

# *Clk1* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Clk1*

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**Project type**

**Cas9-KO**

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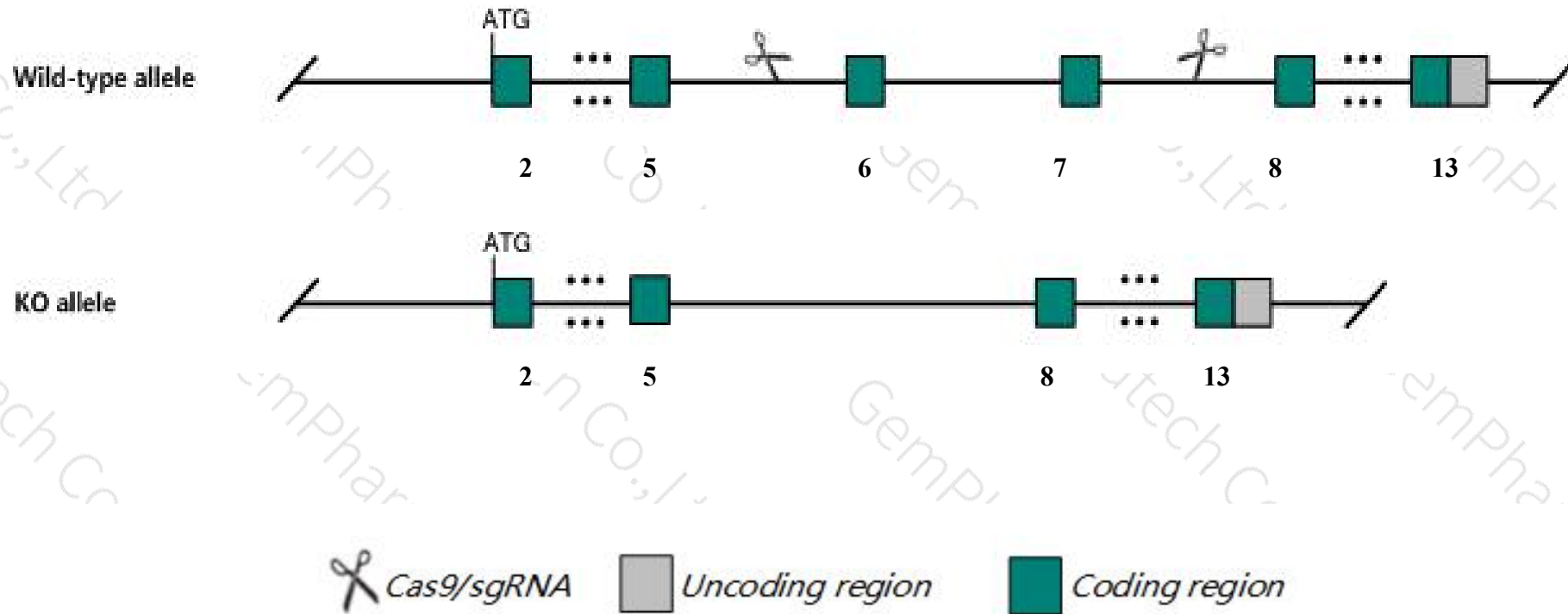
**Strain background**

**C57BL/6J**

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# Knockout strategy

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



- The *Clk1* gene has 13 transcripts. According to the structure of *Clk1* gene, exon6-exon7 of *Clk1-201* (ENSMUST00000034868.13) transcript is recommended as the knockout region. The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clk1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- The *Clk1* 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)

## Clk1 CDC-like kinase 1 [Mus musculus (house mouse)]

Gene ID: 12747, updated on 31-Jan-2019

### Summary



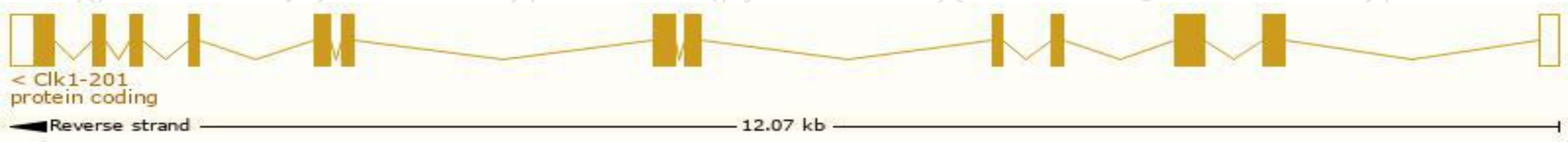
<b>Official Symbol</b>	Clk1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	CDC-like kinase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:107403</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000026034</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	STY
<b>Expression</b>	Broad expression in bladder adult (RPKM 71.4), limb E14.5 (RPKM 59.9) and 23 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

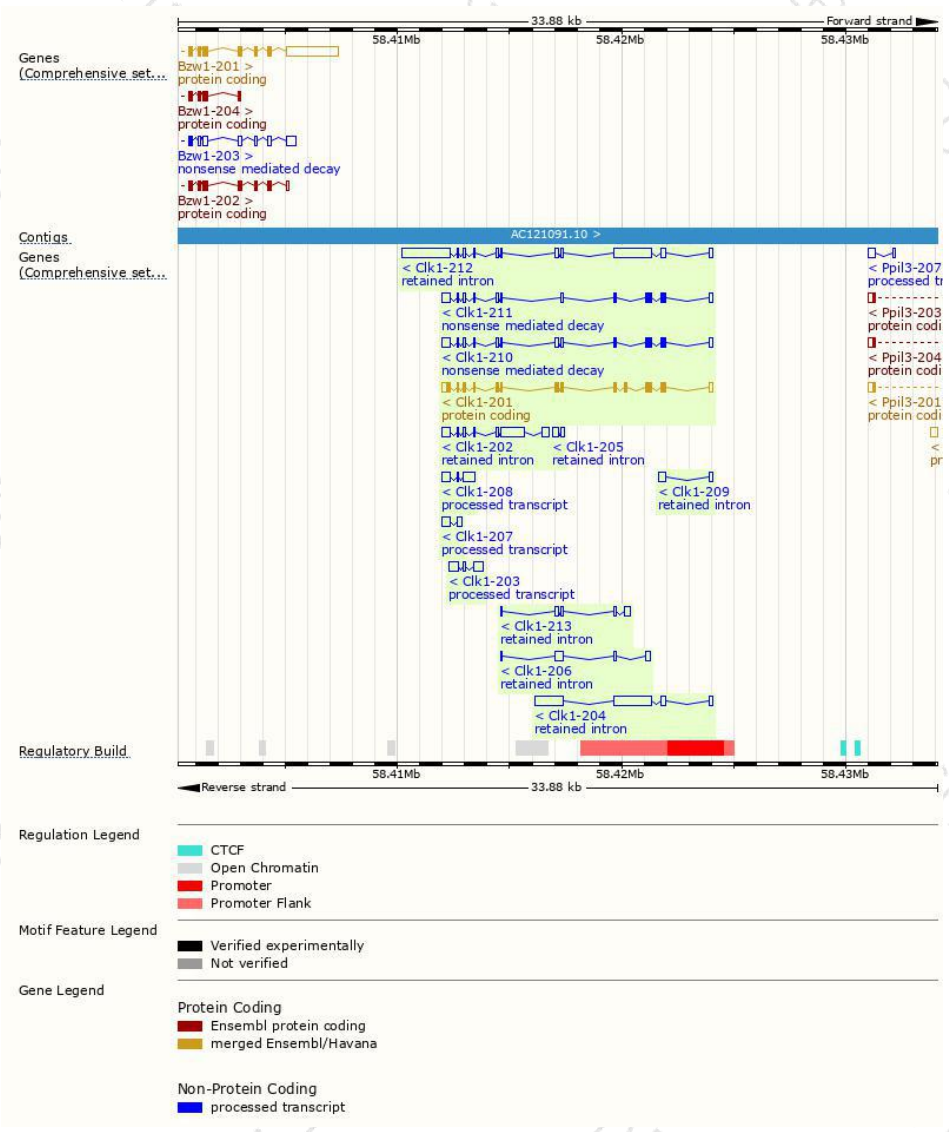
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clk1-201	<a href="#">ENSMUST00000034868.13</a>	1796	<a href="#">483aa</a>	Protein coding	<a href="#">CCDS35577</a>	<a href="#">P22518</a>	TSL:1 GENCODE basic APPRIS P1
Clk1-210	<a href="#">ENSMUST00000148330.7</a>	1705	<a href="#">135aa</a>	Nonsense mediated decay	-	<a href="#">P22518</a>	TSL:1
Clk1-211	<a href="#">ENSMUST00000151338.7</a>	1538	<a href="#">135aa</a>	Nonsense mediated decay	-	<a href="#">P22518</a>	TSL:5
Clk1-203	<a href="#">ENSMUST00000129303.1</a>	938	No protein	Processed transcript	-	-	TSL:3
Clk1-208	<a href="#">ENSMUST00000141570.7</a>	923	No protein	Processed transcript	-	-	TSL:2
Clk1-207	<a href="#">ENSMUST00000139787.7</a>	556	No protein	Processed transcript	-	-	TSL:2
Clk1-212	<a href="#">ENSMUST00000156931.7</a>	4865	No protein	Retained intron	-	-	TSL:2
Clk1-204	<a href="#">ENSMUST00000129577.7</a>	3191	No protein	Retained intron	-	-	TSL:1
Clk1-202	<a href="#">ENSMUST00000123580.7</a>	2102	No protein	Retained intron	-	-	TSL:5
Clk1-213	<a href="#">ENSMUST00000186552.6</a>	724	No protein	Retained intron	-	-	TSL:3
Clk1-206	<a href="#">ENSMUST00000135380.1</a>	684	No protein	Retained intron	-	-	TSL:3
Clk1-209	<a href="#">ENSMUST00000147258.1</a>	456	No protein	Retained intron	-	-	TSL:2
Clk1-205	<a href="#">ENSMUST00000131051.1</a>	430	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Clk1-201* transcript,The transcription is shown below



# Genomic location distribution

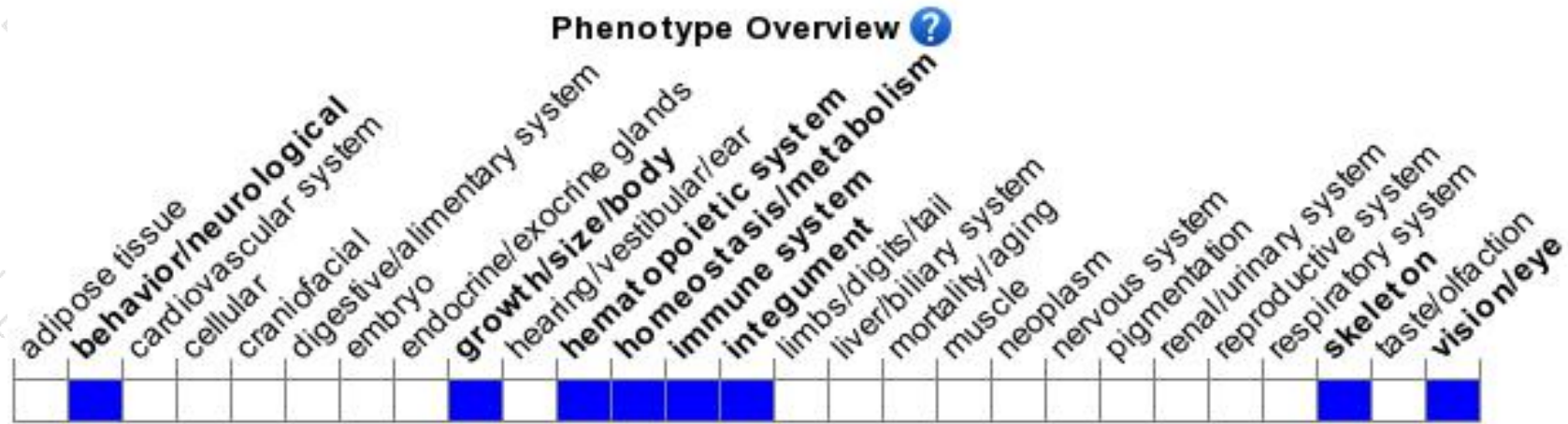




# Protein domain



# Mouse phenotype description(MGI )



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

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

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