Mapk15 Cas9-KO Strategy

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Project Overview

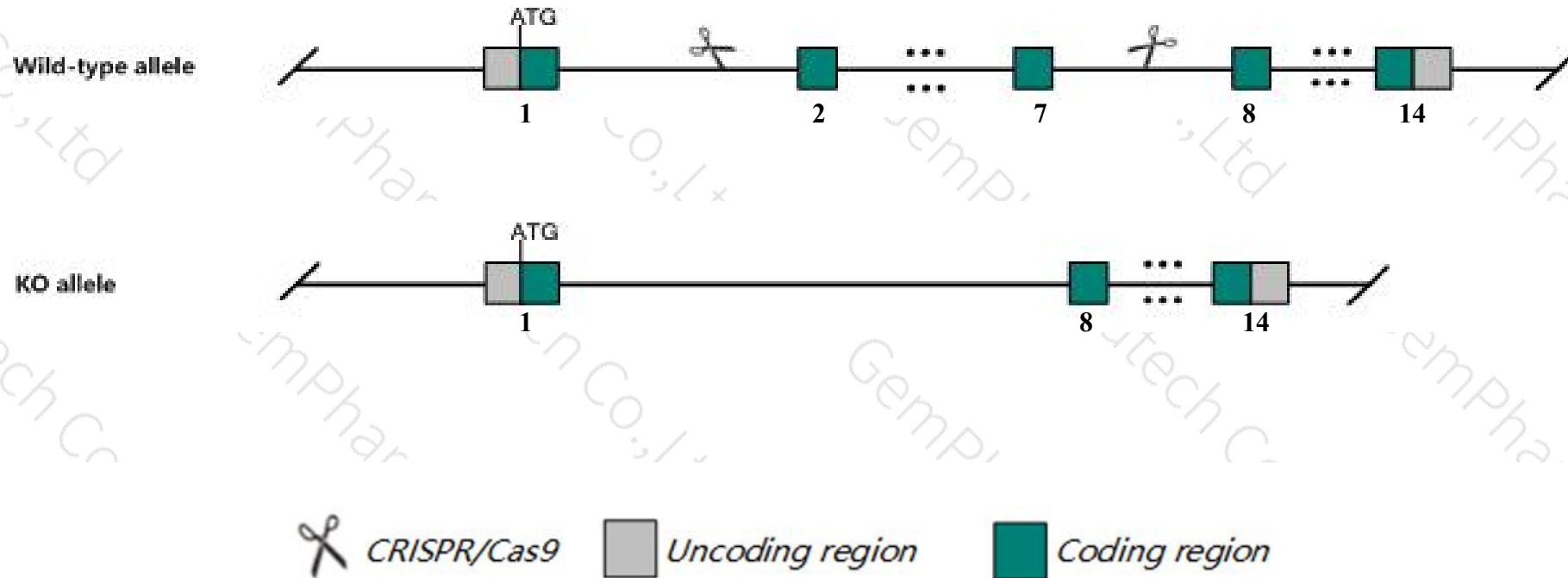|	
Project Name	*Mapk15*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk15* gene. The schematic diagram is as follows:

Technical routes

➢ The *Mapk15* gene has 5 transcripts. According to the structure of *Mapk15* gene, exon2-exon7 of *Mapk15-201*
(ENSMUST00000089669.5) transcript is recommended as the knockout region.The region contains 655bp coding sequence.
Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mapk15* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The *Mapk15* 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.

➢ Transcript *Mapk15*-205 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）

Mapk15 mitogen-activated protein kinase 15 [*Mus musculus* (house mouse)]

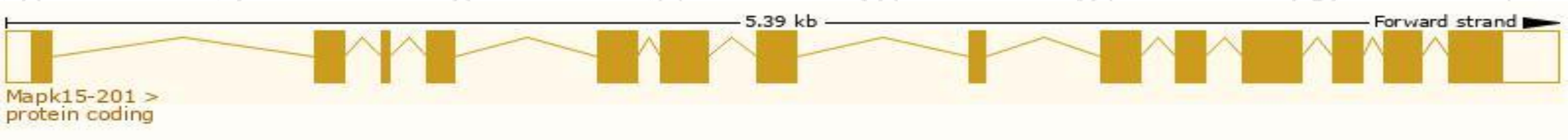Gene ID: 332110, updated on 12-Aug-2019

Summary

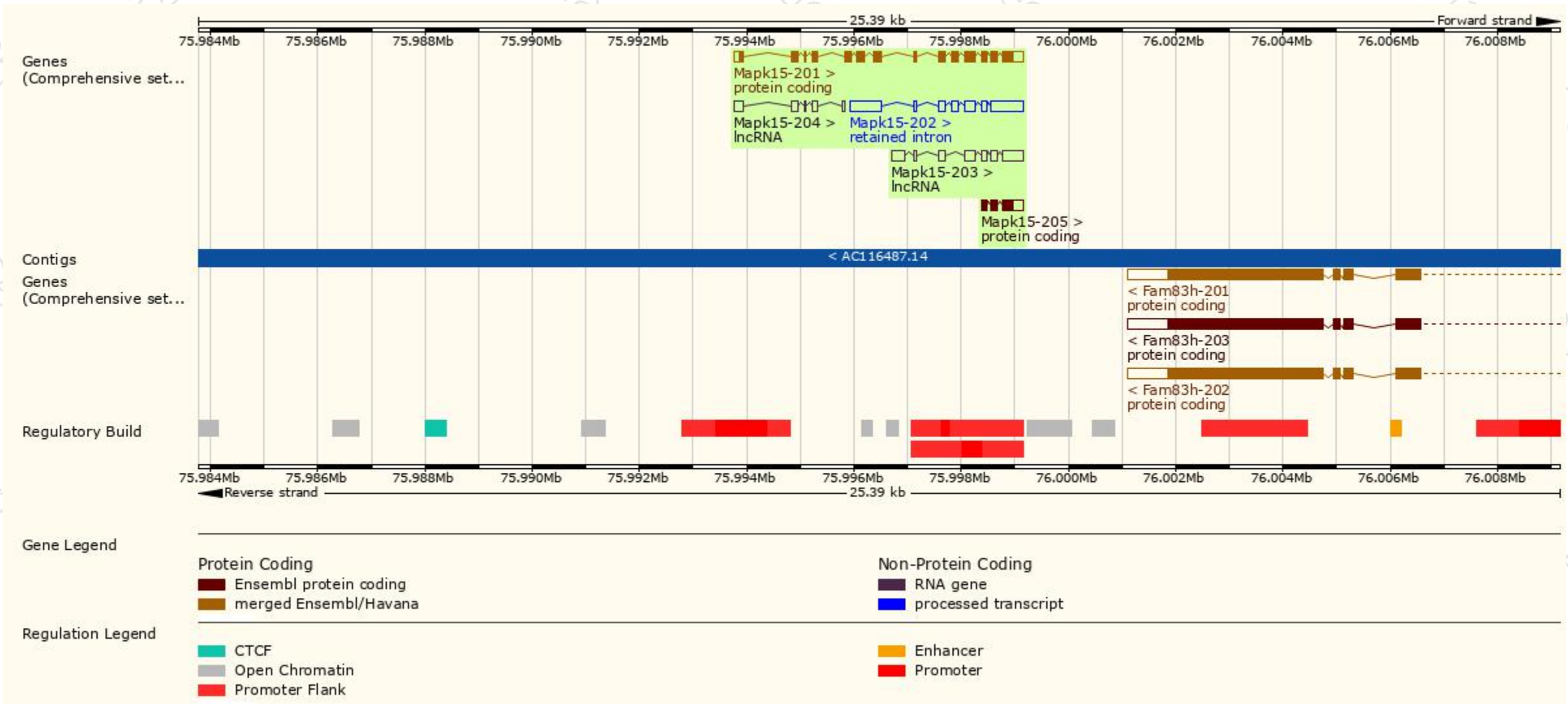|	
Official Symbol	Mapk15 provided by MGI
Official Full Name	mitogen-activated protein kinase 15 provided by MGI
Primary source	MGI:MGI:2652894
See related	Ensembl:ENSMUSG00000063704
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ERK-8; BC048082
Expression	Biased expression in testis adult (RPKM 48.8), lung adult (RPKM 26.9) and 8 other tissues See 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
Mapk15-201	ENSMUST00000089669.5	1931	549aa	Protein coding	CCDS27558	Q80Y86	TSL:1 GENCODE basic APPRIS P1
Mapk15-205	ENSMUST00000230929.1	626	145aa	Protein coding	-	A0A2R8VHA4	CDS 5' incomplete
Mapk15-202	ENSMUST00000160092.8	1788	No protein	Retained intron	-	-	TSL:1
Mapk15-203	ENSMUST00000160637.2	1250	No protein	lncRNA	-	-	TSL:1
Mapk15-204	ENSMUST00000161961.1	419	No protein	lncRNA	-	-	TSL:3

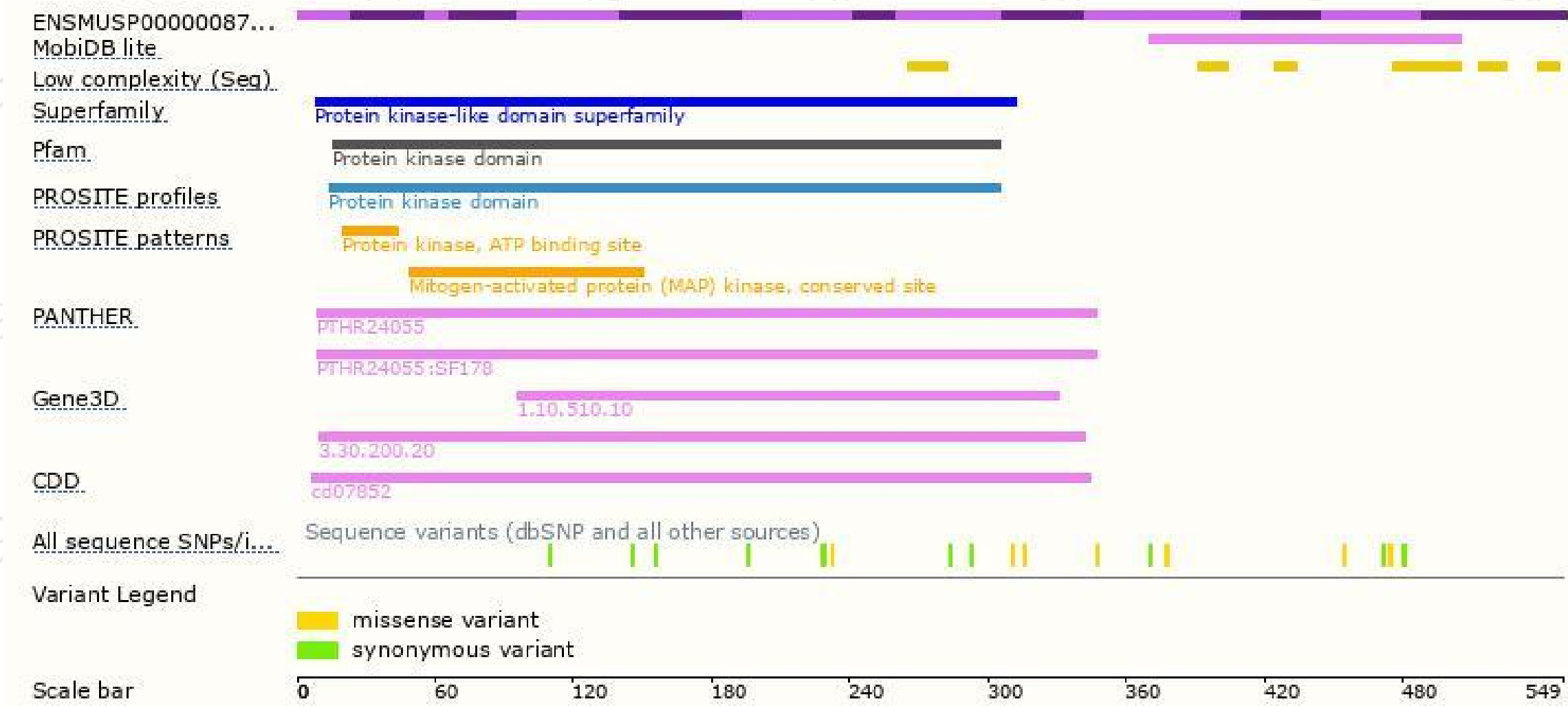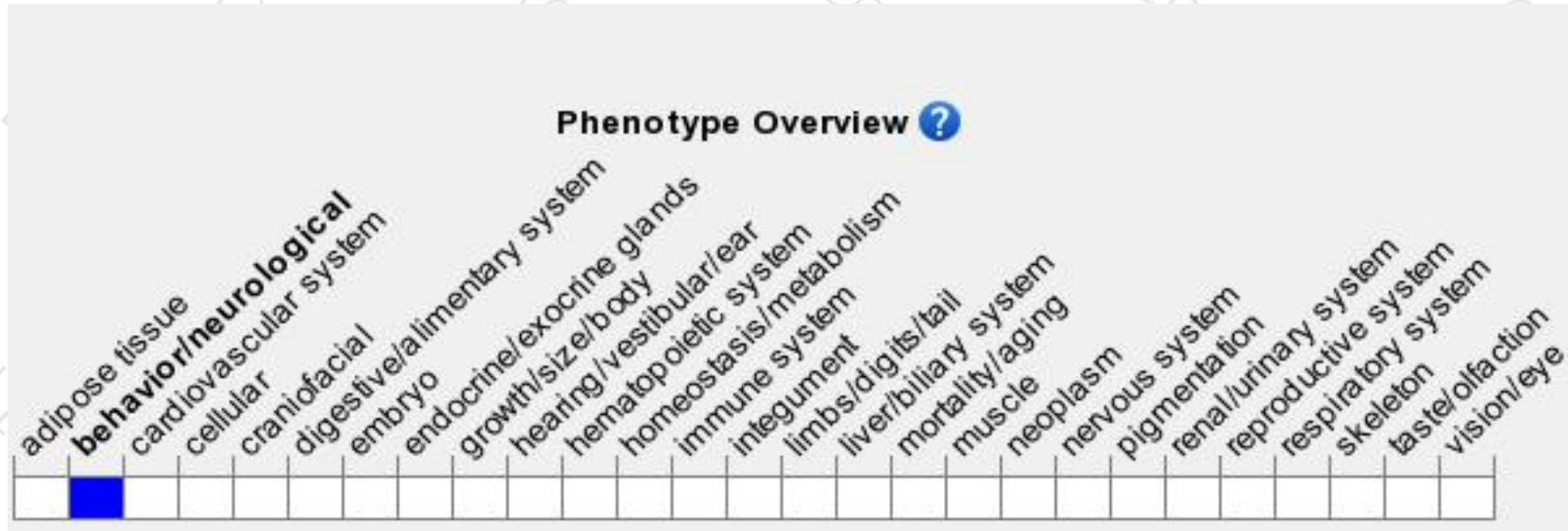The strategy is based on the design of *Mapk15-201* transcript,The transcription is shown below

Genomic location distribution

Protein domain

ENSMUSP0000087...	
MobiDB lite	
Low complexity (Seg)	
Superfamily	Protein kinase-like domain superfamily
Pfam	Protein kinase domain
PROSITE profiles	Protein kinase domain
PROSITE patterns	Protein kinase, ATP binding site
	Mitogen-activated protein (MAP) kinase, conserved site
PANTHER	PTHR24055
	PTHR24055:SF178
Gene3D	1.10.510.10
	3.30.200.20
CDD	cd07852
All sequence SNPs/i....	Sequence variants (dbSNP and all other sources)
Variant Legend	
	▇ missense variant
	▇ synonymous variant

Scale bar

| 0 | 60 | 120 | 180 | 240 | 300 | 360 | 420 | 480 | 549 |

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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