

# ***Bclaf1*** Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-9-30**

# Project Overview

**Project Name**

*Bclaf1*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)

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

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

### Summary



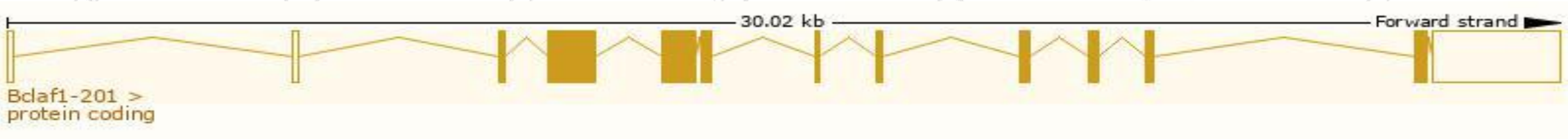
|                           |                                                                                                                                                                           |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Official Symbol</b>    | Bclaf1 provided by <a href="#">MGI</a>                                                                                                                                    |
| <b>Official Full Name</b> | BCL2-associated transcription factor 1 provided by <a href="#">MGI</a>                                                                                                    |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1917580</a>                                                                                                                                           |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG000000037608</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>      | 2610102K23Rik, 2700025J07Rik, 2810454G14Rik, 5730534O06Rik, AI450190, AW556225, Btf, mKIAA0164                                                                            |
| <b>Expression</b>         | Ubiquitous expression in CNS E11.5 (RPKM 24.7), CNS E14 (RPKM 17.4) and 24 other tissues <a href="#">See more</a>                                                         |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

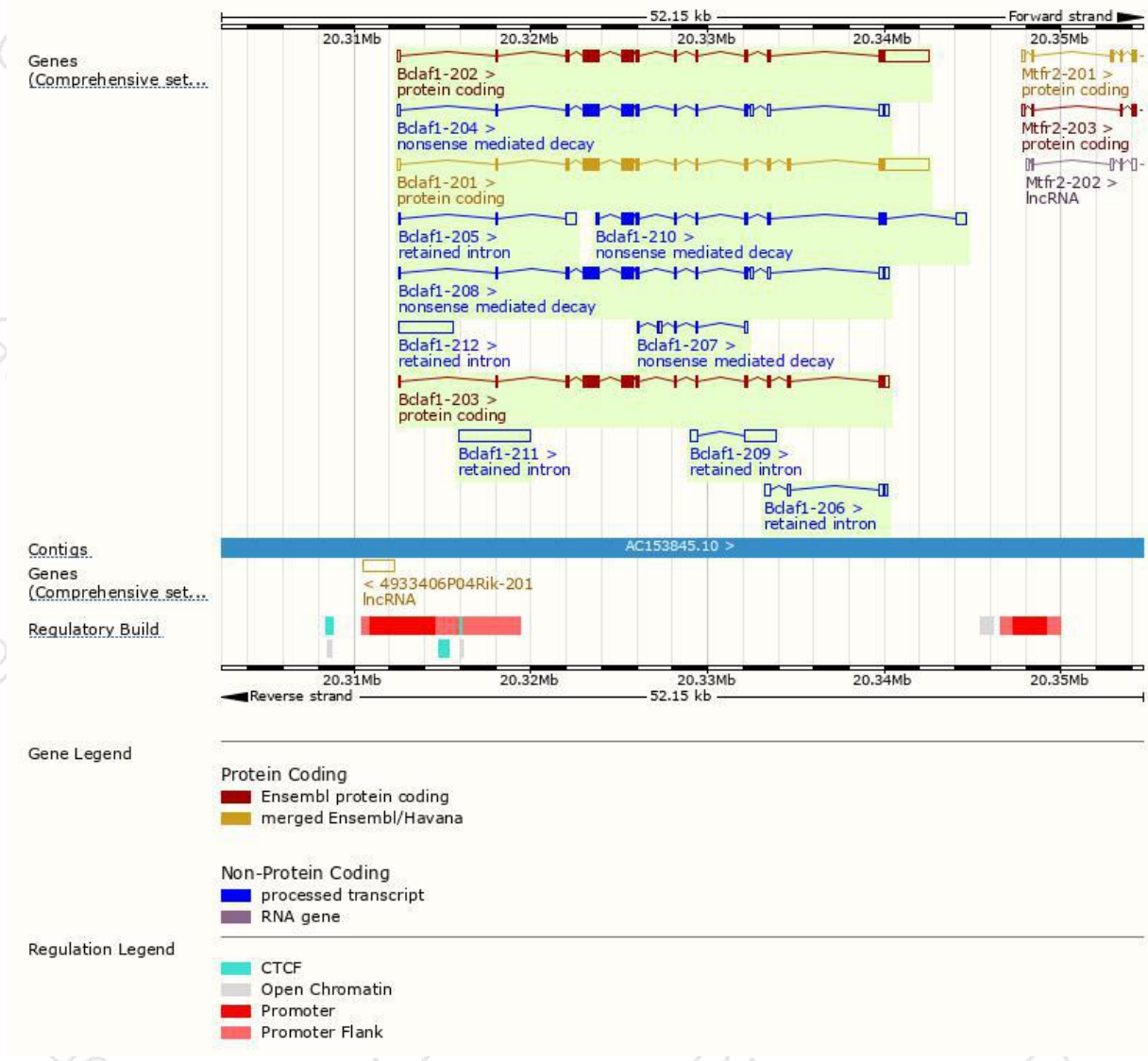
The gene has 12 transcripts,all transcripts are shown below:

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

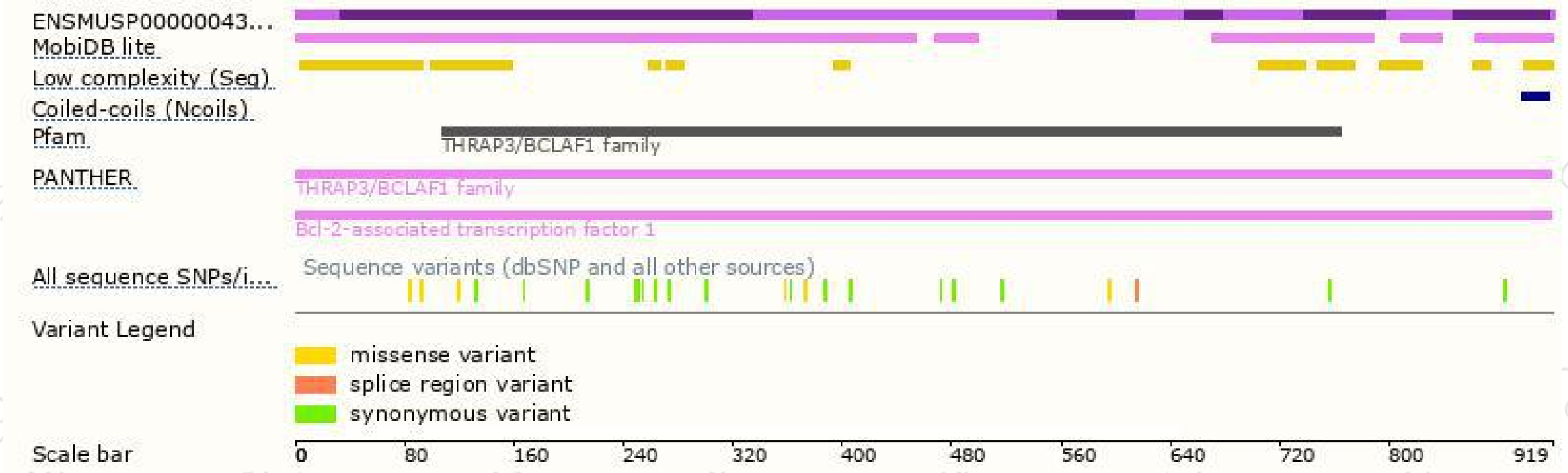
The strategy is based on the design of *Bclaf1-201* transcript,The transcription is shown below



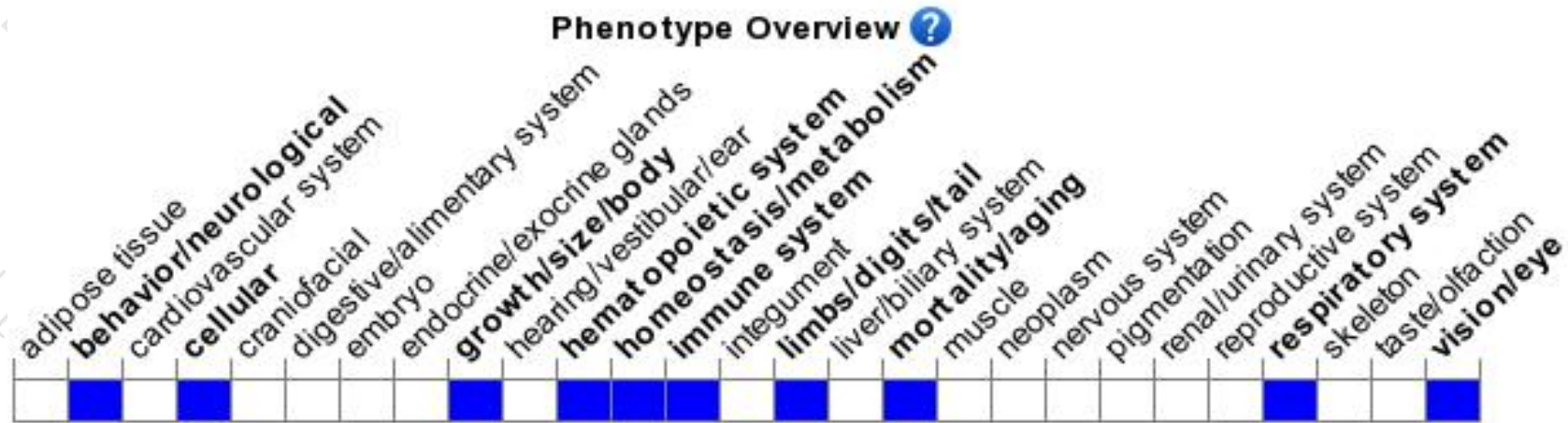
# Genomic location distribution



# 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.

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

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