Map3k10 Cas9-KO Strategy

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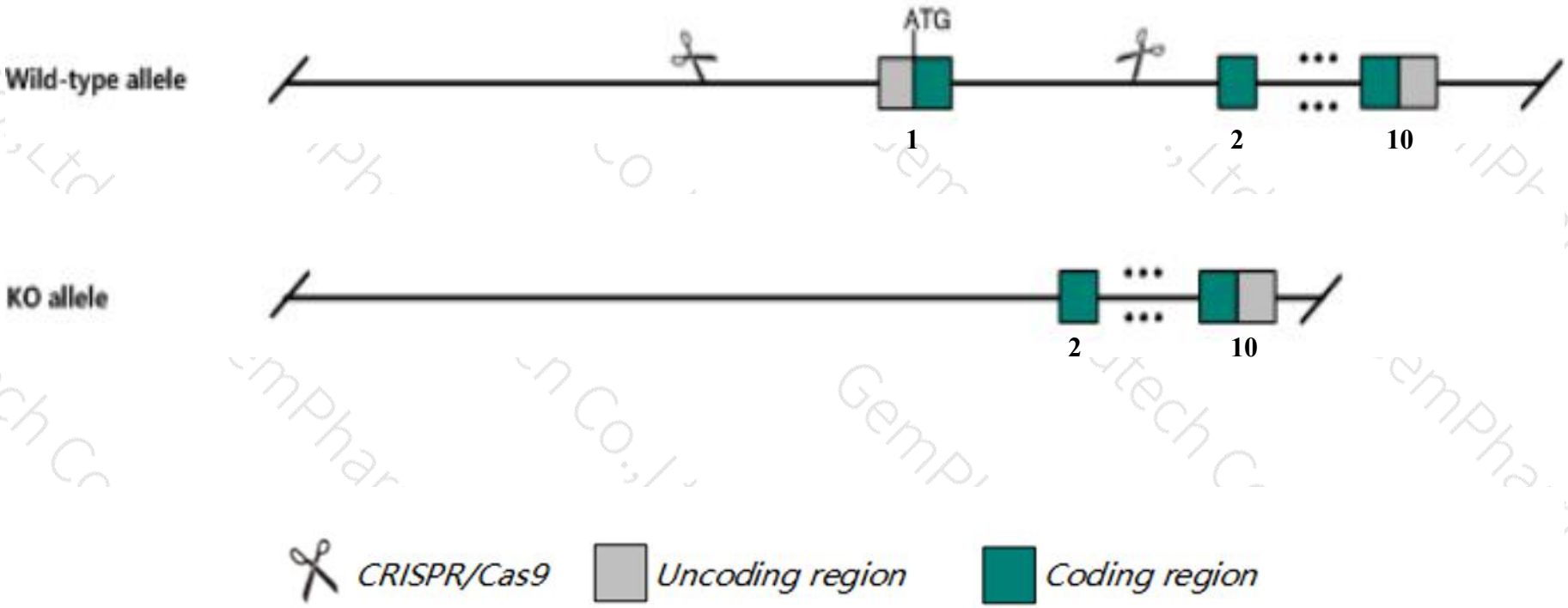
Project Overview

Project Name	***Map3k10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map3k10* gene. The schematic diagram is as follows:



Technical routes

➢ The *Map3k10* gene has 5 transcripts. According to the structure of *Map3k10* gene, exon1 of *Map3k10-201* (ENSMUST00000036453.13) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Map3k10* gene. The brief process is as follows: CRISPR/Cas9 syst

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit normal development, reproduction and lifespan.
- *Gm44684* will be deleted.
- The *Map3k10* 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）

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Map3k10 mitogen-activated protein kinase kinase kinase 10 [Mus musculus (house mouse)]

Gene ID: 269881, updated on 13-Mar-2020

Summary

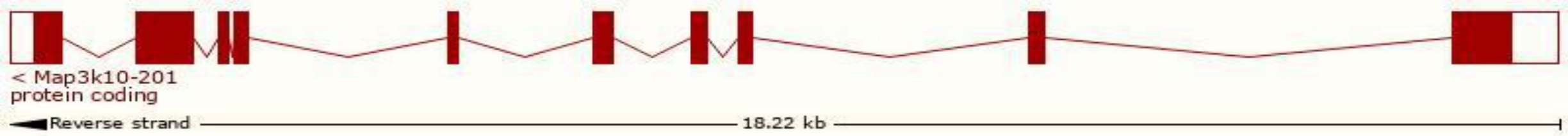
Official Symbol	Map3k10 provided by MGI
Official Full Name	mitogen-activated protein kinase kinase kinase 10 provided byMGI
Primary source	MGI:MGI:1346879
See related	Ensembl:ENSMUSG00000040390
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC028668, BC046514, MST, Mlk2
Expression	Ubiquitous expression in cortex adult (RPKM 23.3), frontal lobe adult (RPKM 19.8) and 25 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

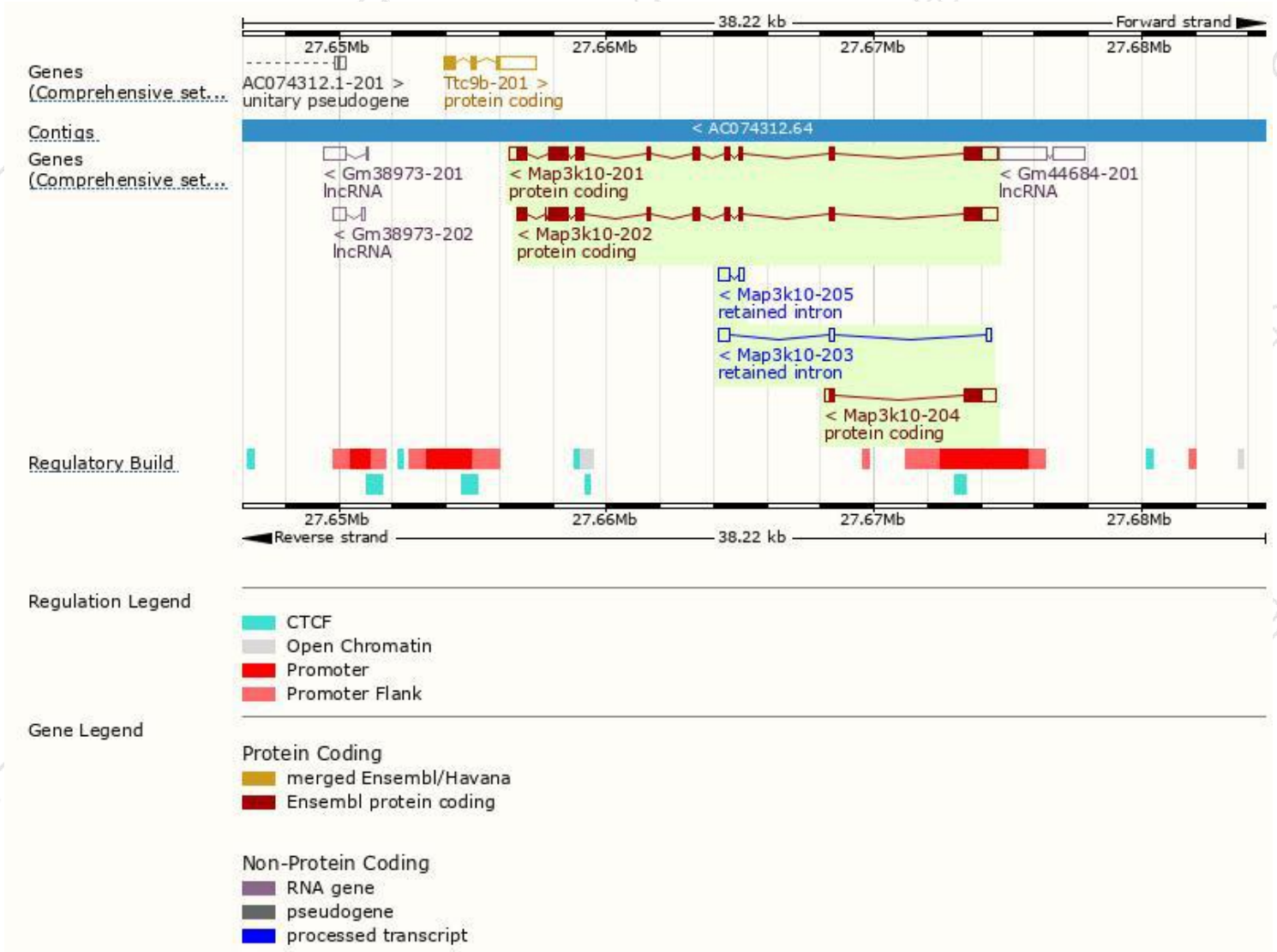
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map3k10-201	ENSMUST00000036453.13	3682	940aa	Protein coding	CCDS39850	Q66L42	TSL:1 GENCODE basic APPRIS P2
Map3k10-202	ENSMUST00000108341.1	3403	942aa	Protein coding	-	D3YXM8	TSL:5 GENCODE basic APPRIS ALT2
Map3k10-204	ENSMUST00000138243.1	1621	289aa	Protein coding	-	A0A0U1RQ74	TSL:1 GENCODE basic
Map3k10-203	ENSMUST00000133551.1	712	No protein	Retained intron	-	-	TSL:3
Map3k10-205	ENSMUST00000152032.1	574	No protein	Retained intron	-	-	TSL:2

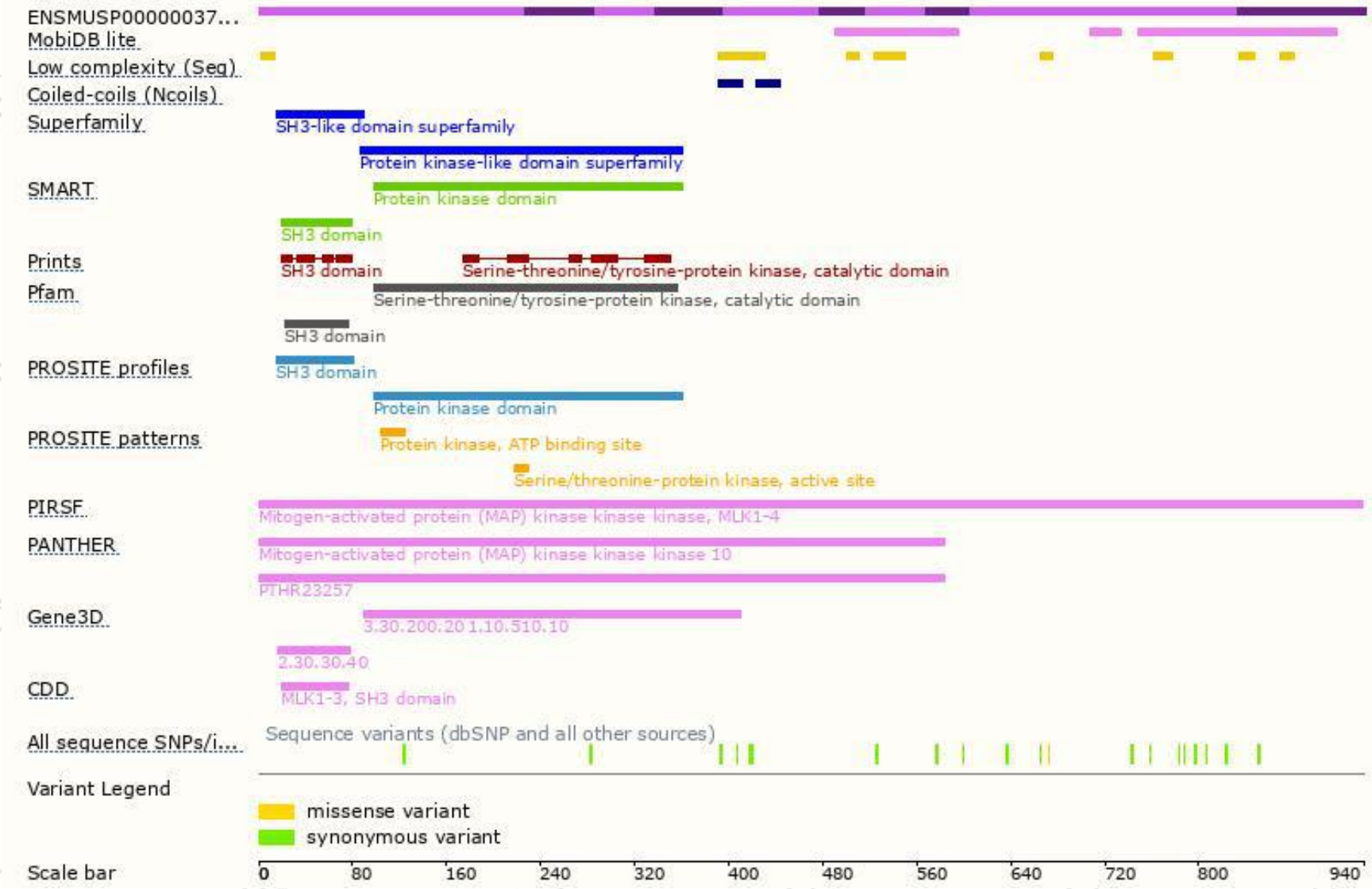
The strategy is based on the design of *Map3k10-201* transcript,the transcription is shown below:



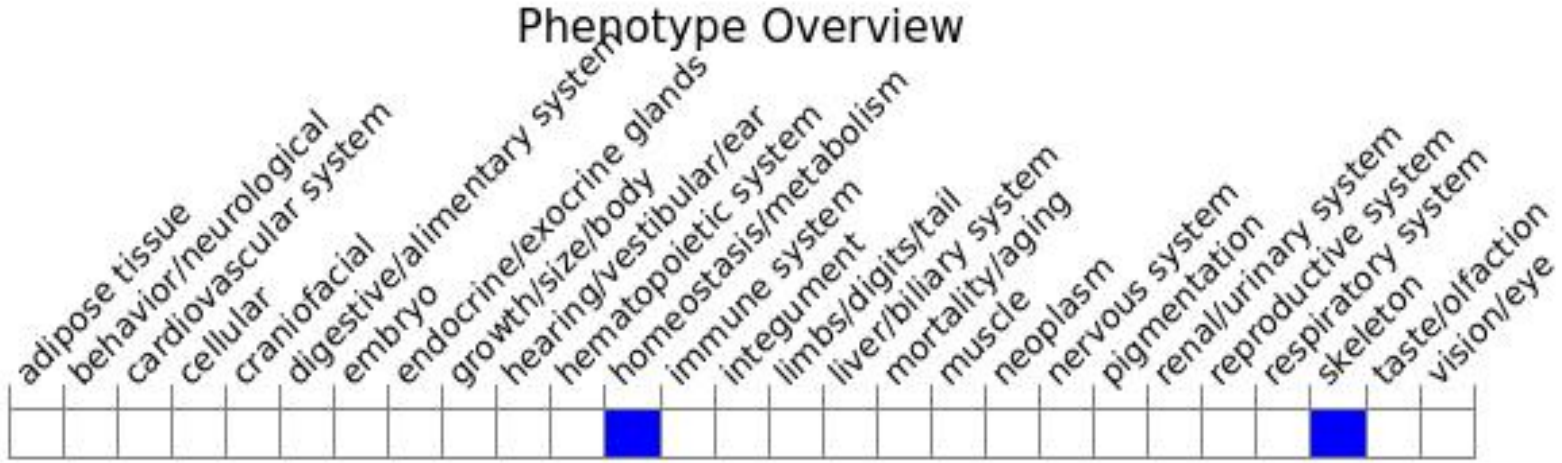
Genomic location distribution



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,mice homozygous for a null allele exhibit normal development, reproduction and lifespan.

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

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