

Zbtb24 Cas9-CKO Strategy

Designer:

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Design Date:

2019-7-29

Project Overview



Project Name

Zbtb24

Project type

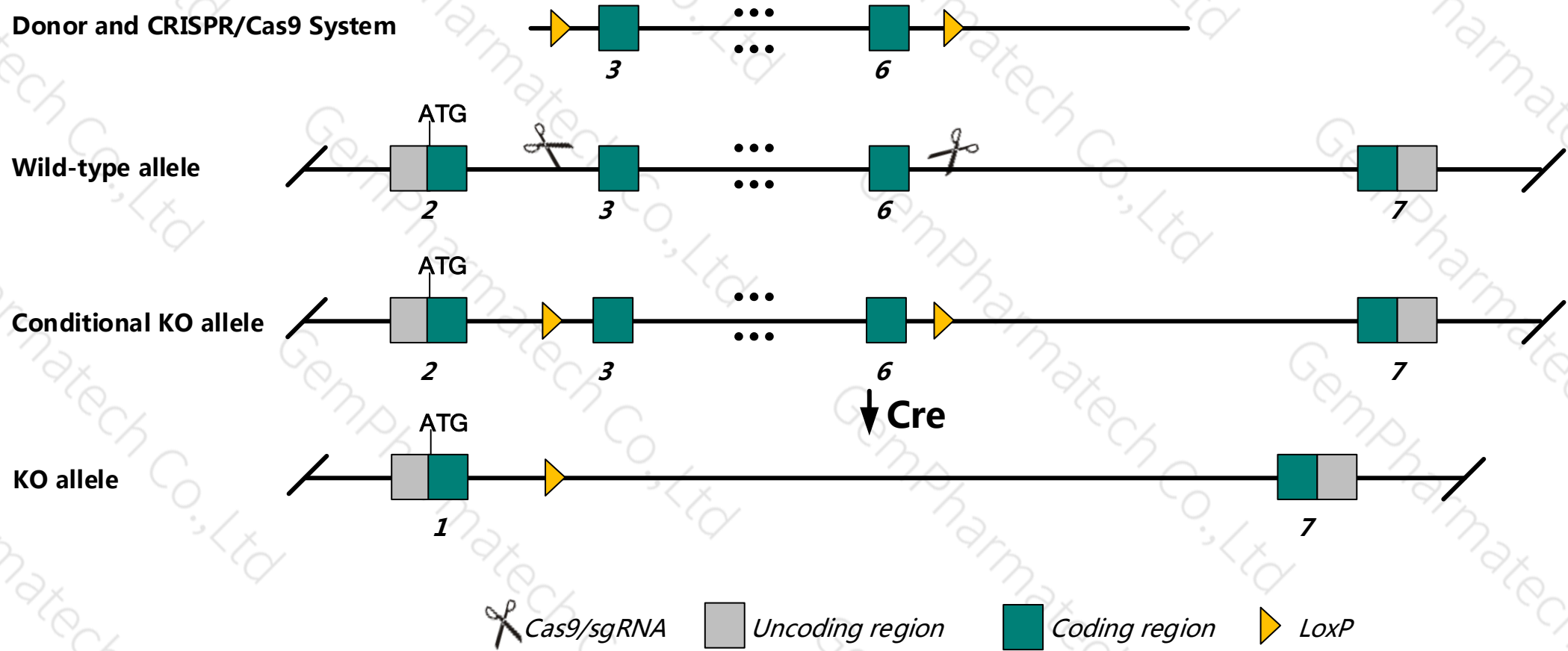
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb24* gene. The schematic diagram is as follows:



- The *Zbtb24* gene has 5 transcript. According to the structure of *Zbtb24* gene, exon3-6 of *Zbtb24*-201 (ENSMUST00000080771.9) transcript is recommended as the knockout region. The region contains 418bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zbtb24* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- According to the existing MGI data , Mice homozygous for a deletion in the BTB domain exhibit embryonic lethality between E4.5 and E9.5.
- Transcript *Zbtb24-205* may not be affected.
- The *Zbtb24* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Zbtb24 zinc finger and BTB domain containing 24 [*Mus musculus* (house mouse)]






Gene ID: 268294, updated on 31-Jan-2019

Summary

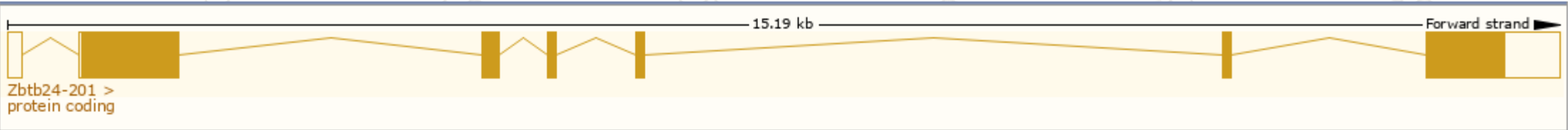
Official Symbol	Zbtb24 provided by MGI
Official Full Name	zinc finger and BTB domain containing 24 provided by MGI
Primary source	MGI:MGI:3039618
See related	Ensembl:ENSMUSG00000019826
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bif1; Bsg1; ZNF450; BC055367
Summary	This gene encodes a protein containing eight C2H2-type zinc fingers and a BTB domain. Expression of this gene is induced by bone morphogenetic protein-2 signaling. Mutation of the related gene in humans causes immunodeficiency-centromeric instability-facial anomalies syndrome-2. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2013]
Expression	Ubiquitous expression in thymus adult (RPKM 6.0), ovary adult (RPKM 5.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

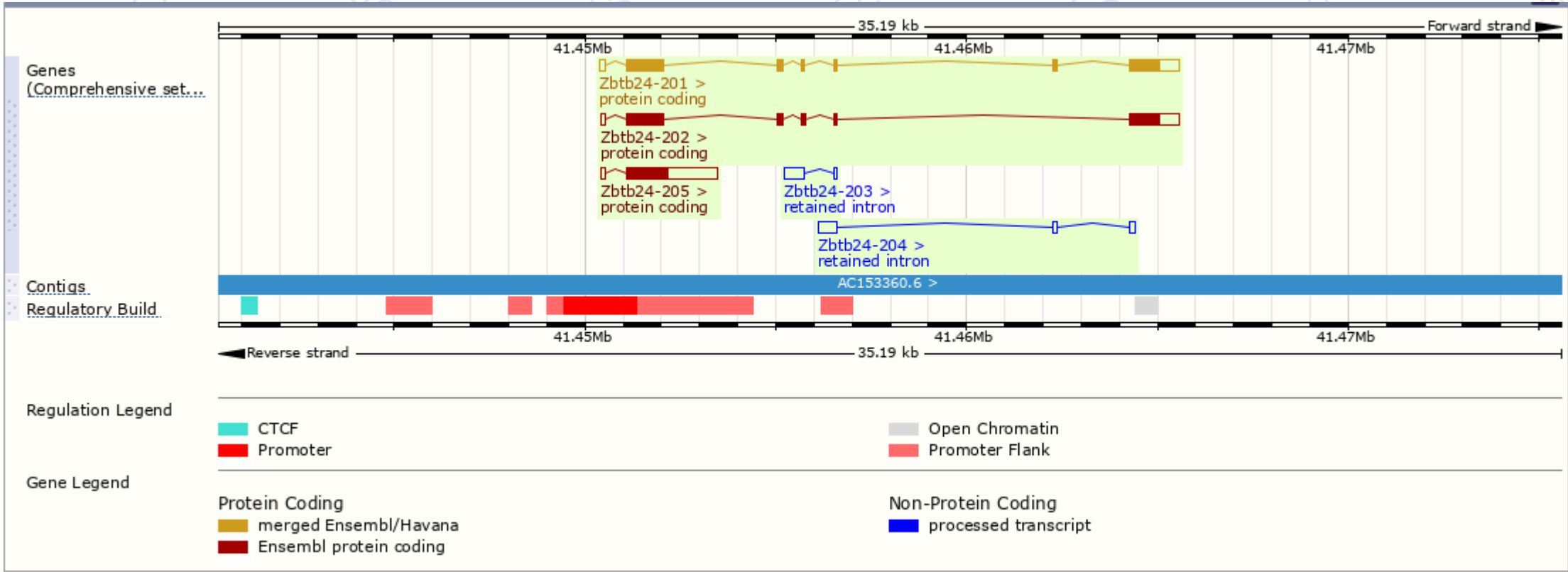
The gene has 5 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb24-201	ENSMUST00000080771.9	2844	710aa	 Protein coding	CCDS23804	Q80X44	TSL:1 GENCODE basic APPRIS P1
Zbtb24-202	ENSMUST00000213797.1	2734	688aa	 Protein coding	-	Q80X44	TSL:1 GENCODE basic
Zbtb24-205	ENSMUST00000216656.1	2476	354aa	 Protein coding	-	Q80X44	TSL:1 GENCODE basic
Zbtb24-204	ENSMUST00000215881.1	719	No protein	 Retained intron	-	-	TSL:2
Zbtb24-203	ENSMUST00000214159.1	623	No protein	 Retained intron	-	-	TSL:3

The strategy is based on the design of *Zbtb24-201* transcript, The transcription is shown below



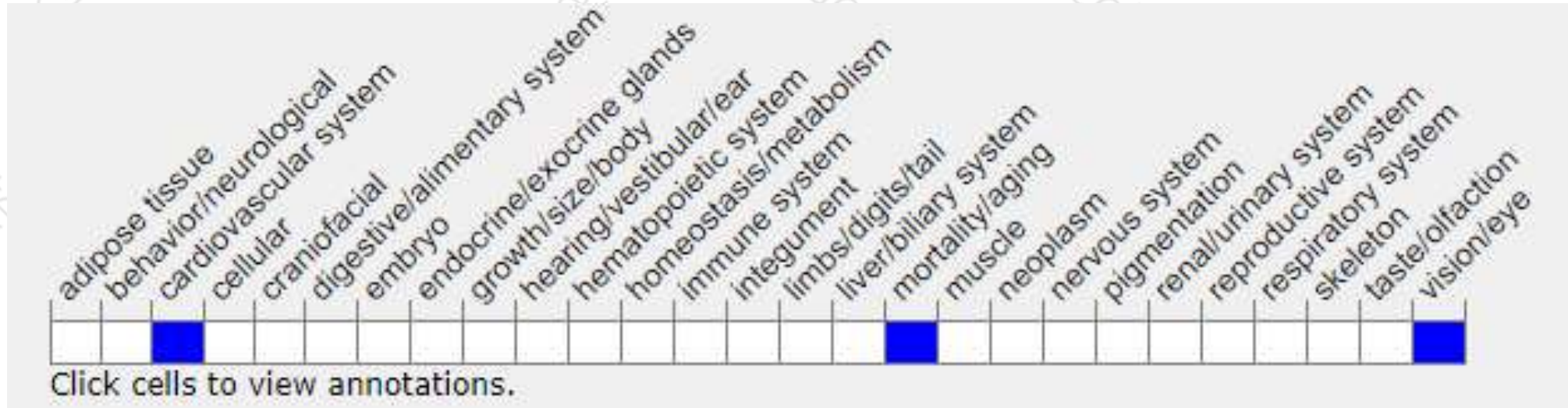
Genomic location distribution



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/>).

Mice homozygous for a deletion in the BTB domain exhibit embryonic lethality between E4.5 and E9.5.

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