

# ***Zbtb14* Cas9-CKO Strategy**

**Designer:**

**Yanhua Shen**

**Reviewer:**

**Xueting Zhang**

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# Project Overview

**Project Name**

***Zbtb14***

**Project type**

**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb14* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Conditional KO allele

KO allele



# Technical routes

- The *Zbtb14* gene has 3 transcripts. According to the structure of *Zbtb14* gene, exon3 of *Zbtb14*-203 (ENSMUST00000112676.3) transcript is recommended as the knockout region. The region contains most 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 *Zbtb14* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for an ENU-induced mutation show exencephaly, cardiac defects including valve abnormalities, double outlet right ventricle, perimembranous ventricular septal defect, and atrioventricular septal defect, and renal anomalies such as duplex kidney, hydronephrosis, and kidney cysts.
- The *Zbtb14* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Zbtb14 zinc finger and BTB domain containing 14 [ *Mus musculus* (house mouse) ]

Gene ID: 22666, updated on 24-Oct-2019

### Summary

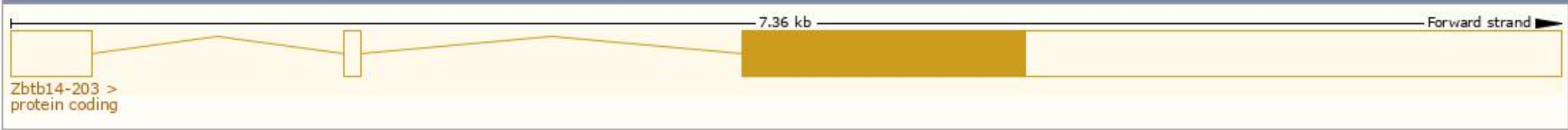
Official Symbol	Zbtb14 provided by MGI
Official Full Name	zinc finger and BTB domain containing 14 provided by MGI
Primary source	<a href="#">MGI:MGI:1195345</a>
See related	<a href="#">Ensembl:ENSMUSG000000049672</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ZF5; Zfp161; b2b1982Clo
Expression	Ubiquitous expression in CNS E11.5 (RPKM 6.3), CNS E14 (RPKM 5.1) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

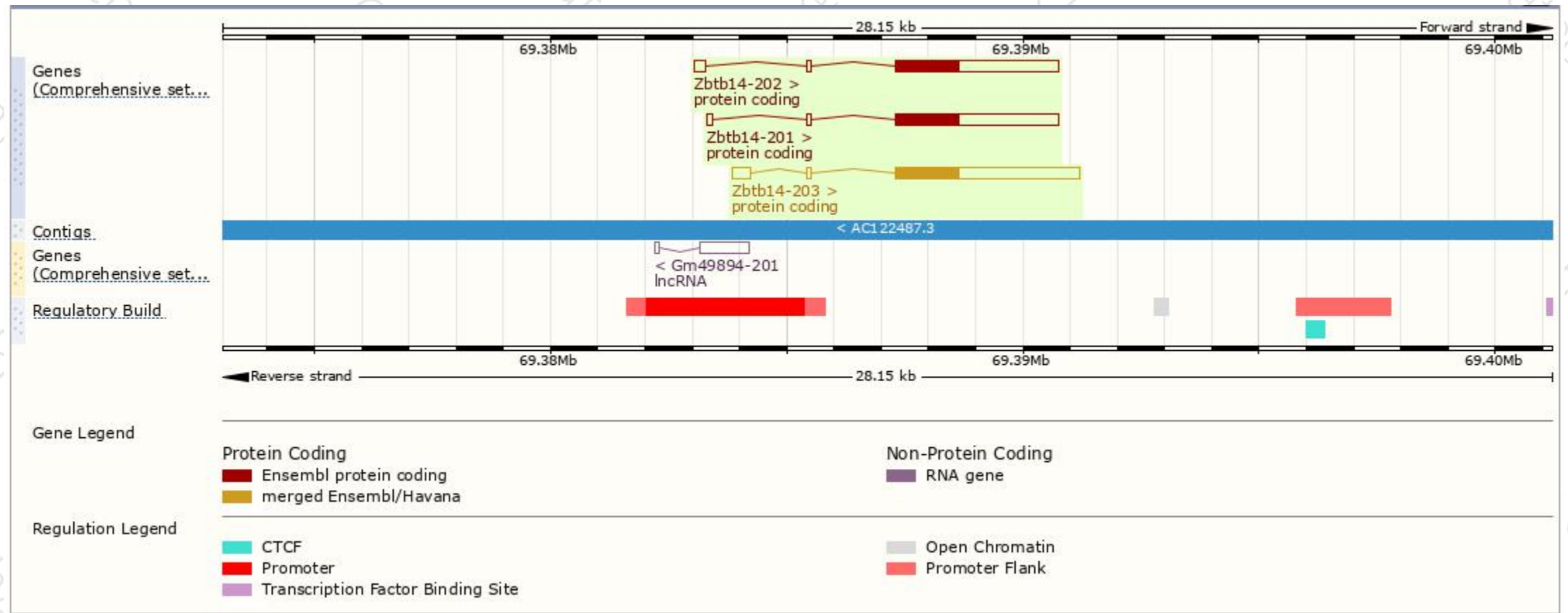
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb14-203	<a href="#">ENSMUST00000112676.3</a>	4358	<a href="#">449aa</a>	Protein coding	<a href="#">CCDS37682</a>	<a href="#">Q08376</a> <a href="#">Q544H8</a>	TSL:1 GENCODE basic APPRIS P1
Zbtb14-202	<a href="#">ENSMUST00000112674.7</a>	3743	<a href="#">449aa</a>	Protein coding	<a href="#">CCDS37682</a>	<a href="#">Q08376</a> <a href="#">Q544H8</a>	TSL:3 GENCODE basic APPRIS P1
Zbtb14-201	<a href="#">ENSMUST00000062369.13</a>	3625	<a href="#">449aa</a>	Protein coding	<a href="#">CCDS37682</a>	<a href="#">Q08376</a> <a href="#">Q544H8</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Zbtb14-203* transcript,The transcription is shown below

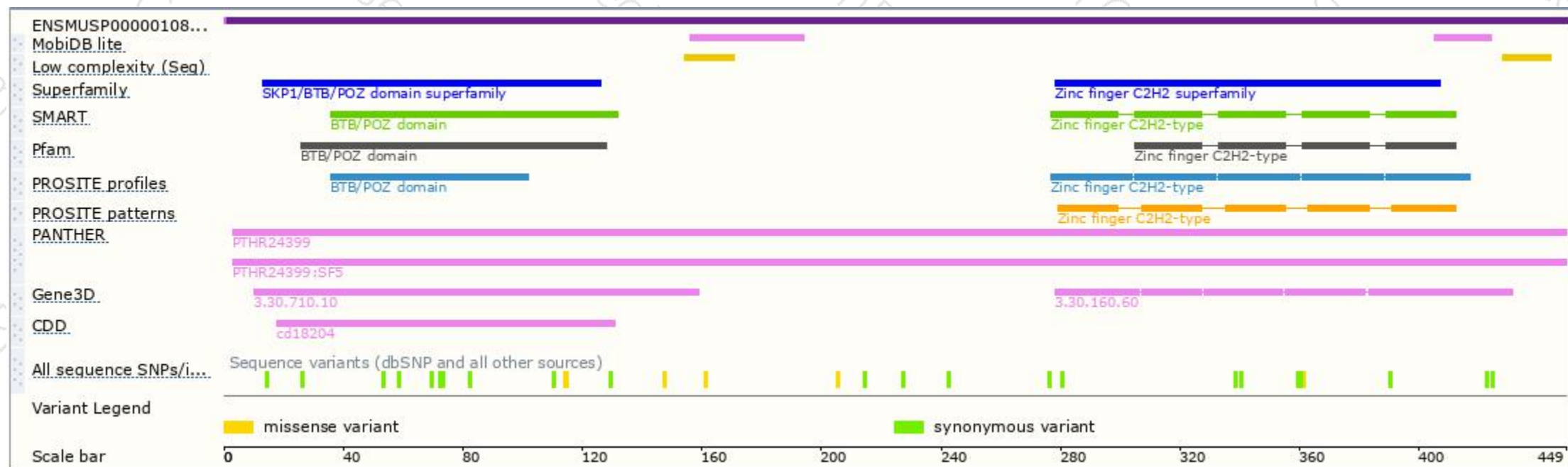


# Genomic location distribution

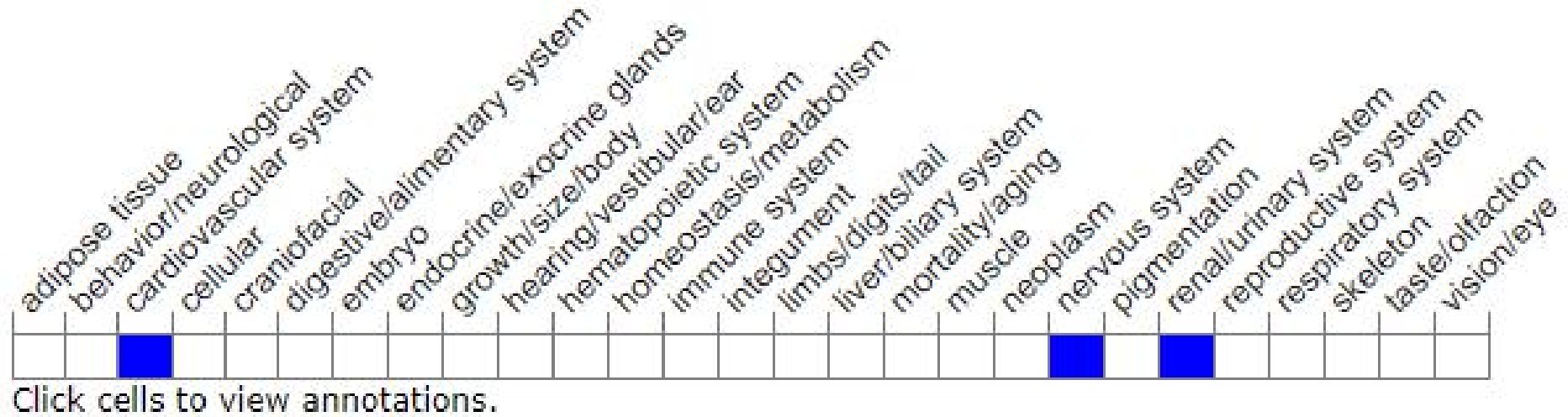




# Protein domain



# Mouse phenotype description(MGI)



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Mice homozygous for an ENU-induced mutation show exencephaly, cardiac defects including valve abnormalities, double outlet right ventricle, perimembranous ventricular septal defect, and atrioventricular septal defect, and renal anomalies such as duplex kidney, hydronephrosis, and kidney cysts.

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

Tel: 400-9660890

