

Zfp354a Cas9-KO Strategy

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Project Overview

Project Name

Zfp354a

Project type

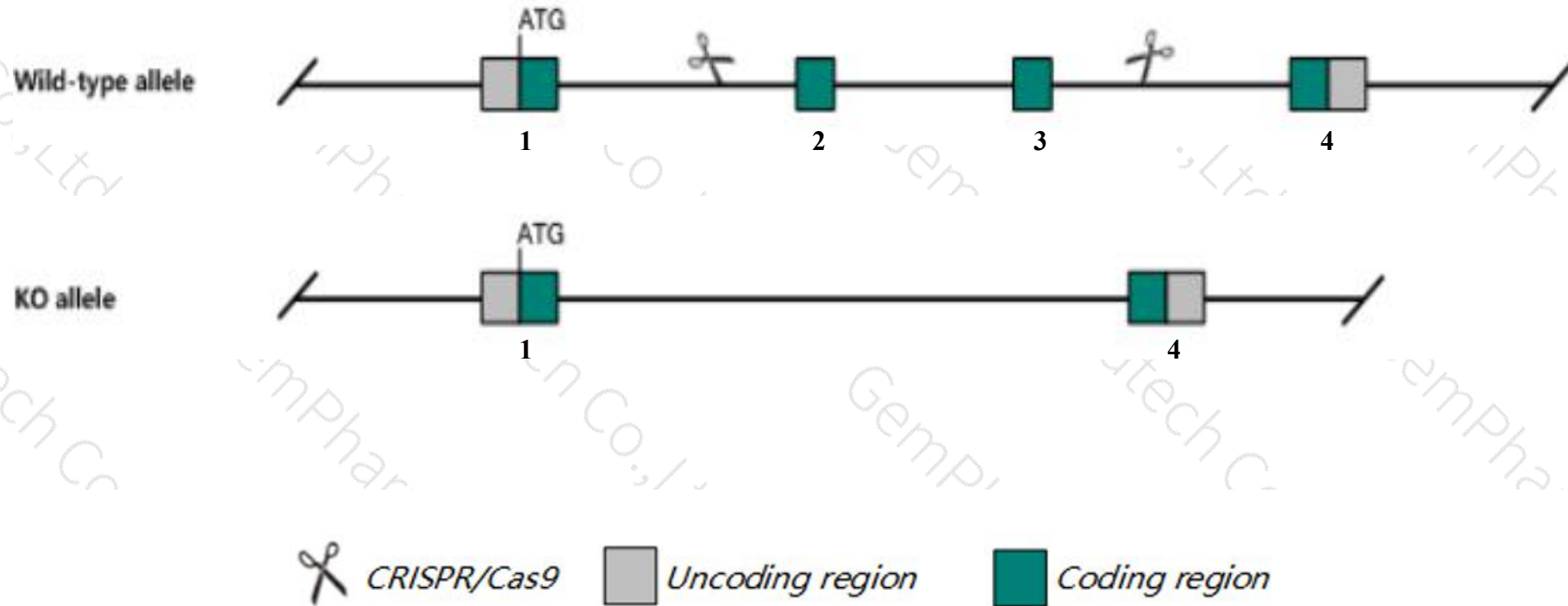
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp354a* gene. The schematic diagram is as follows:



- The *Zfp354a* gene has 5 transcripts. According to the structure of *Zfp354a* gene, exon2-exon3 of *Zfp354a-203* (ENSMUST00000109119.7) transcript is recommended as the knockout region. The region contains 226bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp354a* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zfp354a* 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)

Zfp354a zinc finger protein 354A [Mus musculus (house mouse)]

Gene ID: 21408, updated on 13-Mar-2020

Summary



Official Symbol Zfp354a provided by [MGI](#)

Official Full Name zinc finger protein 354A provided by [MGI](#)

Primary source [MGI:MGI:103172](#)

See related [Ensembl:ENSMUSG00000020364](#)

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 AW488485, Tcf17, Znf354a, kid1

Expression Broad expression in CNS E18 (RPKM 2.5), CNS E14 (RPKM 2.0) and 22 other tissues [See more](#)

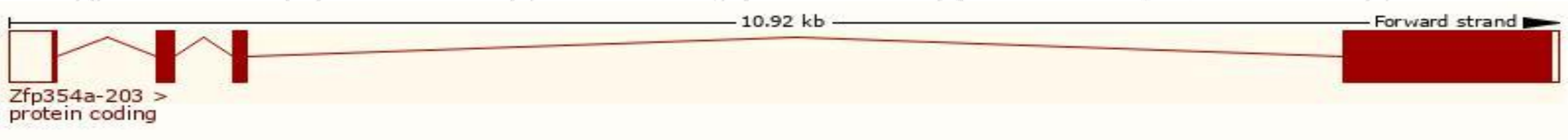
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

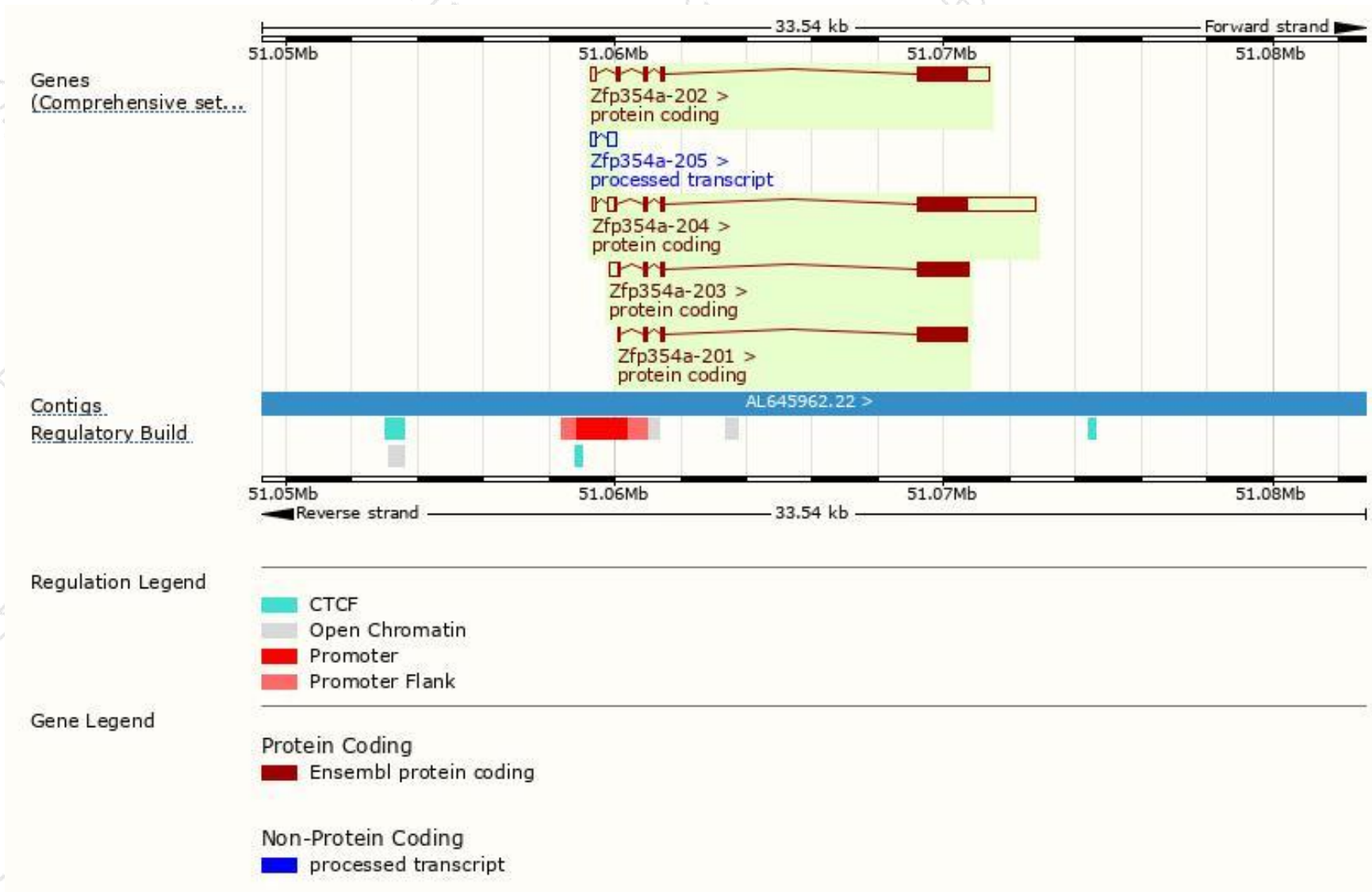
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp354a-204	ENSMUST00000109122.7	4165	571aa	Protein coding	CCDS83802	Q5PPR4	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
Zfp354a-202	ENSMUST00000102766.9	2592	572aa	Protein coding	CCDS24648	Q61751	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
Zfp354a-203	ENSMUST00000109119.7	2078	573aa	Protein coding	CCDS83803	B1ATG3	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
Zfp354a-201	ENSMUST00000020628.5	1719	572aa	Protein coding	CCDS24648	Q61751	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
Zfp354a-205	ENSMUST00000156914.1	430	No protein	Processed transcript	-	-	TSL:3

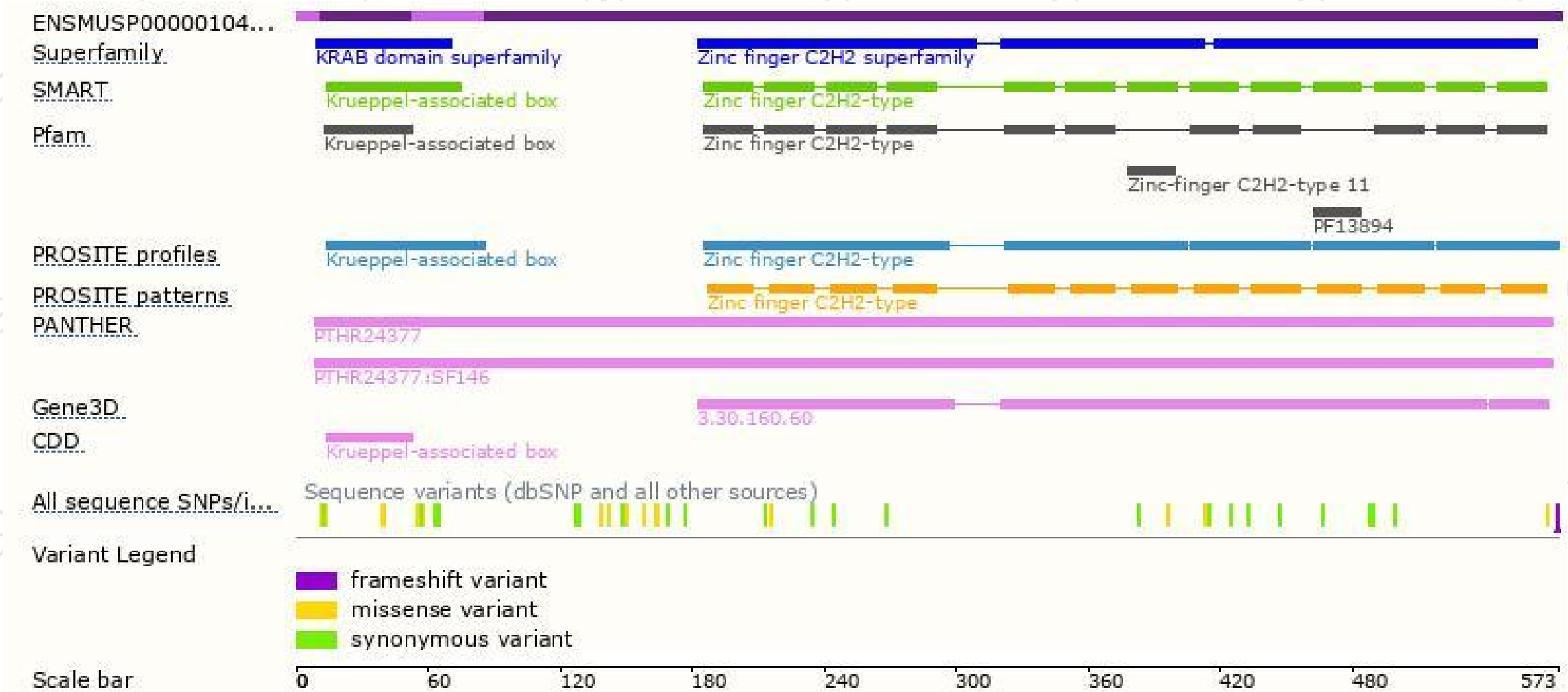
The strategy is based on the design of *Zfp354a-203* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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