

# Klhl1 Cas9-CKO Strategy

**Designer:** 

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**Design Date:** 

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## **Project Overview**



**Project Name** 

Klhl1

**Project type** 

Cas9-CKO

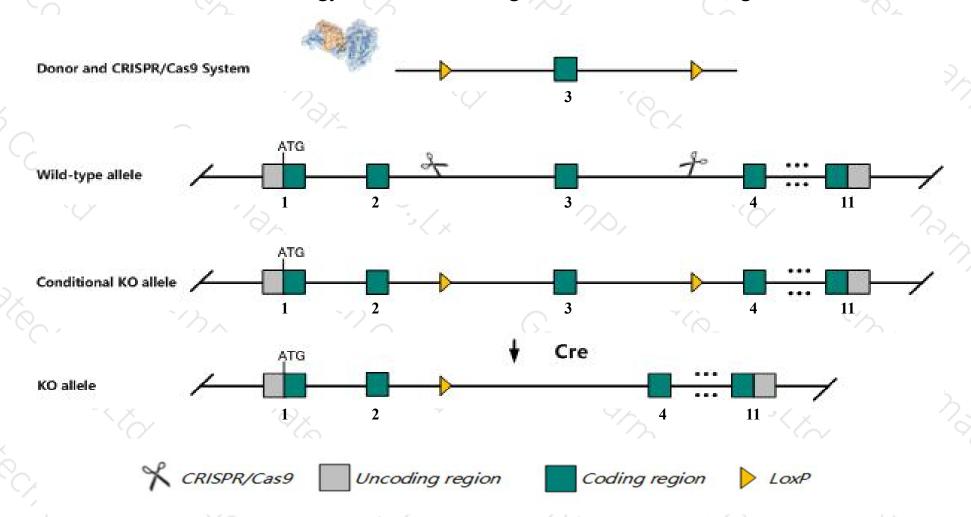
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Klhl1* gene. The schematic diagram is as follows:



### Technical routes



- ➤ The *Klhl1* gene has 1 transcript. According to the structure of *Klhl1* gene, exon3 of *Klhl1-201*(ENSMUST00000022666.8) transcript is recommended as the knockout region. The region contains 137bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Klhl1* 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 both homozygous and heterozygous for disruption of this gene develop abnormalities in gait and defects in motor coordination with time. Dendritic atrophy of Purkinje cells is also seen.
- > The *Klhl1* gene is located on the Chr14. 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)



#### KIhl1 kelch-like 1 [ Mus musculus (house mouse) ]

Gene ID: 93688, updated on 13-Aug-2019

#### Summary



Official Symbol Klhl1 provided by MGI

Official Full Name kelch-like 1 provided by MGI

Primary source MGI:MGI:2136335

See related Ensembl: ENSMUSG00000022076

Gene type protein coding
RefSeq status PROVISIONAL
Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;

Murinae; Mus; Mus

Also known as mKIAA1490

Expression Biased expression in CNS E18 (RPKM 3.1), whole brain E14.5 (RPKM 2.5) and 5 other tissues See more

Orthologs human all

## Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

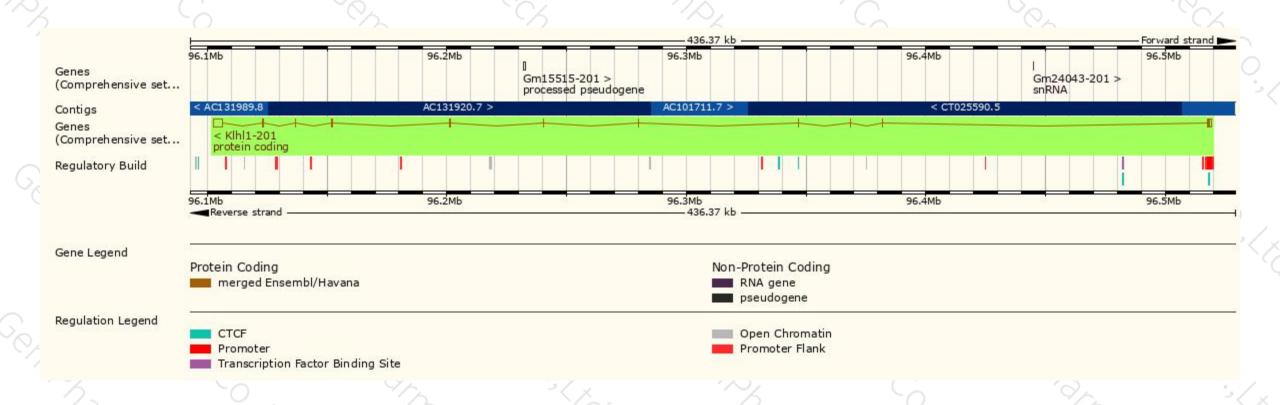
Name 🍦	Transcript ID 👙	bp 🌲	Protein 🍦	Biotype 🔺	CCDS 🍦	UniProt 🌲	Flags		
KIhI1-201	ENSMUST00000022666.8	6645	<u>751aa</u>	Protein coding	CCDS27308 ₽	Q9J174₽	TSL:1	GENCODE basic	APPRIS P1

The strategy is based on the design of *Klhl1-201* transcript, the transcription is shown below:



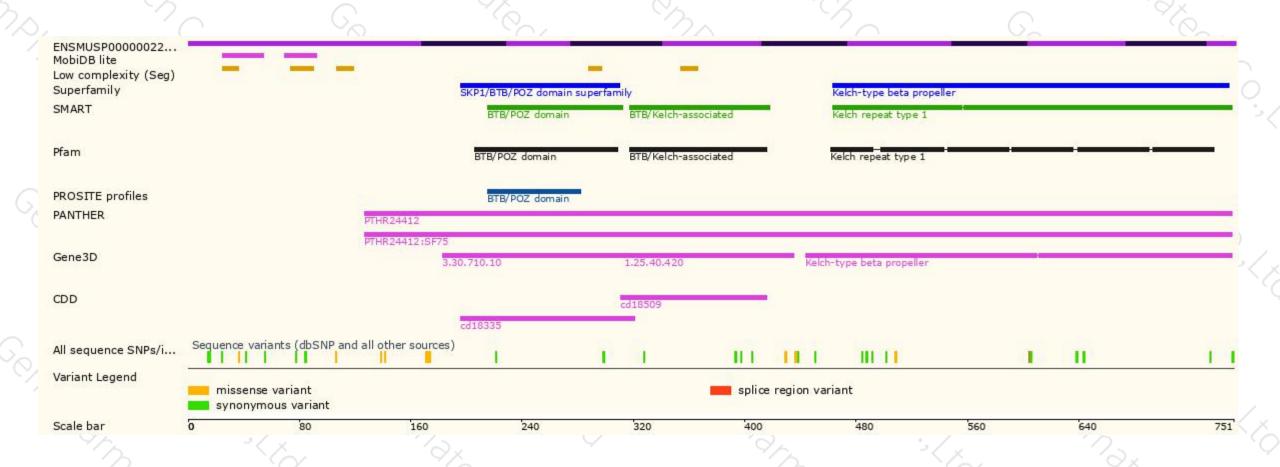
## Genomic location distribution





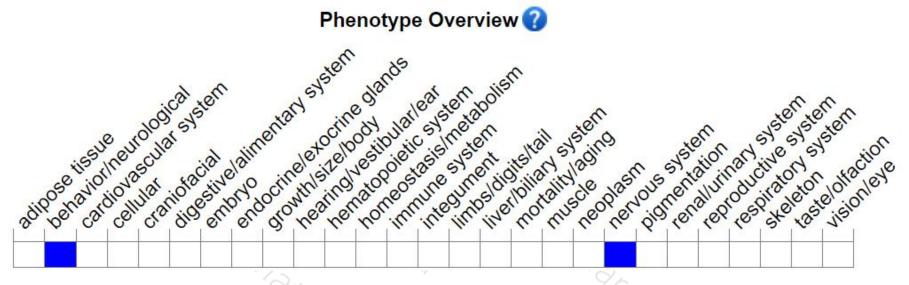
### Protein domain





## 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 both homozygous and heterozygous for disruption of this gene develop abnormalities in gait and defects in motor coordination with time. Dendritic atrophy of Purkinje cells is also seen.



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





