

Map3k5 Cas9-KO Strategy

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Project Overview



Project Name

Map3k5

Project type

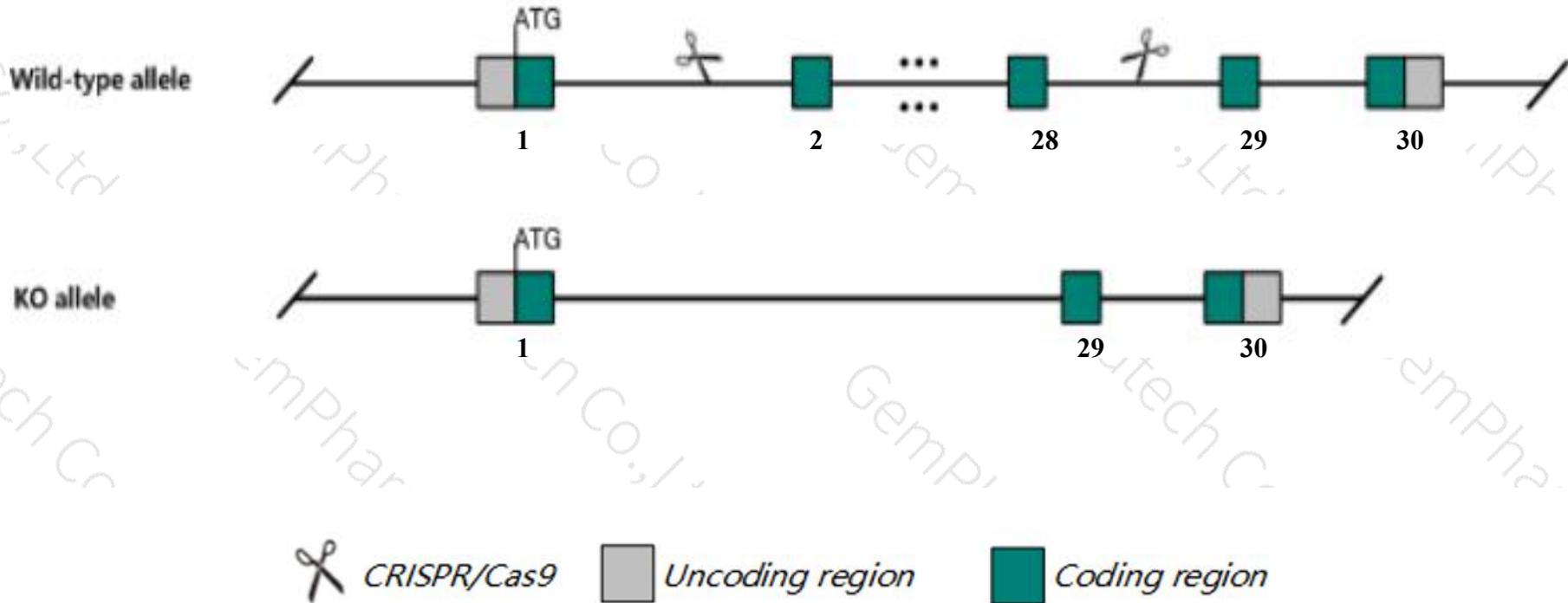
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map3k5* gene. The schematic diagram is as follows:



- The *Map3k5* gene has 6 transcripts. According to the structure of *Map3k5* gene, exon2-exon28 of *Map3k5-201*(ENSMUST00000095806.9) transcript is recommended as the knockout region. The region contains 3539bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map3k5* gene. The brief process is as follows: CRISPR/Cas9 system 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 mutant mice are overtly normal, however apoptosis abnormalities are evident in cultured cells and after induced heart damage.
- The *Map3k5* gene is located on the Chr10. 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)

Map3k5 mitogen-activated protein kinase kinase kinase 5 [Mus musculus (house mouse)]

Gene ID: 26408, updated on 22-Mar-2020

Summary



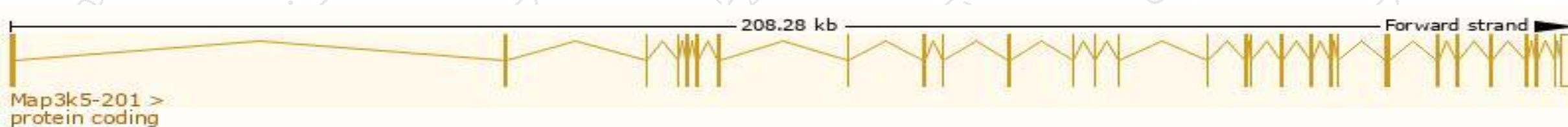
Official Symbol	Map3k5 provided by MGI
Official Full Name	mitogen-activated protein kinase kinase kinase 5 provided by MGI
Primary source	MGI:MGI:1346876
See related	Ensembl:ENSMUSG00000071369
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	7420452D20Rik, A, AS, ASK, ASK1, MAPKKK5, Mekk5
Expression	Ubiquitous expression in bladder adult (RPKM 5.2), cortex adult (RPKM 2.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

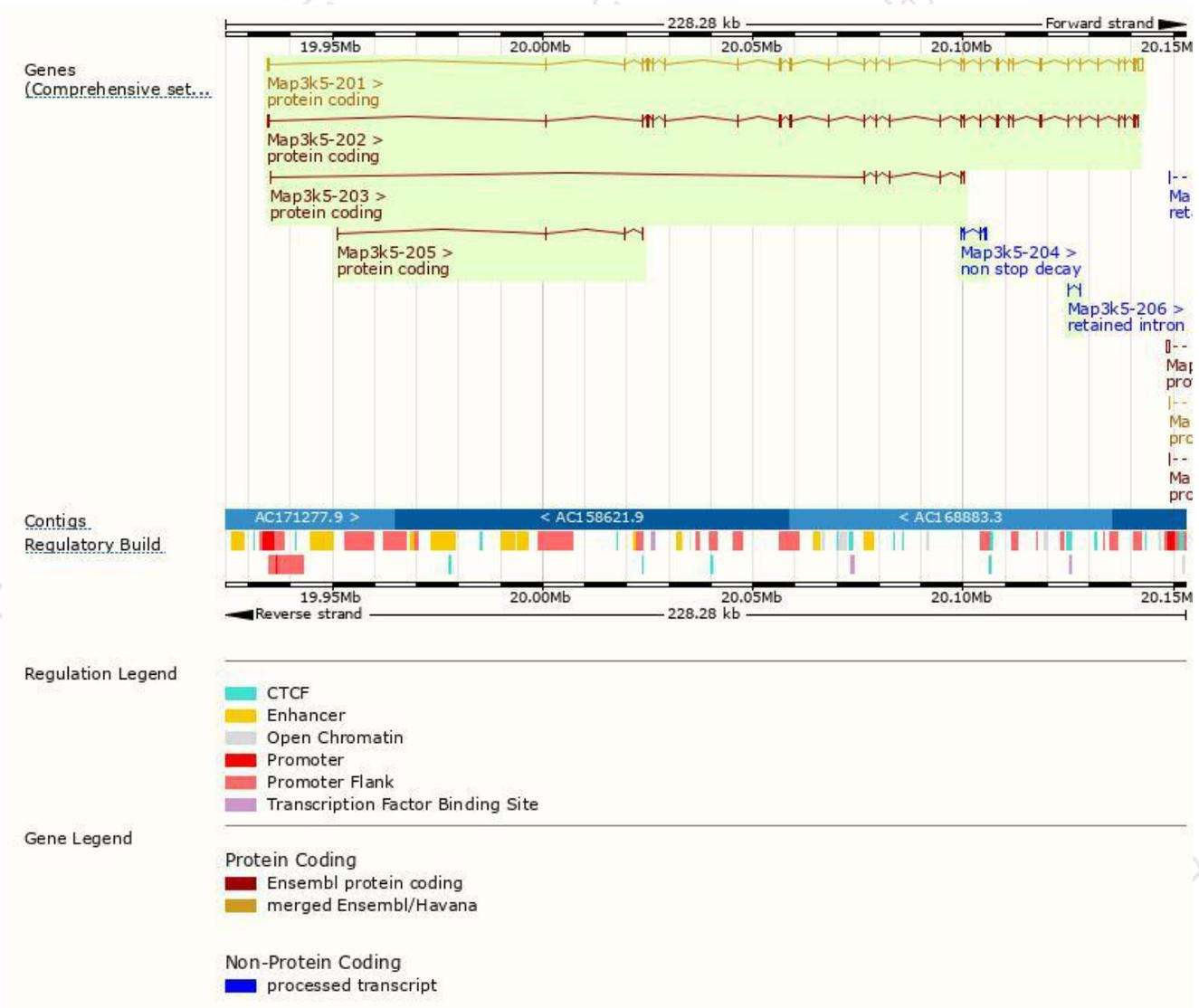
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map3k5-201	ENSMUST00000095806.9	5450	1380aa	Protein coding	CCDS35857	O35099	TSL:1 GENCODE basic APPRIS P2
Map3k5-202	ENSMUST00000120259.7	4289	1372aa	Protein coding	-	E9PWG9	TSL:1 GENCODE basic APPRIS ALT2
Map3k5-203	ENSMUST00000129437.1	789	144aa	Protein coding	-	D3YVC4	CDS 3' incomplete TSL:5
Map3k5-205	ENSMUST00000152533.1	378	79aa	Protein coding	-	D3Z5H1	CDS 3' incomplete TSL:3
Map3k5-204	ENSMUST00000138994.1	513	171aa	Non stop decay	-	A0A1L1ST18	CDS 5' incomplete TSL:3
Map3k5-206	ENSMUST00000156369.1	370	No protein	Retained intron	-	-	TSL:3

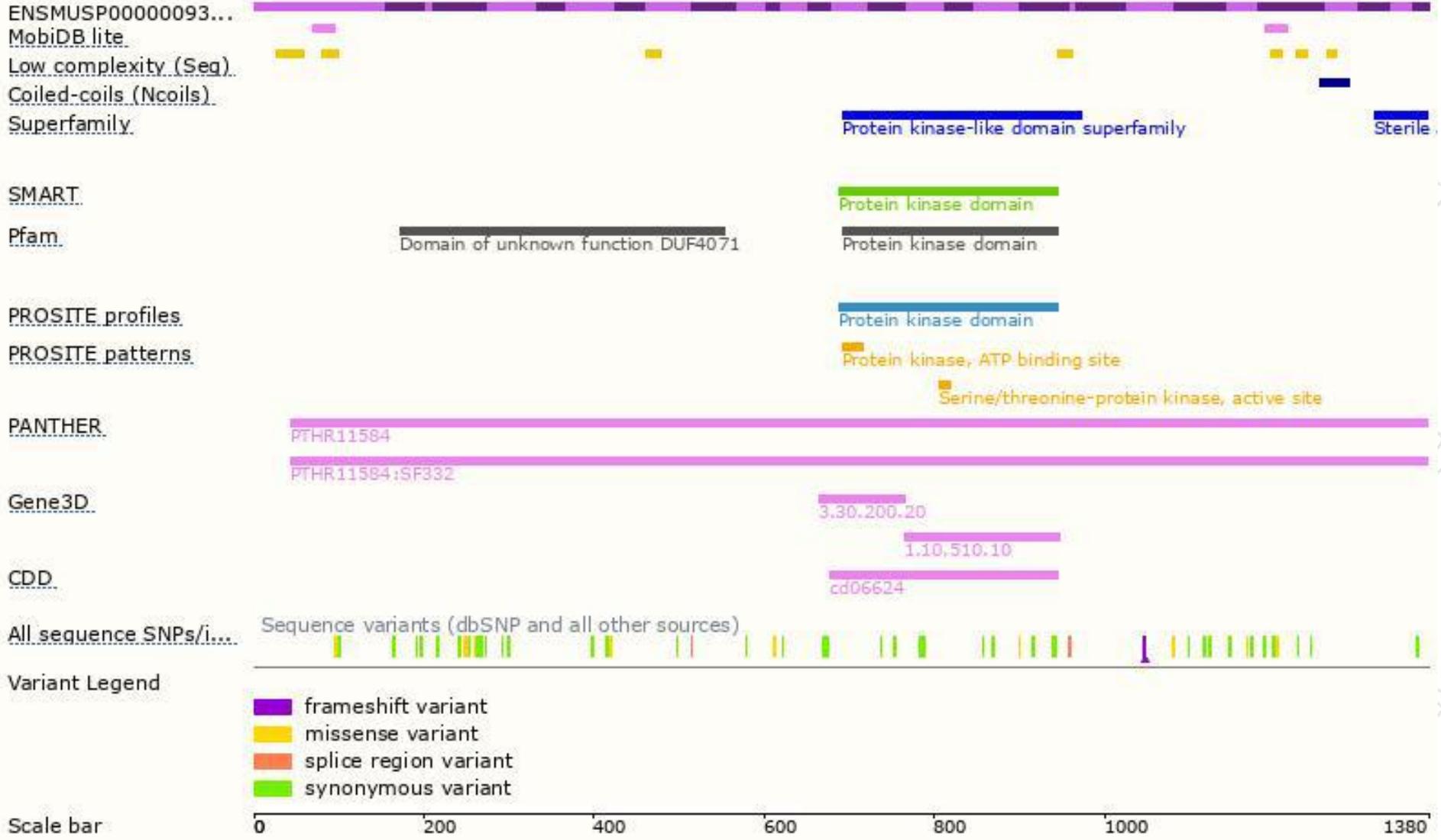
The strategy is based on the design of *Map3k5-201* transcript, the transcription is shown below:



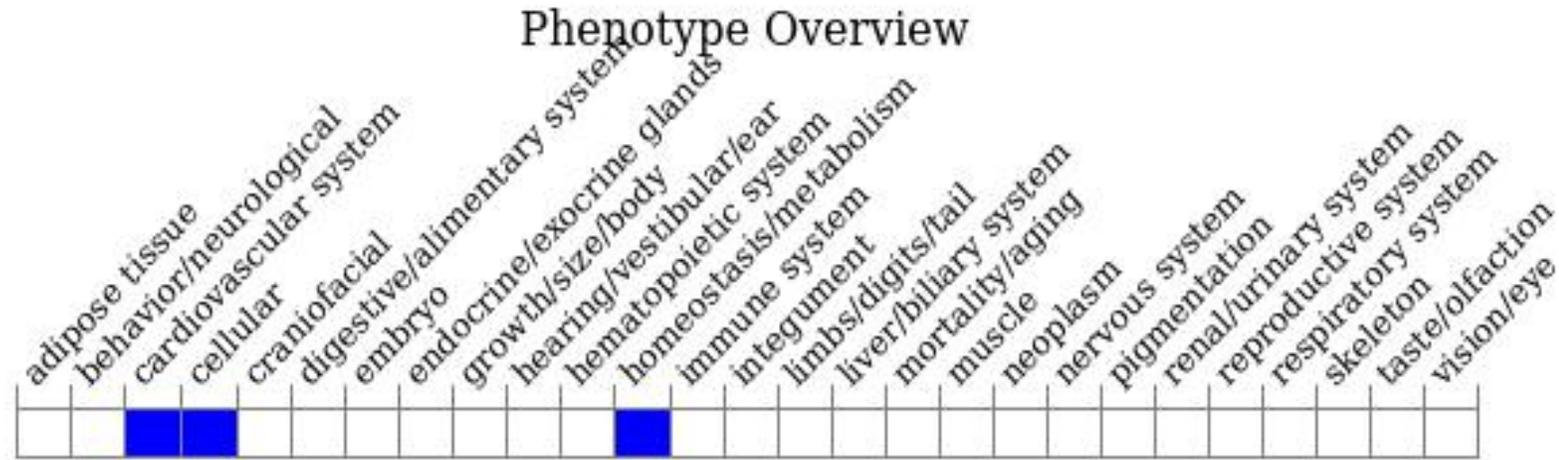
Genomic location distribution



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 mutant mice are overtly normal, however apoptosis abnormalities are evident in cultured cells and after induced heart damage.

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

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