Mapkapk5 Cas9-KO Strategy

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Project Overview

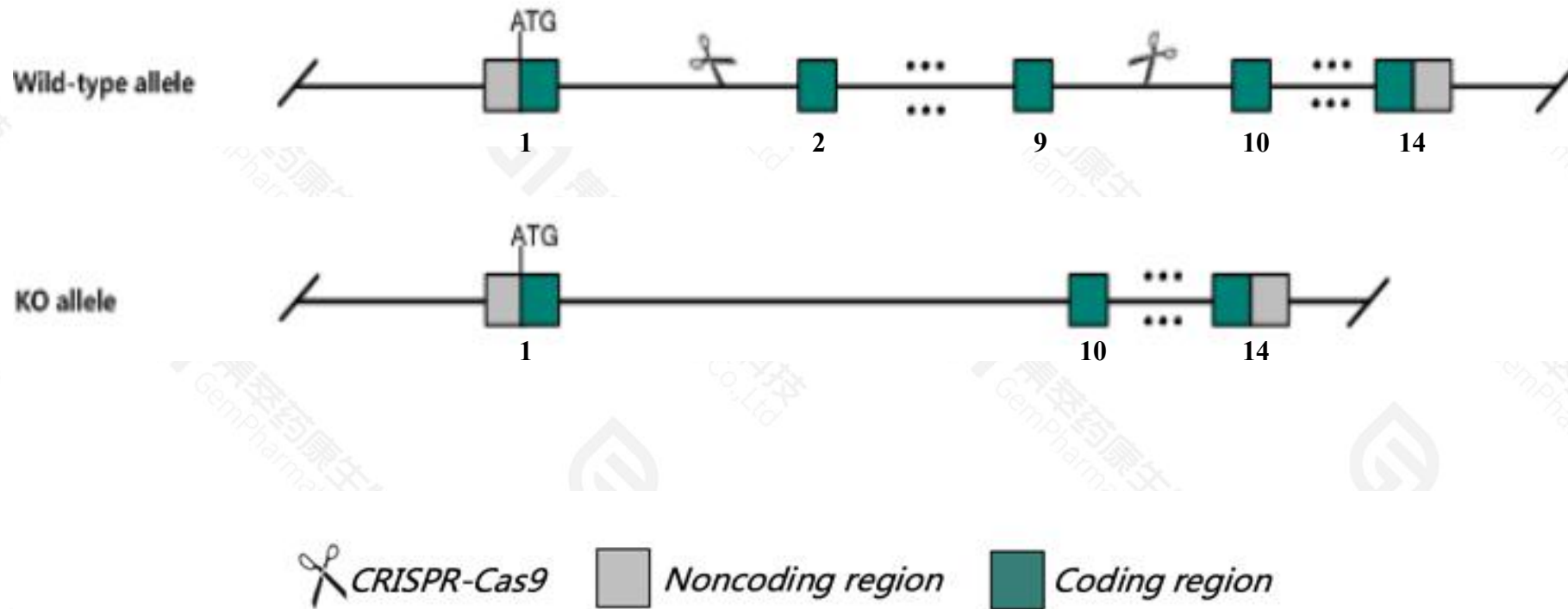|	
Project Name	*Mapkapk5*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Mapkapk5* gene. The schematic diagram is as follows:

Technical routes

➢ The *Mapkapk5* gene has 13 transcripts. According to the structure of *Mapkapk5* gene, exon2-exon9 of *Mapkapk5-201*(ENSMUST00000031410.14) transcript is recommended as the knockout region.The region contains 812bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Mapkapk5* gene. The brief process is as follows: CRISPR-Cas9 system 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.

➢ According to the existing MGI data,homozygous mutant mice are viable, fertile, and show no overt abnormalities.

➢ The *Mapkapk5* gene is located on the Chr5. 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.

➢The gene *Mapkapk5* overlapped with *GM42878*-201-ENSMUST00000125946.8 (Nonsense mediated decay).

➢The transcription of *Mapkapk5*-210 was not damaged.

Gene information （NCBI）

Mapkapk5 MAP kinase-activated protein kinase 5 [Mus musculus (house mouse)]

Gene ID: 17165, updated on 24-Apr-2022

▲ Summary

|	
Official Symbol	Mapkapk5 provided by MGI
Official Full Name	MAP kinase-activated protein kinase 5 provided by MGI
Primary source	MGI:MGI:1333110
See related	Ensembl:ENSMUSG00000029454
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	MK5, PRAK
Expression	Ubiquitous expression in CNS E11.5 (RPKM 21.0), CNS E14 (RPKM 20.7) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapkapk5-201	ENSMUST00000031410.14	2234	473aa	Protein coding	CCDS39248		TSL:1 , GENCODE basic , APPRIS P2 ,
Mapkapk5-204	ENSMUST00000111783.8	1513	471aa	Protein coding	-		TSL:1 , GENCODE basic , APPRIS ALT1 ,
Mapkapk5-205	ENSMUST00000111786.9	975	324aa	Protein coding	-		TSL:1 , GENCODE basic ,
Mapkapk5-203	ENSMUST00000111782.8	969	322aa	Protein coding	-		TSL:1 , GENCODE basic ,
Mapkapk5-213	ENSMUST00000196315.2	592	187aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Mapkapk5-210	ENSMUST00000152270.8	436	114aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Mapkapk5-209	ENSMUST00000151352.3	540	63aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Mapkapk5-202	ENSMUST00000111781.8	1296	No protein	Processed transcript	-		TSL:5 ,
Mapkapk5-211	ENSMUST00000153763.6	1110	No protein	Processed transcript	-		TSL:5 ,
Mapkapk5-208	ENSMUST00000131914.3	366	No protein	Processed transcript	-		TSL:5 ,
Mapkapk5-212	ENSMUST00000154628.2	838	No protein	Retained intron	-		TSL:2 ,
Mapkapk5-206	ENSMUST00000126524.5	578	No protein	Retained intron	-		TSL:2 ,
Mapkapk5-207	ENSMUST00000128782.8	358	No protein	Retained intron	-		TSL:2 ,

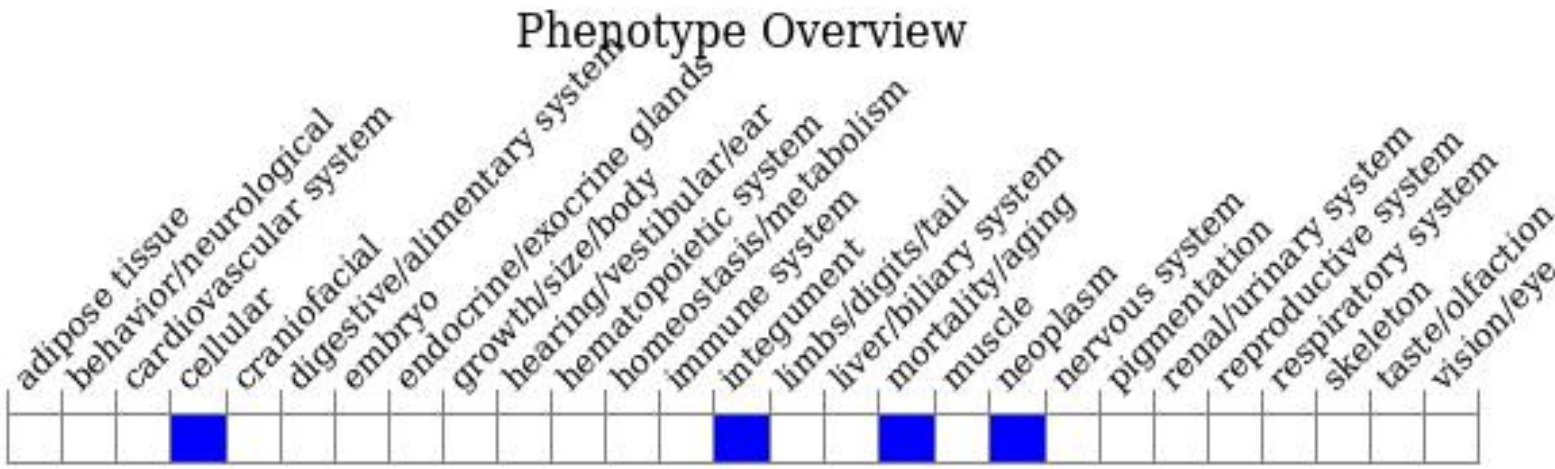The strategy is based on the design of *Mapkapk5-201* transcript,the transcription is shown below:

< Mapkapk5-201
protein coding

◄ Reverse strand

20.87 kb
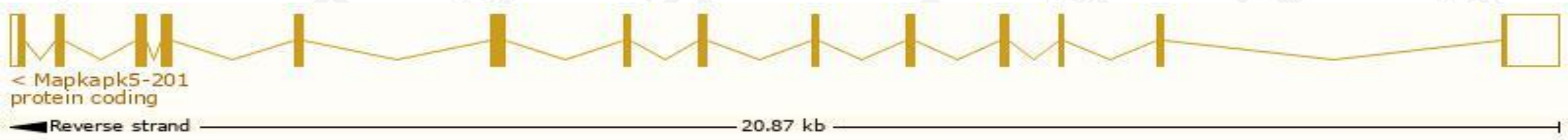
Genomic location distribution
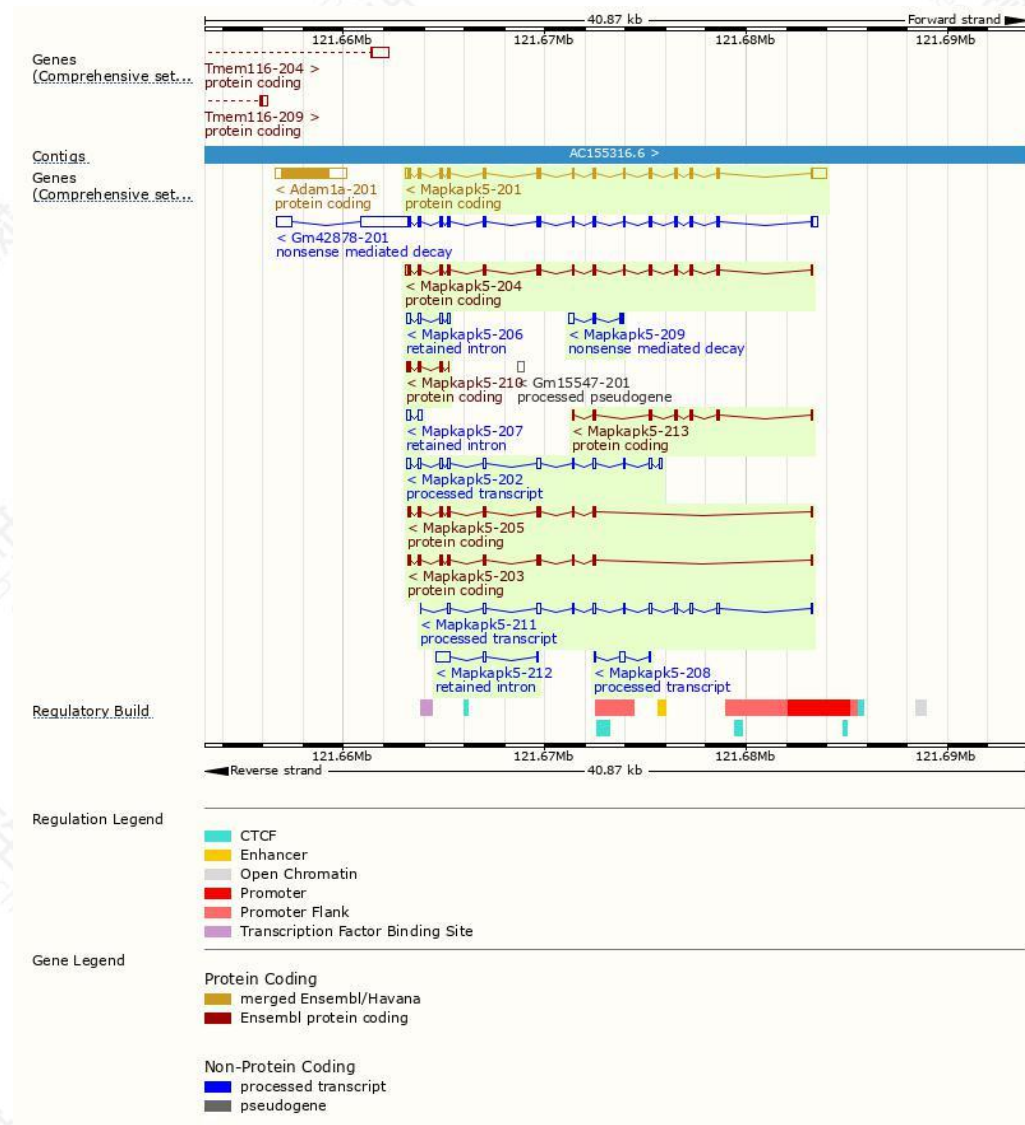
Protein domain
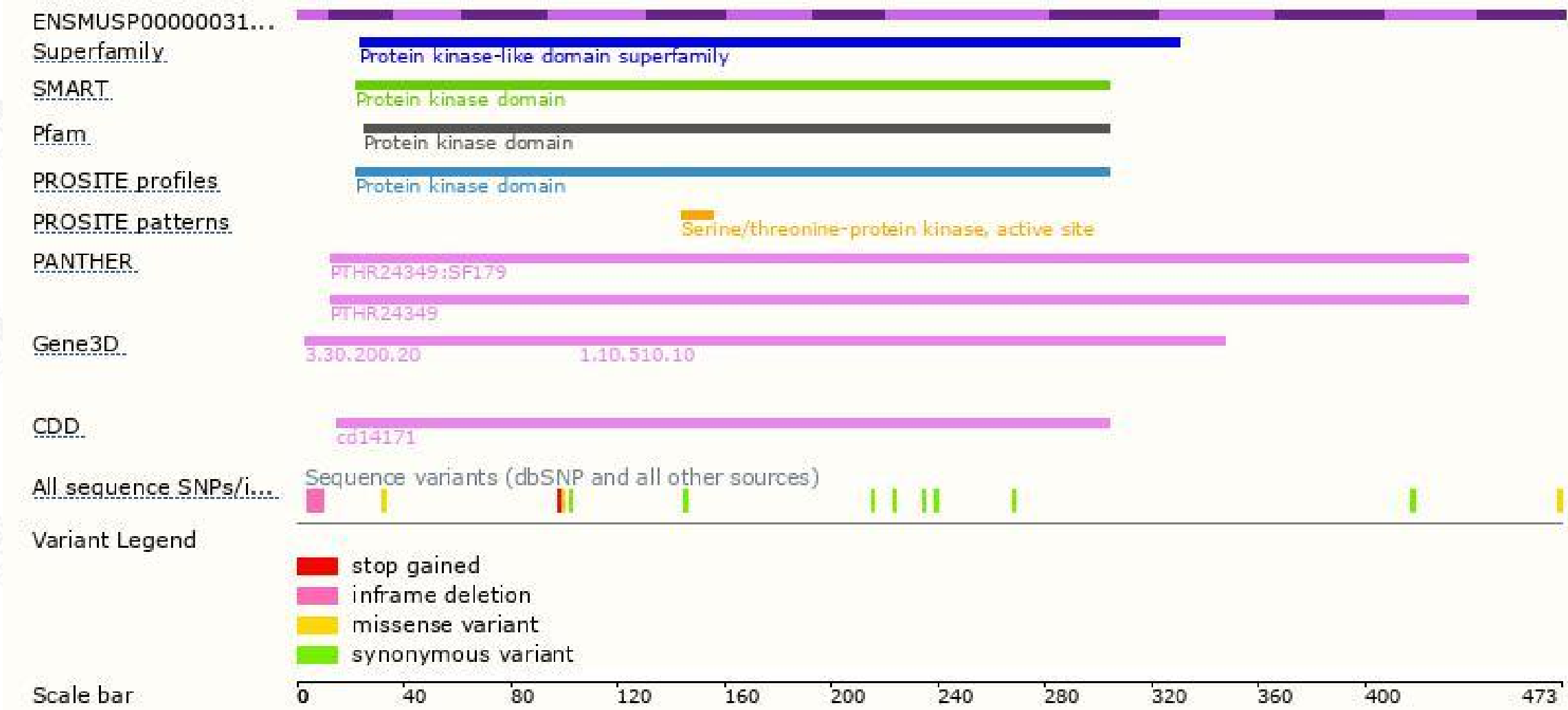
Mouse phenotype description(MGI)

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,homozygous mutant mice are viable, fertile, and show no overt abnormalities.

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