

# ***Mapk10* Cas9-CKO Strategy**

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# Project Overview

**Project Name**

***Mapk10***

**Project type**

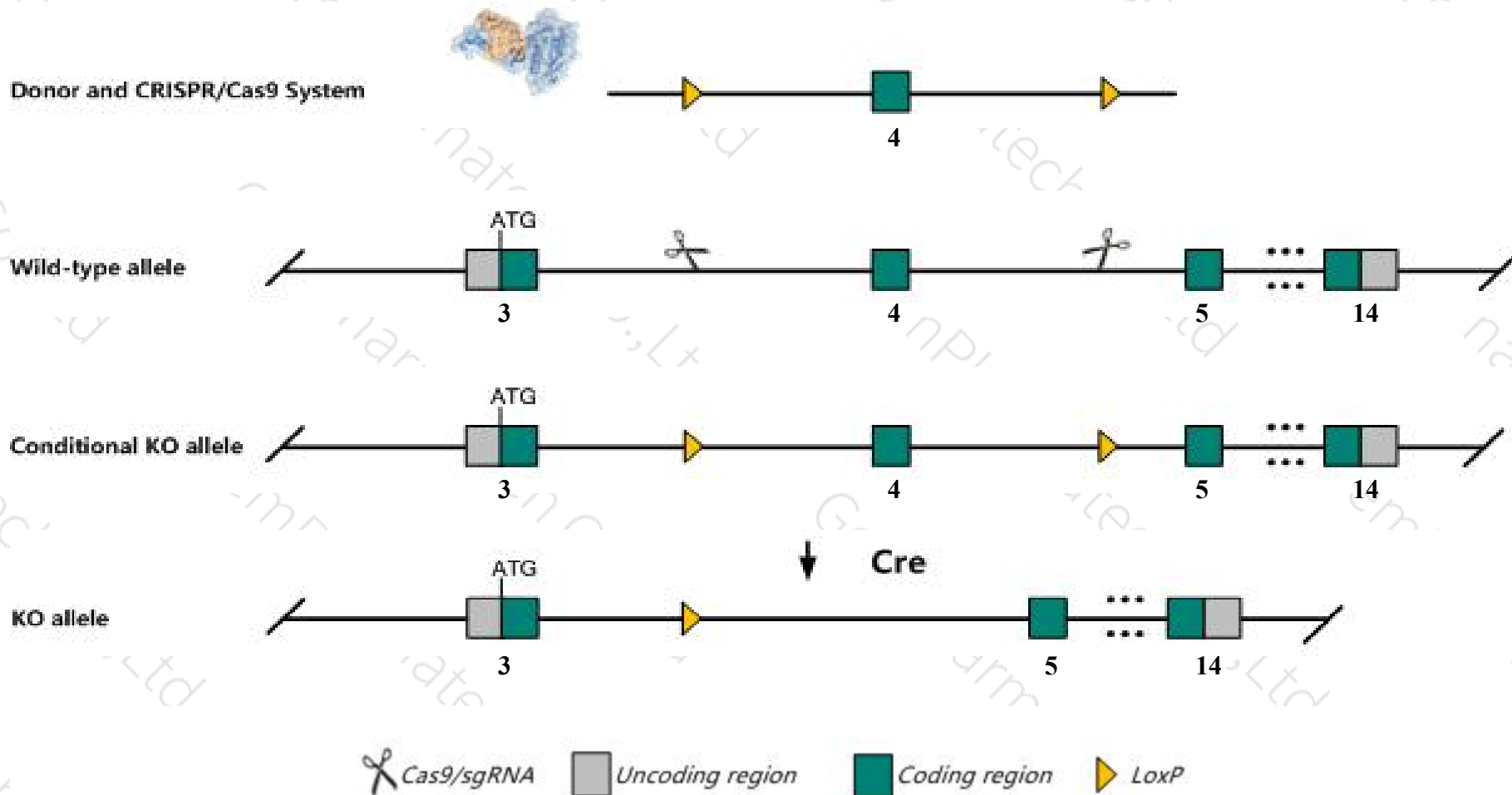
**Cas9-CKO**

**Strain background**

**C57BL/6J**

# Conditional Knockout strategy

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



# Technical routes

- 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: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

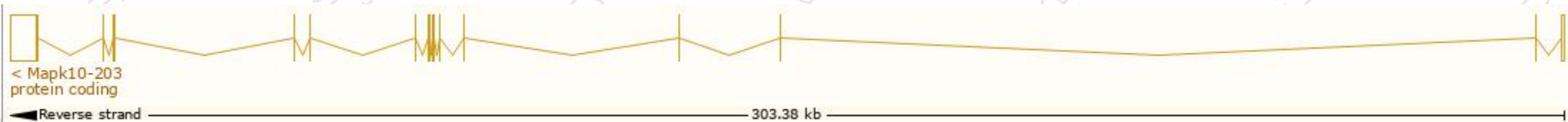
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

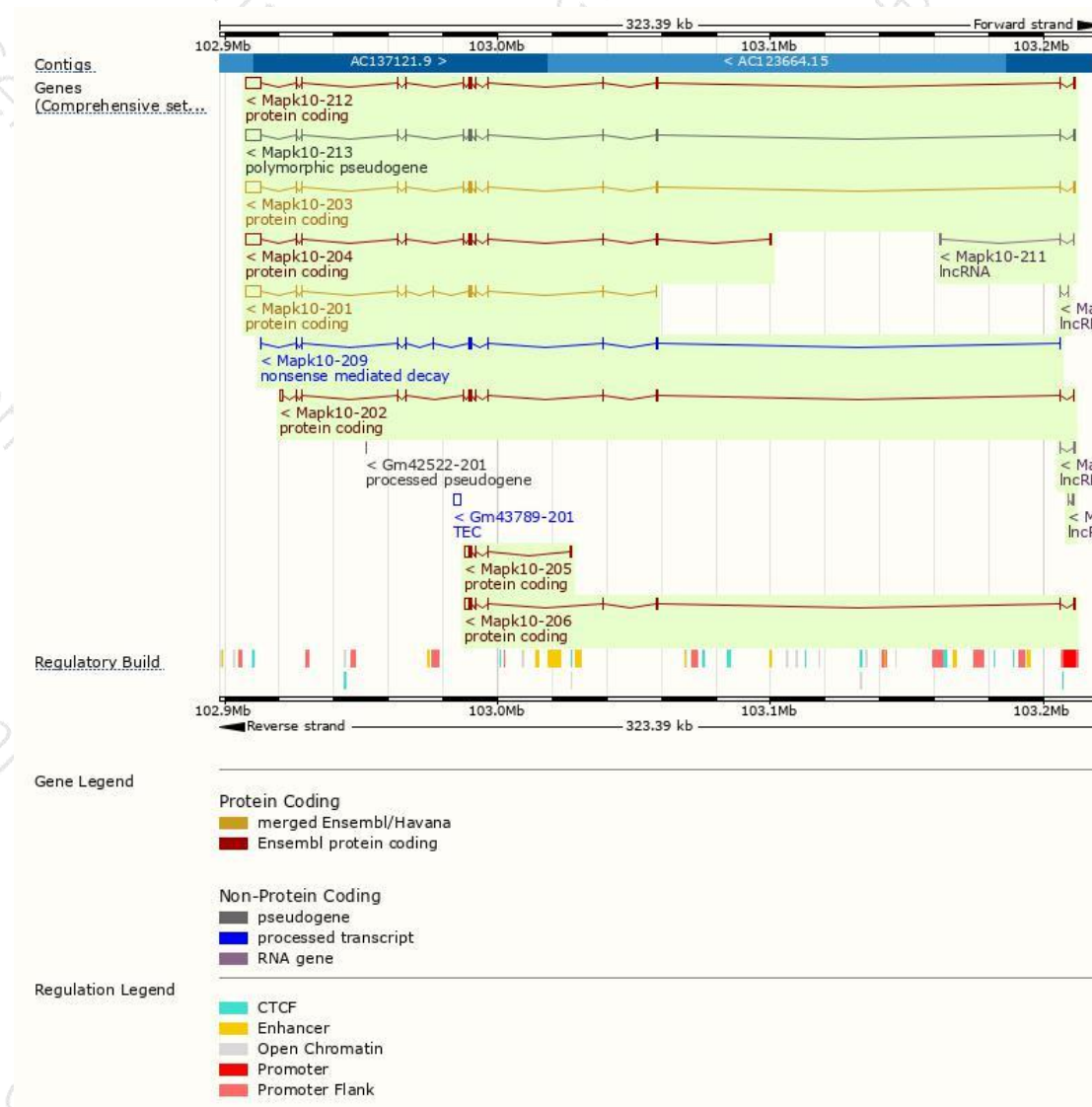
The gene has 13 transcripts,all transcripts are shown below:

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

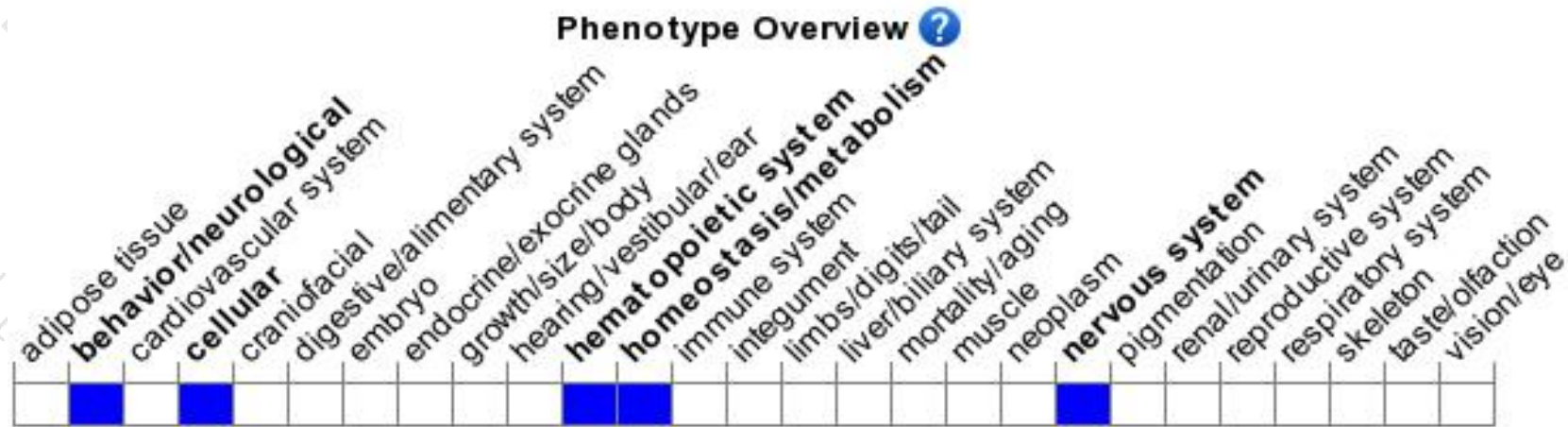




# Protein domain



# 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.

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