

# ***Klhl2* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Klhl2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klhl2* gene. The schematic diagram is as follows:



- The *Klhl2* gene has 5 transcripts. According to the structure of *Klhl2* gene, exon2-exon3 of *Klhl2-201* (ENSMUST00000034017.8) transcript is recommended as the knockout region. The region contains 233bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Klhl2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Klhl2*-202&204 may not be affected.
- The knockout region is near to the N-terminal of *Gm45345* gene, this strategy may influence the regulatory function of the N-terminal of *Gm45345* gene.
- The *Klhl2* gene is located on the Chr8. 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)

## KIHL2 kelch-like 2, Mayven [ *Mus musculus* (house mouse) ]

Gene ID: 77113, updated on 27-Aug-2019

### Summary

Official Symbol	KIHL2 provided by MGI
Official Full Name	kelch-like 2, Mayven provided by MGI
Primary source	MGI:MGI:1924363
See related	Ensembl:ENSMUSG000000031605
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mav; AU020744; ABP-KELCH; 6030411N21Rik; 8530402H02Rik
Annotation information	Annotation category: suggests misassembly
Expression	Broad expression in cortex adult (RPKM 26.9), frontal lobe adult (RPKM 22.8) and 27 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

**Location:** 8; 8 B3.1 [See KIHL2 in Genome Data Viewer](#)

**Exon count:** 16

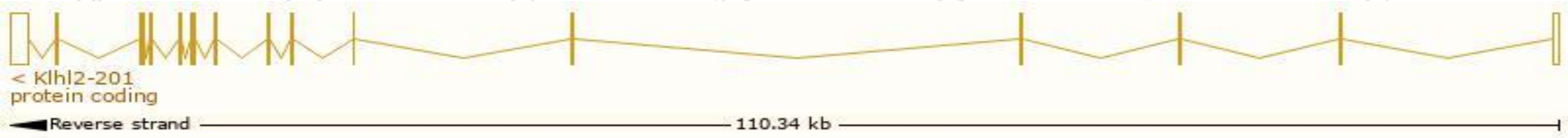
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	8	NC_000074.6 (64739673..64850169, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	8	NC_000074.5 (67335578..67373716, complement)

# Transcript information（Ensembl）

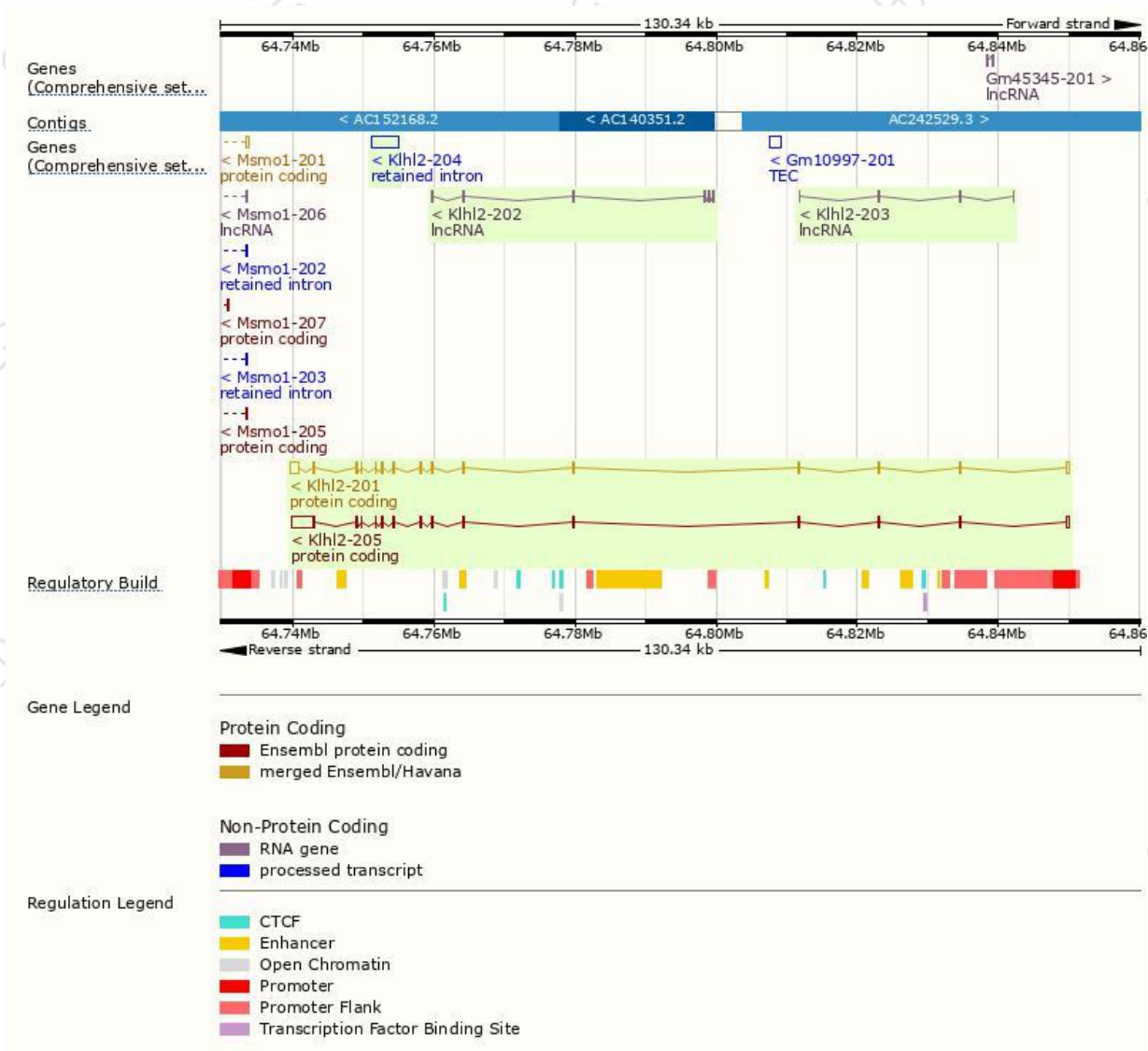
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Klhl2-201	<a href="#">ENSMUST00000034017.8</a>	3412	<a href="#">593aa</a>	Protein coding	<a href="#">CCDS85544</a>	<a href="#">Q8JZP3</a>	TSL:1 GENCODE basic APPRIS P1
Klhl2-205	<a href="#">ENSMUST00000210166.1</a>	5126	<a href="#">603aa</a>	Protein coding	-	<a href="#">A0A1B0GQV2</a>	TSL:1 GENCODE basic
Klhl2-204	<a href="#">ENSMUST00000209919.1</a>	3814	No protein	Retained intron	-	-	TSL:NA
Klhl2-202	<a href="#">ENSMUST00000209458.1</a>	769	No protein	lncRNA	-	-	TSL:5
Klhl2-203	<a href="#">ENSMUST00000209544.1</a>	321	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Klhl2-201* transcript,The transcription is shown below

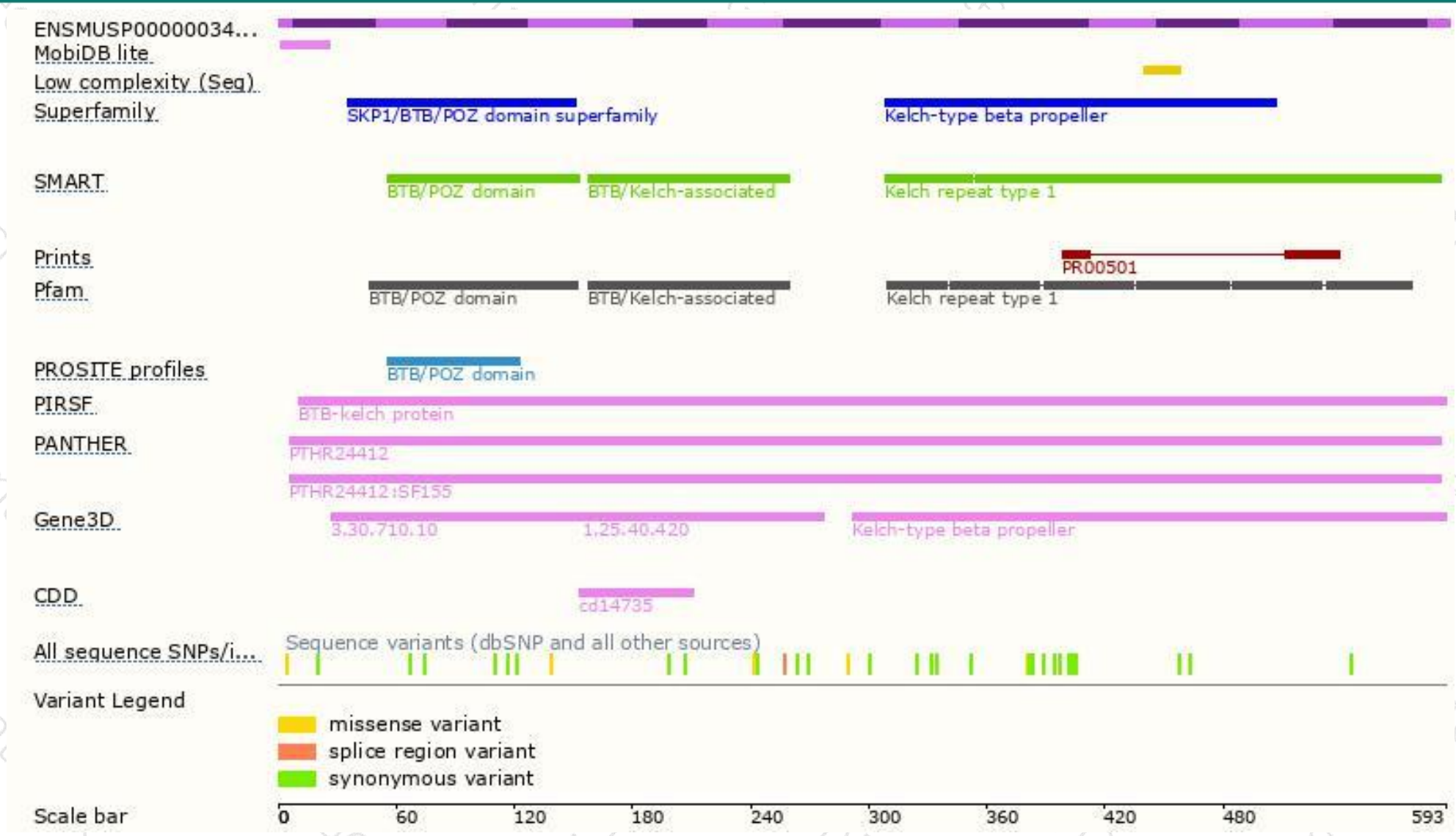


# Genomic location distribution





# Protein domain



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

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