

# ***Clec1b Cas9-CKO Strategy***

**Designer:**

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# Project Overview

**Project Name**

***Clec1b***

**Project type**

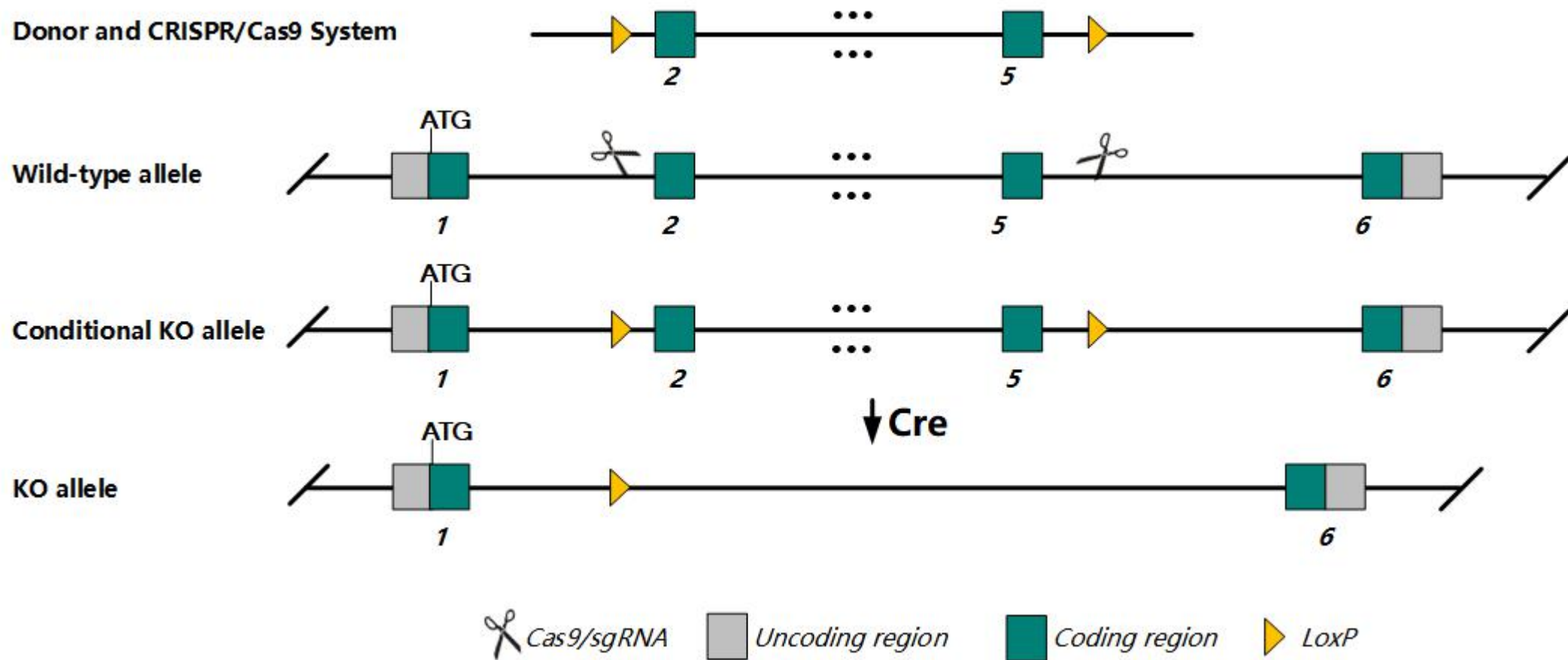
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clec1b* gene. The schematic diagram is as follows:



- The *Clec1b* gene has 4 transcript. According to the structure of *Clec1b* gene, exon2-5 of *Clec1b*-201 transcript is recommended as the knockout region. The region contains 481bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clec1b* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 or cell types.

- According to the existing MGI data , Mice homozygous for a knock-out allele exhibit congestion and hemorrhages during embryogenesis with prenatal and postnatal lethality. Mice homozygous for another knock-out allele exhibit blood-lymph mixing, impaired PDPN-Fc-mediated platelet activation, and intestinal edema.
- The Clec1b gene is located on the Chr6. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information ( NCBI )

## Pax6 paired box 6 [Mus musculus (house mouse)]

Gene ID: 18508, updated on 2-Apr-2019

### Summary



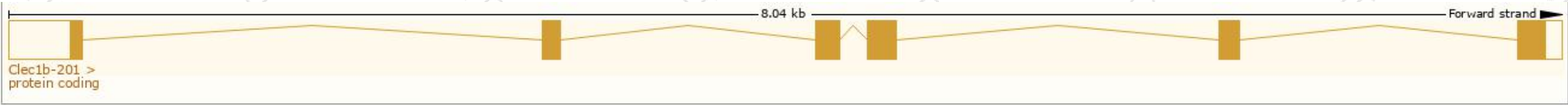
<b>Official Symbol</b>	Pax6 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	paired box 6 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:97490</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027168</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1500038E17Rik, AEY11, Dey, Gsfaey11, Pax-6, Sey
<b>Summary</b>	This gene encodes a homeobox-containing protein that functions as a regulator of transcription. It plays a key role in the development of neural tissues, particularly the eye. Activity of this protein is also required for expression of glucagon in the pancreas. This gene is regulated by multiple enhancers located up to tens or hundreds of kilobases upstream and downstream of the transcription start sites. Mutations in this gene or deletion of these regulatory elements results in severe defects in eye development. Alternative splicing and the use of alternative promoters results in multiple transcript variants, some of which encode proteins that lack the N-terminal paired domain. [provided by RefSeq, Jul 2015]
<b>Expression</b>	Biased expression in cerebellum adult (RPKM 9.1), whole brain E14.5 (RPKM 7.7) and 6 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information ( Ensembl )

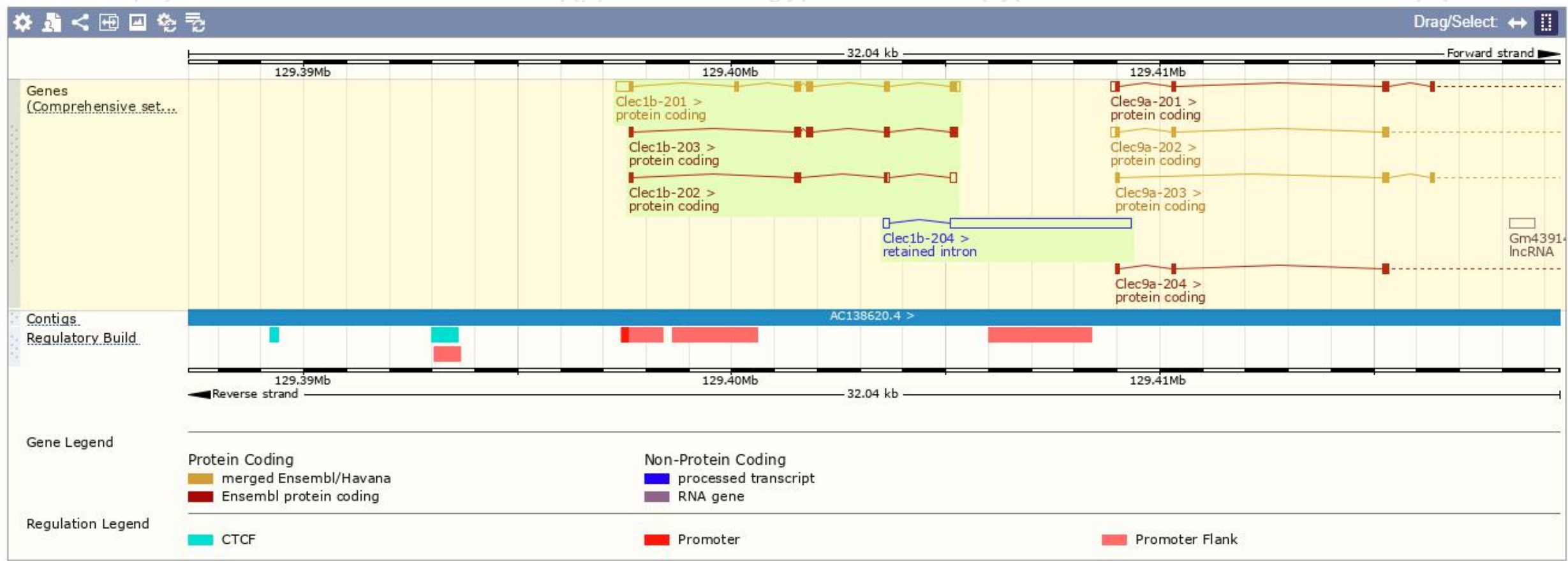
The gene has 4 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clec1b-204	<a href="#">ENSMUST00000133061.1</a>	4347	No protein	Retained intron	-	-	TSL:2
Clec1b-203	<a href="#">ENSMUST00000112081.8</a>	614	<a href="#">197aa</a>	Protein coding	<a href="#">CCDS57452</a>	<a href="#">Q9JL99</a>	TSL:1 GENCODE basic APPRIS ALT2
Clec1b-202	<a href="#">ENSMUST00000112079.2</a>	455	<a href="#">83aa</a>	Protein coding	<a href="#">CCDS57453</a>	<a href="#">A0T1G3</a>	TSL:1 GENCODE basic
Clec1b-201	<a href="#">ENSMUST00000032262.13</a>	1090	<a href="#">229aa</a>	Protein coding	<a href="#">CCDS20586</a>	<a href="#">Q9JL99</a>	TSL:1 GENCODE basic APPRIS P3

The strategy is based on the design of *Clec1b*-201 transcript, The transcription is shown below

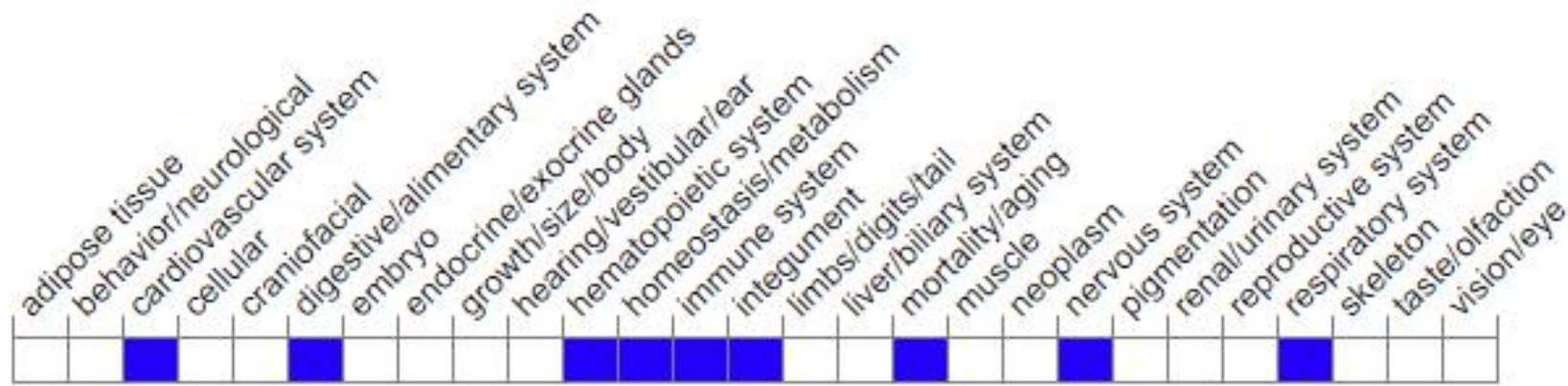


# Genomic location distribution





# Mouse phenotype description(MGI)



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>) .*

Mice homozygous for a knock-out allele exhibit congestion and hemorrhages during embryogenesis with prenatal and postnatal lethality. Mice homozygous for another knock-out allele exhibit blood-lymph mixing, impaired PDPN-Fc-mediated platelet activation, and intestinal edema.

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