

Kif1a Cas9-KO Strategy

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Project Overview

Project Name

Kif1a

Project type

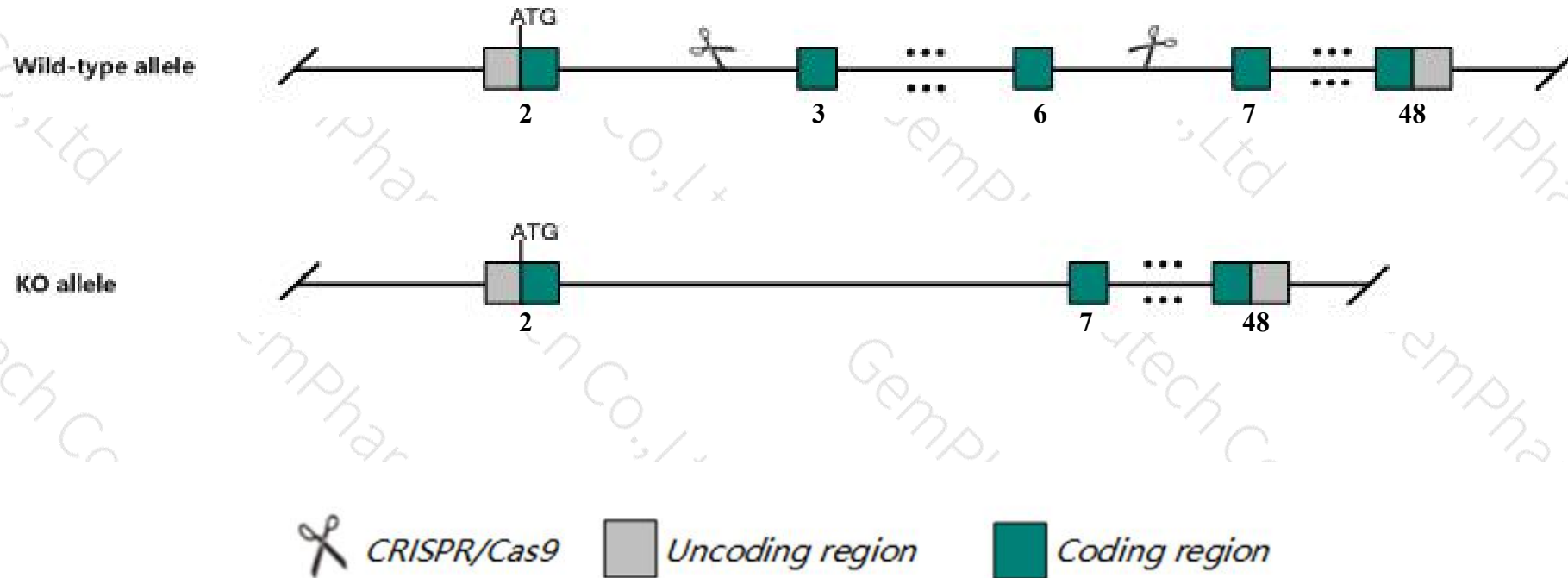
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kif1a* gene. The schematic diagram is as follows:



- The *Kif1a* gene has 11 transcripts. According to the structure of *Kif1a* gene, exon3-exon6 of *Kif1a-202* (ENSMUST00000112958.8) transcript is recommended as the knockout region. The region contains 502bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kif1a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Most mice homozygous for a null allele die within a day of birth, with reduced motor and sensory deficits, decreased synaptic vesicle precursor transport, and significant neuronal degeneration in the central nervous system, but two point mutant alleles cause progressive hindleg paralysis
- The *Kif1a* gene is located on the Chr1. 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)

Kif1a kinesin family member 1A [*Mus musculus* (house mouse)]

Gene ID: 16560, updated on 24-Dec-2019

Summary

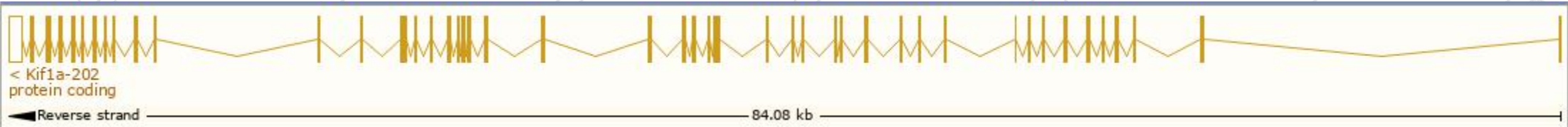
Official Symbol	Kif1a provided by MGI
Official Full Name	kinesin family member 1A provided by MGI
Primary source	MGI:MGI:108391
See related	Ensembl:ENSMUSG00000014602
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ATSV; Kns1; Gm1626; C630002N23Rik
Expression	Biased expression in cortex adult (RPKM 79.2), frontal lobe adult (RPKM 72.1) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

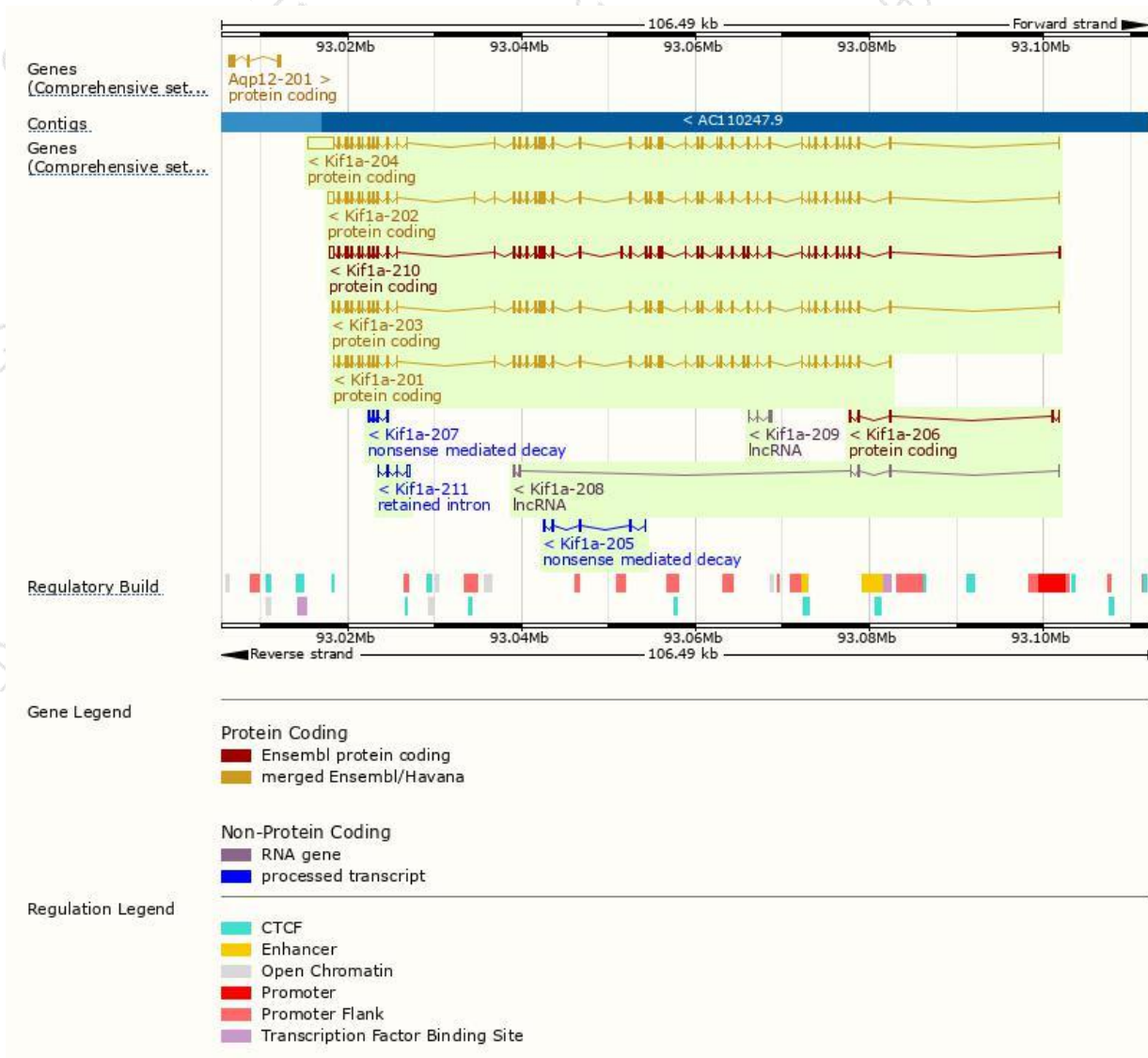
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kif1a-204	ENSMUST00000171796.7	8206	1697aa	Protein coding	CCDS48327	G3UW47	TSL:1 GENCODE basic APPRIS P4
Kif1a-202	ENSMUST00000112958.8	5931	1698aa	Protein coding	CCDS78651	E9Q9G6	TSL:1 GENCODE basic
Kif1a-203	ENSMUST00000171556.7	5391	1689aa	Protein coding	CCDS48326	E9QAN4	TSL:1 GENCODE basic APPRIS ALT 1
Kif1a-201	ENSMUST00000086819.11	5097	1698aa	Protein coding	CCDS78652	Q6TA13	TSL:1 GENCODE basic APPRIS ALT 1
Kif1a-210	ENSMUST00000190723.6	6141	1791aa	Protein coding	-	A0A087WQE8	TSL:5 GENCODE basic APPRIS ALT 1
Kif1a-206	ENSMUST00000186861.1	528	109aa	Protein coding	-	A0A087WSU7	CDS 3' incomplete TSL:2
Kif1a-205	ENSMUST00000186828.1	627	78aa	Nonsense mediated decay	-	A0A087WNM0	CDS 5' incomplete TSL:5
Kif1a-207	ENSMUST00000188136.1	581	46aa	Nonsense mediated decay	-	A0A087WRJ3	CDS 5' incomplete TSL:3
Kif1a-211	ENSMUST00000190854.1	651	No protein	Retained intron	-	-	TSL:3
Kif1a-208	ENSMUST00000188493.1	570	No protein	lncRNA	-	-	TSL:3
Kif1a-209	ENSMUST00000190249.1	325	No protein	lncRNA	-	-	TSL:5

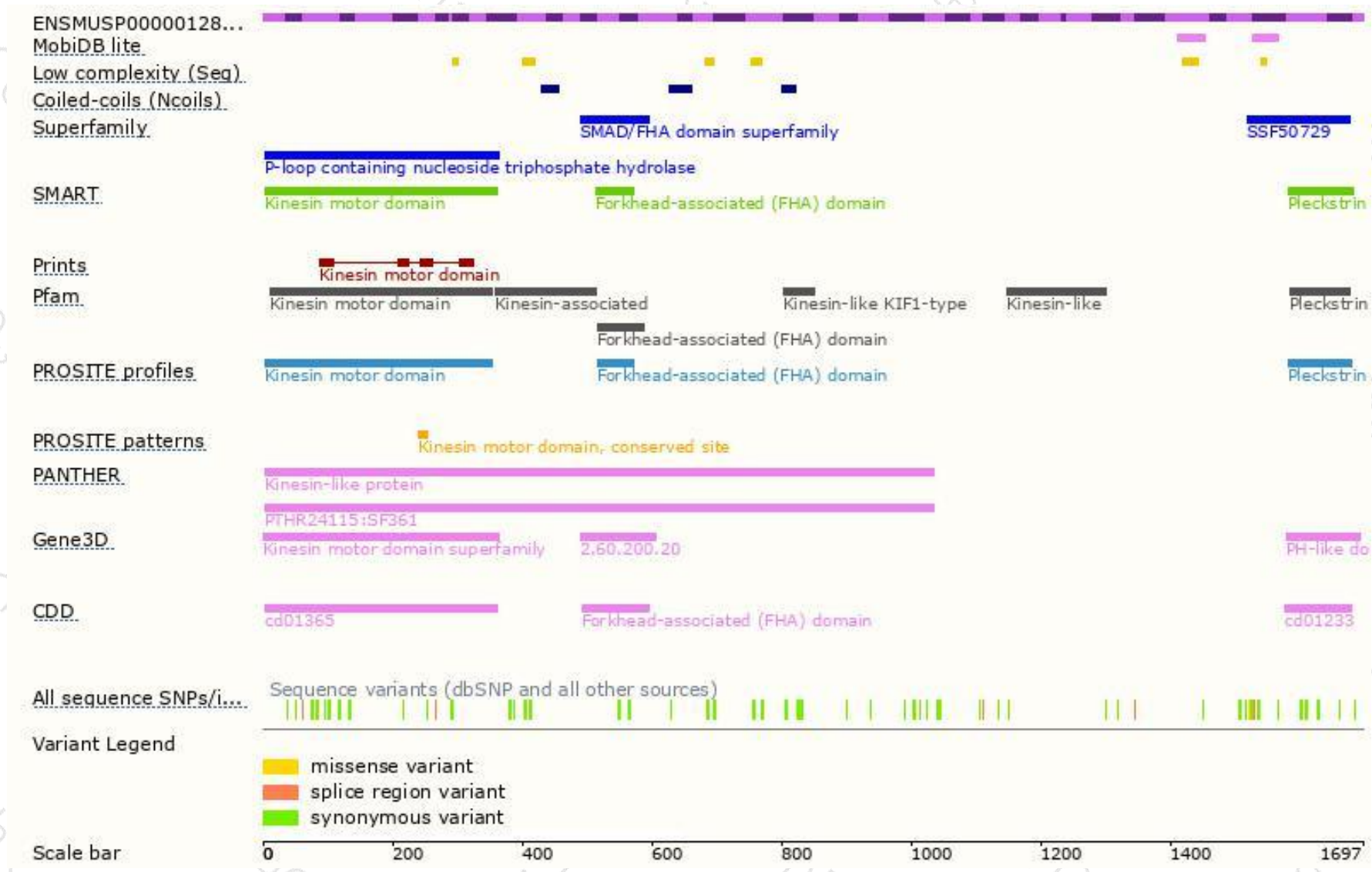
The strategy is based on the design of *Kif1a-202* transcript,The transcription is shown below



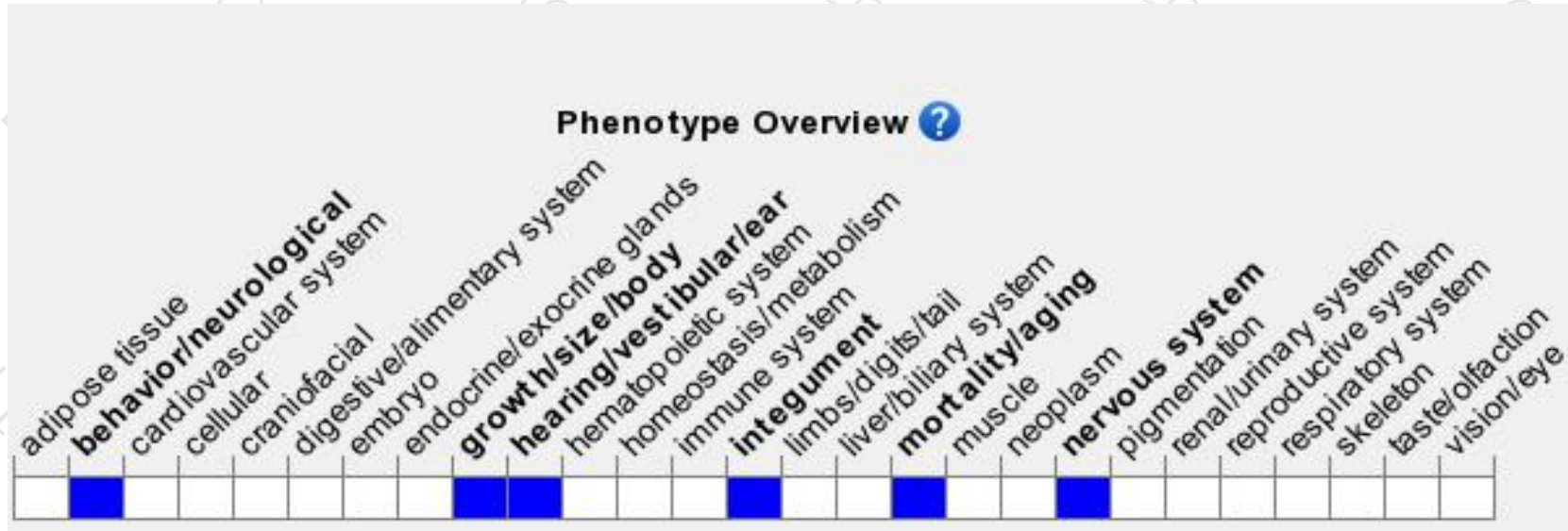
Genomic location distribution



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, Most mice homozygous for a null allele die within a day of birth, with reduced motor and sensory deficits, decreased synaptic vesicle precursor transport, and significant neuronal degeneration in the central nervous system, but two point mutant alleles cause progressive hindleg paralysis

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

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