

# ***Ltbp2*** **Cas9-KO Strategy**

Designer: Yanhua Shen  
Reviewer: Xueting Zhang  
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# Project Overview

**Project Name**

*Ltbp2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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

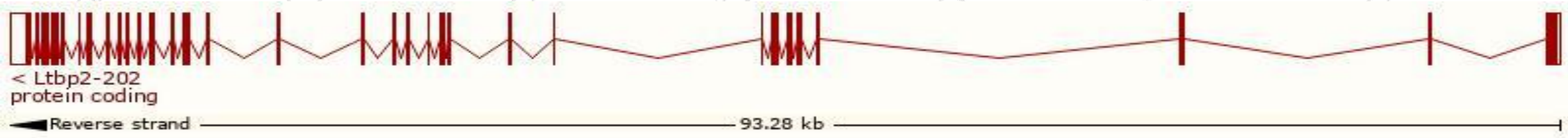
Official Symbol	Ltbp2 provided by MGI
Official Full Name	latent transforming growth factor beta binding protein 2 provided by MGI
Primary source	MGI:MGI:99502
See related	Ensembl:ENSMUSG000000002020
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; 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 <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

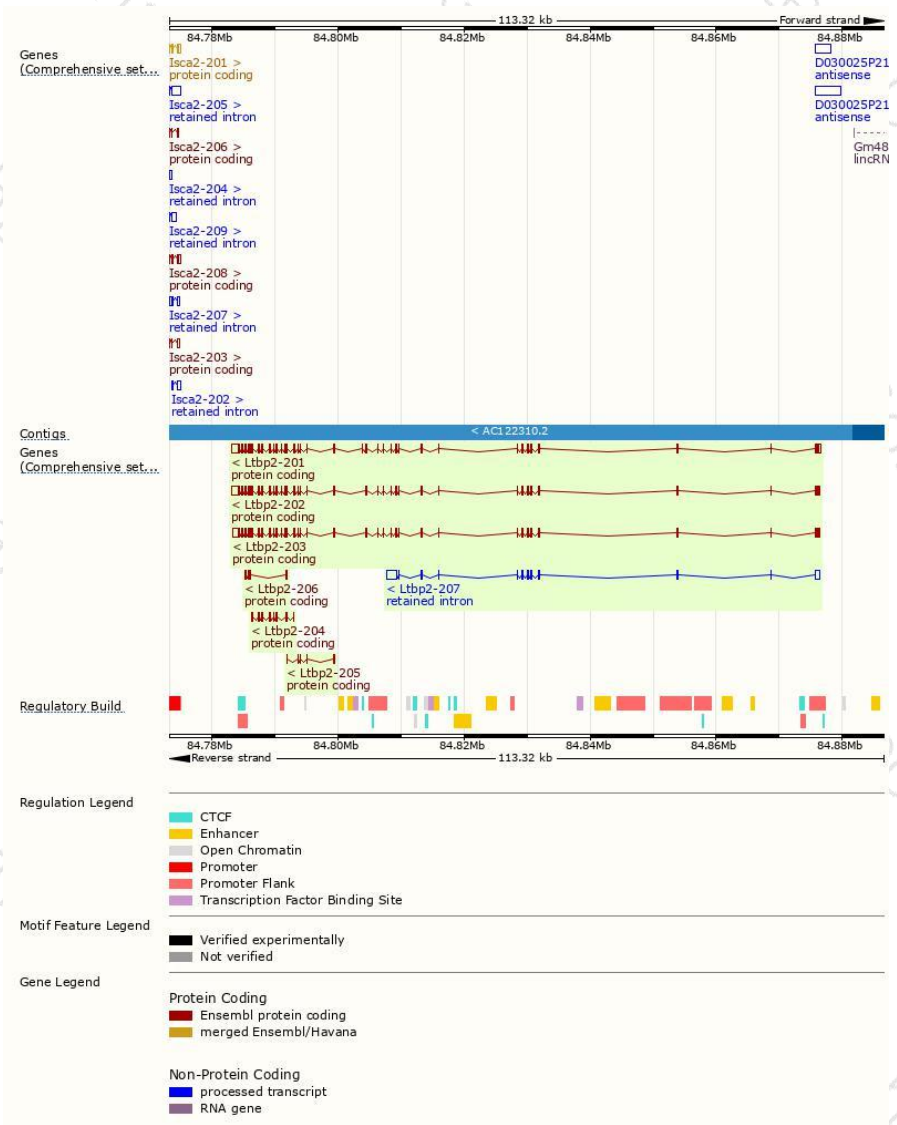
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ltbp2-202	<a href="#">ENSMUST00000110254.8</a>	6602	<a href="#">1786aa</a>	Protein coding	<a href="#">CCDS49112</a>	<a href="#">Q0VD84</a>	TSL:1 GENCODE basic APPRIS P2
Ltbp2-201	<a href="#">ENSMUST00000002073.12</a>	6769	<a href="#">1809aa</a>	Protein coding	-	<a href="#">E9QNQ3</a>	TSL:5 GENCODE basic APPRIS ALT2
Ltbp2-203	<a href="#">ENSMUST00000163189.7</a>	6470	<a href="#">1766aa</a>	Protein coding	-	<a href="#">E9Q1D6</a>	TSL:1 GENCODE basic APPRIS ALT2
Ltbp2-204	<a href="#">ENSMUST00000163214.1</a>	922	<a href="#">307aa</a>	Protein coding	-	<a href="#">F6XGT5</a>	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	<a href="#">ENSMUST00000166383.1</a>	614	<a href="#">204aa</a>	Protein coding	-	<a href="#">F6UFW9</a>	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	<a href="#">ENSMUST00000165141.1</a>	547	<a href="#">183aa</a>	Protein coding	-	<a href="#">F6WSP3</a>	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	<a href="#">ENSMUST00000168699.1</a>	4015	No protein	Retained intron	-	-	TSL:1

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

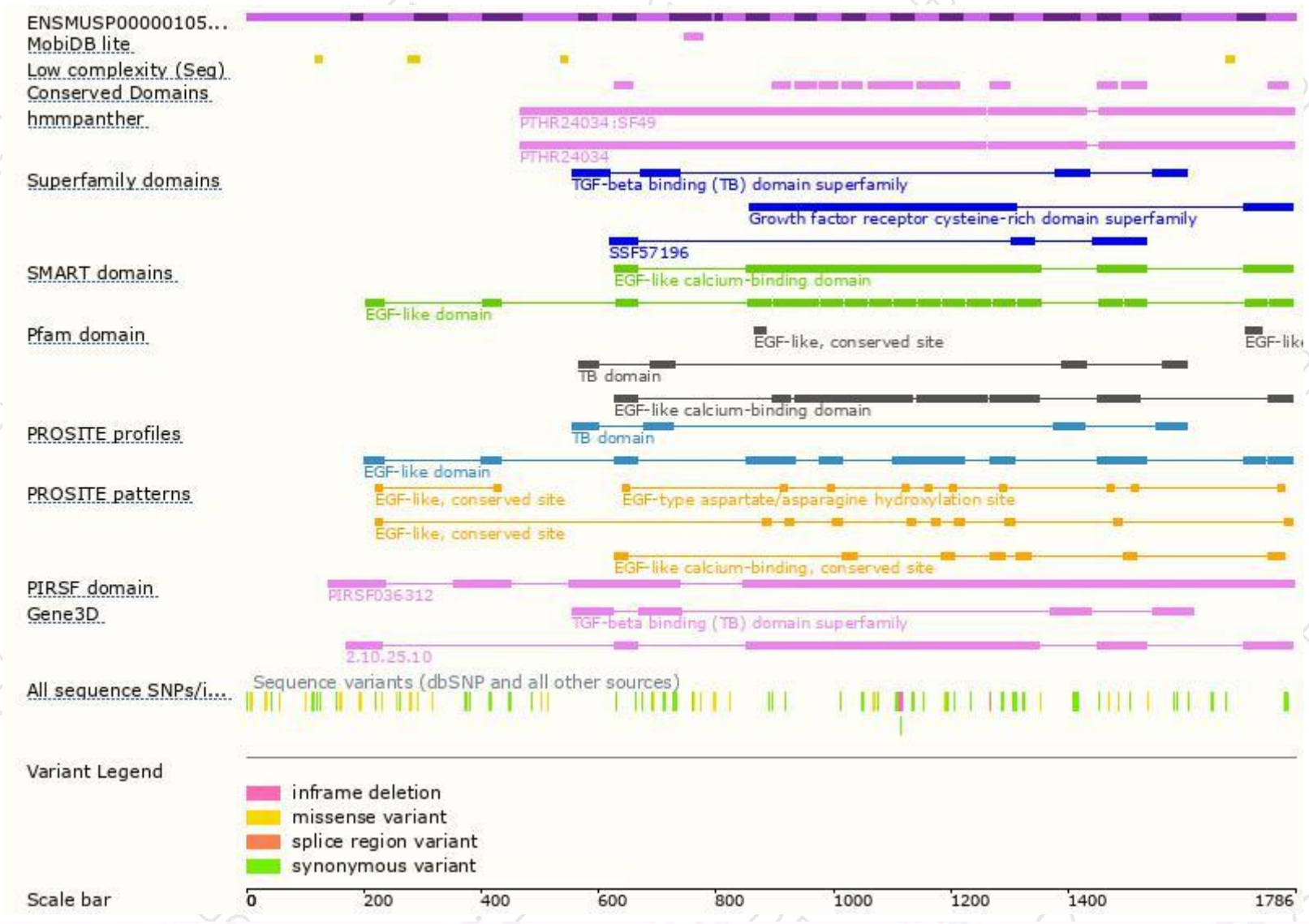


# Genomic location distribution

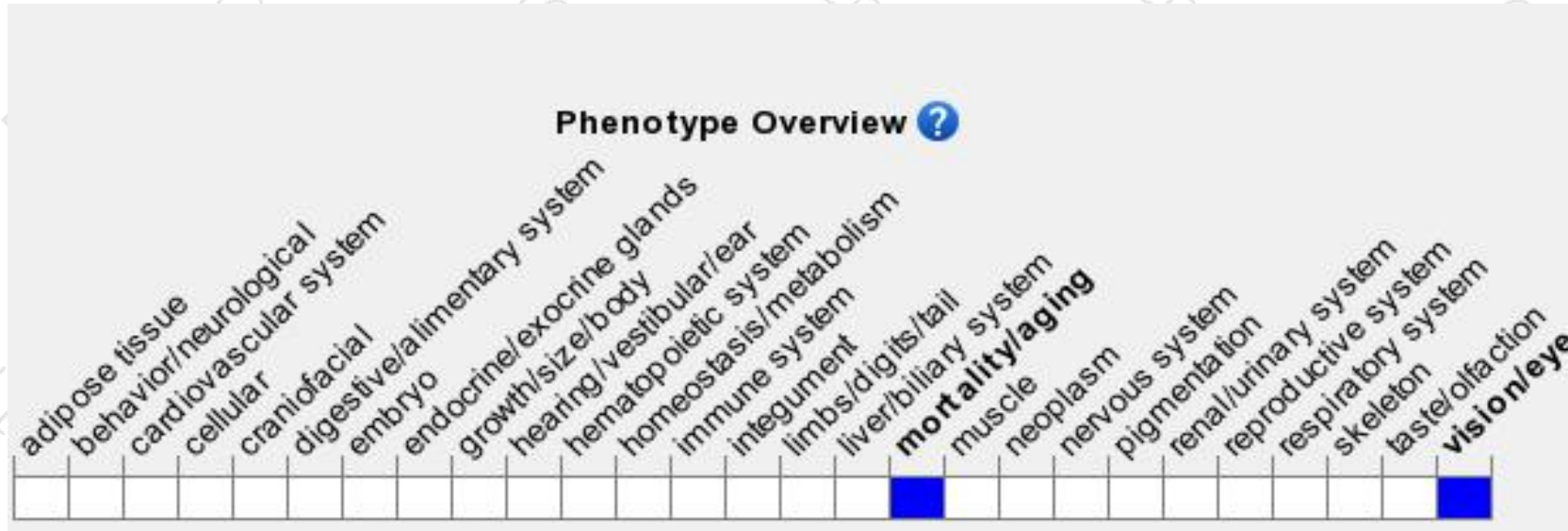




# Protein domain



# 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

