

# ***Itga4 Cas9-CKO Strategy***

**Designer:**

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# Project Overview

**Project Name**

*Itga4*

**Project type**

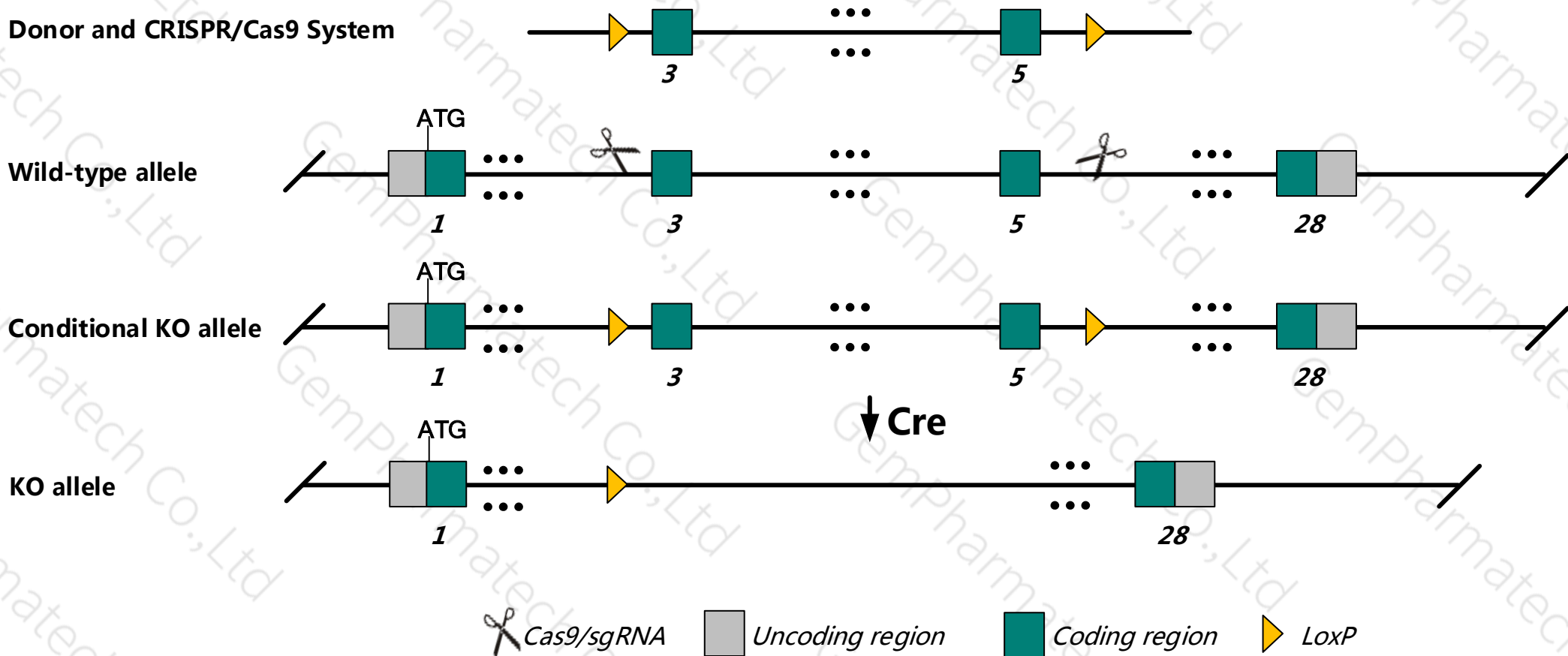
Cas9-CKO

**Animal background**

C57BL/6JGpt

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Itga4* gene. The schematic diagram is as follows:



- The *Itga4* gene has 5 transcripts. According to the structure of *Itga4* gene, exon3-exon5 of *Itga4*-201 transcript is recommended as the knockout region. The region contains 305bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itga4* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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.

- According to the existing MGI data , Mice homozygous for disruptions in this gene exhibit embryonic lethality either due to failure of chorioallantoic fusion or cardiac abnormalities, including hemorrhage around the heart and defects in epicardium formation.
- The *Itga4* gene is located on the Chr2. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

# Gene information ( NCBI )

## Itga4 integrin alpha 4 [ *Mus musculus* (house mouse) ]

Gene ID: 16401, updated on 7-May-2019

### Summary

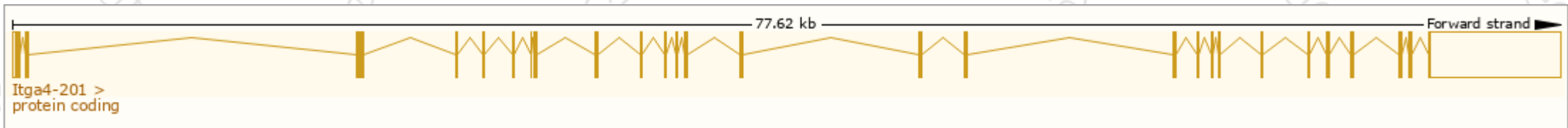
<b>Official Symbol</b>	Itga4 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	integrin alpha 4 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:96603</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000027009</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	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>	CD49D; Itga4B
<b>Expression</b>	Broad expression in liver E14 (RPKM 10.1), liver E14.5 (RPKM 9.6) and 17 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information ( Ensembl )

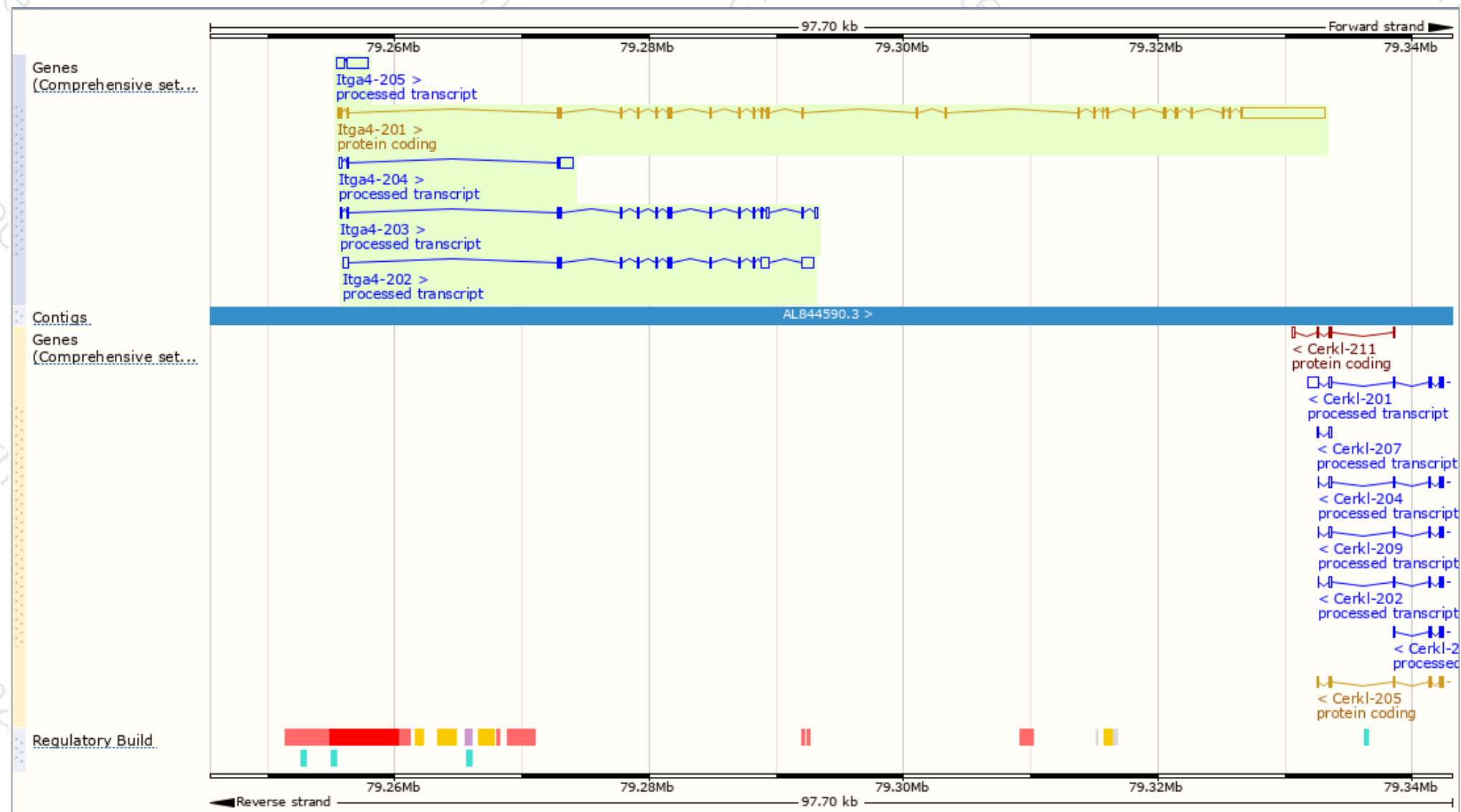
The gene has 5 transcripts, and all transcripts are shown below :

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
<a href="#">Itga4-201</a>	<a href="#">ENSMUST00000099972.4</a>	9767	<a href="#">1032aa</a>	Protein coding	<a href="#">CCDS16168</a>	<a href="#">Q792F9</a>	TSL:1 GENCODE basic APPRIS P1
<a href="#">Itga4-202</a>	<a href="#">ENSMUST00000126312.1</a>	2936	No protein	Processed transcript	-	-	TSL:2
<a href="#">Itga4-205</a>	<a href="#">ENSMUST00000155105.1</a>	2314	No protein	Processed transcript	-	-	TSL:1
<a href="#">Itga4-203</a>	<a href="#">ENSMUST00000135919.7</a>	1826	No protein	Processed transcript	-	-	TSL:1
<a href="#">Itga4-204</a>	<a href="#">ENSMUST00000141094.7</a>	1508	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Itga4-201* transcript, The transcription is shown below



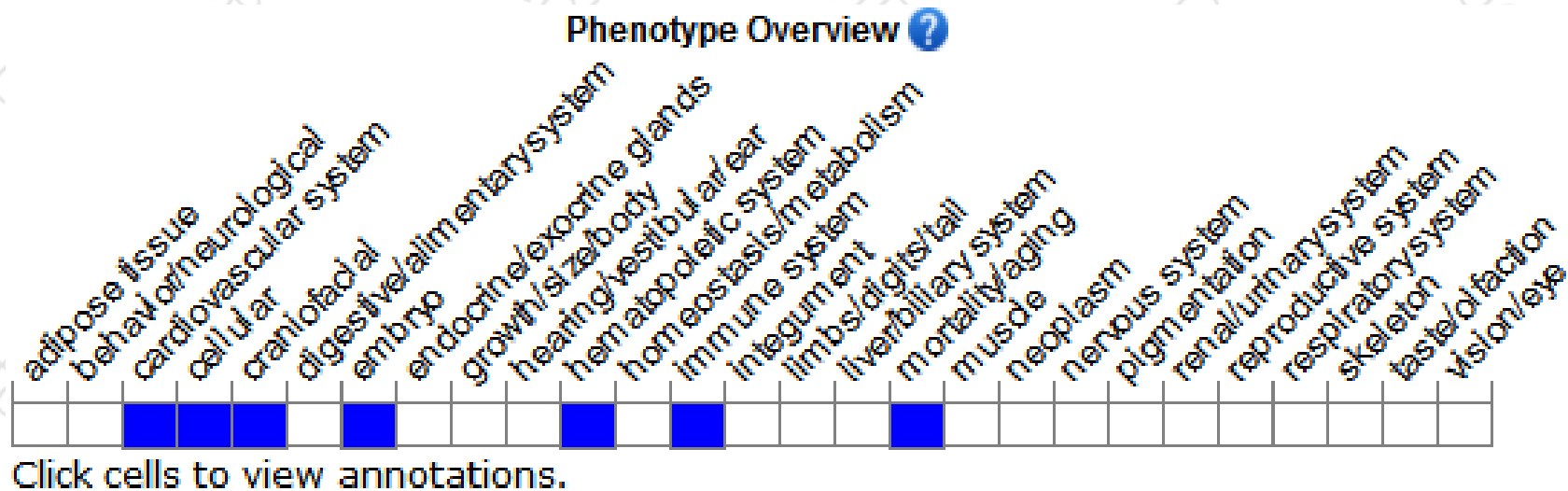
# Genomic location distribution



# 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 disruptions in this gene exhibit embryonic lethality either due to failure of chorioallantoic fusion or cardiac abnormalities, including hemorrhage around the heart and defects in epicardium formation.

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