

Tprkb Cas9-KO Strategy

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Design Date:

2020-5-11

Project Overview

Project Name

Tprkb

Project type

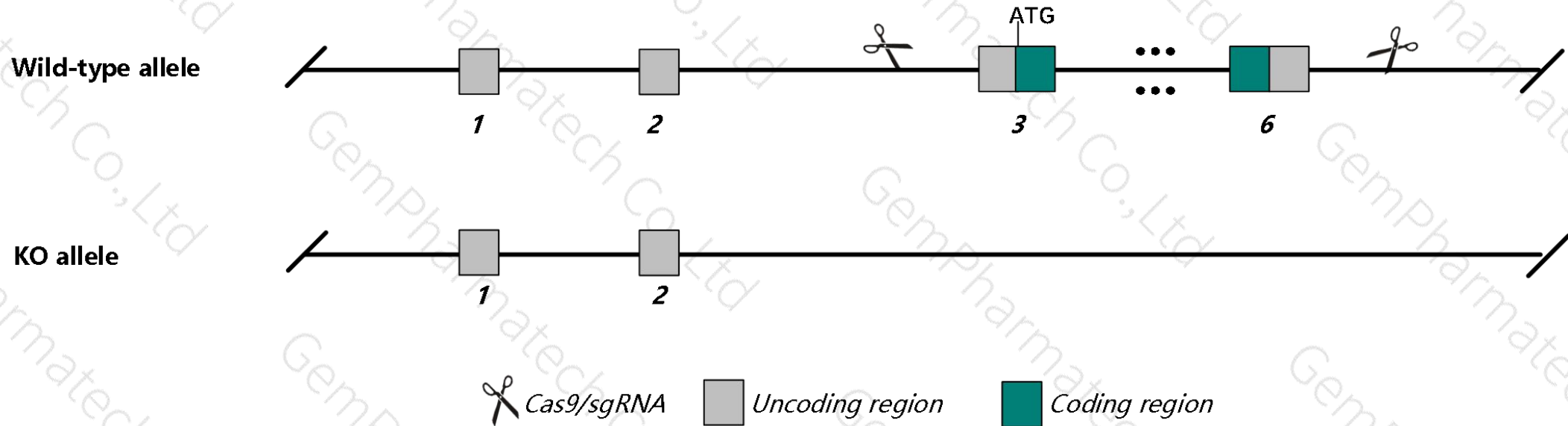
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Tprkb* gene has 14 transcripts. According to the structure of *Tprkb* gene, exon3-exon6 of *Tprkb*-208 (ENSMUST00000200680.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tprkb* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcripts 209,210,212,213 may not be affected.
- The *Tprkb* gene is located on the Chr6. 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)

Tprkb Tp53rk binding protein [Mus musculus (house mouse)]

Gene ID: 69786, updated on 13-Mar-2020

Summary



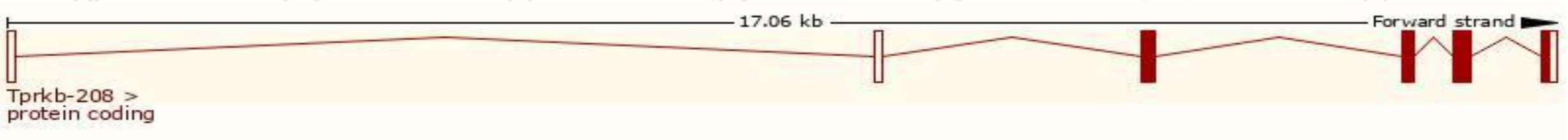
Official Symbol	Tprkb provided by MGI
Official Full Name	Tp53rk binding protein provided by MGI
Primary source	MGI:MGI:1917036
See related	Ensembl:ENSMUSG00000054226
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610033G21Rik, 1810034M08Rik, Cgi-121, DRWMS1, mDRWMS1
Expression	Ubiquitous expression in kidney adult (RPKM 15.1), cerebellum adult (RPKM 12.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

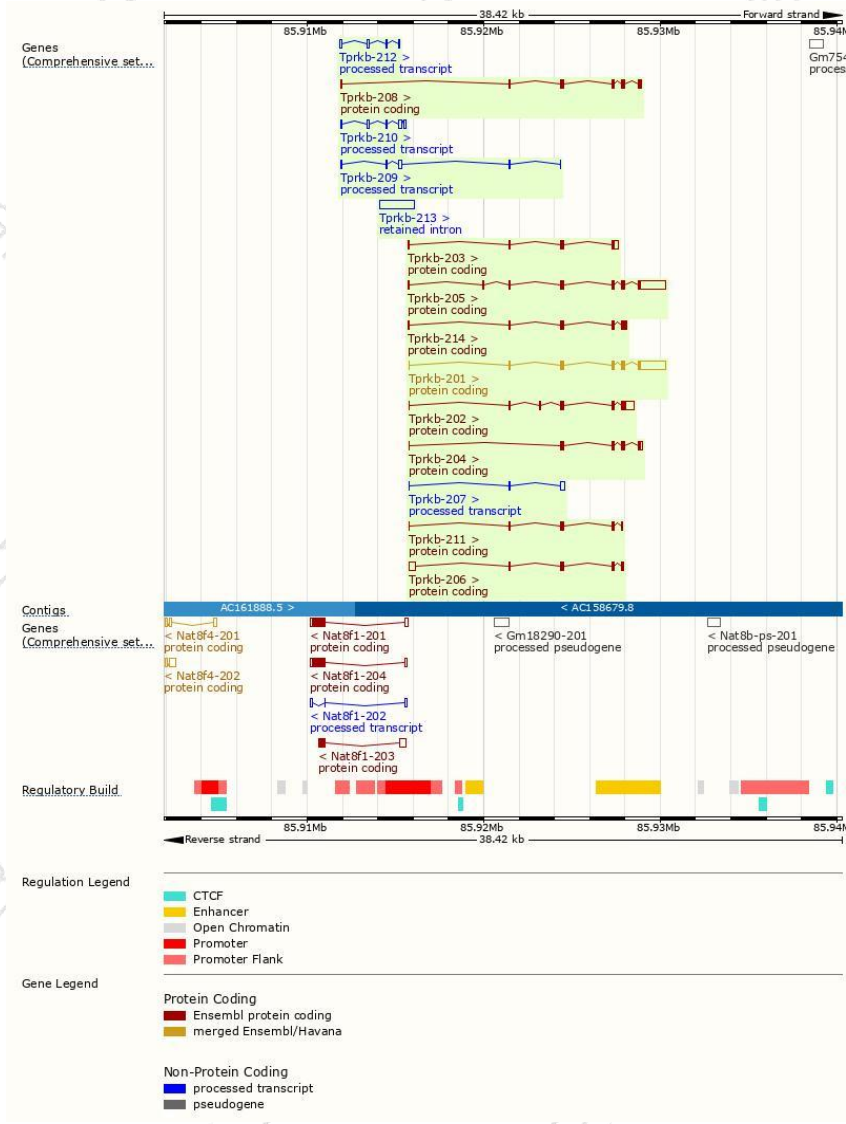
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tprkb-205	ENSMUST00000113753.7	2222	175aa	Protein coding	CCDS20305	Q8QZZ7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Tprkb-201	ENSMUST00000067137.13	2103	175aa	Protein coding	CCDS20305	Q8QZZ7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Tprkb-208	ENSMUST00000200680.3	814	175aa	Protein coding	CCDS20305	Q8QZZ7	TSL:3 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Tprkb-204	ENSMUST00000113752.7	749	175aa	Protein coding	CCDS20305	Q8QZZ7	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Tprkb-202	ENSMUST00000089570.6	1216	158aa	Protein coding	-	G3X9K8	TSL:5 GENCODE basic
Tprkb-206	ENSMUST00000149026.4	818	132aa	Protein coding	-	D3Z5E8	CDS 3' incomplete TSL:3
Tprkb-214	ENSMUST00000202803.3	716	158aa	Protein coding	-	G3X9K8	TSL:1 GENCODE basic
Tprkb-203	ENSMUST00000113751.7	692	91aa	Protein coding	-	D3YXX8	TSL:1 GENCODE basic
Tprkb-211	ENSMUST00000201939.3	475	110aa	Protein coding	-	A0A0J9YVB8	CDS 3' incomplete TSL:3
Tprkb-210	ENSMUST00000201289.3	573	No protein	Processed transcript	-	-	TSL:3
Tprkb-209	ENSMUST00000201217.3	457	No protein	Processed transcript	-	-	TSL:5
Tprkb-207	ENSMUST00000150249.7	381	No protein	Processed transcript	-	-	TSL:3
Tprkb-212	ENSMUST00000202142.3	335	No protein	Processed transcript	-	-	TSL:3
Tprkb-213	ENSMUST00000202588.1	1964	No protein	Retained intron	-	-	TSL:NA

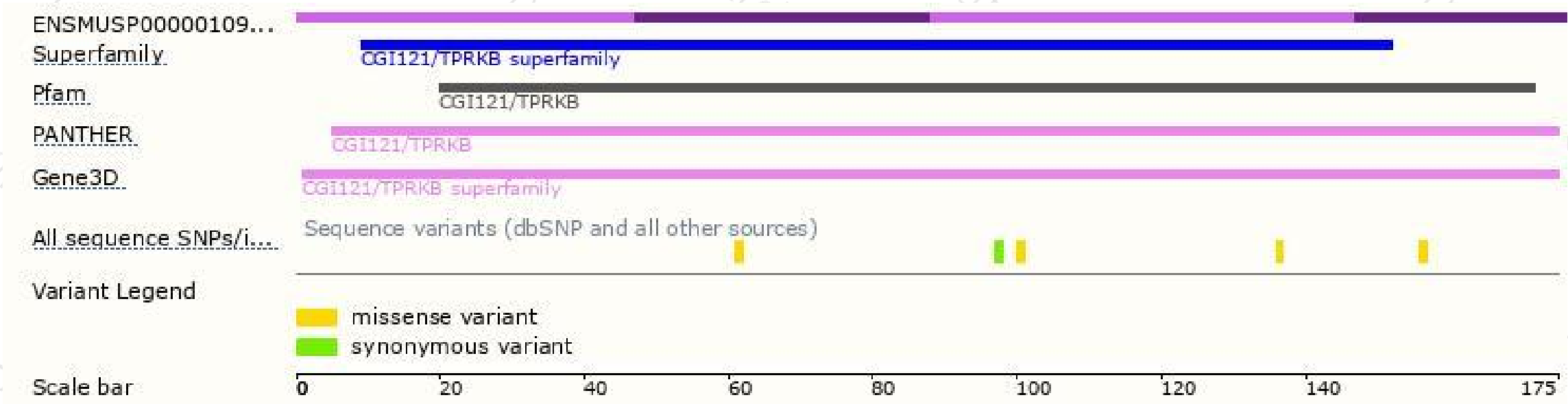
The strategy is based on the design of *Tprkb-208* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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