

Zfp13 Cas9-CKO Strategy

Designer: Xiaojing Li

Reviewer: JiaYu

Design Date: 2020-8-14

Project Overview

Project Name

Zfp13

Project type

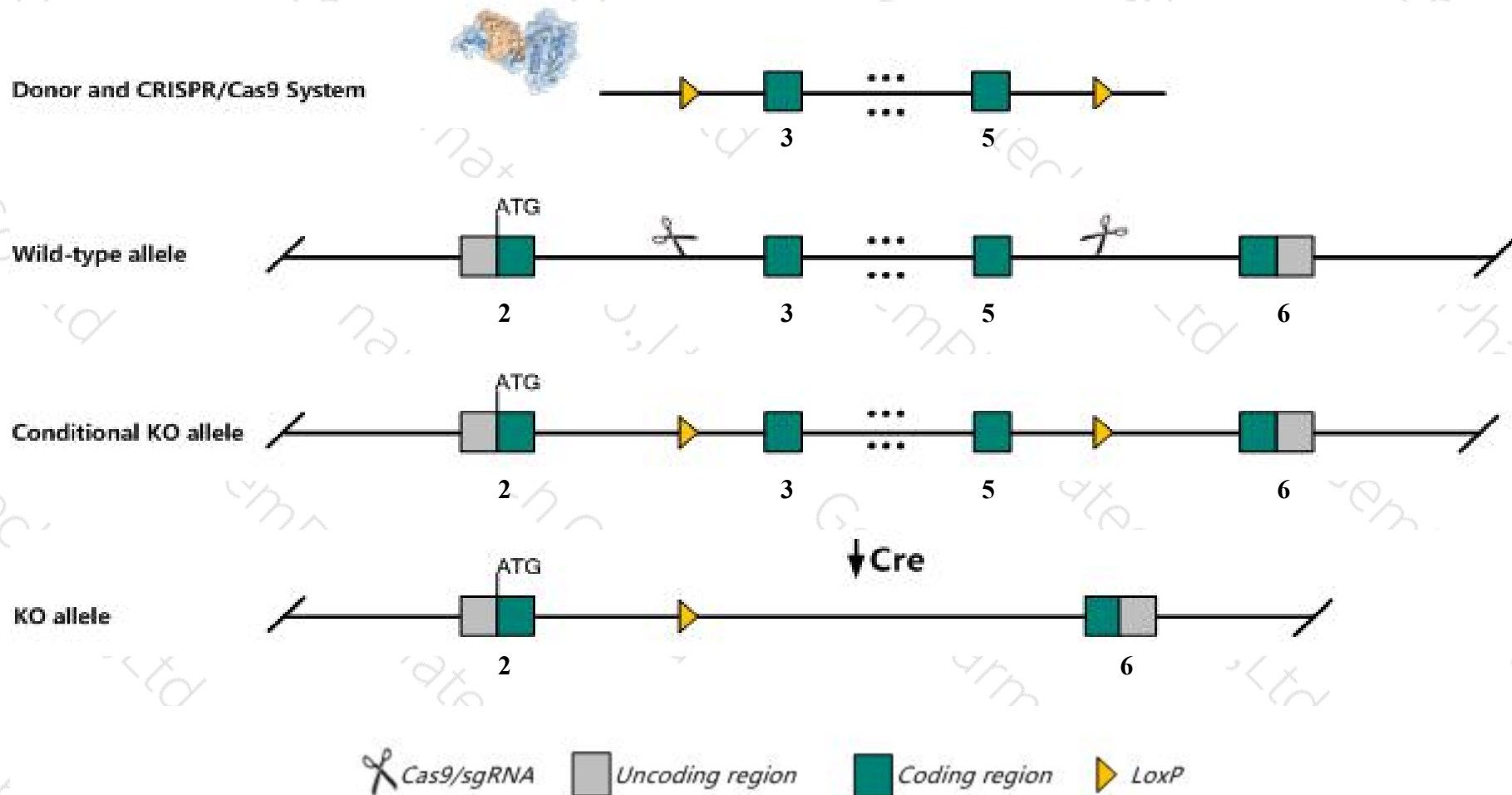
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp13* gene. The schematic diagram is as follows:



Technical routes

- The *Zfp13* gene has 5 transcripts. According to the structure of *Zfp13* gene, exon3-exon5 of *Zfp13-201*(ENSMUST00000057029.4) transcript is recommended as the knockout region. The region contains 406bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp13* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector 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 *Zfp13* 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)

Zfp13 zinc finger protein 13 [Mus musculus (house mouse)]

Gene ID: 22654, updated on 13-Mar-2020

Summary

Official Symbol Zfp13 provided by [MGI](#)

Official Full Name zinc finger protein 13 provided by [MGI](#)

Primary source [MGI:MGI:99159](#)

See related [Ensembl:ENSMUSG00000062012](#)

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 Al835008, Krox-8, Zfp-13

Expression Ubiquitous expression in testis adult (RPKM 18.2), ovary adult (RPKM 12.7) and 25 other tissues [See more](#)

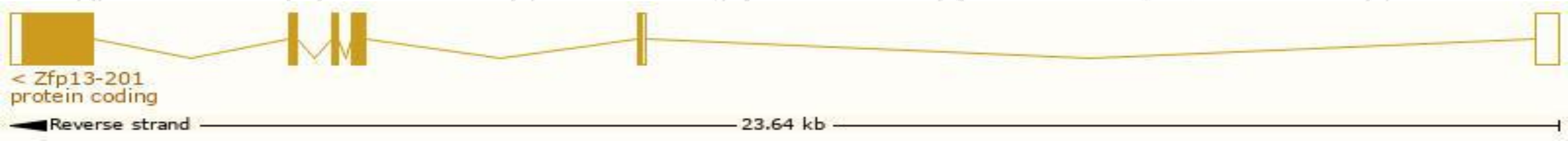
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

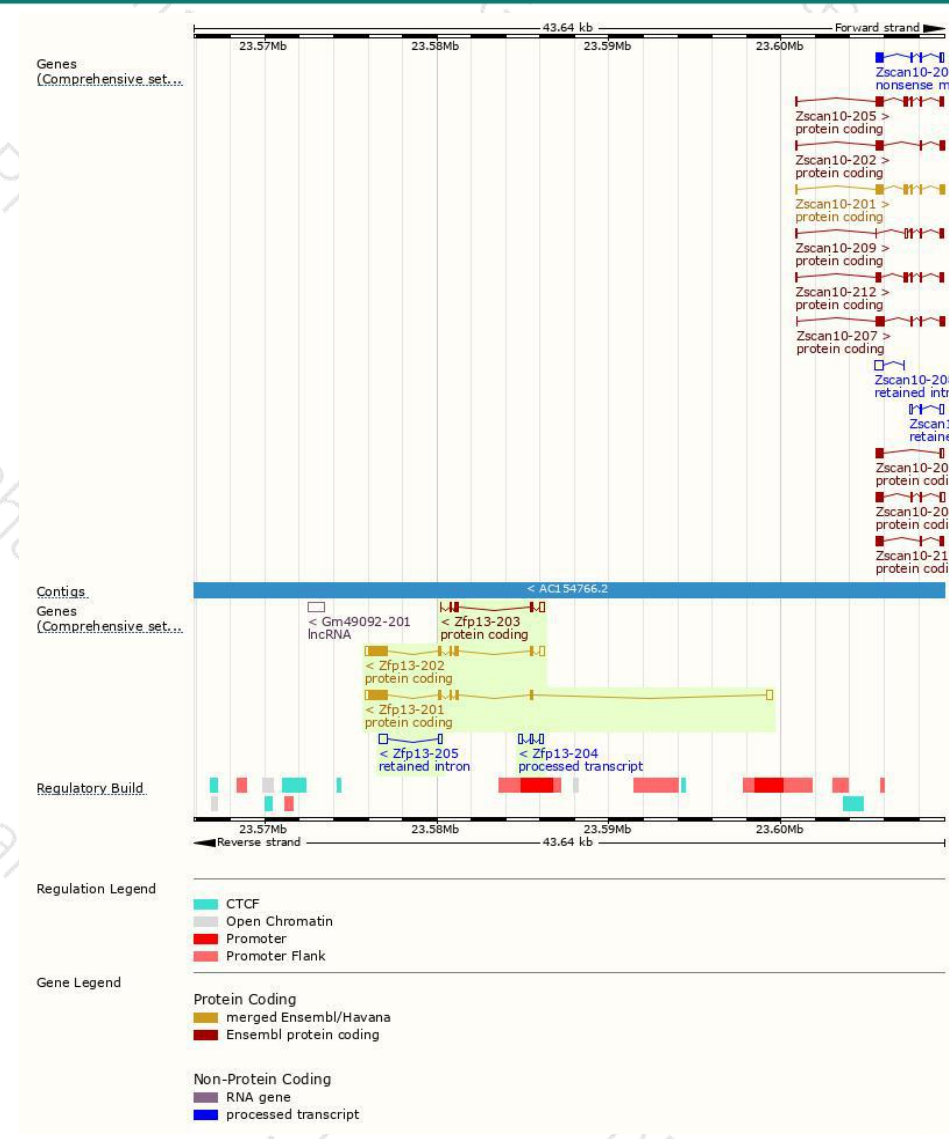
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp13-201	ENSMUST0000057029.4	2139	505aa	Protein coding	CCDS28450	P10754	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 P2
Zfp13-202	ENSMUST00000115516.10	2104	512aa	Protein coding	-	D7F2B3 P10754	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 ALT2
Zfp13-203	ENSMUST00000227952.1	692	118aa	Protein coding	-	A0A2I3BQW3	CDS 3' incomplete
Zfp13-204	ENSMUST00000228298.1	502	No protein	Processed transcript	-	-	
Zfp13-205	ENSMUST00000228942.1	655	No protein	Retained intron	-	-	

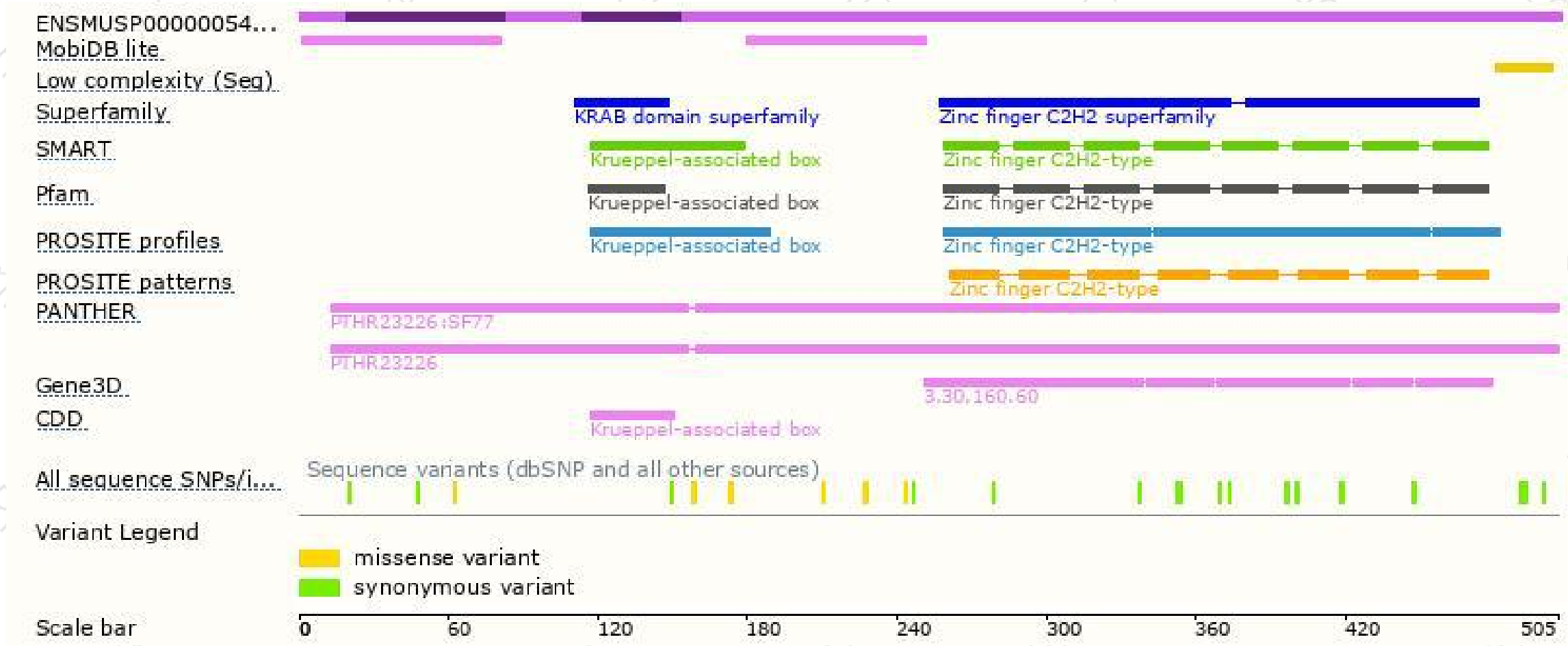
The strategy is based on the design of *Zfp13-201* transcript,the transcription is shown below:



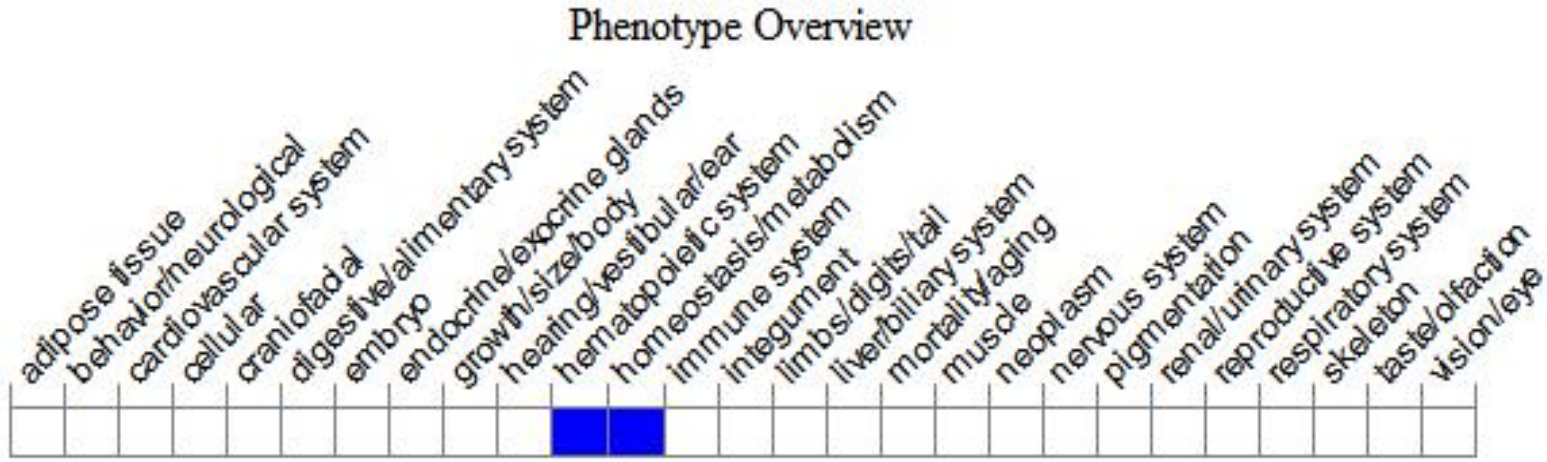
Genomic location distribution



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/>).

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

Tel: 025-5864 1534

