Zbtb7a Cas9-KO Strategy

Designer: Daohua Xu

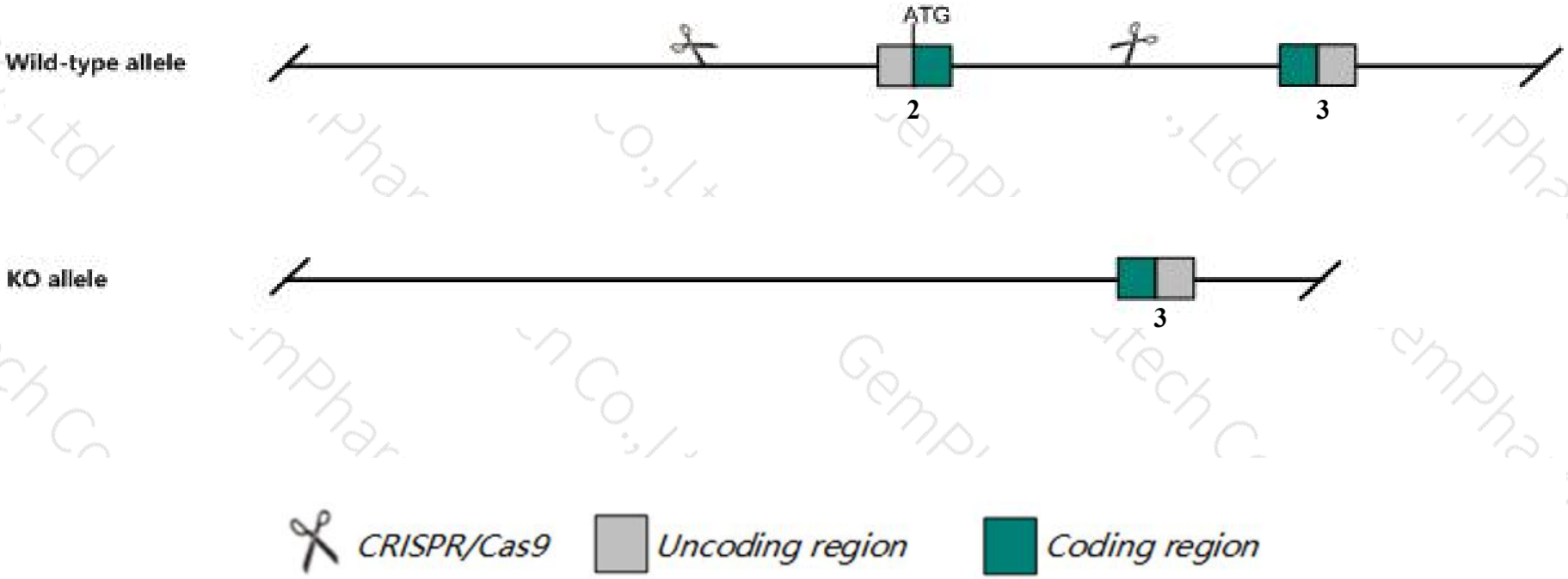
Design Date: 2019-8-12

Project Overview

Project Name	***Zbtb7a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb7a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Zbtb7a* gene has 6 transcripts. According to the structure of *Zbtb7a* gene, exon2 of *Zbtb7a-201* (ENSMUST00000048128.14) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Zbtb7a* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele die around E16.5 due to anemia and exhibit a cell autonomous defect in early B cell development.

➢ The *Zbtb7a* gene is located on the Chr10. 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）

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Zbtb7a zinc finger and BTB domain containing 7a [Mus musculus (house mouse)]

Gene ID: 16969, updated on 31-Jan-2019

Summary

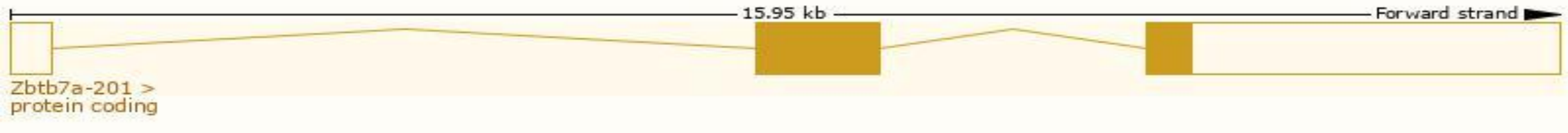
Official Symbol	Zbtb7a provided by MGI
Official Full Name	zinc finger and BTB domain containing 7a provided by MGI
Primary source	MGI:MGI:1335091
See related	Ensembl:ENSMUSG00000035011
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9030619K07Rik, 9130006G12Rik, AI452336, FBI-1, Lrf, Pokemon, Zbtb7
Expression	Broad expression in colon adult (RPKM 50.1), adrenal adult (RPKM 36.3) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

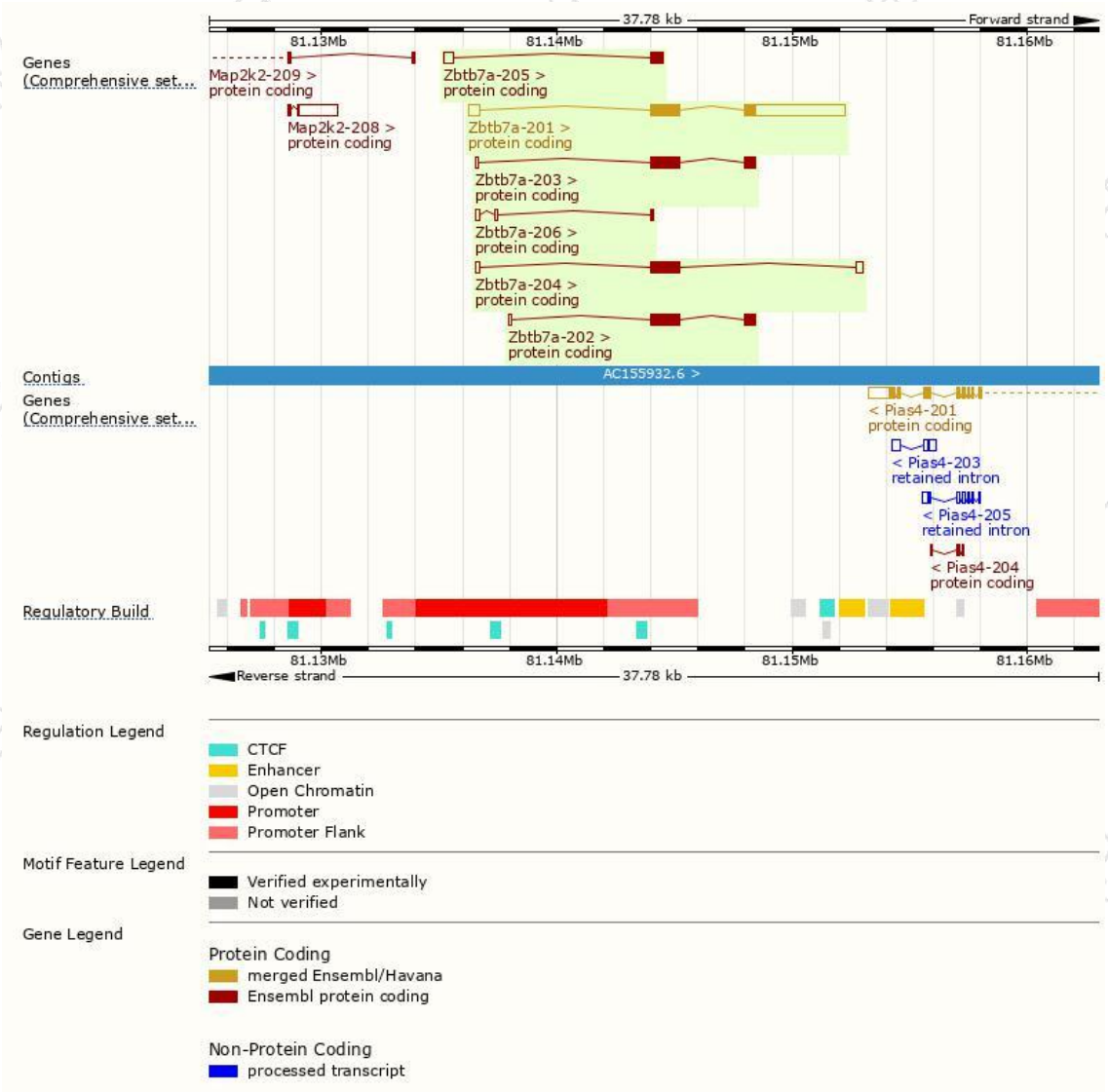
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb7a-201	ENSMUST00000048128.14	5938	569aa	Protein coding	CCDS35991	O88939	TSL:1 GENCODE basic APPRIS P1
Zbtb7a-202	ENSMUST00000117956.1	1863	569aa	Protein coding	CCDS35991	O88939	TSL:1 GENCODE basic APPRIS P1
Zbtb7a-203	ENSMUST00000119606.7	1841	569aa	Protein coding	CCDS35991	O88939	TSL:1 GENCODE basic APPRIS P1
Zbtb7a-204	ENSMUST00000121840.7	1676	415aa	Protein coding	-	D3Z4C3	TSL:1 GENCODE basic
Zbtb7a-205	ENSMUST00000125261.1	907	174aa	Protein coding	-	D3YVF8	CDS 3' incomplete TSL:2
Zbtb7a-206	ENSMUST00000146895.1	362	44aa	Protein coding	-	D3YZI8	CDS 3' incomplete TSL:3

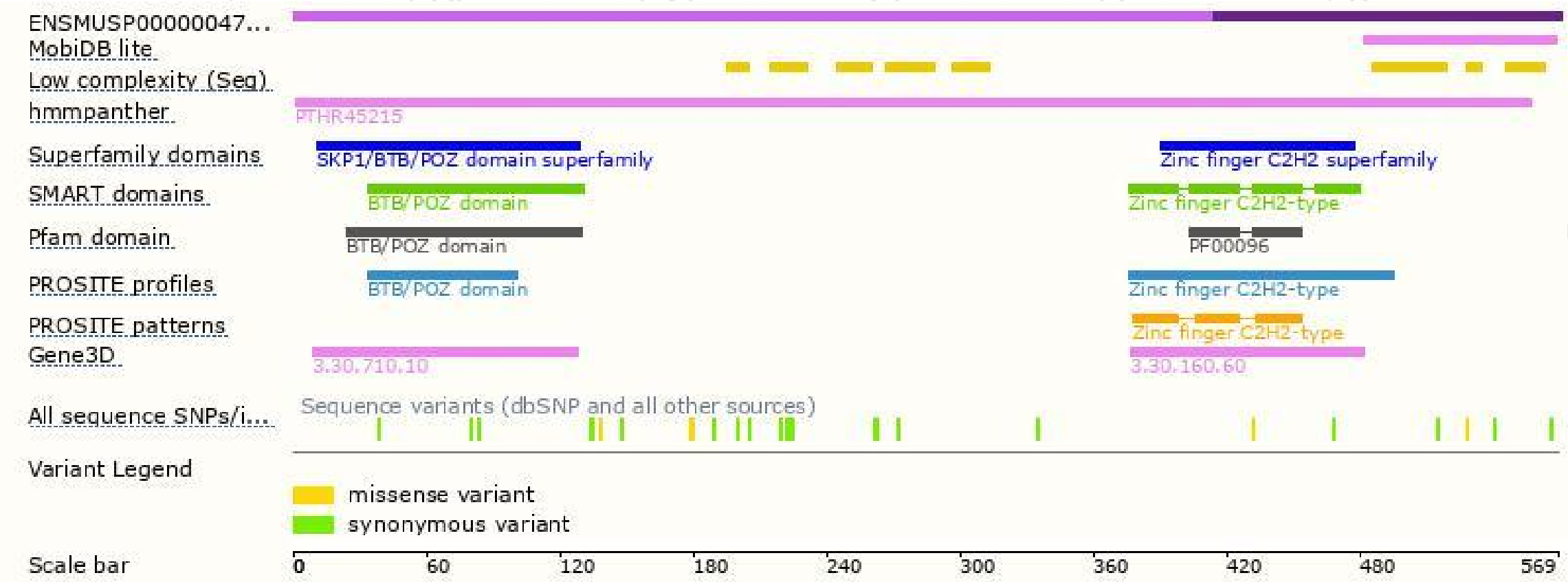
The strategy is based on the design of *Zbtb7a-201* transcript,The transcription is shown below



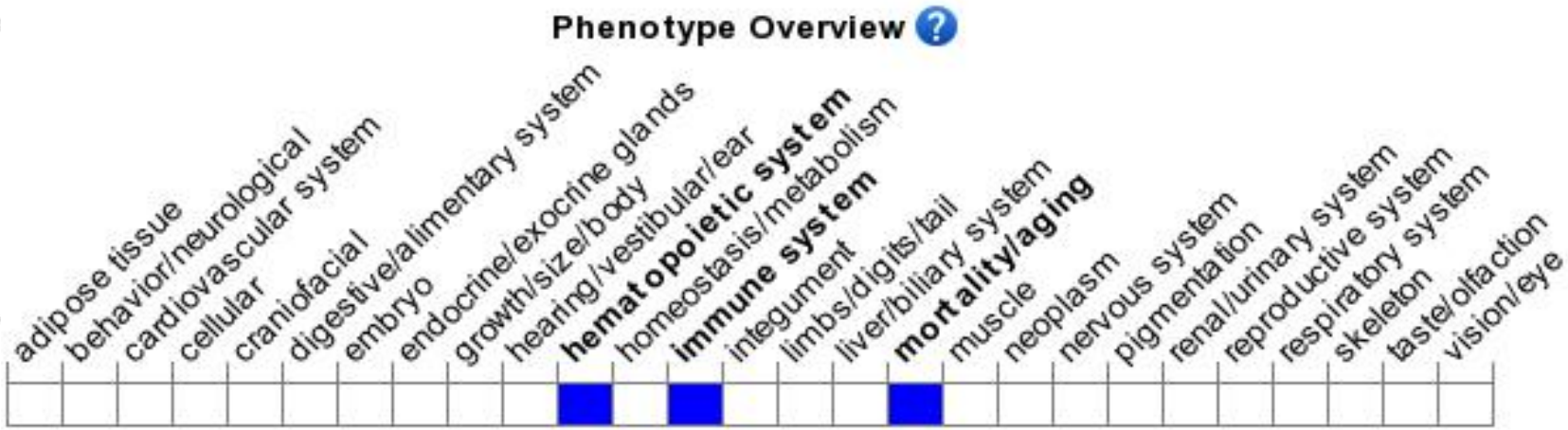
Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for a knock-out allele die around E16.5 due to anemia and exhibit a cell autonomous defect in early B cell development.

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd