Kif18a Cas9-CKO Strategy

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Project Overview

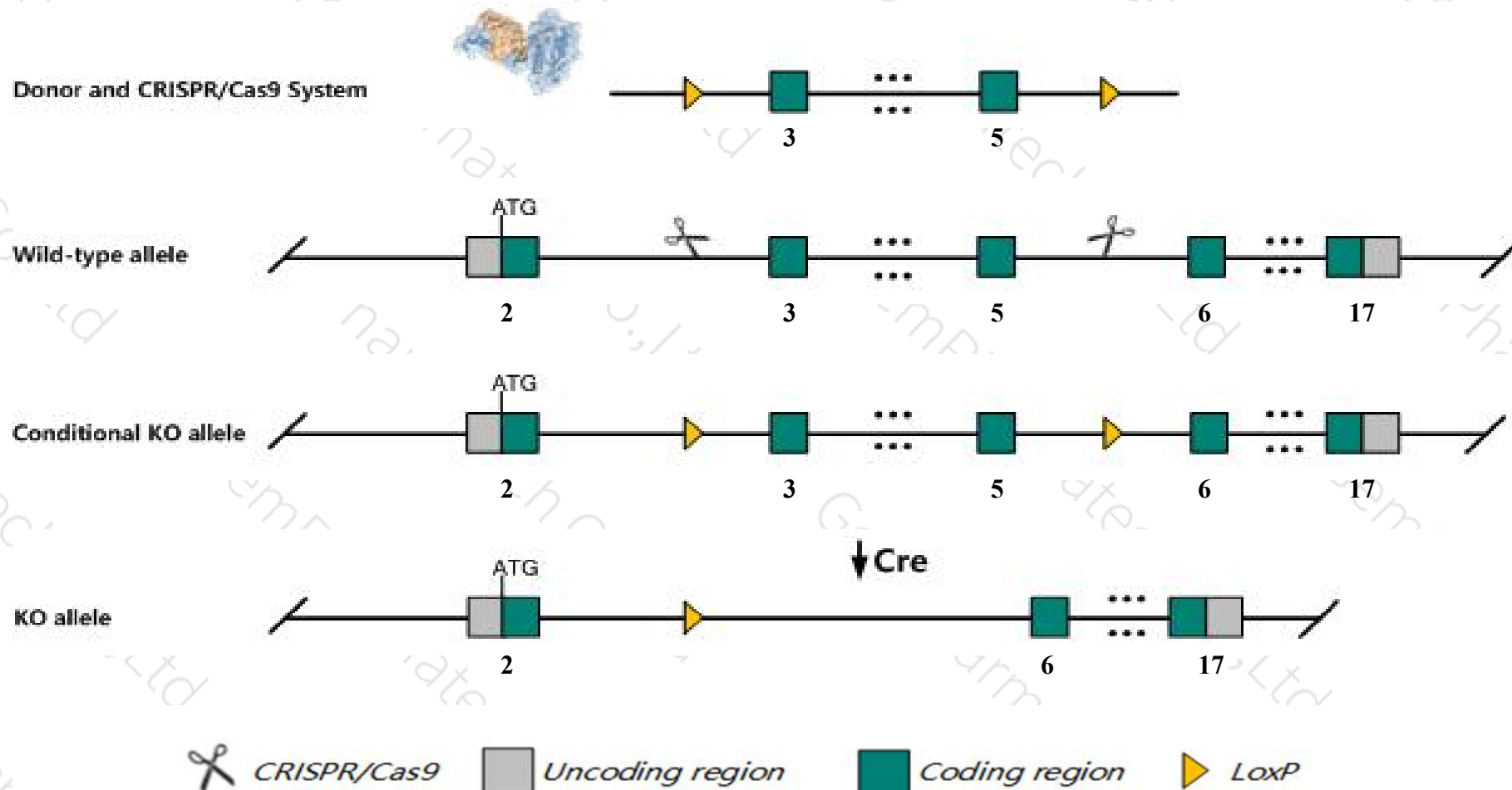|	
Project Name	*Kif18a*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kif18a* gene. The schematic diagram is as follows:

Technical routes

➤ The *Kif18a* gene has 6 transcripts. According to the structure of *Kif18a* gene, exon3-exon5 of *Kif18a-201* (ENSMUST00000028527.7) transcript is recommended as the knockout region.The region contains Ens 374bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Kif18a* 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,Mice homozygous for loss of function alleles exhibit reduced female fertility and male infertility due to primordial germ cell depletion. The sterility phenotype is incompletely penetrant, has variable expressivity, and is modulated by strain background.

➢ The *Kif18a* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Kif18a kinesin family member 18A [Mus musculus (house mouse)]
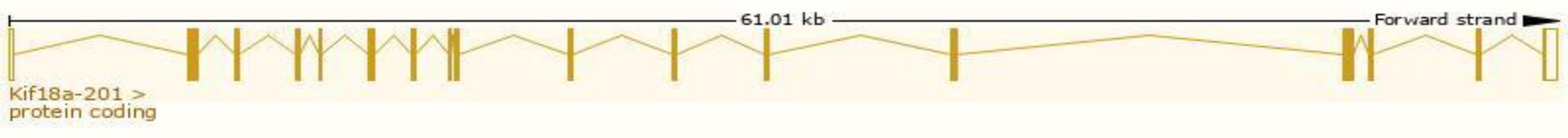
Gene ID: 228421, updated on 13-Mar-2020

▲ Summary

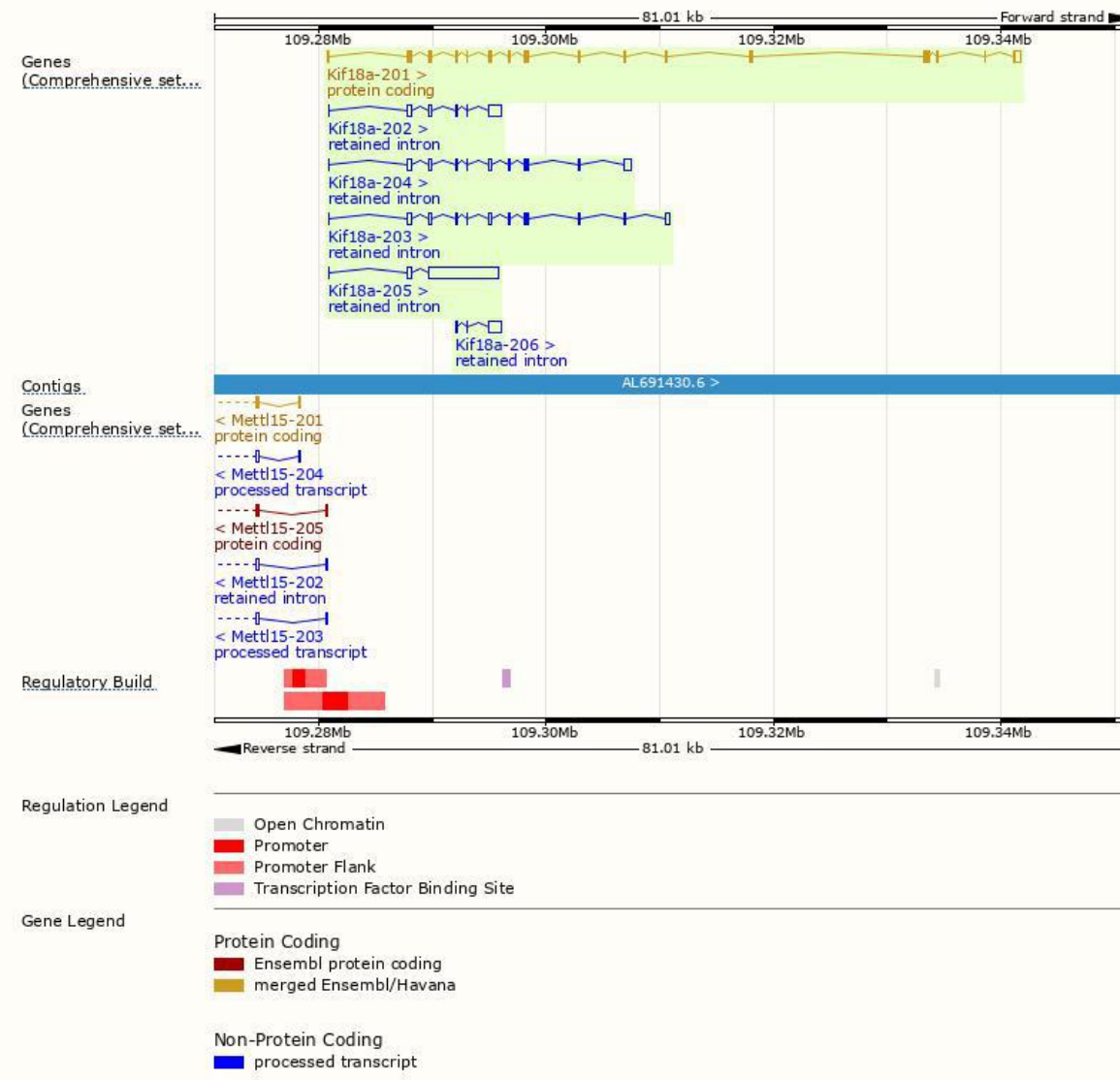|	
Official Symbol	Kif18a provided by MGI
Official Full Name	kinesin family member 18A provided by MGI
Primary source	MGI:MGI:2446977
See related	Ensembl:ENSMUSG00000027115
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU024633, B130001M12Rik, gcd2
Expression	Biased expression in liver E14 (RPKM 8.8), CNS E11.5 (RPKM 7.2) and 10 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kif18a-201	ENSMUST00000028527.7	3369	886aa	Protein coding	CCDS16507	Q91WD7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Kif18a-205	ENSMUST00000152751.1	6509	No protein	Retained intron	-	-	TSL:1
Kif18a-204	ENSMUST00000151395.7	2176	No protein	Retained intron	-	-	TSL:1
Kif18a-203	ENSMUST00000144924.7	1965	No protein	Retained intron	-	-	TSL:1
Kif18a-202	ENSMUST00000130137.7	1934	No protein	Retained intron	-	-	TSL:1
Kif18a-206	ENSMUST00000162515.1	1380	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Kif18a-201* transcript,The transcription is shown below
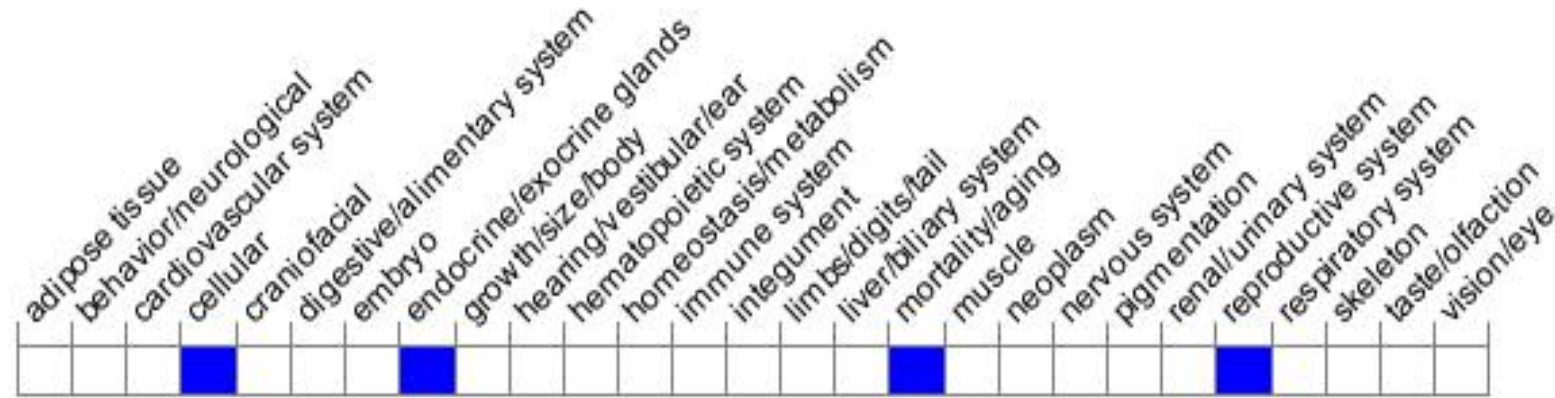
Genomic location distribution

Protein domain

ENSMUSP00000028...											
MobiDB lite											
Low complexity (Seg)											
Coiled-coils (Ncoils)											
Superfamily	P-loop containing nucleoside triphosphate hydrolase										
SMART	Kinesin motor domain										
Prints	Kinesin motor domain										
Pfam	Kinesin motor domain										
PROSITE profiles	Kinesin motor domain										
PROSITE patterns	Kinesin motor domain, conserved site										
PANTHER	Kinesin-like protein										
	PTHR24115:SF399										
Gene3D	Kinesin motor domain superfamily										
CDD	cd01370										
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)										

Variant Legend

■ missense variant
■ synonymous variant

Scale bar	0	80	160	240	320	400	480	560	640	720	800	886

Mouse phenotype description(MGI)

Phenotype Overview

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 loss of function alleles exhibit reduced female fertility and male infertility due to primordial germ cell depletion. The sterility phenotype is incompletely penetrant, has variable expressivity, and is modulated by strain background.

If you have any questions, you are welcome to inquire.
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