

***Mapk10* Cas9-KO Strategy**

Designer: Xiaojing Li
Design Date: 2019-9-19
Reviewer: JiaYu

Project Overview

Project Name

Mapk10

Project type

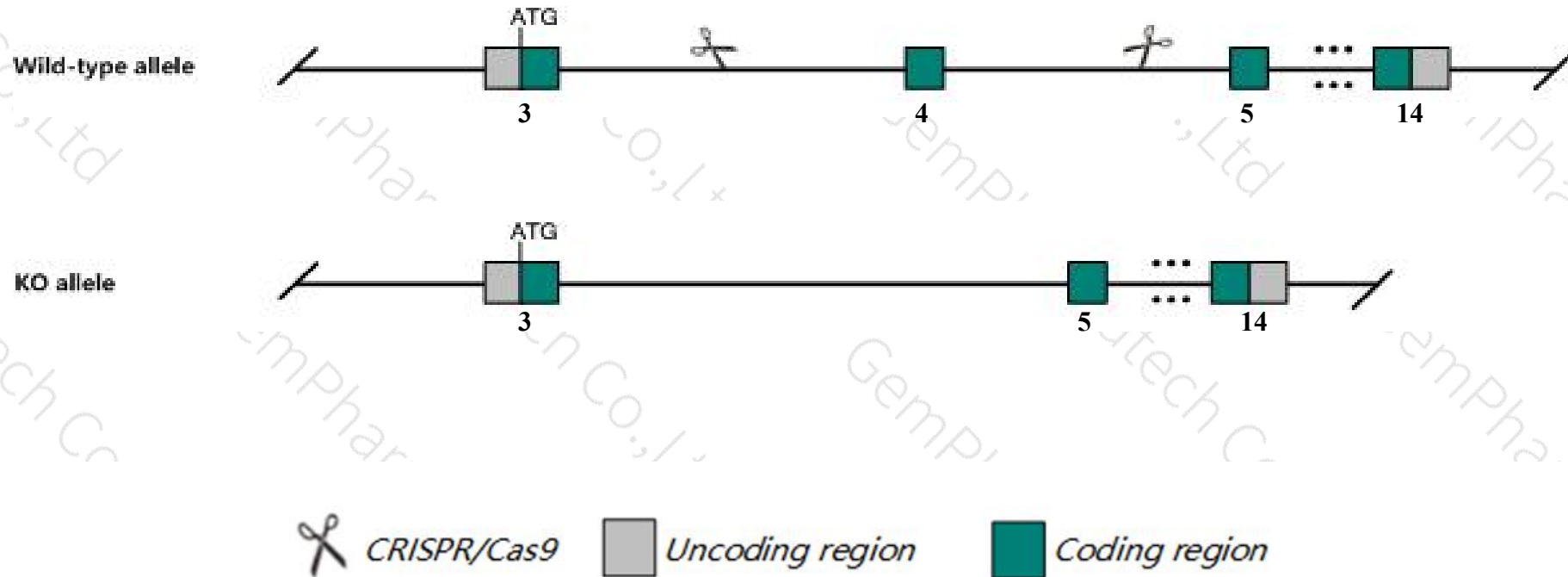
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk10* gene. The schematic diagram is as follows:



- The *Mapk10* gene has 13 transcripts. According to the structure of *Mapk10* gene, exon4 of *Mapk10-203* (ENSMUST00000112847.8) transcript is recommended as the knockout region. The region contains 170bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk10* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 disruptions in this gene display a normal phenotype. They are resistant to kainic acid induced seizures and show increased resistance to MPTP induced Parkinsons disease.
- The *Mapk10* gene is located on the Chr5. 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)

Mapk10 mitogen-activated protein kinase 10 [Mus musculus (house mouse)]

Gene ID: 26414, updated on 10-Feb-2019

Summary

Official Symbol Mapk10 provided by [MGI](#)

Official Full Name mitogen-activated protein kinase 10 provided by [MGI](#)

Primary source [MGI:MGI:1346863](#)

See related [Ensembl:ENSMUSG00000046709](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as C230008H04Rik, JNK3, JNK3B1, JNK3B2, SAPK(beta), Serk2, p493F12, p54bSAPK

Summary The protein encoded by this gene is a member of the MAP kinase family. MAP kinases act as integration points for multiple biochemical signals, and thus are involved in a wide variety of cellular processes, such as proliferation, differentiation, transcription regulation and development. This kinase is specifically expressed in a subset of neurons in the nervous system and is activated by threonine and tyrosine phosphorylation. Targeted deletion of this gene in mice suggests that it may have a role in stress-induced neuronal apoptosis. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. A recent study provided evidence for translational readthrough in this gene, and expression of an additional C-terminally extended isoform via the use of an alternative in-frame translation termination codon. [provided by RefSeq, Dec 2017]

Expression Biased expression in cortex adult (RPKM 28.0), frontal lobe adult (RPKM 20.7) and 7 other tissues [See more](#)

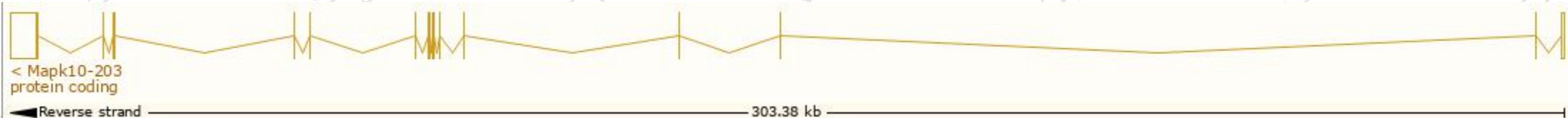
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

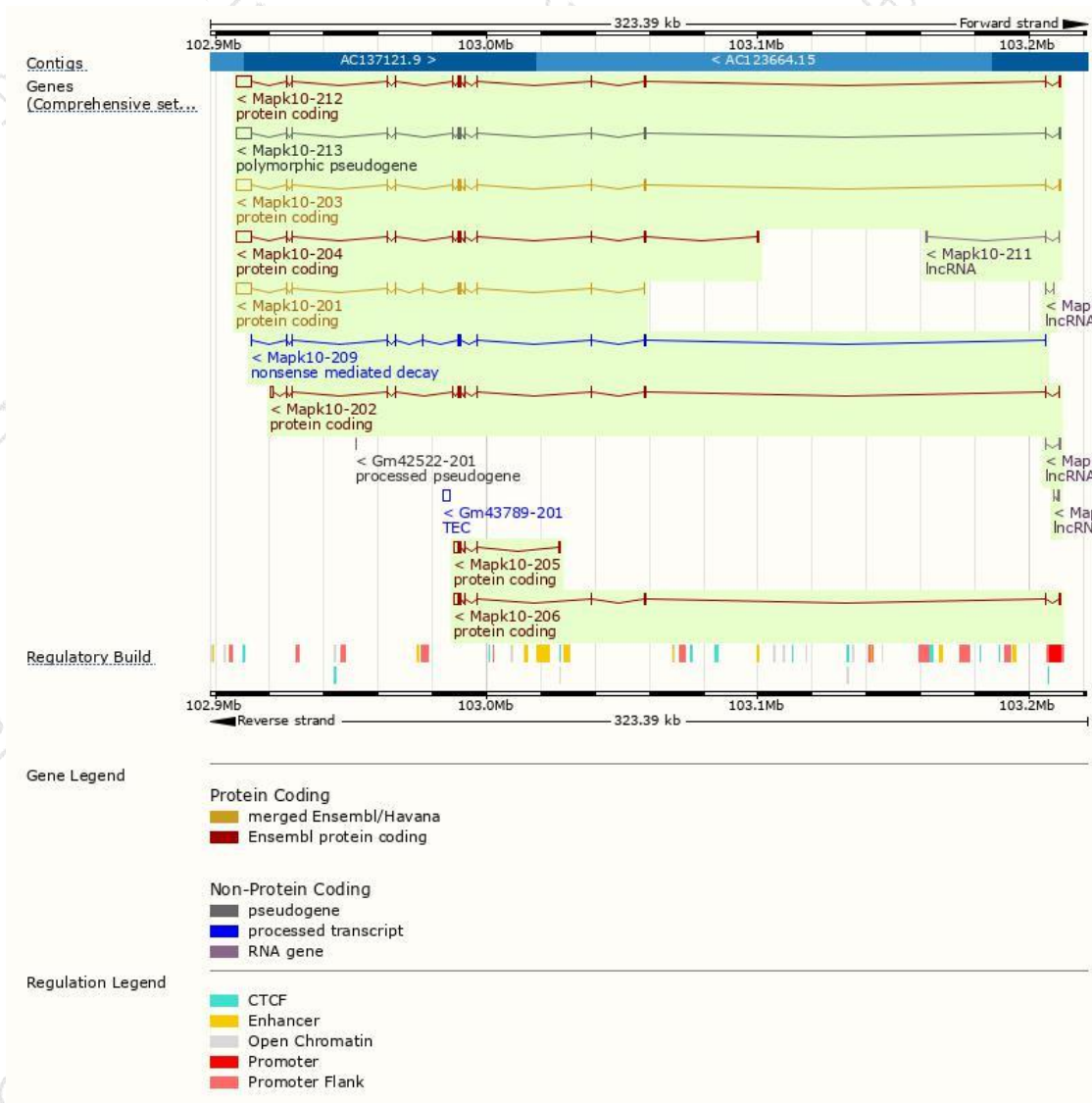
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk10-212	ENSMUST00000170792.8	7198	464aa	Protein coding	CCDS39185	Q80W82	TSL:1 GENCODE basic APPRIS P3
Mapk10-203	ENSMUST00000112847.8	7196	464aa	Protein coding	CCDS39185	Q8C9D4	TSL:1 GENCODE basic APPRIS P3
Mapk10-201	ENSMUST00000086854.9	6630	464aa	Protein coding	CCDS80350	Q80W80	TSL:1 GENCODE basic APPRIS ALT 1
Mapk10-204	ENSMUST00000112848.7	6761	494aa	Protein coding	-	E9QN59	TSL:1 GENCODE basic
Mapk10-206	ENSMUST00000133069.7	2732	252aa	Protein coding	-	A0A0G2JGL2	TSL:2 GENCODE basic
Mapk10-202	ENSMUST00000112846.7	2617	418aa	Protein coding	-	Q3TQZ7	TSL:1 GENCODE basic
Mapk10-205	ENSMUST00000128869.7	2518	178aa	Protein coding	-	A0A0G2JG69	TSL:1 GENCODE basic
Mapk10-209	ENSMUST00000141573.7	1502	173aa	Nonsense mediated decay	-	A0A0G2JEJ8	TSL:5
Mapk10-213	ENSMUST00000238446.1	7196	478aa	Polymorphic pseudogene	-	-	GENCODE basic
Mapk10-211	ENSMUST00000152609.1	968	No protein	lncRNA	-	-	TSL:1
Mapk10-207	ENSMUST00000135134.1	342	No protein	lncRNA	-	-	TSL:3
Mapk10-208	ENSMUST00000136595.1	300	No protein	lncRNA	-	-	TSL:3
Mapk10-210	ENSMUST00000142444.1	265	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Mapk10-203* transcript,The transcription is shown below



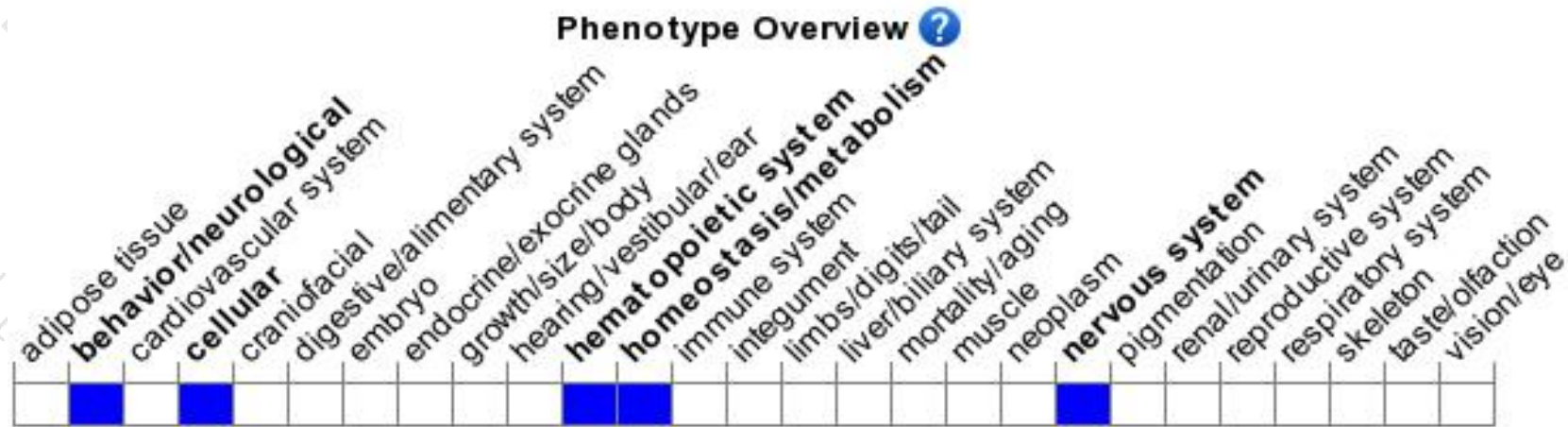
Genomic location distribution



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 display a normal phenotype. They are resistant to kainic acid induced seizures and show increased resistance to MPTP induced Parkinsons disease.

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

Tel: 400-9660890

