

Zfp28 Cas9-KO Strategy

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Project Overview

Project Name

Zfp28

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp28* gene. The schematic diagram is as follows:



- The *Zfp28* gene has 6 transcripts. According to the structure of *Zfp28* gene, exon3-exon6 of *Zfp28-201* (ENSMUST00000081022.8) transcript is recommended as the knockout region. The region contains 499bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp28* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zfp28* gene is located on the Chr7. 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)

Zfp28 zinc finger protein 28 [Mus musculus (house mouse)]

Gene ID: 22690, updated on 13-Mar-2020

Summary



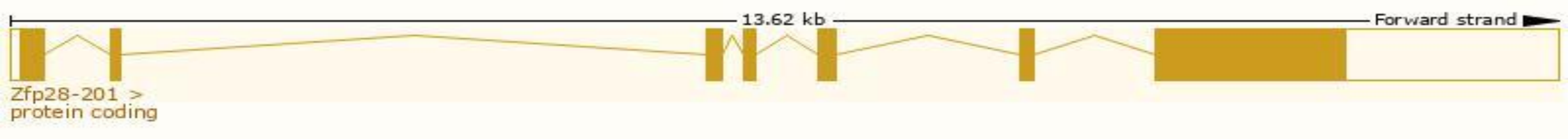
Official Symbol	Zfp28 provided by MGI
Official Full Name	zinc finger protein 28 provided by MGI
Primary source	MGI:MGI:99175
See related	Ensembl:ENSMUSG00000062861
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810438M17Rik, Zfp-28, mkr-5
Expression	Broad expression in CNS E18 (RPKM 4.3), CNS E14 (RPKM 3.9) and 24 other tissues See more

Transcript information (Ensembl)

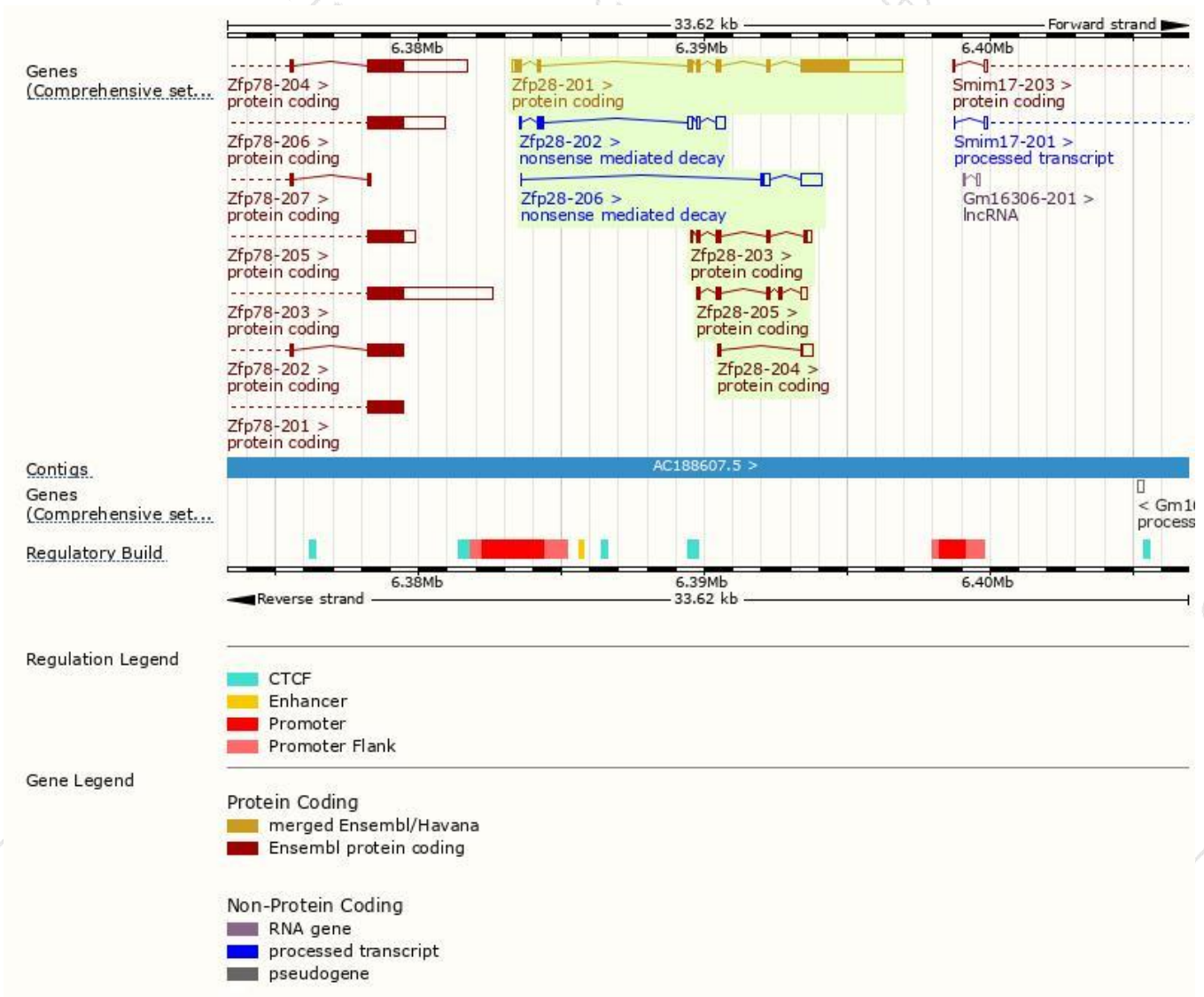
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp28-201	ENSMUST00000081022.8	4447	825aa	Protein coding	CCDS39752	P10078	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
Zfp28-205	ENSMUST00000208338.1	715	161aa	Protein coding	-	A0A140LJ19	CDS 5' incomplete TSL:5
Zfp28-203	ENSMUST00000207465.1	694	171aa	Protein coding	-	A0A140LIA3	CDS 5' incomplete TSL:3
Zfp28-204	ENSMUST00000207809.1	519	56aa	Protein coding	-	A0A140LJB6	CDS 5' incomplete TSL:3
Zfp28-206	ENSMUST00000208949.1	1071	30aa	Nonsense mediated decay	-	A0A140LIS3	CDS 5' incomplete TSL:5
Zfp28-202	ENSMUST00000207086.1	776	58aa	Nonsense mediated decay	-	A0A140LIZ0	CDS 5' incomplete TSL:2

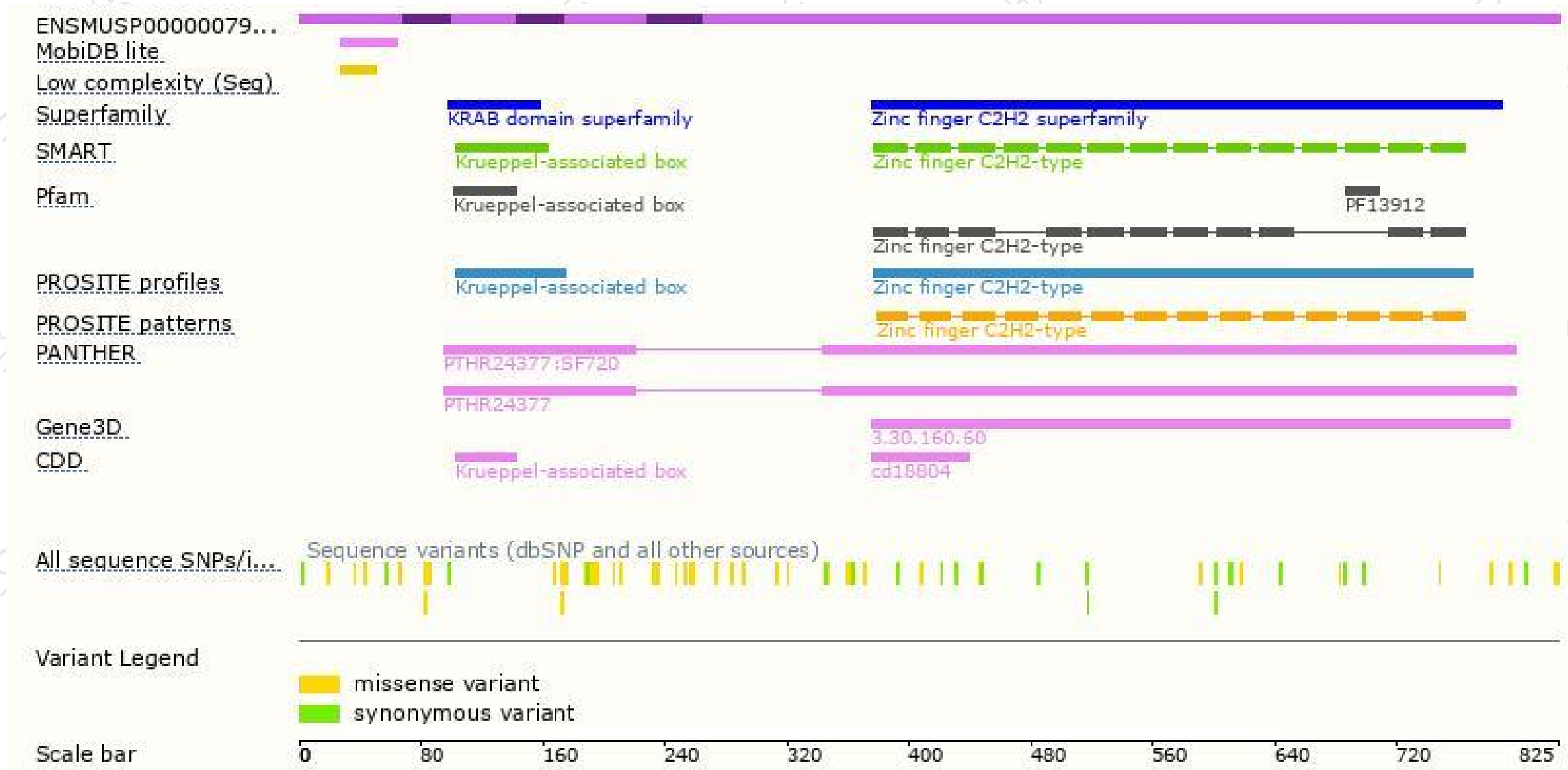
The strategy is based on the design of *Zfp28-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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