

***Mapk12* Cas9-KO Strategy**

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Project Overview

Project Name

Mapk12

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk12* gene. The schematic diagram is as follows:



- The *Mapk12* gene has 7 transcripts. According to the structure of *Mapk12* gene, exon3-exon11 of *Mapk12-201* (ENSMUST00000088827.7) transcript is recommended as the knockout region. The region contains 769bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk12* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice are viable and fertile with no obvious abnormalities. Mice homozygous for a conditional allele activated in muscle cell exhibit decreased endurance exercise-induced mitochondrial biogenesis and angiogenesis.
- The *Mapk12* gene is located on the Chr15. 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)

Mapk12 mitogen-activated protein kinase 12 [Mus musculus (house mouse)]

Gene ID: 29857, updated on 2-Apr-2019

Summary



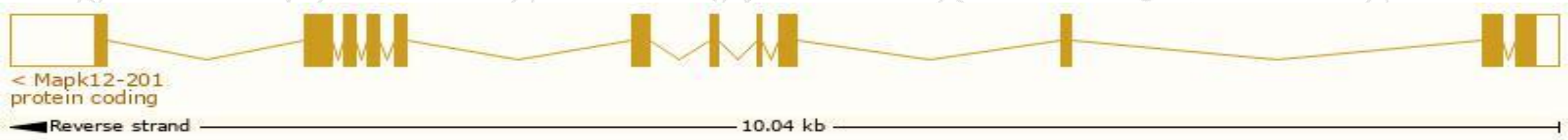
Official Symbol	Mapk12 provided by MGI
Official Full Name	mitogen-activated protein kinase 12 provided by MGI
Primary source	MGI:MGI:1353438
See related	Ensembl:ENSMUSG00000022610
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW123708, Erk6, P38gamma, Prkm12, Sapk3
Expression	Broad expression in cerebellum adult (RPKM 12.5), bladder adult (RPKM 9.4) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

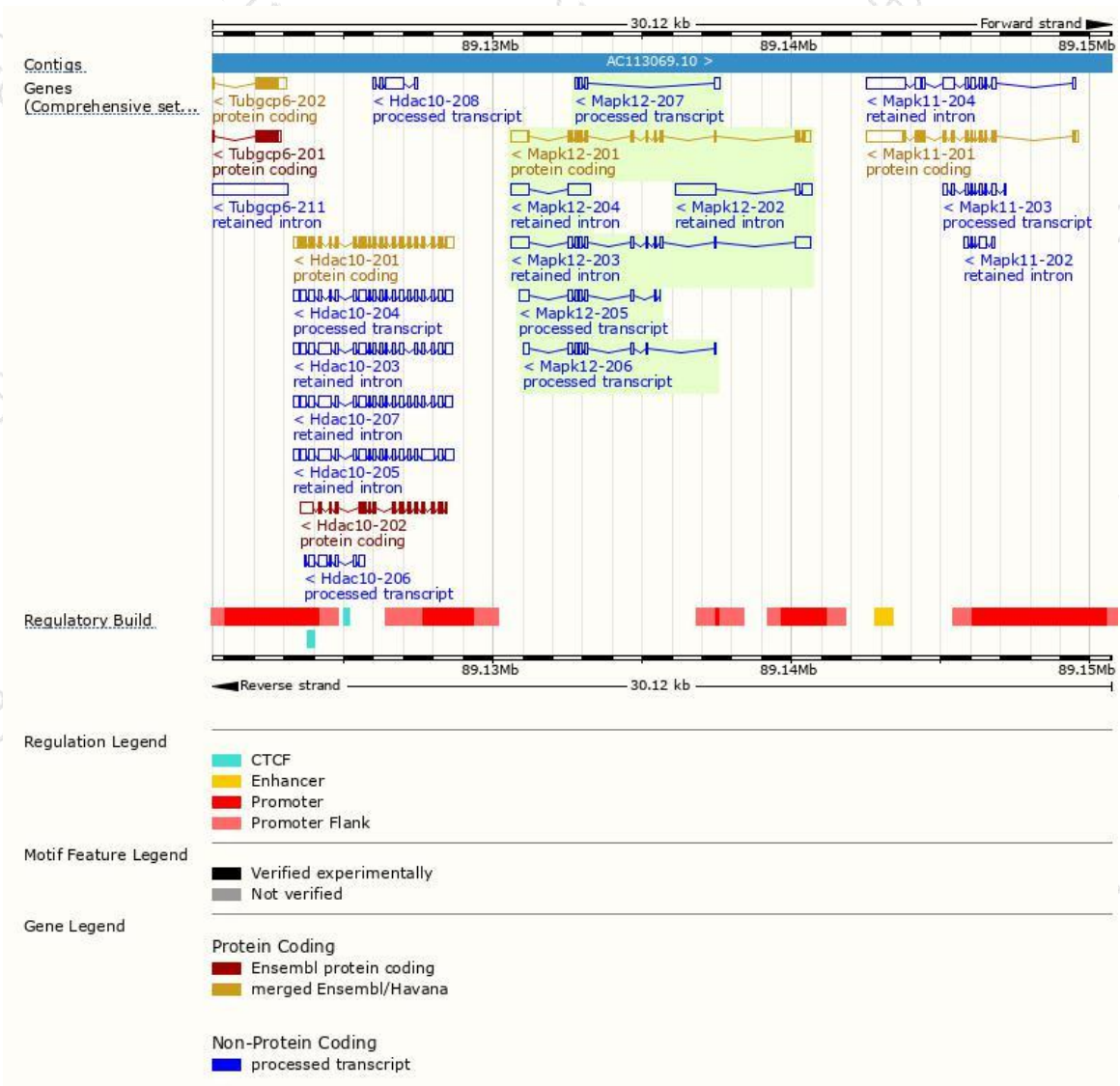
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk12-201	ENSMUST00000088827.7	1808	367aa	Protein coding	CCDS27740	Q08911	TSL:1 GENCODE basic APPRIS P1
Mapk12-205	ENSMUST00000230509.1	930	No protein	Processed transcript	-	-	
Mapk12-206	ENSMUST00000231014.1	793	No protein	Processed transcript	-	-	
Mapk12-207	ENSMUST00000231056.1	445	No protein	Processed transcript	-	-	
Mapk12-203	ENSMUST00000230266.1	1928	No protein	Retained intron	-	-	
Mapk12-202	ENSMUST00000229193.1	1832	No protein	Retained intron	-	-	
Mapk12-204	ENSMUST00000230352.1	1423	No protein	Retained intron	-	-	

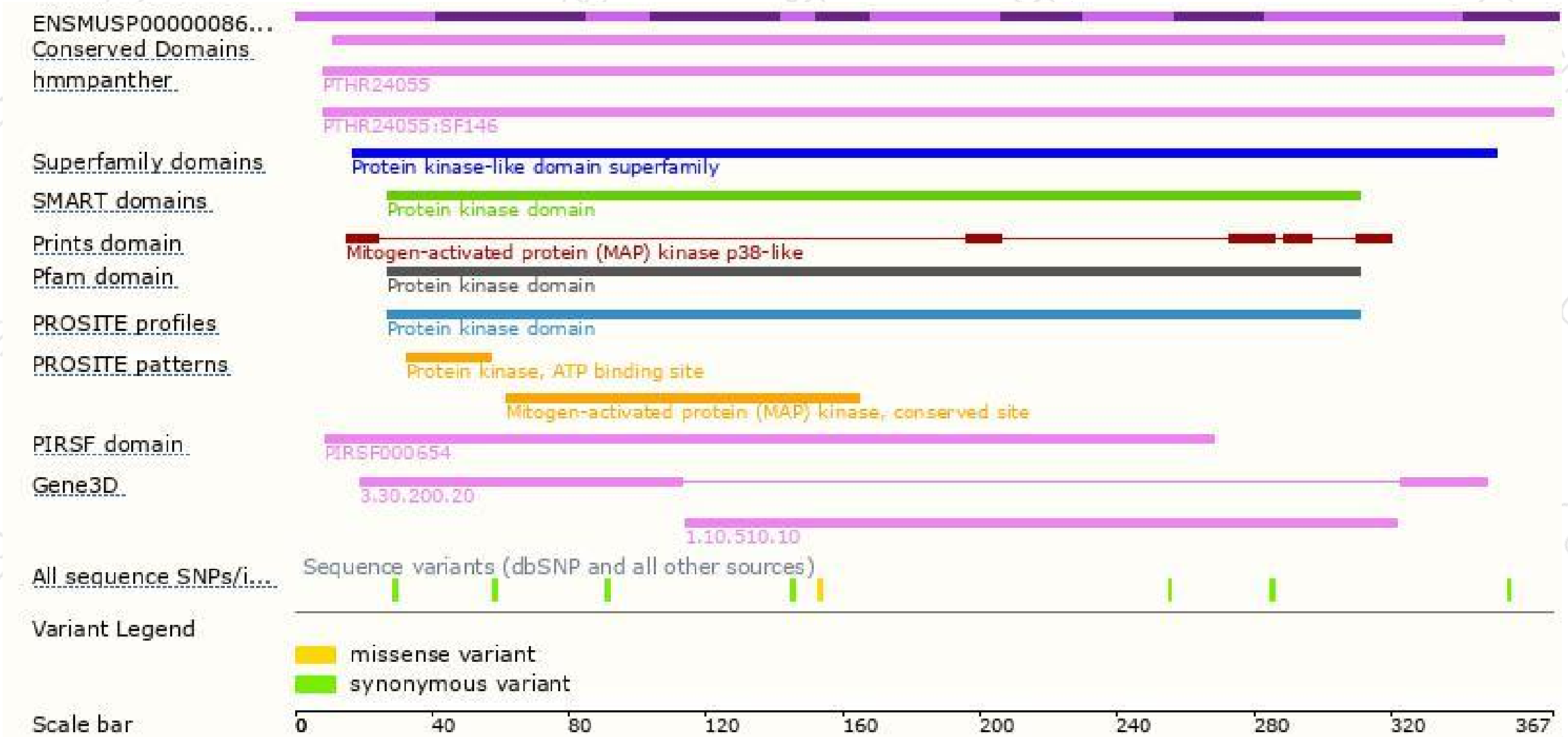
The strategy is based on the design of *Mapk12-201* transcript,The transcription is shown below



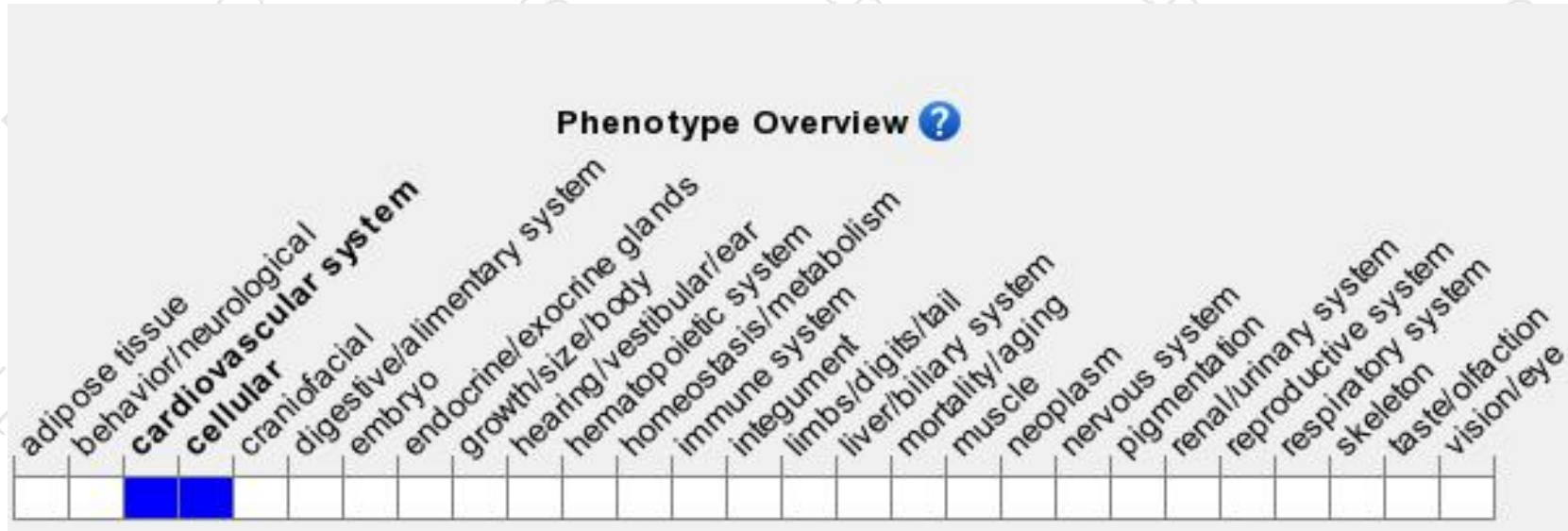
Genomic location distribution



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 null mice are viable and fertile with no obvious abnormalities. Mice homozygous for a conditional allele activated in muscle cell exhibit decreased endurance exercise-induced mitochondrial biogenesis and angiogenesis.

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

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