

Mecom Cas9-CKO Strategy

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Project Overview

Project Name

Mecom

Project type

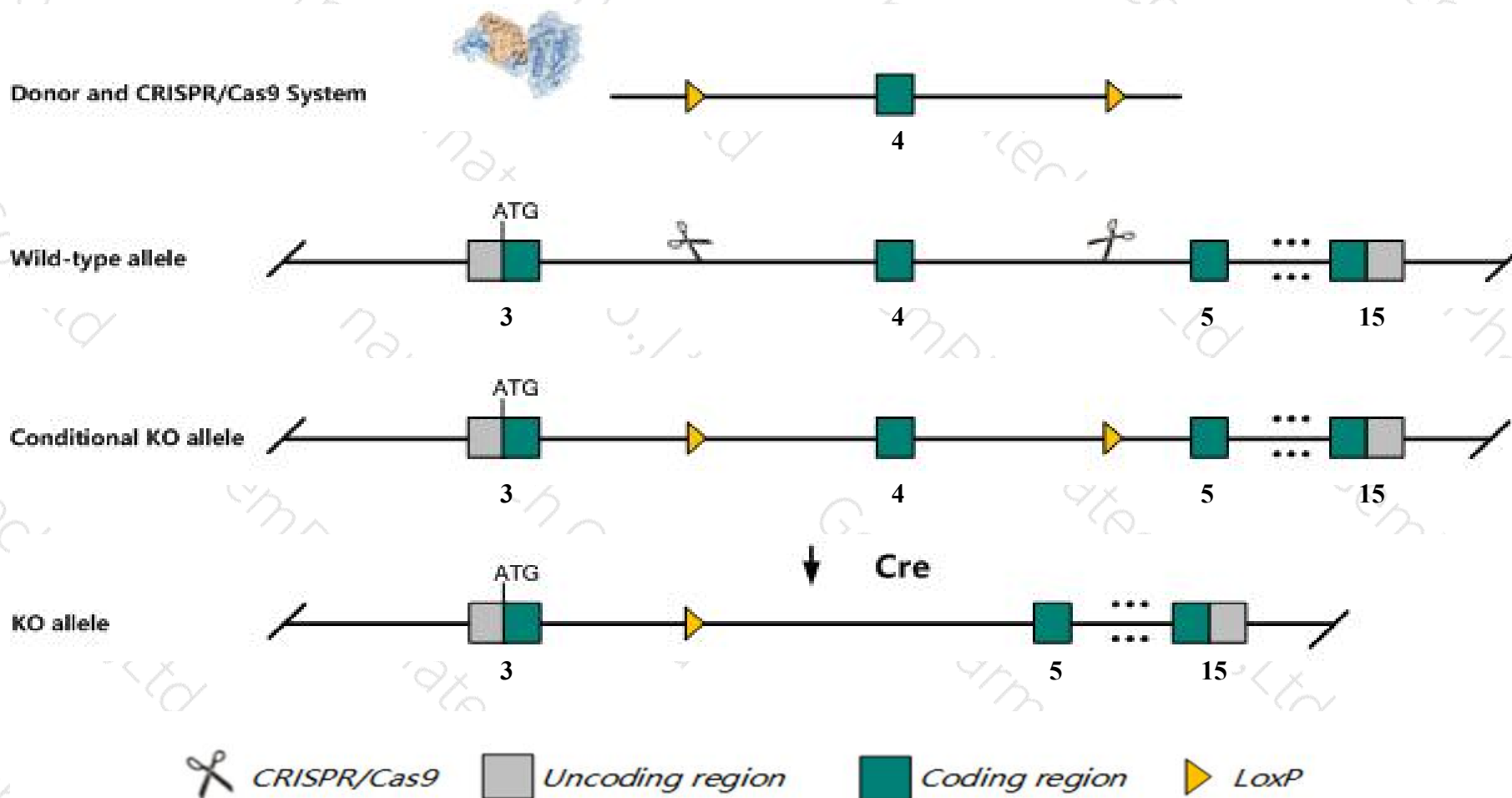
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional 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 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 will be 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.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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)

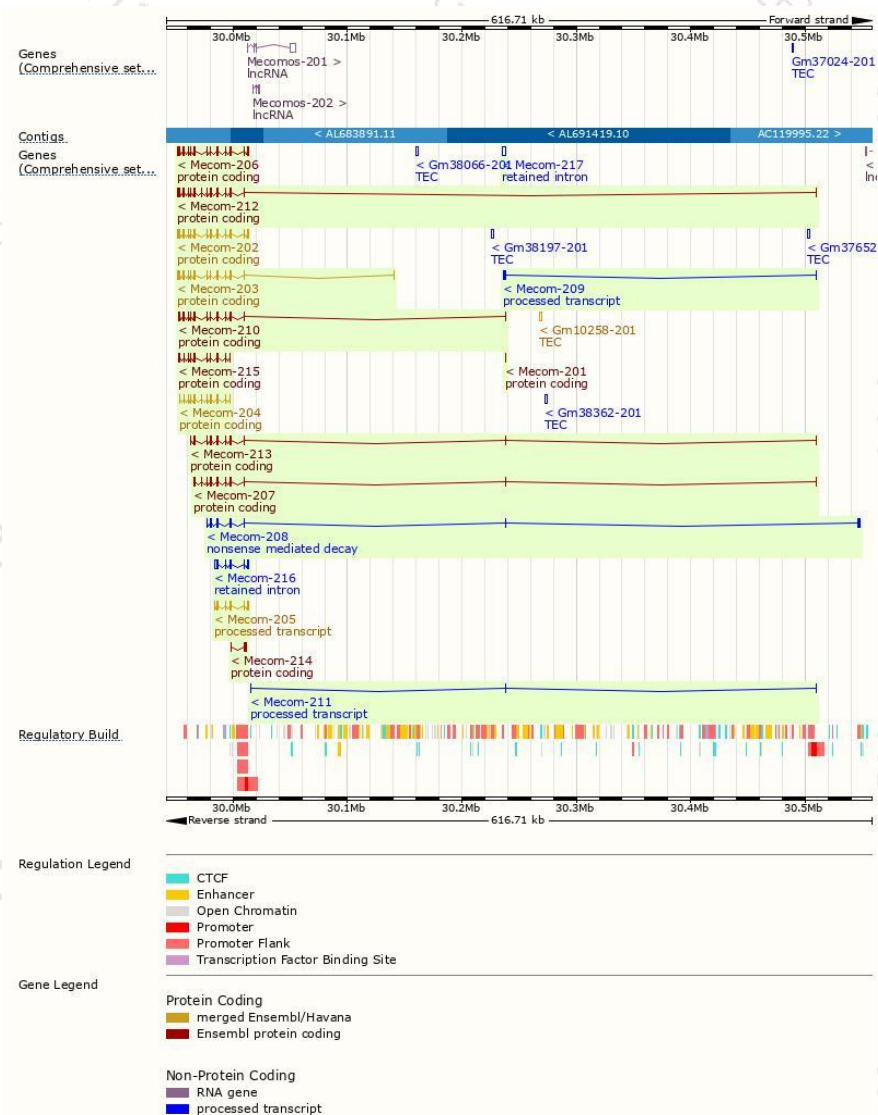
The gene has 17 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mecom-206	ENSMUST00000172694.7	4381	718aa	Protein coding	CCDS17281	G3UZ13	TSL:1 GENCODE basic
Mecom-202	ENSMUST00000108270.9	5692	1042aa	Protein coding	-	H9T841 P14404	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	ENSMUST00000173495.7	5066	1051aa	Protein coding	-	G3UZT5	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	ENSMUST00000108271.9	3851	795aa	Protein coding	-	Q8CCA6	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	ENSMUST00000172697.7	3204	949aa	Protein coding	-	G3UYK2	CDS 3' incomplete TSL:5
Mecom-213	ENSMUST00000173899.7	3031	994aa	Protein coding	-	-	CDS 3' incomplete TSL:5
Mecom-204	ENSMUST00000166001.7	2914	949aa	Protein coding	-	Q35700	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	ENSMUST00000173059.7	2680	843aa	Protein coding	-	G3UWJ0	CDS 5' incomplete TSL:5
Mecom-215	ENSMUST00000174413.7	1942	606aa	Protein coding	-	G3UYY9	CDS 5' incomplete TSL:1
Mecom-214	ENSMUST00000174406.1	524	52aa	Protein coding	-	G3UY46	CDS 3' incomplete TSL:5
Mecom-201	ENSMUST000000061088.6	348	116aa	Protein coding	-	F6SZX1	TSL:NA GENCODE basic
Mecom-208	ENSMUST00000172754.7	3182	45aa	Nonsense mediated decay	-	G3UYN3	TSL:5
Mecom-205	ENSMUST00000170212.7	1586	No protein	Processed transcript	-	-	TSL:1
Mecom-211	ENSMUST00000173411.7	1302	No protein	Processed transcript	-	-	TSL:5
Mecom-209	ENSMUST00000173022.1	1075	No protein	Processed transcript	-	-	TSL:1
Mecom-216	ENSMUST00000174428.1	2803	No protein	Retained intron	-	-	TSL:1
Mecom-217	ENSMUST00000195690.1	2518	No protein	Retained intron	-	-	TSL:NA

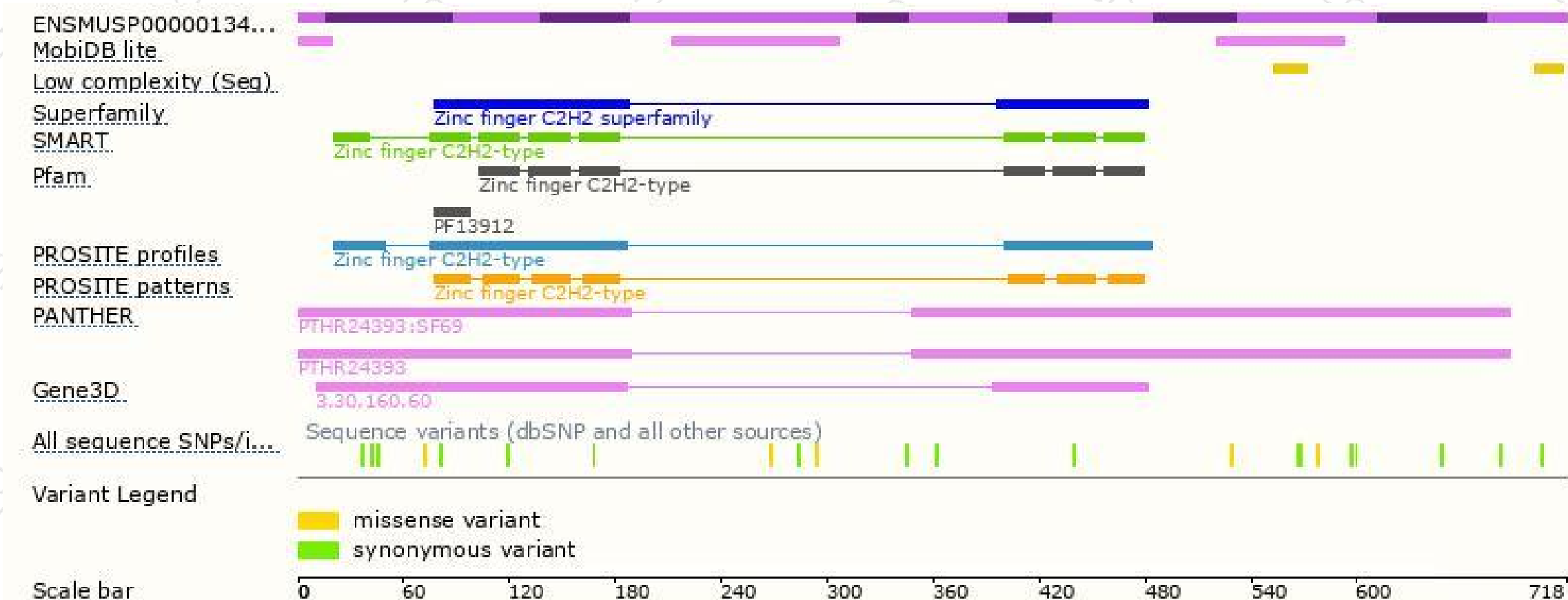
The strategy is based on the design of *Mecom-206* transcript, the transcription is shown below:



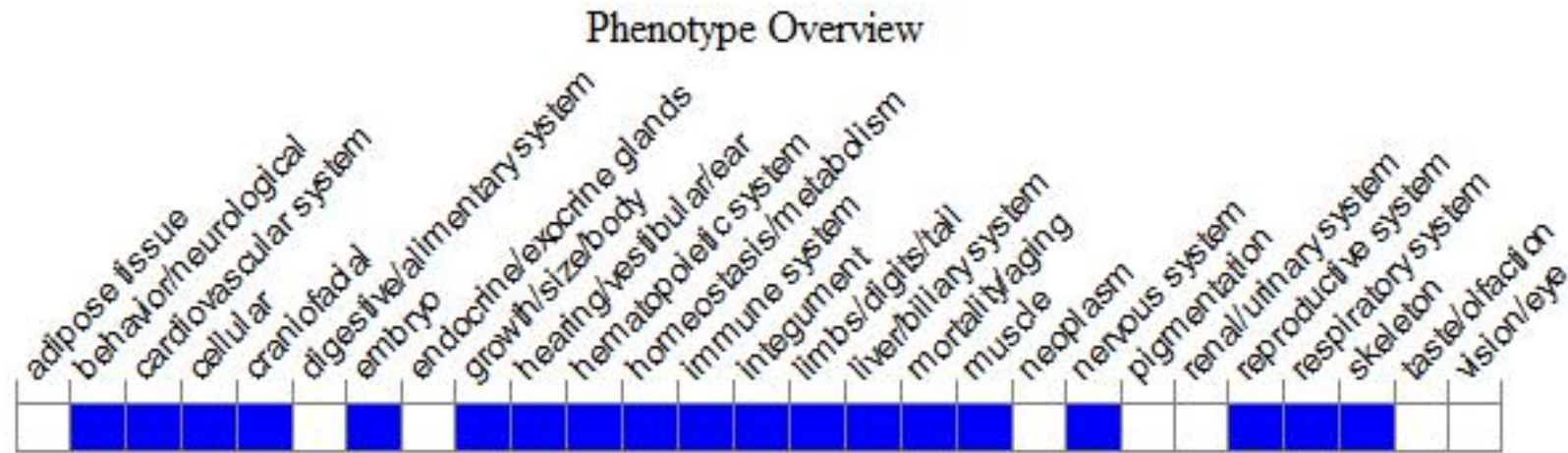
Genomic location distribution



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 cells.

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

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