

Zbtb17 Cas9-KO Strategy

Designer: Keping Yao

Reviewer: Yanhua Shen

Design Date: 2023-05-04

Overview

Target Gene Name

• Zbtb17

Project Type

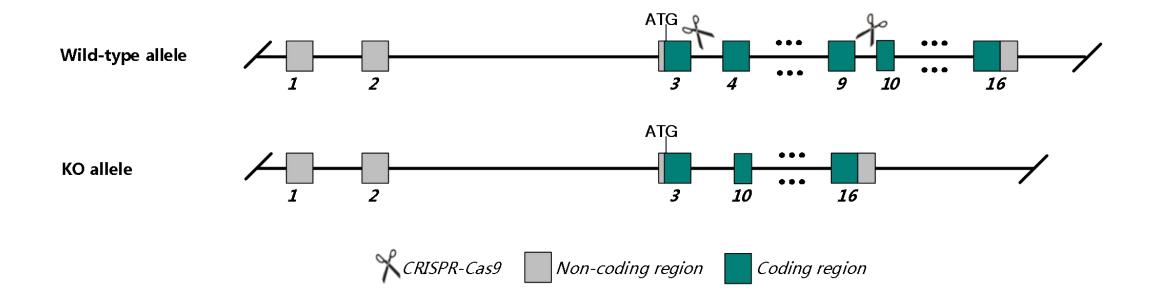
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Zbtb17 gene.



Technical Information

- The *Zbtb17* gene has 7 transcripts. According to the structure of *Zbtb17* gene, exon4 to exon9 of *Zbtb17*-201 (ENSMUST00000006377.13) transcript is recommended as the knockout region. The region contains 1139bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Zbtb17* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



Gene Information

Zbtb17 zinc finger and BTB domain containing 17 [Mus musculus (house mouse)]

♣ Download Datasets

☆ ?

Gene ID: 22642, updated on 12-Apr-2023

Summary

Official Symbol Zbtb17 provided by MGI

Official Full Name zinc finger and BTB domain containing 17 provided by MGI

Primary source MGI:MGI:107410

See related Ensembl:ENSMUSG00000006215 AllianceGenome:MGI:107410

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 Lp-1; Miz1; mZ13; Zfp100

Summary Enables DNA binding activity. Acts upstream of or within ectoderm development; gastrulation with mouth forming second; and positive regulation of transcription, DNA-

templated. Located in nucleus. Is expressed in early conceptus; eye; genitourinary system; limb; and trunk somite. Orthologous to human ZBTB17 (zinc finger and BTB

domain containing 17). [provided by Alliance of Genome Resources, Apr 2022]

Expression Ubiquitous expression in whole brain E14.5 (RPKM 15.8), thymus adult (RPKM 15.4) and 28 other tissues See more

Orthologs human all

Try the new Gene table

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

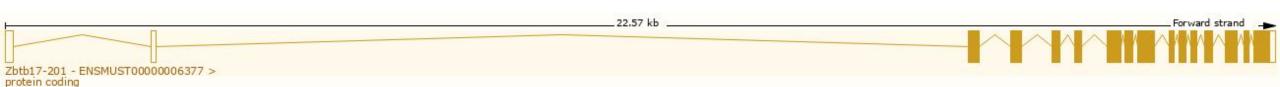


Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

Transcript ID	Name 4	bp 🛔	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000006377.13	Zbtb17-201	2722	<u>794aa</u>	Protein coding	CCDS18875 ₽	<u>Q60821</u> ₽	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000142438.8	Zbtb17-205	3478	No protein	Protein coding CDS not defined		20	TSL:2
ENSMUST00000142020.8	Zbtb17-204	2973	No protein	Protein coding CDS not defined		8)	TSL:2
ENSMUST00000130482.2	Zbtb17-203	867	No protein	Protein coding CDS not defined		=:	TSL:5
ENSMUST00000142695.2	Zbtb17-206	785	No protein	Protein coding CDS not defined		8	TSL:2
ENSMUST00000123477.2	Zbtb17-202	771	No protein	Protein coding CDS not defined		-20	TSL:2
ENSMUST00000144899.2	Zbtb17-207	338	No protein	Protein coding CDS not defined		9	TSL:2

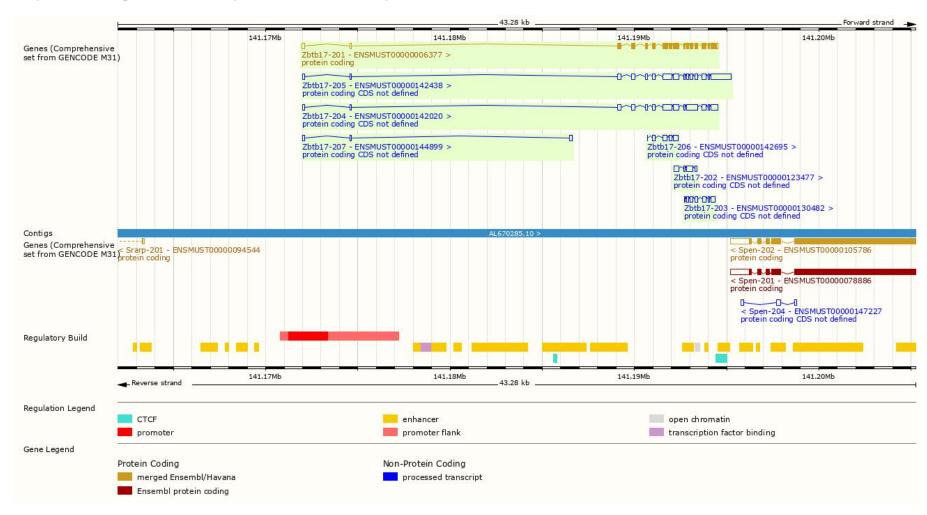
The strategy is based on the design of *Zbtb17*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



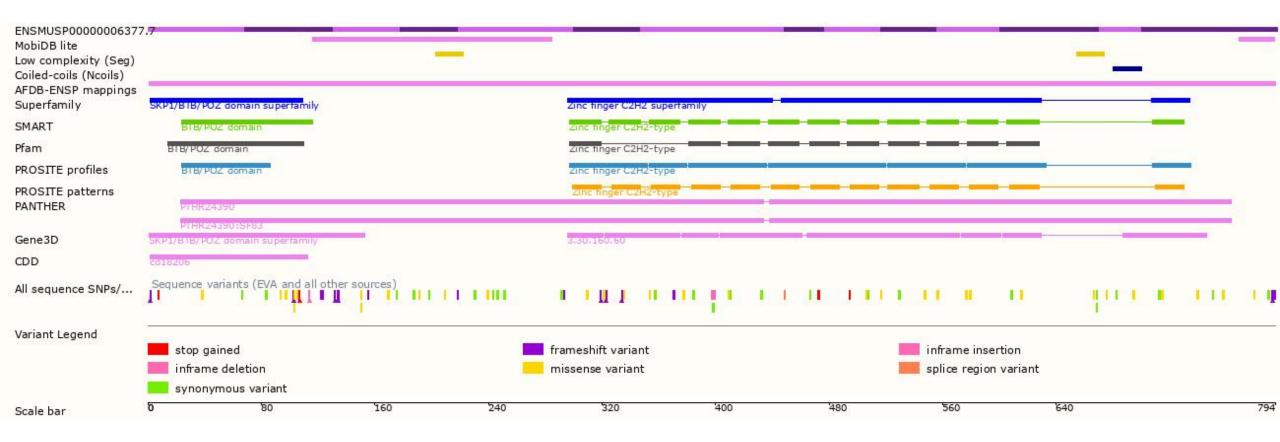
Genomic Information





Source: : https://www.ensembl.org

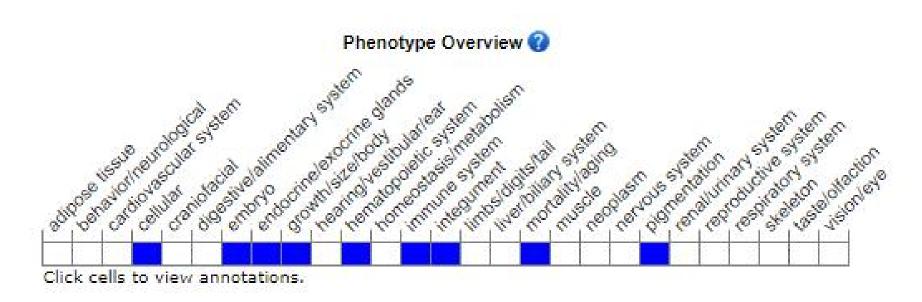
Protein Information





Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



• Embryonic development of homozygous null mice is severely impaired and death occurs prior to E8.5.



Important Information

- Zbtb17 is located on Chr4. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

