

Zfp318 Cas9-CKO Strategy

Designer: Jia Yu

Reviewer: Xiaojing Li

Design Date: 2020-7-28

Project Overview

Project Name

Zfp318

Project type

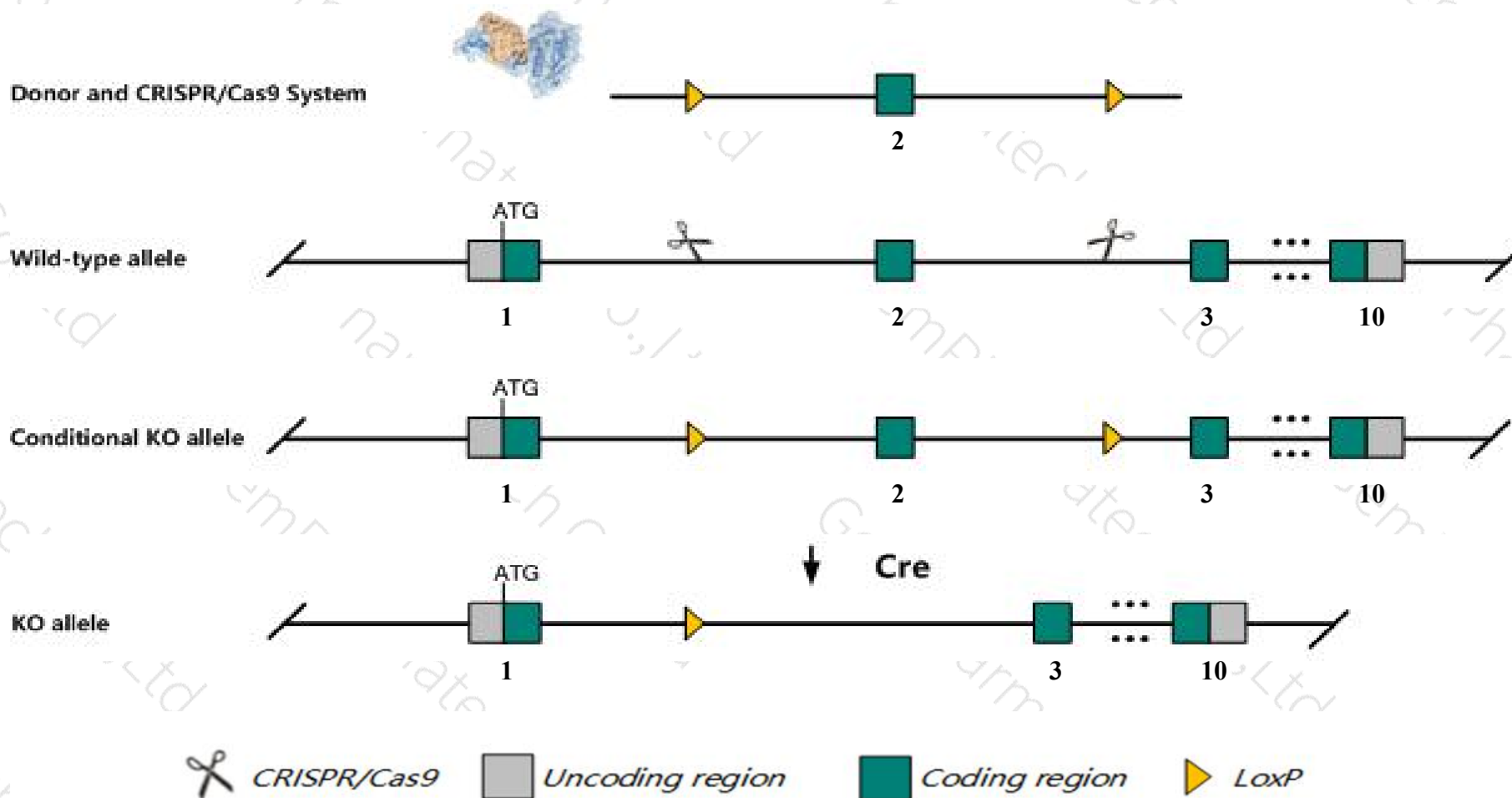
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp318* gene. The schematic diagram is as follows:



Technical routes

- The *Zfp318* gene has 5 transcripts. According to the structure of *Zfp318* gene, exon2 of *Zfp318-201*(ENSMUST00000113481.8) transcript is recommended as the knockout region. The region contains 152bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp318* 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.

- According to the existing MGI data, mice homozygous for an ENU-induced allele exhibit reduced male fertility and altered IgM and IgD levels. Null mutants displayed normal level of circulating B cells with decreased IgD and increased IgM levels.
- The *Zfp318* gene is located on the Chr17. 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)

Zfp318 zinc finger protein 318 [Mus musculus (house mouse)]

Gene ID: 57908, updated on 13-Mar-2020

Summary



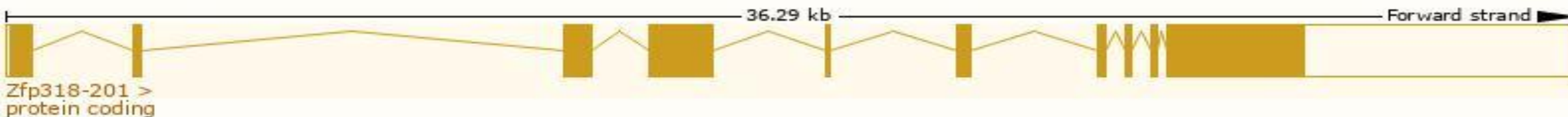
Official Symbol	Zfp318 provided by MGI
Official Full Name	zinc finger protein 318 provided by MGI
Primary source	MGI:MGI:1889348
See related	Ensembl:ENSMUSG00000015597
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610034E08Rik, D530032D06Rik, TZF, Znf318
Expression	Ubiquitous expression in testis adult (RPKM 4.1), CNS E18 (RPKM 3.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

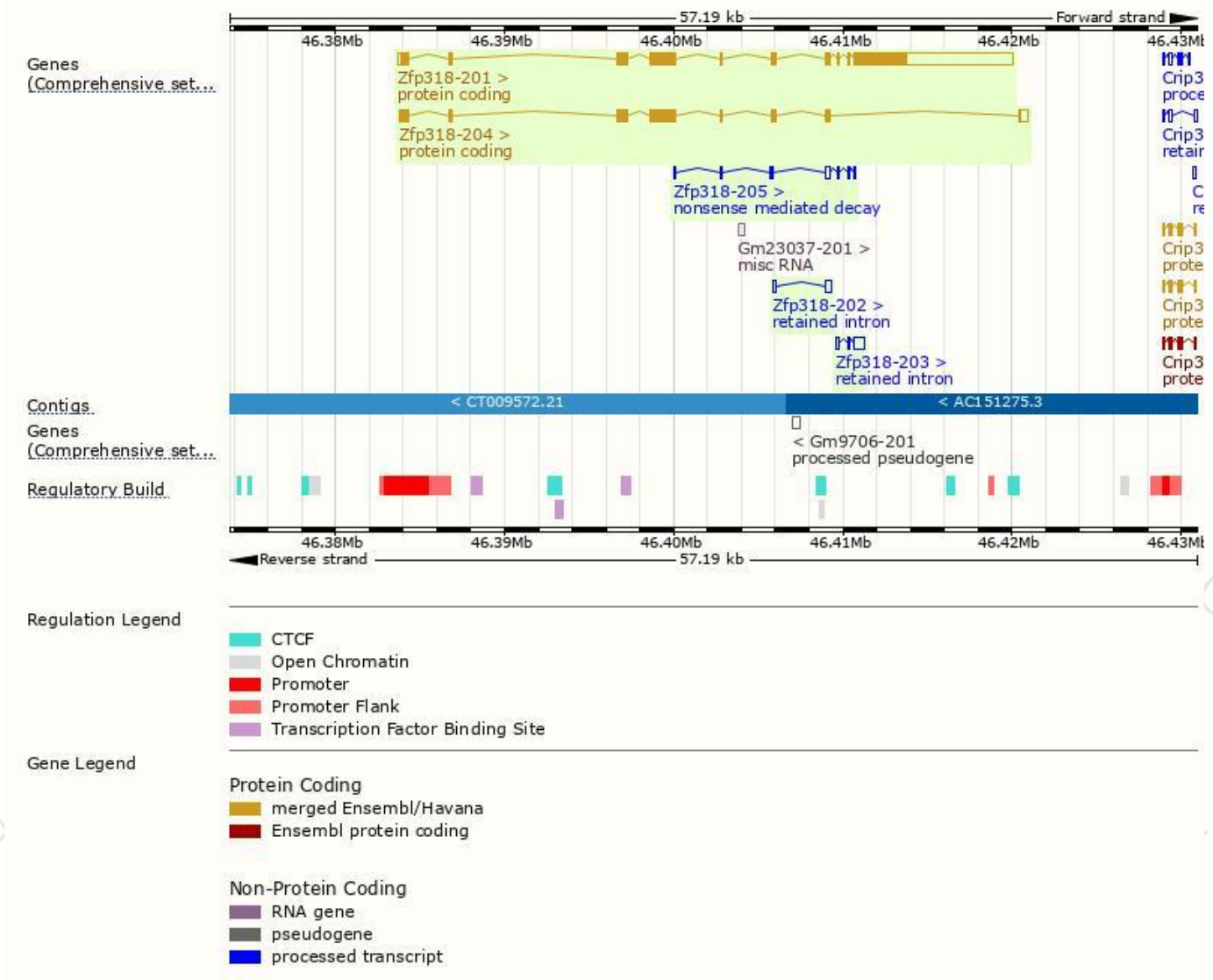
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp318-201	ENSMUST00000113481.8	13060	2237aa	Protein coding	CCDS28827	Q99PP2	TSL:5 GENCODE basic APPRIS P4
Zfp318-204	ENSMUST00000138127.7	3936	1154aa	Protein coding	CCDS28826	Q99PP2	TSL:5 GENCODE basic APPRIS ALT2
Zfp318-205	ENSMUST00000152472.7	748	54aa	Nonsense mediated decay	-	F6R9J2	CDS 5' incomplete TSL:5
Zfp318-203	ENSMUST00000136017.1	958	No protein	Retained intron	-	-	TSL:1
Zfp318-202	ENSMUST00000123733.1	573	No protein	Retained intron	-	-	TSL:3

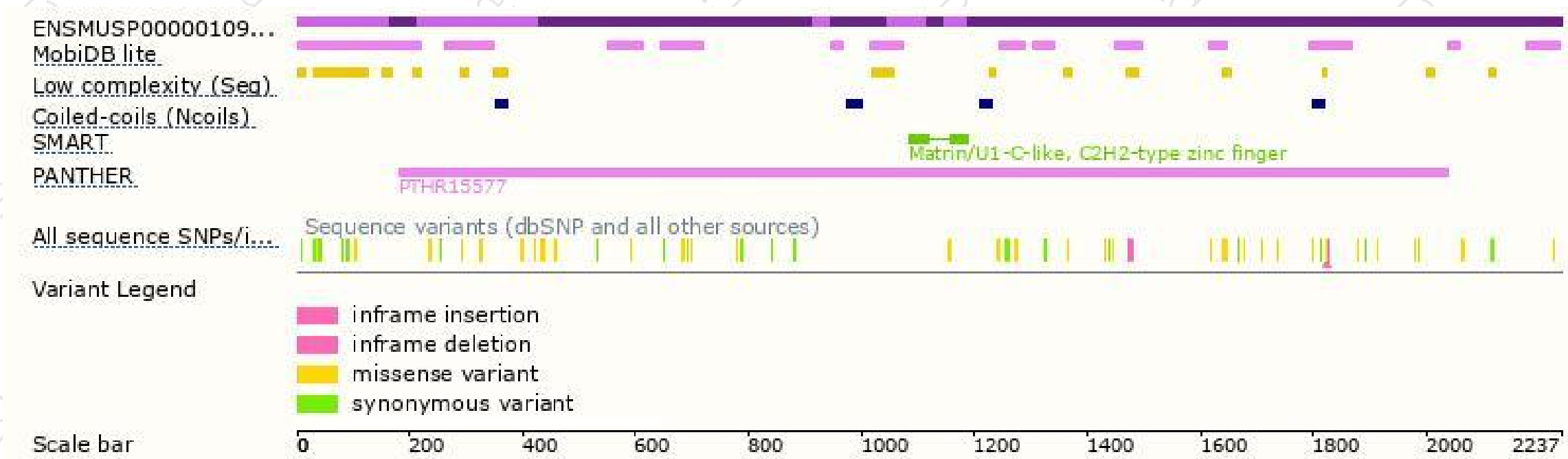
The strategy is based on the design of *Zfp318-201* transcript, the transcription is shown below:



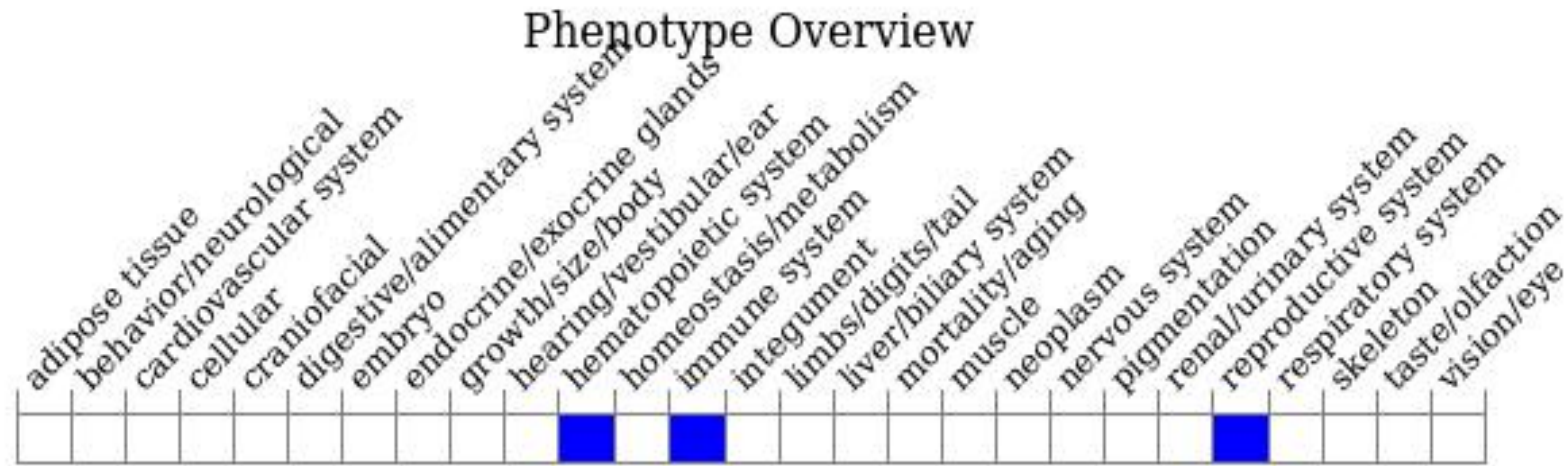
Genomic location distribution



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 an ENU-induced allele exhibit reduced male fertility and altered IgM and IgD levels. Null mutants displayed normal level of circulating B cells with decreased IgD and increased IgM levels.

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

Tel: 400-9660890

