

Map2k2 Cas9-KO Strategy

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Project Overview

Project Name

Map2k2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map2k2* gene. The schematic diagram is as follows:



- The *Map2k2* gene has 9 transcripts. According to the structure of *Map2k2* gene, exon4-exon9 of *Map2k2-207* (ENSMUST00000143517.7) transcript is recommended as the knockout region. The region contains 599bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map2k2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a targeted null mutation are viable, fertile, and apparently normal.
- Transcript *Map2k2*-208 may not be affected . And the effect on transcript *Map2k2*-206&209 is unknown.
- The *Map2k2* 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)

Map2k2 mitogen-activated protein kinase kinase 2 [*Mus musculus* (house mouse)]

Gene ID: 26396, updated on 12-Aug-2019

Summary

- Official Symbol** Map2k2 provided by [MGI](#)
- Official Full Name** mitogen-activated protein kinase kinase 2 provided by [MGI](#)
- Primary source** [MGI:MGI:1346867](#)
- See related** [Ensembl:ENSMUSG00000035027](#)
- 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** MK2; MEK2; Prkmk2; AA589381
- Expression** Ubiquitous expression in duodenum adult (RPKM 230.0), adrenal adult (RPKM 218.2) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10 C1; 10 39.72 cM [See Map2k2 in Genome Data Viewer](#)

Exon count: 11

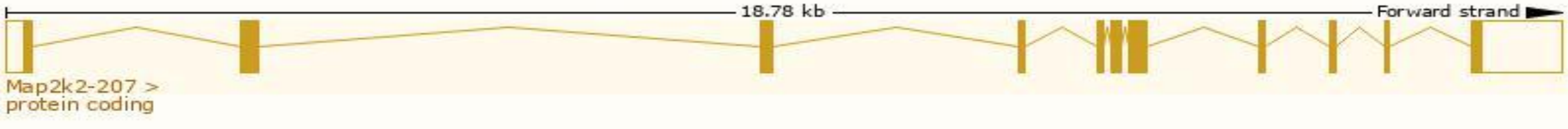
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (81105913..81124697)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (80568692..80587442)

Transcript information (Ensembl)

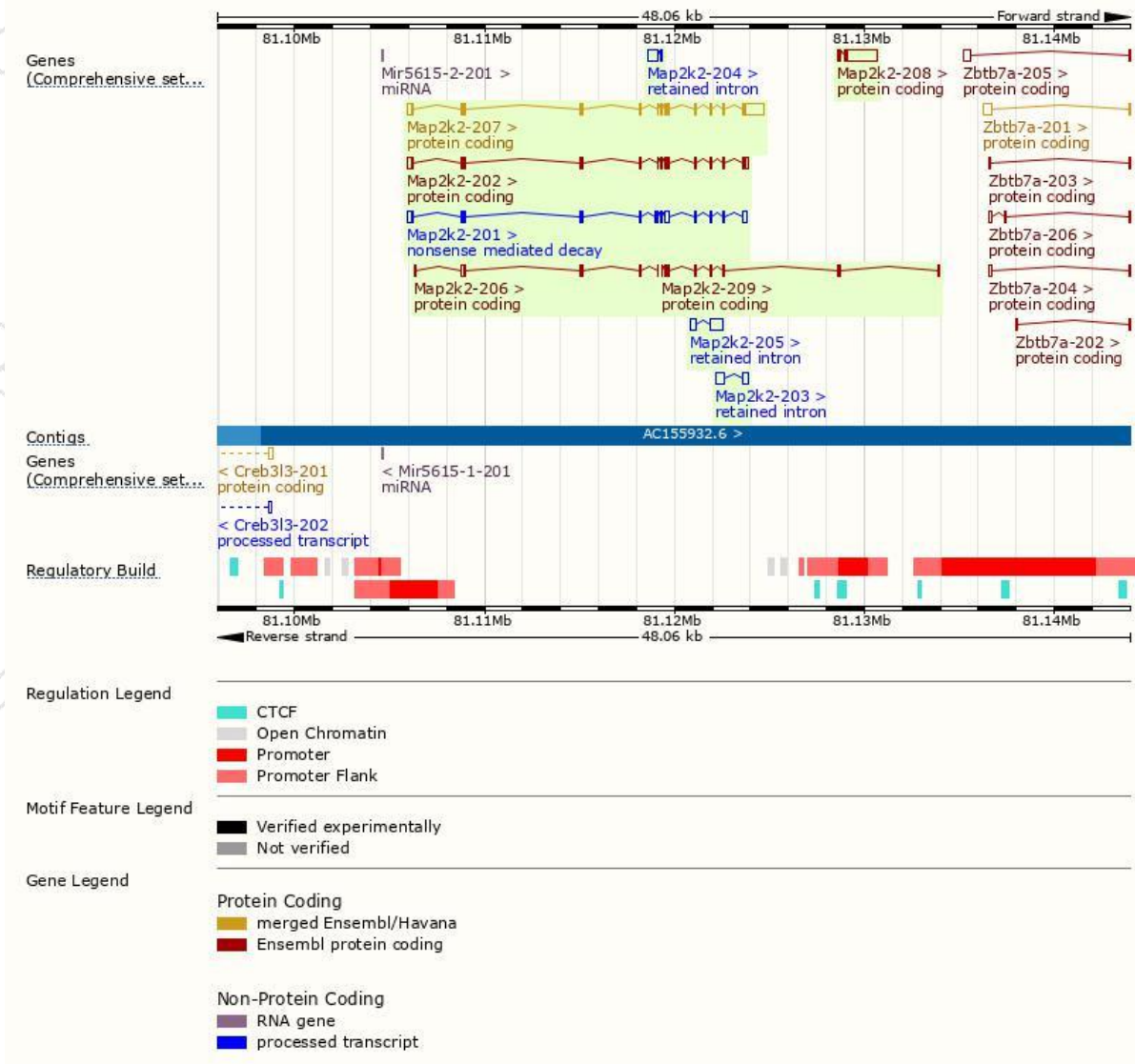
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map2k2-207	ENSMUST00000143517.7	2405	401aa	Protein coding	CCDS24044	Q63932	TSL:1 GENCODE basic APPRIS P3
Map2k2-202	ENSMUST00000105331.7	1556	400aa	Protein coding	CCDS83734	Q91YS7	TSL:1 GENCODE basic APPRIS ALT1
Map2k2-208	ENSMUST00000218571.1	1803	65aa	Protein coding	-	A0A1W2P769	CDS 5' incomplete TSL:3
Map2k2-209	ENSMUST00000220329.1	662	196aa	Protein coding	-	A0A1W2P7V9	CDS 5' incomplete TSL:3
Map2k2-206	ENSMUST00000136743.1	482	84aa	Protein coding	-	D3Z446	CDS 3' incomplete TSL:5
Map2k2-201	ENSMUST00000048223.13	1625	203aa	Nonsense mediated decay	-	M0QWN2	TSL:1
Map2k2-205	ENSMUST00000128937.1	917	No protein	Retained intron	-	-	TSL:2
Map2k2-203	ENSMUST00000123241.1	761	No protein	Retained intron	-	-	TSL:2
Map2k2-204	ENSMUST00000123888.1	620	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Map2k2-207* transcript,The transcription is shown below



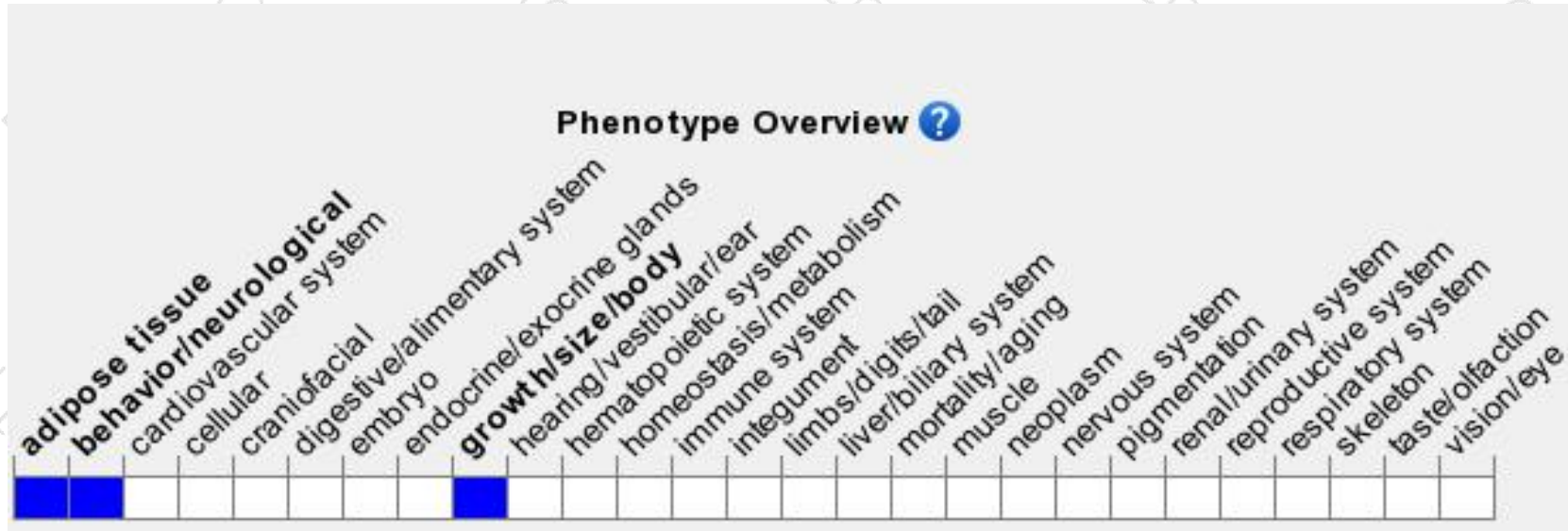
Genomic location distribution



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 targeted null mutation are viable, fertile, and apparently normal.

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

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