

Zfp637 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Zfp637

Project type

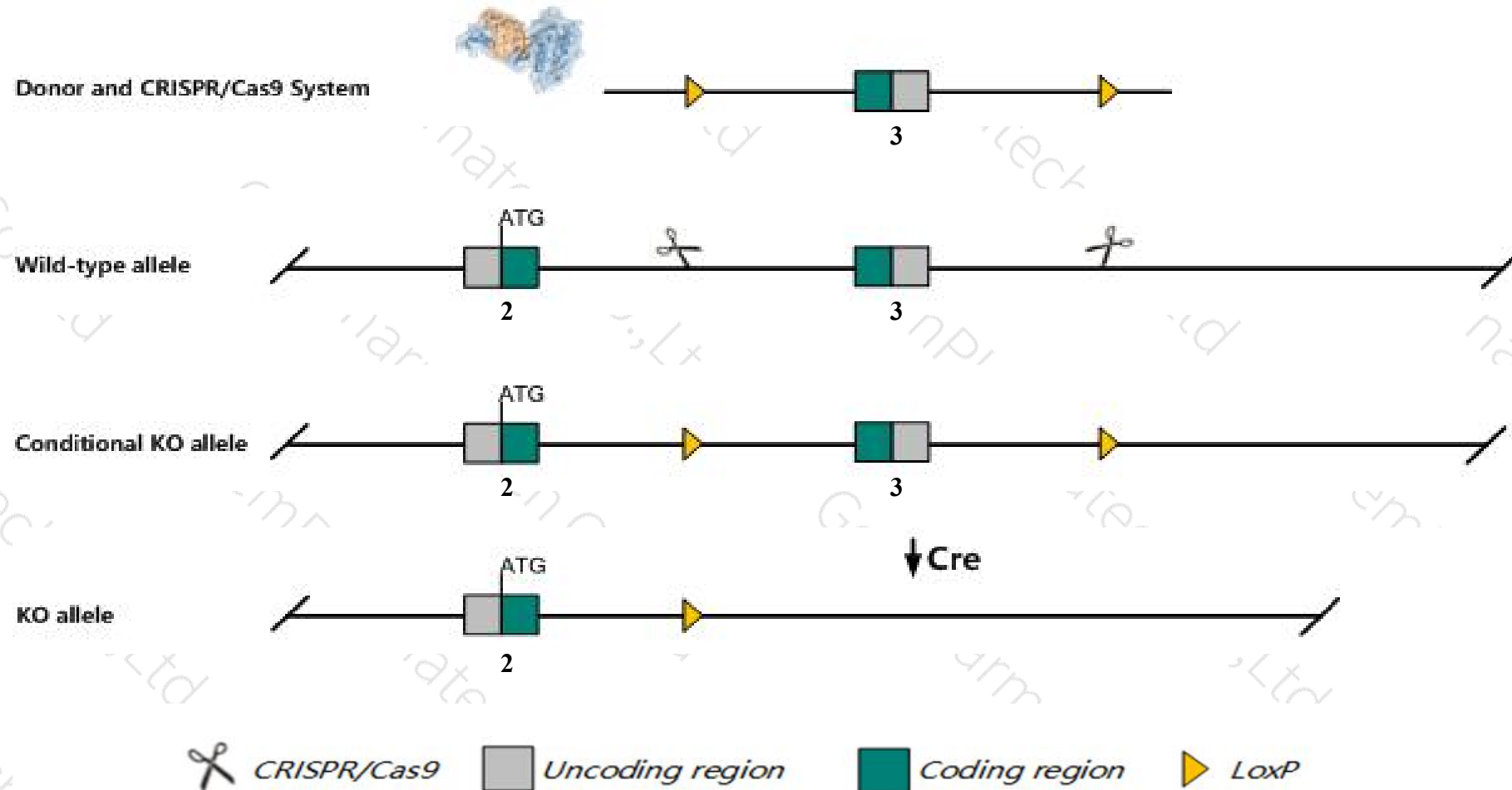
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp637* gene. The schematic diagram is as follows:



- The *Zfp637* gene has 11 transcripts. According to the structure of *Zfp637* gene, exon3 of *Zfp637-203* (ENSMUST00000112860.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp637* 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 *Zfp637* gene is located on the Chr6. 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)

Zfp637 zinc finger protein 637 [Mus musculus (house mouse)]

Gene ID: 232337, updated on 31-Jan-2019

Summary



Official Symbol	Zfp637 provided by MGI
Official Full Name	zinc finger protein 637 provided by MGI
Primary source	MGI:MGI:2448537
See related	Ensembl:ENSMUSG00000059689
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	AI646709, BC021601, Znf32
Expression	Ubiquitous expression in CNS E18 (RPKM 16.4), CNS E14 (RPKM 16.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

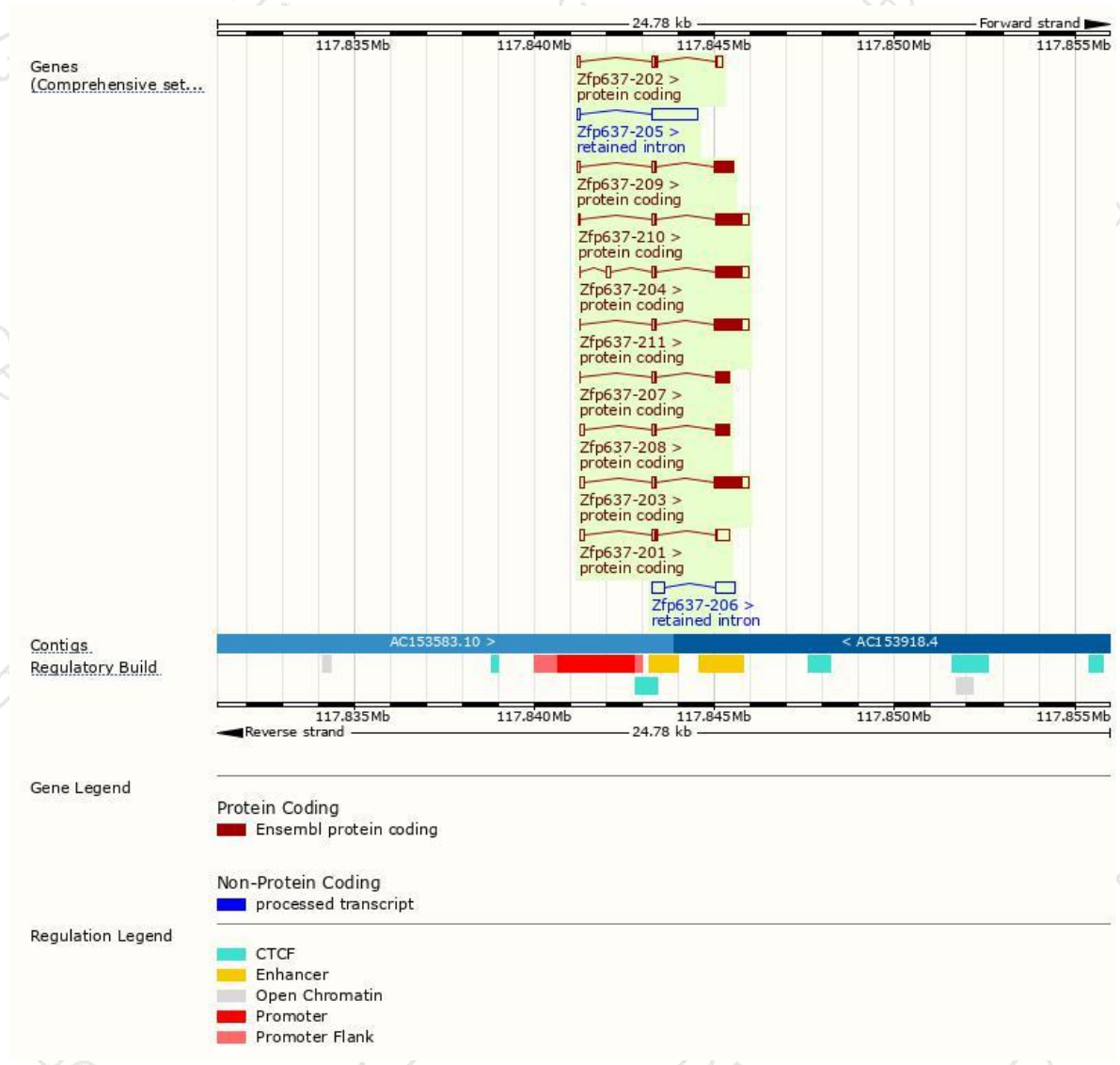
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp637-203	ENSMUST00000112860.1	1231	286aa	Protein coding	CCDS85139	Q80V23	TSL:1 GENCODE basic
Zfp637-204	ENSMUST00000112861.7	1202	272aa	Protein coding	CCDS39607	Q80V23	TSL:2 GENCODE basic APPRIS P1
Zfp637-211	ENSMUST00000223041.1	1128	286aa	Protein coding	CCDS85139	Q80V23	TSL:1 GENCODE basic
Zfp637-210	ENSMUST00000164472.7	1098	272aa	Protein coding	CCDS39607	Q80V23	TSL:1 GENCODE basic APPRIS P1
Zfp637-209	ENSMUST00000137224.7	765	202aa	Protein coding	-	D3Z0E5	CDS 3' incomplete TSL:1
Zfp637-208	ENSMUST00000136889.7	659	153aa	Protein coding	-	D3YYX3	CDS 3' incomplete TSL:3
Zfp637-201	ENSMUST00000112858.7	650	33aa	Protein coding	-	D3Z3T2	TSL:2 GENCODE basic
Zfp637-207	ENSMUST00000134526.7	543	153aa	Protein coding	-	D3YYX3	CDS 3' incomplete TSL:5
Zfp637-202	ENSMUST00000112859.7	421	33aa	Protein coding	-	D3Z3T2	TSL:2 GENCODE basic
Zfp637-205	ENSMUST00000127593.7	1355	No protein	Retained intron	-	-	TSL:1
Zfp637-206	ENSMUST00000132644.1	905	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Zfp637-203* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000108...

[Superfamily](#)

[SMART](#)

[Pfam](#)

[PROSITE profiles](#)

[PROSITE patterns](#)

[PANTHER](#)

Zinc finger C2H2 superfamily

Zinc finger C2H2-type

Zinc finger C2H2-type

Zinc finger C2H2-type

Zinc finger C2H2-type

PTHR23226:SF214

PTHR23226

[Gene3D](#)

3.30.160.60

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

Sequence variants (dbSNP and all other sources)

Variant Legend

frameshift variant

missense variant

synonymous variant

Scale bar

0 40 80 120 160 200 240 286

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

Tel: 400-9660890

