

Zfp821 Cas9-CKO Strategy

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Project Overview

Project Name

Zfp821

Project type

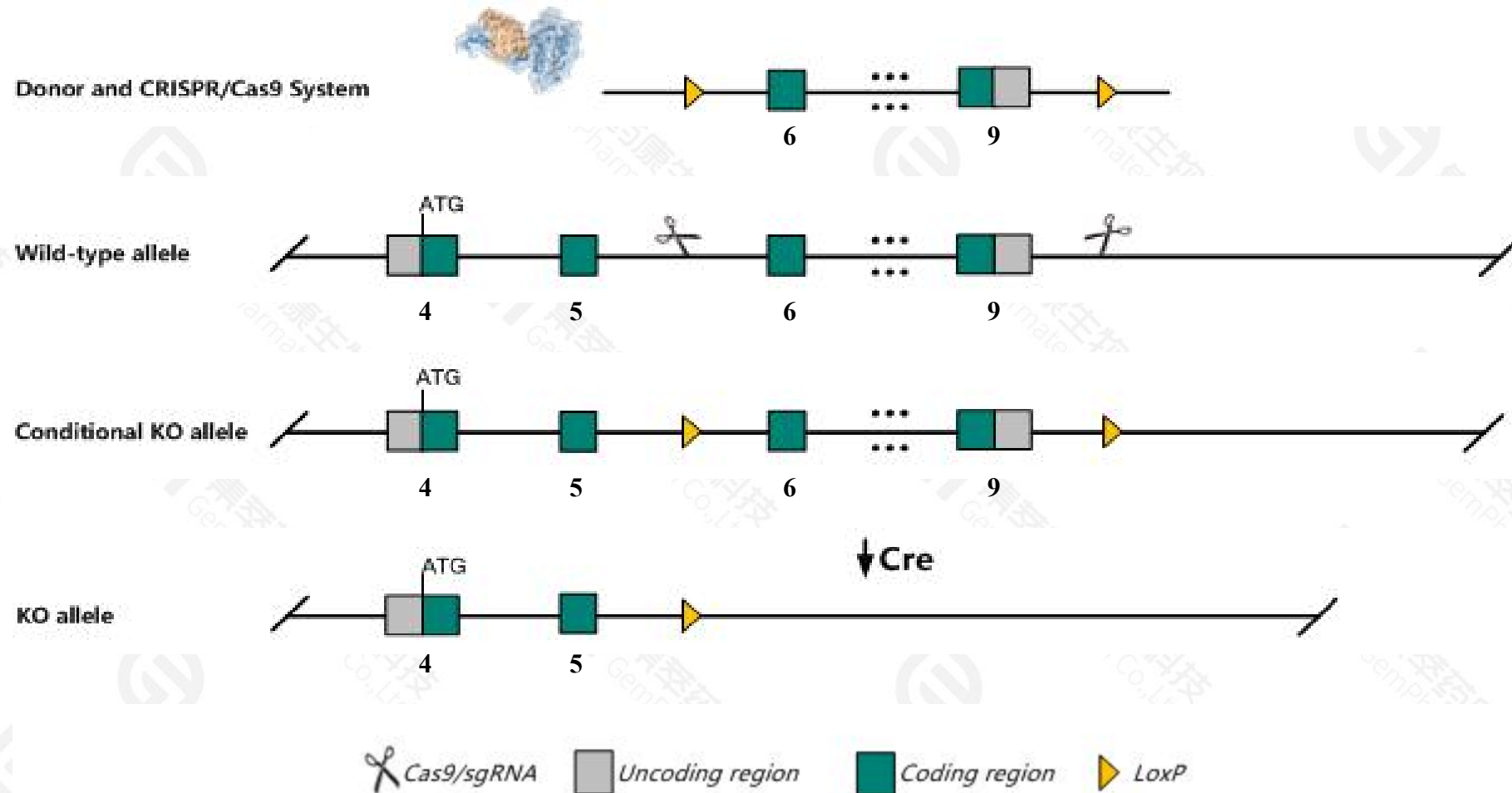
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp821* gene. The schematic diagram is as follows:



- The *Zfp821* gene has 6 transcripts. According to the structure of *Zfp821* gene, exon6-exon9 of *Zfp821-201*(ENSMUST00000034163.9) transcript is recommended as the knockout region. The region contains most coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp821* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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.

- The *Zfp821* 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.

Gene information (NCBI)

Zfp821 zinc finger protein 821 [Mus musculus (house mouse)]

Gene ID: 75871, updated on 13-Dec-2020

Summary



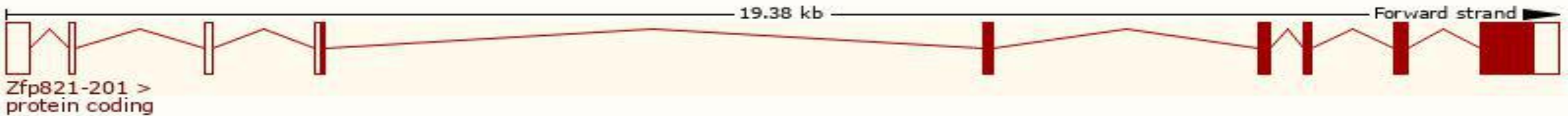
Official Symbol	Zfp821 provided by MGI
Official Full Name	zinc finger protein 821 provided by MGI
Primary source	MGI:MGI:1923121
See related	Ensembl:ENSMUSG00000031728
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930566A11Rik, Znf821
Expression	Broad expression in CNS E14 (RPKM 11.3), testis adult (RPKM 11.1) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

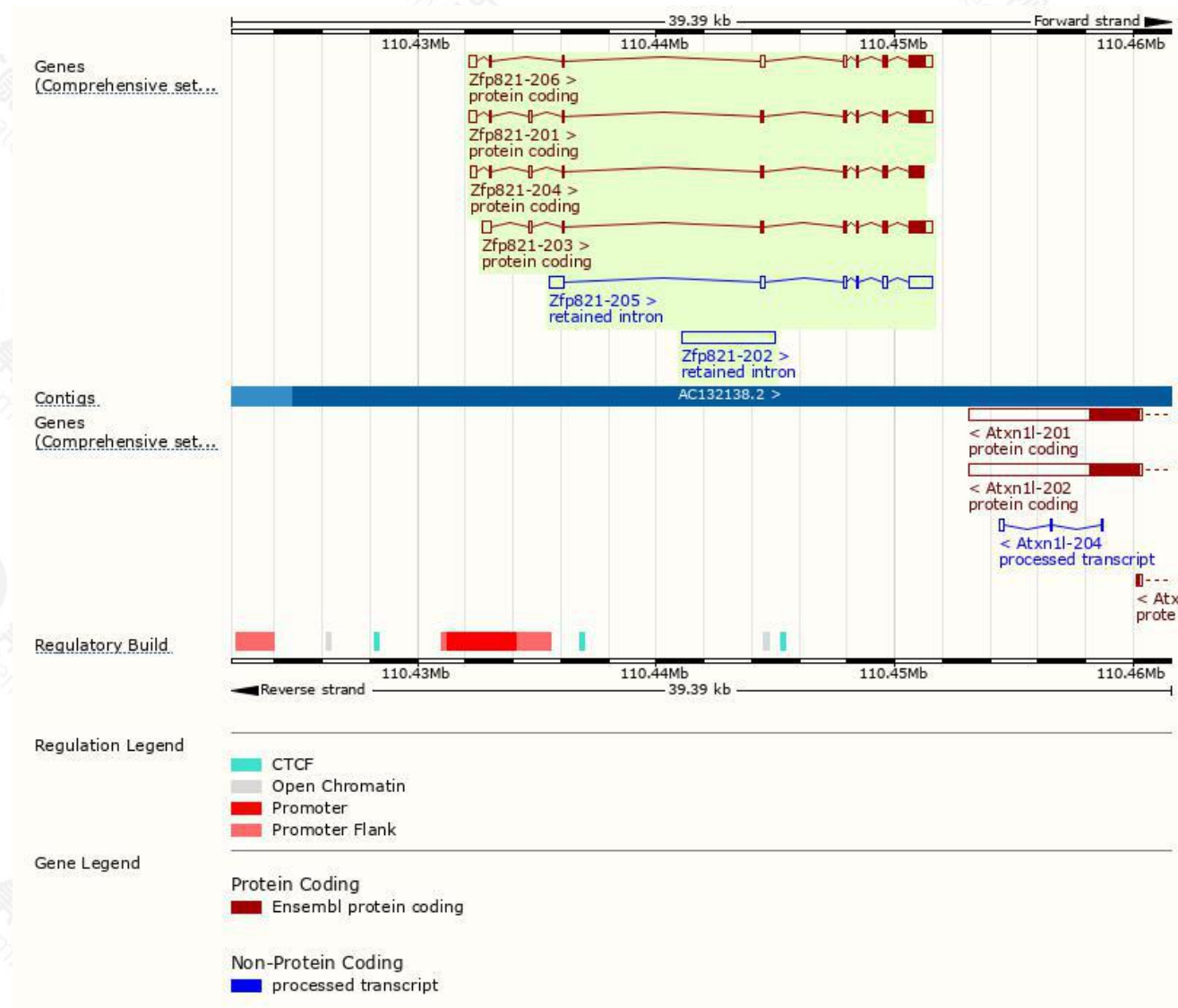
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp821-201	ENSMUST00000034163.9	2127	413aa	Protein coding	CCDS40473		TSL:1 , GENCODE basic , APPRIS P1 ,
Zfp821-203	ENSMUST00000212000.2	2081	413aa	Protein coding	CCDS40473		TSL:1 , GENCODE basic , APPRIS P1 ,
Zfp821-206	ENSMUST00000212964.2	2033	262aa	Protein coding	CCDS85609		TSL:1 , GENCODE basic ,
Zfp821-204	ENSMUST00000212192.2	1713	404aa	Protein coding	-		CDS 3' incomplete , TSL:1 ,
Zfp821-202	ENSMUST00000211918.2	3879	No protein	Retained intron	-		TSL:NA ,
Zfp821-205	ENSMUST00000212233.2	2149	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Zfp821-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain

ENSMUSP000000034...

[MobiDB lite](#)

[Low complexity \(Seq\)](#)

[Coiled-coils \(Ncoils\)](#)

[Superfamily](#)

[SMART](#)

[PROSITE profiles](#)

[PROSITE patterns](#)

[PANTHER](#)

PTHR24404

PTHR24404:SF1



[Gene3D](#)

3.30.160.60

[All sequence SNPs/i...](#)

Sequence variants (dbSNP and all other sources)

[Variant Legend](#)

-  missense variant
-  synonymous variant

[Scale bar](#)

0 40 80 120 160 200 240 280 320 360 413

Zinc finger C2H2 superfamily

Zinc finger C2H2-type

Zinc finger C2H2-type

Zinc finger C2H2-type

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

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