

# *Map2k3* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Map2k3*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map2k3* gene. The schematic diagram is as follows:



- The *Map2k3* gene has 6 transcripts. According to the structure of *Map2k3* gene, exon2-exon5 of *Map2k3-201* (ENSMUST00000019076.9) transcript is recommended as the knockout region. The region contains 350bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map2k3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene are viable and fertile but display abnormalities in cytokine production.
- Transcript 204 is unaffected.
- The *Map2k3* 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)

## Map2k3 mitogen-activated protein kinase kinase 3 [ *Mus musculus* (house mouse) ]

Gene ID: 26397, updated on 12-Aug-2019

### Summary

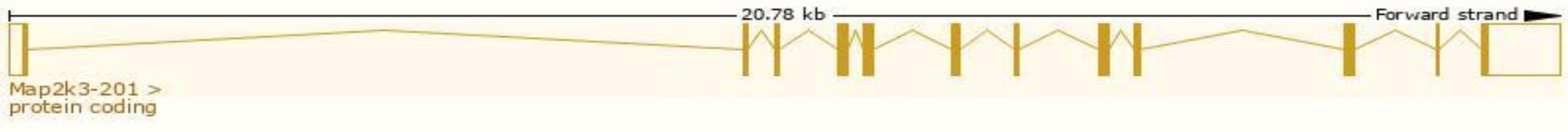
|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Map2k3 provided by <a href="#">MGI</a>                                                                                                                                    |
| Official Full Name | mitogen-activated protein kinase kinase 3 provided by <a href="#">MGI</a>                                                                                                 |
| Primary source     | <a href="#">MGI:MGI:1346868</a>                                                                                                                                           |
| See related        | <a href="#">Ensembl:ENSMUSG00000018932</a>                                                                                                                                |
| Gene type          | protein coding                                                                                                                                                            |
| RefSeq status      | VALIDATED                                                                                                                                                                 |
| Organism           | <a href="#">Mus musculus</a>                                                                                                                                              |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as      | MEK3; MKK3; MKK3b; Prkmk3; MAPKK 3; AW212142                                                                                                                              |
| Expression         | Ubiquitous expression in large intestine adult (RPKM 35.9), small intestine adult (RPKM 30.3) and 28 other tissues <a href="#">See more</a>                               |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

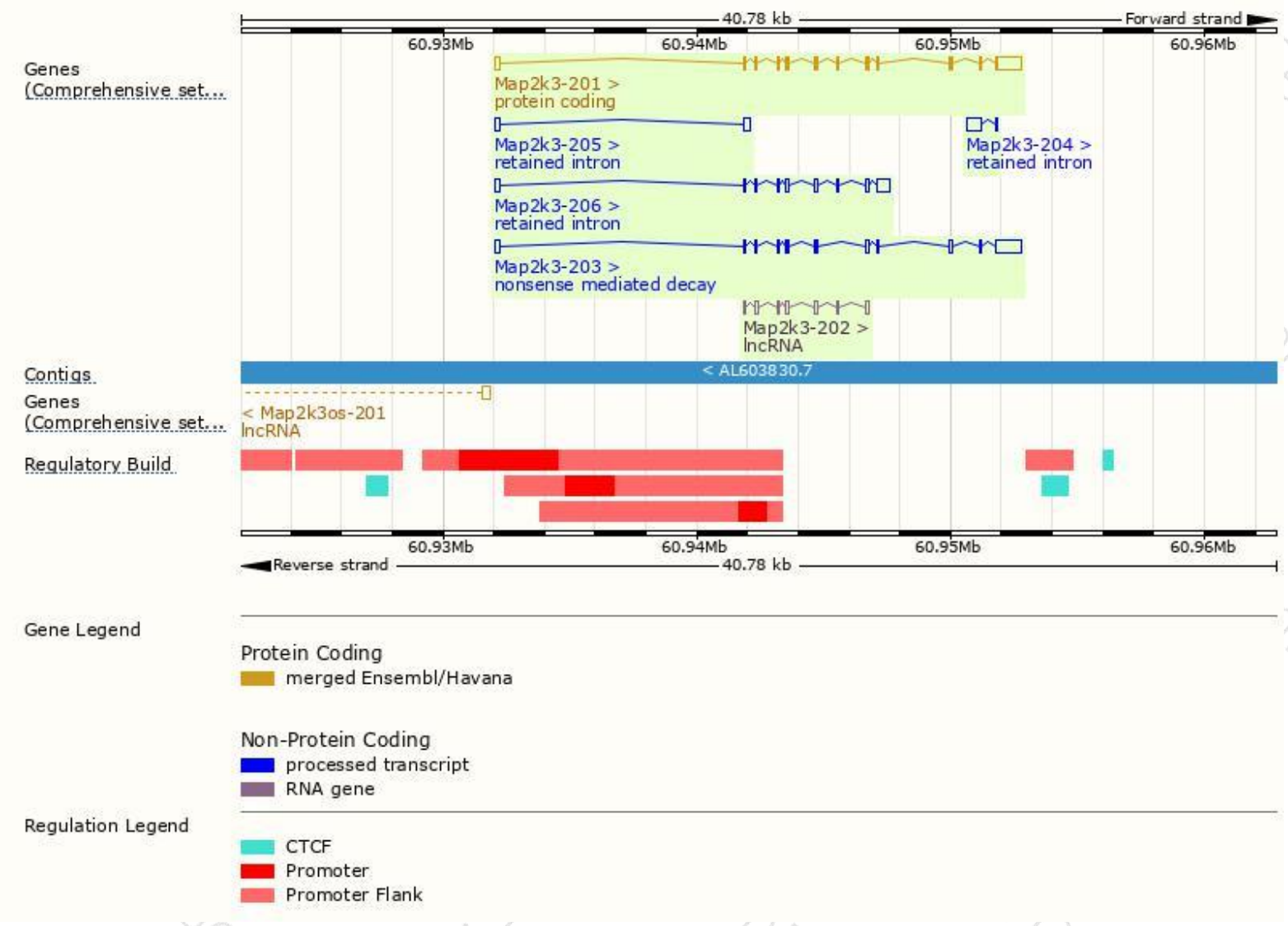
The gene has 6 transcripts,all transcripts are shown below:

| Name       | Transcript ID                        | bp   | Protein               | Biotype                 | CCDS                      | UniProt                       | Flags                         |
|------------|--------------------------------------|------|-----------------------|-------------------------|---------------------------|-------------------------------|-------------------------------|
| Map2k3-201 | <a href="#">ENSMUST00000019076.9</a> | 2198 | <a href="#">347aa</a> | Protein coding          | <a href="#">CCDS24804</a> | <a href="#">O09110 Q5SWN9</a> | TSL:1 GENCODE basic APPRIS P1 |
| Map2k3-203 | <a href="#">ENSMUST00000130269.1</a> | 2096 | <a href="#">173aa</a> | Nonsense mediated decay | -                         | <a href="#">A0A0R4J1Q6</a>    | TSL:1                         |
| Map2k3-206 | <a href="#">ENSMUST00000145828.7</a> | 1346 | No protein            | Retained intron         | -                         | -                             | TSL:1                         |
| Map2k3-204 | <a href="#">ENSMUST00000137609.1</a> | 600  | No protein            | Retained intron         | -                         | -                             | TSL:2                         |
| Map2k3-205 | <a href="#">ENSMUST00000137739.1</a> | 455  | No protein            | Retained intron         | -                         | -                             | TSL:2                         |
| Map2k3-202 | <a href="#">ENSMUST00000126043.1</a> | 694  | No protein            | lncRNA                  | -                         | -                             | TSL:5                         |

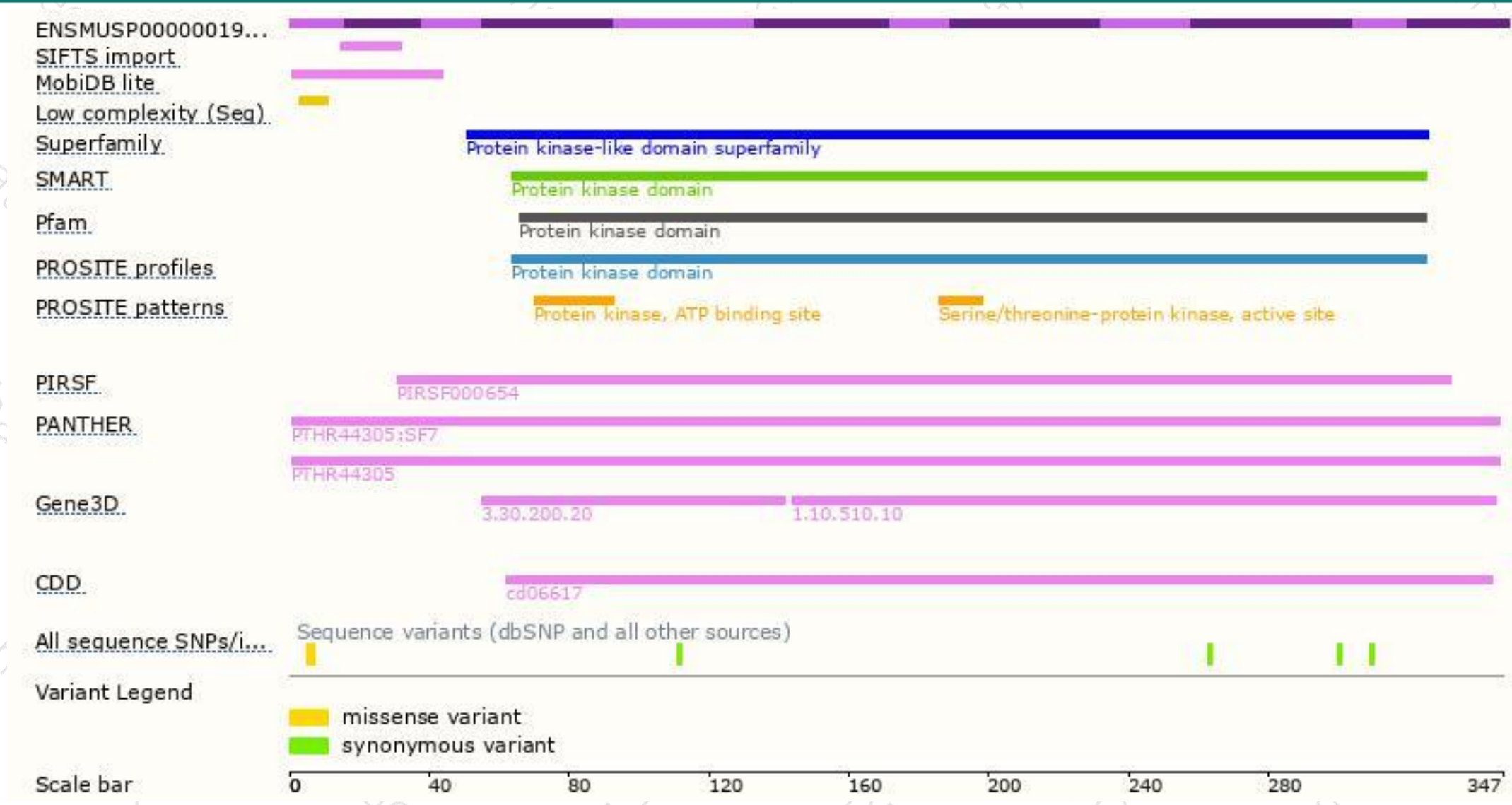
The strategy is based on the design of *Map2k3-201* transcript,The transcription is shown below



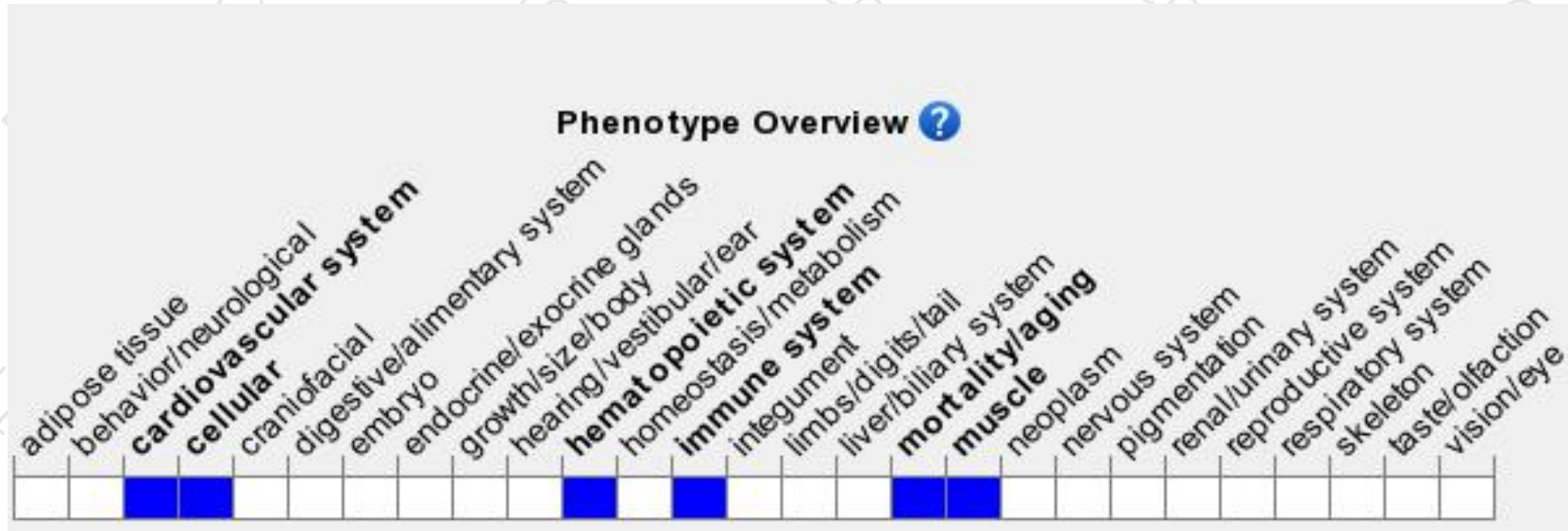
# Genomic location distribution



# 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 are viable and fertile but display abnormalities in cytokine production.

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

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