

***Ltbp2* Cas9-CKO Strategy**

Designer: Yanhua Shen
Reviewer: Xueting Zhang
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Project Overview

Project Name

Ltbp2

Project type

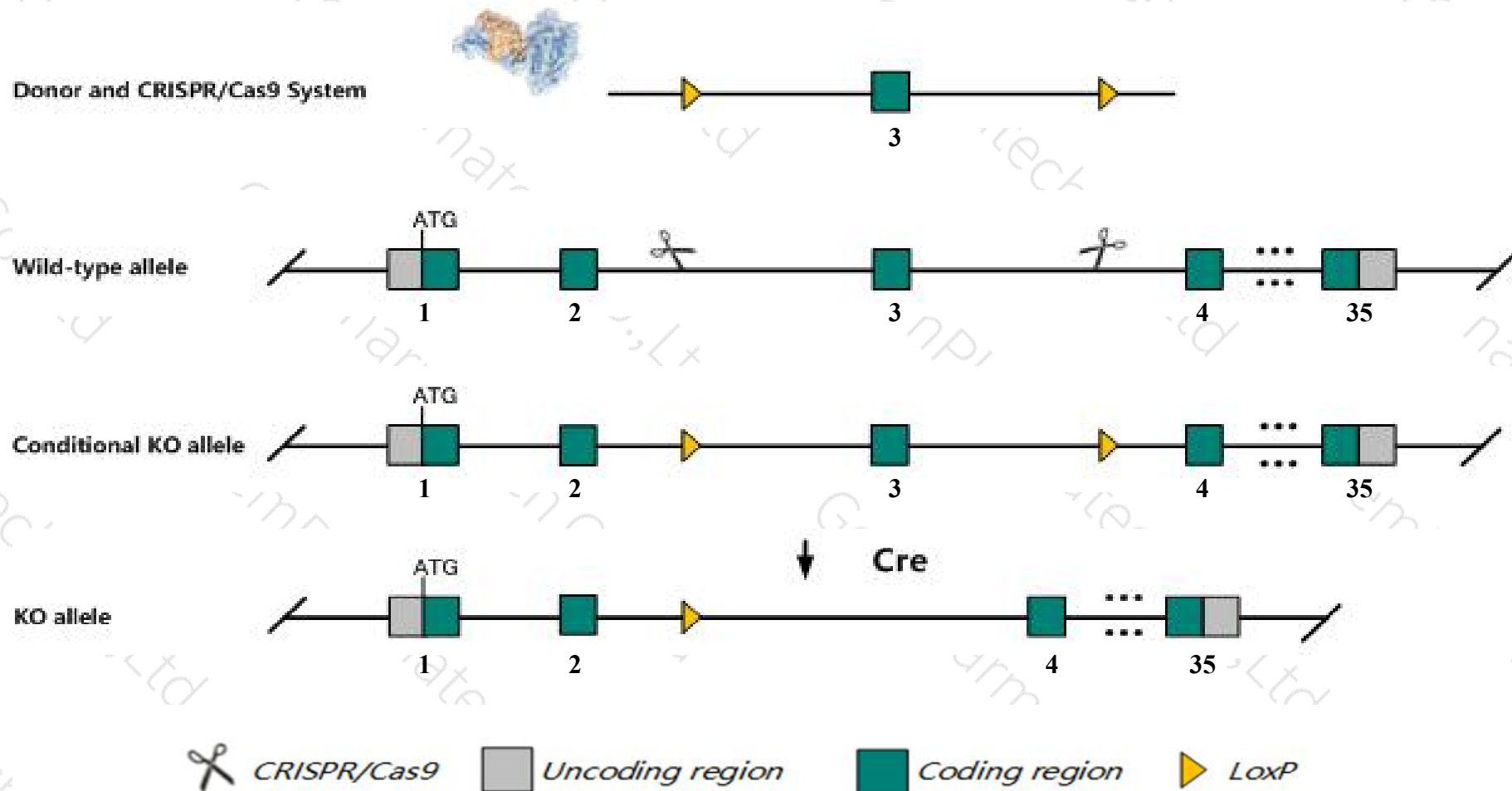
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ltbp2* gene. The schematic diagram is as follows:



- The *Ltbp2* gene has 7 transcripts. According to the structure of *Ltbp2* gene, exon3 of *Ltbp2*-202 (ENSMUST00000110254.8) transcript is recommended as the knockout region. The region contains 253bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ltbp2* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a null allele exhibit early embryonic lethality prior to E6.5. Mice homozygous for a different null allele are viable, fertile, and developmentally normal but develop lens dislocations due to ciliary zonule fragmentation.
- There are more amino acid residues at the N-terminus.
- Transcripts 204,205,206 maybe unaffected.
- The *Ltbp2* gene is located on the Chr12. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ltbp2 latent transforming growth factor beta binding protein 2 [*Mus musculus* (house mouse)]

Gene ID: 16997, updated on 12-Aug-2019

Summary

Official Symbol Ltbp2 provided by [MGI](#)

Official Full Name latent transforming growth factor beta binding protein 2 provided by [MGI](#)

Primary source [MGI:MGI:99502](#)

See related [Ensembl:ENSMUSG000000002020](#)

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 AW208642

Expression Biased expression in lung adult (RPKM 25.3), mammary gland adult (RPKM 11.8) and 10 other tissues [See more](#)

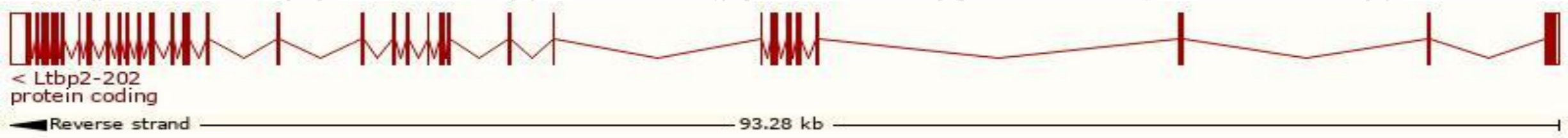
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

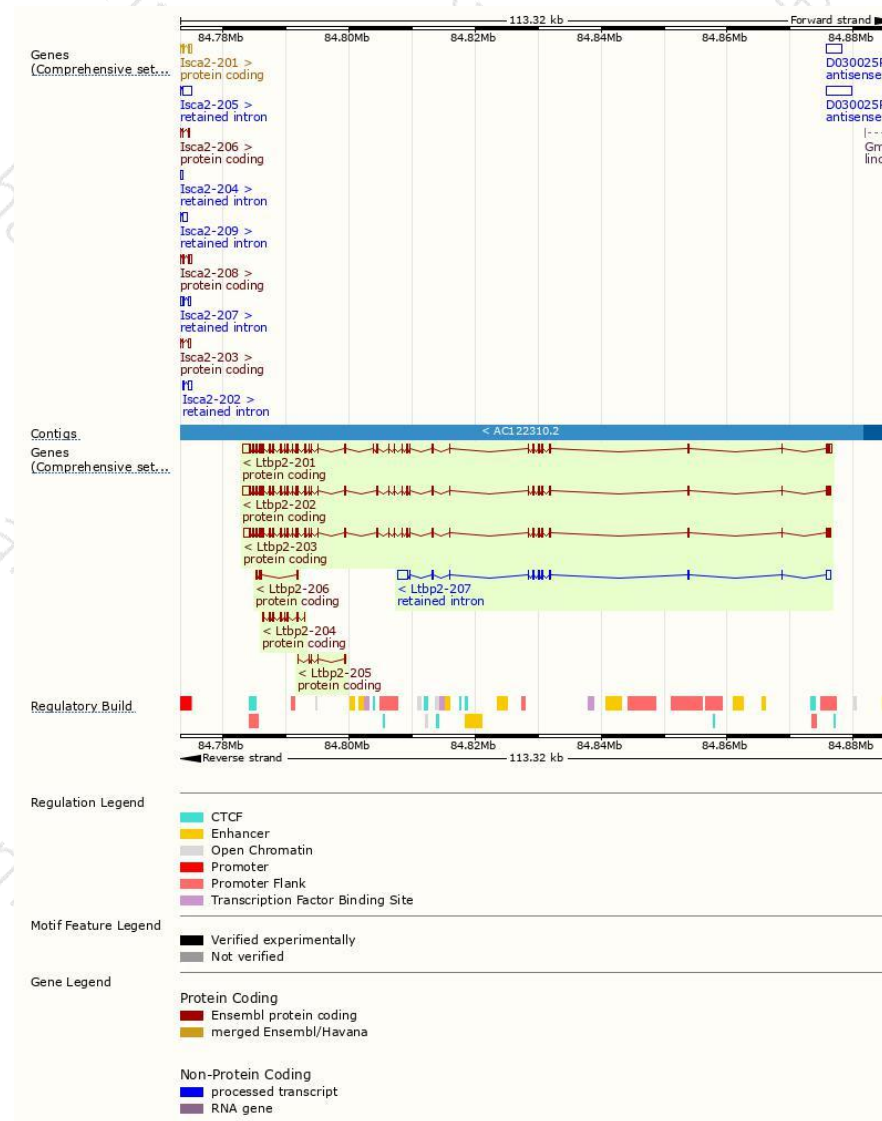
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ltbp2-202	ENSMUST00000110254.8	6602	1786aa	Protein coding	CCDS49112	Q0VD84	TSL:1 GENCODE basic APPRIS P2
Ltbp2-201	ENSMUST00000002073.12	6769	1809aa	Protein coding	-	E9QNQ3	TSL:5 GENCODE basic APPRIS ALT2
Ltbp2-203	ENSMUST00000163189.7	6470	1766aa	Protein coding	-	E9Q1D6	TSL:1 GENCODE basic APPRIS ALT2
Ltbp2-204	ENSMUST00000163214.1	922	307aa	Protein coding	-	F6XGT5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ltbp2-206	ENSMUST00000166383.1	614	204aa	Protein coding	-	F6UFW9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ltbp2-205	ENSMUST00000165141.1	547	183aa	Protein coding	-	F6WSP3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ltbp2-207	ENSMUST00000168699.1	4015	No protein	Retained intron	-	-	TSL:1

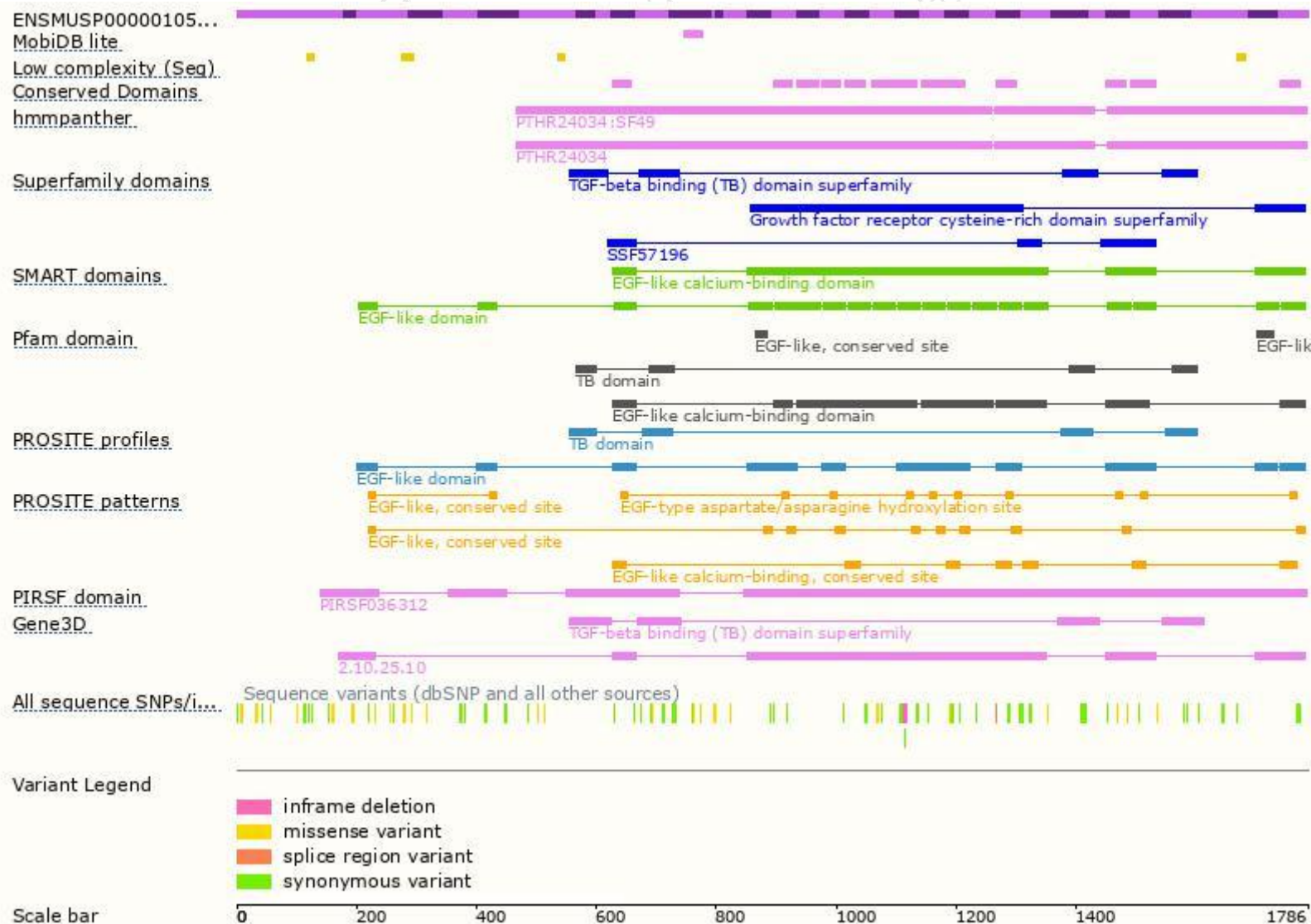
The strategy is based on the design of *Ltbp2-202* transcript,The transcription is shown below



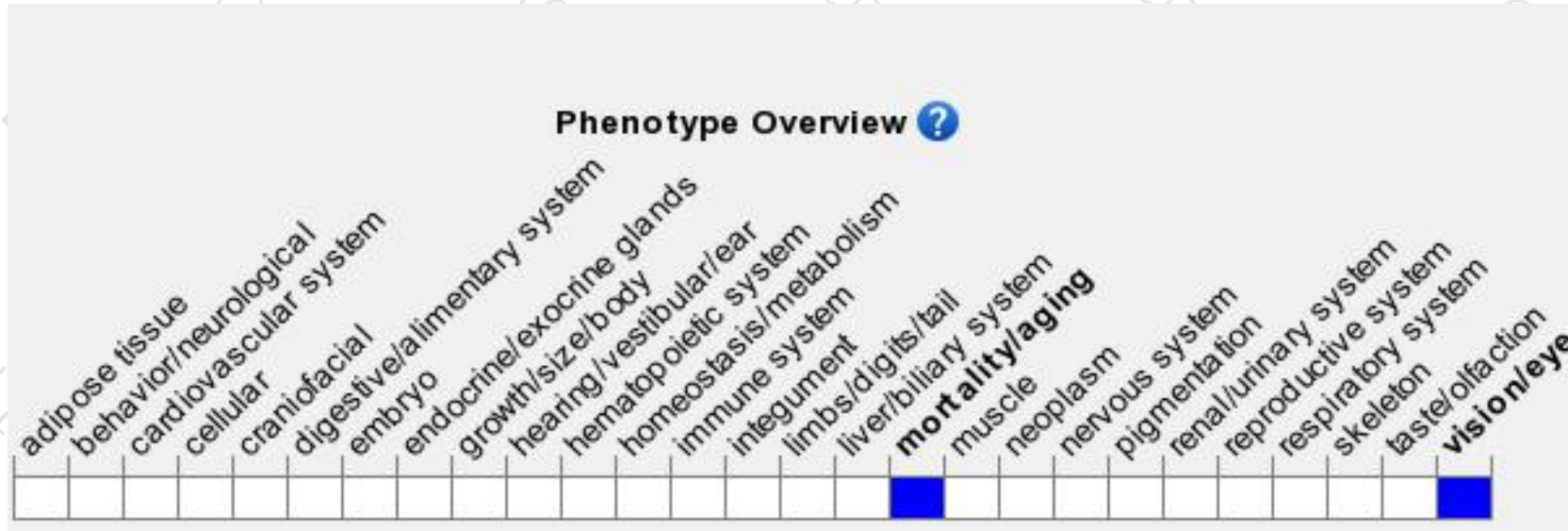
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a null allele exhibit early embryonic lethality prior to E6.5.

Mice homozygous for a different null allele are viable, fertile, and developmentally normal but develop lens dislocations due to ciliary zonule fragmentation.

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

Tel: 400-9660890

