

Mcf2 Cas9-KO Strategy

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Project Overview

Project Name

Mcf2

Project type

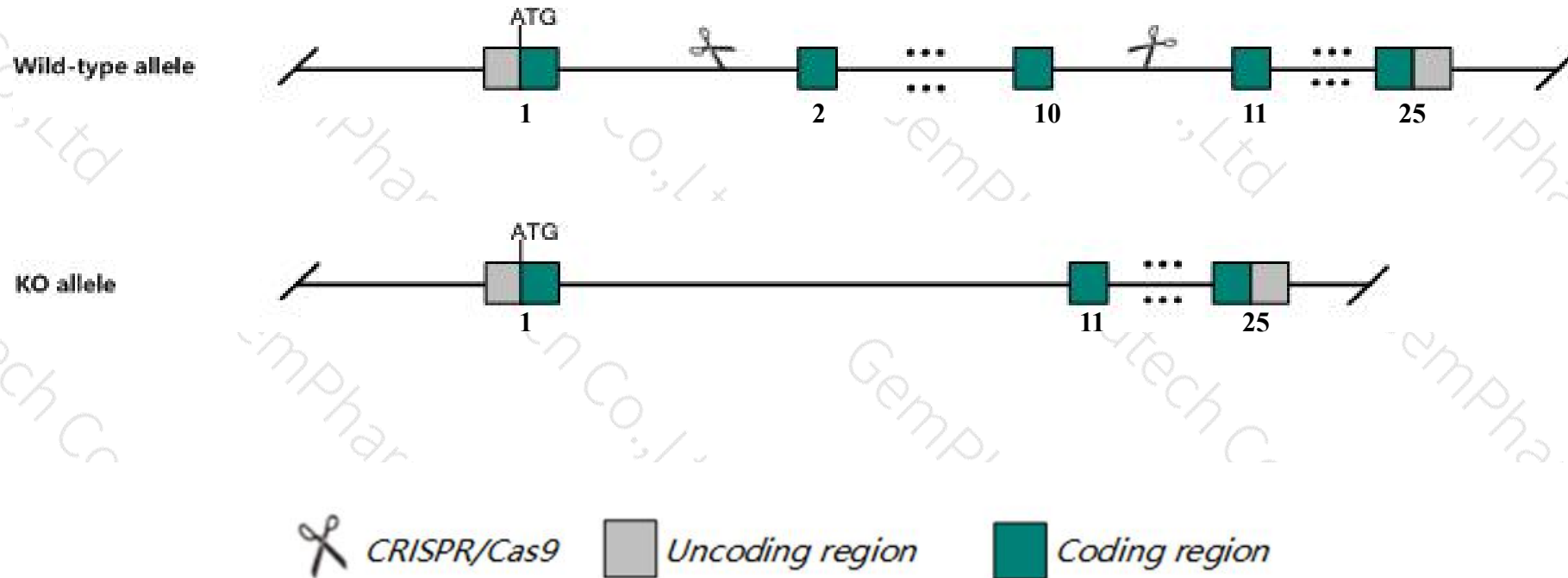
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcf2* gene. The schematic diagram is as follows:



- The *Mcf2* gene has 4 transcripts. According to the structure of *Mcf2* gene, exon2-exon10 of *Mcf2*-203 (ENSMUST00000101531.9) transcript is recommended as the knockout region. The region contains 1312bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mcf2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous and hemizygous null mice are viable, fertile and behaviorally normal, exhibit normal gonad and brain development and neuronal migration, but show a significant reduction of basal dendritic length in distinct subpopulations of cortical pyramidal neurons.
- The *Mcf2* gene is located on the ChrX. 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)

Mcf2 mcf.2 transforming sequence [Mus musculus (house mouse)]

Gene ID: 109904, updated on 31-Jan-2019

Summary



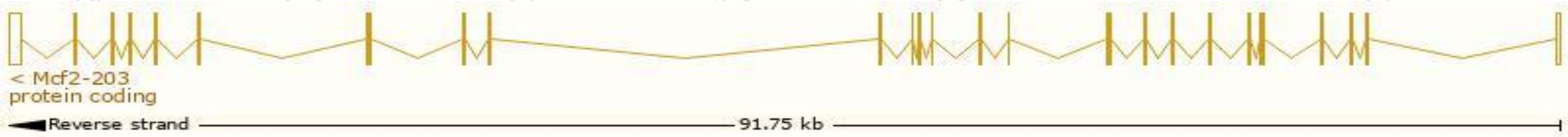
Official Symbol	Mcf2 provided by MGI
Official Full Name	mcf.2 transforming sequence provided by MGI
Primary source	MGI:MGI:96932
See related	Ensembl:ENSMUSG000000031139
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B230117G22Rik, Dbl, Mcf-2
Expression	Biased expression in cerebellum adult (RPKM 1.2), cortex adult (RPKM 0.7) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

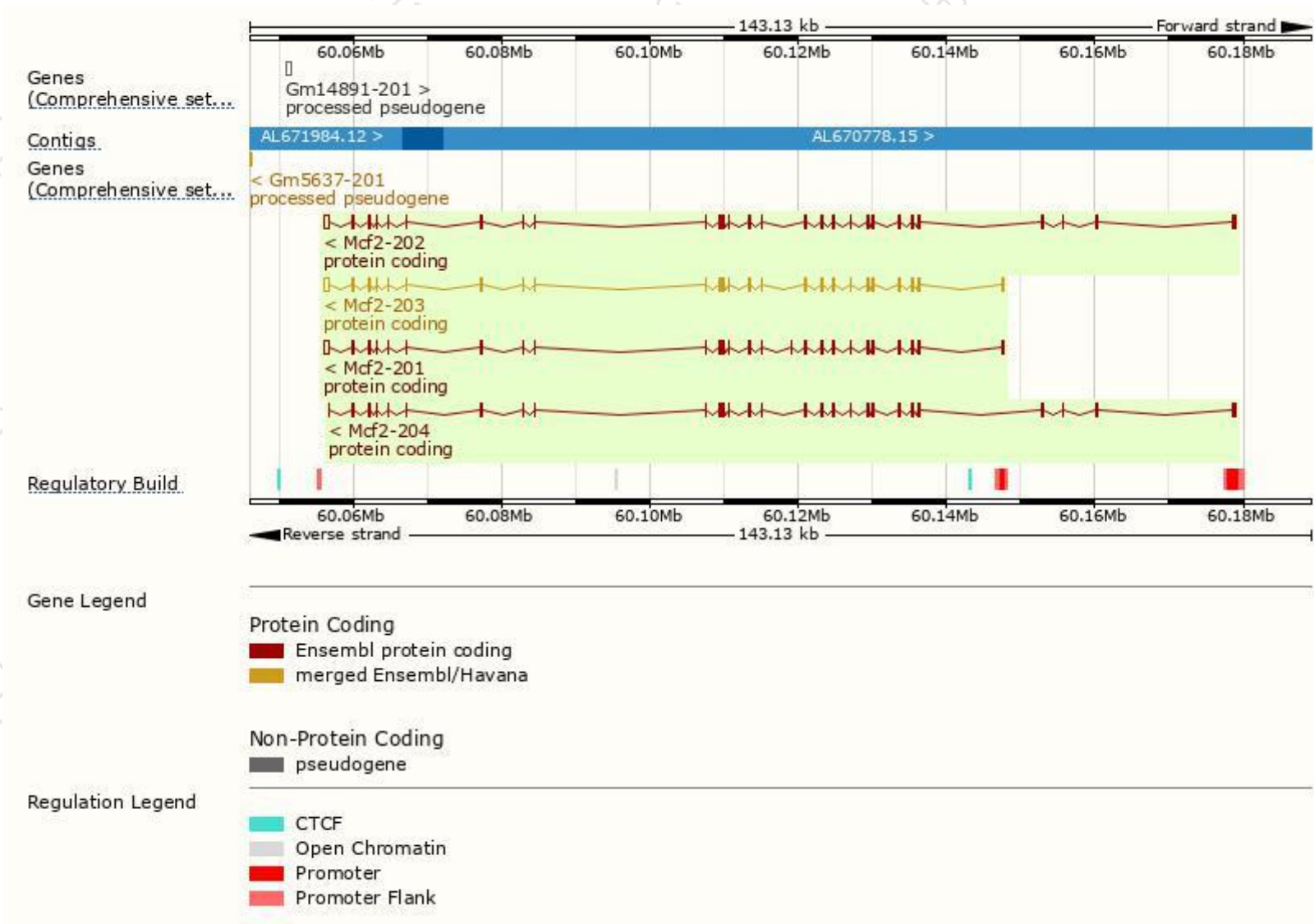
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcf2-203	ENSMUST00000101531.9	3671	928aa	Protein coding	CCDS30160	Q8C067	TSL:1 GENCODE basic APPRIS P3
Mcf2-201	ENSMUST00000033478.4	3659	944aa	Protein coding	CCDS81129	A2AET8	TSL:1 GENCODE basic APPRIS ALT2
Mcf2-204	ENSMUST00000228150.1	3336	1111aa	Protein coding	CCDS72384	A0A2I3BR92	GENCODE basic APPRIS ALT2
Mcf2-202	ENSMUST00000063507.10	4227	1031aa	Protein coding	-	Q8BLE2	TSL:1 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Mcf2-203* transcript,The transcription is shown below



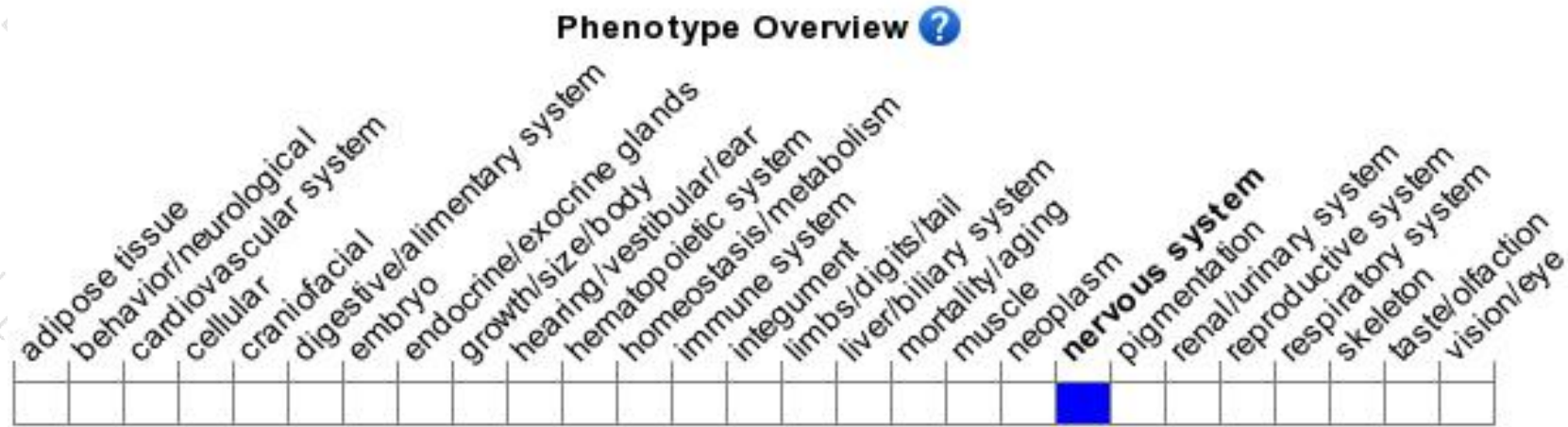
Genomic location distribution



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, Homozygous and hemizygous null mice are viable, fertile and behaviorally normal, exhibit normal gonad and brain development and neuronal migration, but show a significant reduction of basal dendritic length in distinct subpopulations of cortical pyramidal neurons.

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

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