

***Zbtb48* Cas9-KO Strategy**

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Project Overview

Project Name

Zbtb48

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb48* gene. The schematic diagram is as follows:



- The *Zbtb48* gene has 8 transcripts. According to the structure of *Zbtb48* gene, exon4-exon11 of *Zbtb48-201* (ENSMUST00000066715.10) transcript is recommended as the knockout region. The region contains 1135bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zbtb48* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zbtb48* gene is located on the Chr4. 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.
- The n-terminal amino acid residues are about half of the total, and the function of the protein may be preserved.
- 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)

Zbtb48 zinc finger and BTB domain containing 48 [Mus musculus (house mouse)]

Gene ID: 100090, updated on 31-Jan-2019

Summary



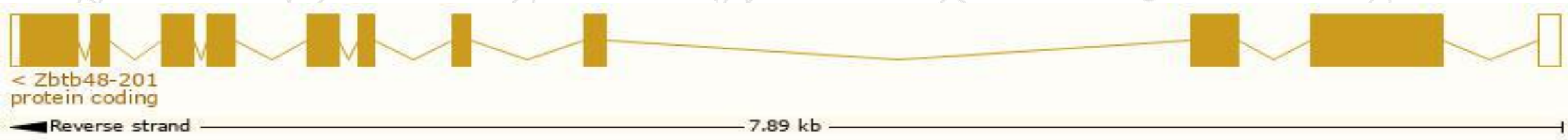
Official Symbol	Zbtb48 provided by MGI
Official Full Name	zinc finger and BTB domain containing 48 provided by MGI
Primary source	MGI:MGI:2140248
See related	Ensembl:ENSMUSG00000028952
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610011D15Rik, AI327031, Hkr3, TZAP
Expression	Ubiquitous expression in thymus adult (RPKM 8.7), limb E14.5 (RPKM 7.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

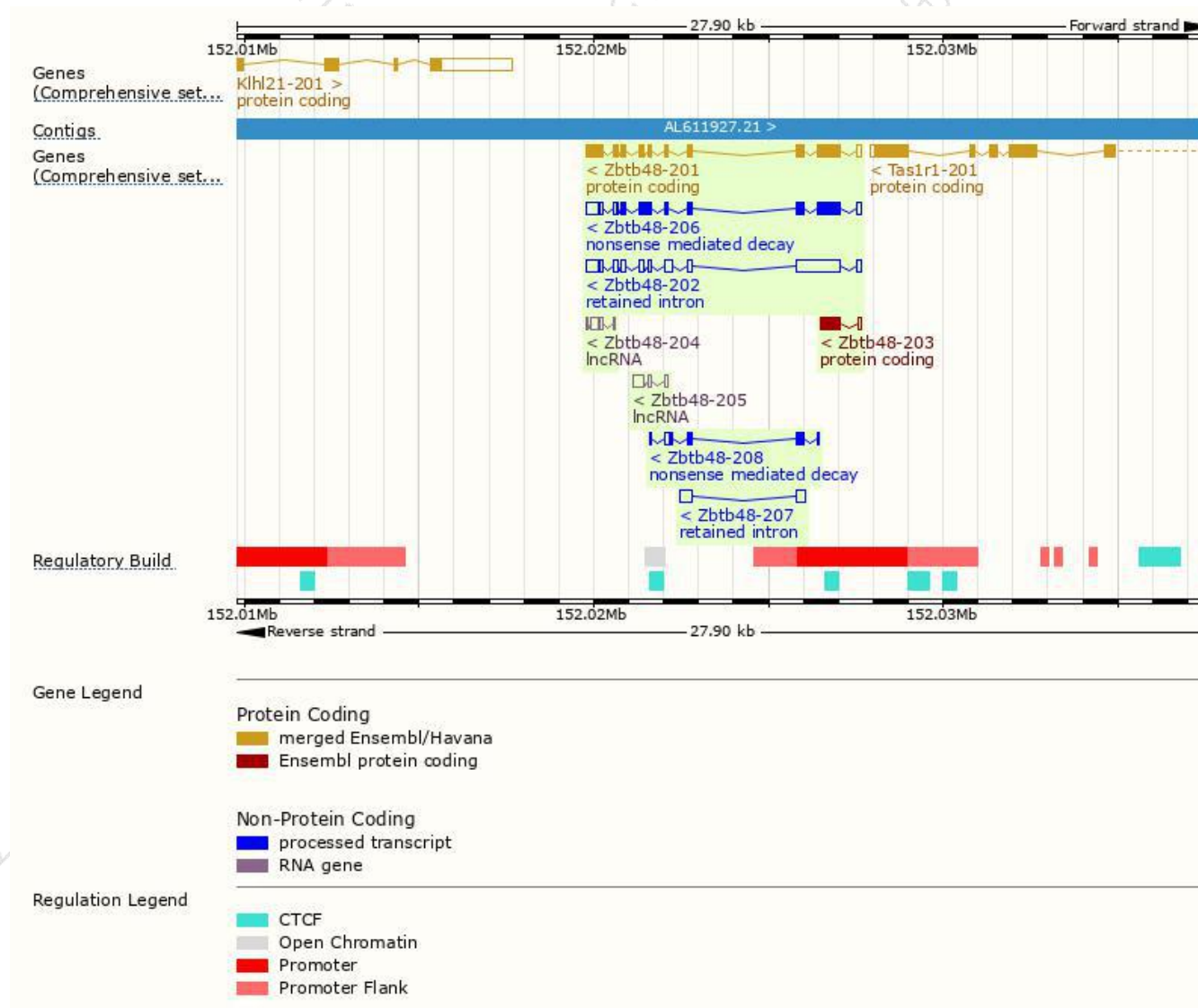
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb48-201	ENSMUST00000066715.10	2218	681aa	Protein coding	CCDS38982	Q1H9T6	TSL:1 GENCODE basic APPRIS P1
Zbtb48-203	ENSMUST00000131935.1	655	193aa	Protein coding	-	A0A0A0MQG8	CDS 3' incomplete TSL:3
Zbtb48-206	ENSMUST00000155389.7	2312	547aa	Nonsense mediated decay	-	Q1H9T6	TSL:2
Zbtb48-208	ENSMUST00000156748.1	656	164aa	Nonsense mediated decay	-	F6ZA56	CDS 5' incomplete TSL:3
Zbtb48-202	ENSMUST00000123696.7	2709	No protein	Retained intron	-	-	TSL:1
Zbtb48-207	ENSMUST00000155441.1	592	No protein	Retained intron	-	-	TSL:3
Zbtb48-205	ENSMUST00000147895.1	502	No protein	lncRNA	-	-	TSL:3
Zbtb48-204	ENSMUST00000136212.1	406	No protein	lncRNA	-	-	TSL:3

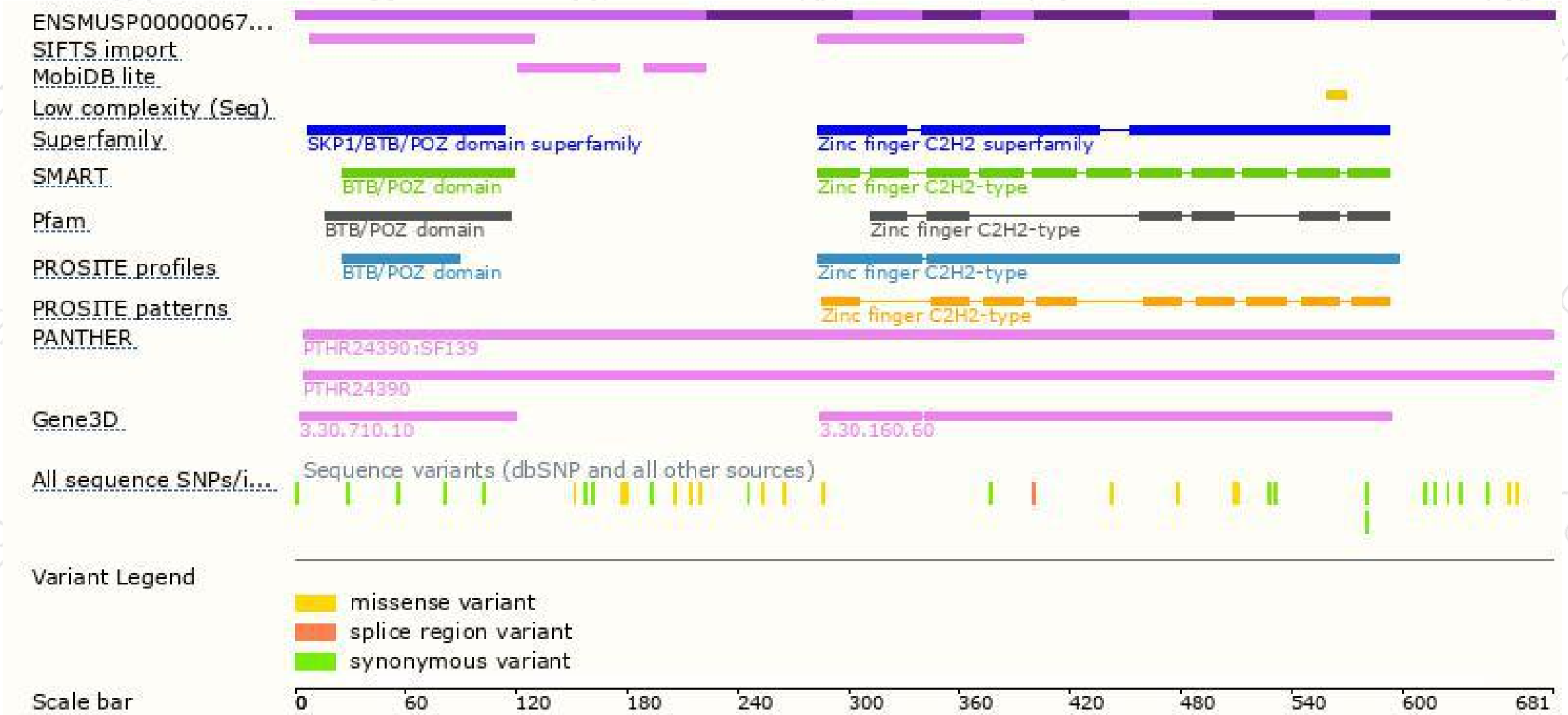
The strategy is based on the design of *Zbtb48-201* transcript,The transcription is shown below



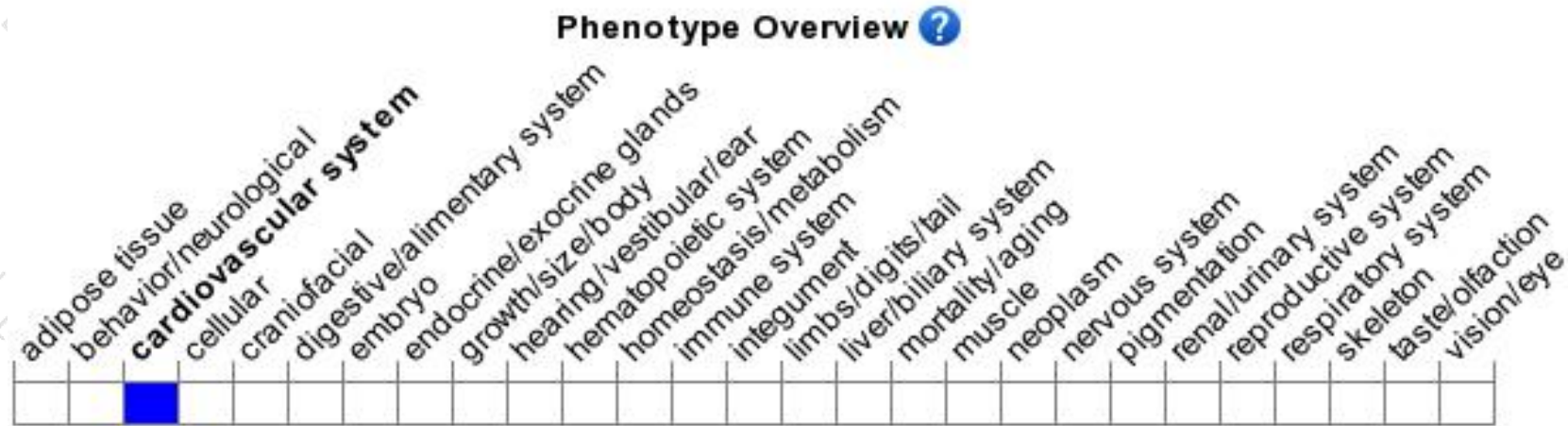
Genomic location distribution



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/>).

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

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