# Ptk7-P690R cas9-ki(PM) Mouse Model Strategy -CRISPR/Cas9 technology

Designer: Xiaojing Li

Reviewer: Jia Yu

**Design Date: 2021-8-9** 

# **Project Overview**



Project Name Ptk7-P690R

Project type cas9-ki(PM)

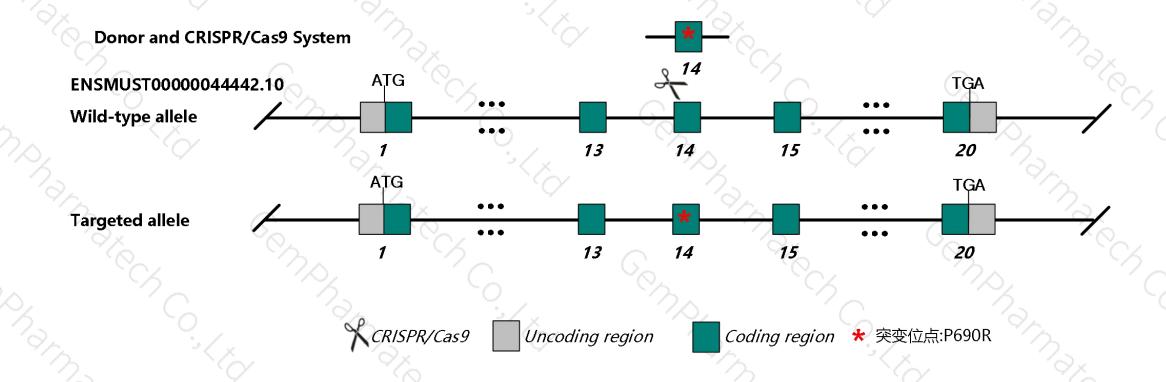
Strain background C57BL/6JGpt

**Project cycles** 5-8 months

# Strategy



This model uses CRISPR/Cas9 technology to edit the *Ptk7* gene and the schematic diagram is as follow:



## **Technical Description**

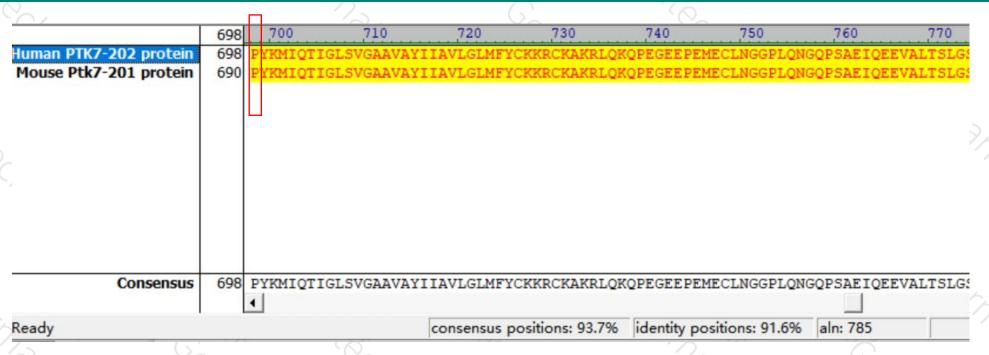


- The mouse *Ptk7* gene has 2 transcripts. The human *PTK7* gene has 20 transcripts.
- According to the structure of *Ptk7* gene and requirements of customer, the 698th amino acid(P) of human *PTK7*202(NM\_002821.5) gene corresponds to the 690th amino acid(P) of mouse *Ptk7* gene after comparing homology of mouse

  Ptk7 gene and human *PTK7* gene. This project produced *Ptk7*-P690R point mutation on exon14 of the transcript of *Ptk7*201(ENSMUST00000044442.10, NM\_175168.4). The 690th amino acids will be mutated from P to R, and the
  corresponding codon will be mutated to CGC by the CCA.
- The mouse *Ptk7*-201 transcript contains 20 exons. The translation initiation site ATG is located at exon1, and the translation termination site TGA is located at exon20, encoding 1062aa.
- In this project, *Ptk7* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, CRISPR/Cas9 system and Donor 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.



#### A comparison of the aa homology of human and mouse Ptk7 gene



The 698th amino acid(P) of human *PTK7* gene corresponds to the 690th amino acid(P) of mouse *Ptk7* gene after comparing homology of mouse *Ptk7* gene and human *PTK7* gene.

### **Mutation Site**



#### **Before mutation**

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		GACAGG	ACTG	GA	AGAG	GCAC	A CA	GAG	AATC <mark>T</mark>	GTT	CGGI	CAC	TACC	TTCTG	A GC	CTCC	CGGG	TCC	GTCG	GGA	GGG	GGT	ATGT	TCTA	CTAG	GGT	CTGG	TAG	CCC
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	57101	CTGTCG	GTGG	GC	GCA	GCGG	r AG	CCT	ACATC	ATC	GCGG	STCC	TGGG	CCTCA	T GT	TCTA	CTGC	AAG	AAGC	GGT	GTA	AAG	CCAA	GCGG	CTGC	CAG	AAAC	AGC	CTG
		GACAGO	CACC	CG	CGT	CGCCI	A TC	GGA:	IGTAG	TAG	CGCC	CAGG	ACCC	GGAGT	A CA	AGAT	GACG	TTC	TTCG	CCA	CAT	TTC	GGTT	CGCC	GACG	STC	TTTG	TCG	GAC
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	57201	AGGGGG	AGGA	GC	CAG	AGAT	G GA	AGTG	CCTCA	ATG	GTGG	GTC	CCCC	TGTAG	C GG	GAGG	TGGA	CCG	GTCI	GGG	TAC	AGA	GCAC	CCTC	CCGI	rgc	CAGC	TGT	GGA
Y.		TCCCCC	TCCT	CG	GTC	TCTA	CT	CAC	GGAGT	TAC	CACC	CAG	GGGG	ACATO	G CC	CTCC	ACCT	GGC	CAGA	CCC	ATG	TCT	CGTG	GGAG	GGCA	ACG	GTCG	ACAC	CCT
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9	•2		TGAC	CI		CGTGT GCACI			TTAG <mark>A</mark> AATC <mark>T</mark>			GTG	ATG				u , r	AGG	S CAGO GTCO		P CCC GGG		Y TACA ATGT	15 15	GAT	CCA	GACC CTGG		000
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-	57001	CTGTCC	TGAC ACTG	CI GA			A CA	AGAGA A		GTT	GCCZ	AGTG CAC V	TACC	SAAGAC CTTCTG	A GC	CTCC F Y	GCCC	AGG TCC K	GTC0	GGA	GGG	GCG K		AGAI TCTA	GATO CTAO	CCA GGT Q	01100	TAG	CCC P E?
-	57001	CTGTCC GACAGG	TGAC ACTG V	G GC	AGAG	GCACI A GCGGT	A CA V r AG	AGAGA A CCTA	AATC <mark>T</mark>	GTT	GCGI	AGTG CAC V GTCC	TACO	GAAGAC CTTCTG	A GC M T GI	CTCC F Y	GGCCC CCGGG CCGGG	AGG TCC K AAG	GTCG K AAGG	GGA R GGT	GGG C GTA	GCG K AAG	ATGT	AGAT TCTA	GATO CTAO L	CCA GGT Q CAG	CTGG	Q (	CCC P E?
-	57001	CTGTCC GACAGG	TGAC ACTG V	G GC	AGAG A CGCA CGCT	GCACI A GCGGT	A CA V I AG A TC	AGAGI A GCCTI GGGA	AATC <mark>T</mark> Y I ACATC	GTT	GCGI	AGTG CAC V GTCC	TACO	GAAGAC CTTCTG	A GC M T GI	CTCC F Y	GGCCC CCGGG CCGGG	AGG TCC K AAG	GTCG K AAGG	GGA R GGT	GGG C GTA	GCG K AAG	ATGT A K	AGAT TCTA	GATO CTAO L	CCA GGT Q CAG	CTGG K AAAG	Q (	CCC P E?
7	57001 •2 57101	CTGTCC GACAGO L S CTGTCC GACAGO	TGAC ACTG V GTGG CCACC	G GC	A GCA GCGT	GCACI A GCGGT CGCCI	A CA V F AG A TC	AGAGI A GCCTI GGGA	AATC <mark>T</mark> Y I ACATC	ATC TAG	GCGI	AGTG CAC V GTCC CAGG	TACO	GAAGAC CTTCTG	A GC M T GI A CA	CTCC F Y TCTA AGAT	GGCCC CCGGG CCGGG	AGG TCC K AAG TTC	K AAGO	GGA R GGT	GGG C GTA CAT	K AAG TTC	ATGT A K	AGAT TCTA R GCGG CGCG	GATO L GCTGO	CCA GGT Q CAG GTC	CTGG K AAAG	Q (AGC)	CCC P E? CTG GAC

The yellow region is exon14 of *Ptk7-201*, the red region represents the mutation site.

### **Notice**



- According to the data of MGI, Mice homozygous for a gene trapped allele die perinatally with defects in neural tube closure and planar cell polarity in the ear. ENU-induced mutant mice show omphalocele, impaired neural tube, heart and lung development, rib defects, polydactyly, failed eyelid closure and altered cell polarity.
- > One or Two synonymous mutations of amino acids will be intronduced on exon14 of Ptk7.
- Mouse *Ptk7* gene is located on Chr17. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr17, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

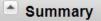
# Gene name and location (NCBI)



#### Ptk7 PTK7 protein tyrosine kinase 7 [ Mus musculus (house mouse) ]

♣ Download Datasets

Gene ID: 71461, updated on 23-Jun-2021



△ ?

Official Symbol Ptk7 provided by MGI

Official Full Name PTK7 protein tyrosine kinase 7 provided by MGI

Primary source MGI:MGI:1918711

See related Ensembl:ENSMUSG00000023972

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 chz; mPTK7/CCK; mPTK7/CCK4; 8430404F20Rik

Expression Broad expression in limb E14.5 (RPKM 30.4), ovary adult (RPKM 29.7) and 22 other tissues See more

Orthologs human all

#### 

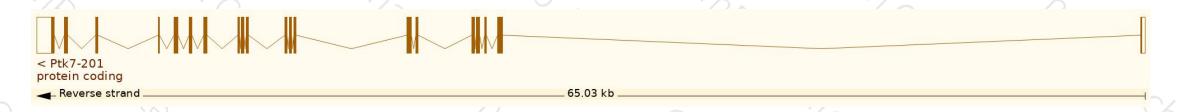
# Transcript information (Ensembl)



The gene has 2 transcripts, and all transcripts are shown below:

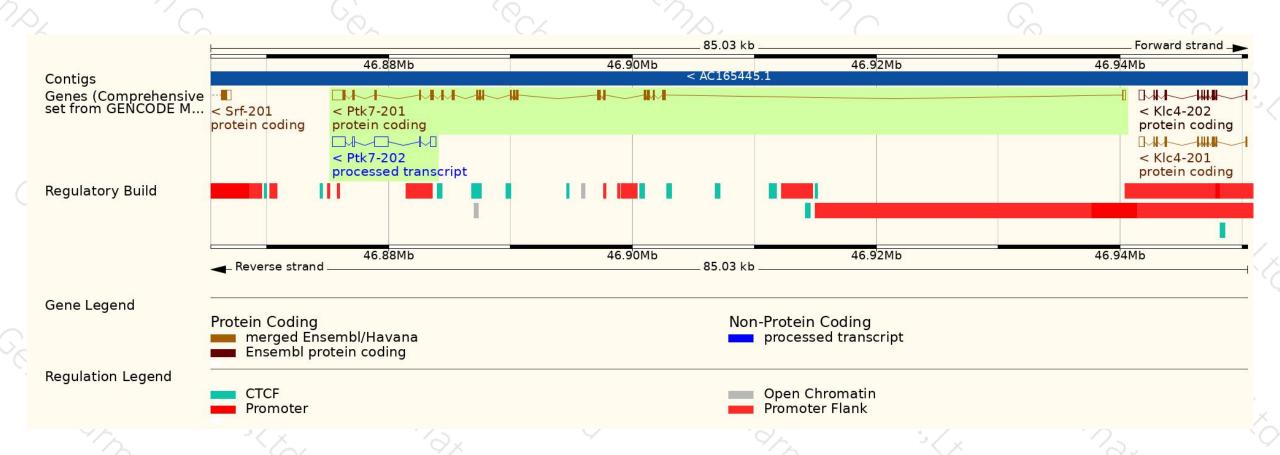
Name 🍦	Transcript ID 🔺	bp 🌲	Protein 🍦	Biotype	CCDS 🍦	UniProt Match 🌲	Flags				
Ptk7-201	ENSMUST00000044442.10	4235	<u>1062aa</u>	Protein coding	CCDS37637&	Q8BKG3虚	GENCODE basic APPRIS P1 TSL:1				
Ptk7-202	ENSMUST00000232855.2	2819	No protein	Processed transcript	-	-	-				

The strategy is based on the design of Ptk7-201 transcript, the transcription is shown below:



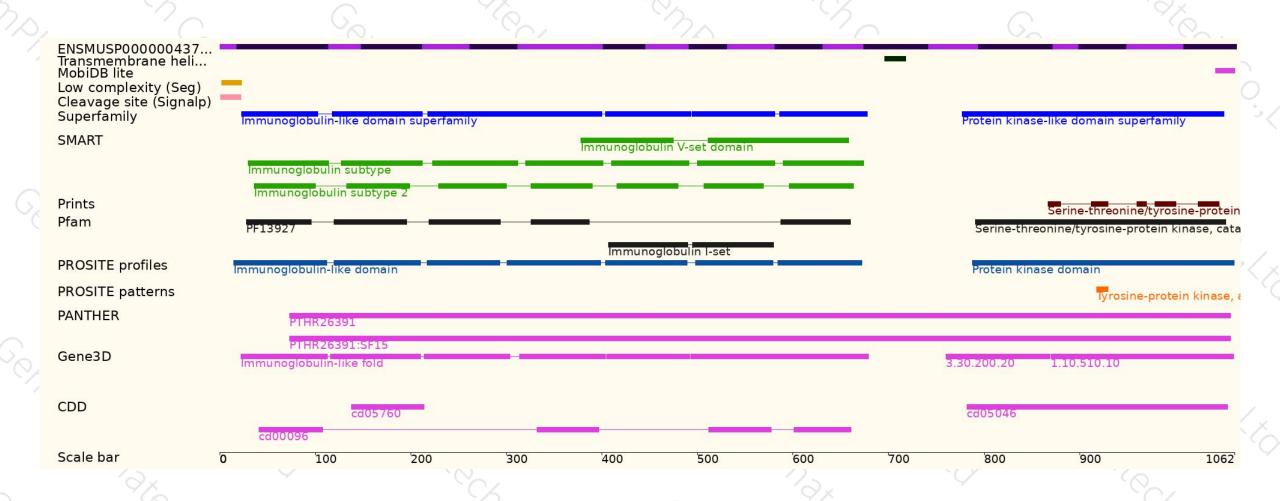
### Genomic location distribution





#### Protein domain



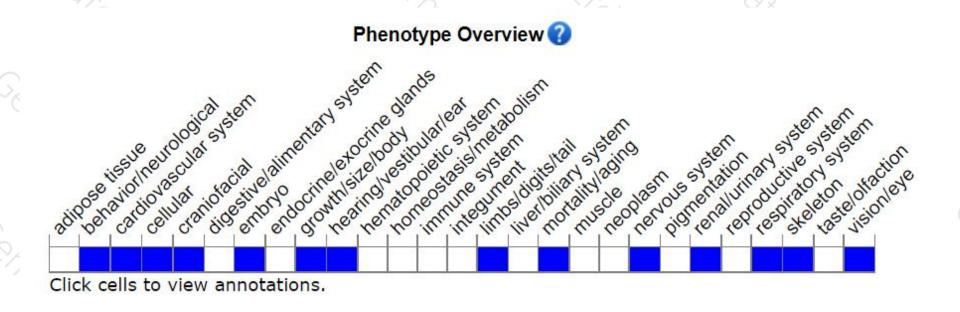


### Mouse phenotype description(MGI)



URL link is as follows:

http://www.informatics.jax.org/marker/MGI:1918711



Mice homozygous for a gene trapped allele die perinatally with defects in neural tube closure and planar cell polarity in the ear. ENU-induced mutant mice show omphalocele, impaired neural tube, heart and lung development, rib defects, polydactyly, failed eyelid closure and altered cell polarity.

If you have any questions, please feel free to contact us. Tel: 025-5864 1534





