

# Cdk10 Cas9-KO Strategy

Designer: Longyun Hu

Reviewer: Shanhong Tao

Design Date: 2022-12-6

# Overview

## Target Gene Name

- Cdk10

## Project Type

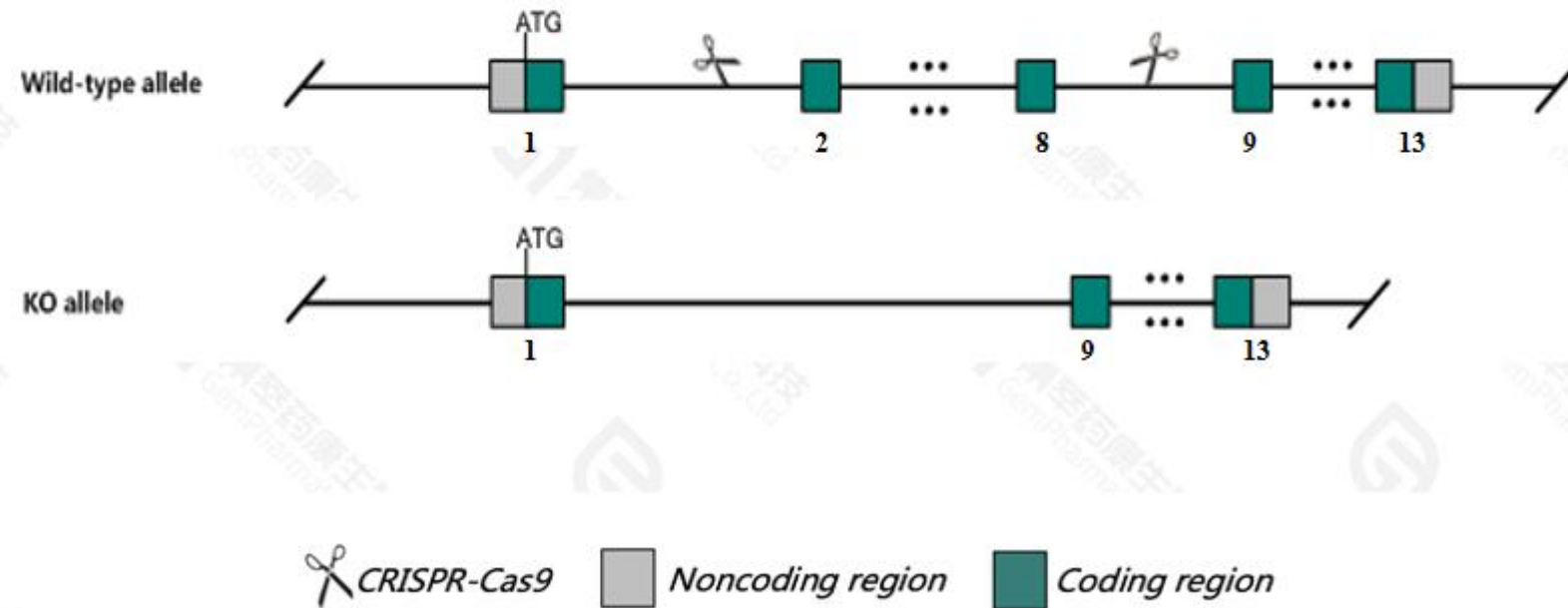
- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy

This model will use CRISPR-Cas9 technology to edit the *Cdk10* gene. The schematic diagram is as follows:



Schematic representation of CRISPR-Cas9 engineering used to edit the *Cdk10* gene.

# Technical Information

- The *Cdk10* gene has 12 transcripts. According to the structure of *Cdk10* gene, exon2-exon8 of *Cdk10-201*(ENSMUST00000036880.8) transcript is recommended as the knockout region. The region contains 521bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cdk10* gene. The brief process is as follows: CRISPR-Cas9 system 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.

# Gene Information

## Cdk10 cyclin-dependent kinase 10 [Mus musculus (house mouse)]

Gene ID: 234854, updated on 24-Apr-2022

### Summary

<b>Official Symbol</b>	Cdk10 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	cyclin-dependent kinase 10 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2448549</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033862</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>	BC017131
<b>Summary</b>	The protein encoded by this gene belongs to the CDK (cyclin-dependent kinase) subfamily of the Ser/Thr protein kinase family. The CDK subfamily members are highly similar to the gene products of <i>S. cerevisiae</i> cdc28, and <i>S. pombe</i> cdc2, and are known to be essential for cell cycle progression. The human ortholog has been shown to play a role in cellular proliferation. Multiple transcript variants encoding different isoforms have been found for this gene. A related pseudogene exists on chromosome 1. [provided by RefSeq, Jan 2010]
<b>Expression</b>	Ubiquitous expression in cortex adult (RPKM 24.7), limb E14.5 (RPKM 24.3) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

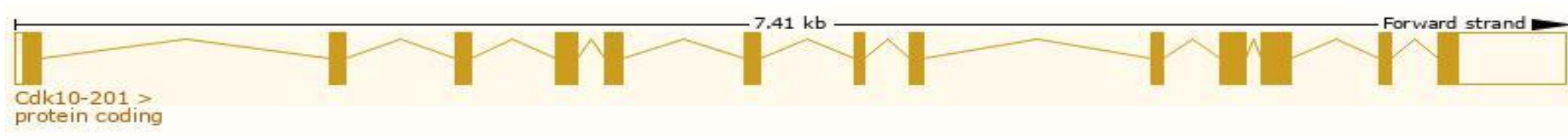
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 12 transcripts, all transcripts are shown below:

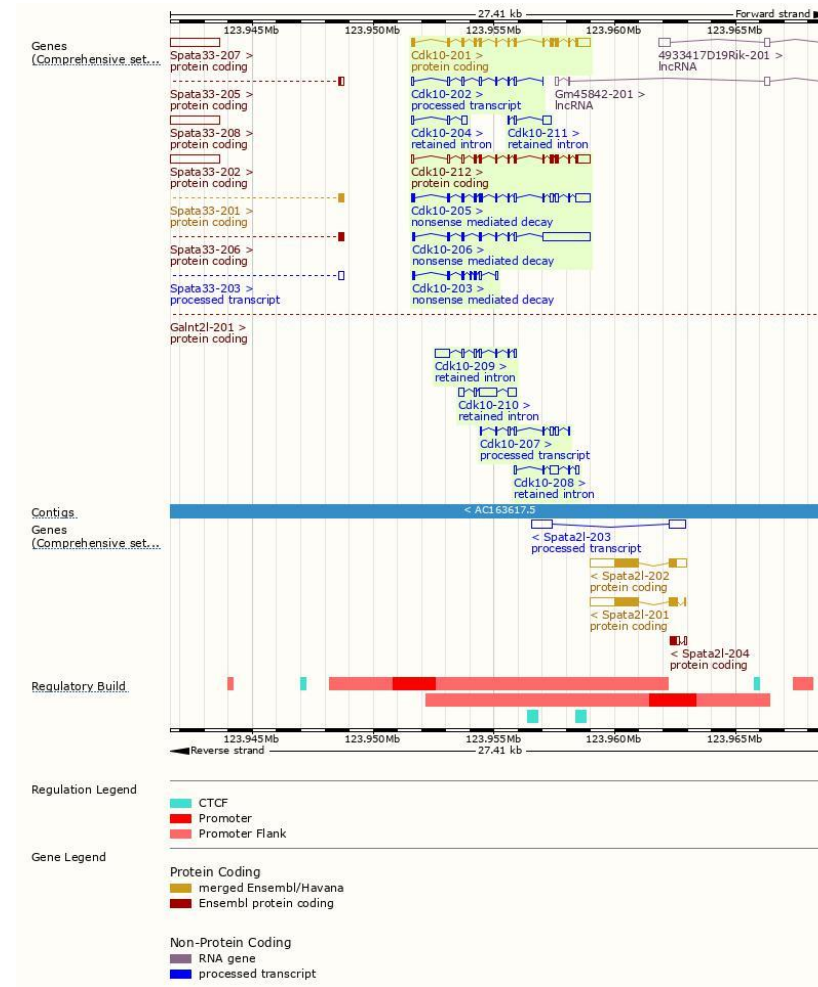
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
<b>Cdk10-201</b>	<a href="#">ENSMUST00000036880.8</a>	1642	<a href="#">360aa</a>	Protein coding	<a href="#">CCDS22751</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
<b>Cdk10-212</b>	<a href="#">ENSMUST00000213005.2</a>	1580	<a href="#">289aa</a>	Protein coding	<a href="#">CCDS85629</a>		TSL:1 , GENCODE basic ,
<b>Cdk10-206</b>	<a href="#">ENSMUST00000212361.2</a>	2498	<a href="#">129aa</a>	Nonsense mediated decay	-		TSL:1 ,
<b>Cdk10-205</b>	<a href="#">ENSMUST00000212193.2</a>	1638	<a href="#">140aa</a>	Nonsense mediated decay	-		TSL:2 ,
<b>Cdk10-203</b>	<a href="#">ENSMUST00000212028.2</a>	528	<a href="#">115aa</a>	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
<b>Cdk10-207</b>	<a href="#">ENSMUST00000212497.2</a>	648	No protein	Processed transcript	-		TSL:3 ,
<b>Cdk10-202</b>	<a href="#">ENSMUST00000212021.2</a>	518	No protein	Processed transcript	-		TSL:5 ,
<b>Cdk10-210</b>	<a href="#">ENSMUST00000212784.2</a>	1379	No protein	Retained intron	-		TSL:1 ,
<b>Cdk10-209</b>	<a href="#">ENSMUST00000212749.2</a>	1054	No protein	Retained intron	-		TSL:2 ,
<b>Cdk10-208</b>	<a href="#">ENSMUST00000212532.2</a>	676	No protein	Retained intron	-		TSL:3 ,
<b>Cdk10-211</b>	<a href="#">ENSMUST00000212904.2</a>	454	No protein	Retained intron	-		TSL:3 ,
<b>Cdk10-204</b>	<a href="#">ENSMUST00000212035.2</a>	359	No protein	Retained intron	-		TSL:3 ,

The strategy is based on the design of *Cdk10-201* transcript, the transcription is shown below:



Source: <https://www.ensembl.org>

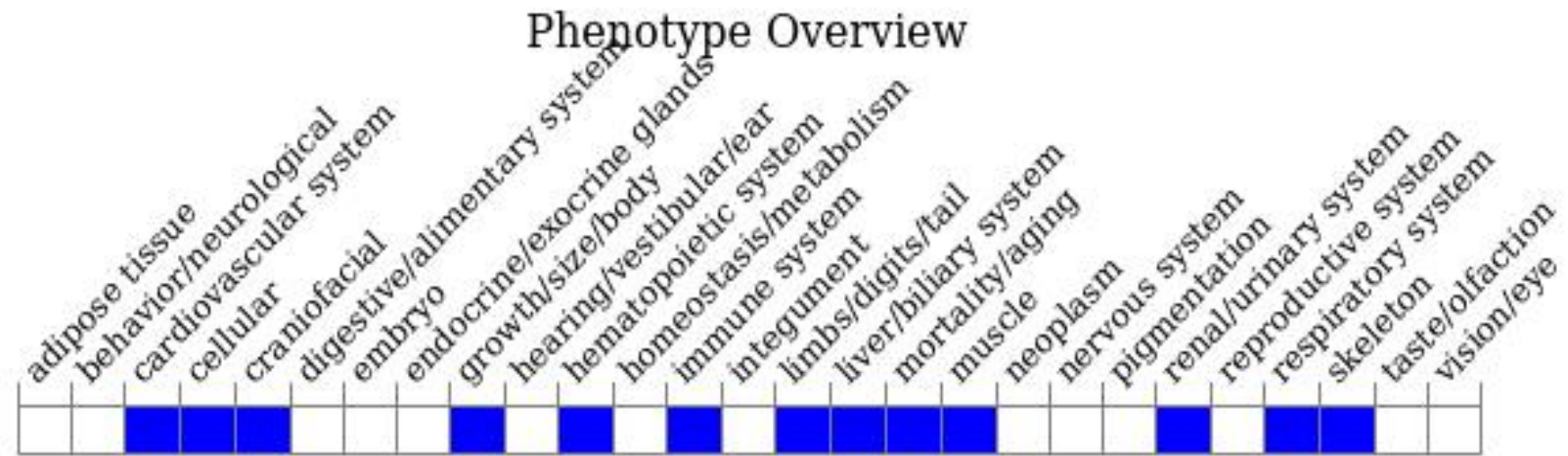
# Genomic Information



# Protein Information



# Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Cdk10* gene are marked in blue. Mice homozygous for a knock-out allele exhibit severe growth retardation, neonatal lethality, spine malformations and defects in lung, heart, liver and spleen.

# Important Information

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit severe growth retardation, neonatal lethality, spine malformations and defects in lung, heart, liver and spleen.
- The KO region is about 1.6 kb away from the N-terminus of the Gm45842 gene, this strategy may influence the regulatory function of the N-terminal of Gm45842 gene.
- The *Cdk10* 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.