Cdk10 Cas9-CKO Strategy

Designer: Longyun Hu

Reviewer: Shanhong Tao

Design Date: 2022-12-6

Overview

Target Gene Name

- Cdk10
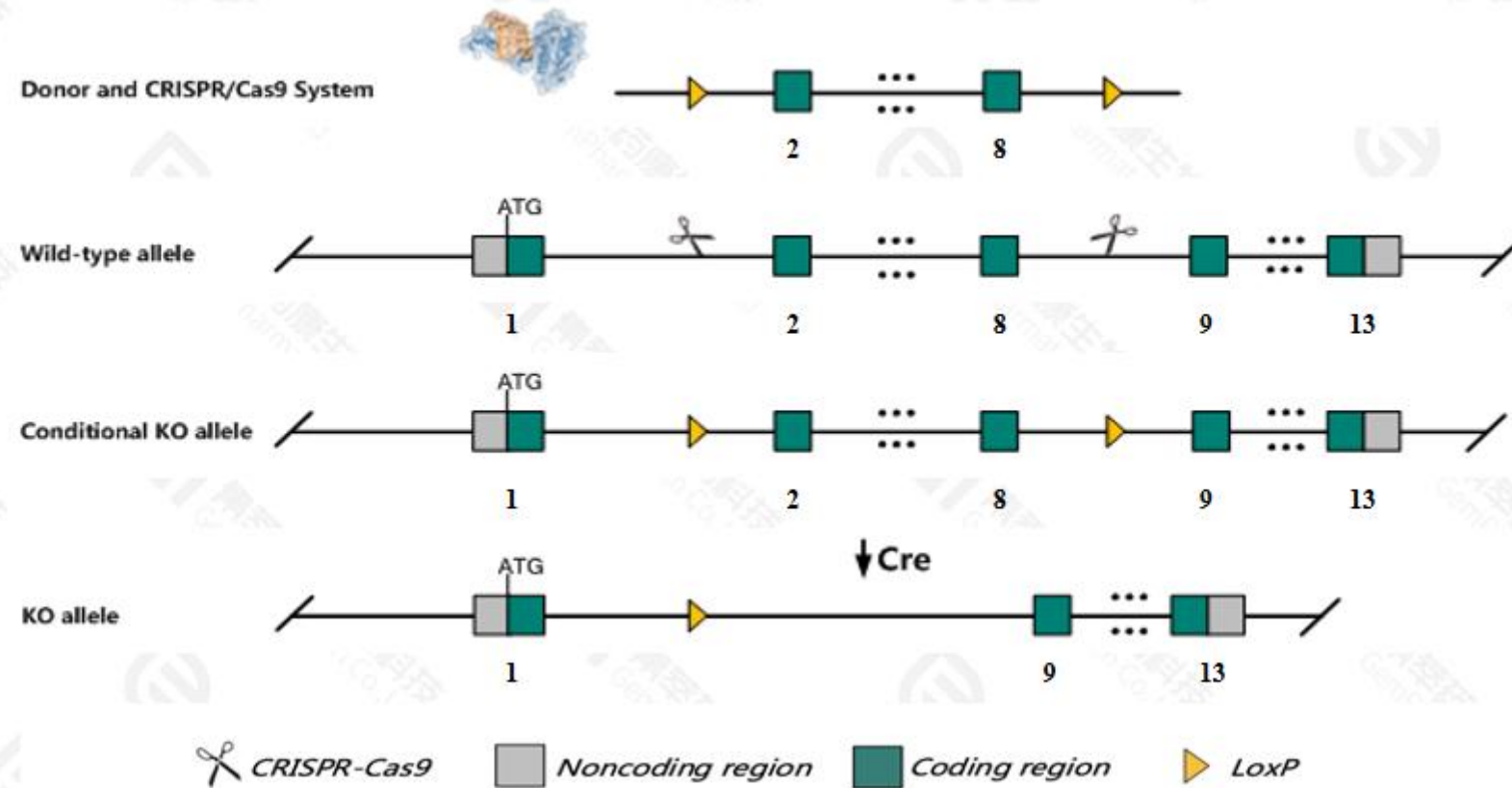
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

GemPharmatech™

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 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.

Gene Information

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

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

▲ Summary

|	
Official Symbol	Cdk10 provided by MGI
Official Full Name	cyclin-dependent kinase 10 provided by MGI
Primary source	MGI:MGI:2448549
See related	Ensembl:ENSMUSG00000033862
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC017131
Summary	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 S. cerevisiae cdc28, and S. pombe 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]
Expression	Ubiquitous expression in cortex adult (RPKM 24.7), limb E14.5 (RPKM 24.3) and 28 other tissues See more
Orthologs	human all

GemPharmatech™

Transcript Information

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

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

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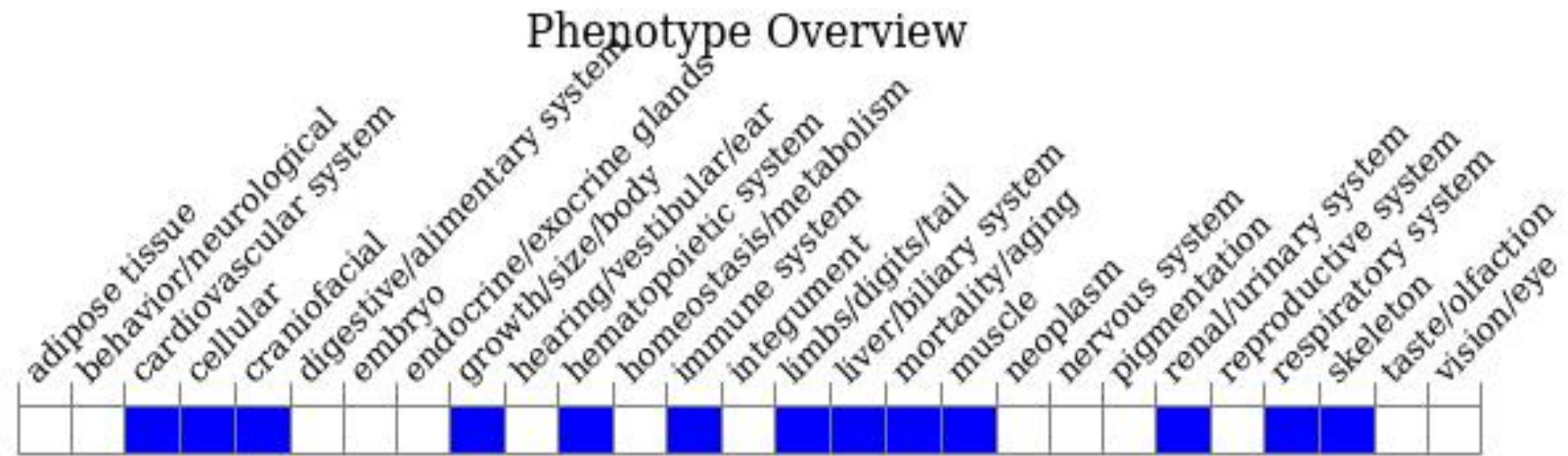

Source: https://www.ensembl.org

GemPharmatech™
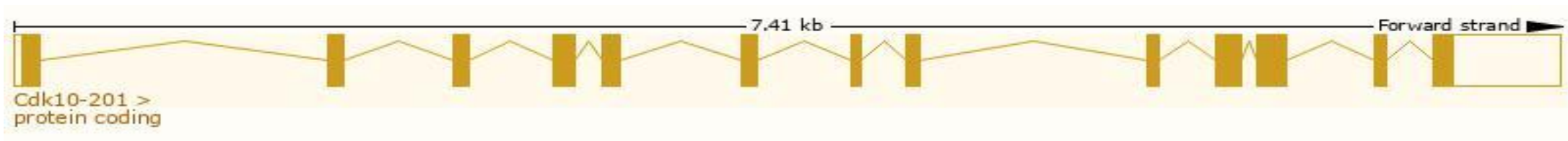
Genomic Information

GemPharmatech™

Protein Information

Source: : https://www.ensembl.org
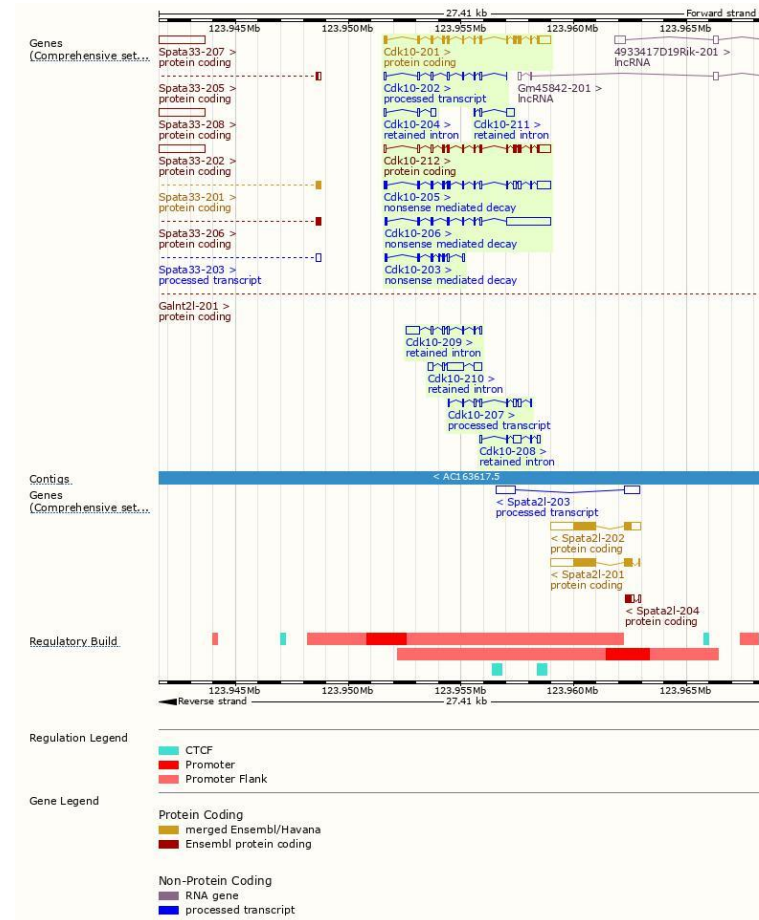
Mouse Phenotype Information (MGI)

• 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.

Source: https://www.informatics.jax.org

GemPharmatech™

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 flox 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.