

Rnf121 Cas9-CKO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

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Project Overview

Project Name

Rnf121

Project type

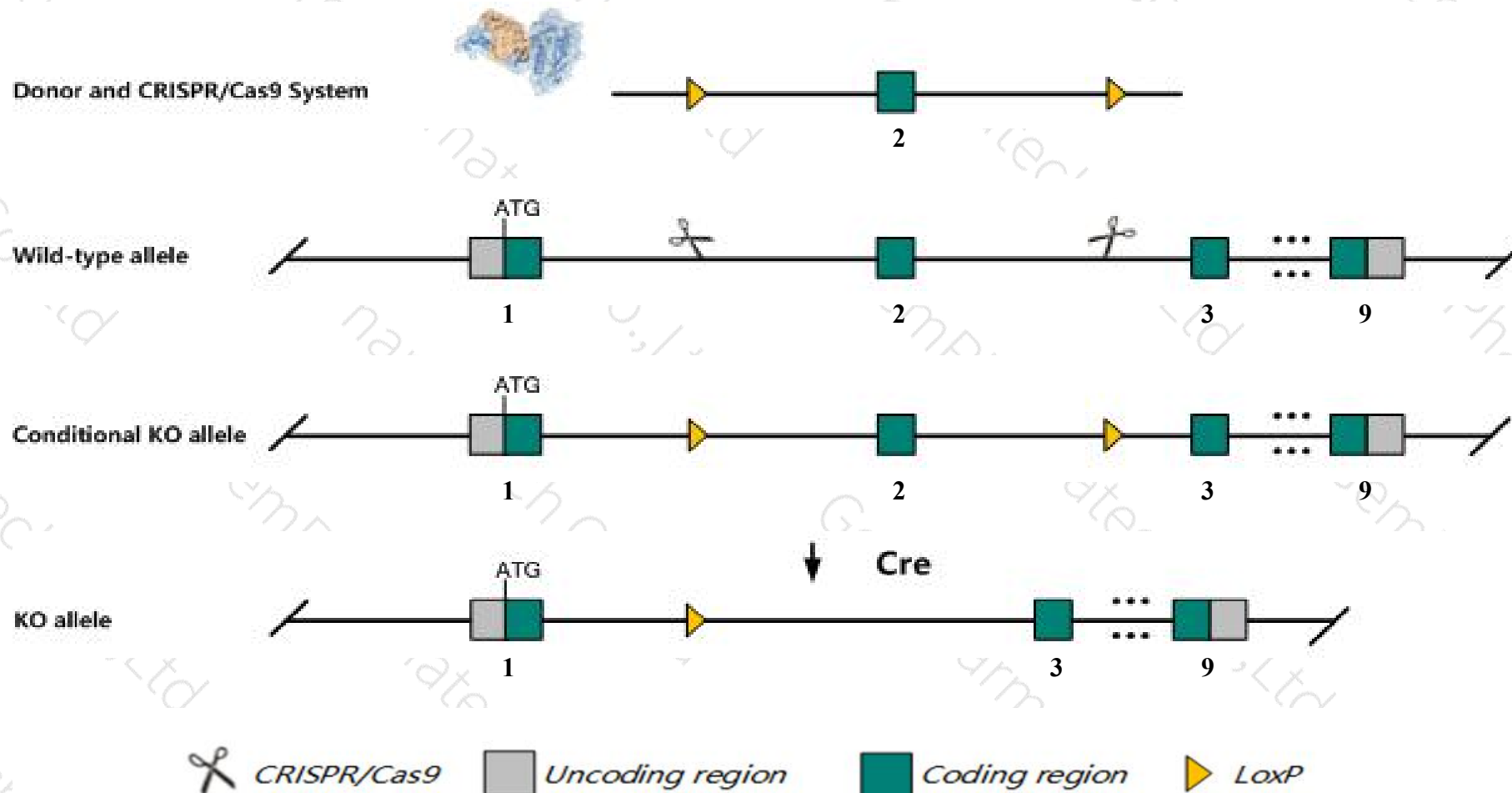
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnfl21* gene. The schematic diagram is as follows:



Technical routes

- The *Rnf121* gene has 7 transcripts. According to the structure of *Rnf121* gene, exon2 of *Rnf121-202* (ENSMUST00000096639.11) transcript is recommended as the knockout region. The region contains 38bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnf121* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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

- Transcript *Rnf121-206* may not be affected.
- The *Rnf121* 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)

Rnf121 ring finger protein 121 [Mus musculus (house mouse)]

Gene ID: 75212, updated on 13-Mar-2020

Summary



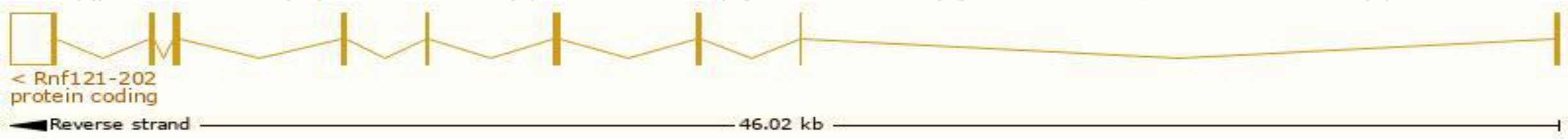
Official Symbol	Rnf121 provided by MGI
Official Full Name	ring finger protein 121 provided by MGI
Primary source	MGI:MGI:1922462
See related	Ensembl:ENSMUSG00000070426
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930544L10Rik
Expression	Ubiquitous expression in placenta adult (RPKM 13.4), large intestine adult (RPKM 13.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

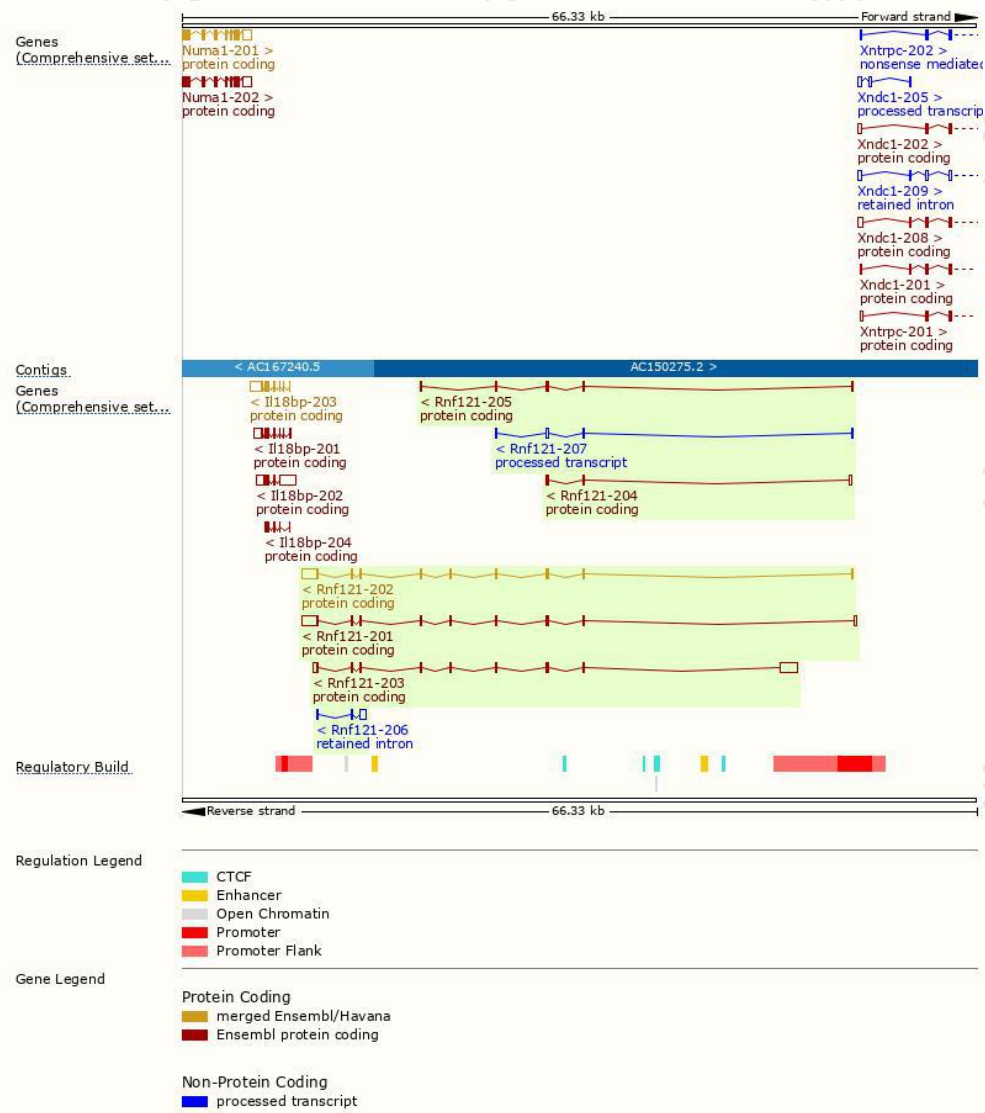
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf121-202	ENSMUST00000096639.11	2249	327aa	Protein coding	CCDS21523	Q8R1Z9	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Rnf121-203	ENSMUST00000106953.7	2545	310aa	Protein coding	-	Q8R1Z9	TSL:1 GENCODE basic
Rnf121-201	ENSMUST00000089052.10	2344	304aa	Protein coding	-	K4DI70	TSL:1 GENCODE basic
Rnf121-205	ENSMUST00000131104.2	508	170aa	Protein coding	-	F6XTP0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Rnf121-204	ENSMUST00000130074.1	446	57aa	Protein coding	-	D3YWK0	CDS 3' incomplete TSL:3
Rnf121-207	ENSMUST00000156119.1	364	No protein	Processed transcript	-	-	TSL:2
Rnf121-206	ENSMUST00000149976.1	619	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Rnf121-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

