	<a href="#">ENSMUST00000172754.7</a>	3182	<a href="#">45aa</a>	Nonsense mediated decay	-	<a href="#">G3UYN3</a>	TSL:5
Mecom-205	<a href="#">ENSMUST00000170212.7</a>	1586	No protein	Processed transcript	-	-	TSL:1
Mecom-211	<a href="#">ENSMUST00000173411.7</a>	1302	No protein	Processed transcript	-	-	TSL:5
Mecom-209	<a href="#">ENSMUST00000173022.1</a>	1075	No protein	Processed transcript	-	-	TSL:1
Mecom-216	<a href="#">ENSMUST00000174428.1</a>	2803	No protein	Retained intron	-	-	TSL:1
Mecom-217	<a href="#">ENSMUST00000195690.1</a>	2518	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Mecom-206* transcript,the transcription is shown below:

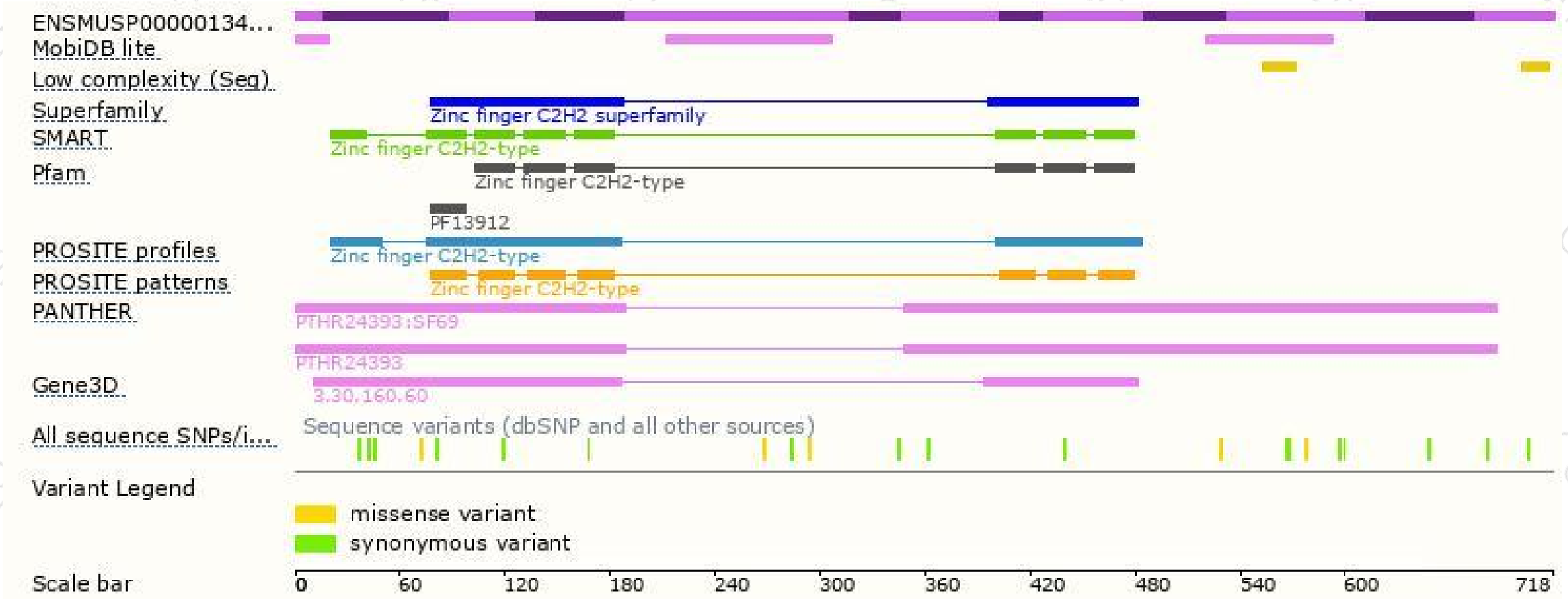


# Genomic location distribution

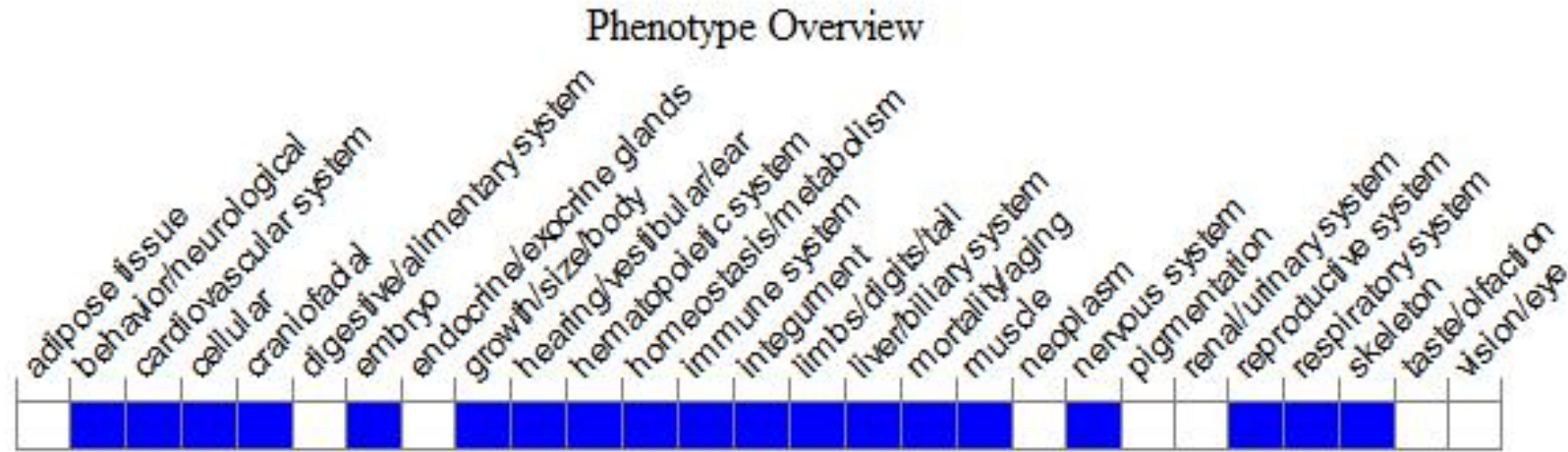




# Protein domain



# 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, embryos homozygous for a targeted null mutation die at 10.5 dpc displaying widespread hypocellularity, hemorrhage, and disruption in the development of the heart, somites, and neural crest-derived cell

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

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