

Zfp512 Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Yumeng Wang

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Project Overview

Project Name

Zfp512

Project type

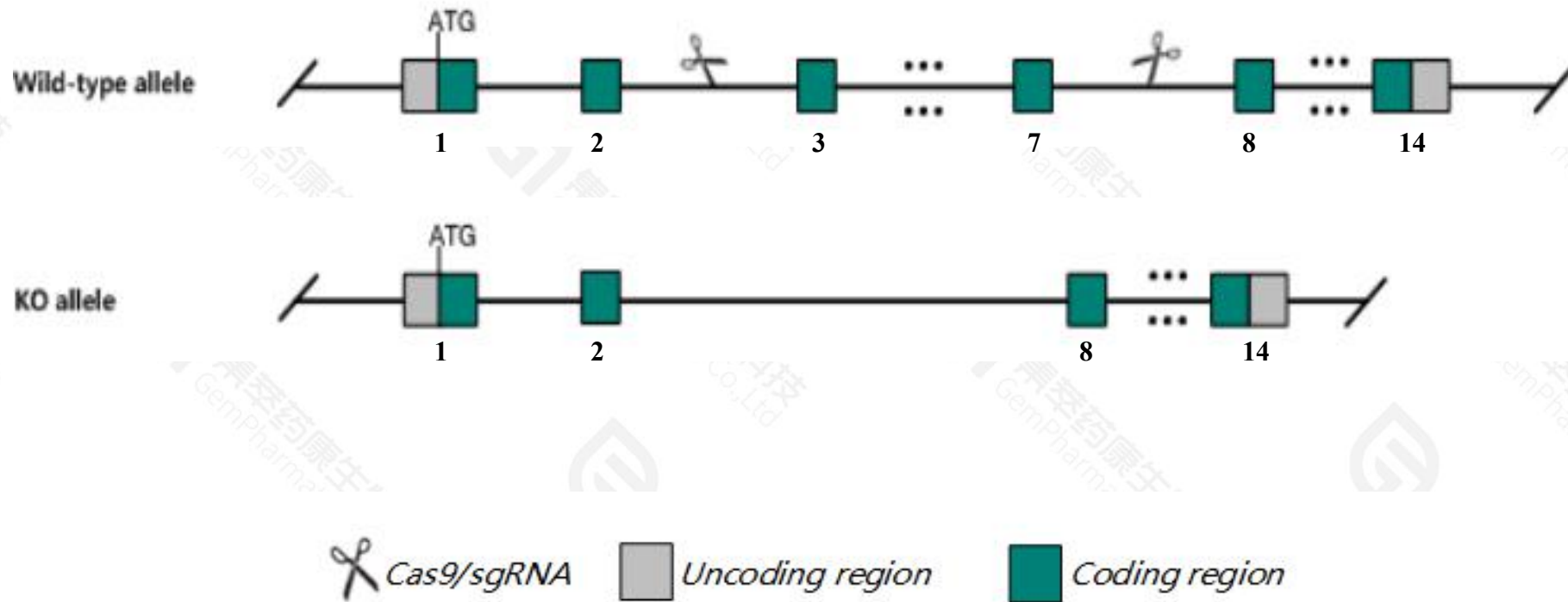
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp512* gene. The schematic diagram is as follows:



- The *Zfp512* gene has 8 transcripts. According to the structure of *Zfp512* gene, exon3-exon7 of *Zfp512-201*(ENSMUST00000076264.8) transcript is recommended as the knockout region. The region contains 589bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp512* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Zfp512* gene is located on the Chr5. 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)

Zfp512 zinc finger protein 512 [Mus musculus (house mouse)]

Gene ID: 269639, updated on 13-Mar-2020

Summary



Official Symbol	Zfp512 provided by MGI
Official Full Name	zinc finger protein 512 provided by MGI
Primary source	MGI:MGI:1917345
See related	Ensembl:ENSMUSG00000062761
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	2500002M11Rik, AI450173, D230008H22, Znf512
Expression	Broad expression in CNS E18 (RPKM 24.0), CNS E14 (RPKM 21.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

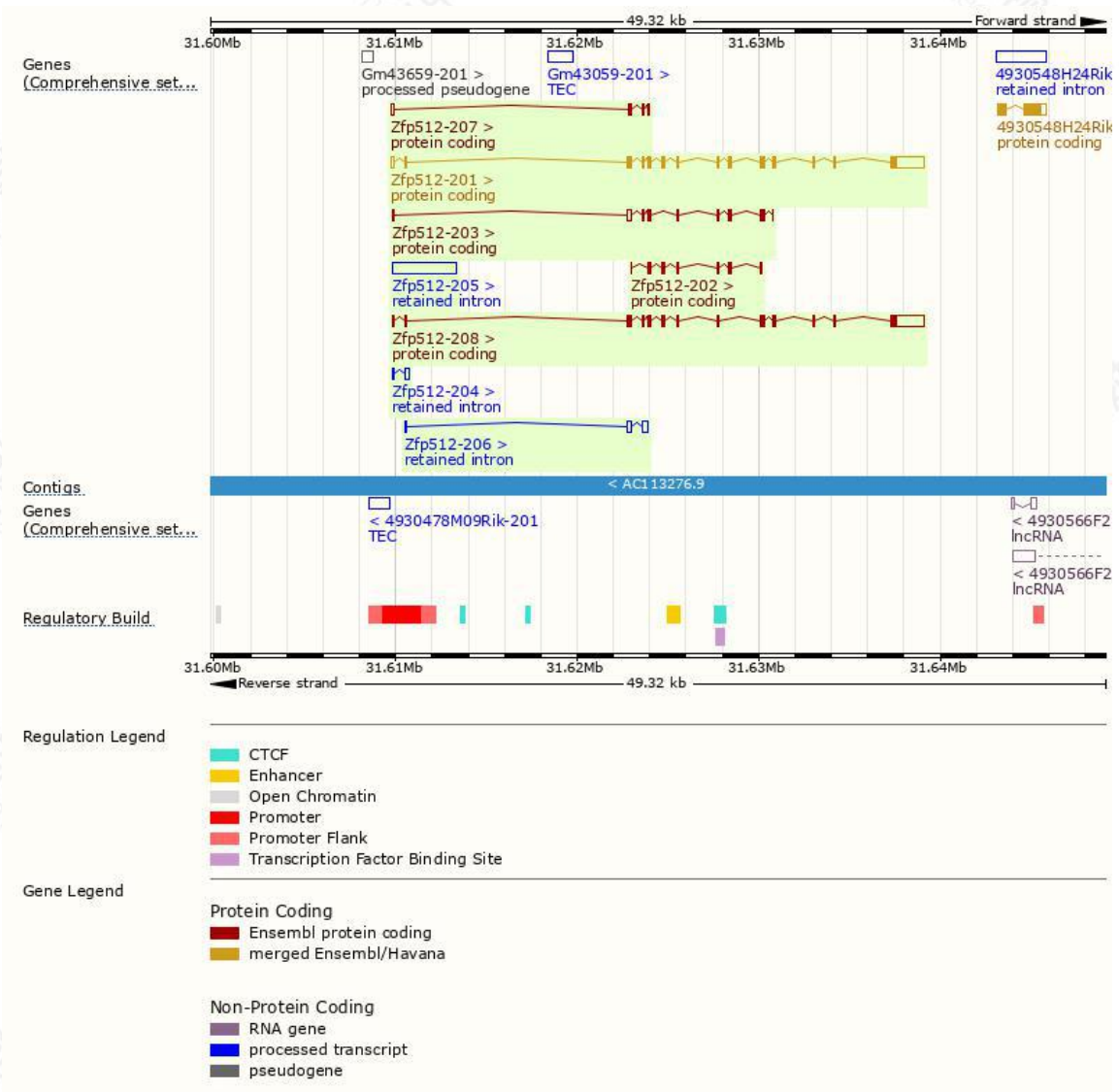
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp512-201	ENSMUST00000076264.7	3299	562aa	Protein coding	CCDS19183	Q69Z99	TSL:1 GENCODE basic APPRIS P1
Zfp512-208	ENSMUST00000202244.3	3045	506aa	Protein coding	-	A0A0J9YTU9	TSL:1 GENCODE basic
Zfp512-203	ENSMUST00000201450.3	1055	226aa	Protein coding	-	A0A0J9YV10	CDS 3' incomplete TSL:5
Zfp512-202	ENSMUST00000200782.1	668	222aa	Protein coding	-	A0A0J9YTW0	CDS 5' and 3' incomplete TSL:3
Zfp512-207	ENSMUST00000202061.3	500	72aa	Protein coding	-	A0A0J9YU29	CDS 3' incomplete TSL:2
Zfp512-205	ENSMUST00000201859.1	3522	No protein	Retained intron	-	-	TSL:NA
Zfp512-206	ENSMUST00000201945.1	570	No protein	Retained intron	-	-	TSL:3
Zfp512-204	ENSMUST00000201599.1	331	No protein	Retained intron	-	-	TSL:3

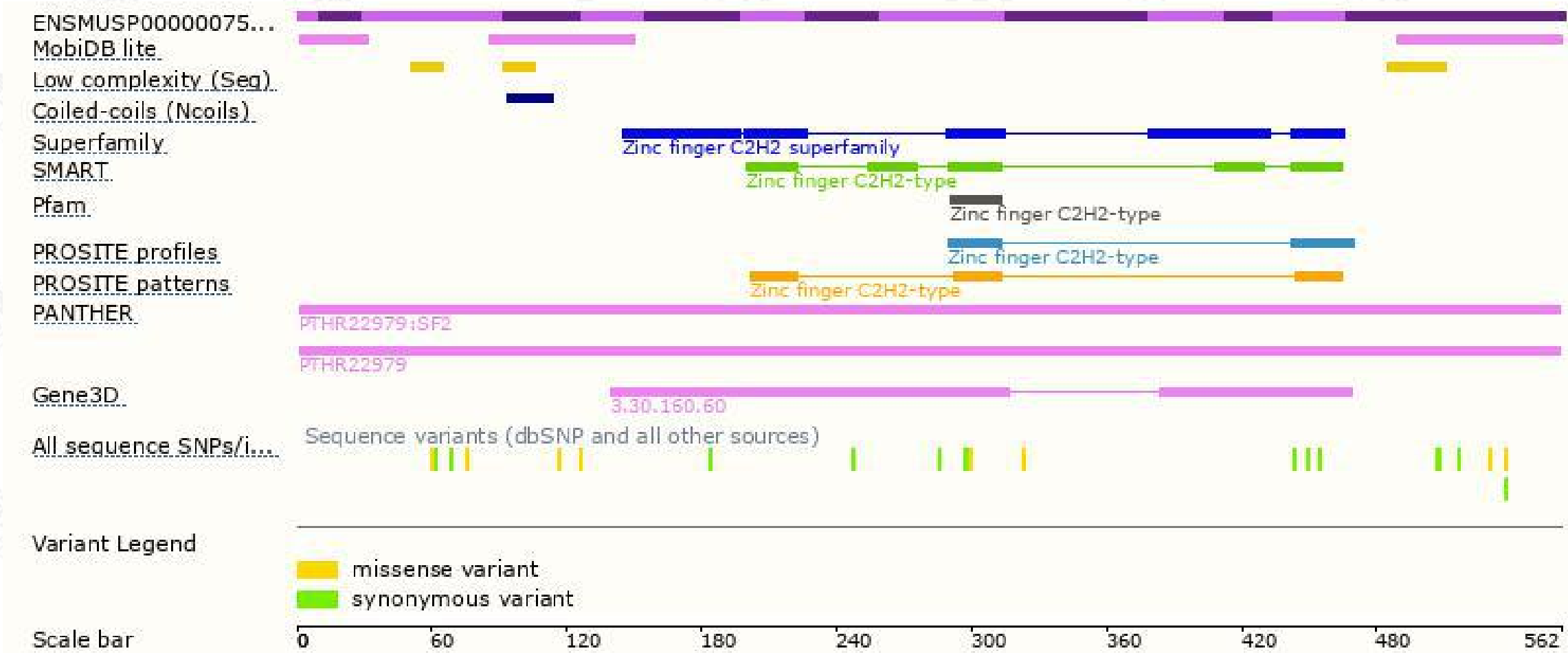
The strategy is based on the design of *Zfp512-201* transcript,the transcription is shown below:



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

