

Zfp2 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2020-4-8

Project Overview

Project Name

Zfp2

Project type

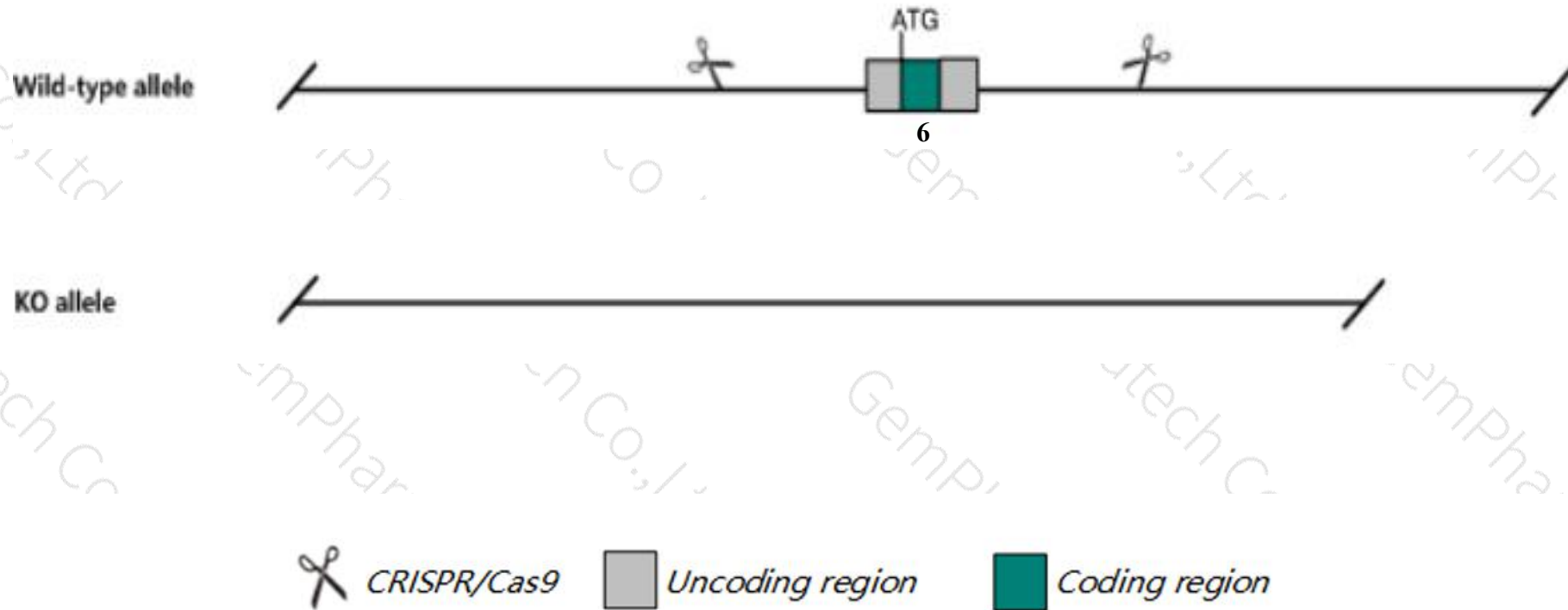
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp2* gene. The schematic diagram is as follows:



- The *Zfp2* gene has 6 transcripts. According to the structure of *Zfp2* gene, exon6 of *Zfp2*-203 (ENSMUST00000116378.7) transcript is recommended as the knockout region. The region contains all 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 *Zfp2* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Zfp2* gene is located on the Chr11. 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)

Zfp2 zinc finger protein 2 [Mus musculus (house mouse)]

Gene ID: 22678, updated on 13-Mar-2020

Summary



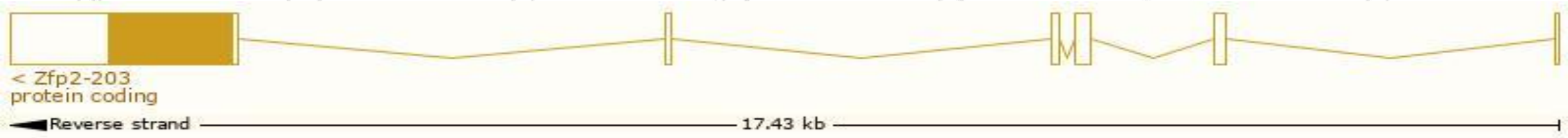
Official Symbol	Zfp2 provided by MGI
Official Full Name	zinc finger protein 2 provided by MGI
Primary source	MGI:MGI:99167
See related	Ensembl:ENSMUSG00000049321
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9930007F06Rik, Fnp-2, Zfp-2, mKR2, mkr-2, mszf87
Expression	Broad expression in CNS E18 (RPKM 2.3), whole brain E14.5 (RPKM 2.2) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

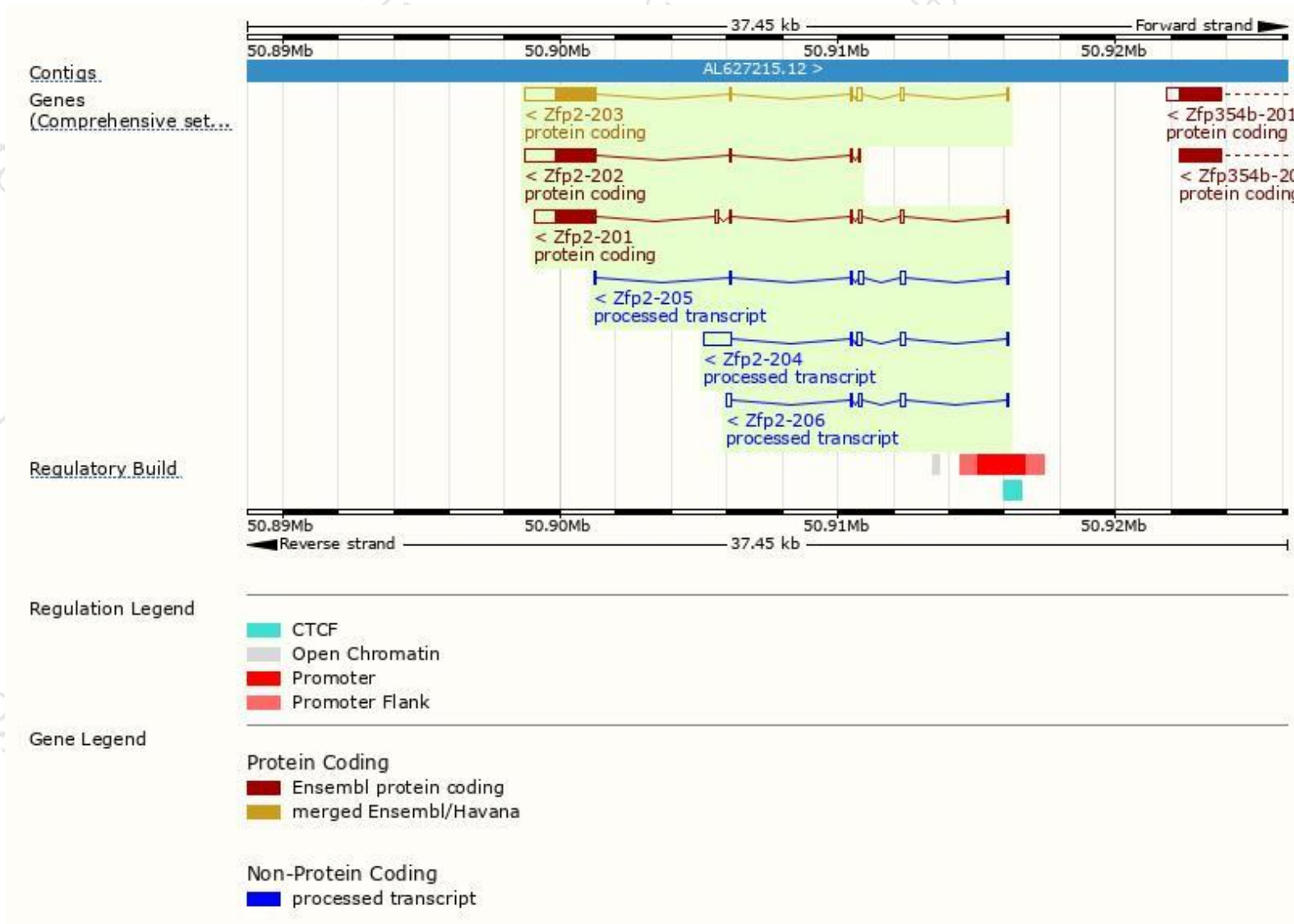
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp2-203	ENSMUST00000116378.7	3069	459aa	Protein coding	CCDS36148	P08043	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 P1
Zfp2-202	ENSMUST00000109129.7	2803	459aa	Protein coding	CCDS36148	P08043	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 P1
Zfp2-201	ENSMUST00000109128.7	2782	459aa	Protein coding	CCDS36148	P08043	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 P1
Zfp2-204	ENSMUST00000124748.7	1407	No protein	Processed transcript	-	-	TSL:1
Zfp2-206	ENSMUST00000151027.1	539	No protein	Processed transcript	-	-	TSL:5
Zfp2-205	ENSMUST00000150903.7	501	No protein	Processed transcript	-	-	TSL:5

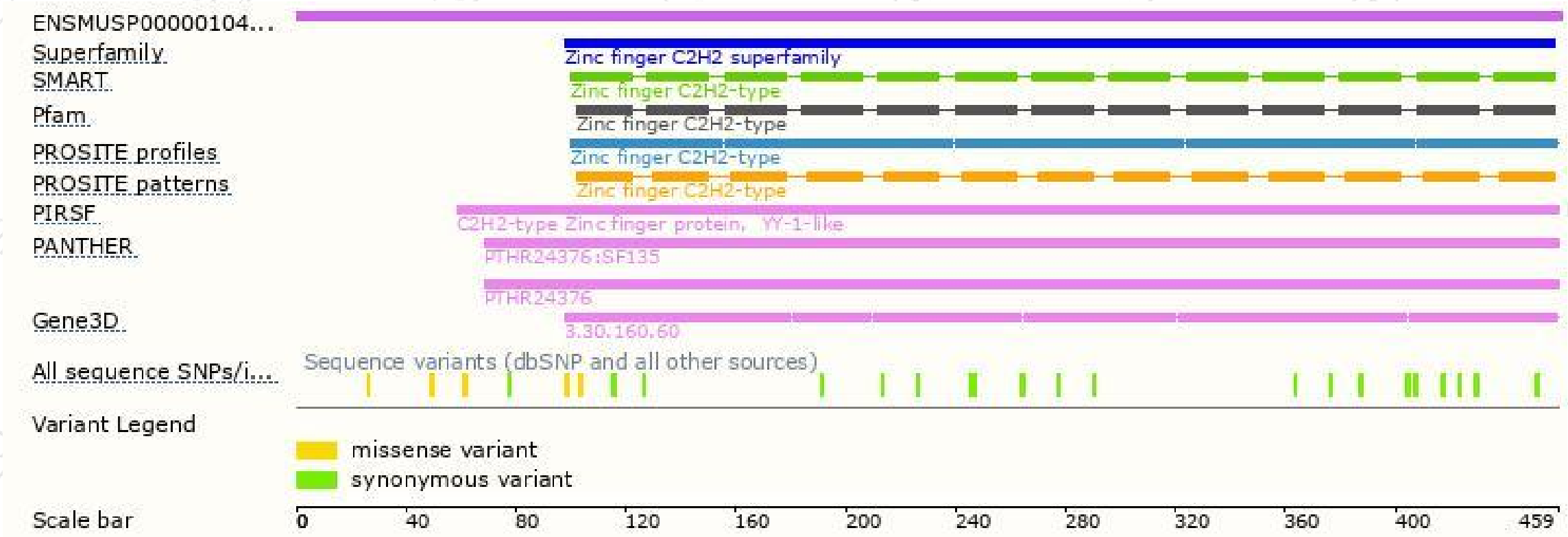
The strategy is based on the design of *Zfp2-203* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

