

Pkp4 Cas9-KO Strategy

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Project Overview



Project Name

Pkp4

Project type

Cas9-KO

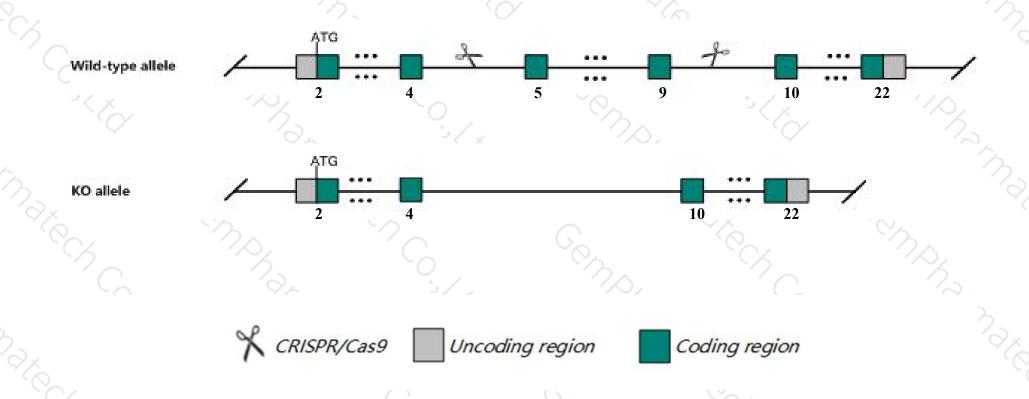
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Pkp4* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Pkp4* gene has 14 transcripts. According to the structure of *Pkp4* gene, exon5-exon9 of *Pkp4-202*(ENSMUST00000102754.10) transcript is recommended as the knockout region. The region contains 1279bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Pkp4* gene. The brief process is as follows: CRISPR/Cas9 system were

Notice



- > According to the existing MGI data, an uncharacterized gene trap insertion does not result in an obvious phenotype during the observation period early in life, although abnormalities may still develop at older age.
- The *Pkp4* gene is located on the Chr2. 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)



Pkp4 plakophilin 4 [Mus musculus (house mouse)]

Gene ID: 227937, updated on 24-Oct-2019

▲ Summary

Official Symbol Pkp4 provided by MGI

Official Full Name plakophilin 4 provided by MGI

Primary source MGI:MGI:109281

See related Ensembl: ENSMUSG00000026991

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 Armrp; p0071; 5031422109Rik; 9430019K17Rik

Expression Ubiquitous expression in kidney adult (RPKM 42.6), cerebellum adult (RPKM 33.0) and 28 other tissues See more

Orthologs <u>human</u> all

- Genomic context

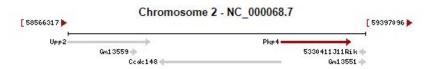
☆ ?

Location: 2; 2 C1.1

See Pkp4 in Genome Data Viewer

Exon count: 25

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (5916085059355205)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (5899890759193262)



Transcript information (Ensembl)



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

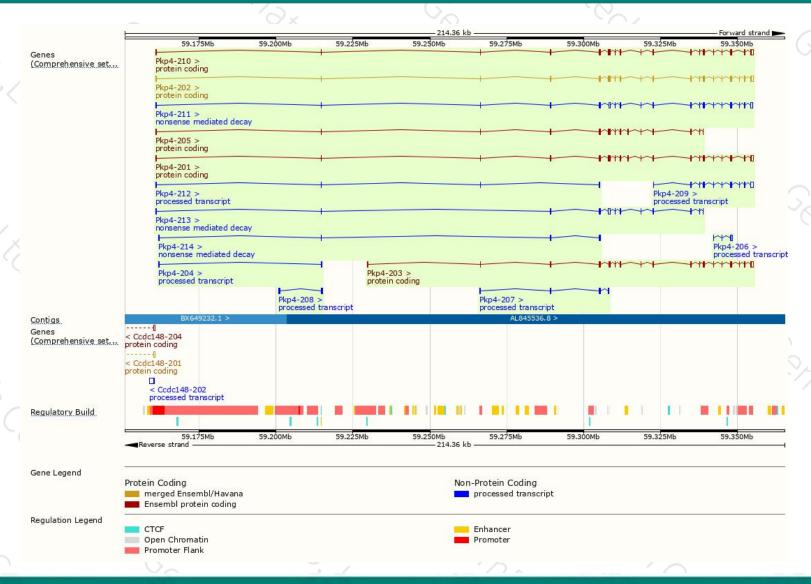
Name	Transcript ID	bp 🛊	Protein	Biotype	CCDS	UniProt 🍦	Flags
Pkp4-202	ENSMUST00000102754.10	4614	<u>1190aa</u>	Protein coding	CCDS16052 ₽	Q68FH0₽	TSL:1 GENCODE basic APPRIS P3
Pkp4-210	ENSMUST00000168631.7	4484	<u>1147aa</u>	Protein coding	CCDS50588 ₽	Q68FH0₽	TSL:1 GENCODE basic APPRIS ALT1
Pkp4-201	ENSMUST00000037903.14	4378	<u>1163aa</u>	Protein coding	121	A2AS45₺	TSL:5 GENCODE basic
Pkp4-203	ENSMUST00000112577.7	4222	849aa	Protein coding	7.2	A2AS47₺	TSL:5 GENCODE basic
Pkp4-205	ENSMUST00000123908.7	2663	803aa	Protein coding	853	A2AS44₽	CDS 3' incomplete TSL:1
Pkp4-211	ENSMUST00000183359.7	4122	215aa	Nonsense mediated decay	976	V9GXG7₽	TSL:5
Pkp4-213	ENSMUST00000184332.7	2344	<u>46aa</u>	Nonsense mediated decay	170	V9GWY7₽	TSL:5
Pkp4-214	ENSMUST00000184705.7	437	<u>46aa</u>	Nonsense mediated decay	(t + 3)	V9GWY7₽	TSL:3
Pkp4-209	ENSMUST00000151452.7	2505	No protein	Processed transcript	(4)	-	TSL:5
Pkp4-207	ENSMUST00000124725.1	806	No protein	Processed transcript	1940	-	TSL:3
Pkp4-208	ENSMUST00000126749.1	679	No protein	Processed transcript	121	2	TSL:1
Pkp4-206	ENSMUST00000124127.1	661	No protein	Processed transcript	12	2	TSL:2
Pkp4-212	ENSMUST00000183625.7	428	No protein	Processed transcript	85		TSL:5
Pkp4-204	ENSMUST00000122888.7	306	No protein	Processed transcript	959	5	TSL:5

The strategy is based on the design of *Pkp4-202* transcript, the transcription is shown below:



Genomic location distribution





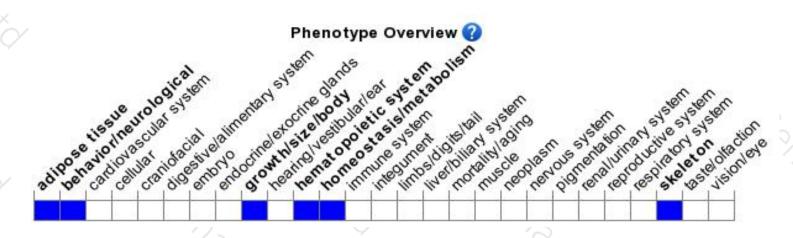
Protein domain





Mouse phenotype description(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, an uncharacterized gene trap insertion does not result in an obvious phenotype during the observation period early in life, although abnormalities may still develop at older age.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





