

Pkp3 Cas9-KO Strategy

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Project Overview



Project Name

Pkp3

Project type

Cas9-KO

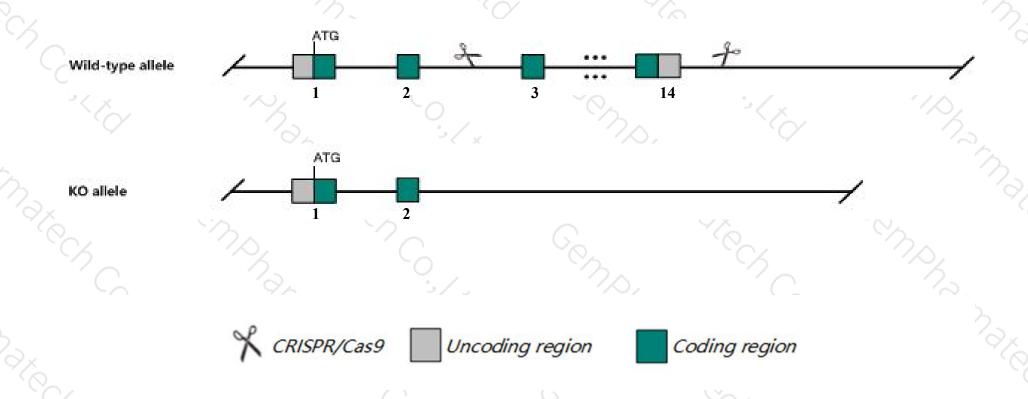
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Pkp3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Pkp3* gene has 9 transcripts. According to the structure of *Pkp3* gene, exon3-exon14 of *Pkp3-202* (ENSMUST00000106039.8) transcript is recommended as the knockout region. The region contains most 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 *Pkp3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for a null allele exhibit retarded hair growth, epidermal thickening and abnormal hair follicles that lead to secondary alopecia and acute dermatitis.
- The knockout region is near to the C-terminal of *Sigirr* gene, this strategy may influence the regulatory function of the C-terminal of *Sigirr* gene.
- > The *Pkp3* gene is located on the Chr7. 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)



Pkp3 plakophilin 3 [Mus musculus (house mouse)]

Gene ID: 56460, updated on 3-Sep-2019

Summary

☆ ?

Official Symbol Pkp3 provided by MGI

Official Full Name plakophilin 3 provided by MGI

Primary source MGI:MGI:1891830

See related Ensembl: ENSMUSG00000054065

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 2310056L12Rik

Expression Biased expression in small intestine adult (RPKM 54.7), colon adult (RPKM 49.3) and 13 other tissues See more

Orthologs <u>human</u> <u>all</u>

Genomic context



Location: 7; 7 F5

See Pkp3 in Genome Data Viewer

Exon count: 15

Annotation release	Status	Assembly	Chr	Location	
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (141078229141090511)	
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (148264128148276409)	

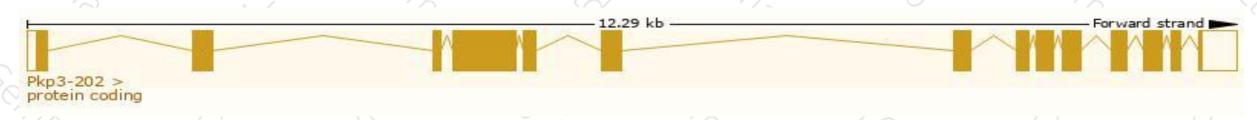
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

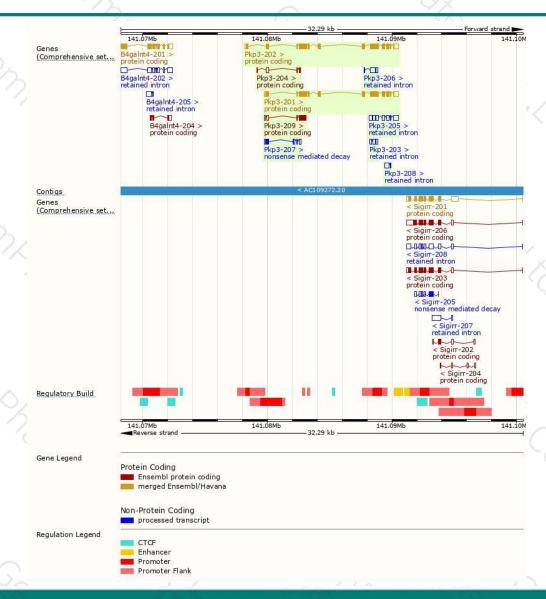
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000106039.8	2919	822aa	Protein coding	CCDS52437	Q9QY23	TSL:1 GENCODE basic APPRIS ALT2
ENSMUST00000066873.4	2848	<u>797aa</u>	Protein coding	CCDS21999	Q9QY23	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000163041.1	866	215aa	Protein coding	ų.	E0CY75	CDS 3' incomplete TSL:2
ENSMUST00000159375.7	417	<u>56aa</u>	Protein coding	2	E0CY06	CDS 3' incomplete TSL:2
ENSMUST00000160869.1	670	<u>87aa</u>	Nonsense mediated decay	ā	E0CYP0	TSL:3
ENSMUST00000160403.7	1425	No protein	Retained intron		* .	TSL:1
ENSMUST00000160615.1	557	No protein	Retained intron	ū.	-	TSL:3
ENSMUST00000159253.1	458	No protein	Retained intron	2	20	TSL:3
ENSMUST00000161142.1	412	No protein	Retained intron	8	=	TSL:3
	ENSMUST00000106039.8 ENSMUST00000066873.4 ENSMUST00000163041.1 ENSMUST00000159375.7 ENSMUST00000160869.1 ENSMUST00000160403.7 ENSMUST00000160615.1 ENSMUST00000159253.1	ENSMUST00000106039.8 2919 ENSMUST00000066873.4 2848 ENSMUST00000163041.1 866 ENSMUST00000159375.7 417 ENSMUST00000160869.1 670 ENSMUST00000160403.7 1425 ENSMUST00000160615.1 557 ENSMUST00000159253.1 458	ENSMUST0000016039.8 2919 822aa ENSMUST00000066873.4 2848 797aa ENSMUST00000163041.1 866 215aa ENSMUST00000159375.7 417 56aa ENSMUST00000160869.1 670 87aa ENSMUST00000160403.7 1425 No protein ENSMUST00000160615.1 557 No protein ENSMUST00000159253.1 458 No protein	ENSMUST00000106039.8 2919 822aa Protein coding ENSMUST00000066873.4 2848 797aa Protein coding ENSMUST00000163041.1 866 215aa Protein coding ENSMUST00000159375.7 417 56aa Protein coding ENSMUST00000160869.1 670 87aa Nonsense mediated decay ENSMUST00000160403.7 1425 No protein Retained intron ENSMUST00000160615.1 557 No protein Retained intron ENSMUST00000159253.1 458 No protein Retained intron	ENSMUST00000106039.8 2919 822aa Protein coding CCDS52437 ENSMUST00000066873.4 2848 797aa Protein coding CCDS21999 ENSMUST00000163041.1 866 215aa Protein coding - ENSMUST00000159375.7 417 56aa Protein coding - ENSMUST00000160869.1 670 87aa Nonsense mediated decay - ENSMUST00000160403.7 1425 No protein Retained intron - ENSMUST00000160615.1 557 No protein Retained intron - ENSMUST00000159253.1 458 No protein Retained intron -	ENSMUST00000106039.8 2919 822aa Protein coding CCDS52437 Q9QY23 ENSMUST00000066873.4 2848 797aa Protein coding CCDS21999 Q9QY23 ENSMUST00000163041.1 866 215aa Protein coding - E0CY75 ENSMUST00000159375.7 417 56aa Protein coding - E0CY06 ENSMUST00000160869.1 670 87aa Nonsense mediated decay - E0CYP0 ENSMUST00000160403.7 1425 No protein Retained intron - - ENSMUST00000160615.1 557 No protein Retained intron - - ENSMUST00000159253.1 458 No protein Retained intron - -

The strategy is based on the design of *Pkp3-202* transcript, The transcription is shown below



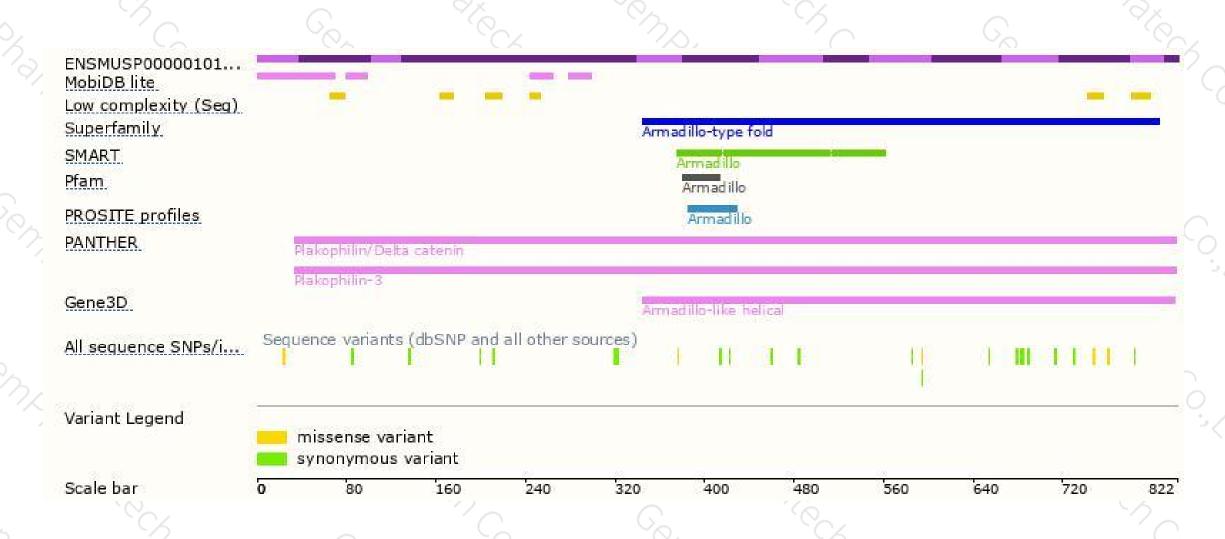
Genomic location distribution





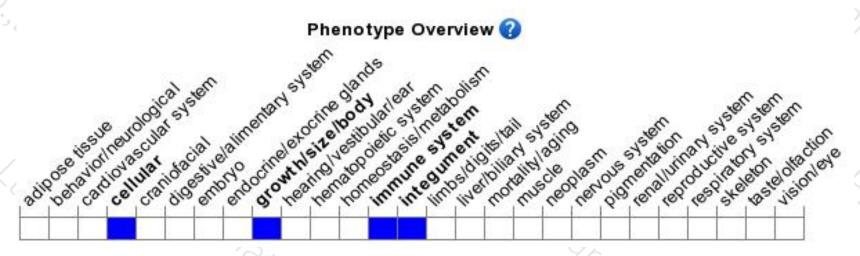
Protein domain





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, Mice homozygous for a null allele exhibit retarded hair growth, epidermal thickening and abnormal hair follicles that lead to secondary alopecia and acute dermatitis.



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





