GemPharmatech™

Ptk2 Cas9-KO Strategy

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Design Date: 2022-10-27

Overview

Target Gene Name

- *Ptk2*

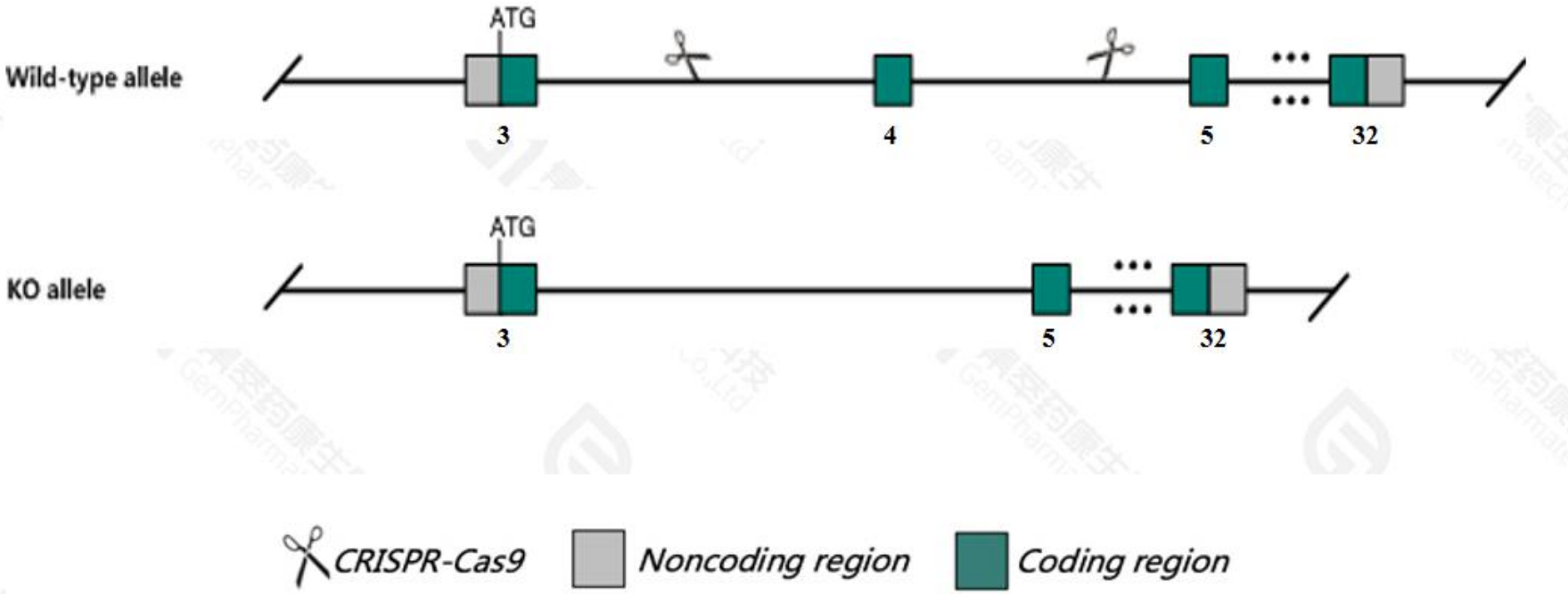
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ptk2* gene.

Technical Information

- The *Ptk2* gene has 16 transcripts. According to the structure of *Ptk2* gene, exon4 of *Ptk2-201*(ENSMUST00000110036.11) transcript is recommended as the knockout region. The region contains 167bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ptk2* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Ptk2 PTK2 protein tyrosine kinase 2 [Mus musculus (house mouse)]

Gene ID: 14083, updated on 15-Mar-2020

Summary

Official Symbol	Ptk2 provided by MGI
Official Full Name	PTK2 protein tyrosine kinase 2 provided byMGI
Primary source	MGI:MGI:95481
See related	Ensembl:ENSMUSG00000022607
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	FADK 1, FAK, FRNK, Fadk, p125FAK
Expression	Ubiquitous expression in cortex adult (RPKM 12.3), CNS E11.5 (RPKM 11.8) and 28 other tissuesSee more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

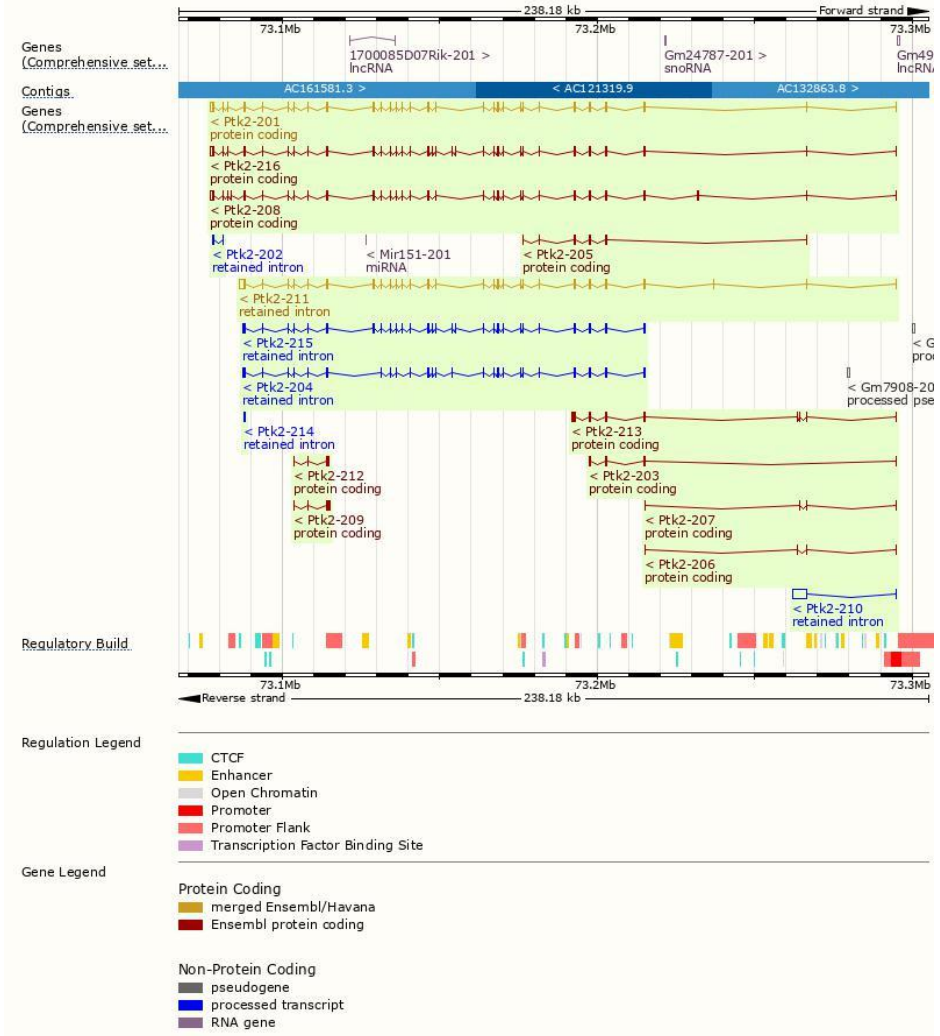
Transcript Information

The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptk2-201	ENSMUST00000110036.10	4417	1052aa	Protein coding	CCDS37099	P34152	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 P2
Ptk2-208	ENSMUST00000226988.2	4675	1055aa	Protein coding	-	P34152	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 ALT2
Ptk2-216	ENSMUST00000239146.1	4540	1093aa	Protein coding	-	-	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 ALT1
Ptk2-213	ENSMUST00000228180.2	1333	198aa	Protein coding	-	P34152	GENCODE basic
Ptk2-205	ENSMUST00000226791.1	517	119aa	Protein coding	-	A0A2I3BRG7	CDS 3' incomplete
Ptk2-209	ENSMUST00000227395.1	498	81aa	Protein coding	-	A0A2I3BR46	CDS 3' incomplete
Ptk2-203	ENSMUST00000226466.1	488	126aa	Protein coding	-	A0A2I3BQ85	CDS 3' incomplete
Ptk2-212	ENSMUST00000227686.1	485	114aa	Protein coding	-	A0A2I3BPK4	CDS 3' incomplete
Ptk2-206	ENSMUST00000226848.1	364	14aa	Protein coding	-	Q2VQT9	CDS 3' incomplete
Ptk2-207	ENSMUST00000226893.1	318	14aa	Protein coding	-	Q2VQT9	CDS 3' incomplete
Ptk2-211	ENSMUST00000227569.1	4678	No protein	Retained intron	-	-	
Ptk2-210	ENSMUST00000227435.1	4580	No protein	Retained intron	-	-	
Ptk2-215	ENSMUST00000228628.1	3254	No protein	Retained intron	-	-	
Ptk2-204	ENSMUST00000226742.1	2820	No protein	Retained intron	-	-	
Ptk2-202	ENSMUST00000226454.1	542	No protein	Retained intron	-	-	
Ptk2-214	ENSMUST00000228457.1	259	No protein	Retained intron	-	-	

The strategy is based on the design of *Ptk2-201* transcript,the transcription is shown below:

Genomic Information



Source: : https://www.ensembl.org

Protein Information

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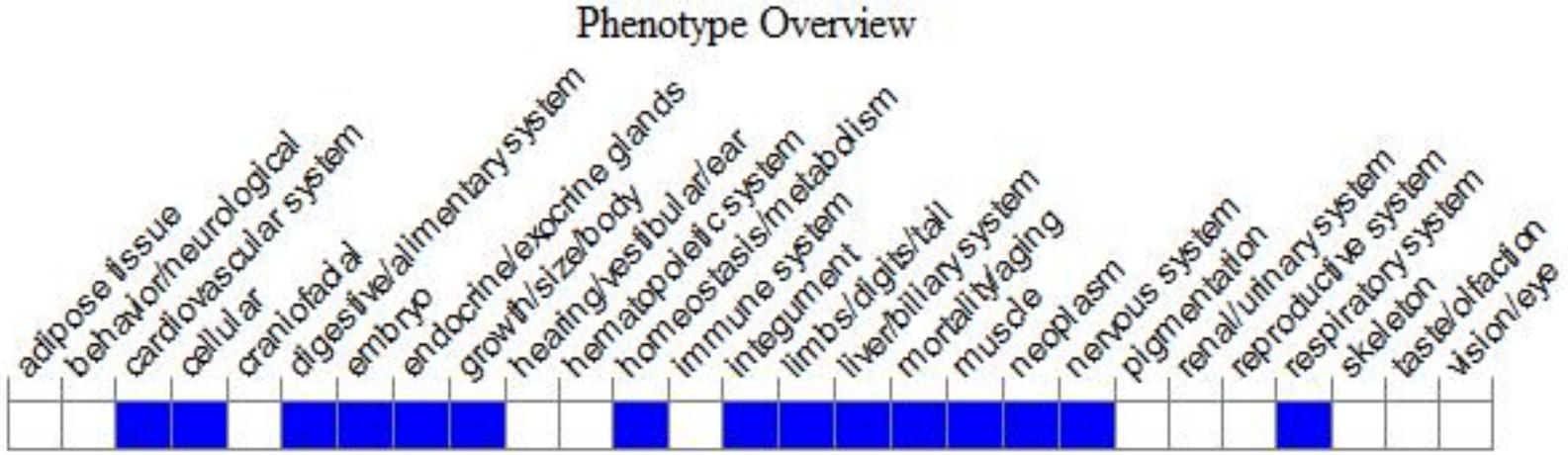
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



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 a null allele die before or during organogenesis with growth retardation, abnormal embryonic and extra embryonic tissue development, and abnormal vascular development.

Source: https://www.informatics.jax.org

Important Information

➢ According to the existing MGI data,mice homozygous for a null allele die before or during organogenesis with growth retardation, abnormal embryonic and extra embryonic tissue development, and abnormal vascular development.

➢ The *Ptk2* 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.

➢Transcripts Ptk2-206, 207,209,212 may not be disrupted.

➢ This strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes,all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.