

# **Ltb4r1 Cas9-CKO Strategy**

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GemPharmatech

# Project Overview

**Project Name**

***Ltb4rl***

**Project type**

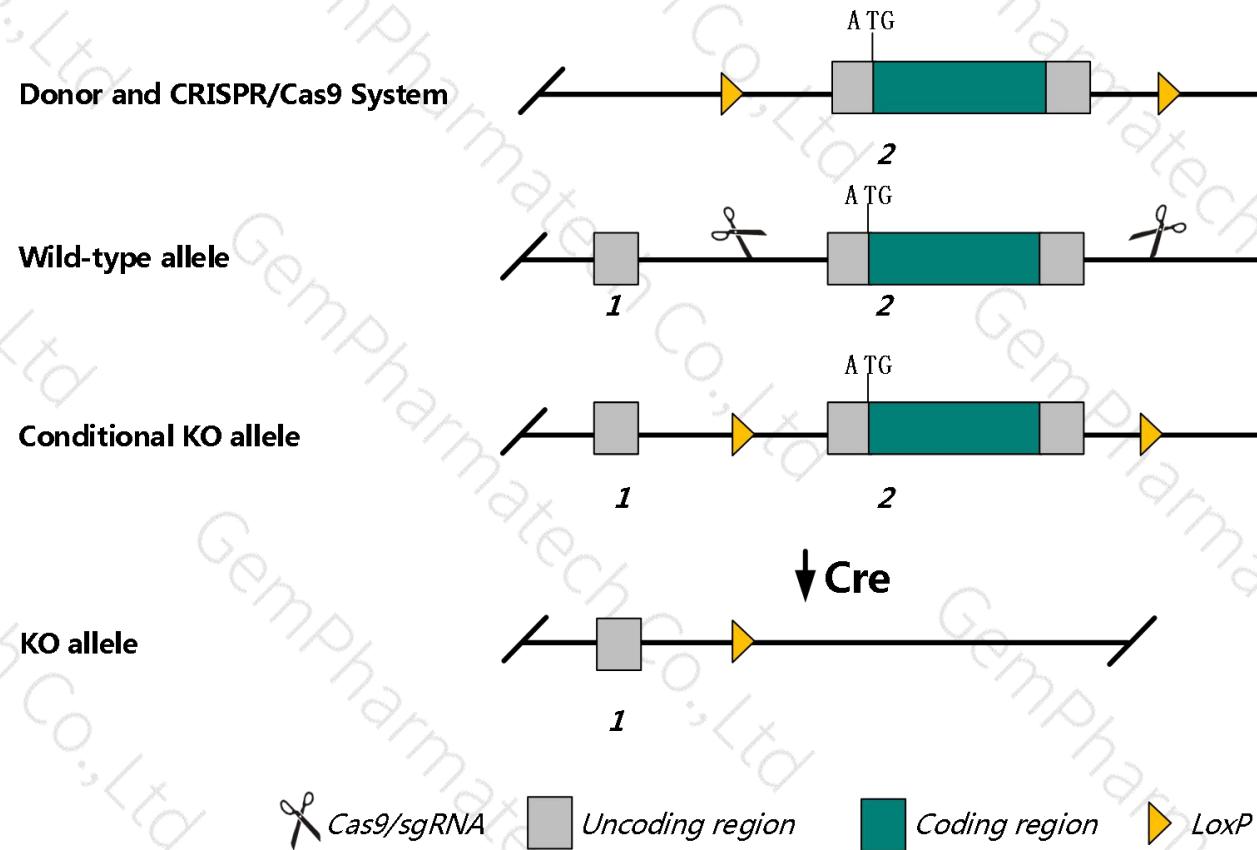
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ltb4rl* gene. The schematic diagram is as follows:



# Technical routes



- The *Ltb4rl* gene has 1 transcript. According to the structure of *Ltb4rl* gene, exon 2 of *Ltb4rl*-201 (ENSMUST00000057569.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ltb4rl* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 or cell types.

# Notice

- According to the existing MGI data , Nullizygous mutations cause impaired Ltb4-driven chemotaxis and adhesion. Homozygous null phenotypes include attenuated autoAb-driven arthritis, adoptive transfer-induced uveitis, airway hyperresponsiveness and Th2-type immune responses, and reduced eosinophil recruitment in induced peritonitis.
- The CKO region contains functional region of the *Adcy4* gene.Knockout the region may affect the function of *Adcy4* gene.
- The *Ltb4rl* gene is located on the Chr 14. 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 )

## Ltb4r1 leukotriene B4 receptor 1 [ *Mus musculus* (house mouse) ]

Gene ID: 16995, updated on 30-Apr-2019

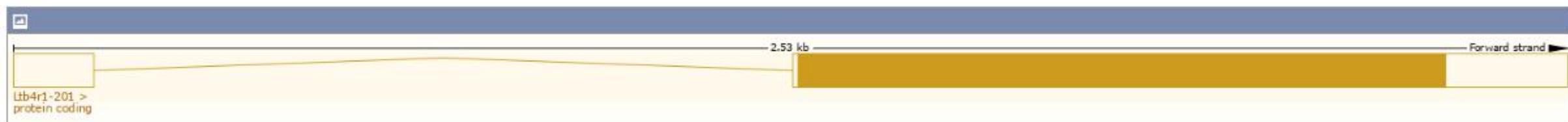
Summary	
Official Symbol	Ltb4r1 provided by <a href="#">MGI</a>
Official Full Name	leukotriene B4 receptor 1 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1309472</a>
See related	<a href="#">Ensembl:ENSMUSG00000046908</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BLT1; BLTR; Ltb4r; mBLTR
Expression	Biased expression in duodenum adult (RPKM 10.3), small intestine adult (RPKM 8.5) and 12 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information ( Ensembl )

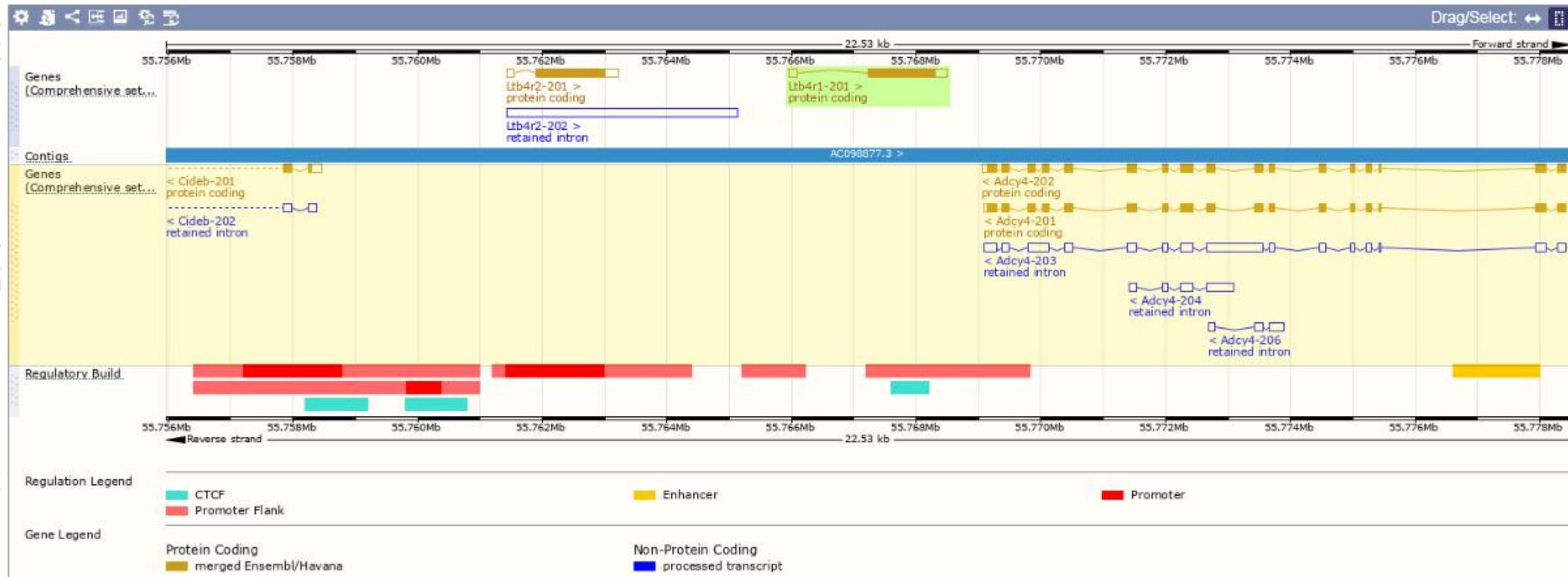
The gene has 1 transcript, and the transcript is shown below:

Show/hide columns (1 hidden)										Filter	Export
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags				
Ltb4r1-201	ENSMUST00000057569.3	1394	351aa	Protein coding	CCDS27129	A7VJD3 O88855	TSL:1 GENCODE basic APPRIS P1				

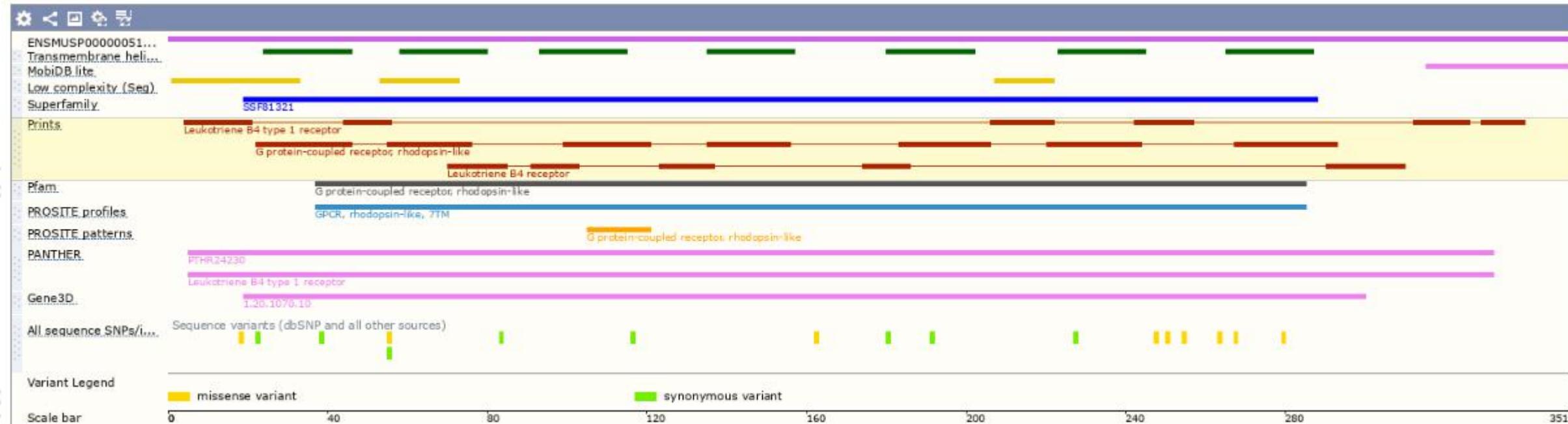
The strategy is based on the design of *Ltb4r1-201* transcript, The transcription is shown below



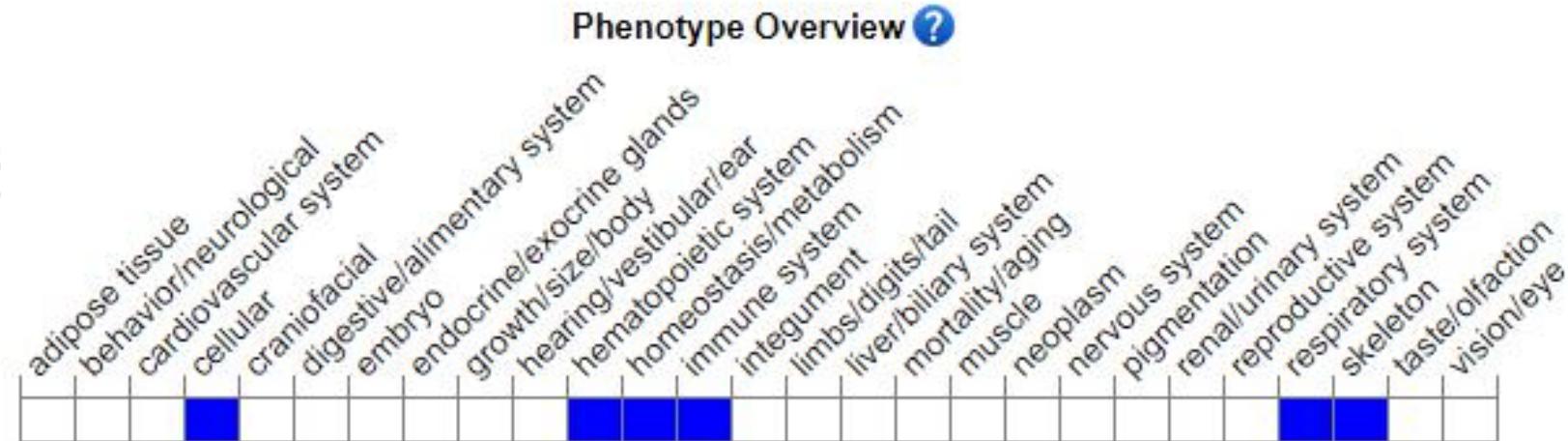
# Genomic location distribution



# 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, Mutations in this locus affect cell-cycle regulation and apoptosis. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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