

Map3k3 Cas9-KO Strategy

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Project Overview

Project Name

Map3k3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map3k3* gene. The schematic diagram is as follows:



- The *Map3k3* gene has 3 transcripts. According to the structure of *Map3k3* gene, exon3 of *Map3k3-201* (ENSMUST00000002044.9) transcript is recommended as the knockout region. The region contains 41bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map3k3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene die as embryos before E11.5. vascular remodeling does not take place normally.
- The *Map3k3* 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)

Map3k3 mitogen-activated protein kinase kinase kinase 3 [*Mus musculus* (house mouse)]

Gene ID: 26406, updated on 7-Dec-2019

Summary

- Official Symbol

Map3k3 provided by [MGI](#)
- Official Full Name

mitogen-activated protein kinase kinase kinase 3 provided by [MGI](#)
- Primary source

[MGI:MGI:1346874](#)
- See related

[Ensembl:ENSMUSG00000020700](#)
- 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

Mekk3; MAPKKK3; AW548911; mKIAA4031
- Expression

Ubiquitous expression in lung adult (RPKM 22.2), subcutaneous fat pad adult (RPKM 19.2) and 28 other tissues [See more](#)
- Orthologs

[human](#) [all](#)

Genomic context

Location: 11; 11 E1

See Map3k3 in [Genome Data Viewer](#)

Exon count: 18

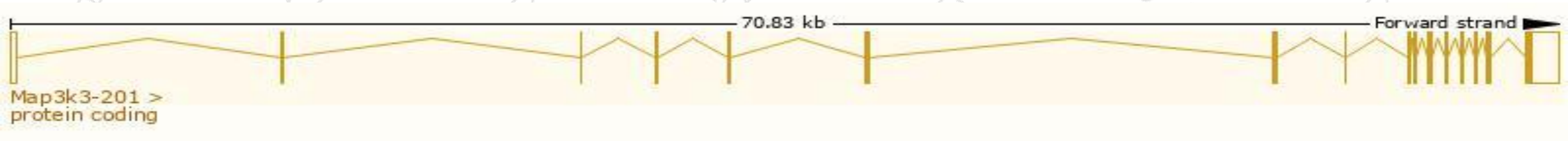
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (106084902..106156650)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (105946216..106016760)

Transcript information (Ensembl)

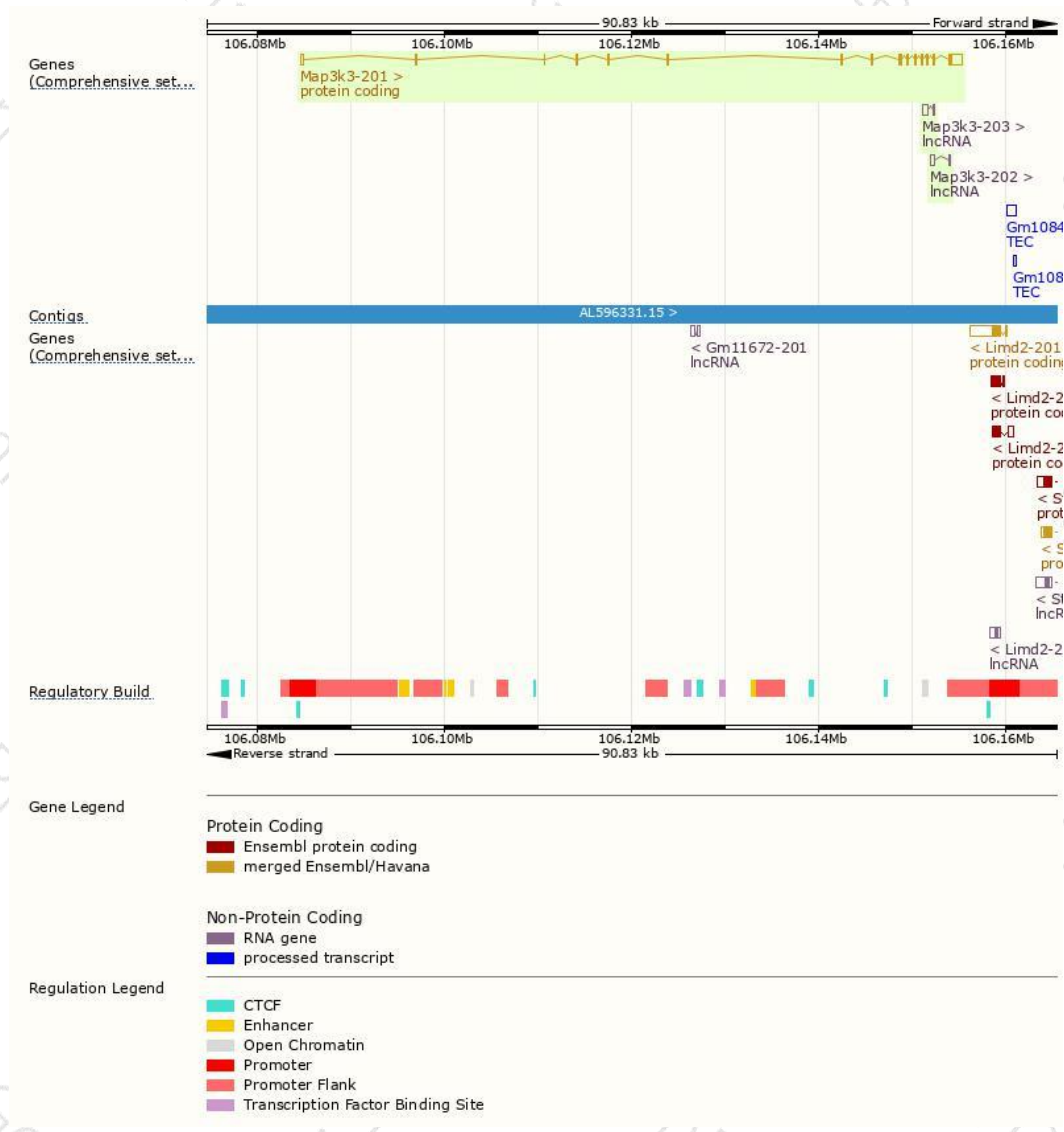
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map3k3-201	ENSMUST00000002044.9	3450	626aa	Protein coding	CCDS25548	Q61084	TSL:1 GENCODE basic APPRIS P1
Map3k3-203	ENSMUST00000129793.1	698	No protein	lncRNA	-	-	TSL:3
Map3k3-202	ENSMUST00000124449.1	520	No protein	lncRNA	-	-	TSL:3

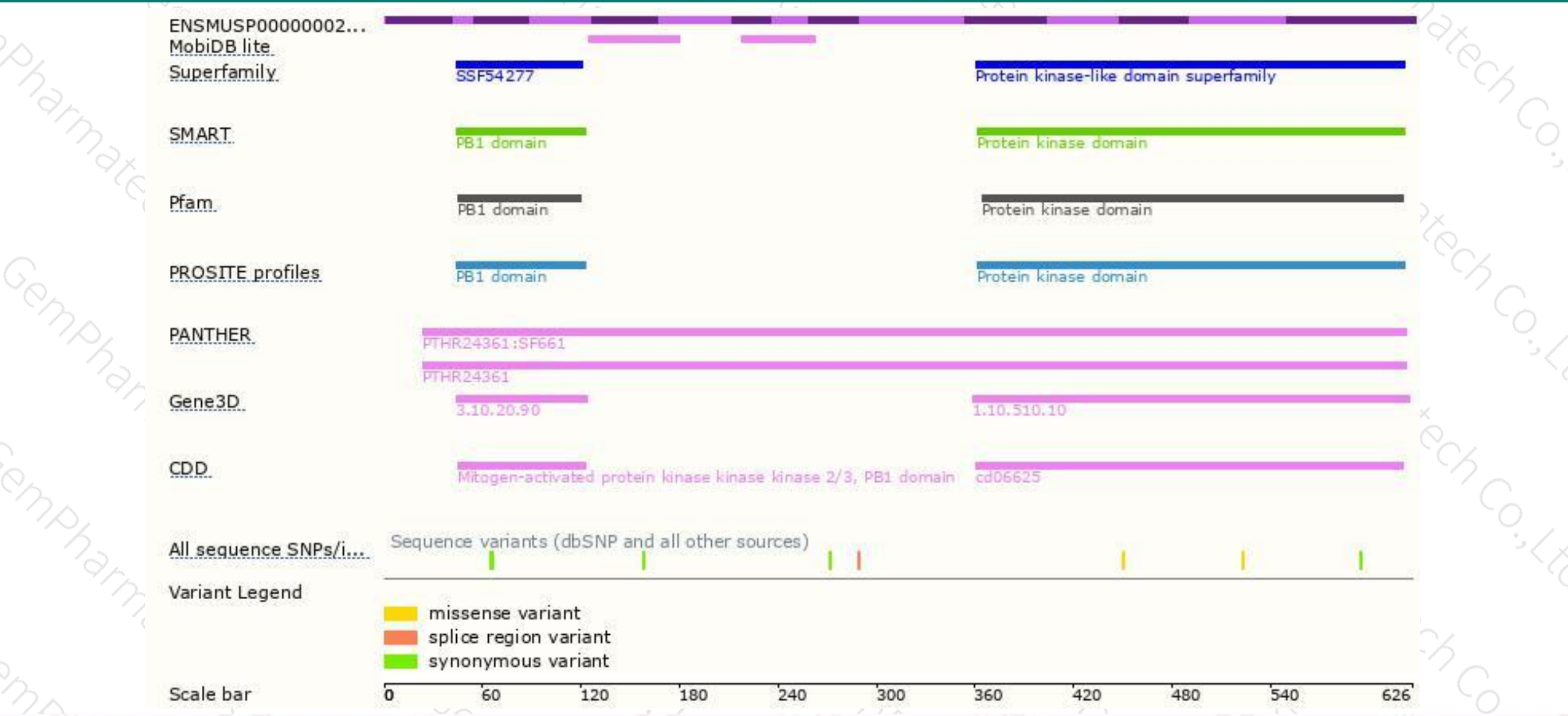
The strategy is based on the design of *Map3k3-201* transcript,The transcription is shown below



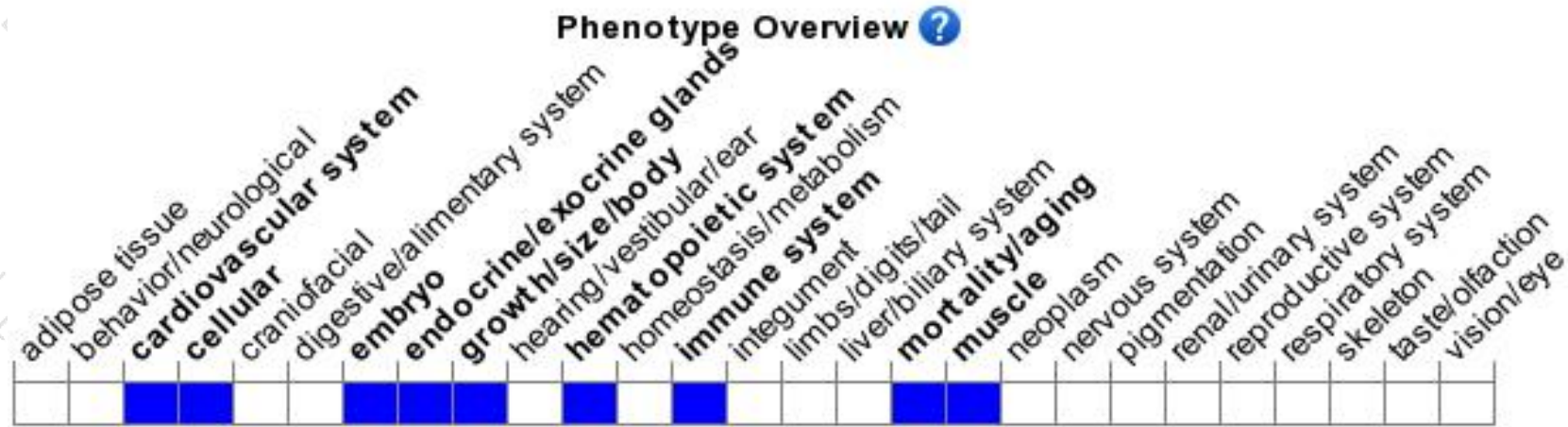
Genomic location distribution



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, Mice homozygous for disruptions in this gene die as embryos before E11.5. vascular remodeling does not take place normally.

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

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