

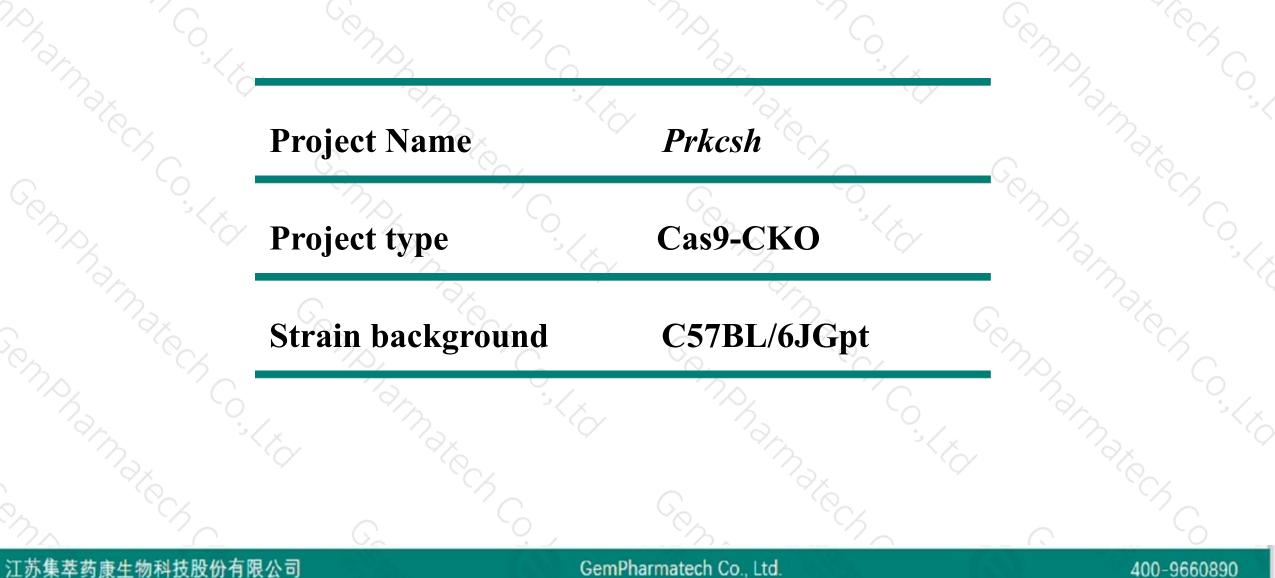
Prkcsh Cas9-CKO Strategy

Designer: Reviewer Design Date: Ruirui Zhang Huimin Su

2019-8-15

Project Overview





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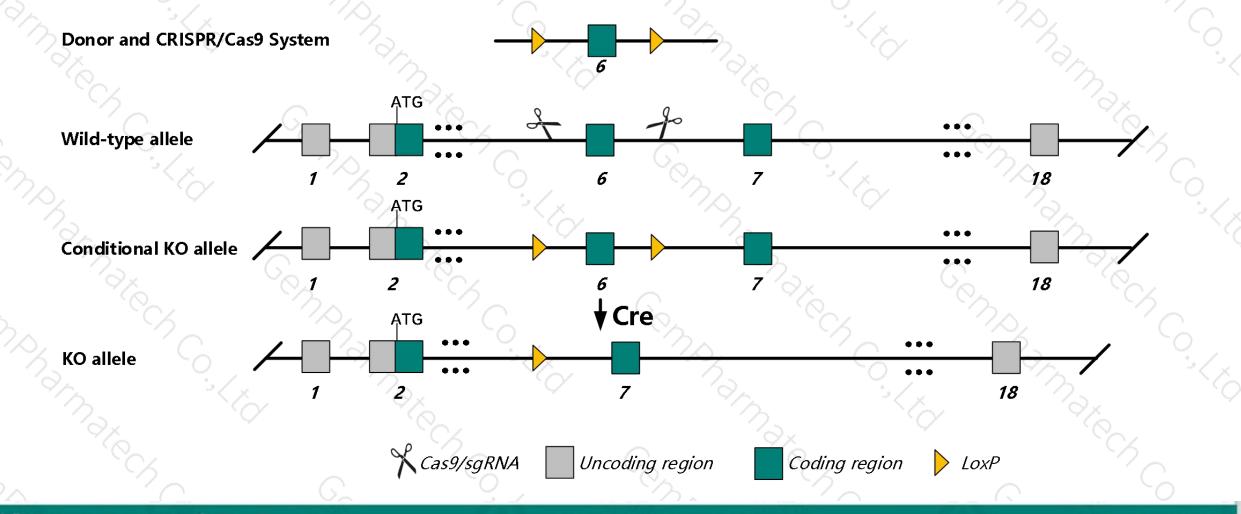
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Conditional Knockout strategy



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



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The Prkcsh gene has 5 transcripts. According to the structure of Prkcsh gene, exon6 of Prkcsh-201 (ENSMUST0000003493.8) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Prkcsh* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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.

The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice



- According to the existing MGI data, mice homozygous for a knock-out allele exhibit embryonic lethality during organogenesis. Mice homozygous for a conditional allele activated in the kidneys or ubiquitously develop polycystic kidney and liver phenotypes, respectively.
- The distance of *Ccdc151* gene from exon6 of *Prkcsh* gene is about 3.9kb, this strategy may affect the regulatory function of the 5-terminals of Ccdc151 gene.
- The *Prkcsh* gene is located on the Chr9. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

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Gene information (NCBI)



Prkcsh protein kinase C substrate 80K-H [Mus musculus (house mouse)]

Gene ID: 19089, updated on 12-Aug-2019

Summary

Official Symbol	Prkcsh provided by MGI								
Official Full Name	protein kinase C substrate 80K-H provided by MGI								
Primary source	MGI:MGI:107877								
See related	Ensembl:ENSMUSG0000003402								
Gene type	protein coding								
RefSeq status	VALIDATED								
Organism	Mus musculus								
Lineage	ge Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;								
	Murinae; Mus; Mus								
Also known as	80K-H; PKCSH								
Expression	Ubiquitous expression in adrenal adult (RPKM 75.3), duodenum adult (RPKM 65.8) and 28 other tissues See more								
Orthologs	gs <u>human all</u>								
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Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Prkcsh-205	ENSMUST00000216344.1	2228	<u>521aa</u>	Protein coding	CCDS22918	<u>008795 Q3U518</u>	TSL:1 GENCODE basic APPRIS P3	
Prkcsh-201	ENSMUST0000003493.8	2012	<u>521aa</u>	Protein coding	CCDS22918	008795 Q3U518	TSL:1 GENCODE basic APPRIS P3	
Prkcsh-202	ENSMUST00000115331.9	1983	<u>528aa</u>	Protein coding	CCDS80967	008795	TSL:1 GENCODE basic APPRIS ALT2	
Prkcsh-204	ENSMUST00000215795.1	601	<u>119aa</u>	Protein coding	20	A0A1L1ST83	CDS 3' incomplete TSL:2	
Prkcsh-203	ENSMUST00000214565.1	T00000214565.1 2092 No protein Retained intron		TSL:1				

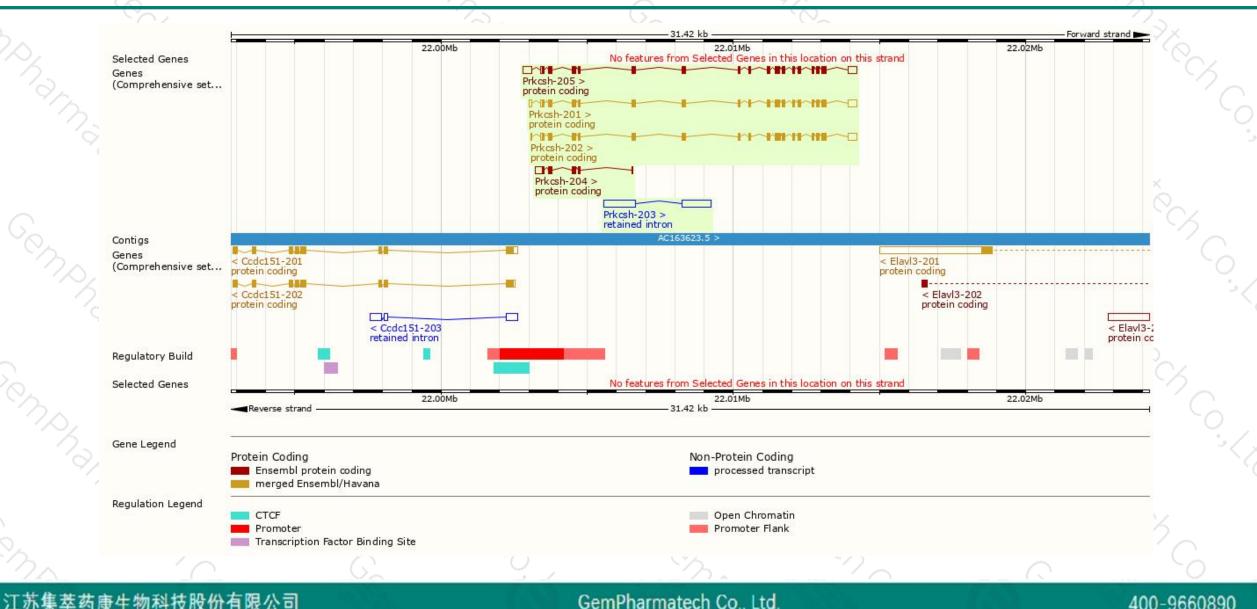
11.21 kb

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

Prkcsh-201 > protein coding Forward strand

Genomic location distribution

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Protein domain



9	ENSMUSP00000003 SIFTS import	<u> </u>				`%.		<u> </u>		
	MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils) Cleavage site (Sign Superfamily	LDL rece	ptor-like superfamily	EF-har	nd domain pair	_		SSF50911		
	Pfam	Glucosidase II beta subunit, N-ter	minal	EF-	hand domain		Glu cos idas	e 2 subunit beta-like		
Z	PROSITE profiles PROSITE patterns PANTHER				od domain F-Hand 1, calcium-bi	nding site				
	Gene3D	Glucosidase 2 subunit beta Glucosidase II beta subunit-like LDL receptor-like super	family	1.10.238,	10			Mannose-6-phosphate re	aceptor binding domain su	
	All sequence SNPs/i	Sequence variants (dbSNP and a	ll other sources)	i ii iiii	6.6		î.	1.0		
	Variant Legend inframe insertion missense variant				inframe deletion synonymous variant					
	Scale bar	io ico	120	180	240	300	360	420	521	
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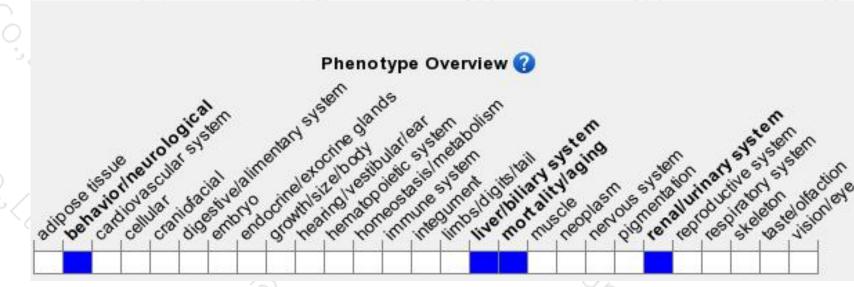
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Mouse phenotype description(MGI)





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 knock-out allele exhibit embryonic lethality during organogenesis. Mice homozygous for a conditional allele activated in the kidneys or ubiquitously develop polycystic kidney a liver phenotypes, respectively.

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



