

# Ulk4 Cas9-CKO Strategy

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Reviewer: Huimin Su

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## **Project Overview**



**Project Name** 

Ulk4

**Project type** 

Cas9-CKO

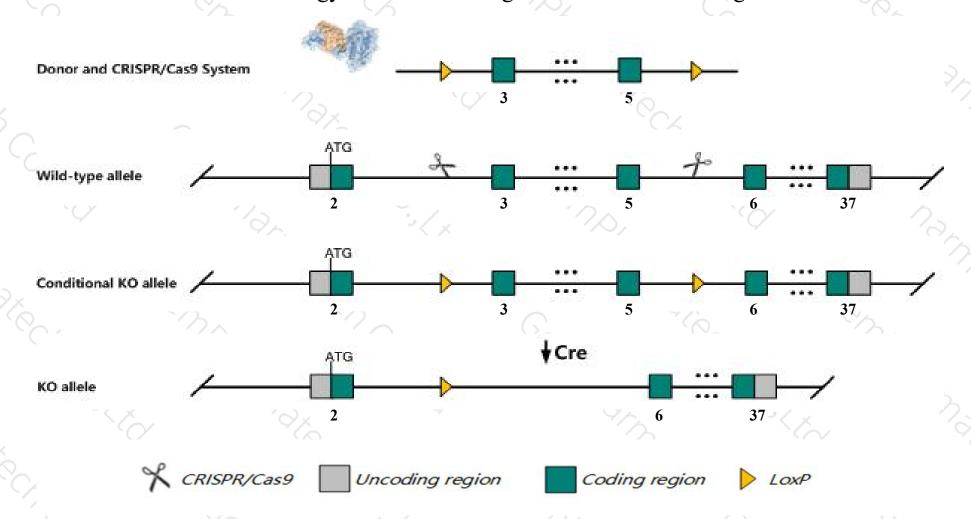
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Ulk4* gene. The schematic diagram is as follows:



### Technical routes



- ➤ The *Ulk4* gene has 10 transcripts. According to the structure of *Ulk4* gene, exon3-exon5 of *Ulk4-209*(ENSMUST00000171923.7) transcript is recommended as the knockout region. The region contains 403bp coding sequence.

  Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ulk4* gene. The brief process is as follows:CRISPR/Cas9 system 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, Homozygotes for a null allele show reduced body size, hydrocephaly, dilated brain ventricles, otitis media, and premature death. Hypomorphic mice show partial corpus callosum aplasia, hydrocephaly, subcommissural organ and ependymal motile ciliary defects, aqueduct stenosis, and impaired CSF flow.
- The *Ulk4* 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.

## Gene information (NCBI)



#### Ulk4 unc-51-like kinase 4 [Mus musculus (house mouse)]

Gene ID: 209012, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Ulk4 provided by MGI

Official Full Name unc-51-like kinase 4 provided by MGI

Primary source MGI:MGI:1921622

See related Ensembl:ENSMUSG00000040936

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 4932415A06Rik, A730098P15

Expression Biased expression in testis adult (RPKM 56.7) and ovary adult (RPKM 3.4)See more

Orthologs <u>human</u> all

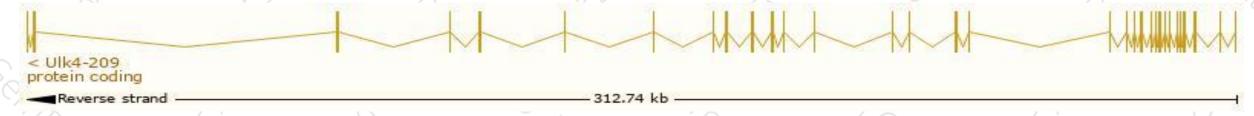
## Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

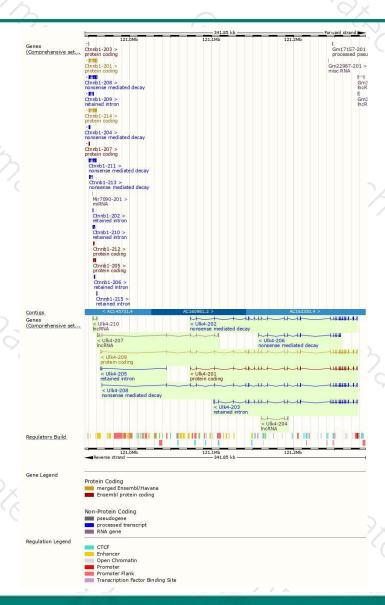
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ulk4-209	ENSMUST00000171923.7	4103	<u>1275aa</u>	Protein coding	CCDS52967	E9Q2P5	TSL:5 GENCODE basic APPRIS P2
Ulk4-201	ENSMUST00000051479.12	3898	<u>1188aa</u>	Protein coding	(#K	E9QKJ7	TSL:1 GENCODE basic APPRIS ALT2
UIk4-202	ENSMUST00000051565.12	4200	<u>54aa</u>	Nonsense mediated decay	320	H7BX20	TSL:1
UIk4-208	ENSMUST00000171061.7	3900	910aa	Nonsense mediated decay	127	Q3V129	TSL:5
Ulk4-206	ENSMUST00000170237.7	1751	<u>139aa</u>	Nonsense mediated decay	-	E9Q220	TSL:1
UIk4-203	ENSMUST00000164336.7	4629	No protein	Retained intron	(#K	-	TSL:1
UIk4-205	ENSMUST00000169176.1	528	No protein	Retained intron	323	ů.	TSL:3
Ulk4-207	ENSMUST00000170406.7	2639	No protein	IncRNA	N <u>-</u> 3	2	TSL:1
Ulk4-210	ENSMUST00000213408.1	759	No protein	IncRNA	151		TSL:3
Ulk4-204	ENSMUST00000164969.1	546	No protein	IncRNA	681	-	TSL:3
			77				

The strategy is based on the design of *Ulk4-209* transcript, The transcription is shown below



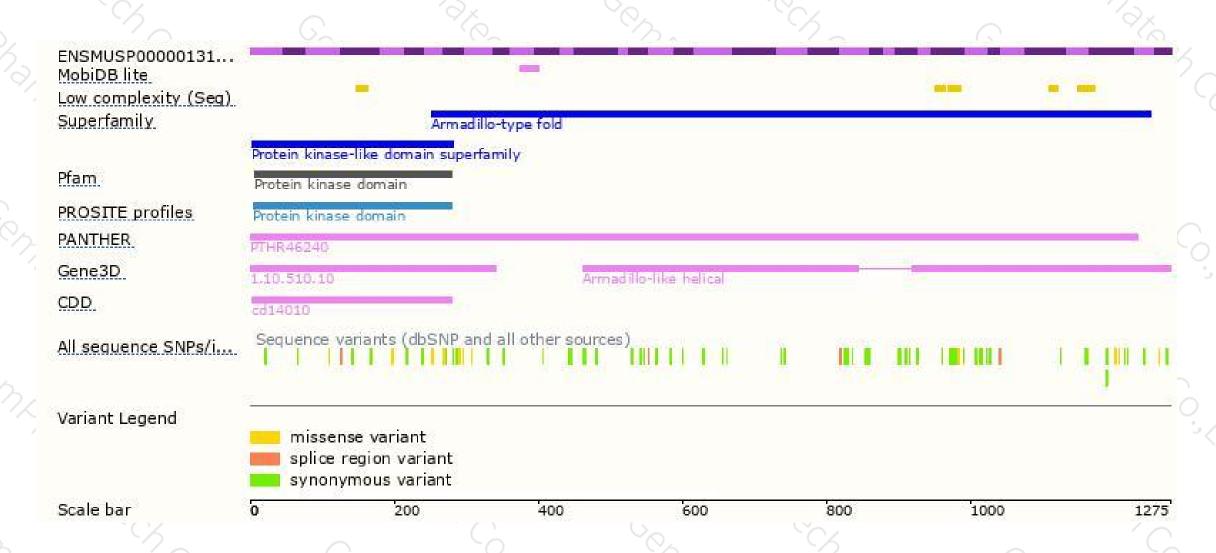
## Genomic location distribution





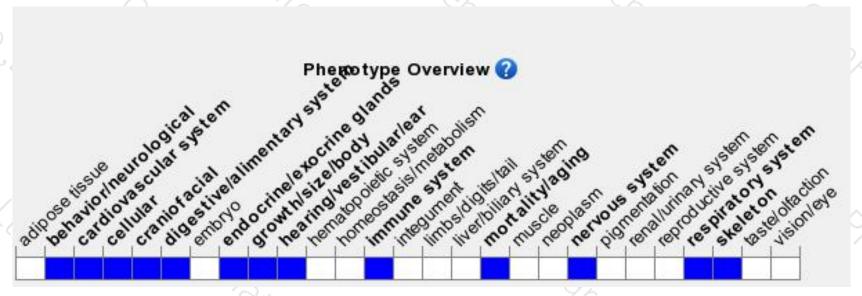
### Protein domain





## 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, Homozygotes for a null allele show reduced body size, hydrocephaly, dilated brain ventricles, otitis media, and premature death. Hypomorphic mice show partial corpus callosum aplasia, hydrocephaly, subcommissural organ and ependymal motile ciliary defects, aqueduct stenosis, and impaired CSF flow.



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





