

Ltbp1 Cas9-KO Strategy

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Project Overview



Project Name

Ltbp1

Project type

Cas9-KO

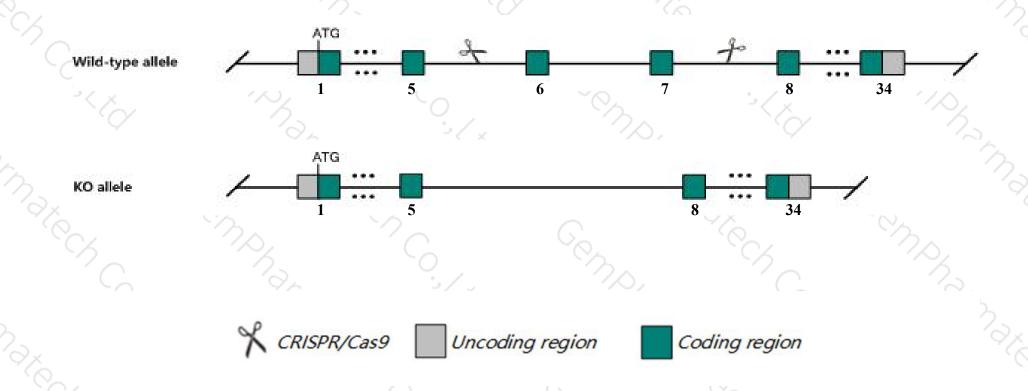
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Ltbp1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Ltbp1* gene has 10 transcripts. According to the structure of *Ltbp1* gene, exon6-exon7 of *Ltbp1-201*(ENSMUST0000001927.11) transcript is recommended as the knockout region. The region contains 500bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ltbp1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Mice homozygous for a null allele exhibit embryonic and neonatal lethality associated with defects in the aortic arch and outflow tract.
- ➤ Transcript *Ltbp1-209* may not be affected.
- The *Ltbp1* gene is located on the Chr17. 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)



Ltbp1 latent transforming growth factor beta binding protein 1 [Mus musculus (house mouse)]

Gene ID: 268977, updated on 3-Feb-2019

Summary



Official Symbol Ltbp1 provided by MGI

Official Full Name latent transforming growth factor beta binding protein 1 provided by MGI

Primary source MGI:MGI:109151

See related Ensembl: ENSMUSG00000001870

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 9430031G15Rik, 9830146M04, Ltbp-1, Ltbp1L, TGF-beta1-BP-1, Tgfb, b2b1000Clo

Expression Broad expression in ovary adult (RPKM 29.6), limb E14.5 (RPKM 18.7) and 16 other tissuesSee more

Orthologs <u>human</u> all

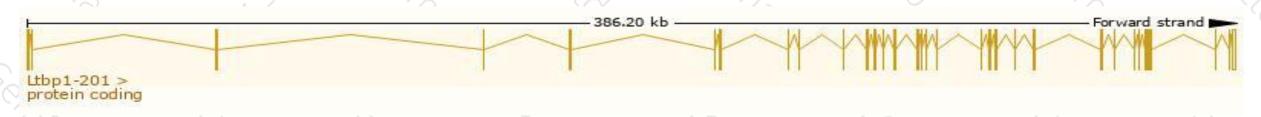
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000001927.11	6671	<u>1712aa</u>	Protein coding	CCDS28973	Q8CG19	TSL:5 GENCODE basic
ENSMUST00000112516.7	5140	<u>1394aa</u>	Protein coding	CCDS37694	Q8CG19	TSL:5 GENCODE basic
ENSMUST00000112514.1	4870	<u>1341aa</u>	Protein coding	CCDS84336	Q8CG19	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000234490.1	6235	<u>1713aa</u>	Protein coding	12	2	GENCODE basic
ENSMUST00000135447.7	3114	980aa	Protein coding		B1B1E2	CDS 3' incomplete TSL:1
ENSMUST00000234327.1	246	<u>82aa</u>	Protein coding		-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
ENSMUST00000135750.1	3277	No protein	Retained intron	1/4	ų.	TSL:1
ENSMUST00000127458.1	1905	No protein	Retained intron	12	2	TSL:1
ENSMUST00000234008.1	823	No protein	IncRNA			
ENSMUST00000146839.1	519	No protein	IncRNA	19-	-	TSL:2
	ENSMUST0000001927.11 ENSMUST00000112516.7 ENSMUST00000112514.1 ENSMUST00000234490.1 ENSMUST00000135447.7 ENSMUST00000234327.1 ENSMUST00000135750.1 ENSMUST00000127458.1 ENSMUST00000234008.1	ENSMUST0000001927.11 6671 ENSMUST00000112516.7 5140 ENSMUST00000112514.1 4870 ENSMUST00000234490.1 6235 ENSMUST00000135447.7 3114 ENSMUST00000234327.1 246 ENSMUST00000135750.1 3277 ENSMUST00000127458.1 1905 ENSMUST000000234008.1 823	ENSMUST00000001927.11 6671 1712aa ENSMUST00000112516.7 5140 1394aa ENSMUST00000112514.1 4870 1341aa ENSMUST00000234490.1 6235 1713aa ENSMUST00000135447.7 3114 980aa ENSMUST00000234327.1 246 82aa ENSMUST00000135750.1 3277 No protein ENSMUST00000127458.1 1905 No protein ENSMUST00000234008.1 823 No protein	ENSMUST00000001927.11 6671 1712aa Protein coding ENSMUST00000112516.7 5140 1394aa Protein coding ENSMUST00000112514.1 4870 1341aa Protein coding ENSMUST00000234490.1 6235 1713aa Protein coding ENSMUST00000135447.7 3114 980aa Protein coding ENSMUST00000234327.1 246 82aa Protein coding ENSMUST00000135750.1 3277 No protein Retained intron ENSMUST00000127458.1 1905 No protein Retained intron ENSMUST00000234008.1 823 No protein IncRNA	ENSMUST00000001927.11 6671 1712aa Protein coding CCDS28973 ENSMUST00000112516.7 5140 1394aa Protein coding CCDS37694 ENSMUST00000112514.1 4870 1341aa Protein coding CCDS84336 ENSMUST00000234490.1 6235 1713aa Protein coding - ENSMUST00000135447.7 3114 980aa Protein coding - ENSMUST00000135750.1 3277 No protein Retained intron - ENSMUST00000127458.1 1905 No protein Retained intron - ENSMUST00000234008.1 823 No protein IncRNA -	ENSMUST00000001927.11 6671 1712aa Protein coding CCDS28973 Q8CG19 ENSMUST00000112516.7 5140 1394aa Protein coding CCDS37694 Q8CG19 ENSMUST00000112514.1 4870 1341aa Protein coding CCDS84336 Q8CG19 ENSMUST00000234490.1 6235 1713aa Protein coding - - ENSMUST00000135447.7 3114 980aa Protein coding - B1B1E2 ENSMUST00000135750.1 3277 No protein Retained intron - - ENSMUST00000127458.1 1905 No protein Retained intron - - ENSMUST00000234008.1 823 No protein IncRNA - -

The strategy is based on the design of *Ltbp1-201* transcript, The transcription is shown below



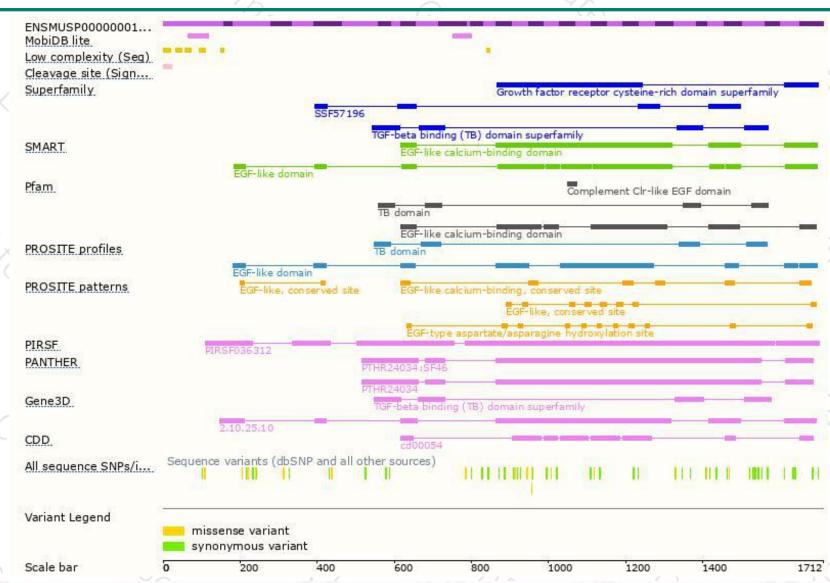
Genomic location distribution





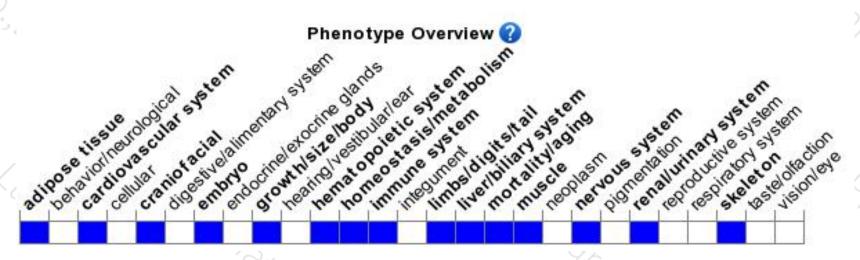
Protein domain





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 null allele exhibit embryonic and neonatal lethality associated with defects in the aortic arch and outflow tract.



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





