Kat8 Cas9-CKO Strategy

Designer: Huan Wang

Reviewer: Fengjuan Wang

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集萃药康 GemPharmatech
GemPharmatech Co.,Ltd

Project Overview

Project Name	***Kat8***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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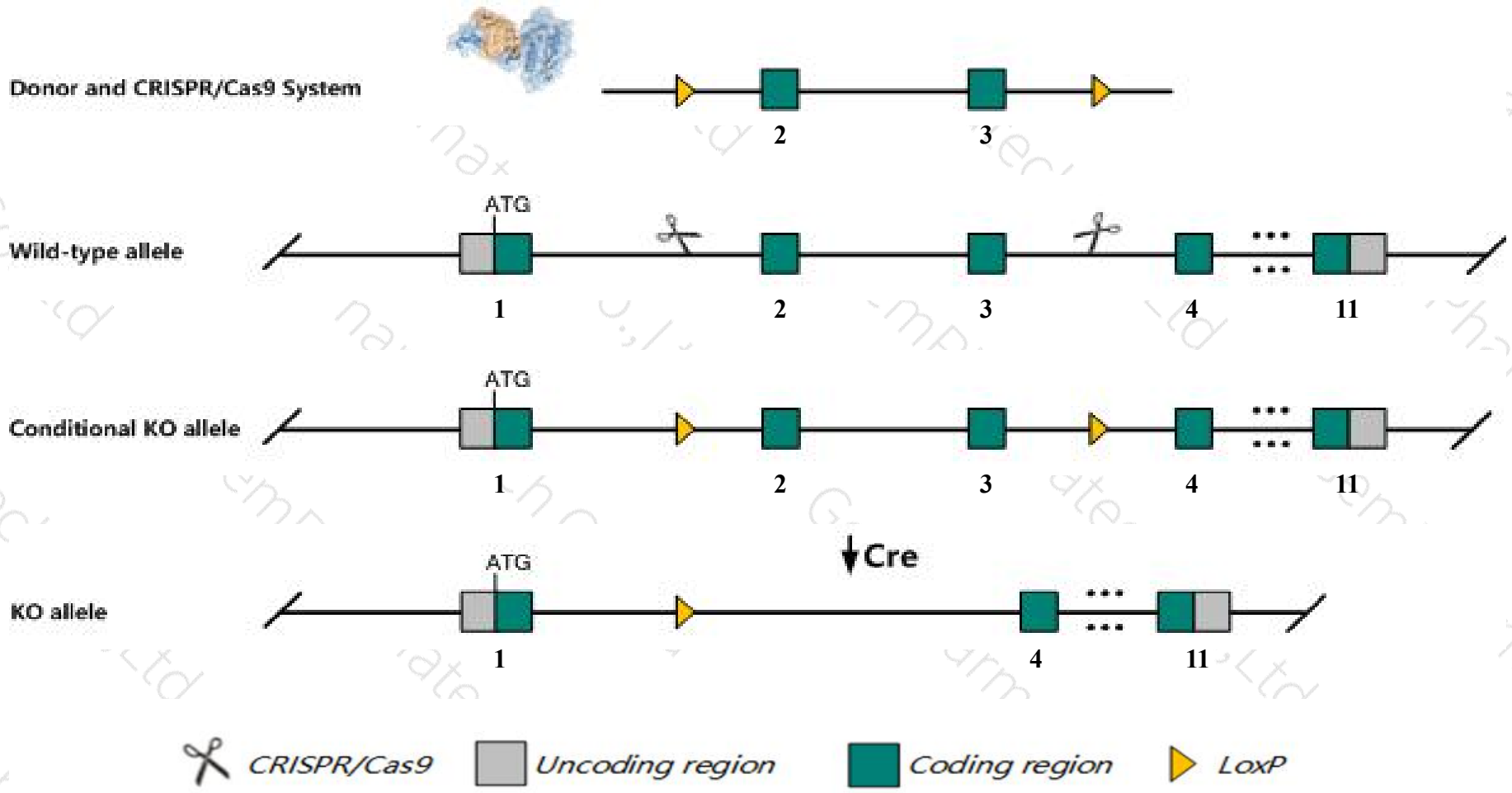
This model will use CRISPR/Cas9 technology to edit the *Kat8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kat8* gene has 4 transcripts. According to the structure of *Kat8* gene, exon2-exon3 of *Kat8-201*(ENSMUST00000033070.8) transcript is recommended as the knockout region.The region contains 251bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Kat8* 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

➢ According to the existing MGI data,mice homozygous for a null allele die prior to gastrulation.

➢ The *Kat8* gene is located on the Chr7. 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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Kat8 K(lysine) acetyltransferase 8 [Mus musculus (house mouse)]

Gene ID: 67773, updated on 13-Mar-2020

Summary

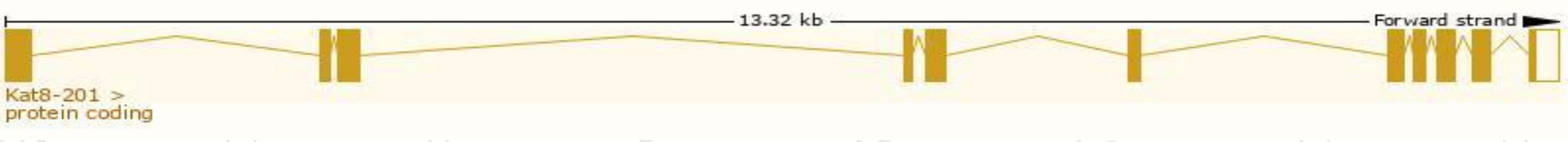
Official Symbol	Kat8 provided by MGI
Official Full Name	K(lysine) acetyltransferase 8 provided byMGI
Primary source	MGI:MGI:1915023
See related	Ensembl:ENSMUSG00000030801
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2010203C02Rik, 5830450F21Rik, D7Ertd629e, MOF, MYST-1, Myst1
Expression	Ubiquitous expression in testis adult (RPKM 32.3), CNS E11.5 (RPKM 9.8) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

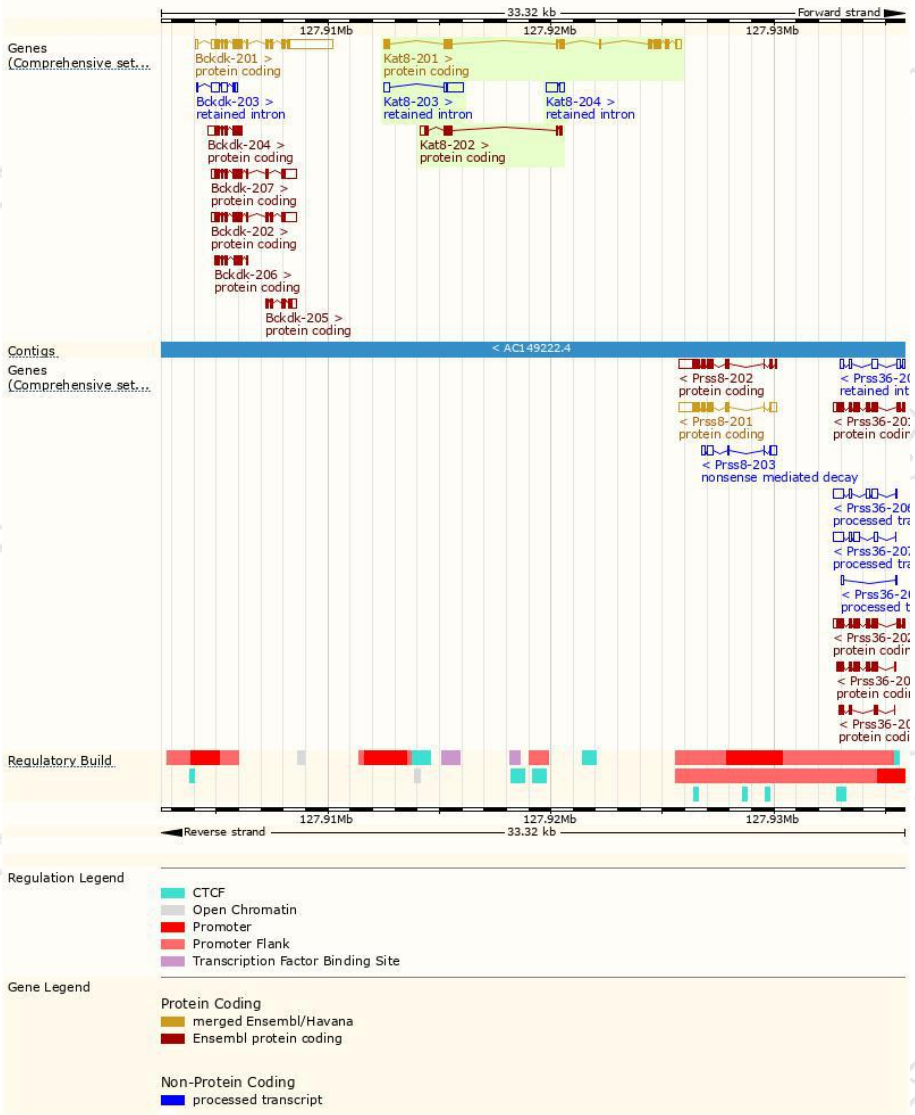
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kat8-201	ENSMUST00000033070.8	1579	458aa	Protein coding	CCDS21885	Q9D1P2	TSL:1 GENCODE basic APPRIS P1
Kat8-202	ENSMUST00000205357.1	723	176aa	Protein coding	-	A0A0U1RNW7	CDS 3' incomplete TSL:5
Kat8-203	ENSMUST00000206071.1	1014	No protein	Retained intron	-	-	TSL:1
Kat8-204	ENSMUST00000206364.1	660	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Kat8-201* transcript,the transcription is shown below:

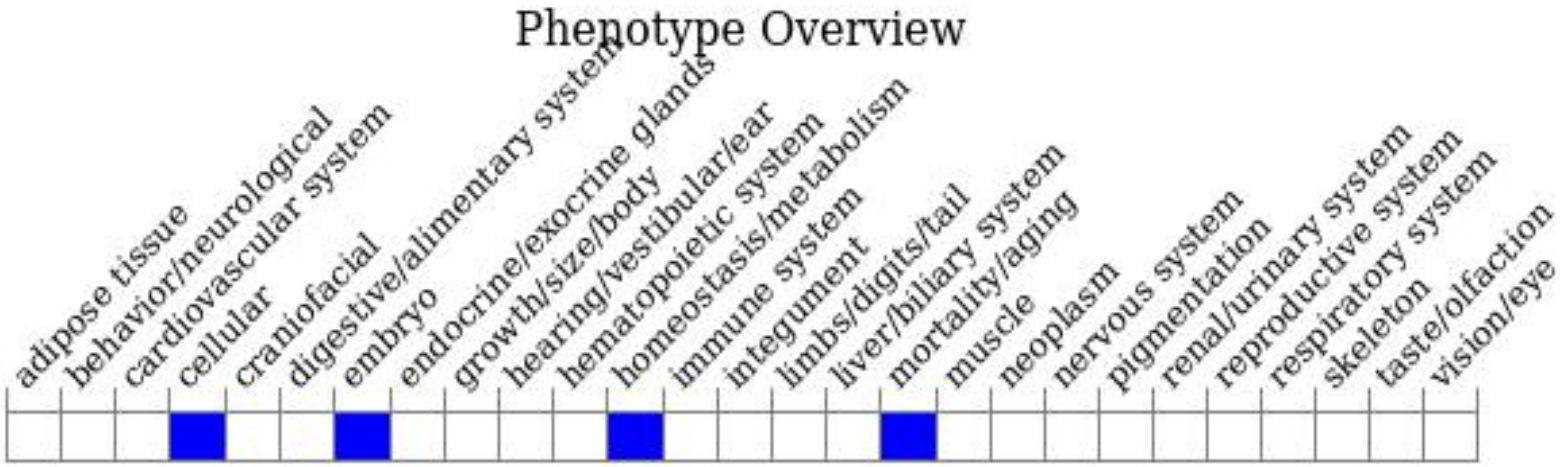


Genomic location distribution



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/).

According to the existing MGI data,mice homozygous for a null allele die prior to gastrulation.

集萃药康
GemPharmatech

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd