

# *Itgal* Cas9-KO Strategy

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# Project Overview



**Project Name**

***Itgal***

**Project type**

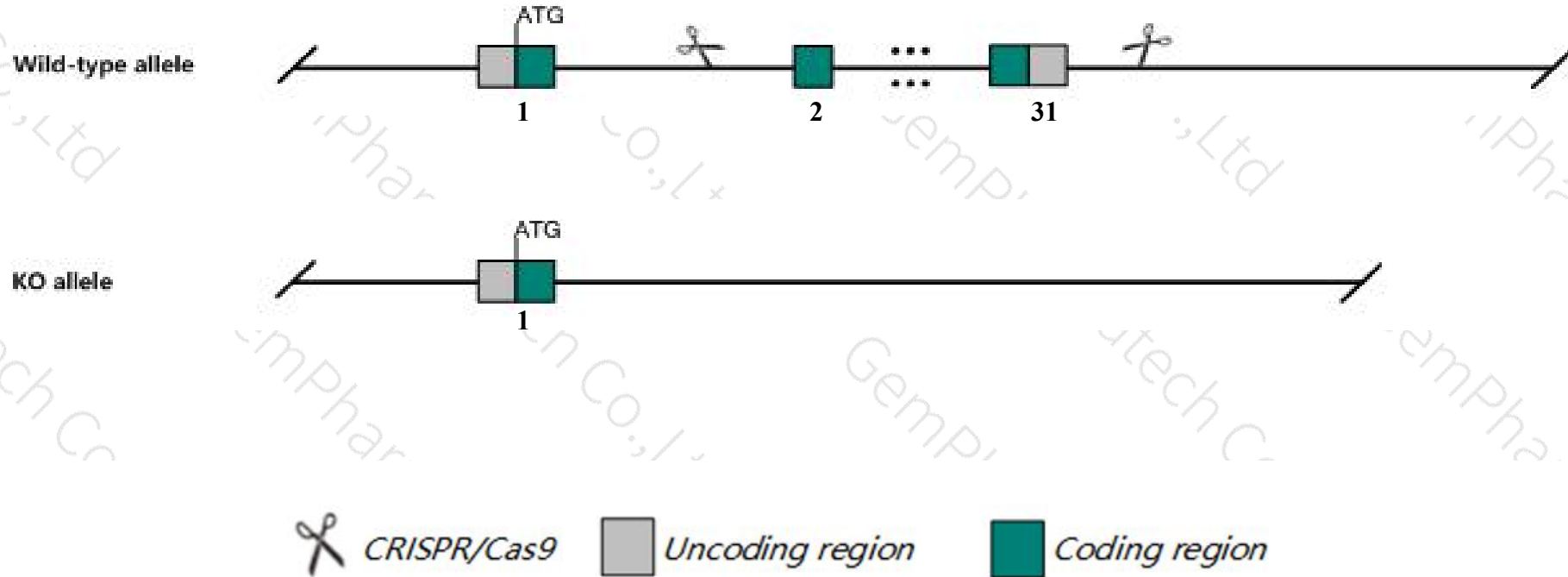
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Itgal* gene has 6 transcripts. According to the structure of *Itgal* gene, exon2-exon31 of *Itgal-201* (ENSMUST00000106306.8) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itgal* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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, Nullizygous mutations of this gene lead to increased leukocyte cell number, alter T cell activation, leukocyte migration and adhesion, spleen and lymph node morphology, and may affect humoral immune responses, metastatic potential, and susceptibility to endotoxin shock.
- The *Itgal* gene is located on the Chr7. 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)

## Itgal integrin alpha L [Mus musculus (house mouse)]

Gene ID: 16408, updated on 12-Feb-2019

### Summary



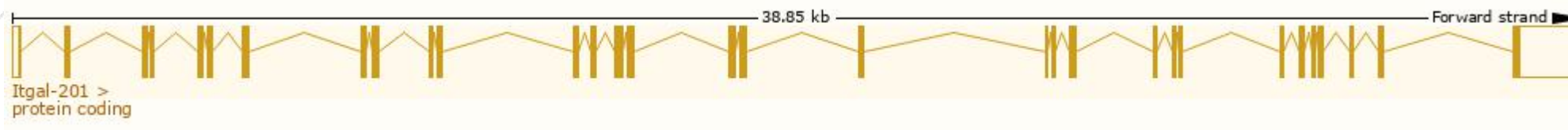
<b>Official Symbol</b>	Itgal provided by <a href="#">MGI</a>
<b>Official Full Name</b>	integrin alpha L provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:96606</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030830</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	(p180), Cd11a, LFA-1, LFA-1A, Ly-15, Ly-21
<b>Expression</b>	Biased expression in thymus adult (RPKM 94.8), spleen adult (RPKM 38.1) and 2 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

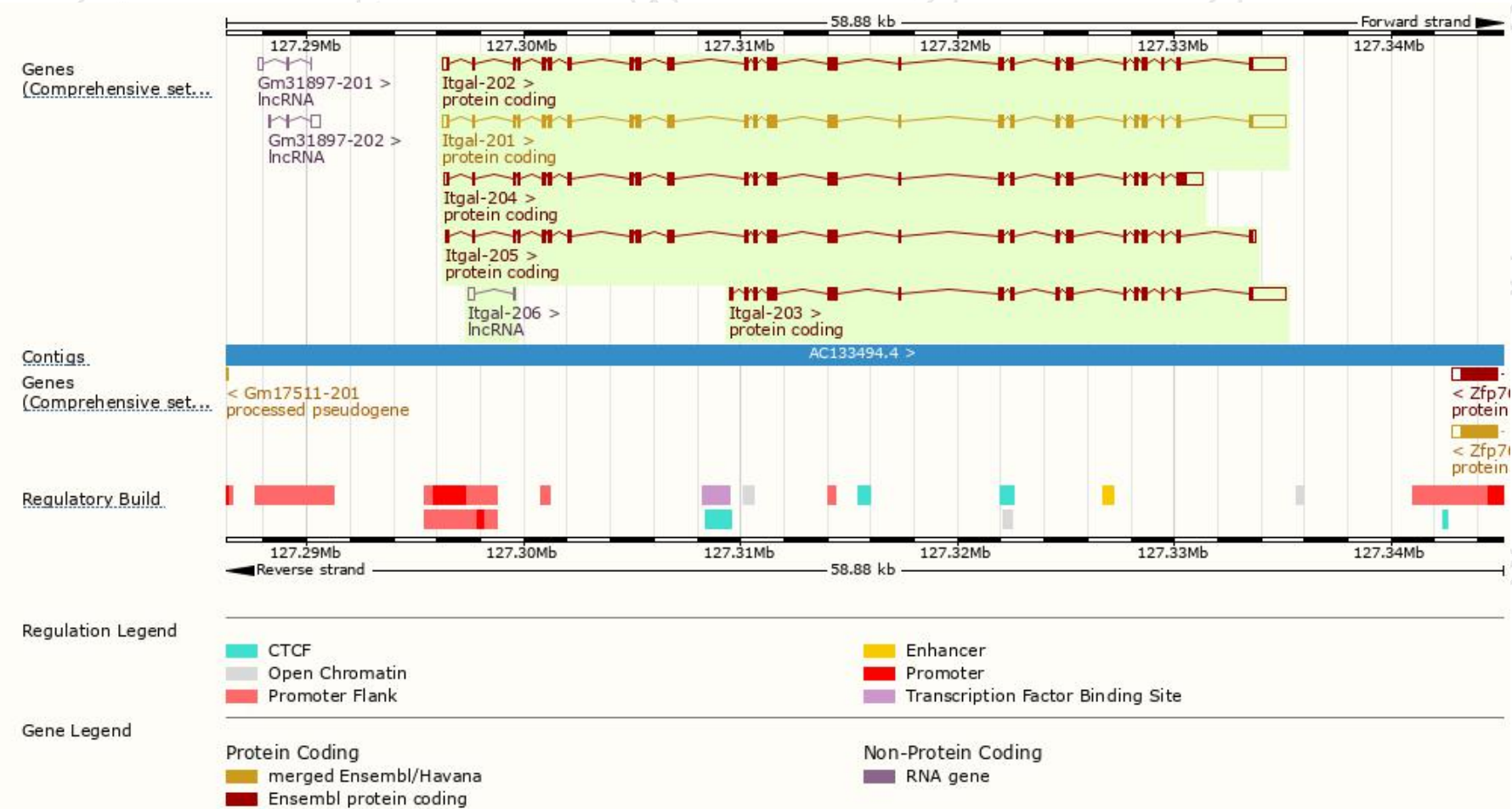
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
<b>Itgal-202</b>	<a href="#">ENSMUST00000117762.7</a>	5222	<a href="#">1161aa</a>	Protein coding	<a href="#">CCDS57588</a>	<a href="#">E9QNL8</a>	TSL:1 GENCODE basic APPRIS ALT2
<b>Itgal-201</b>	<a href="#">ENSMUST00000106306.8</a>	5195	<a href="#">1162aa</a>	Protein coding	<a href="#">CCDS57589</a>	<a href="#">E9Q5M7</a>	TSL:1 GENCODE basic APPRIS P4
<b>Itgal-204</b>	<a href="#">ENSMUST00000120857.7</a>	4533	<a href="#">1201aa</a>	Protein coding	-	<a href="#">D3Z627</a>	TSL:1 GENCODE basic APPRIS ALT2
<b>Itgal-203</b>	<a href="#">ENSMUST00000118405.1</a>	3909	<a href="#">765aa</a>	Protein coding	-	<a href="#">D3YW95</a>	TSL:1 GENCODE basic
<b>Itgal-205</b>	<a href="#">ENSMUST00000170971.7</a>	3662	<a href="#">1163aa</a>	Protein coding	-	<a href="#">P24063</a>	TSL:5 GENCODE basic APPRIS ALT2
<b>Itgal-206</b>	<a href="#">ENSMUST00000205695.1</a>	330	No protein	Processed transcript	-	-	TSL:3

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



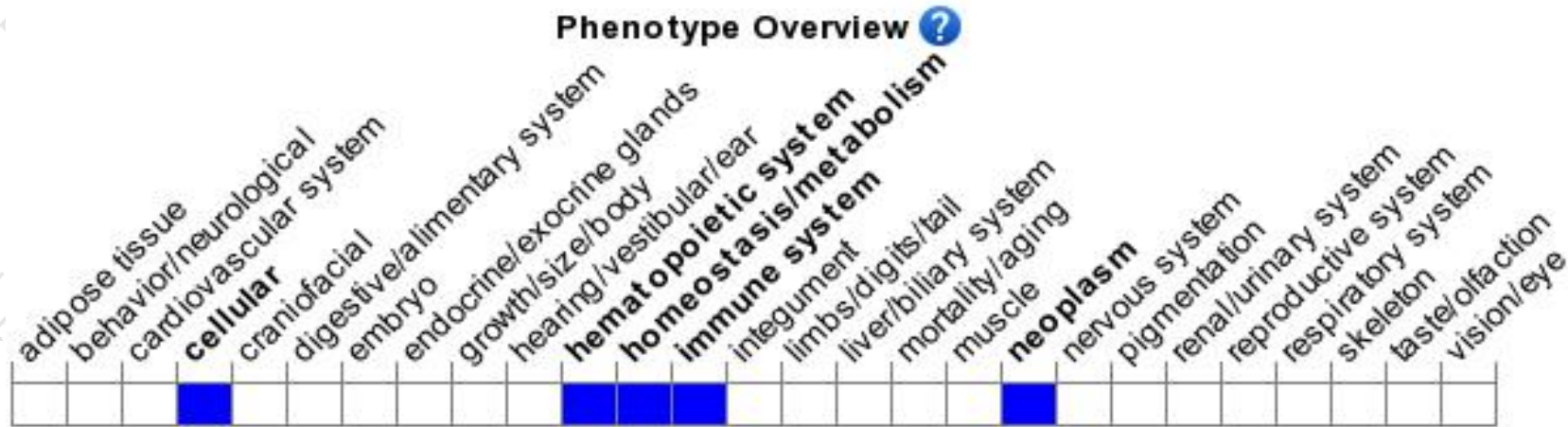
# Genomic location distribution



# 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, Nullizygous mutations of this gene lead to increased leukocyte cell number, alter T cell activation, leukocyte migration and adhesion, spleen and lymph node morphology, and may affect humoral immune responses, metastatic potential, and susceptibility to endotoxin shock.