

Bcl11a Cas9-CKO Strategy

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Project Overview

Project Name

Bcl11a

Project type

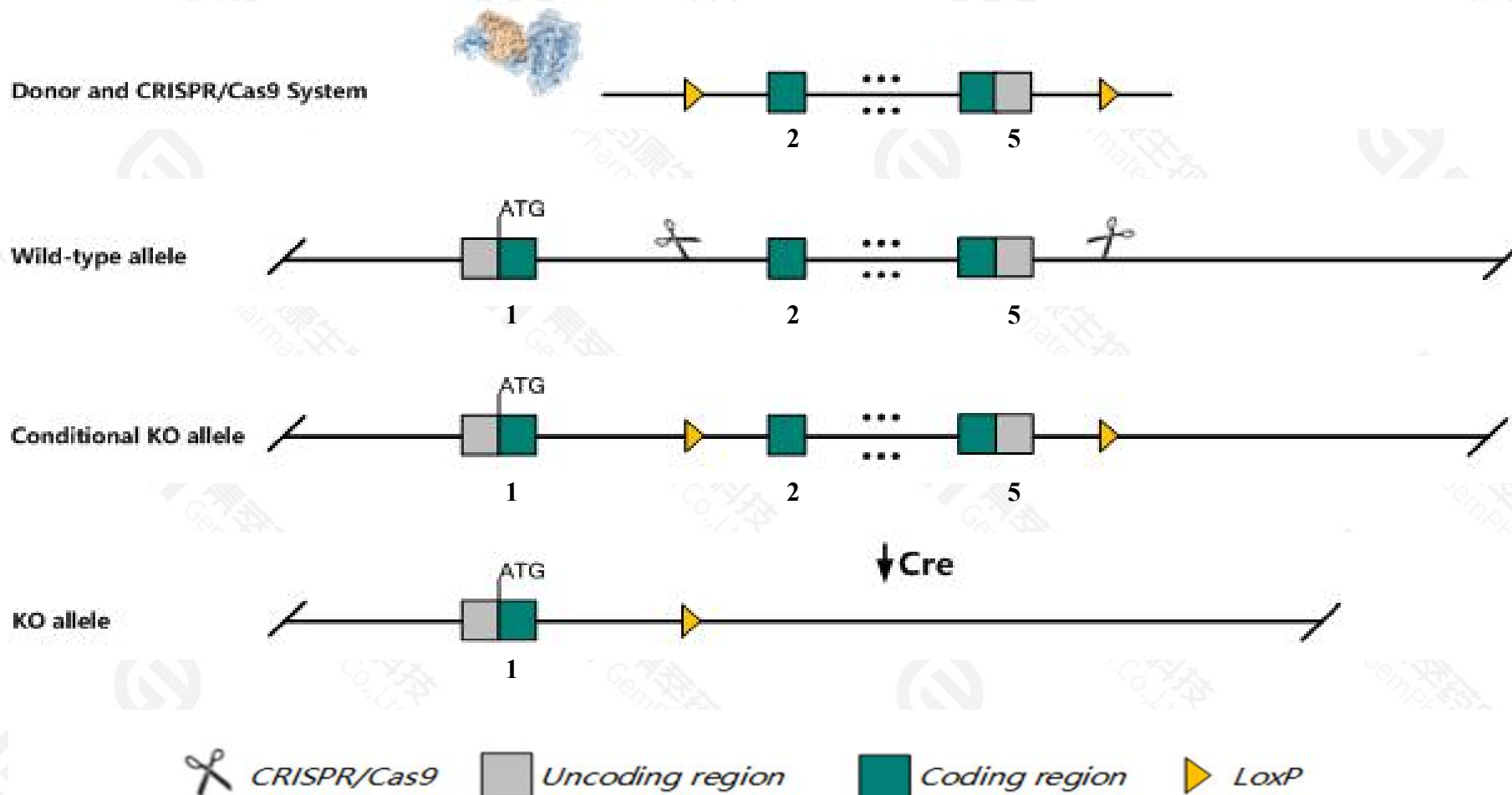
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bcl11a* gene. The schematic diagram is as follows:



- The *Bcl11a* gene has 6 transcripts. According to the structure of *Bcl11a* gene, exon2-exon5 of *Bcl11a-201*(ENSMUST00000000881.13) transcript is recommended as the knockout region. The region contains 2267bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bcl11a* 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 and cell types.

- According to the existing MGI data, homozygous mutation of this gene results in B cell deficiency, alteration of T cell types, and neonatal lethality.
- The KO region contains functional region of *Gm12064*, *4930538E20Rik*, *4930538E20Rik* gene. Knockout the region may affect the function of *Gm12064*, *4930538E20Rik*, *4930538E20Rik* gene.
- The *Bcl11a* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Bcl11a B cell CLL/lymphoma 11A (zinc finger protein) [Mus musculus (house mouse)]

Gene ID: 14025, updated on 13-Mar-2020

Summary

Official Symbol Bcl11a provided by [MGI](#)

Official Full Name B cell CLL/lymphoma 11A (zinc finger protein) provided by [MGI](#)

Primary source [MGI:MGI:106190](#)

See related [Ensembl:ENSMUSG000000000861](#)

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 2810047E18Rik, BCL-11A, Ctip1, D930021L15Rik, Evi9, Evi9a, Evi9b, Evi9c, mKIAA1809

Expression Biased expression in CNS E14 (RPKM 11.6), CNS E18 (RPKM 11.0) and 13 other tissues [See more](#)

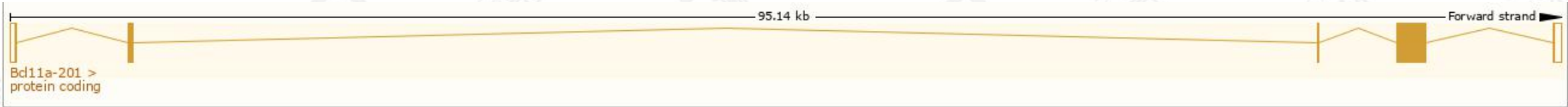
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

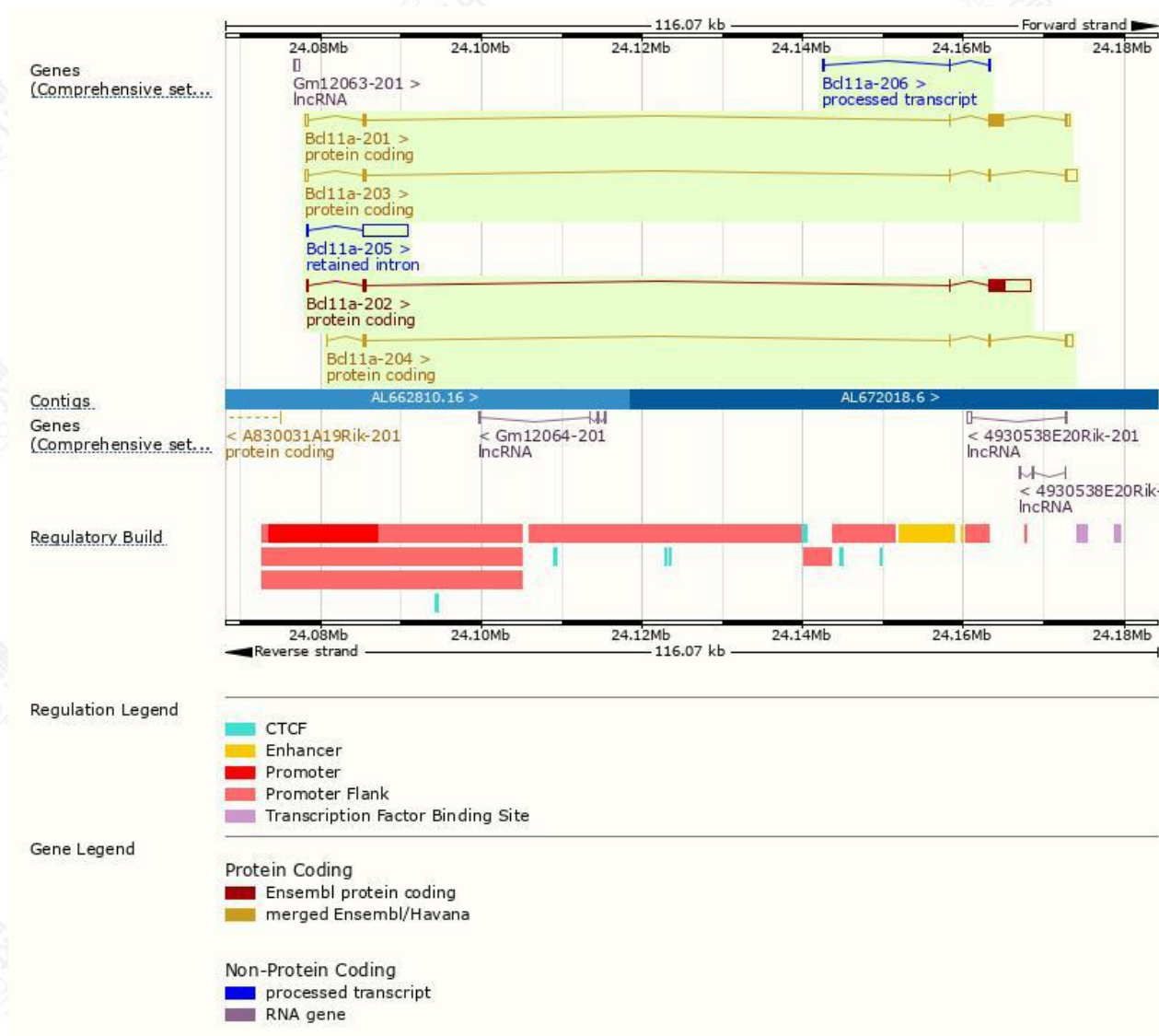
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bcl11a-202	ENSMUST00000109514.7	5989	835aa	Protein coding	CCDS56764	Q5STS9	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
Bcl11a-201	ENSMUST00000000881.12	3061	773aa	Protein coding	CCDS24483	Q9QYE3	TSL:1 GENCODE basic
Bcl11a-203	ENSMUST00000109516.7	2329	243aa	Protein coding	CCDS48758	Q9QYE3	TSL:1 GENCODE basic
Bcl11a-204	ENSMUST00000118955.1	1505	191aa	Protein coding	CCDS48759	Q9QYE3	TSL:1 GENCODE basic
Bcl11a-206	ENSMUST00000127494.1	566	No protein	Processed transcript	-	-	TSL:5
Bcl11a-205	ENSMUST00000124148.1	5885	No protein	Retained intron	-	-	TSL:1

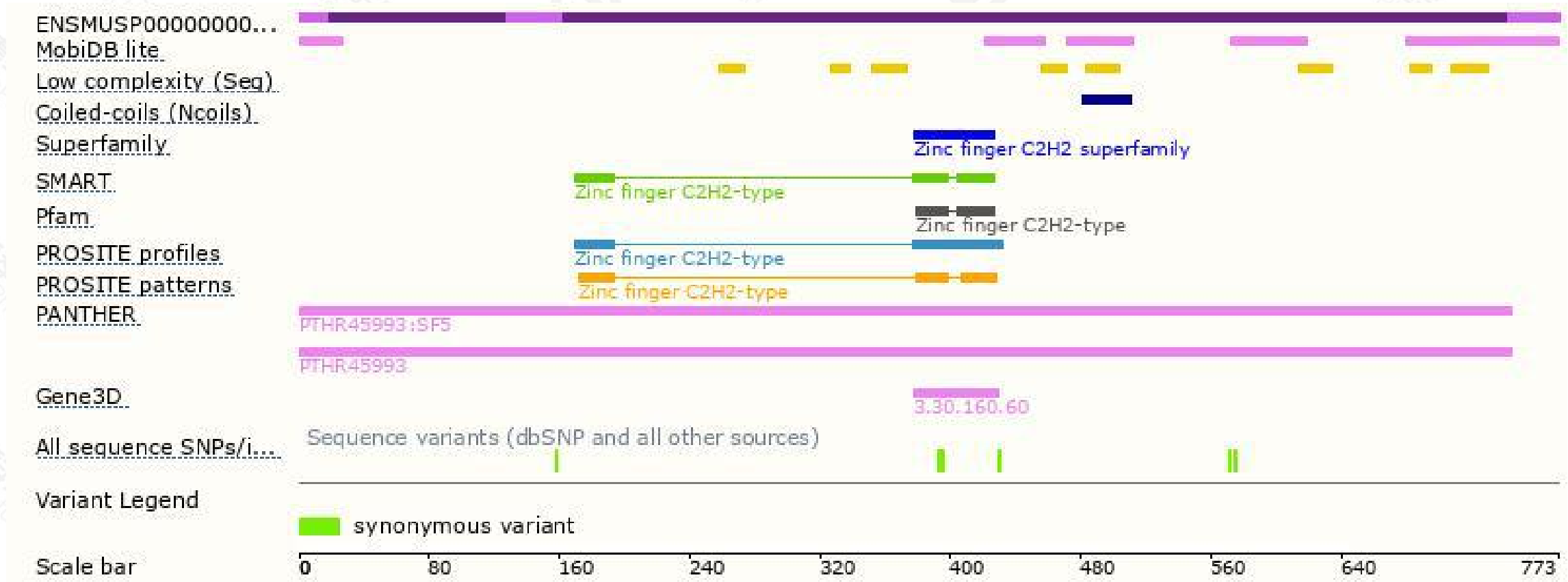
The strategy is based on the design of *Bcl11a-201* transcript,the transcription is shown below:



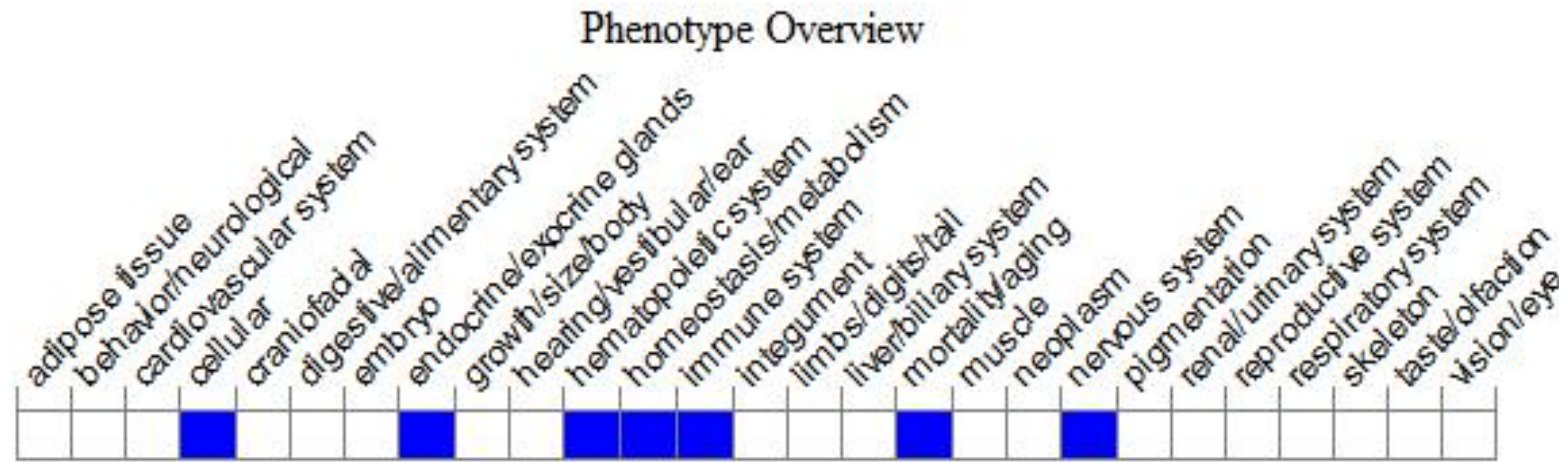
Genomic location distribution



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 mutation of this gene results in B cell deficiency, alteration of T cell types, and neonatal lethality.

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

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