

# Ltbp3 Cas9-KO Strategy

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## **Project Overview**



**Project Name** 

Ltbp3

**Project type** 

Cas9-KO

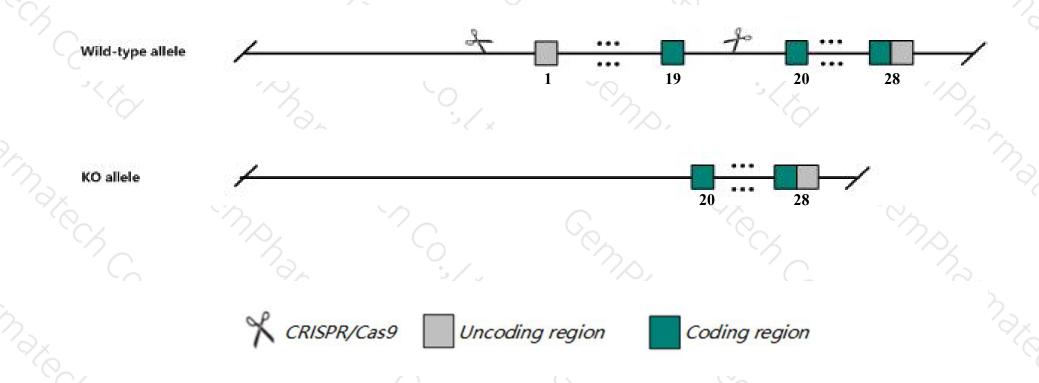
Strain background

C57BL/6JGpt

## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Ltbp3* gene. The schematic diagram is as follows:



### **Technical routes**



➤ The *Ltbp3* gene has 12 transcripts. According to the structure of *Ltbp3* gene, exon1-exon19 of *Ltbp3-201* (ENSMUST00000081496.5) 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 Ltbp3 gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- ➤ According to the existing MGI data, Homozygotes for a targeted null mutation exhibit craniofacial malformations including an overshot mandible and ossification of synchondroses. Mutants develop osteosclerosis of long bones and osteoarthritis, and, in some cases, high corticosterone levels.
- ➤ Transcript *Ltbp3* may not be affected.
- ➤ This strategy may affect the 5-terminal regulation of the target gene and the *Znrd2* gene.
- > The *Ltbp3* gene is located on the Chr19. 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)



#### Ltbp3 latent transforming growth factor beta binding protein 3 [Mus musculus (house mouse)]

Gene ID: 16998, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Ltbp3 provided by MGI

Official Full Name latent transforming growth factor beta binding protein 3 provided by MGI

Primary source MGI:MGI:1101355

See related Ensembl:ENSMUSG00000024940

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 Ltbp2, mFLJ00070

Expression Biased expression in adrenal adult (RPKM 141.5), ovary adult (RPKM 97.4) and 14 other tissuesSee more

Orthologs human all

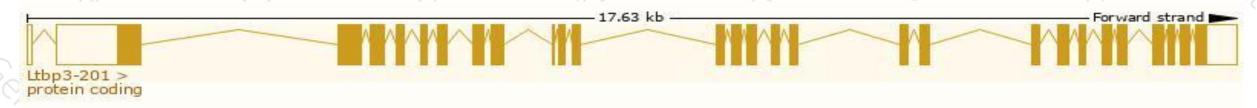
## Transcript information (Ensembl)



The gene has 12 transcripts, all transcripts are shown below:

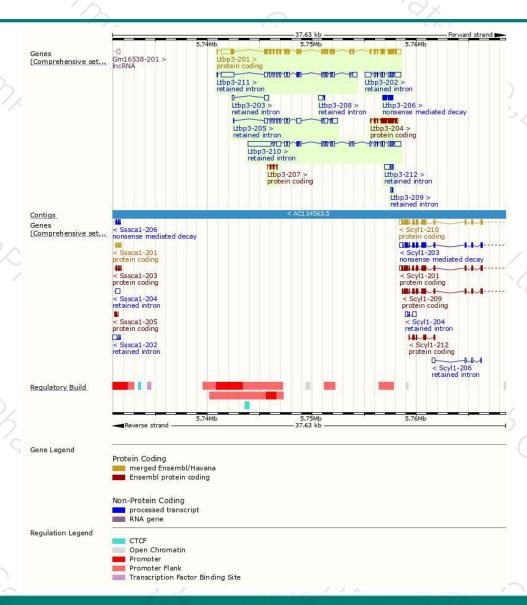
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ltbp3-201	ENSMUST00000081496.5	5190	<u>1253aa</u>	Protein coding	CCDS37891	Q61810	TSL:5 GENCODE basic APPRIS P1
Ltbp3-204	ENSMUST00000236130.1	1387	415aa	Protein coding	-		CDS 5' incomplete
Ltbp3-207	ENSMUST00000236617.1	356	118aa	Protein coding		1920	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Ltbp3-206	ENSMUST00000236529.1	580	<u>153aa</u>	Nonsense mediated decay	-	-	CDS 5' incomplete
Ltbp3-210	ENSMUST00000237280.1	5729	No protein	Retained intron		-	
Ltbp3-211	ENSMUST00000237317.1	3857	No protein	Retained intron			
Ltbp3-205	ENSMUST00000236258.1	2673	No protein	Retained intron	0	1343	
Ltbp3-202	ENSMUST00000235336.1	2099	No protein	Retained intron	-	-	
Ltbp3-212	ENSMUST00000237327.1	704	No protein	Retained intron	5	-	
Ltbp3-203	ENSMUST00000235898.1	650	No protein	Retained intron	-		
Ltbp3-208	ENSMUST00000237128.1	498	No protein	Retained intron	-	8 <b>2</b> 8	
Ltbp3-209	ENSMUST00000237180.1	156	No protein	Retained intron	-	-	
	7 30%		79		74 2 7		

The strategy is based on the design of *Ltbp3-201* transcript, The transcription is shown below



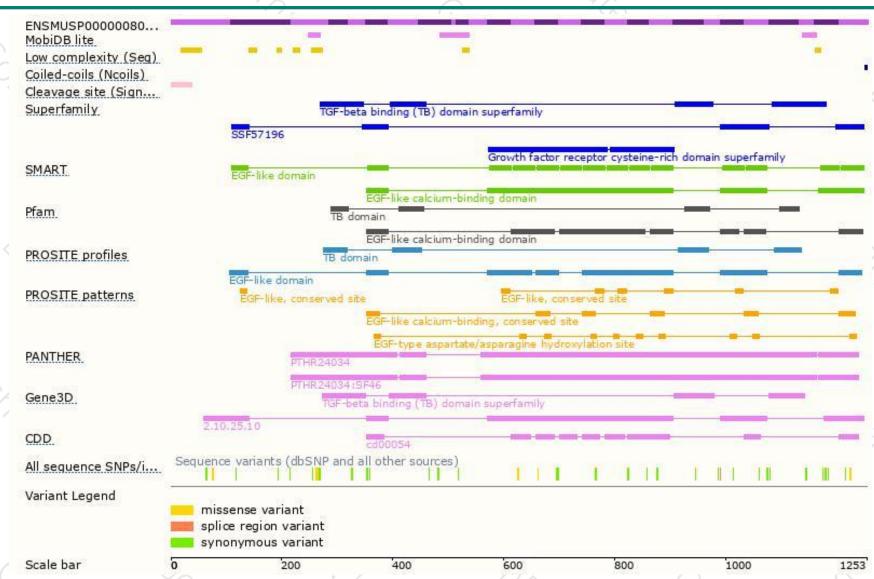
### Genomic location distribution





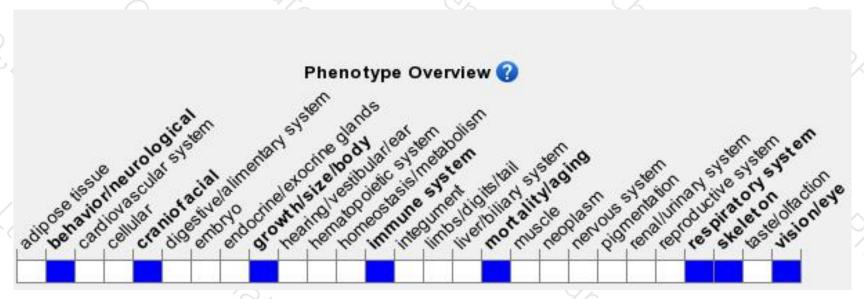
### Protein domain





## 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, Homozygotes for a targeted null mutation exhibit craniofacial malformations including an overshot mandible and ossification of synchondroses. Mutants develop osteosclerosis of long bones and osteoarthritis, and, in some cases, high corticosterone levels.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





