Mapk14 Cas9-KO Strategy

Designer: Jing Jin

Reviewer: Yang Zeng

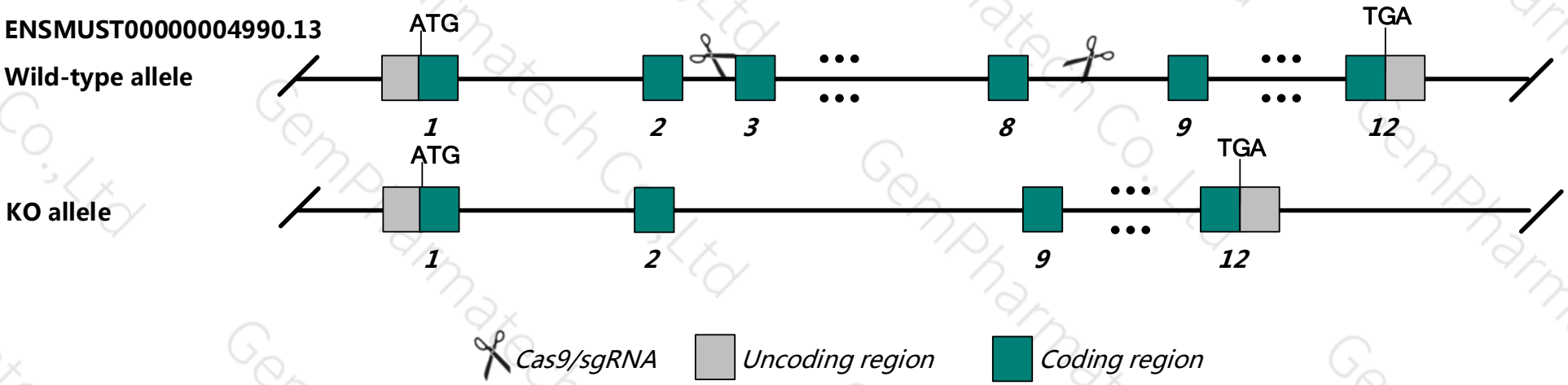
Design Date: 2018-6-8

Project Overview

Project Name	***Mapk14***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk14* gene. The schematic diagram is as follows:



Technical routes

- The *Mapk14* gene has 10 transcripts. According to the structure of *Mapk14* gene, exon3-exon8 of *Mapk14-201* (ENSMUST00000004990.13) transcript is recommended as the knockout region.The region contains 436bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Mapk14* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

- According to the existing MGI data, Mice homozygous for various null mutations are embryonic to perinatal lethal showing multiple organ system defects. Mice homozygous for a knock-out mutation exhibit abnormal myoblast differentiation and delayed myofiber growth and maturation.

- The *Mapk14* gene is located on the Chr17. 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.

- The KO region overlaps *Gm4356* gene. Knockout the region may affect the function of *Gm4356* gene. Transcript *Mapk14-207* may not be affected.

- 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）

集萃药康 GemPharmatech

Mapk14 mitogen-activated protein kinase 14 [*Mus musculus* (house mouse)]

Gene ID: 26416, updated on 15-Aug-2019

Summary

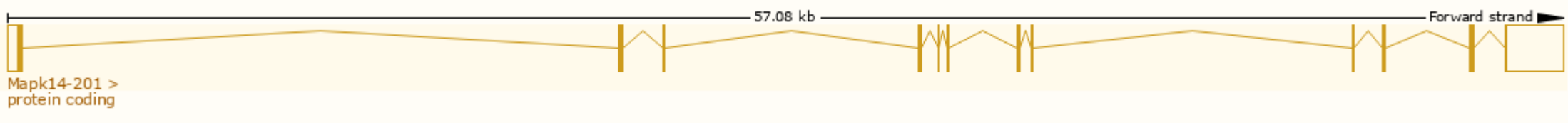
Official Symbol	Mapk14 provided by MGI
Official Full Name	mitogen-activated protein kinase 14 provided by MGI
Primary source	MGI:MGI:1346865
See related	Ensembl:ENSMUSG00000053436
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	p38; Crk1; Mxi2; p38a; CSBP2; Csbp1; PRKM14; PRKM15; p38MAPK; p38alpha; p38-alpha
Expression	Ubiquitous expression in spleen adult (RPKM 35.2), thymus adult (RPKM 34.4) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

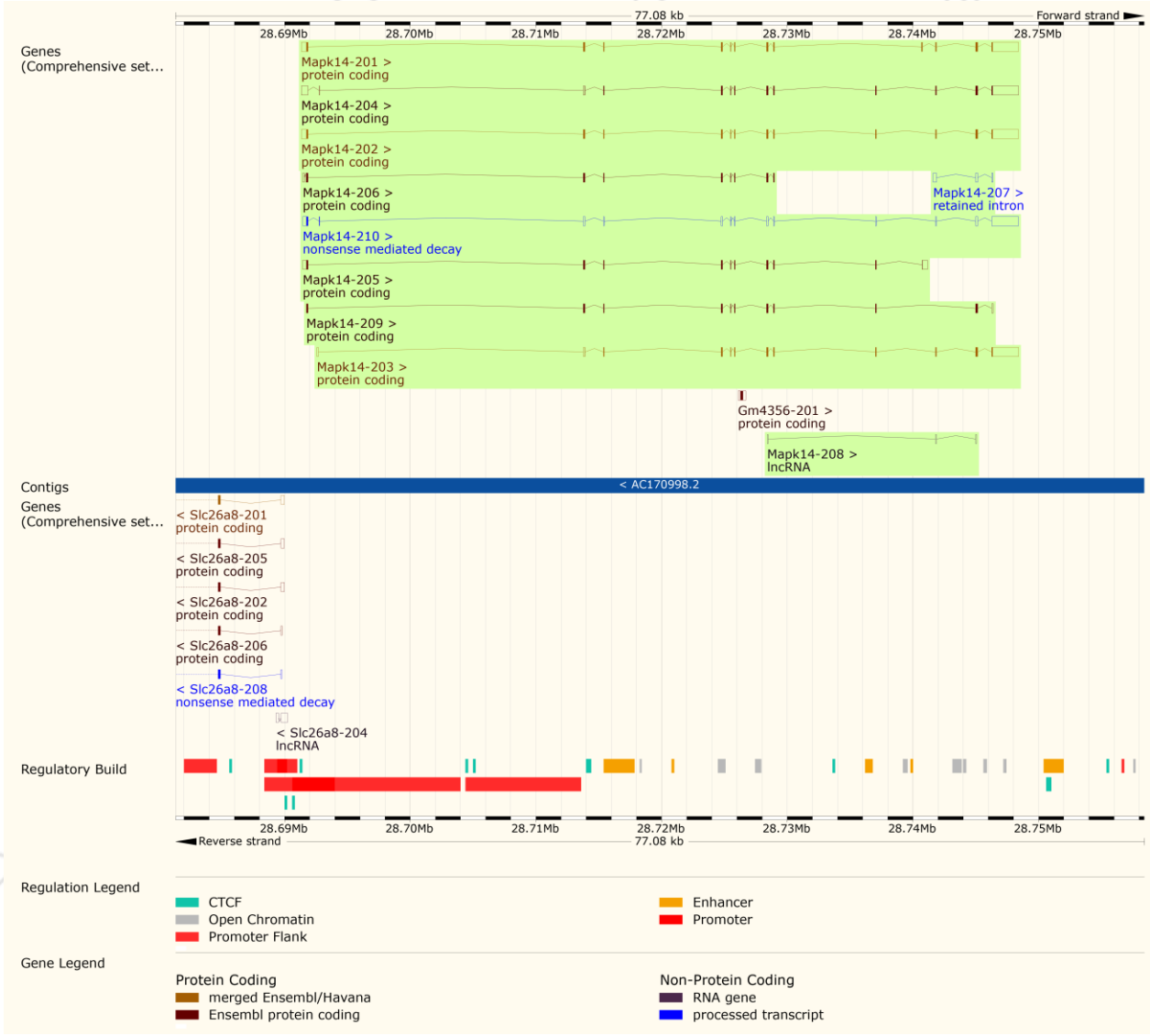
The gene has 10 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Mapk14-201	ENSMUST00000004990.13	3562	360aa	ENSMUSP00000004990.6	Protein coding	CCDS50048	P47811 Q5U421	TSL:1 GENCODE basic APPRIS ALT1
Mapk14-202	ENSMUST00000062694.15	3548	360aa	ENSMUSP00000061958.8	Protein coding	CCDS28583	P47811	TSL:1 GENCODE basic APPRIS P3
Mapk14-203	ENSMUST00000114752.2	3148	283aa	ENSMUSP00000110400.1	Protein coding	CCDS50049	P47811	TSL:1 GENCODE basic
Mapk14-204	ENSMUST00000114754.7	3592	283aa	ENSMUSP00000110402.1	Protein coding	CCDS50049	P47811	TSL:1 GENCODE basic
Mapk14-205	ENSMUST00000114758.8	1478	258aa	ENSMUSP00000110406.1	Protein coding	-	B2KF35 P47811	TSL:1 GENCODE basic
Mapk14-206	ENSMUST00000124886.8	866	227aa	ENSMUSP00000116914.2	Protein coding	-	B2KF34	CDS 3' incomplete TSL:3
Mapk14-207	ENSMUST00000151613.1	509	No protein	-	Retained intron	-	-	TSL:2
Mapk14-208	ENSMUST00000233095.1	223	No protein	-	lncRNA	-	-	-
Mapk14-209	ENSMUST00000233250.1	1066	307aa	ENSMUSP00000156692.1	Protein coding	-	A0A3B2WB60	GENCODE basic
Mapk14-210	ENSMUST00000233811.1	3490	50aa	ENSMUSP00000156603.1	Nonsense mediated decay	-	A0A3B2WAZ7	-

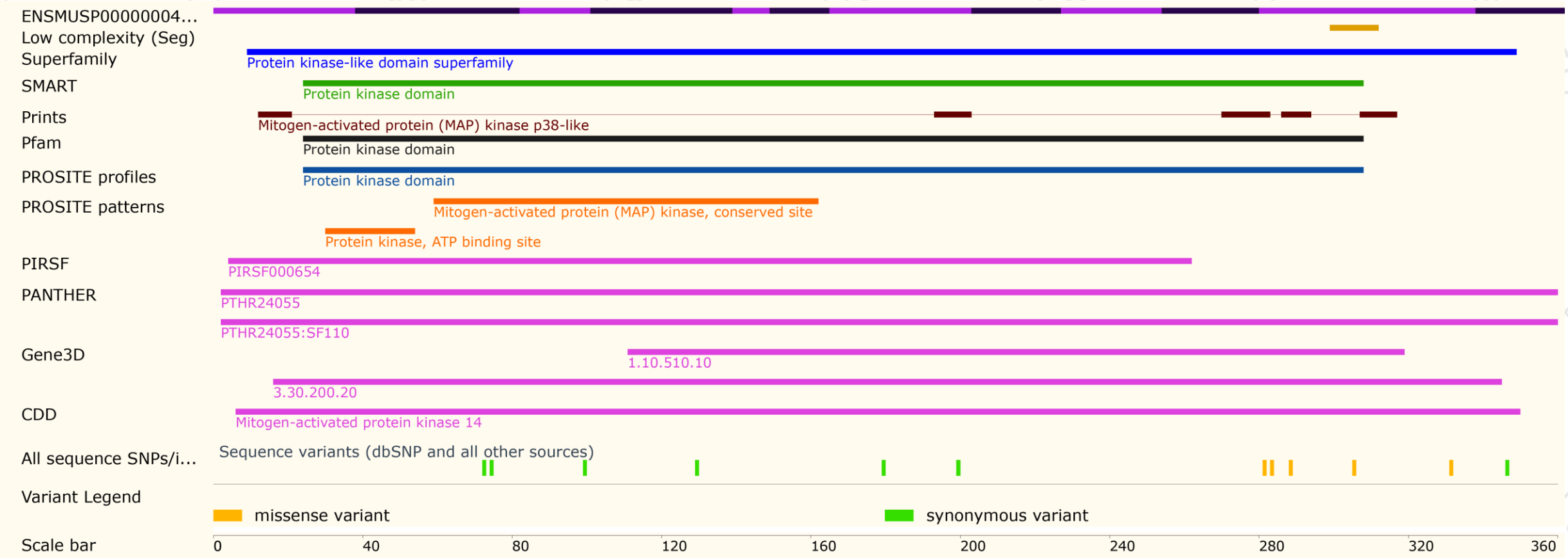
The strategy is based on the design of *Mapk14-201* transcript,The transcription is shown below



Genomic location distribution



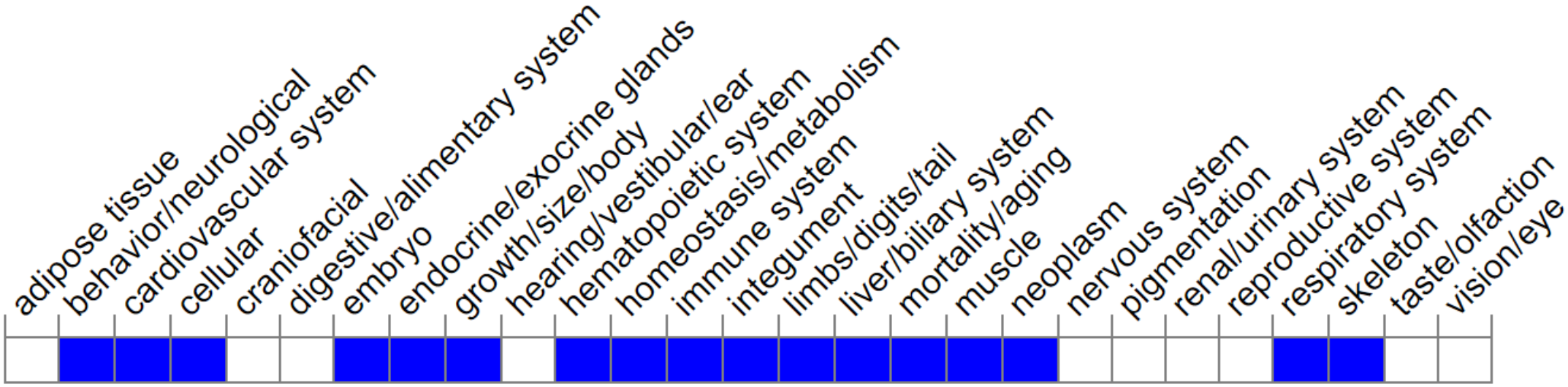
Protein domain



Mouse phenotype description(MGI)

集萃药康 GemPharmatech

Phenotype Overview



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 various null mutations are embryonic to perinatal lethal showing multiple organ system defects. Mice homozygous for a knock-out mutation exhibit abnormal myoblast differentiation and delayed myofiber growth and maturation.

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd