

Map2k1 Cas9-KO Strategy

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Design Date:

2019-11-14

Project Overview

Project Name

Map2k1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map2k1* gene. The schematic diagram is as follows:



- The *Map2k1* gene has 4 transcripts. According to the structure of *Map2k1* gene, exon2 of *Map2k1-201* (ENSMUST00000005066.8) transcript is recommended as the knockout region. The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map2k1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous inactivation of this gene leads to reduced embryo size and midgestational lethality due to impaired development and hypovascularization of the placenta with decreased labyrinth cell proliferation and enhanced cell apoptosis. Mutant MEFs fail to exhibit fibronectin-induced migration.
- The *Map2k1* gene is located on the Chr9. 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)

Map2k1 mitogen-activated protein kinase kinase 1 [Mus musculus (house mouse)]

Gene ID: 26395, updated on 7-Apr-2019

Summary



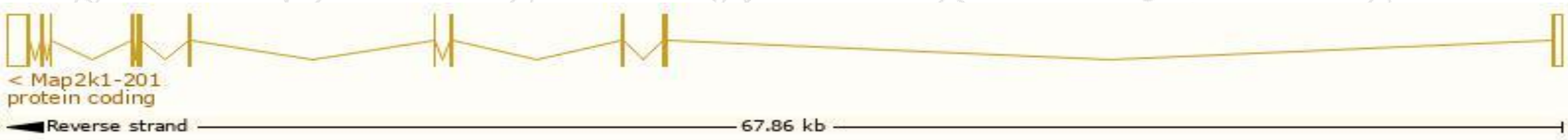
Official Symbol	Map2k1 provided by MGI
Official Full Name	mitogen-activated protein kinase kinase 1 provided by MGI
Primary source	MGI:MGI:1346866
See related	Ensembl:ENSMUSG000000004936
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MAPKK1, MEKK1, Mek1, Prkmk1
Expression	Ubiquitous expression in frontal lobe adult (RPKM 50.3), cortex adult (RPKM 32.1) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

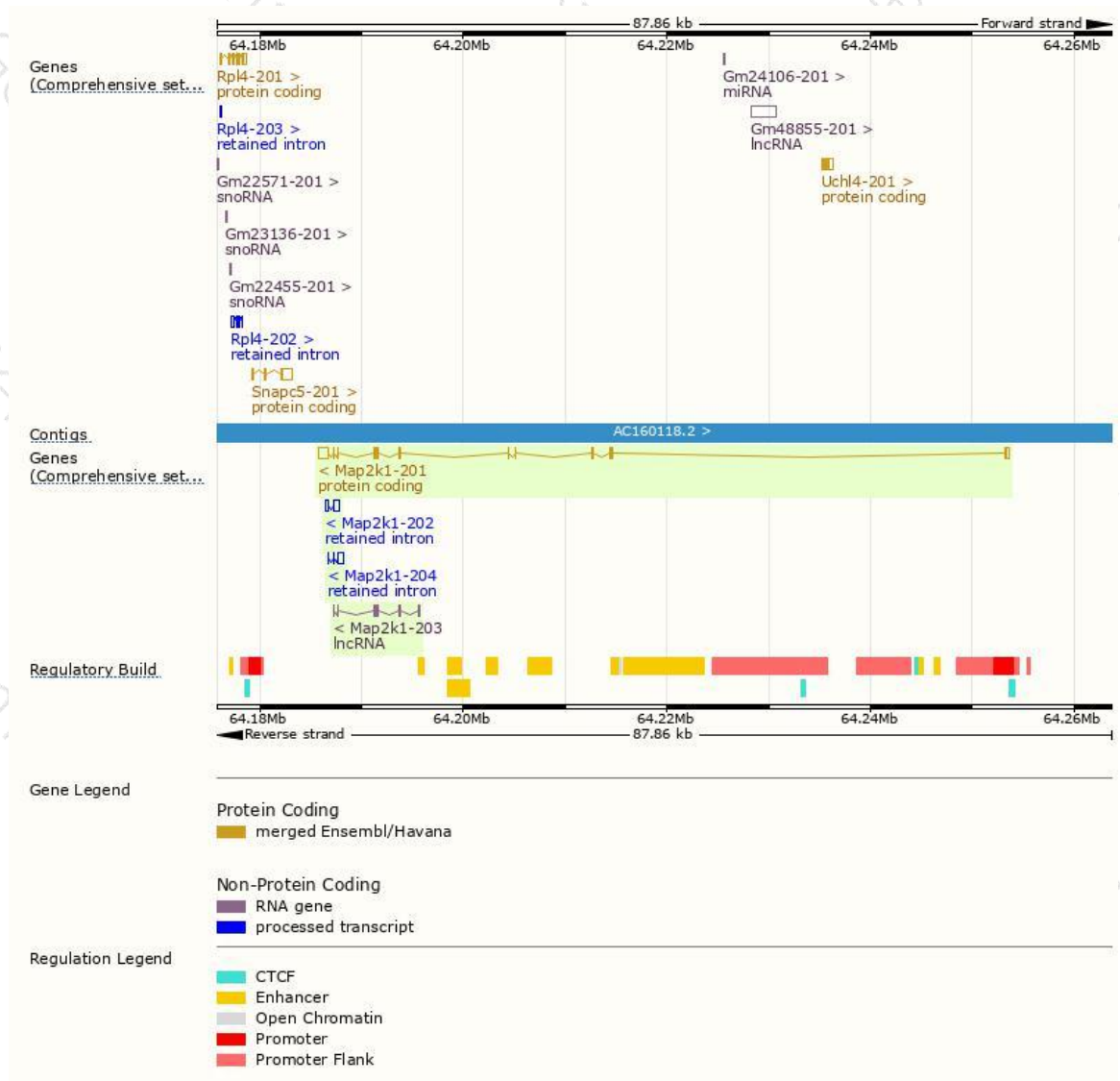
The gene has 4 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Map2k1-201	ENSMUST00000005066.8	2436	393aa	Protein coding	CCDS23277	P31938 Q3TMJ8	NM_008927 NP_032953	TSL:1	GENCODE basic APPRIS P1
Map2k1-203	ENSMUST00000152535.1	597	No protein	Processed transcript	-	-	-	TSL:3	
Map2k1-202	ENSMUST00000147796.1	844	No protein	Retained intron	-	-	-	TSL:3	
Map2k1-204	ENSMUST00000152675.1	688	No protein	Retained intron	-	-	-	TSL:2	

The strategy is based on the design of *Map2k1-201* transcript,The transcription is shown below



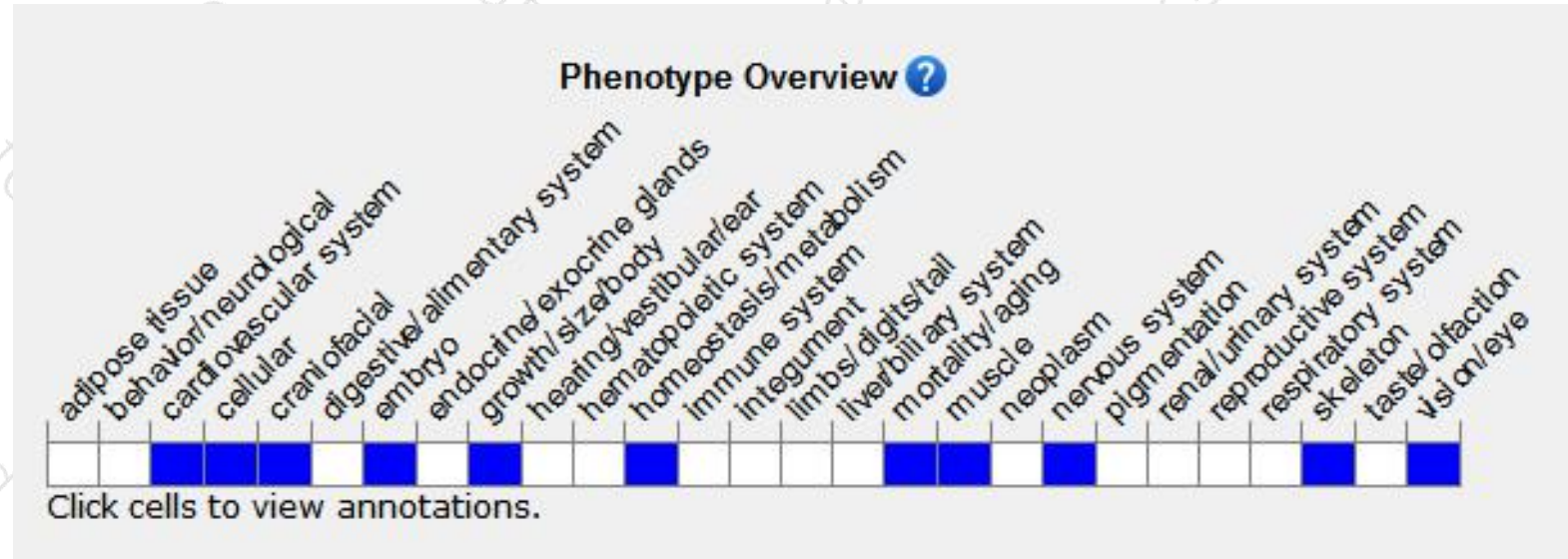
Genomic location distribution



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 reduced embryo size and midgestational lethality due to impaired development and hypovascularization of the placenta with decreased labyrinth cell proliferation and enhanced cell apoptosis. Mutant MEFs fail to exhibit fibronectin-induced migration.

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

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