

***Zfp142* Cas9-KO Strategy**

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-5-18

Project Overview

Project Name

Zfp142

Project type

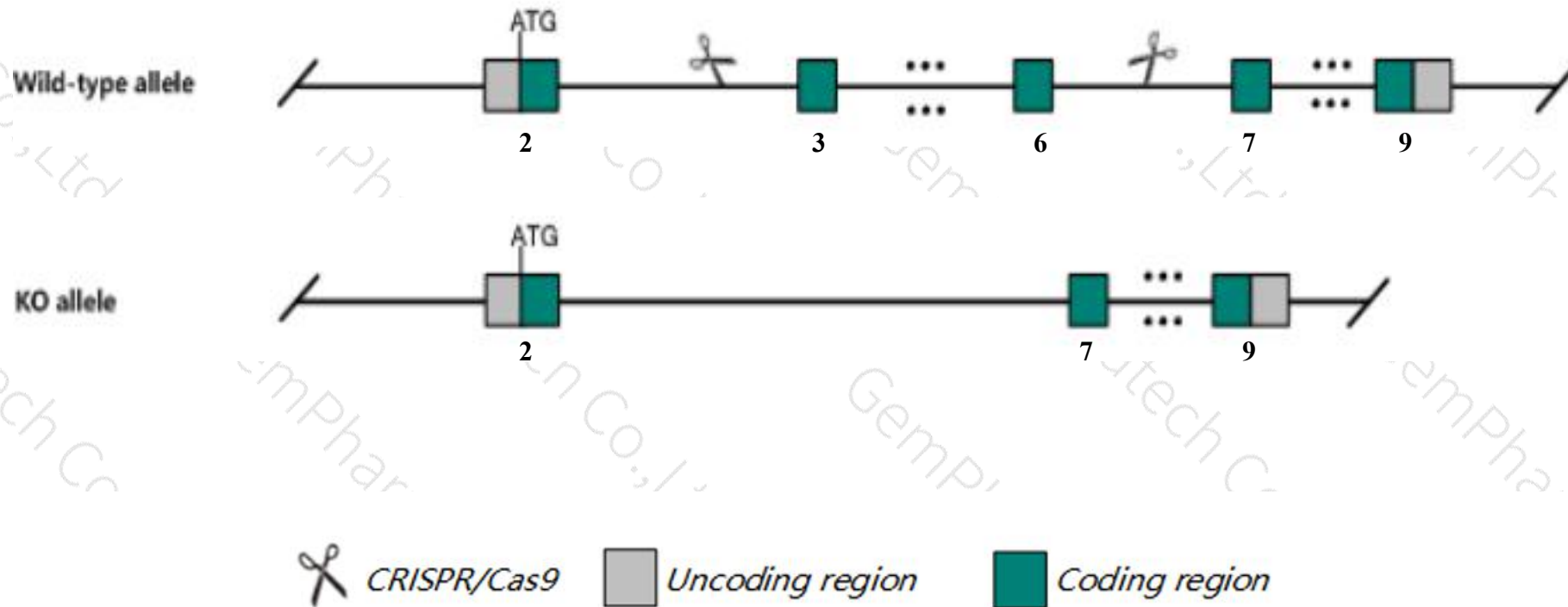
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp142* gene. The schematic diagram is as follows:



- The *Zfp142* gene has 8 transcripts. According to the structure of *Zfp142* gene, exon3-exon6 of *Zfp142-201* (ENSMUST00000027315.13) transcript is recommended as the knockout region. The region contains 1771bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp142* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Zfp142* gene is located on the Chr1. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Zfp142 zinc finger protein 142 [Mus musculus (house mouse)]

Gene ID: 77264, updated on 13-Mar-2020

Summary



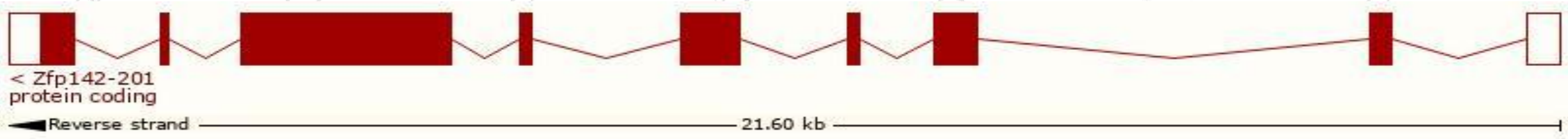
Official Symbol	Zfp142 provided by MGI
Official Full Name	zinc finger protein 142 provided by MGI
Primary source	MGI:MGI:1924514
See related	Ensembl:ENSMUSG00000026135
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9330177B18Rik, BB154236, Znf142, mKIAA0236
Expression	Ubiquitous expression in ovary adult (RPKM 10.5), thymus adult (RPKM 9.6) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

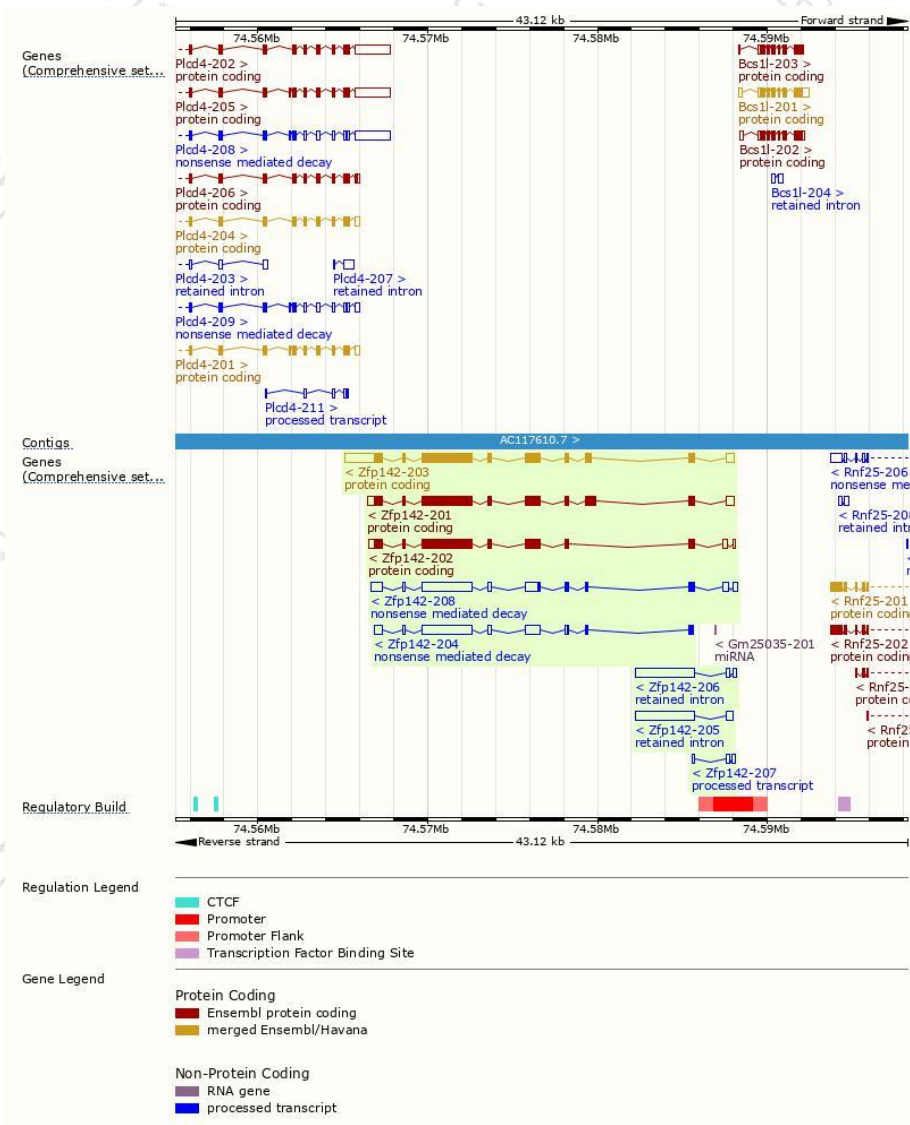
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp142-203	ENSMUST00000113737.7	7473	1740aa	Protein coding	CCDS35618	-	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 P3
Zfp142-201	ENSMUST00000027315.13	6480	1843aa	Protein coding	CCDS78619	G5E869	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
Zfp142-202	ENSMUST00000066986.12	5756	1642aa	Protein coding	-	-	TSL:5 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
Zfp142-208	ENSMUST00000156613.7	5902	219aa	Nonsense mediated decay	-	M0QWZ4	TSL:5
Zfp142-204	ENSMUST00000127921.1	5020	132aa	Nonsense mediated decay	-	M0QWM7	TSL:1
Zfp142-207	ENSMUST00000147011.2	510	No protein	Processed transcript	-	-	TSL:3
Zfp142-206	ENSMUST00000136865.7	3876	No protein	Retained intron	-	-	TSL:1
Zfp142-205	ENSMUST00000130112.1	3855	No protein	Retained intron	-	-	TSL:1

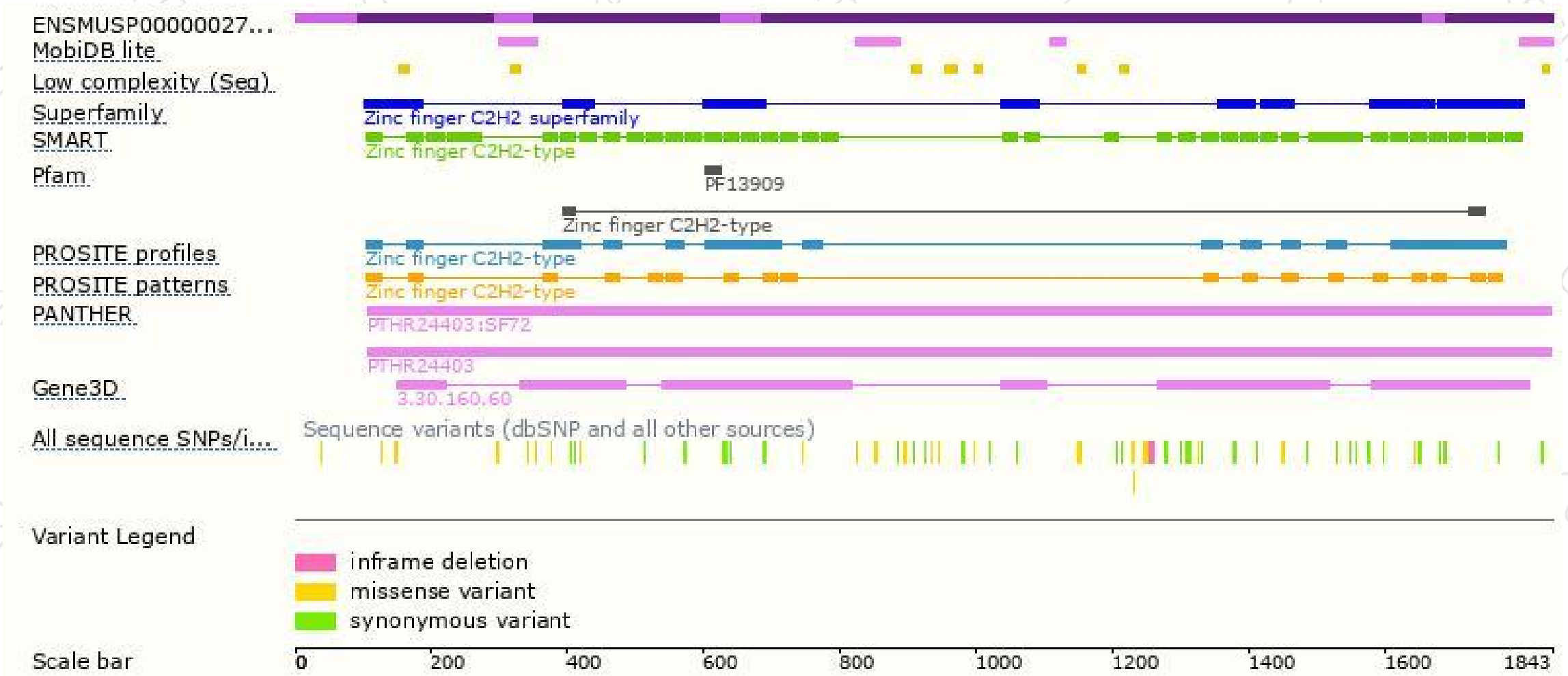
The strategy is based on the design of *Zfp142-201* transcript,The transcription is shown below



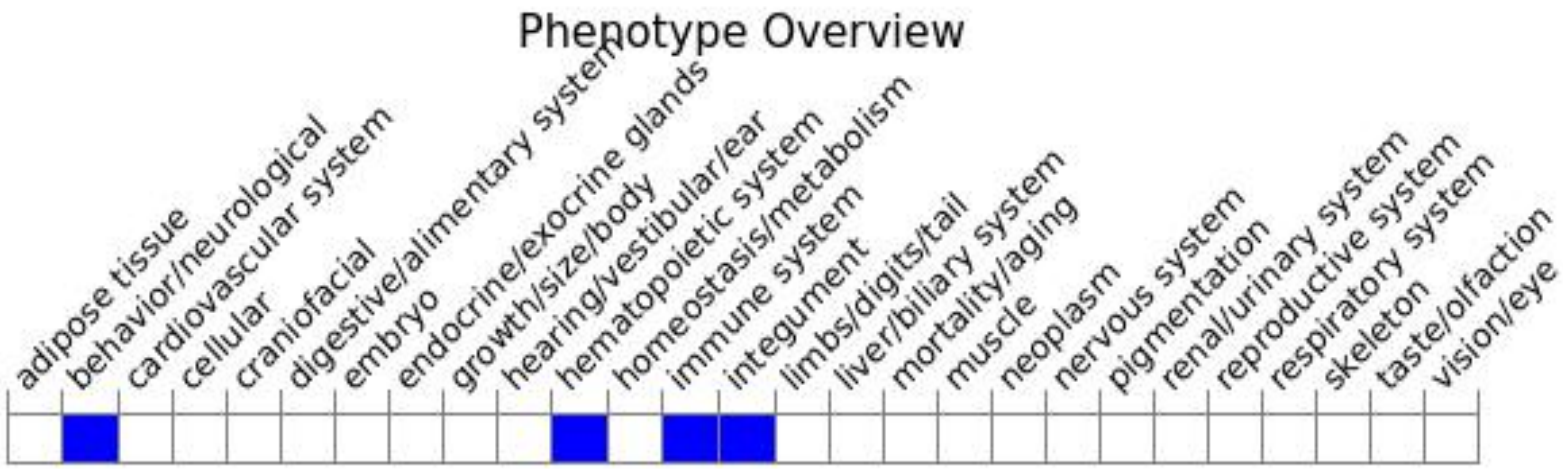
Genomic location distribution



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: 400-9660890

