

Itgb7 Cas9-KO Strategy

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Project Overview

Project Name

Itgb7

Project type

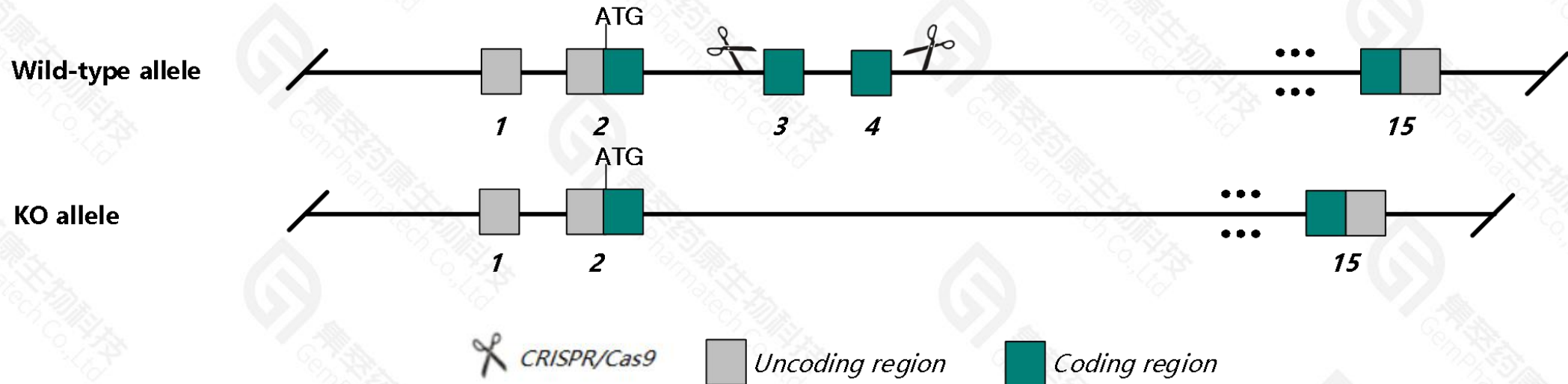
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Itgb7* gene. The schematic diagram is as follows:



- The *Itgb7* gene has 5 transcripts. According to the structure of *Itgb7* gene, exon3-exon4 of *Itgb7*-201(ENSMUST00000001327.11) transcript is recommended as the knockout region. The region contains 373bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itgb7* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mice display hypoplasia of gut-associated lymph tissue due to defects in lymphocyte migration
- The *Itgb7* gene is located on the Chr15. 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)

Itgb7 integrin beta 7 [Mus musculus (house mouse)]

Gene ID: 16421, updated on 13-Mar-2020

Summary

Official Symbol Itgb7 provided by [MGI](#)

Official Full Name integrin beta 7 provided by [MGI](#)

Primary source [MGI:MGI:96616](#)

See related [Ensembl:ENSMUSG00000001281](#)

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 Ly69

Expression Biased expression in spleen adult (RPKM 26.7), mammary gland adult (RPKM 11.9) and 7 other tissues [See more](#)

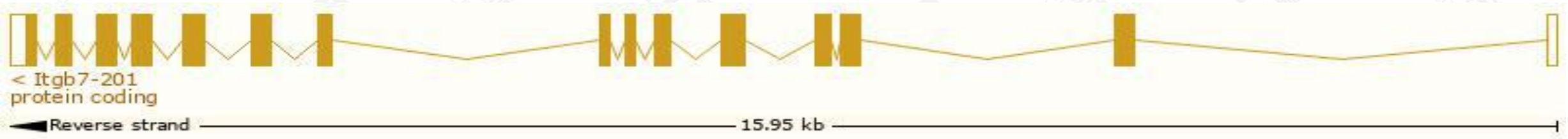
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

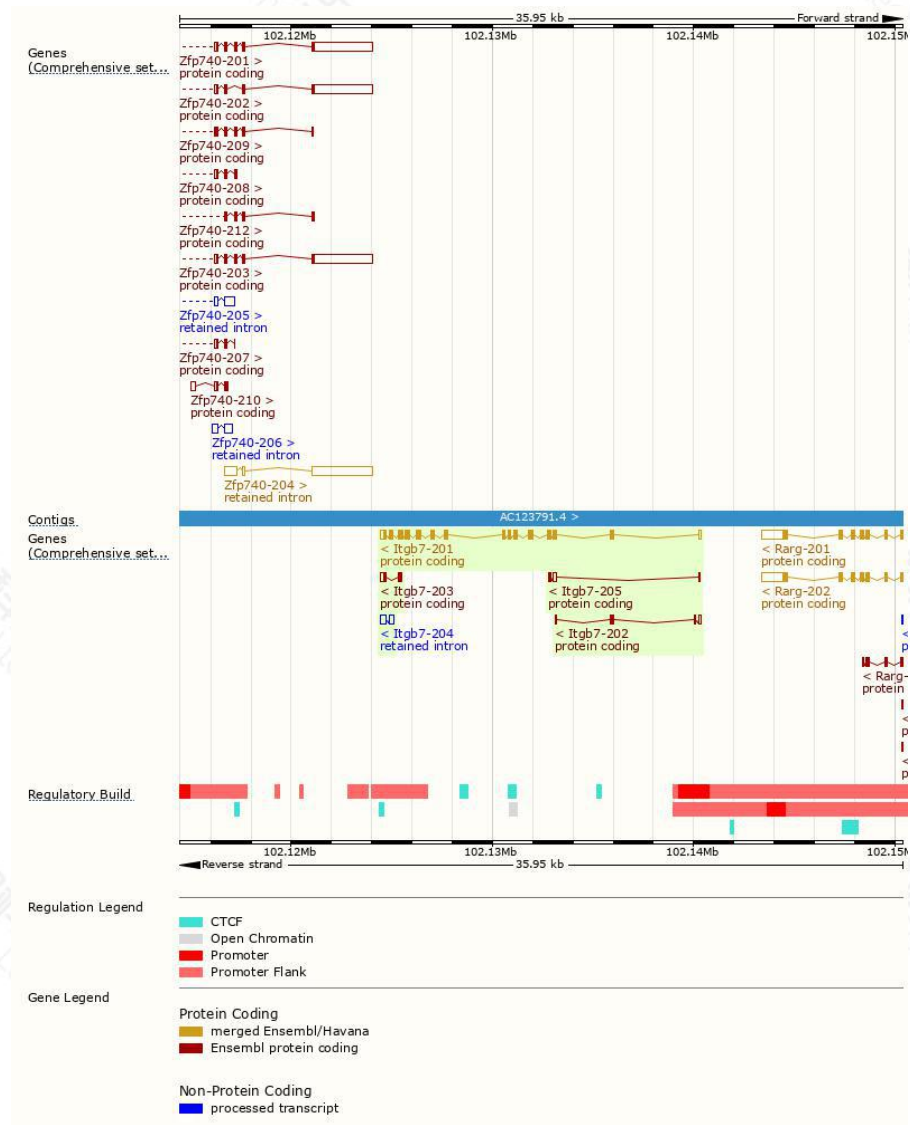
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Itgb7-201	ENSMUST0000001327.10	2683	806aa	Protein coding	CCDS49740	P26011	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Itgb7-203	ENSMUST00000229440.1	455	98aa	Protein coding	-	A0A2R8VI55	CDS 5' incomplete
Itgb7-202	ENSMUST00000127014.2	406	83aa	Protein coding	-	D3Z0L2	CDS 3' incomplete TSL:3
Itgb7-205	ENSMUST00000230652.1	358	10aa	Protein coding	-	A0A2R8VI38	CDS 3' incomplete
Itgb7-204	ENSMUST00000230550.1	449	No protein	Retained intron	-	-	

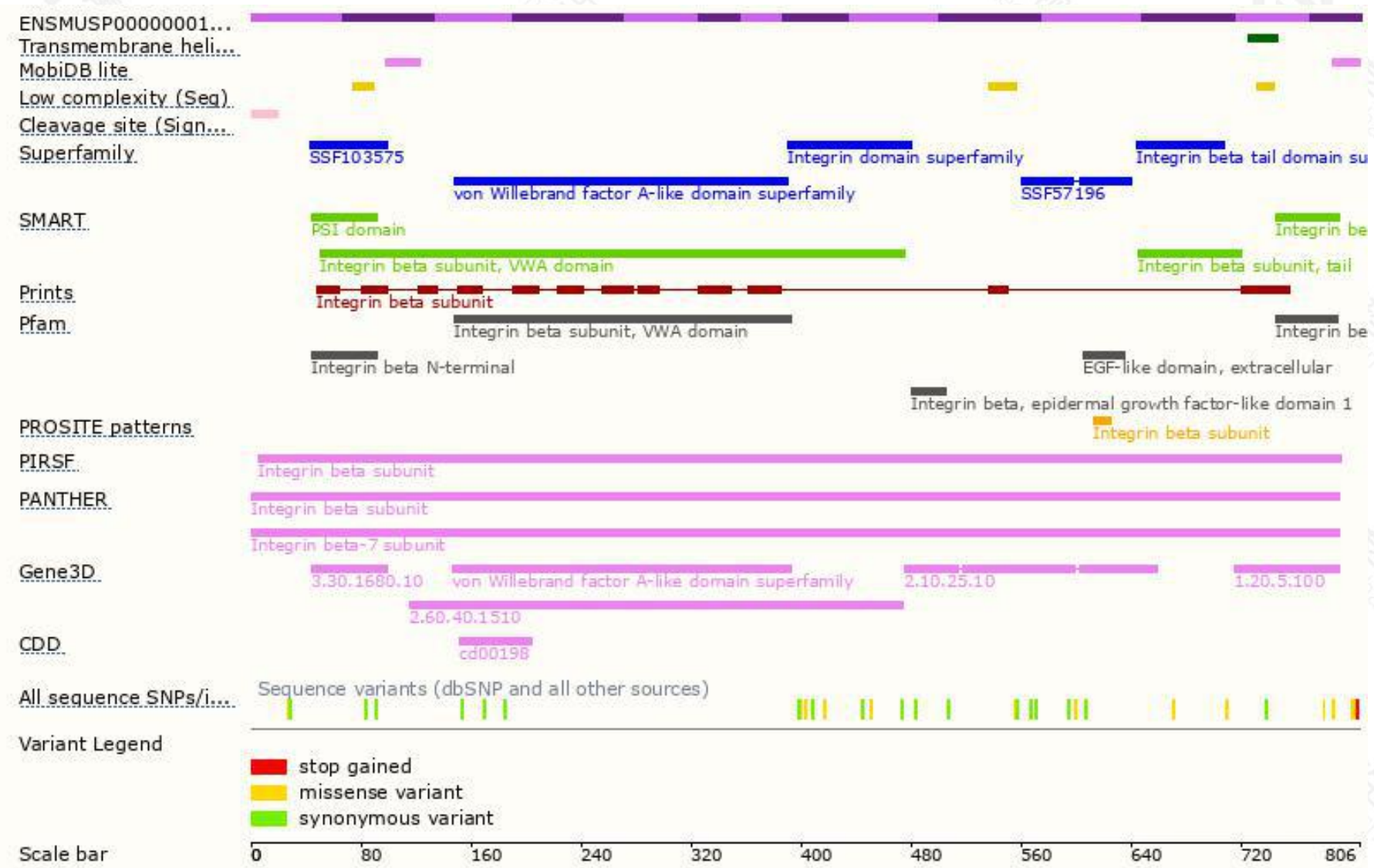
The strategy is based on the design of *Itgb7-201* transcript,the transcription is shown below:



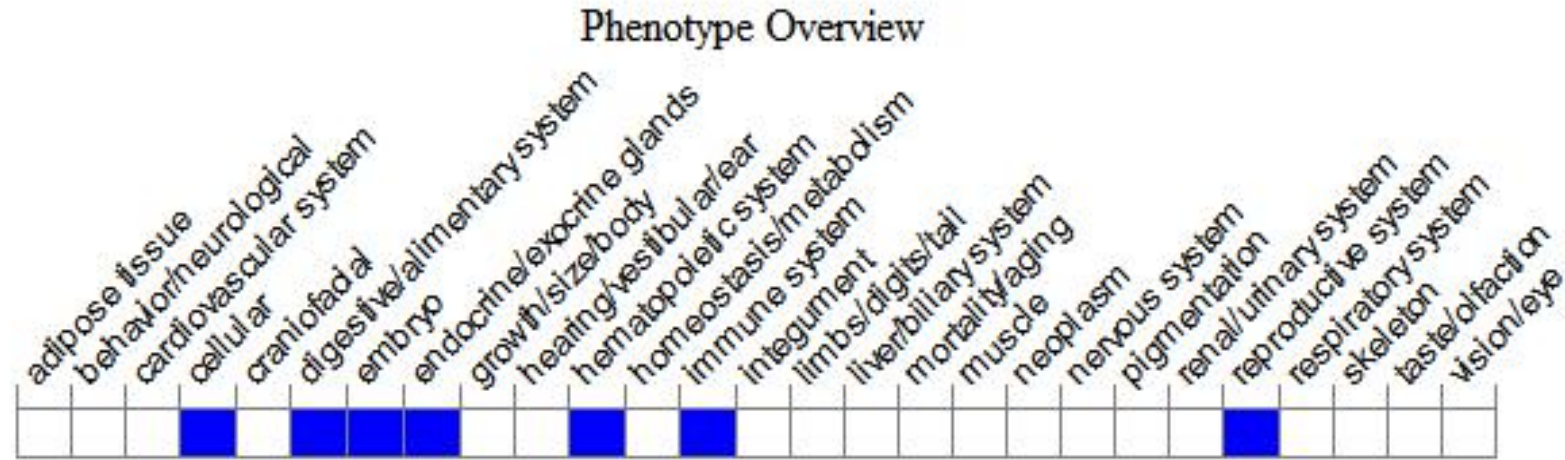
Genomic location distribution



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, homozygous null mice display hypoplasia of gut-associated lymph tissue due to defects in lymphocyte migration

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