

***Zfp445* Cas9-KO Strategy**

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-4-20

Project Overview

Project Name

Zfp445

Project type

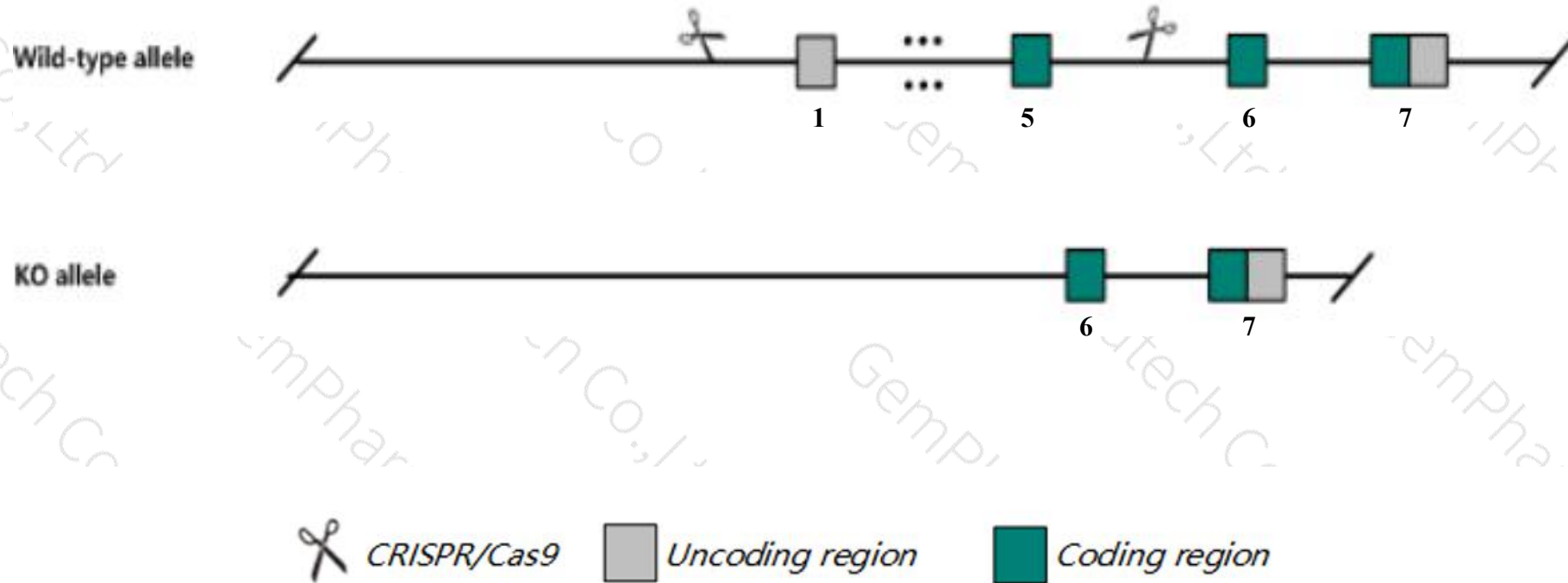
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp445* gene. The schematic diagram is as follows:



- The *Zfp445* gene has 8 transcripts. According to the structure of *Zfp445* gene, exon1-exon5 of *Zfp445-206* (ENSMUST00000216063.1) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp445* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zfp445* gene is located on the Chr9. 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)

Zfp445 zinc finger protein 445 [Mus musculus (house mouse)]

Gene ID: 235682, updated on 13-Mar-2020

Summary



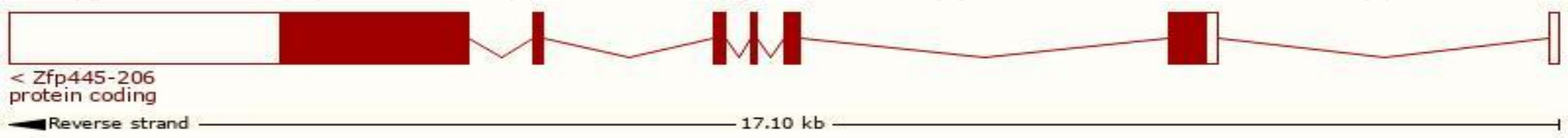
Official Symbol	Zfp445 provided by MGI
Official Full Name	zinc finger protein 445 provided by MGI
Primary source	MGI:MGI:2143340
See related	Ensembl:ENSMUSG00000047036
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW610627, ZNF168, Znf445, mszf29, mszf50
Expression	Broad expression in CNS E18 (RPKM 31.5), CNS E14 (RPKM 28.7) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

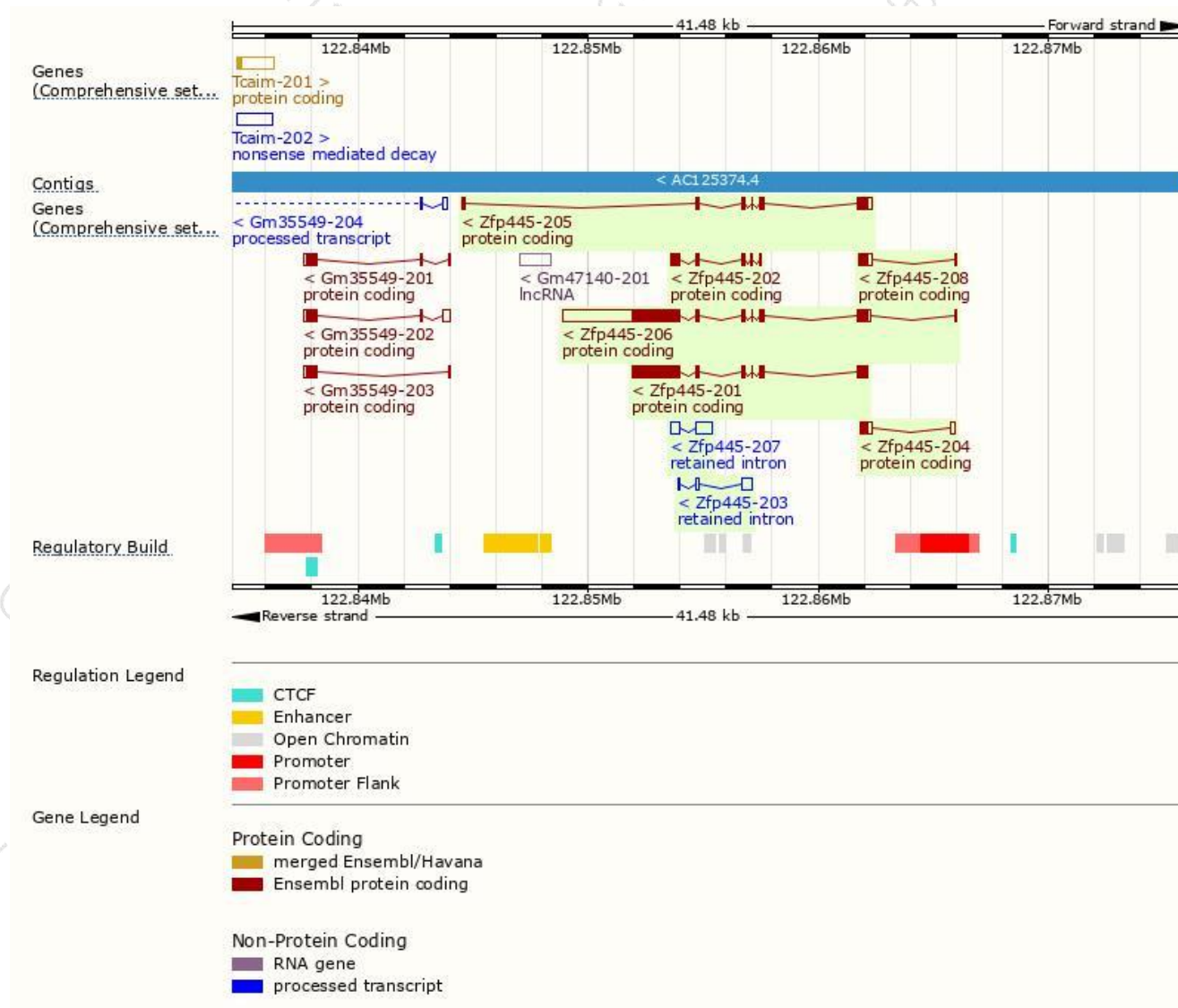
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp445-206	ENSMUST00000216063.1	6189	986aa	Protein coding	CCDS23648	Q8R2V3	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
Zfp445-201	ENSMUST00000056467.7	2961	986aa	Protein coding	CCDS23648	Q8R2V3	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
Zfp445-205	ENSMUST00000214626.1	1220	303aa	Protein coding	-	A0A1L1SQ84	TSL:5 GENCODE basic
Zfp445-202	ENSMUST00000213971.1	758	252aa	Protein coding	-	A0A1L1SSQ0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Zfp445-204	ENSMUST00000214558.1	747	111aa	Protein coding	-	A0A1L1STL2	CDS 3' incomplete TSL:5
Zfp445-208	ENSMUST00000216721.1	645	119aa	Protein coding	-	A0A1L1STQ8	CDS 3' incomplete TSL:2
Zfp445-207	ENSMUST00000216243.1	1064	No protein	Retained intron	-	-	TSL:2
Zfp445-203	ENSMUST00000214162.1	604	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Zfp445-206* transcript,the transcription is shown below:



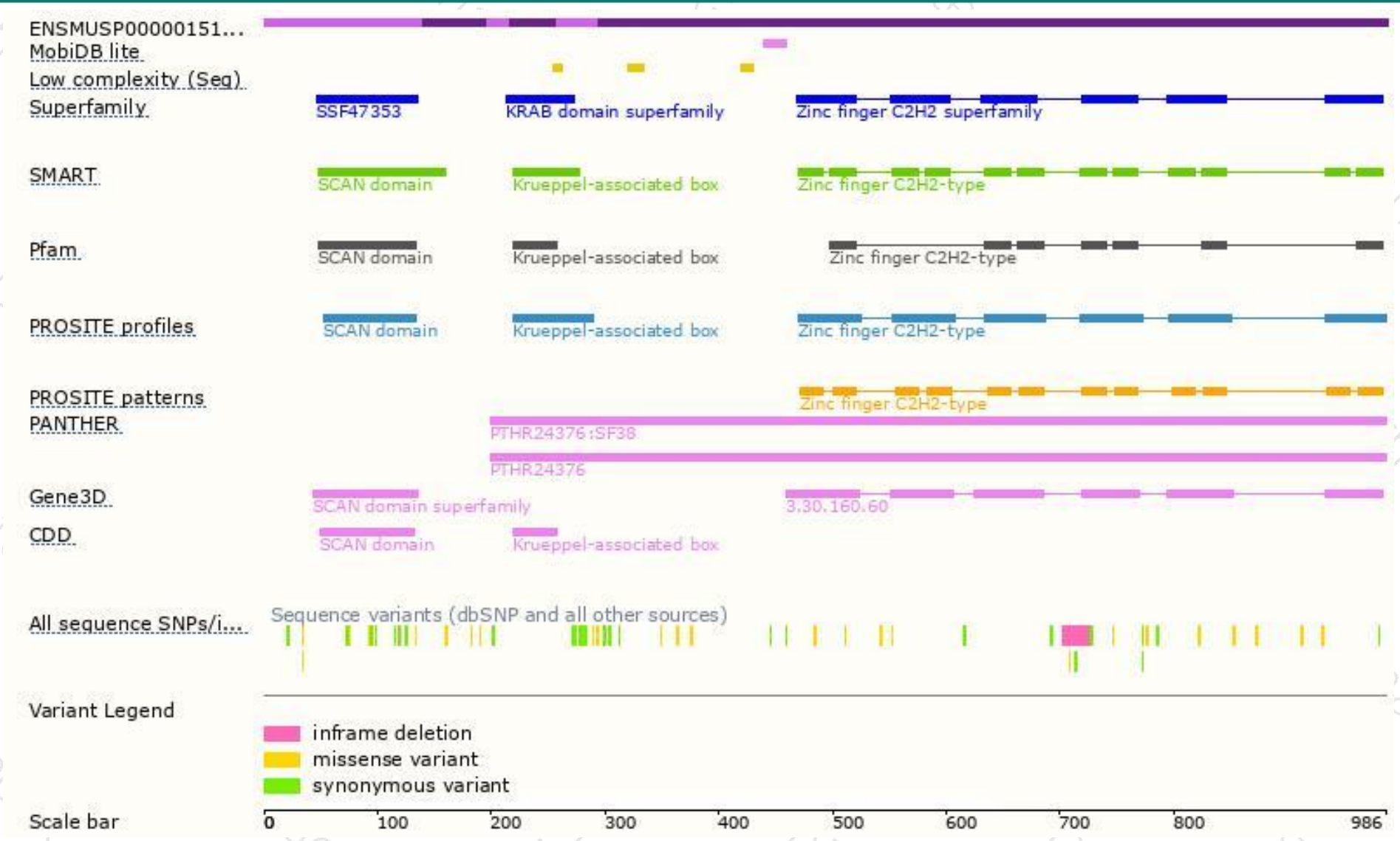
Genomic location distribution



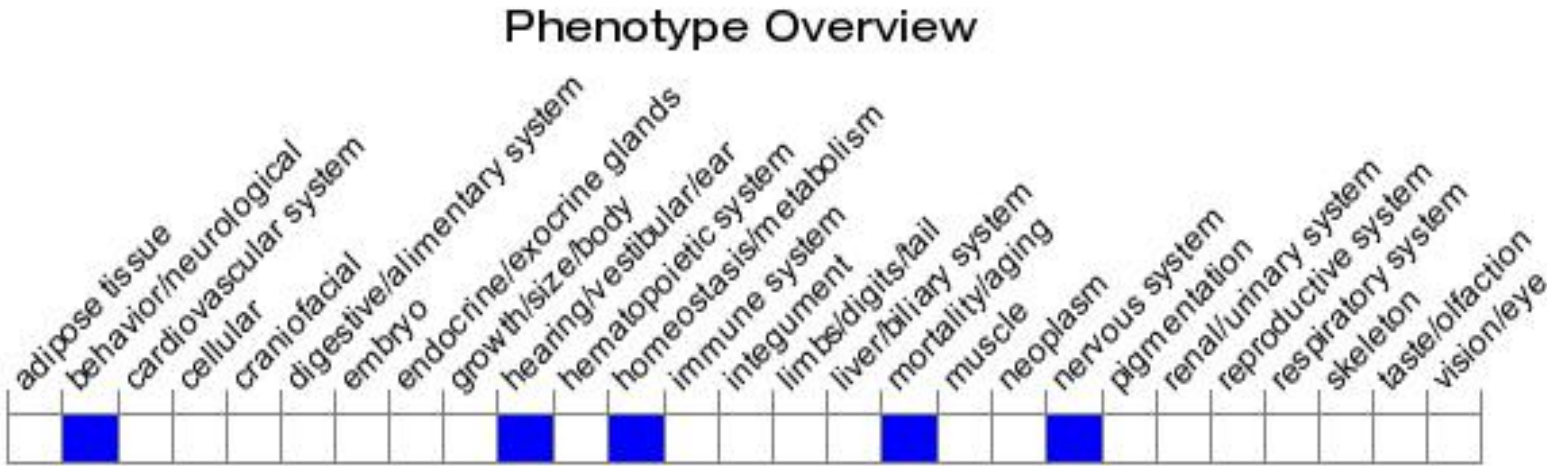
Protein domain



集萃药康
GemPharmatech



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

