

Mre11a Cas9-CKO Strategy

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Project Overview

Project Name

Mrell1a

Project type

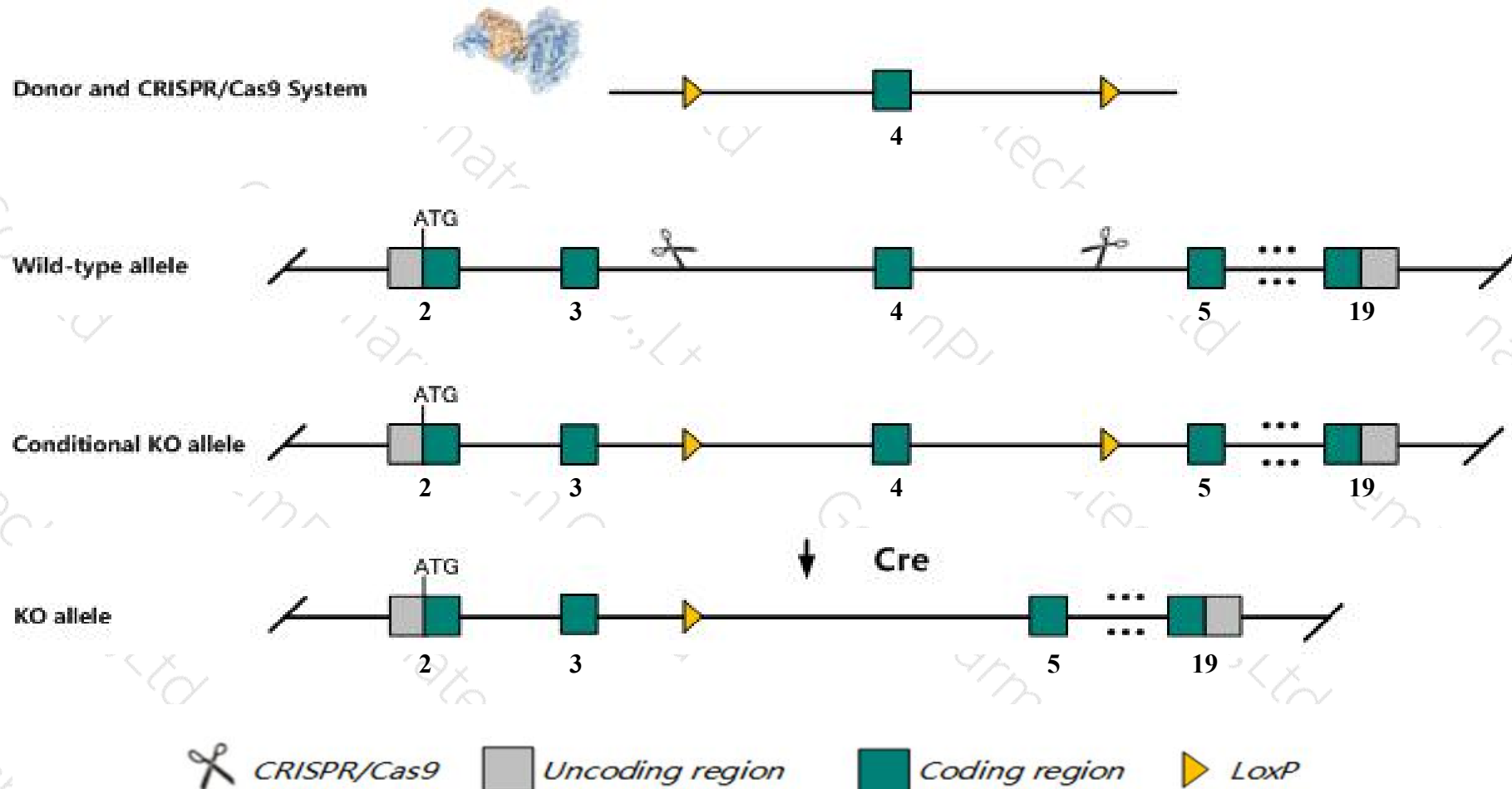
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mre11a* gene. The schematic diagram is as follows:



- The *Mrell1a* gene has 6 transcripts. According to the structure of *Mrell1a* gene, exon4 of *Mrell1a-201* (ENSMUST00000034405.10) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mrell1a* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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, Though mutation of this locus affected chromosome stability, mutant mice were no more susceptible to tumorigenesis than wild-type mice. Mutant female mice showed reduced fertility.
- The *Mrell1a* gene is located on the Chr9. 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)

Mre11a MRE11A homolog A, double strand break repair nuclease [Mus musculus (house mouse)]

Gene ID: 17535, updated on 7-Apr-2019

Summary



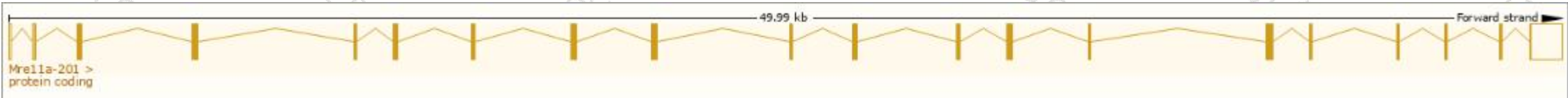
Official Symbol	Mre11a provided by MGI
Official Full Name	MRE11A homolog A, double strand break repair nuclease provided by MGI
Primary source	MGI:MGI:1100512
See related	Ensembl:ENSMUSG000000031928
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mre11, Mre11b
Expression	Ubiquitous expression in CNS E11.5 (RPKM 5.2), liver E14 (RPKM 3.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

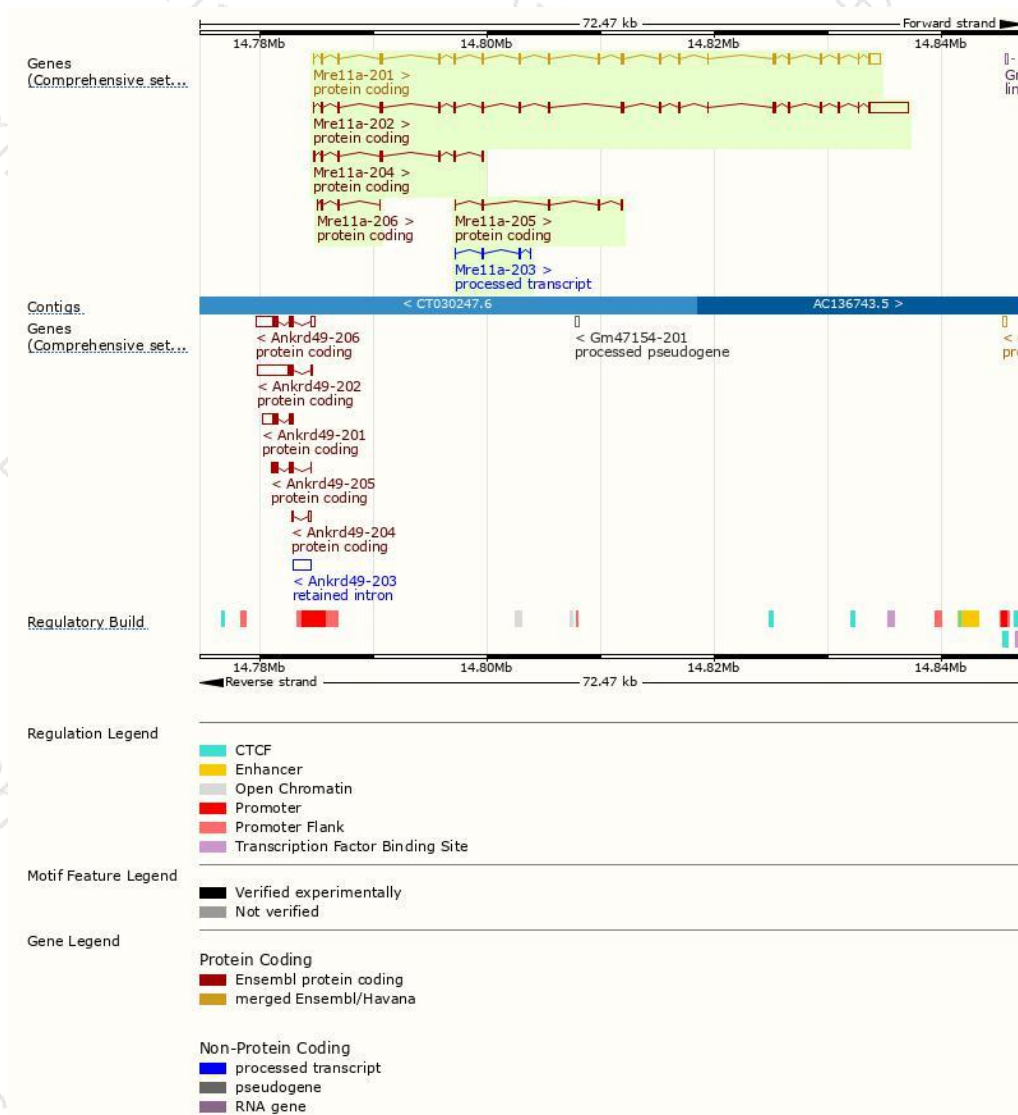
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mre11a-202	ENSMUST00000115632.9	5660	679aa	Protein coding	CCDS80958	Q61216	TSL:1 GENCODE basic
Mre11a-201	ENSMUST00000034405.10	3286	706aa	Protein coding	CCDS22827	Q3URU4 Q61216	TSL:1 GENCODE basic APPRIS P1
Mre11a-204	ENSMUST00000147305.1	793	203aa	Protein coding	-	B2KF76	CDS 3' incomplete TSL:3
Mre11a-205	ENSMUST00000147676.7	510	170aa	Protein coding	-	F6RX99	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Mre11a-206	ENSMUST00000215820.1	274	57aa	Protein coding	-	A0A1L1SQT7	CDS 3' incomplete TSL:5
Mre11a-203	ENSMUST00000136568.1	409	No protein	Processed transcript	-	-	TSL:5

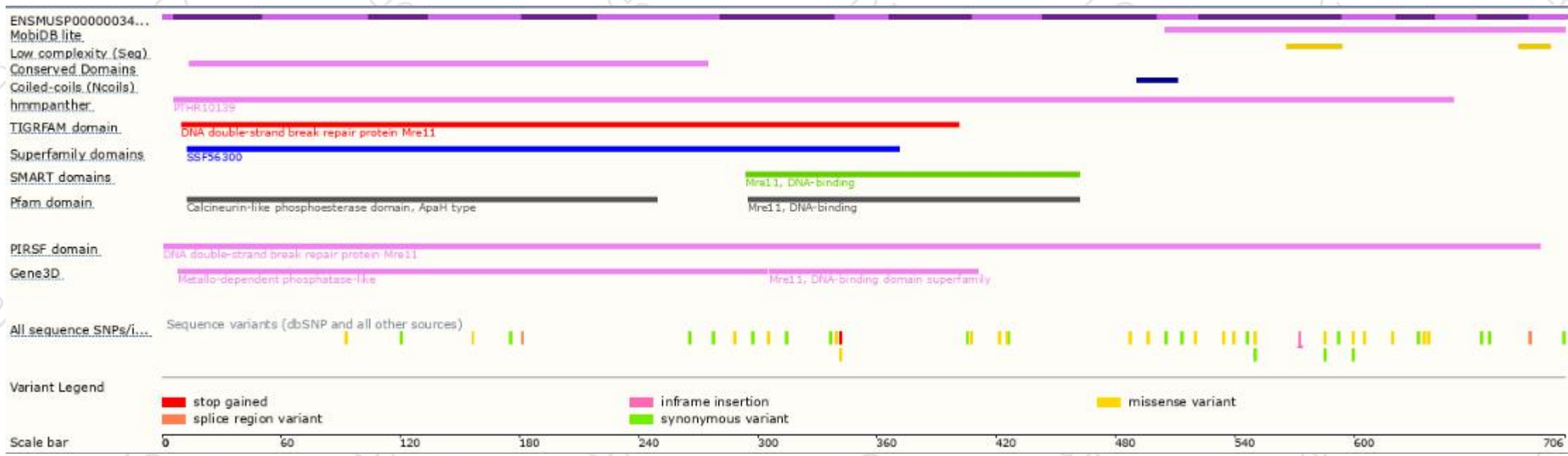
The strategy is based on the design of *Mre11a-201* transcript,The transcription is shown below



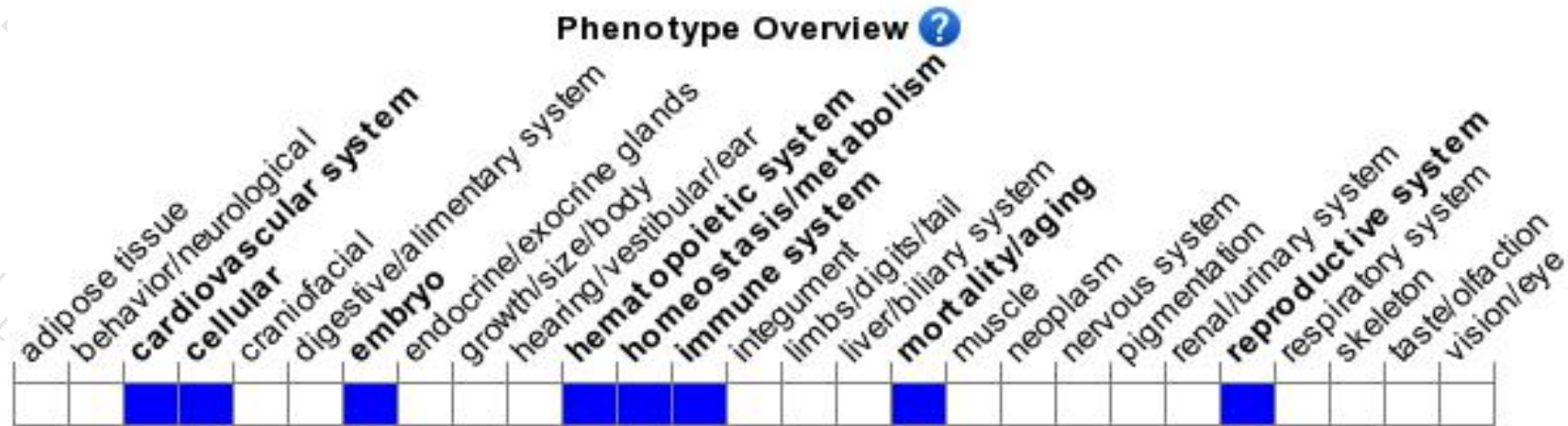
Genomic location distribution



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, Though mutation of this locus affected chromosome stability, mutant mice were no more susceptible to tumorigenesis than wild-type mice. Mutant female mice showed reduced fertility.

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

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