Cdk14 Cas9-CKO Strategy

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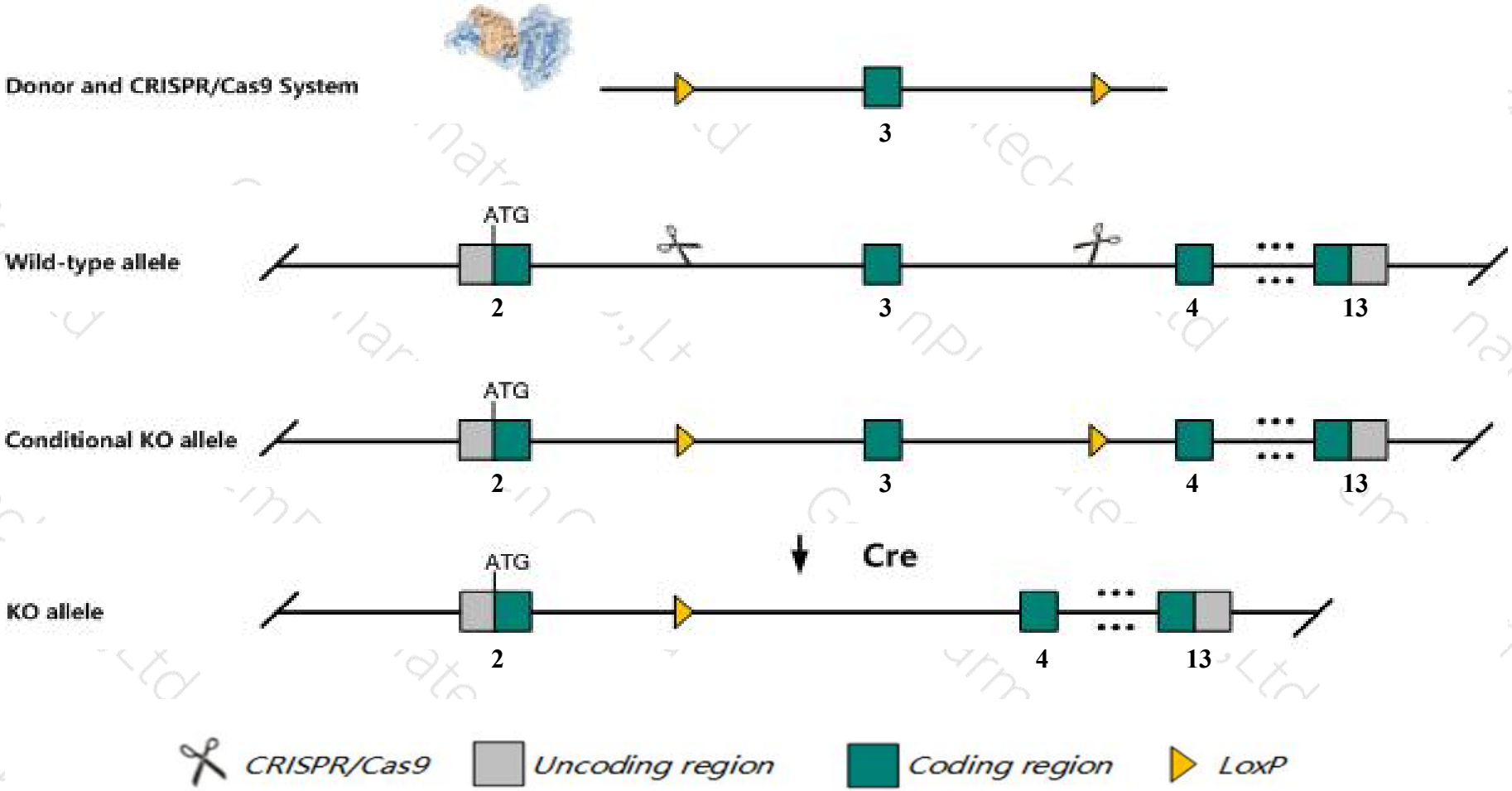
Project Overview

Project Name	***Cdk14***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdk14* gene. The schematic diagram is as follows:



Technical routes

- The *Cdk14* gene has 15 transcripts. According to the structure of *Cdk14* gene, exon3 of *Cdk14-203* (ENSMUST00000115451.7) transcript is recommended as the knockout region.The region contains 95bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cdk14* 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.

Notice

- The effect on transcript *Cdk14*-205&215 is unknown.
- Transcript *Cdk14*-209&211&213&214&215 may not be affected.
- The *Cdk14* gene is located on the Chr5. 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.

Gene information （NCBI）

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Cdk14 cyclin-dependent kinase 14 [*Mus musculus* (house mouse)]

Gene ID: 18647, updated on 10-Oct-2019

Summary

Official Symbol	Cdk14 provided by MGI
Official Full Name	cyclin-dependent kinase 14 provided by MGI
Primary source	MGI:MGI:894318
See related	Ensembl:ENSMUSG00000028926
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Pftk1; mKIAA0834
Expression	Biased expression in frontal lobe adult (RPKM 18.7), cortex adult (RPKM 14.0) and 13 other tissues See more
Orthologs	human all

Genomic context

Location: 5 A1; 5 2.61 cM

See Cdk14 in Genome Data Viewer

Exon count: 19

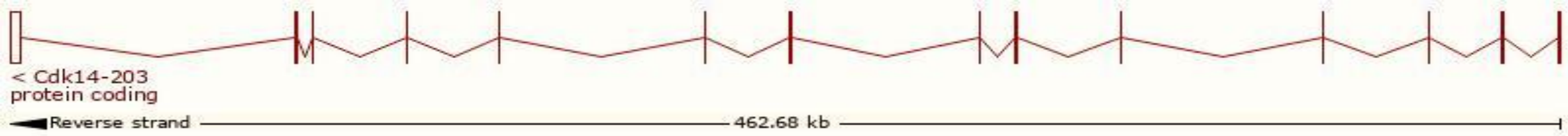
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (4803384..5380251, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (4803385..5380251, complement)

Transcript information（Ensembl）

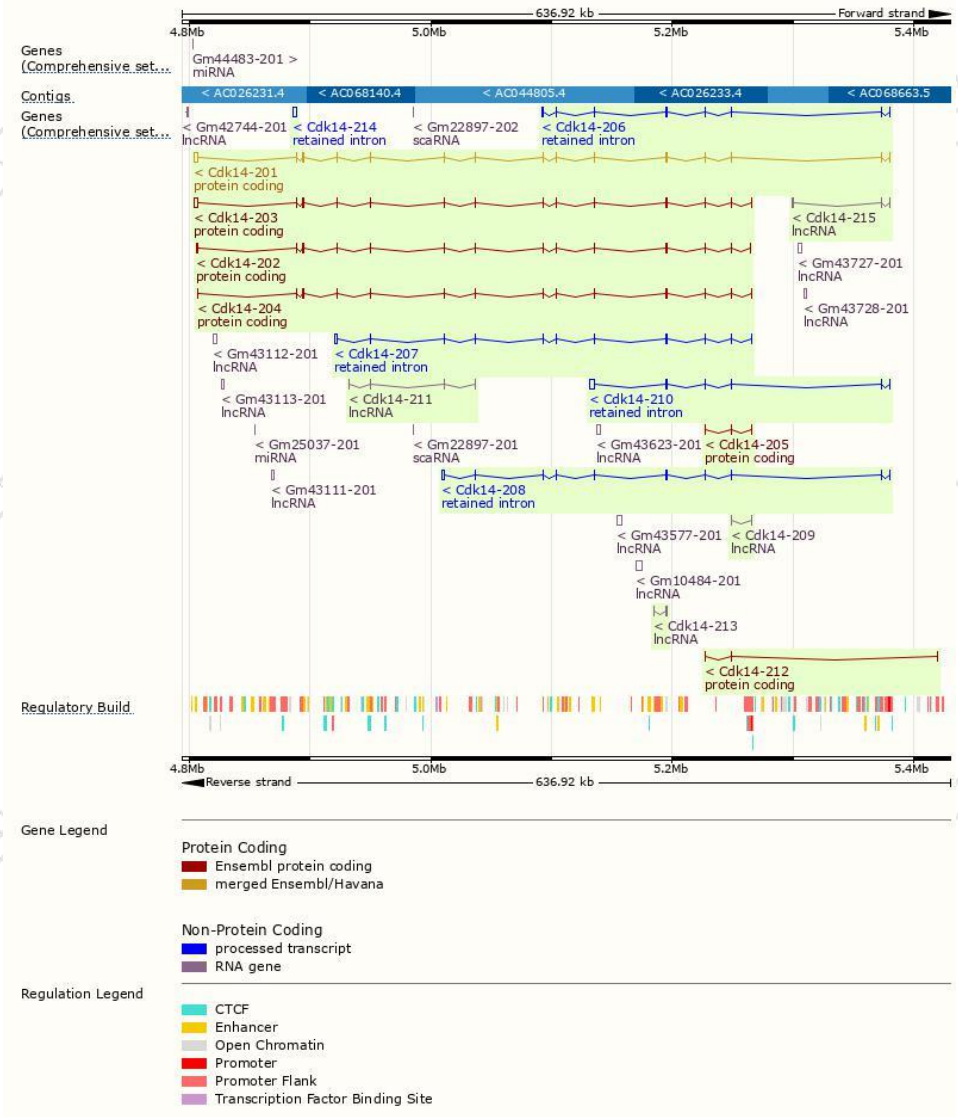
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cdk14-203	ENSMUST00000115451.7	5145	423aa	Protein coding	CCDS80203	O35495 Q6NVF8	TSL:1 GENCODE basic
Cdk14-201	ENSMUST00000030763.12	4851	469aa	Protein coding	CCDS19073	O35495	TSL:1 GENCODE basic APPRIS P1
Cdk14-202	ENSMUST00000115450.7	2386	423aa	Protein coding	CCDS80203	O35495 Q6NVF8	TSL:1 GENCODE basic
Cdk14-204	ENSMUST00000115452.7	1567	451aa	Protein coding	-	E9PVC7	TSL:5 GENCODE basic
Cdk14-205	ENSMUST00000131392.7	559	92aa	Protein coding	-	D3YV23	CDS 3' incomplete TSL:5
Cdk14-212	ENSMUST00000167567.1	534	167aa	Protein coding	-	E9Q9M2	CDS 3' incomplete TSL:3
Cdk14-210	ENSMUST00000153331.5	4150	No protein	Retained intron	-	-	TSL:2
Cdk14-207	ENSMUST00000133465.7	3446	No protein	Retained intron	-	-	TSL:1
Cdk14-214	ENSMUST00000199623.1	3419	No protein	Retained intron	-	-	TSL:NA
Cdk14-208	ENSMUST00000134867.7	3122	No protein	Retained intron	-	-	TSL:2
Cdk14-206	ENSMUST00000132390.7	2296	No protein	Retained intron	-	-	TSL:1
Cdk14-211	ENSMUST00000156660.1	631	No protein	lncRNA	-	-	TSL:3
Cdk14-209	ENSMUST00000137554.1	510	No protein	lncRNA	-	-	TSL:5
Cdk14-215	ENSMUST00000200637.1	381	No protein	lncRNA	-	-	TSL:3
Cdk14-213	ENSMUST00000171119.1	194	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Cdk14-203* transcript,The transcription is shown below

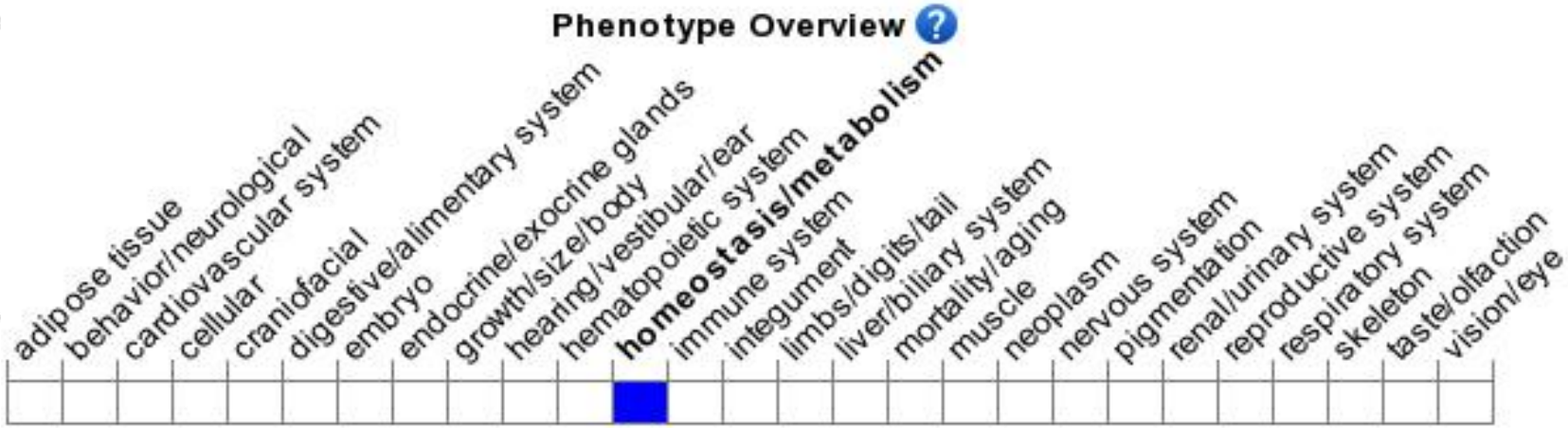


Genomic location distribution



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/).

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

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