

***Mapk7* Cas9-KO Strategy**

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Project Overview

Project Name

Mapk7

Project type

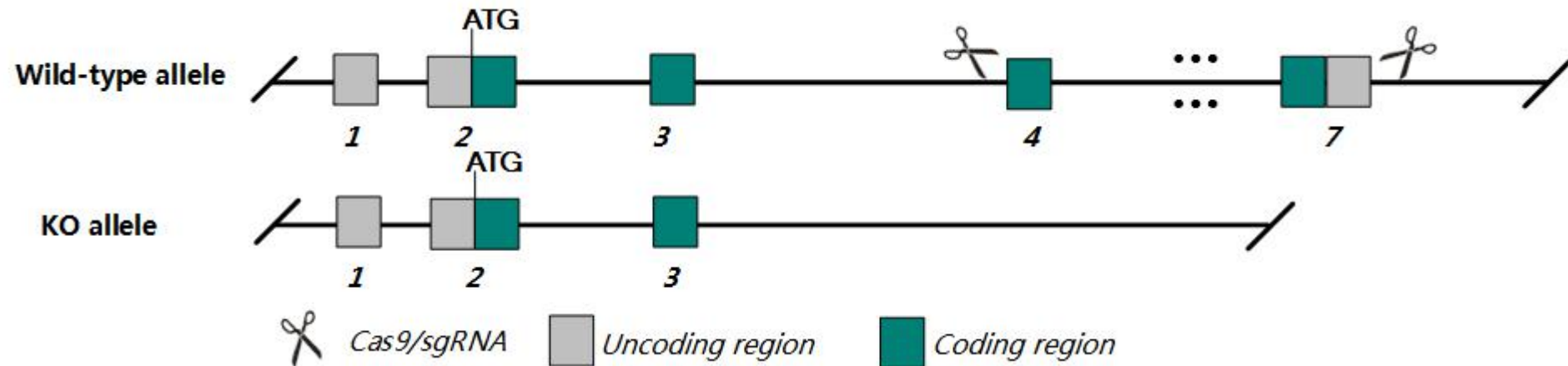
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk7* gene. The schematic diagram is as follows:



- The *Mapk7* gene has 14 transcripts. According to the structure of *Mapk7* gene, exon4-exon7 of *Mapk1-202* (ENSMUST00000079080.12) transcript is recommended as the knockout region. The region contains 2023bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk7* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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, Homozygous inactivation of this gene leads to embryonic growth retardation and midgestational lethality due to multiple developmental anomalies and vascular remodelling, cardiac development, and placental defects.
- The strategy can directly destroy the 3'UTR of *Mfap4* gene.
- The *Mapk7* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Mapk7 mitogen-activated protein kinase 7 [Mus musculus (house mouse)]

Gene ID: 23939, updated on 31-Jan-2019

Summary



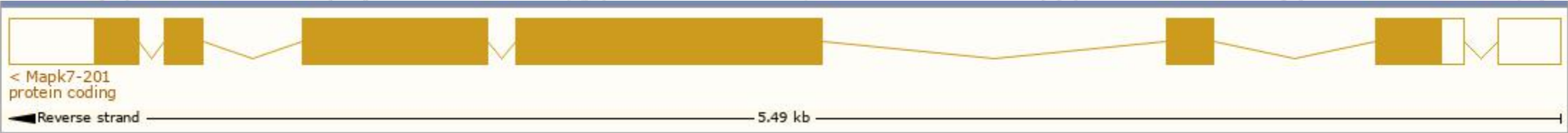
Official Symbol	Mapk7 provided by MGI
Official Full Name	mitogen-activated protein kinase 7 provided by MGI
Primary source	MGI:MGI:1346347
See related	Ensembl:ENSMUSG00000001034
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BMK-1, BMK1, ERK-5, ERK5, Erk5-T, PRKM7, b2b2346Clo
Expression	Ubiquitous expression in limb E14.5 (RPKM 31.7), whole brain E14.5 (RPKM 29.9) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

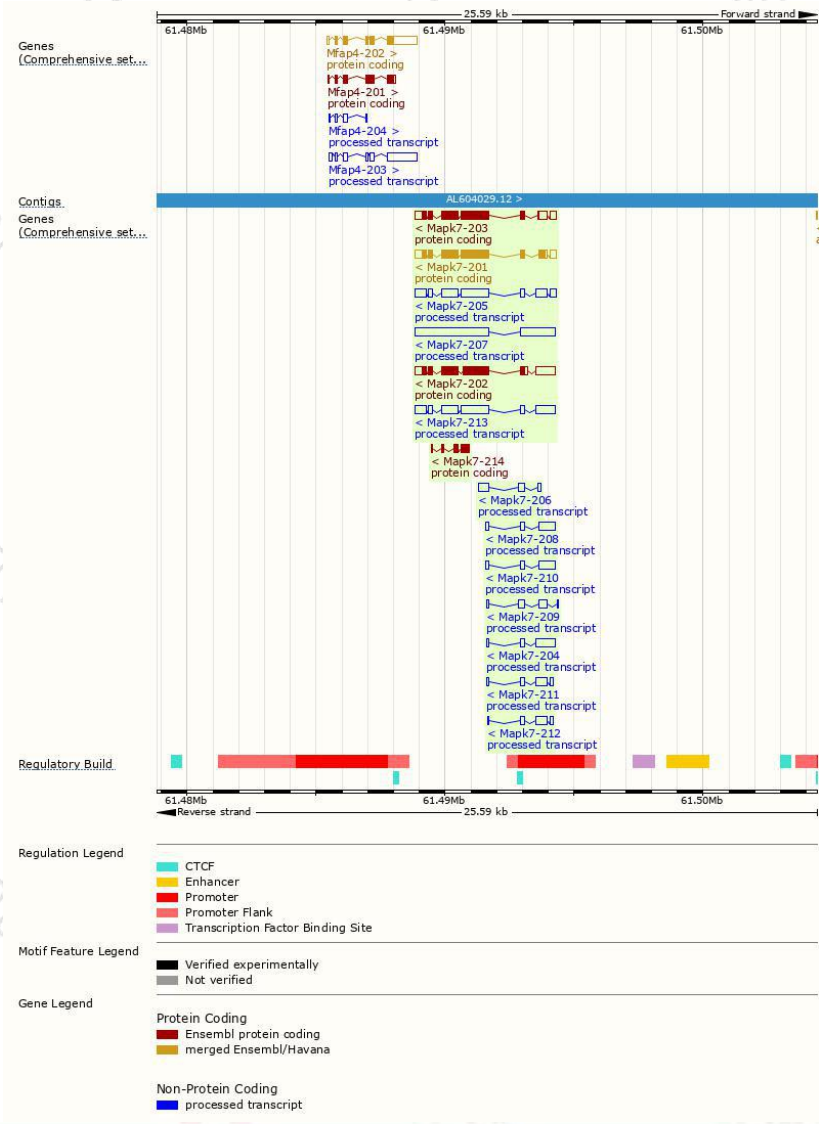
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk7-202	ENSMUST00000101085.8	3254	703aa	Protein coding	CCDS78963	Q5NCN8	TSL:1 GENCODE basic
Mapk7-203	ENSMUST00000108714.1	3069	737aa	Protein coding	CCDS70205	Q9WVS8	TSL:1 GENCODE basic
Mapk7-201	ENSMUST00000079080.12	3019	806aa	Protein coding	CCDS24814	Q9WVS8	TSL:1 GENCODE basic APPRIS P1
Mapk7-214	ENSMUST00000153441.1	609	203aa	Protein coding	-	Z4YLV8	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
Mapk7-207	ENSMUST00000128478.1	4238	No protein	Processed transcript	-	-	TSL:2
Mapk7-213	ENSMUST00000152755.7	3255	No protein	Processed transcript	-	-	TSL:1
Mapk7-205	ENSMUST00000125840.7	3134	No protein	Processed transcript	-	-	TSL:1
Mapk7-204	ENSMUST00000123360.7	990	No protein	Processed transcript	-	-	TSL:2
Mapk7-208	ENSMUST00000129272.7	909	No protein	Processed transcript	-	-	TSL:3
Mapk7-210	ENSMUST00000139663.7	895	No protein	Processed transcript	-	-	TSL:1
Mapk7-211	ENSMUST00000139932.7	787	No protein	Processed transcript	-	-	TSL:5
Mapk7-212	ENSMUST00000140779.1	769	No protein	Processed transcript	-	-	TSL:5
Mapk7-206	ENSMUST00000126495.7	714	No protein	Processed transcript	-	-	TSL:2
Mapk7-209	ENSMUST00000135521.1	691	No protein	Processed transcript	-	-	TSL:3

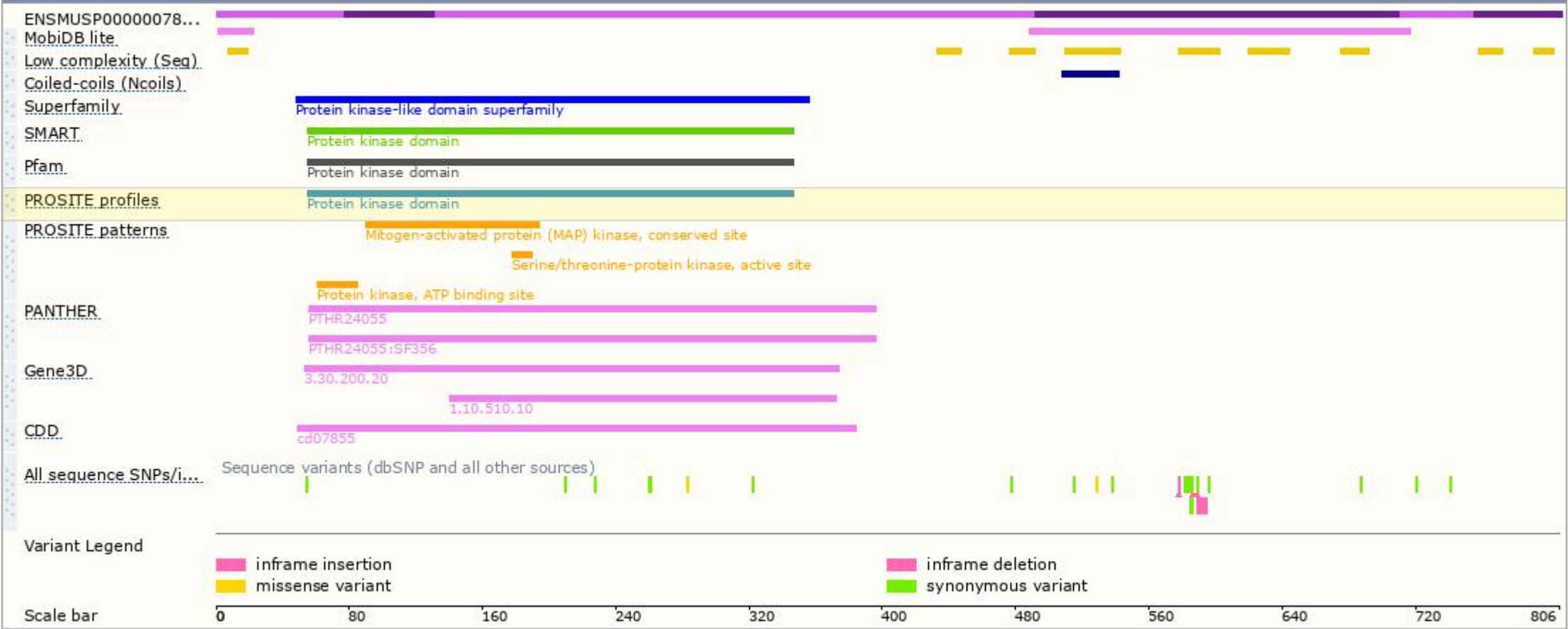
The strategy is based on the design of *Mapk7-201* transcript,The transcription is shown below



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, Homozygous inactivation of this gene leads to embryonic growth retardation and midgestational lethality due to multiple developmental anomalies and vascular remodelling, cardiac development, and placental defects.

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

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