Zbtb32 Cas9-KO *Strategy*

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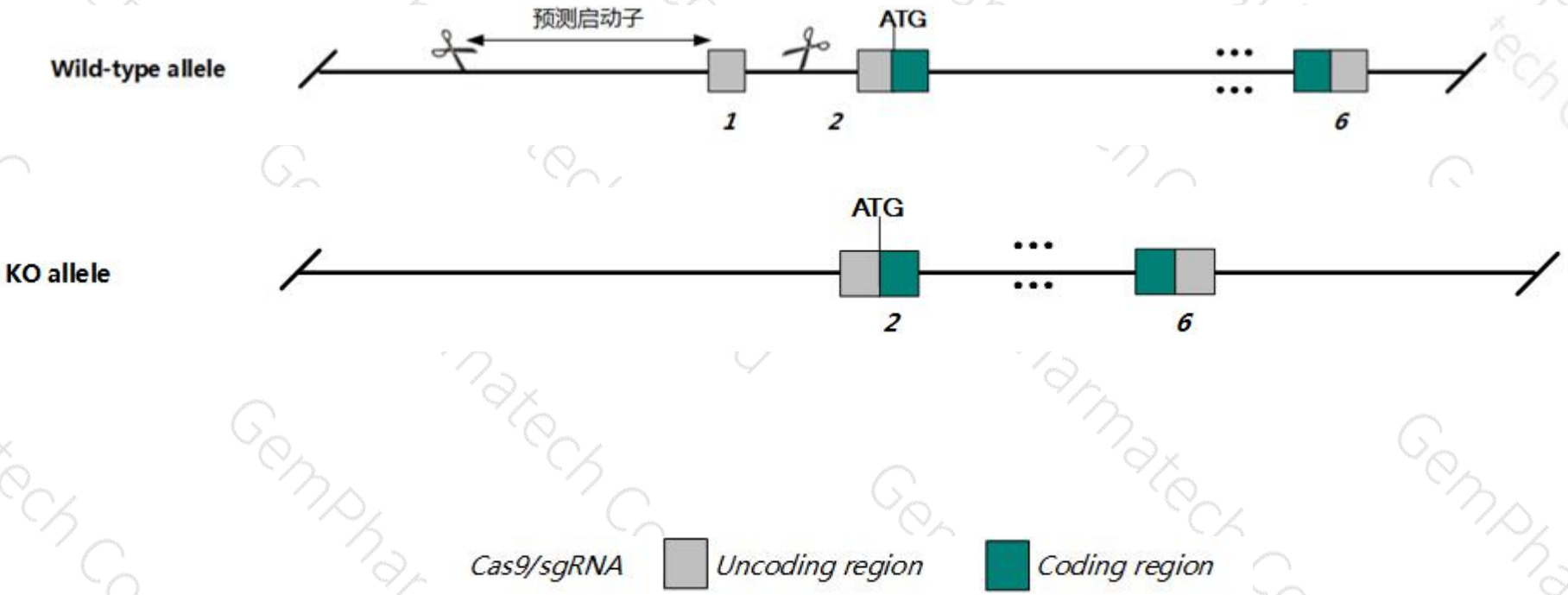
Design Date: **2019-7-29**

Project Overview

Project Name	***Zbtb32***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb32* gene. The schematic diagram is as follows:



Technical routes

- The *Zbtb32* gene has 3 transcripts, According to the structure of *Zbtb32* gene, the predicted [romoter and exon1 of *Zbtb32*-202 transcript is recommended as the knockout region.The region contains the predicted promoter region seqence. Knock out the region,result in destruction of protein.

- In this project we use CRISPR/Cas9 technology to modify *Zbtb32* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

- According to the existing MGI data: Homozygous null mice display increased T cell proliferation and increased cytokine secretion.

- The *Zbtb32* gene is located on the Chr7. 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）

集萃药康 GemPharmatech

Zbtb32 zinc finger and BTB domain containing 32 [*Mus musculus* (house mouse)]

Gene ID: 58206, updated on 8-Dec-2018

Summary

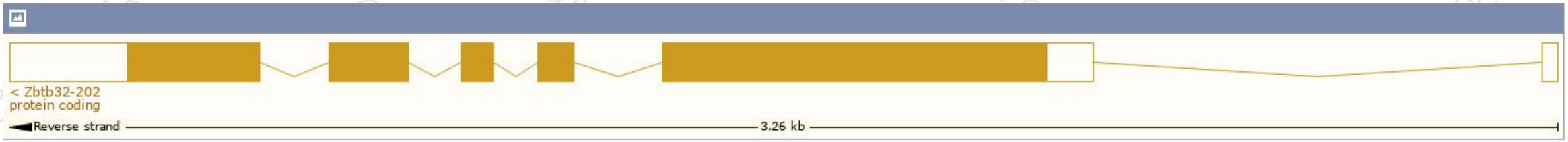
Official Symbol	Zbtb32 provided by MGI
Official Full Name	zinc finger and BTB domain containing 32 provided by MGI
Primary source	MGI:MGI:1891838
See related	Ensembl:ENSMUSG00000006310
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Rog; FAXF; FAZF; PLZP; Tzfp; 4930524C15Rik
Expression	Biased expression in testis adult (RPKM 43.9), spleen adult (RPKM 2.9) and 1 other tissue See more
Orthologs	human all

Transcript information（Ensembl）

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

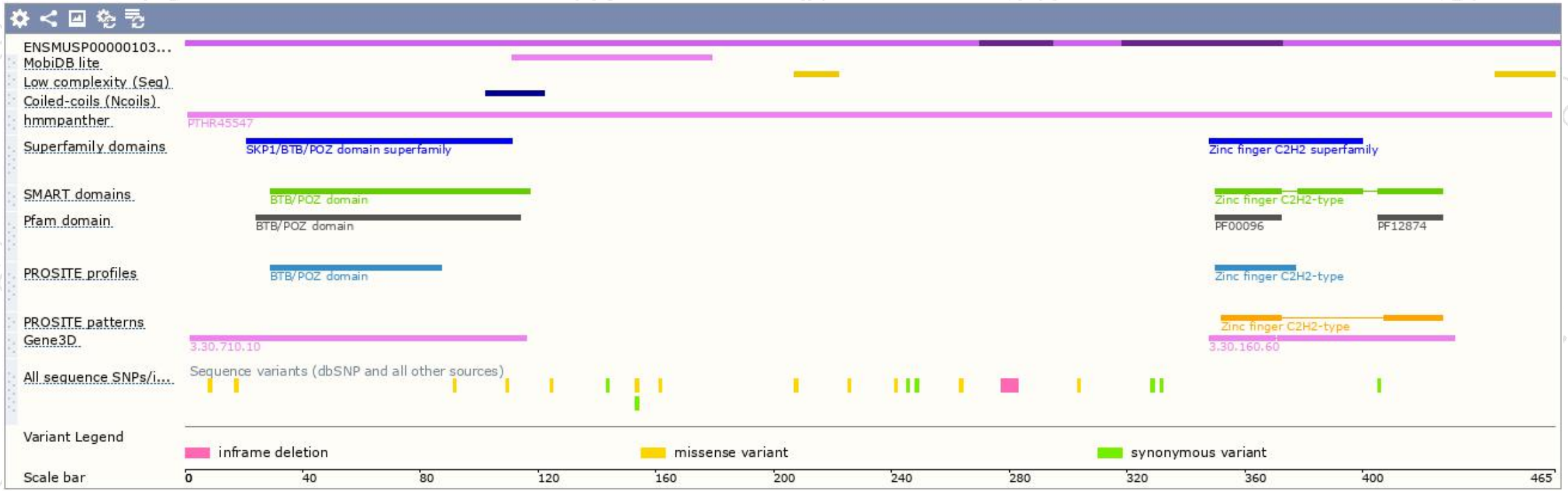
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb32-201	ENSMUST00000108150.1	854	101aa	Protein coding	-	Q9JKD9	TSL:1 GENCODE basic
Zbtb32-202	ENSMUST00000108151.2	1775	465aa	Protein coding	CCDS21102	B2RQ06	TSL:5 GENCODE basic APPRIS P1
Zbtb32-203	ENSMUST00000144532.1	582	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Zbtb32*-202 transcript,The transcription is shown below

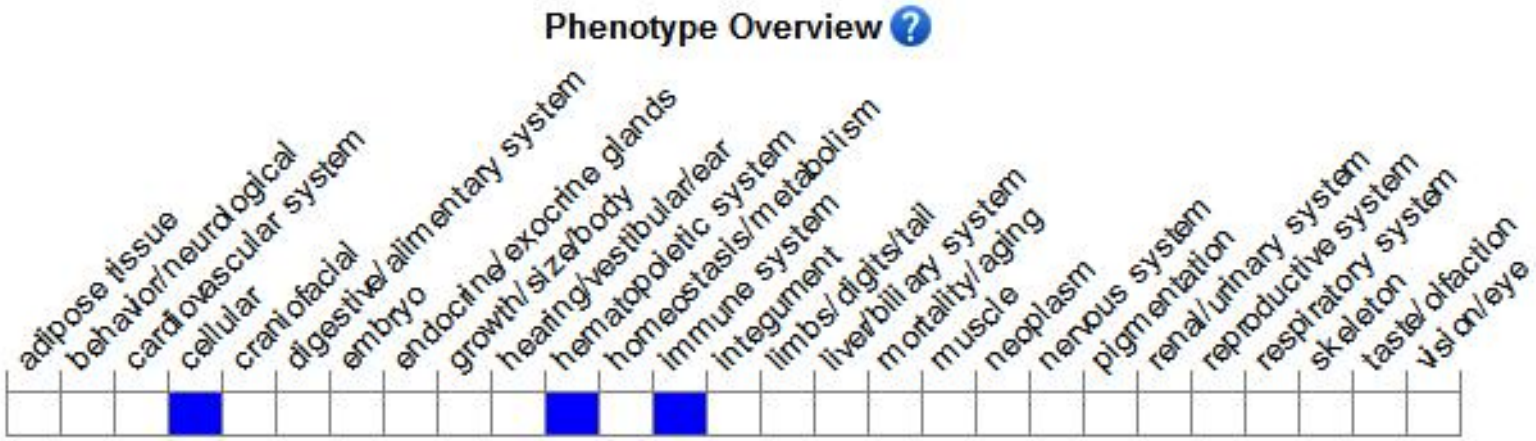


Genomic location distribution

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/) .

Homozygous null mice display increased T cell proliferation and increased cytokine secretion.

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