

Mapk9 Cas9-CKO Strategy

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Project Overview

Project Name

Mapk9

Project type

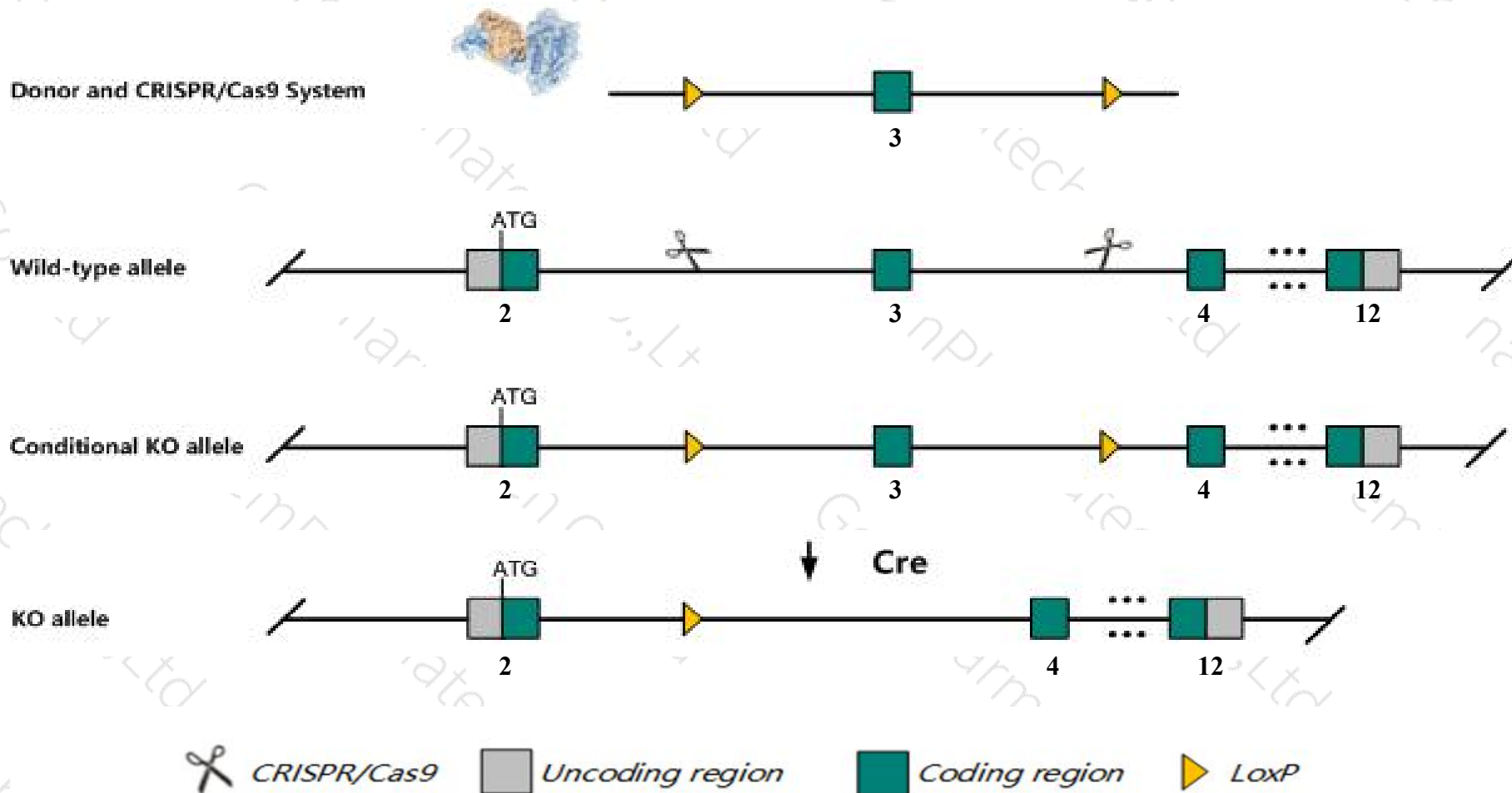
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk9* gene. The schematic diagram is as follows:



Technical routes

- The *Mapk9* gene has 10 transcripts. According to the structure of *Mapk9* gene, exon3 of *Mapk9-201* (ENSMUST00000020634.13) transcript is recommended as the knockout region. The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk9* 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, Homozygotes for a null allele show resistance to TNF-induced liver injury, impaired TH1 cell differentiation, and enhanced epidermal differentiation and proliferation. Homozygotes for a reporter allele show impaired T-cell activation and apoptosis, resistance to I-R cardiac injury, and reduced LTP.
- The *Mapk9* gene is located on the Chr11. 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)

Mapk9 mitogen-activated protein kinase 9 [Mus musculus (house mouse)]

Gene ID: 26420, updated on 19-Mar-2019

Summary



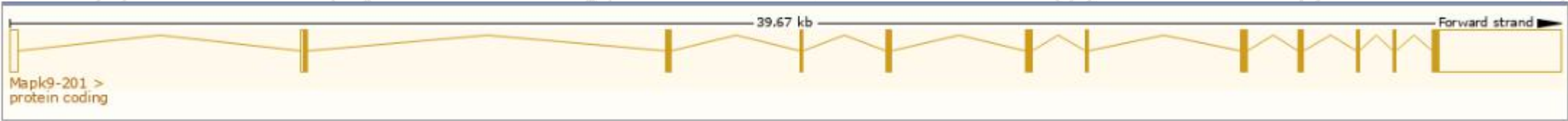
Official Symbol	Mapk9 provided by MGI
Official Full Name	mitogen-activated protein kinase 9 provided by MGI
Primary source	MGI:MGI:1346862
See related	Ensembl:ENSMUSG00000020366
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI851083, JNK2, Prkm9, p54aSAPK
Expression	Ubiquitous expression in cerebellum adult (RPKM 32.4), cortex adult (RPKM 26.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

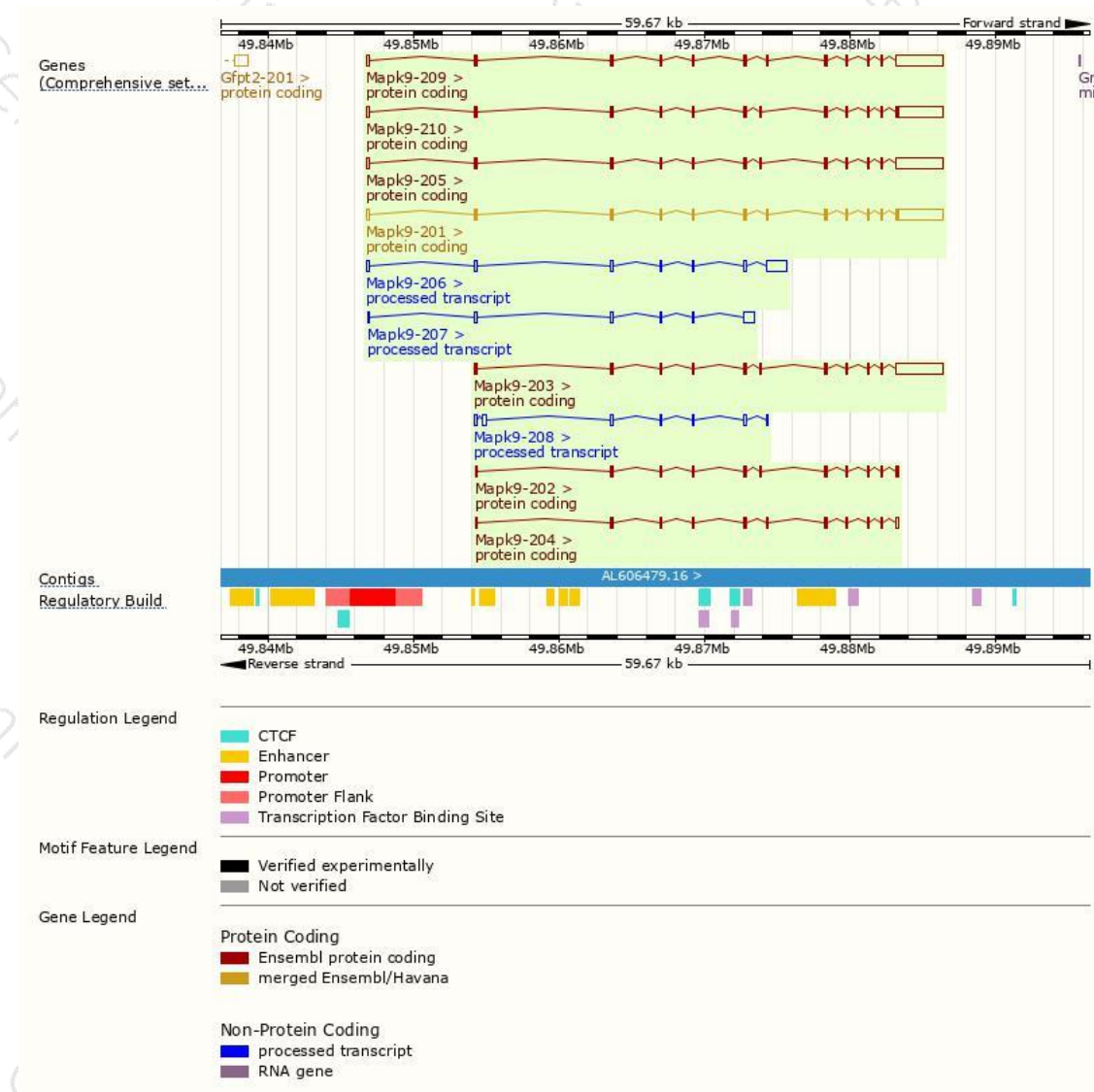
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk9-205	ENSMUST00000109179.8	4682	381aa	Protein coding	CCDS24624	Q9WTU6	TSL:5 GENCODE basic APPRIS ALT 1
Mapk9-209	ENSMUST00000164643.7	4682	381aa	Protein coding	CCDS48783	Q9WTU6	TSL:5 GENCODE basic APPRIS ALT 1
Mapk9-210	ENSMUST00000178543.7	4677	423aa	Protein coding	CCDS48782	Q9WTU6	TSL:5 GENCODE basic APPRIS ALT 1
Mapk9-201	ENSMUST00000020634.13	4675	423aa	Protein coding	CCDS24623	Q5NCK8 Q9WTU6	TSL:1 GENCODE basic APPRIS P4
Mapk9-203	ENSMUST00000102778.7	4447	381aa	Protein coding	CCDS24624	Q9WTU6	TSL:1 GENCODE basic APPRIS ALT 1
Mapk9-204	ENSMUST00000109178.7	1302	381aa	Protein coding	CCDS48783	Q9WTU6	TSL:1 GENCODE basic APPRIS ALT 1
Mapk9-202	ENSMUST00000043321.5	1297	423aa	Protein coding	CCDS48782	Q9WTU6	TSL:1 GENCODE basic APPRIS ALT 1
Mapk9-206	ENSMUST00000144857.7	2192	No protein	Processed transcript	-	-	TSL:1
Mapk9-207	ENSMUST00000148274.7	1245	No protein	Processed transcript	-	-	TSL:1
Mapk9-208	ENSMUST00000151695.1	950	No protein	Processed transcript	-	-	TSL:5

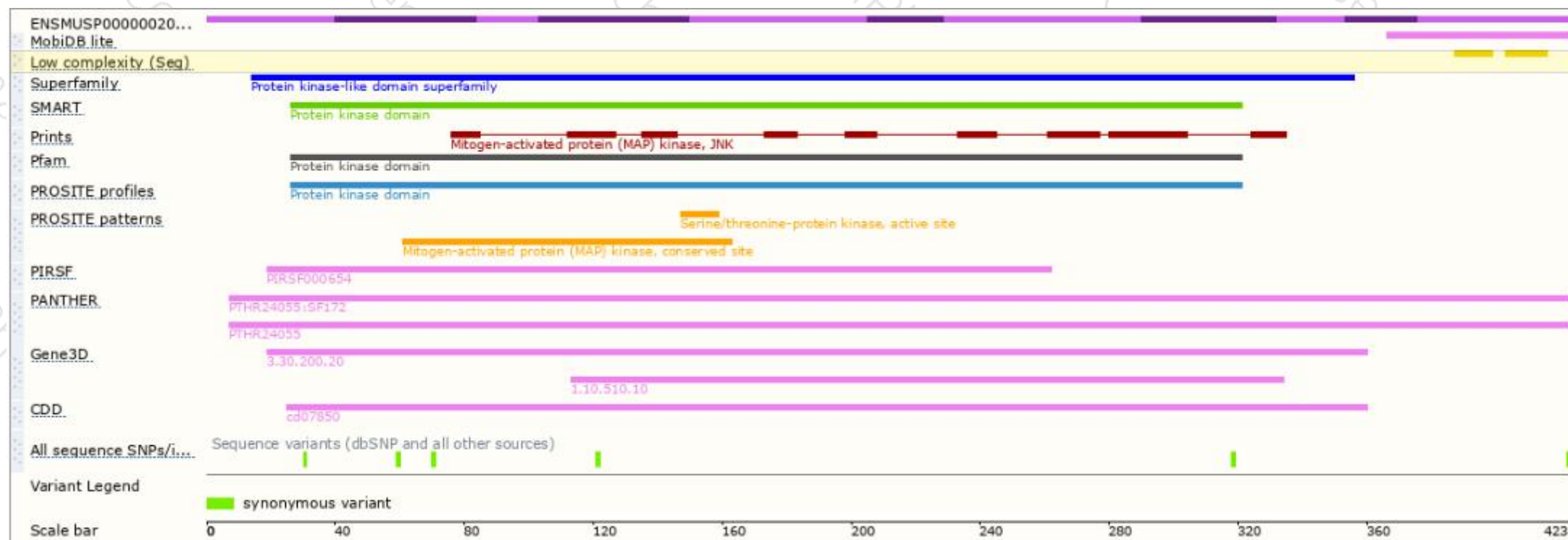
The strategy is based on the design of *Mapk9-201* transcript,The transcription is shown below



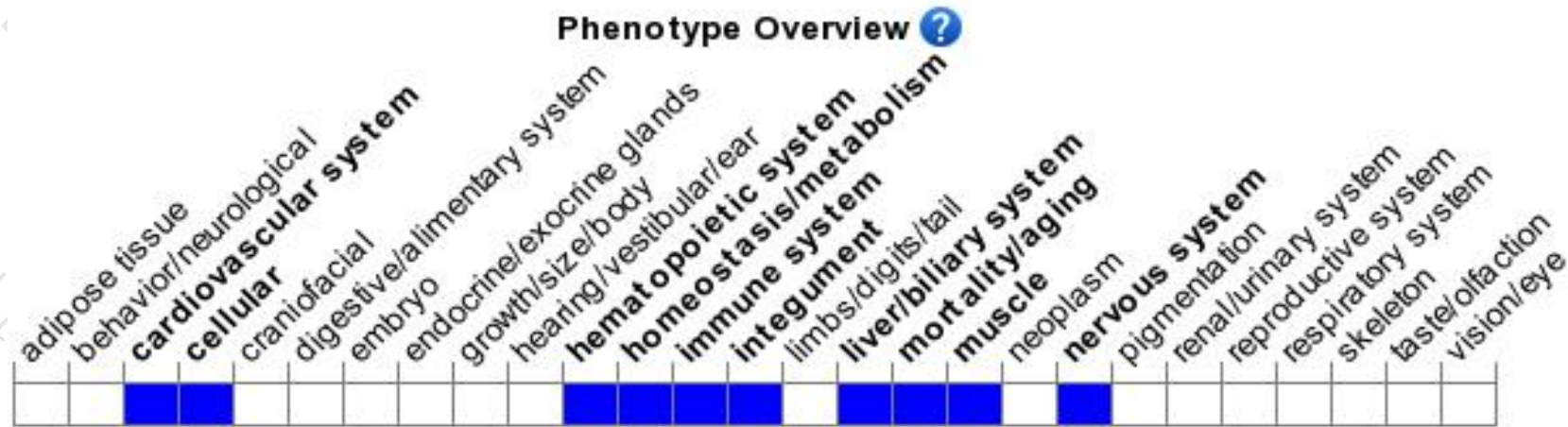
Genomic location distribution



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, Homozygotes for a null allele show resistance to TNF-induced liver injury, impaired TH1 cell differentiation, and enhanced epidermal differentiation and proliferation. Homozygotes for a reporter allele show impaired T-cell activation and apoptosis, resistance to I-R cardiac injury, and reduced LTP.

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

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