

Pacrgl Cas9-CKO Strategy

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Project Overview



Project Name Pacrgl

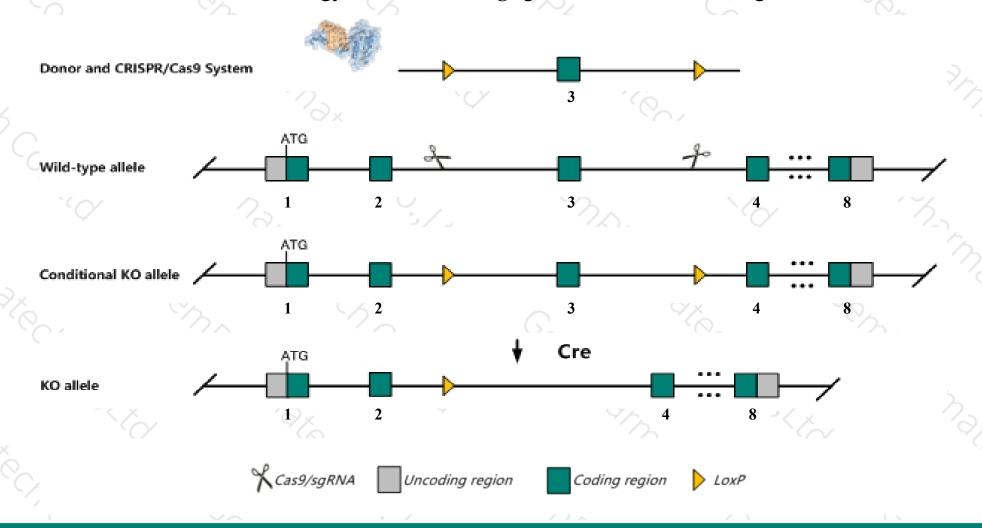
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



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



Technical routes



- ➤ The *Pacrgl* gene has 9 transcripts. According to the structure of *Pacrgl* gene, exon3 of *5730480H06Rik-205*(ENSMUST00000196950.4) transcript is recommended as the knockout region. The region contains 68bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Pacrgl* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was 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



- ➤ The KO region contains functional region of the Pacrgl gene. Knockout the region may affect the function of 5730480H06Rik gene.
- The *Pacrgl* gene is located on the Chr5. 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.

Gene information (NCBI)



Pacrgl PARK2 co-regulated-like [Mus musculus (house mouse)]

Gene ID: 66768, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Pacrgl provided by MGI

Official Full Name PARK2 co-regulated-like provided by MGI

Primary source MGI:MGI:1914018

See related Ensembl:ENSMUSG00000029089

Gene type protein coding
RefSeq status PROVISIONAL
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 4933428G09Rik

Expression Broad expression in testis adult (RPKM 12.7), CNS E11.5 (RPKM 4.1) and 21 other tissuesSee more

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

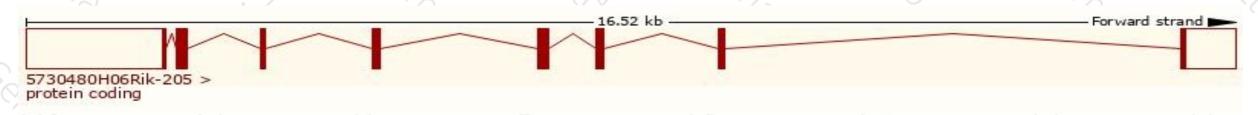
Transcript information (Ensembl)



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

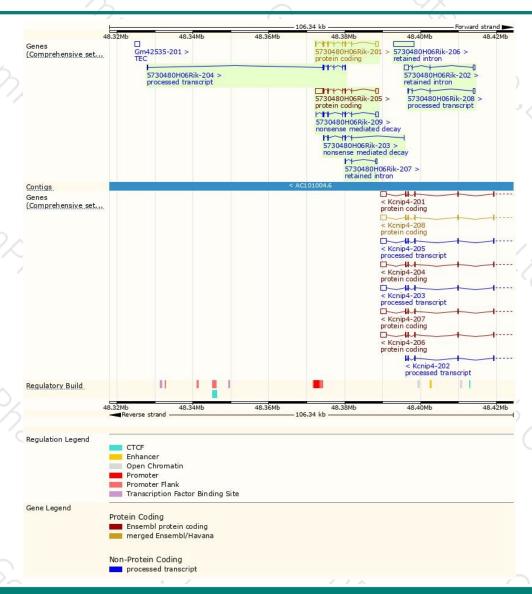
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000196950.4	3300	<u>248aa</u>	Protein coding	CCDS19281	Q9D3X5	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000030968.6	1616	248aa	Protein coding	CCDS19281	Q9D3X5	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000200566.4	1422	<u>93aa</u>	Nonsense mediated decay	-	A0A0G2JE33	TSL:5
ENSMUST00000195960.4	549	<u>59aa</u>	Nonsense mediated decay	-	A0A0G2JE98	CDS 5' incomplete TSL:2
ENSMUST00000196604.1	705	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000199818.1	587	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000197072.1	5405	No protein	Retained intron	-	-	TSL:NA
ENSMUST00000176521.5	1702	No protein	Retained intron	-	-	TSL:1
ENSMUST00000197915.1	648	No protein	Retained intron	-	-	TSL:3
	ENSMUST00000196950.4 ENSMUST00000030968.6 ENSMUST00000200566.4 ENSMUST00000195960.4 ENSMUST00000196604.1 ENSMUST00000199818.1 ENSMUST00000197072.1 ENSMUST00000176521.5	ENSMUST00000196950.4 3300 ENSMUST00000030968.6 1616 ENSMUST00000200566.4 1422 ENSMUST00000195960.4 549 ENSMUST00000196604.1 705 ENSMUST00000199818.1 587 ENSMUST00000197072.1 5405 ENSMUST00000176521.5 1702	ENSMUST00000196950.4 3300 248aa ENSMUST00000030968.6 1616 248aa ENSMUST00000200566.4 1422 93aa ENSMUST00000195960.4 549 59aa ENSMUST00000196604.1 705 No protein ENSMUST00000199818.1 587 No protein ENSMUST00000197072.1 5405 No protein ENSMUST00000176521.5 1702 No protein	ENSMUST00000196950.4 3300 248aa Protein coding ENSMUST00000030968.6 1616 248aa Protein coding ENSMUST00000200566.4 1422 93aa Nonsense mediated decay ENSMUST00000195960.4 549 59aa Nonsense mediated decay ENSMUST00000196604.1 705 No protein Processed transcript ENSMUST00000199818.1 587 No protein Processed transcript ENSMUST00000197072.1 5405 No protein Retained intron ENSMUST000000176521.5 1702 No protein Retained intron	ENSMUST00000196950.4 3300 248aa Protein coding CCDS19281 ENSMUST00000030968.6 1616 248aa Protein coding CCDS19281 ENSMUST00000200566.4 1422 93aa Nonsense mediated decay - ENSMUST00000195960.4 549 59aa Nonsense mediated decay - ENSMUST00000196604.1 705 No protein Processed transcript - ENSMUST00000199818.1 587 No protein Processed transcript - ENSMUST00000197072.1 5405 No protein Retained intron - ENSMUST00000176521.5 1702 No protein Retained intron -	ENSMUST00000196950.4 3300 248aa Protein coding CCDS19281 Q9D3X5 ENSMUST00000030968.6 1616 248aa Protein coding CCDS19281 Q9D3X5 ENSMUST00000200566.4 1422 93aa Nonsense mediated decay - A0A0G2JE33 ENSMUST00000195960.4 549 59aa Nonsense mediated decay - A0A0G2JE98 ENSMUST00000196604.1 705 No protein Processed transcript - - ENSMUST00000199818.1 587 No protein Processed transcript - - ENSMUST00000197072.1 5405 No protein Retained intron - - ENSMUST00000176521.5 1702 No protein Retained intron - -

The strategy is based on the design of 5730480H06Rik-205 transcript, the transcription is shown below:



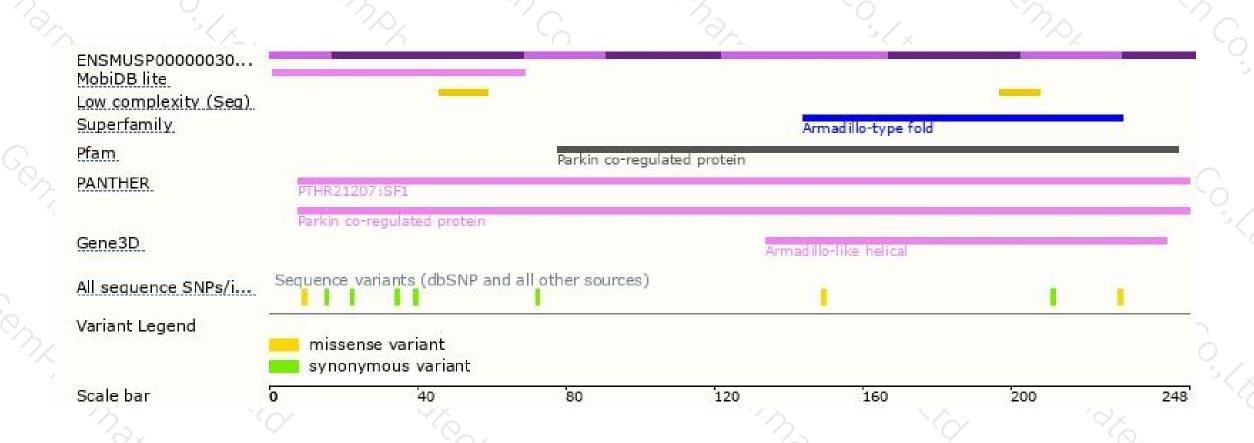
Genomic location distribution





Protein domain







If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





