

Kif21b Cas9-KO Strategy

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Project Overview



Project Name

Kif21b

Project type

Cas9-KO

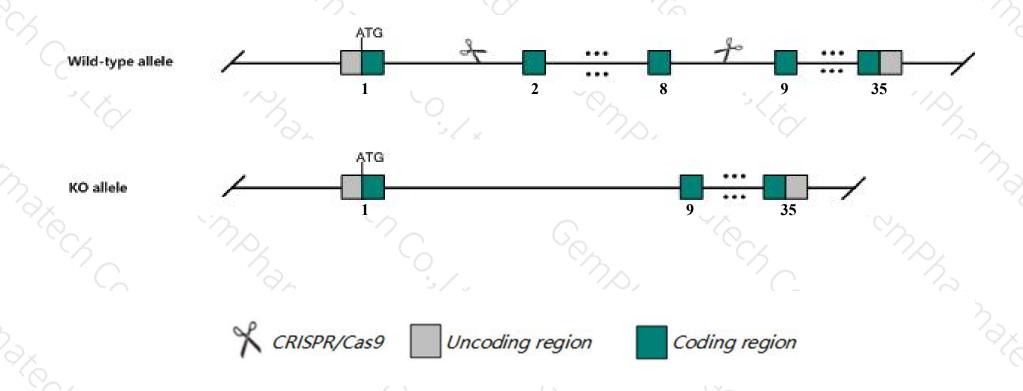
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Kif21b* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Kif21b* gene has 6 transcripts. According to the structure of *Kif21b* gene, exon2-exon8 of *Kif21b-201*(ENSMUST00000075164.10) transcript is recommended as the knockout region. The region contains 1174bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Kif21b* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Homozygous KO reduces dendrite branching and spine density as a result of reduced microtubule growth, resulting in impaired spatial learning and cued conditioning behavior.
- The *Kif21b* 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)



Kif21b kinesin family member 21B [Mus musculus (house mouse)]

Gene ID: 16565, updated on 19-Mar-2019

Summary

☆ ?

Official Symbol Kif21b provided by MGI

Official Full Name kinesin family member 21B provided by MGI

Primary source MGI:MGI:109234

See related Ensembl: ENSMUSG00000041642

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 2610511N21Rik, mKIAA0449

Expression Broad expression in thymus adult (RPKM 74.1), whole brain E14.5 (RPKM 48.8) and 15 other tissuesSee more

Orthologs <u>human</u> all

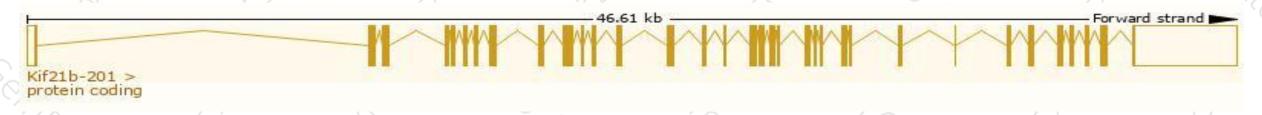
Transcript information (Ensembl)



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

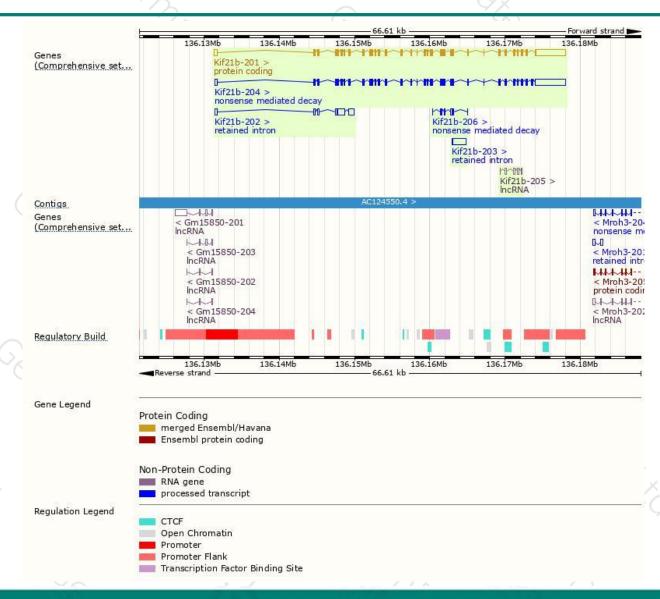
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Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
ENSMUST00000075164.10	9115	<u>1624aa</u>	Protein coding	CCDS15324	F8VQE2	TSL:2 GENCODE basic APPRIS P1	
ENSMUST00000130864.8	9254	<u>1639aa</u>	Nonsense mediated decay	3.43	E9Q0A4	TSL:1	
ENSMUST00000171381.1	583	<u>78aa</u>	Nonsense mediated decay	828	F6ZSF2	CDS 5' incomplete TSL:5	
ENSMUST00000122892.1	2606	No protein	Retained intron	3528	90	TSL:1	
ENSMUST00000127624.2	1802	No protein	Retained intron	127	-	TSL:2	
ENSMUST00000165333.1	701	No protein	IncRNA	363	8-	TSL:5	
	ENSMUST00000130864.8 ENSMUST00000171381.1 ENSMUST00000122892.1 ENSMUST00000127624.2	ENSMUST000000130864.8 9254 ENSMUST00000171381.1 583 ENSMUST00000122892.1 2606 ENSMUST00000127624.2 1802	ENSMUST000000130864.8 9254 1639aa ENSMUST00000171381.1 583 78aa ENSMUST00000122892.1 2606 No protein ENSMUST00000127624.2 1802 No protein	ENSMUST00000075164.10 9115 1624aa Protein coding ENSMUST00000130864.8 9254 1639aa Nonsense mediated decay ENSMUST00000171381.1 583 78aa Nonsense mediated decay ENSMUST00000122892.1 2606 No protein Retained intron ENSMUST00000127624.2 1802 No protein Retained intron	ENSMUST00000075164.10 9115 1624aa Protein coding CCDS15324 ENSMUST00000130864.8 9254 1639aa Nonsense mediated decay - ENSMUST00000171381.1 583 78aa Nonsense mediated decay - ENSMUST00000122892.1 2606 No protein Retained intron - ENSMUST00000127624.2 1802 No protein Retained intron -	ENSMUST00000075164.10 9115 1624aa Protein coding CCDS15324 F8VQE2 ENSMUST00000130864.8 9254 1639aa Nonsense mediated decay - E9Q0A4 ENSMUST00000171381.1 583 78aa Nonsense mediated decay - F6ZSF2 ENSMUST00000122892.1 2606 No protein Retained intron - - ENSMUST00000127624.2 1802 No protein Retained intron - -	

The strategy is based on the design of *Kif21b-201* transcript, The transcription is shown below



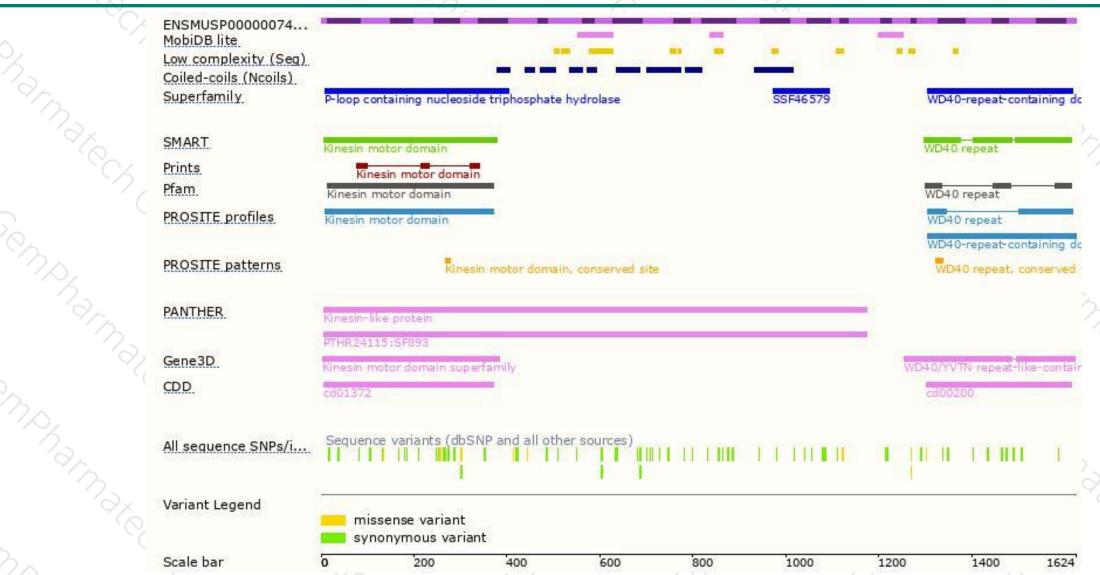
Genomic location distribution





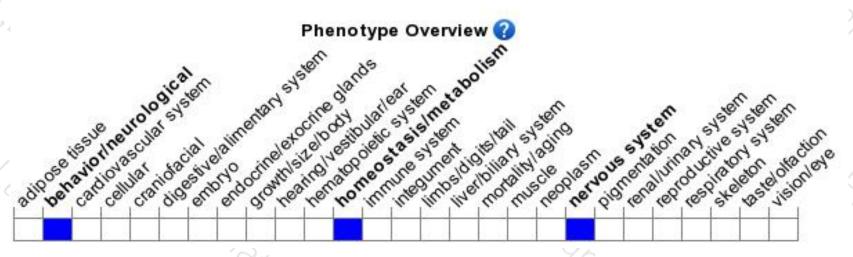
Protein domain





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, Homozygous KO reduces dendrite branching and spine density as a result of reduced microtubule growth, resulting in impaired spatial learning and cued conditioning behavior.



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





