Bclaf1 Cas9-CKO Strategy

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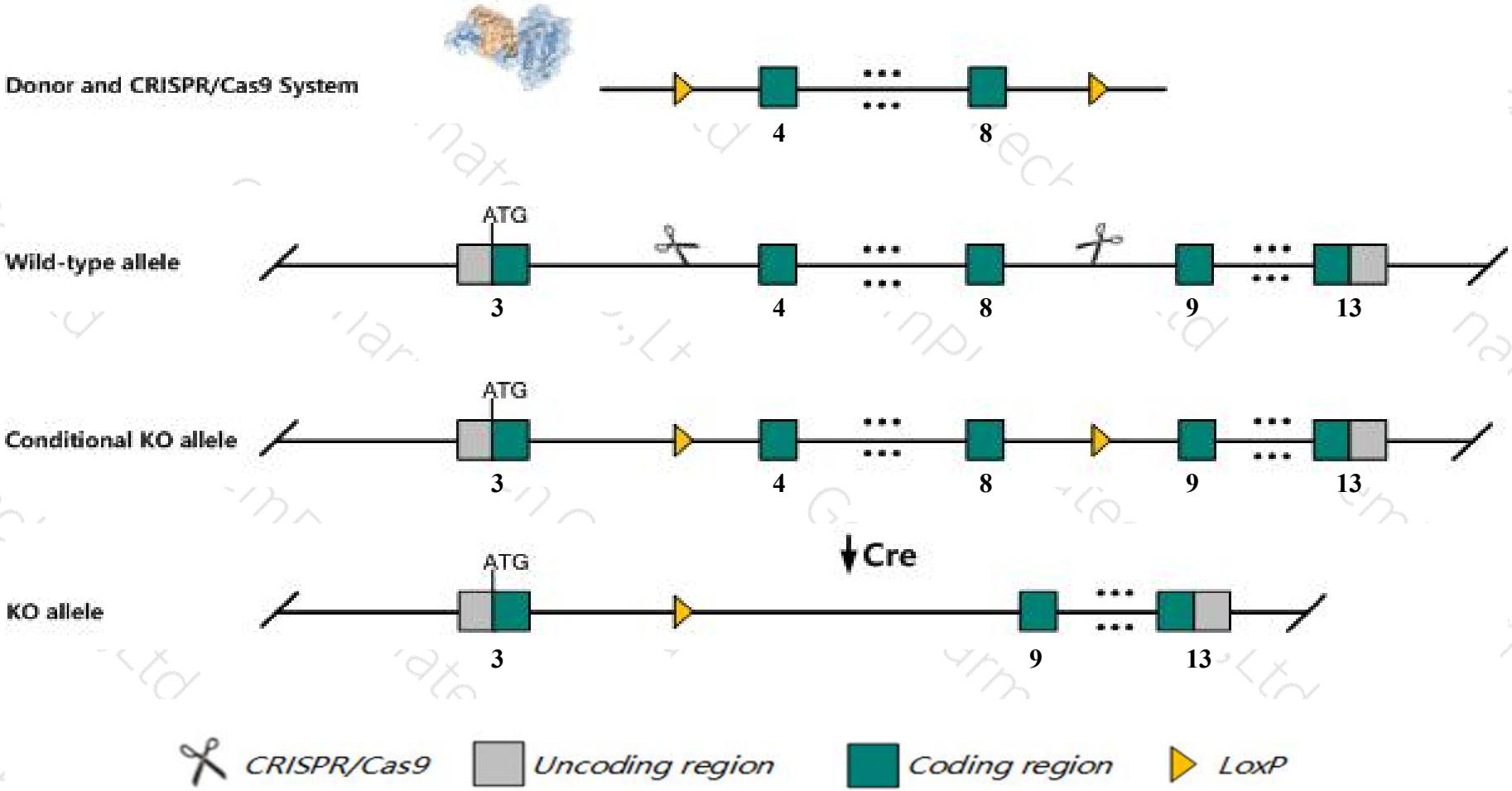
Project Overview

Project Name	***Bclaf1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bclaf1* gene. The schematic diagram is as follows:



Technical routes

- The *Bclaf1* gene has 12 transcripts. According to the structure of *Bclaf1* gene, exon4-exon8 of *Bclaf1-201* (ENSMUST00000043881.11) transcript is recommended as the knockout region.The region contains 1933bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Bclaf1* gene. The brief process is as follows:CRISPR/Cas9 system 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.

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit postnatal lethality, impaired lung development, and T cell and B cell homeostasis abnormalities.

- The *Bclaf1* gene is located on the Chr10. 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）

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Bclaf1 BCL2-associated transcription factor 1 [Mus musculus (house mouse)]

Gene ID: 72567, updated on 31-Jan-2019

Summary

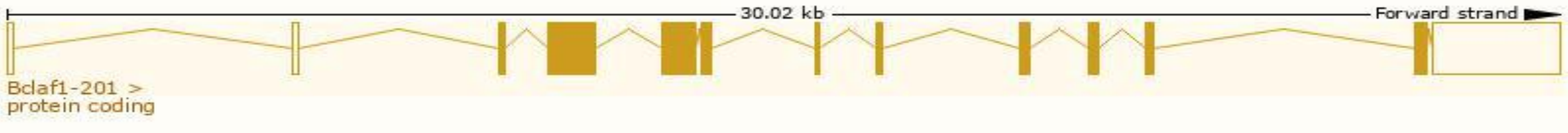
Official Symbol	Bclaf1 provided by MGI
Official Full Name	BCL2-associated transcription factor 1 provided by MGI
Primary source	MGI:MGI:1917580
See related	Ensembl:ENSMUSG00000037608
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610102K23Rik, 2700025J07Rik, 2810454G14Rik, 5730534O06Rik, AI450190, AW556225, Btf, mKIAA0164
Expression	Ubiquitous expression in CNS E11.5 (RPKM 24.7), CNS E14 (RPKM 17.4) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

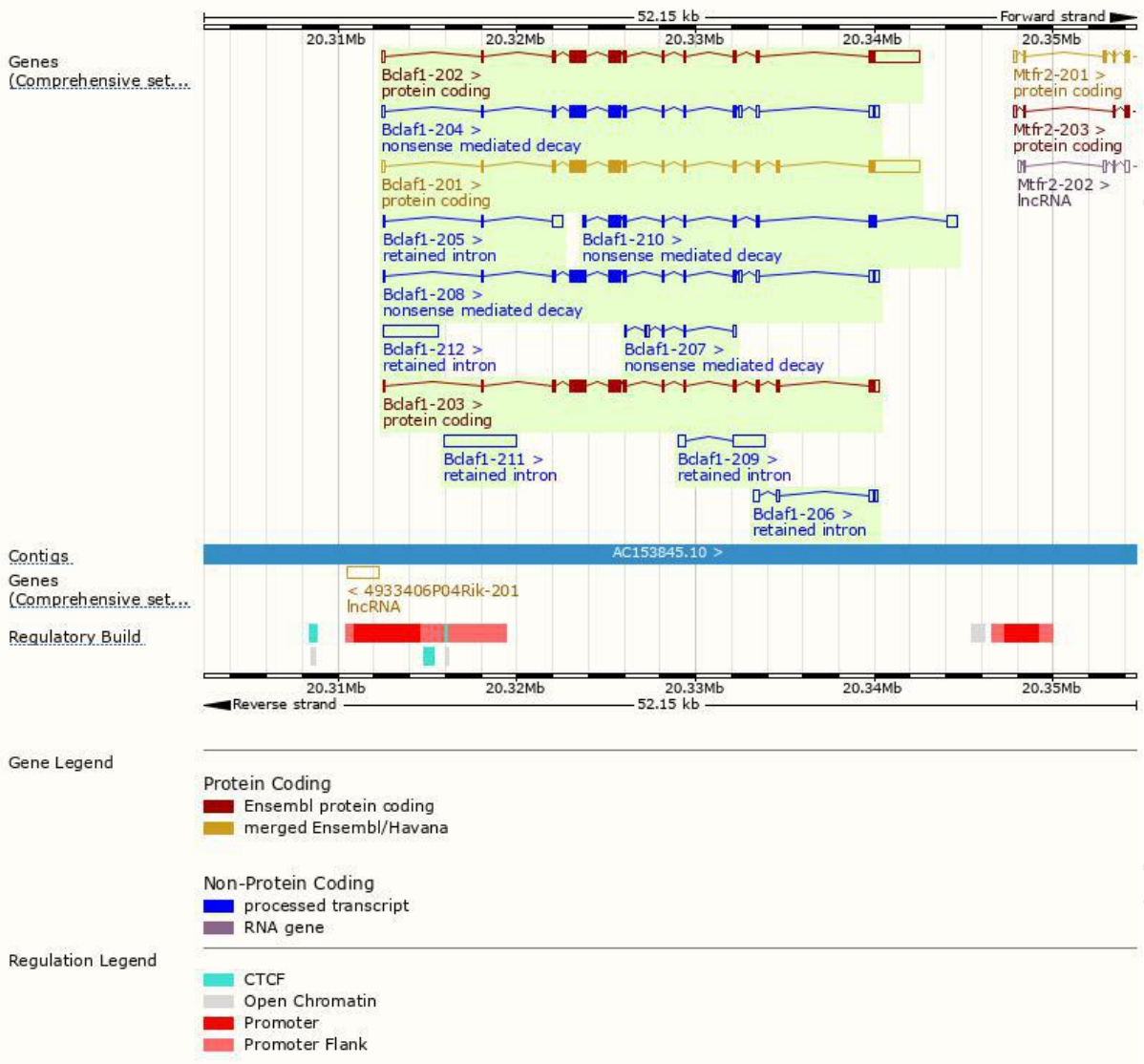
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bclaf1-201	ENSMUST00000043881.11	5437	919aa	Protein coding	CCDS35858	Q8K019	TSL:1 GENCODE basic APPRIS ALT2
Bclaf1-202	ENSMUST00000092678.9	5307	870aa	Protein coding	CCDS23721	F8WI22	TSL:1 GENCODE basic APPRIS P3
Bclaf1-203	ENSMUST00000185800.6	3142	917aa	Protein coding	CCDS78798	Q8K019	TSL:1 GENCODE basic APPRIS ALT2
Bclaf1-204	ENSMUST00000186100.6	3231	750aa	Nonsense mediated decay	-	A0A087WQA0	TSL:1
Bclaf1-208	ENSMUST00000190156.6	3164	748aa	Nonsense mediated decay	-	Q8K019	TSL:1
Bclaf1-210	ENSMUST00000191438.1	2383	583aa	Nonsense mediated decay	-	A0A087WRN1	CDS 5' incomplete TSL:1
Bclaf1-207	ENSMUST00000189158.1	647	43aa	Nonsense mediated decay	-	A0A087WRF8	CDS 5' incomplete TSL:3
Bclaf1-211	ENSMUST00000215262.1	3988	No protein	Retained intron	-	-	TSL:NA
Bclaf1-212	ENSMUST00000216560.1	3064	No protein	Retained intron	-	-	TSL:NA
Bclaf1-209	ENSMUST00000191143.1	2151	No protein	Retained intron	-	-	TSL:1
Bclaf1-206	ENSMUST00000188546.1	834	No protein	Retained intron	-	-	TSL:1
Bclaf1-205	ENSMUST00000187338.6	774	No protein	Retained intron	-	-	TSL:2

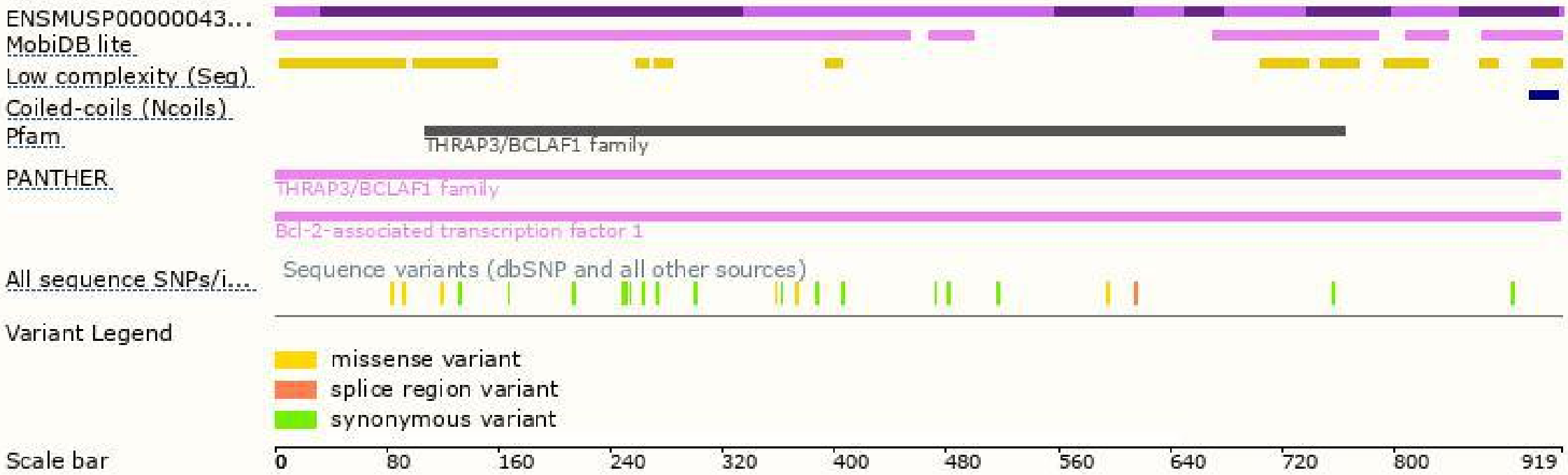
The strategy is based on the design of *Bclaf1-201* transcript,The transcription is shown below



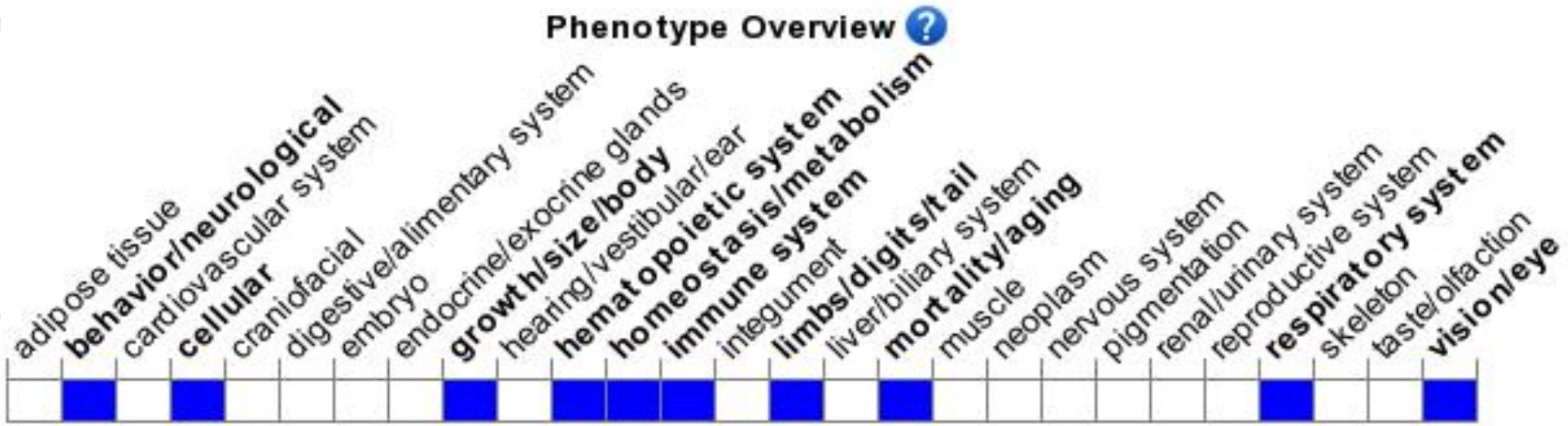
Genomic location distribution



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 a knock-out allele exhibit postnatal lethality, impaired lung development, and T cell and B cell homeostasis abnormalities.

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

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