

Kif18a Cas9-KO Strategy

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Reviewer:

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Project Overview



Project Name

Kif18a

Project type

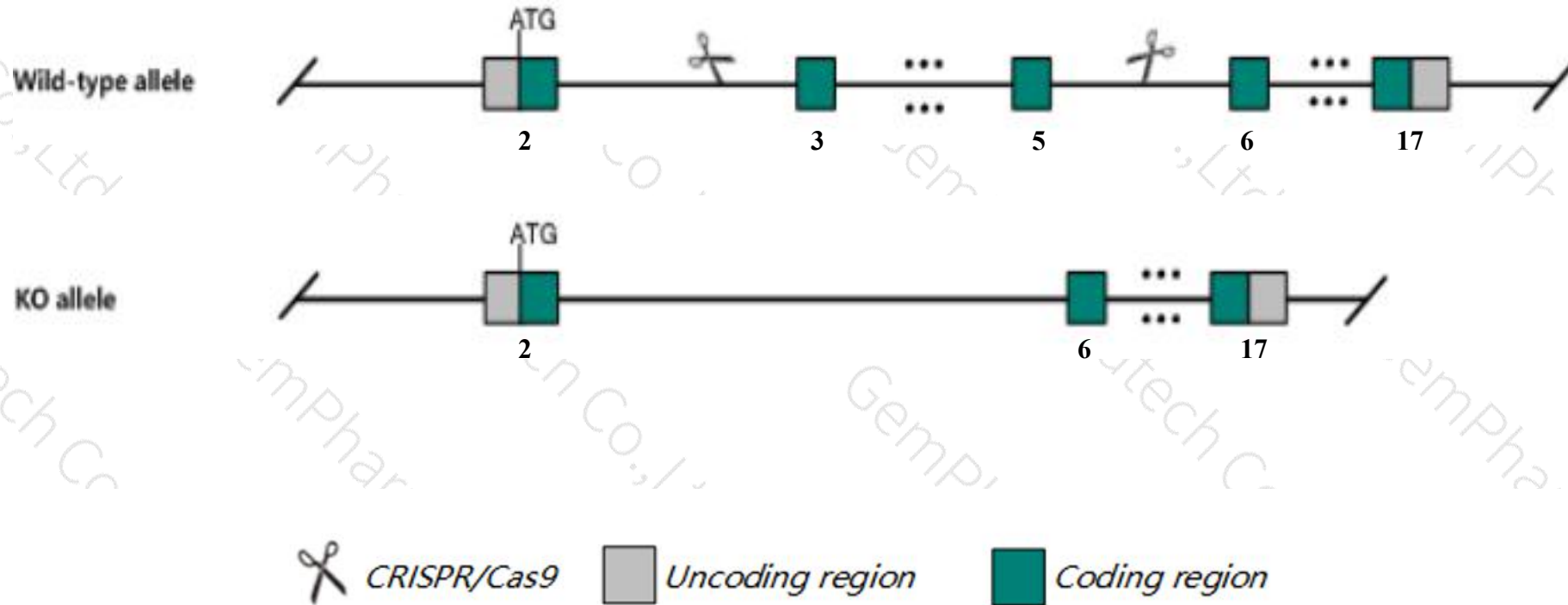
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Kif18a kinesin family member 18A [Mus musculus (house mouse)]

Gene ID: 228421, updated on 13-Mar-2020

Summary



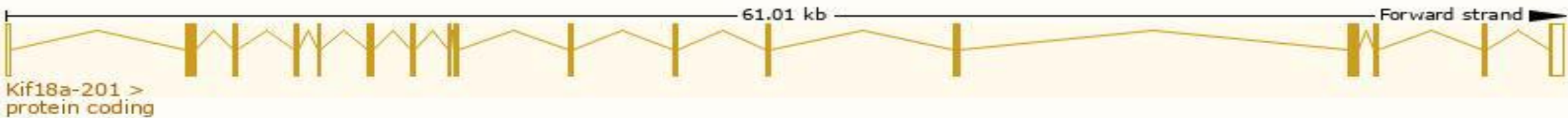
Official Symbol	Kif18a provided by MGI
Official Full Name	kinesin family member 18A provided by MGI
Primary source	MGI:MGI:2446977
See related	Ensembl:ENSMUSG00000027115
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 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 tissues See more
Orthologs	human all

Transcript information (Ensembl)

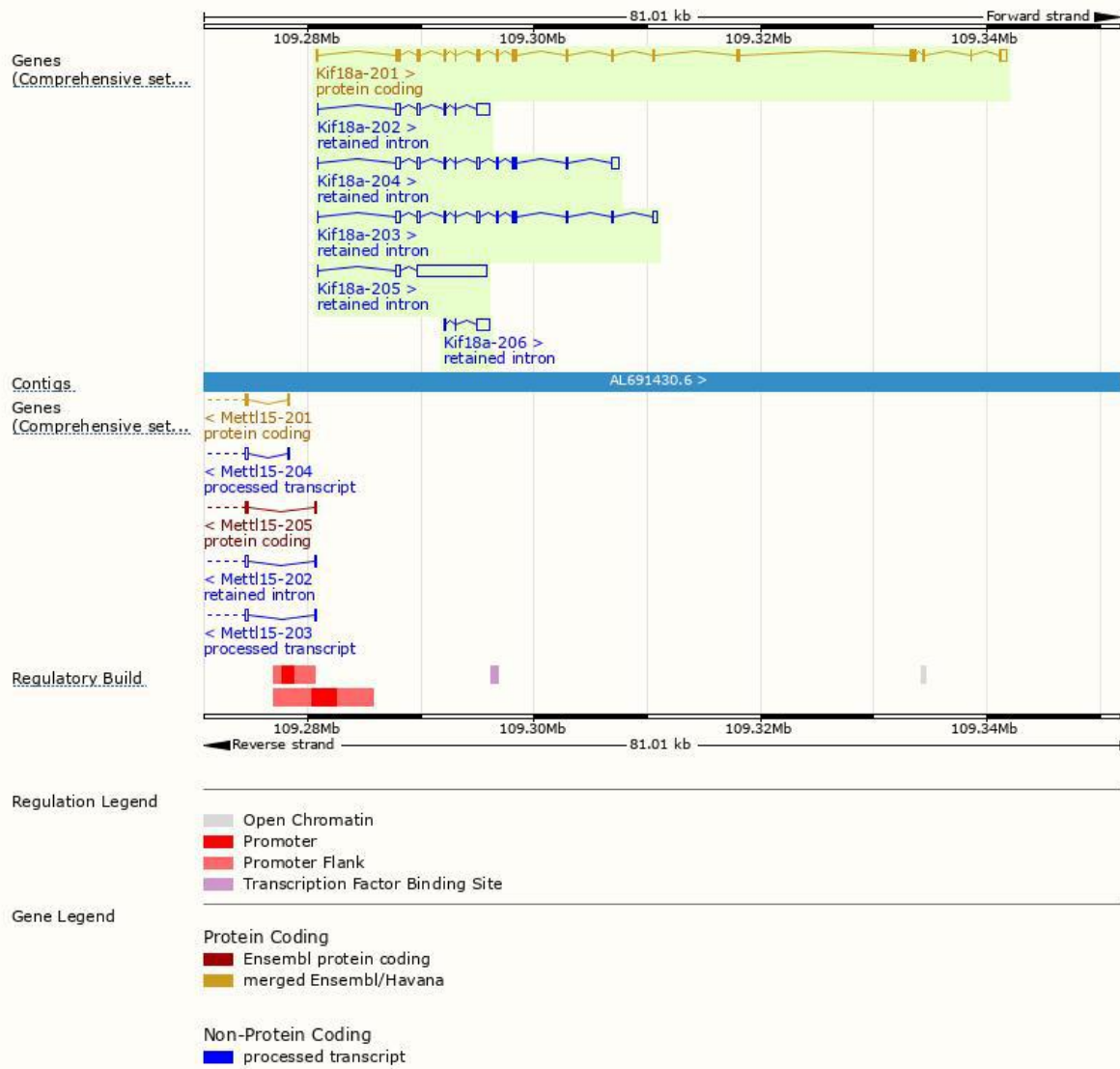
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kif18a-201	ENSMUST00000028527.7	3369	886aa	Protein coding	CCDS16507	Q91WDZ	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

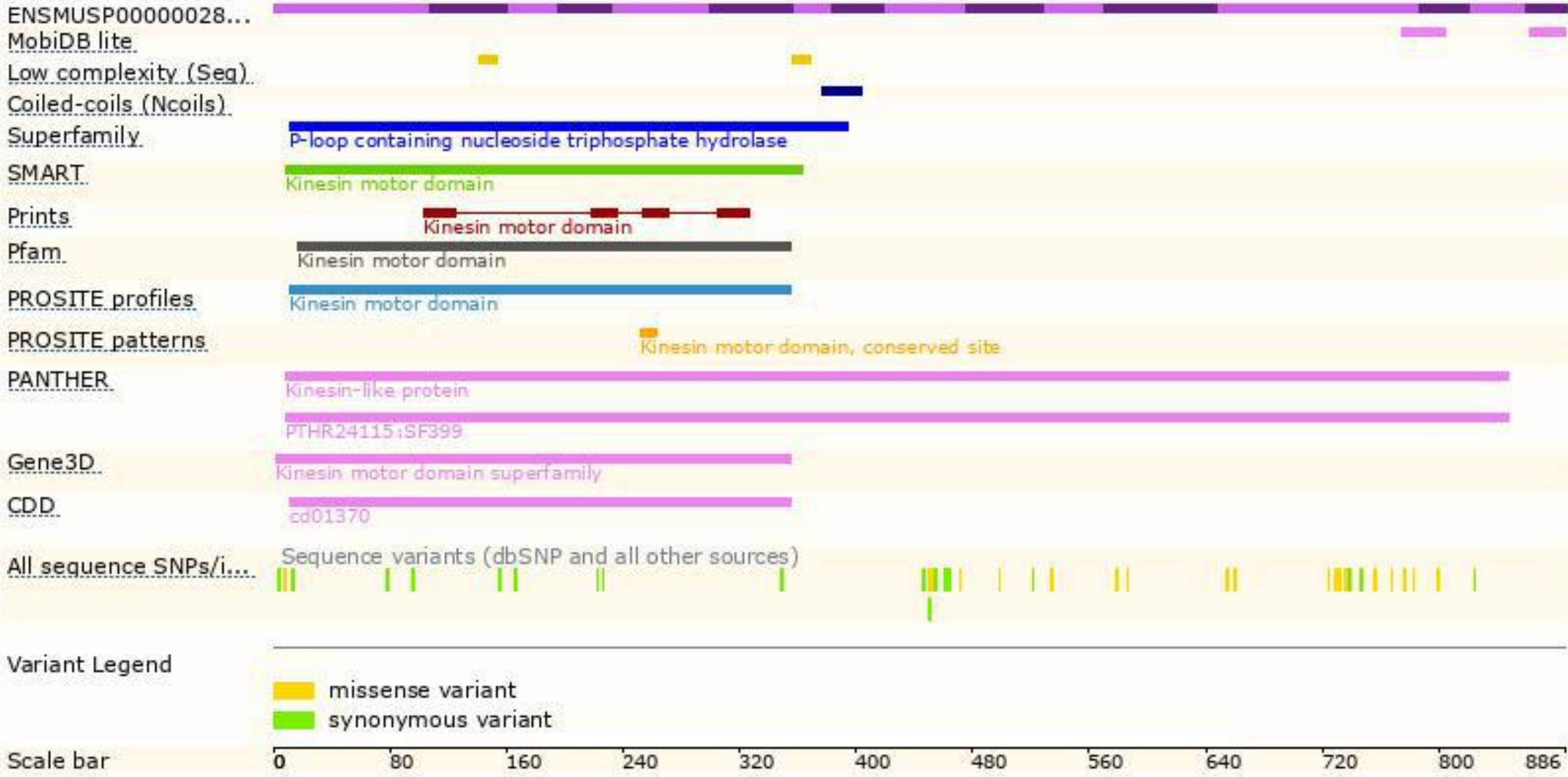
The strategy is based on the design of *Kif18a-201* transcript, The transcription is shown below



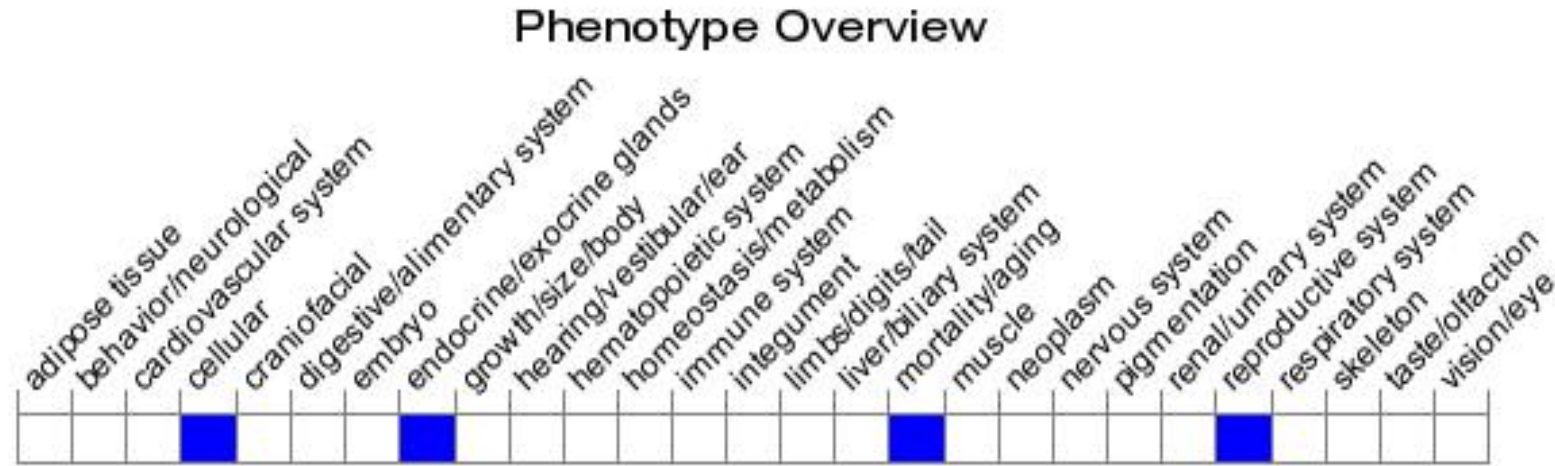
Genomic location distribution



Protein domain



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 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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