

# *Cd79a* Cas9-KO Strategy

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# Project Overview



**Project Name**

***Cd79a***

**Project type**

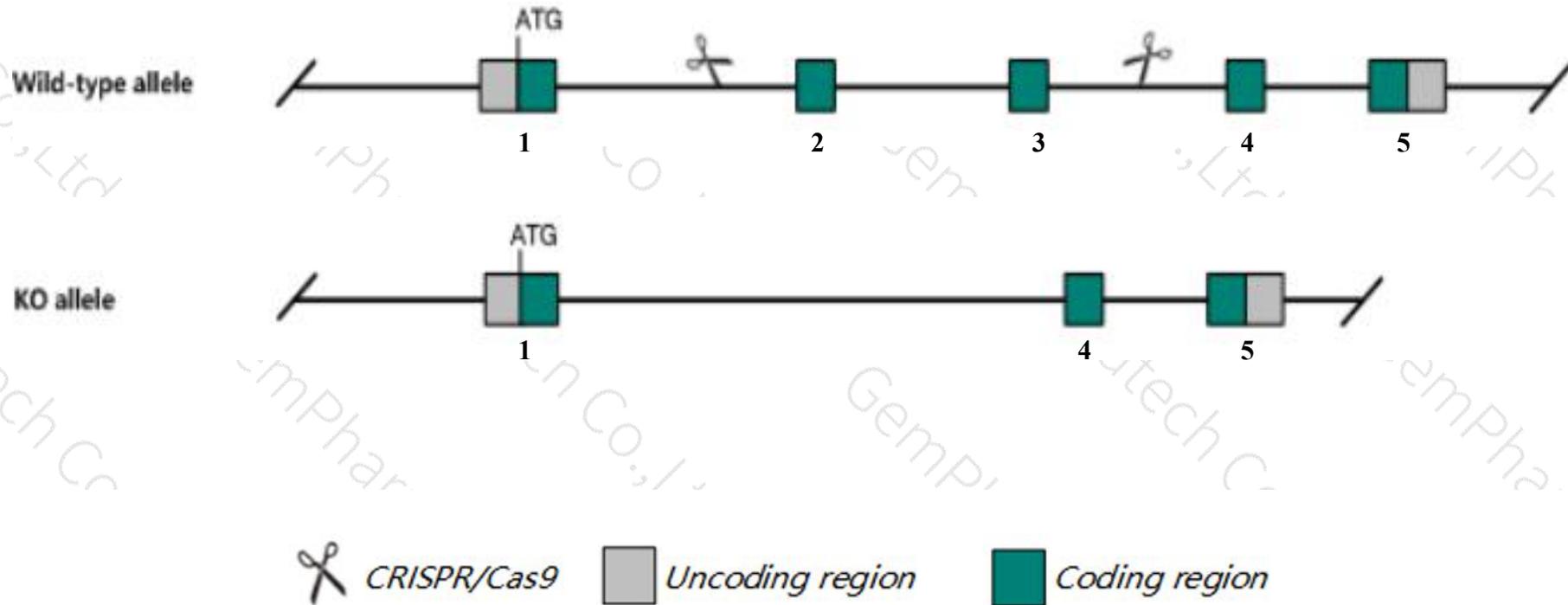
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd79a* gene. The schematic diagram is as follows:



- The *Cd79a* gene has 1 transcript. According to the structure of *Cd79a* gene, exon2-exon3 of *Cd79a-201* (ENSMUST00000003469.7) transcript is recommended as the knockout region. The region contains 413bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd79a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygotes for targeted null mutations exhibit arrested development of b cells at the pro-b cell stage due to diminished signaling of the b cell receptor.
- The KO region is 3kb away from *Arhgef1* gene, so *Arhgef1* gene may be affected.
- The *Cd79a* 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)

## Cd79a CD79A antigen (immunoglobulin-associated alpha) [Mus musculus (house mouse)]

Gene ID: 12518, updated on 13-Mar-2020

### Summary



**Official Symbol** Cd79a provided by [MGI](#)

**Official Full Name** CD79A antigen (immunoglobulin-associated alpha) provided by [MGI](#)

**Primary source** [MGI:MGI:101774](#)

**See related** [Ensembl:ENSMUSG00000003379](#)

**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** Ig-alpha, Iga, Igalpha, Ly-54, Ly54, mb-1

**Expression** Biased expression in spleen adult (RPKM 536.2), mammary gland adult (RPKM 128.1) and 1 other tissue [See more](#)

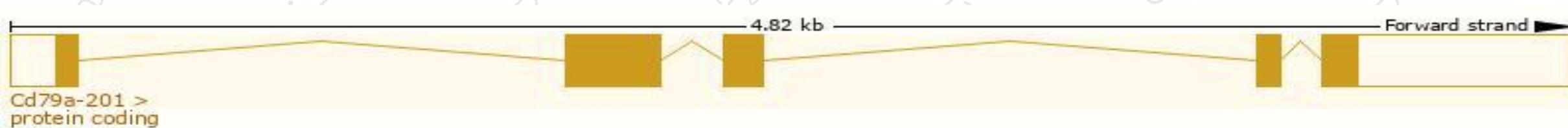
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

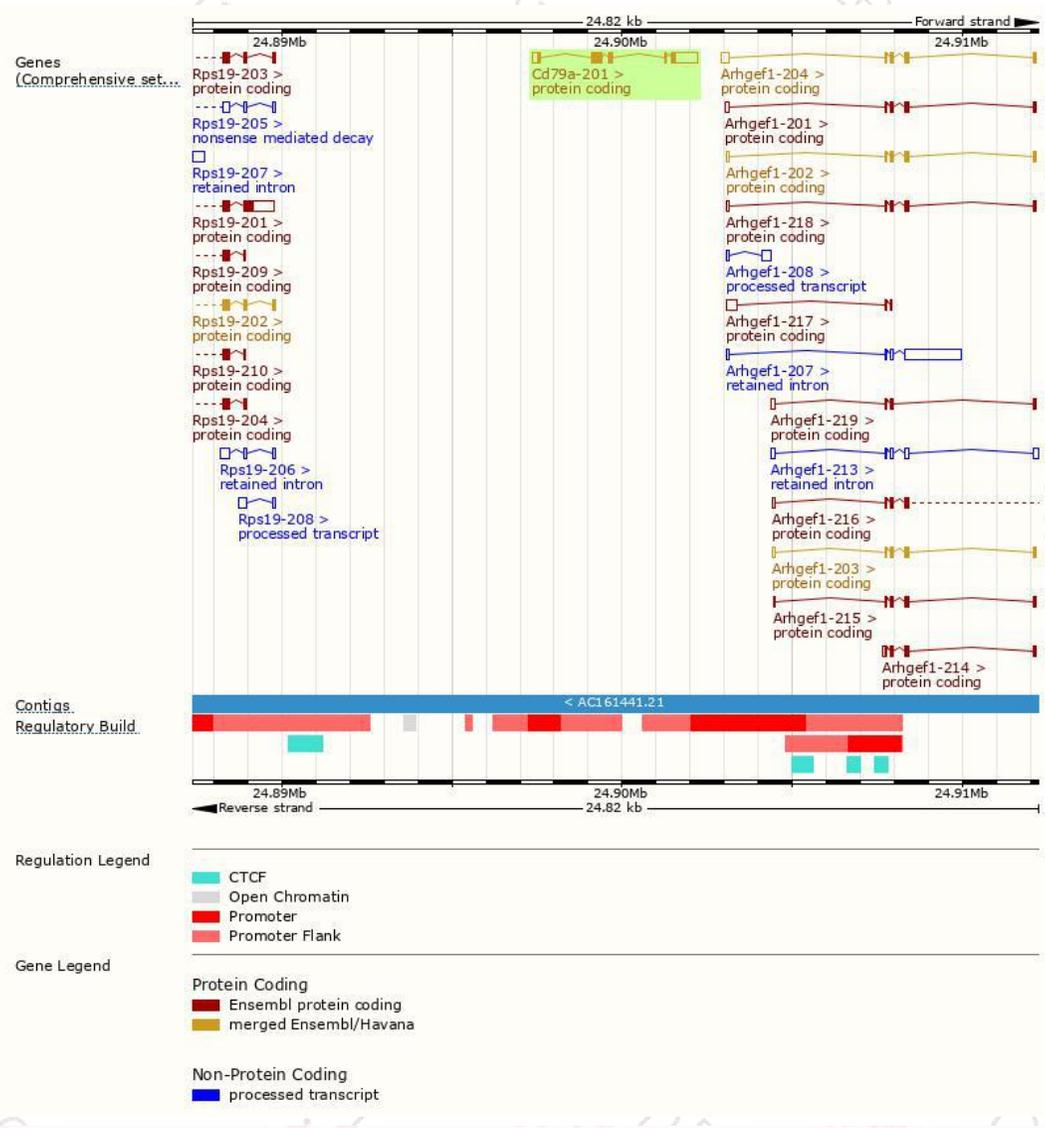
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd79a-201	<a href="#">ENSMUST00000003469.7</a>	1457	<a href="#">220aa</a>	Protein coding	<a href="#">CCDS20967</a>	<a href="#">P11911</a>	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

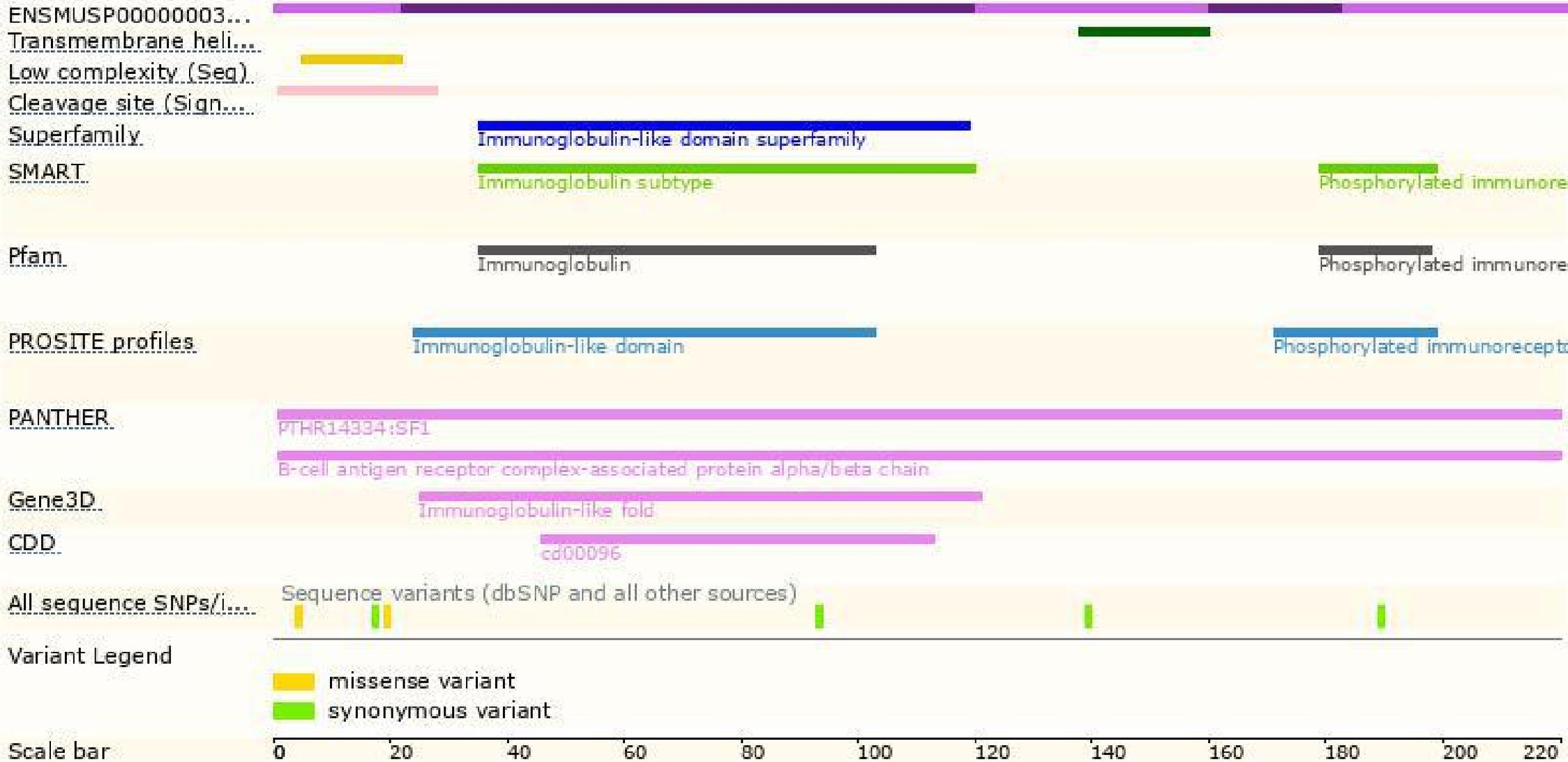
The strategy is based on the design of *Cd79a-201* transcript, the transcription is shown below



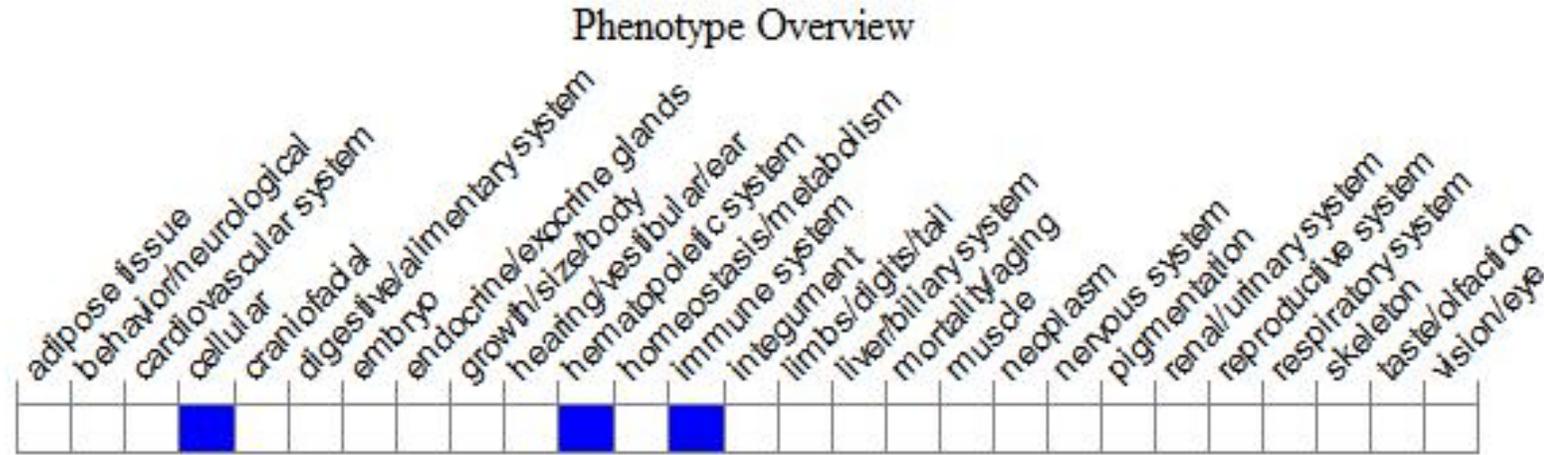
# Genomic location distribution



# 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, homozygotes for targeted null mutations exhibit arrested development of B cells at the pro-B cell stage due to diminished signaling of the B cell receptor.

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

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