

***Zbtb5* Cas9-KO Strategy**

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Design Date: 2020-5-14

Project Overview

Project Name

Zbtb5

Project type

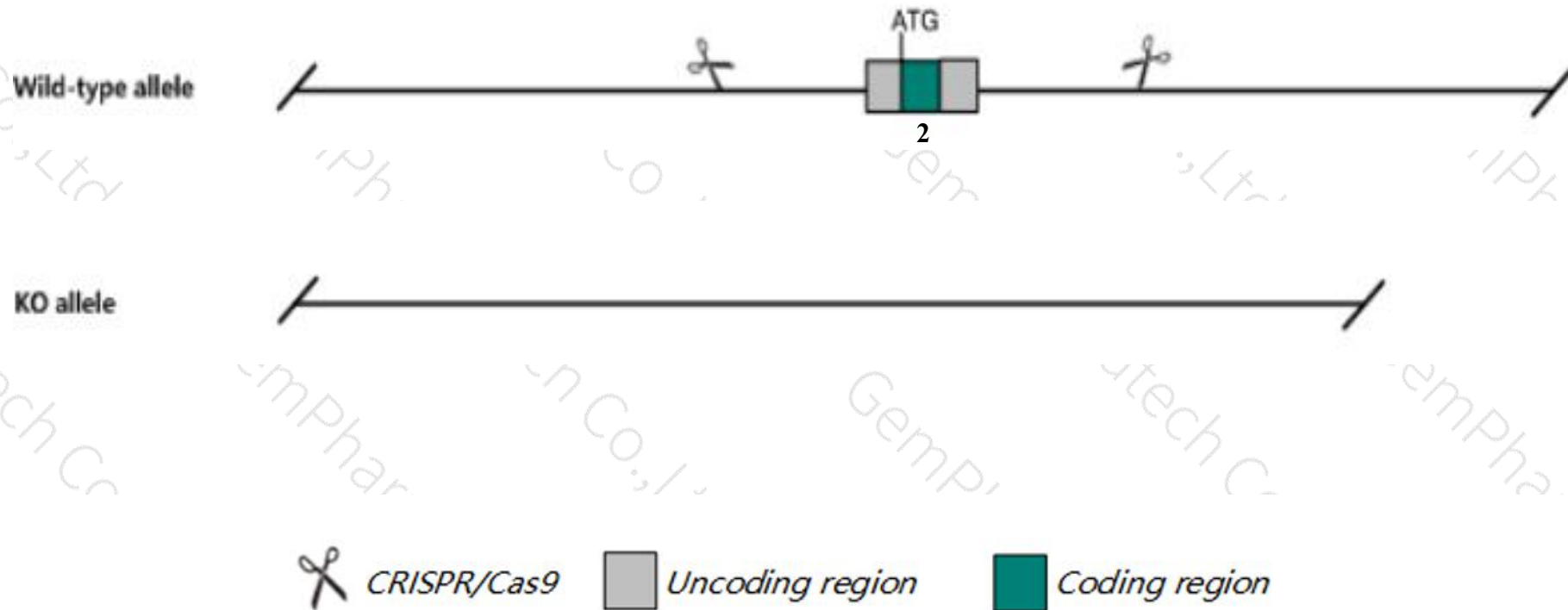
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb5* gene. The schematic diagram is as follows:



- The *Zbtb5* gene has 4 transcripts. According to the structure of *Zbtb5* gene, exon2 of *Zbtb5-204* (ENSMUST00000180217.1) transcript is recommended as the knockout region. The region contains all 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 *Zbtb5* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zbtb5* 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.
- 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)

Zbtb5 zinc finger and BTB domain containing 5 [Mus musculus (house mouse)]

Gene ID: 230119, updated on 13-Mar-2020

Summary



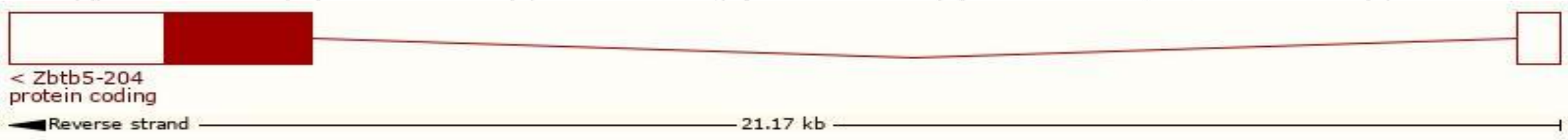
Official Symbol	Zbtb5 provided by MGI
Official Full Name	zinc finger and BTB domain containing 5 provided by MGI
Primary source	MGI:MGI:1924601
See related	Ensembl:ENSMUSG00000049657
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5930421I10, 9430083K24Rik, A1646847, mKIAA0354
Expression	Ubiquitous expression in testis adult (RPKM 8.9), whole brain E14.5 (RPKM 8.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

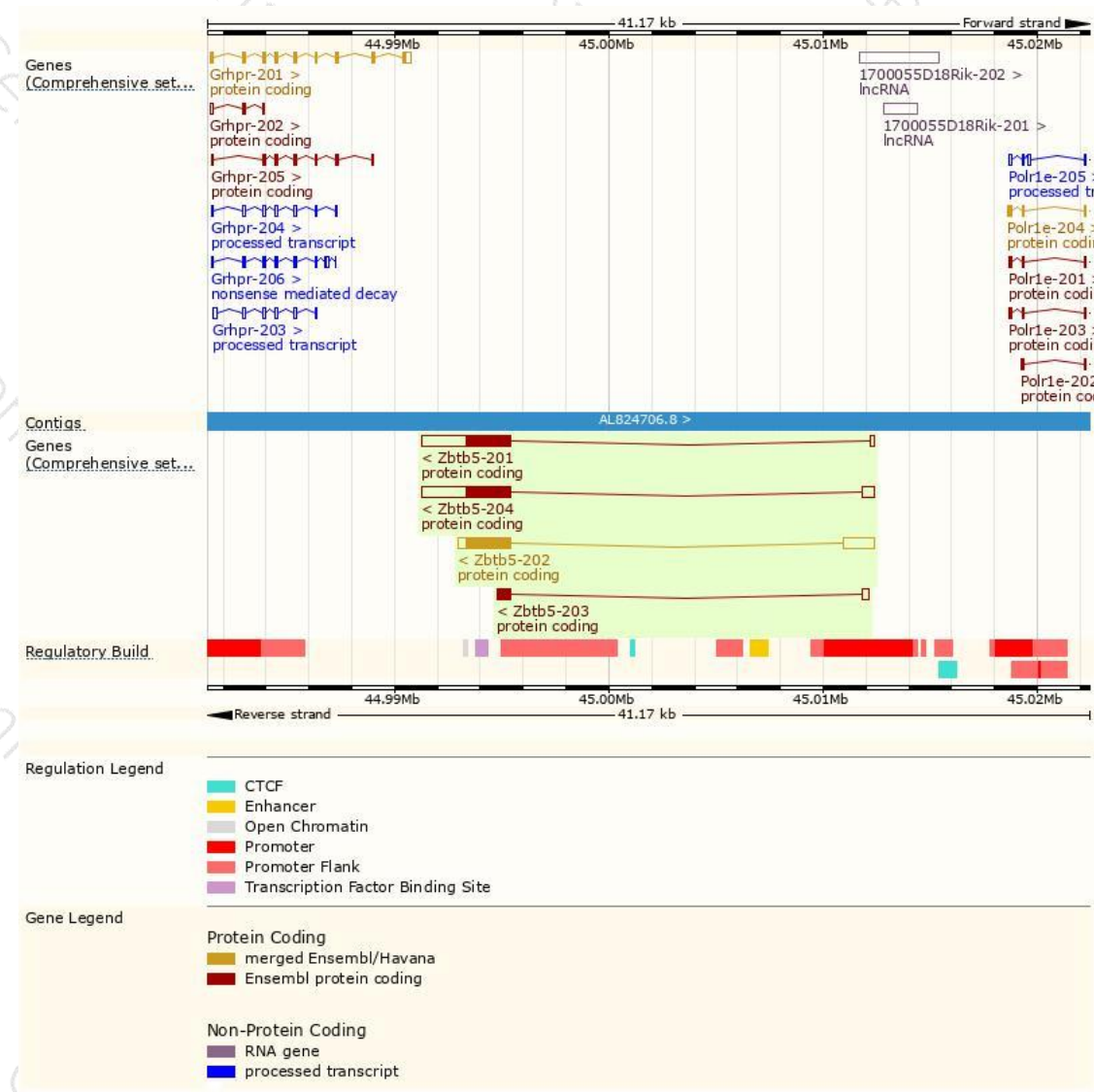
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb5-204	ENSMUST00000180217.1	4708	670aa	Protein coding	CCDS18129	Q7TQG0	TSL:2 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
Zbtb5-201	ENSMUST00000055028.8	4316	670aa	Protein coding	CCDS18129	Q7TQG0	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
Zbtb5-202	ENSMUST00000107817.2	3867	670aa	Protein coding	CCDS18129	Q7TQG0	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
Zbtb5-203	ENSMUST00000131991.1	872	189aa	Protein coding	-	B1AXQ4	CDS 3' incomplete TSL:2

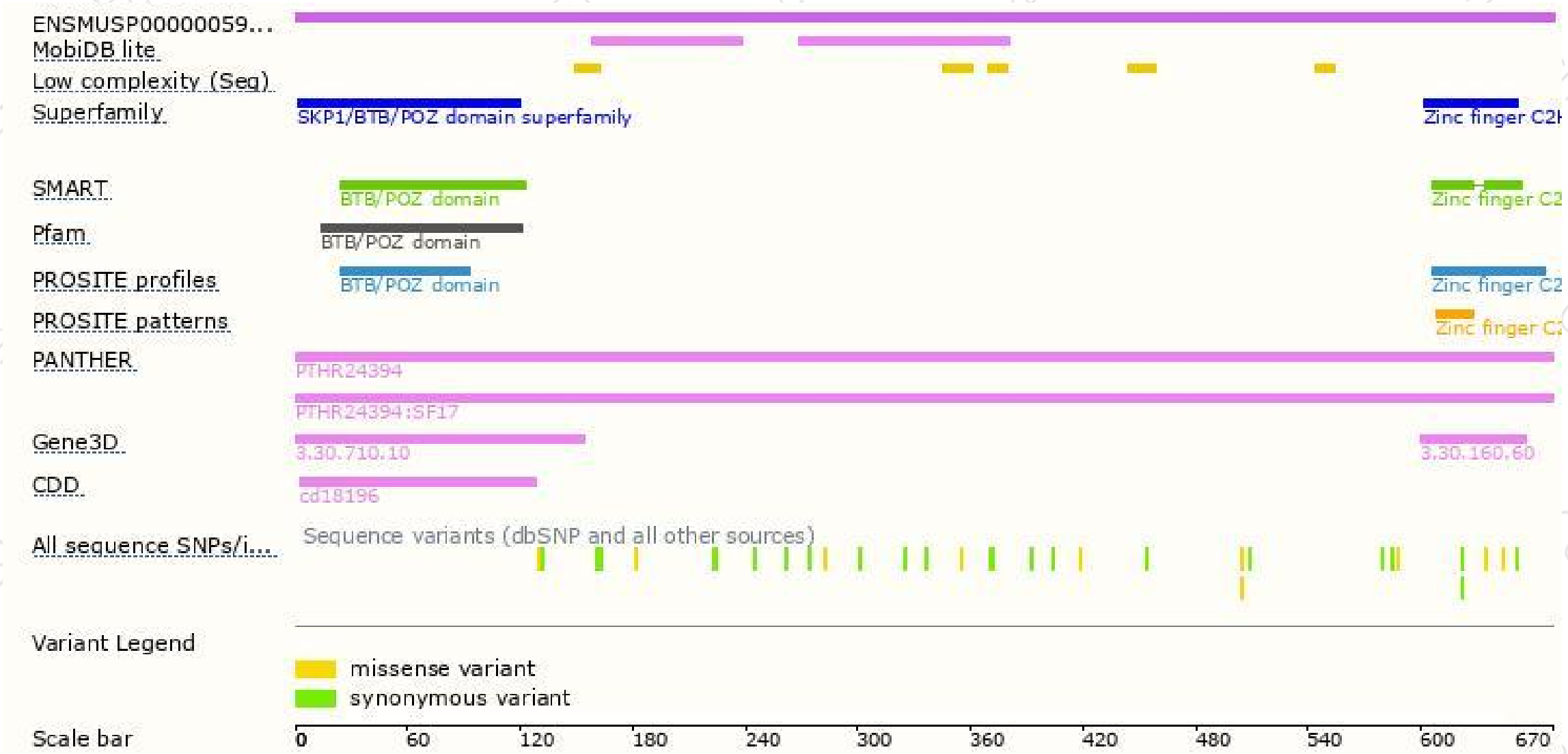
The strategy is based on the design of *Zbtb5-204* transcript,The transcription is shown below



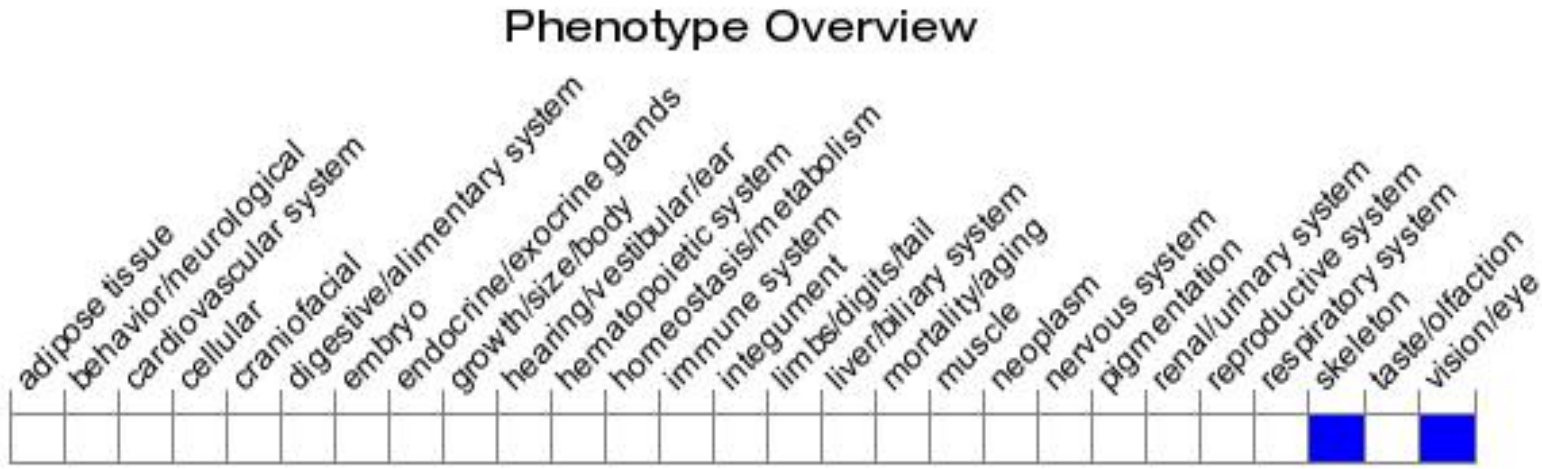
Genomic location distribution



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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