

Mapk3 Cas9-KO Strategy

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Project Overview

Project Name

Mapk3

Project type

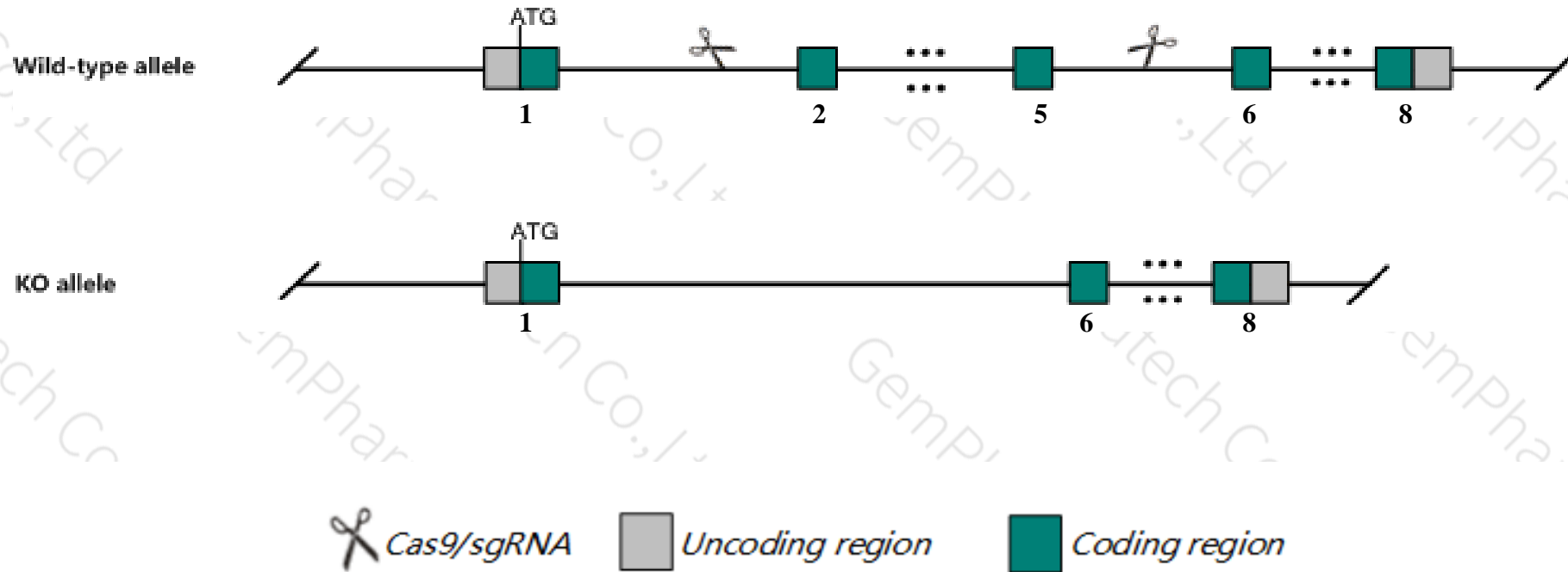
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk3* gene. The schematic diagram is as follows:



- The *Mapk3* gene has 8 transcripts. According to the structure of *Mapk3* gene, exon2-exon5 of *Mapk3-202* (ENSMUST00000057669.15) transcript is recommended as the knockout region. The region contains 605bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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, Mice homozygous for a targeted null mutation are hyperactive with impaired T cell maturation and proliferation. Mice homozygous for a knock-out allele on a CD-1 background exhibit normal Mendelian ratios, growth, and no obvious abnormalities.
- The knockout region is near to the N-terminal of *Gdpc3* gene, this strategy may influence the regulatory function of the N-terminal of *Gdpc3* gene.
- The *Mapk3* gene is located on the Chr7. 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)

Mapk3 mitogen-activated protein kinase 3 [Mus musculus (house mouse)]

Gene ID: 26417, updated on 19-Mar-2019

Summary



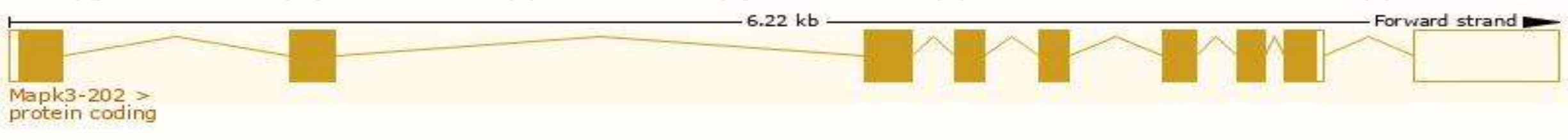
Official Symbol	Mapk3 provided by MGI
Official Full Name	mitogen-activated protein kinase 3 provided by MGI
Primary source	MGI:MGI:1346859
See related	Ensembl:ENSMUSG00000063065
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Erk-1, Erk1, Er12, Esrk1, Mnk1, Mtap2k, Prkm3, p44, p44erk1, p44mapk
Expression	Ubiquitous expression in colon adult (RPKM 245.8), large intestine adult (RPKM 217.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

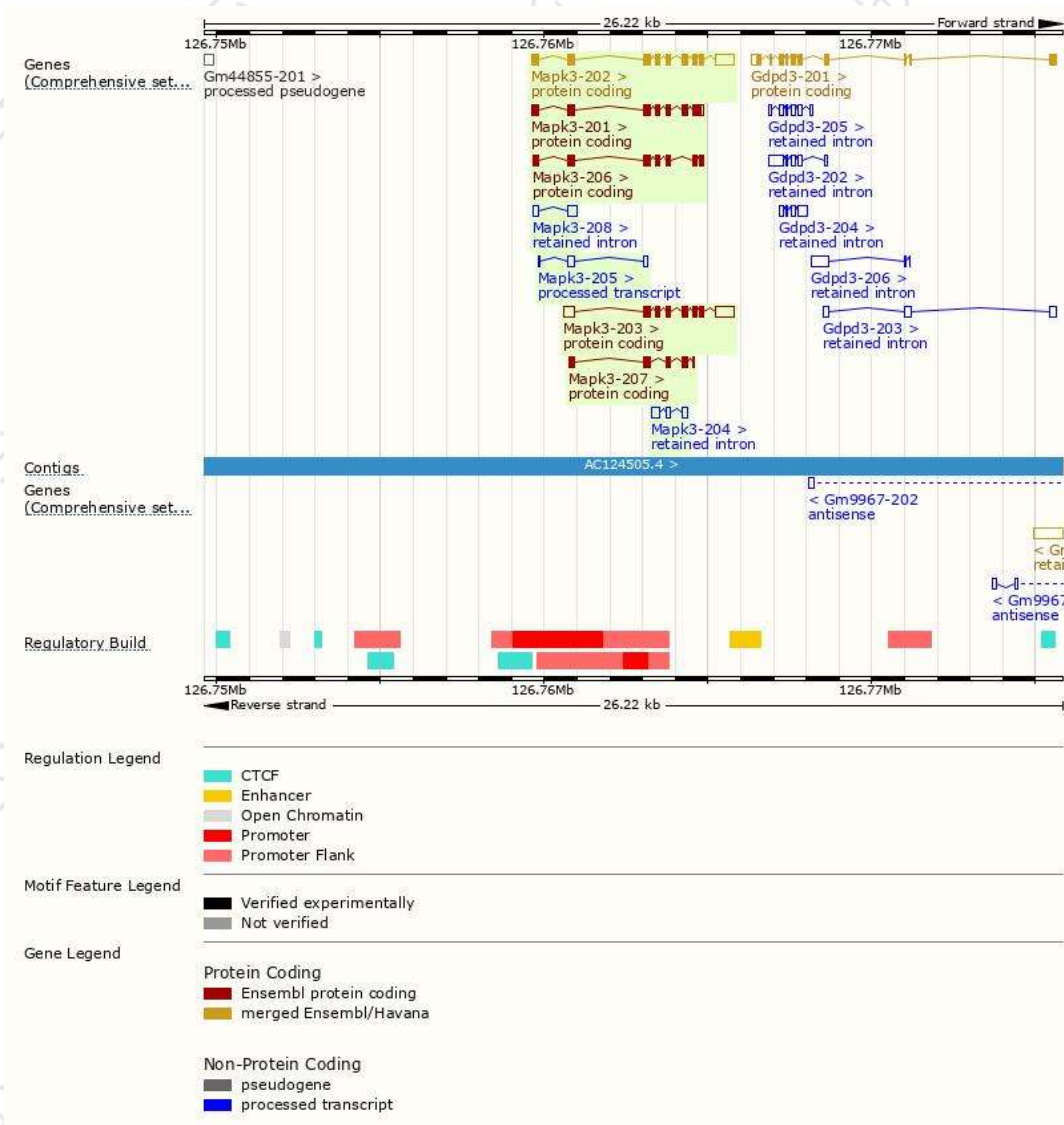
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk3-202	ENSMUST00000057669.15	1800	380aa	Protein coding	CCDS21841	Q63844	TSL:1 GENCODE basic APPRIS P2
Mapk3-203	ENSMUST00000091328.3	1716	265aa	Protein coding	-	D3Z6D8	TSL:1 GENCODE basic
Mapk3-201	ENSMUST00000050201.10	1267	380aa	Protein coding	-	D3Z3G6	TSL:3 GENCODE basic APPRIS ALT2
Mapk3-206	ENSMUST00000205657.1	1005	335aa	Protein coding	-	A0A0U1RPX4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 APPRIS ALT2
Mapk3-207	ENSMUST00000206272.1	641	214aa	Protein coding	-	A0A0U1RPZ0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mapk3-205	ENSMUST00000145965.1	337	No protein	Processed transcript	-	-	TSL:5
Mapk3-204	ENSMUST00000135649.1	480	No protein	Retained intron	-	-	TSL:3
Mapk3-208	ENSMUST00000206875.1	436	No protein	Retained intron	-	-	TSL:2

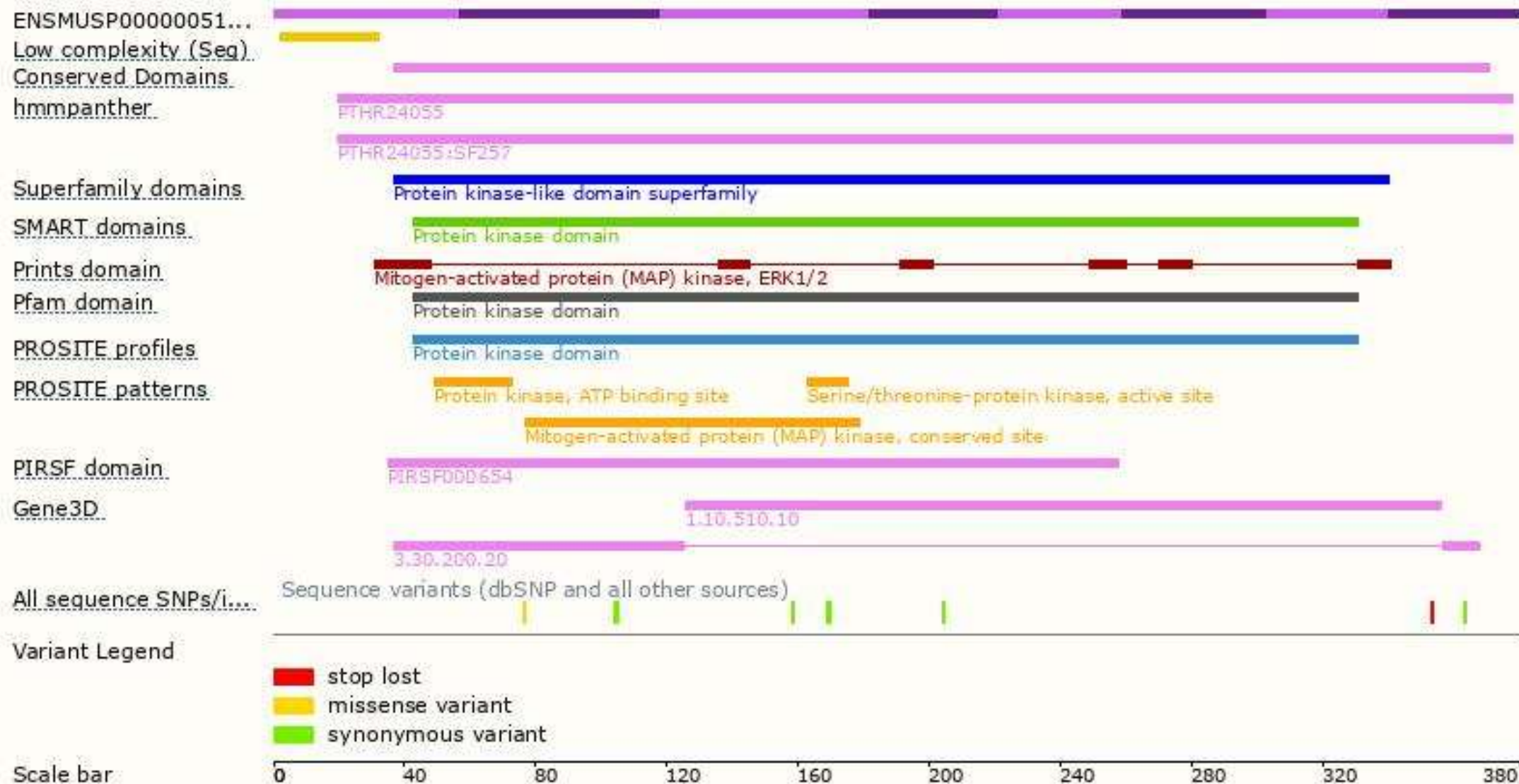
The strategy is based on the design of *Mapk3-202* transcript,The transcription is shown below



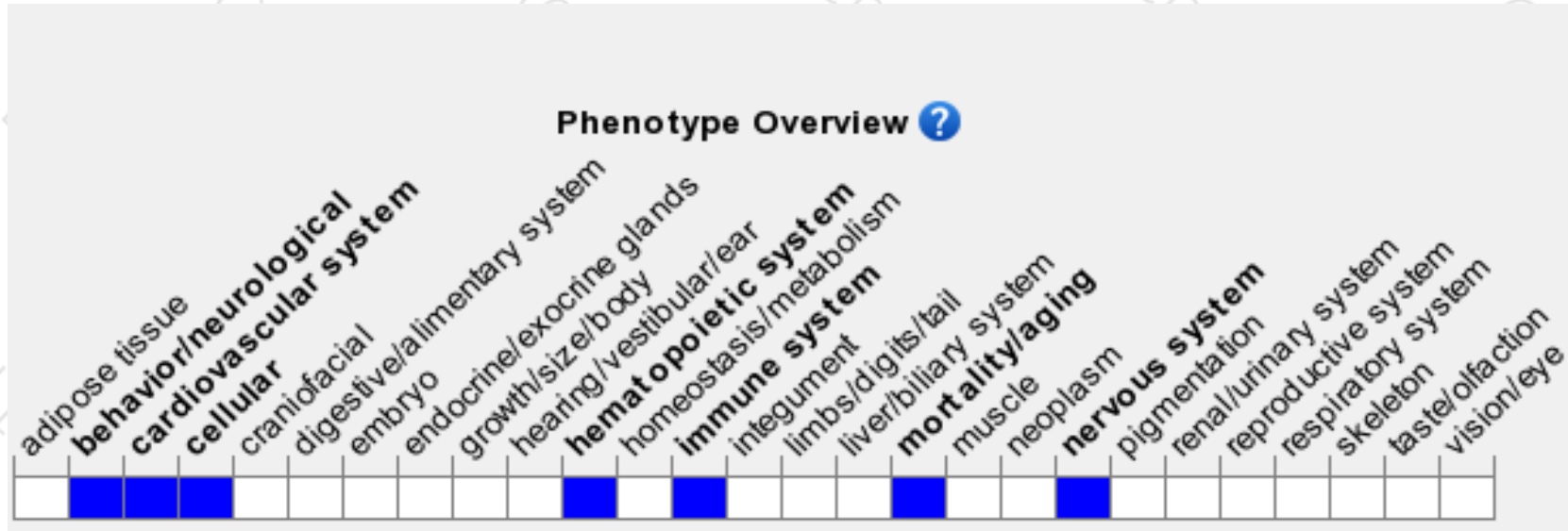
Genomic location distribution



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 a targeted null mutation are hyperactive with impaired T cell maturation and proliferation. Mice homozygous for a knock-out allele on a CD-1 background exhibit normal Mendelian ratios, growth, and no obvious abnormalities.

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

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