

Cbll1 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

Design Date:

2020-4-17

Project Overview

Project Name

Cbll1

Project type

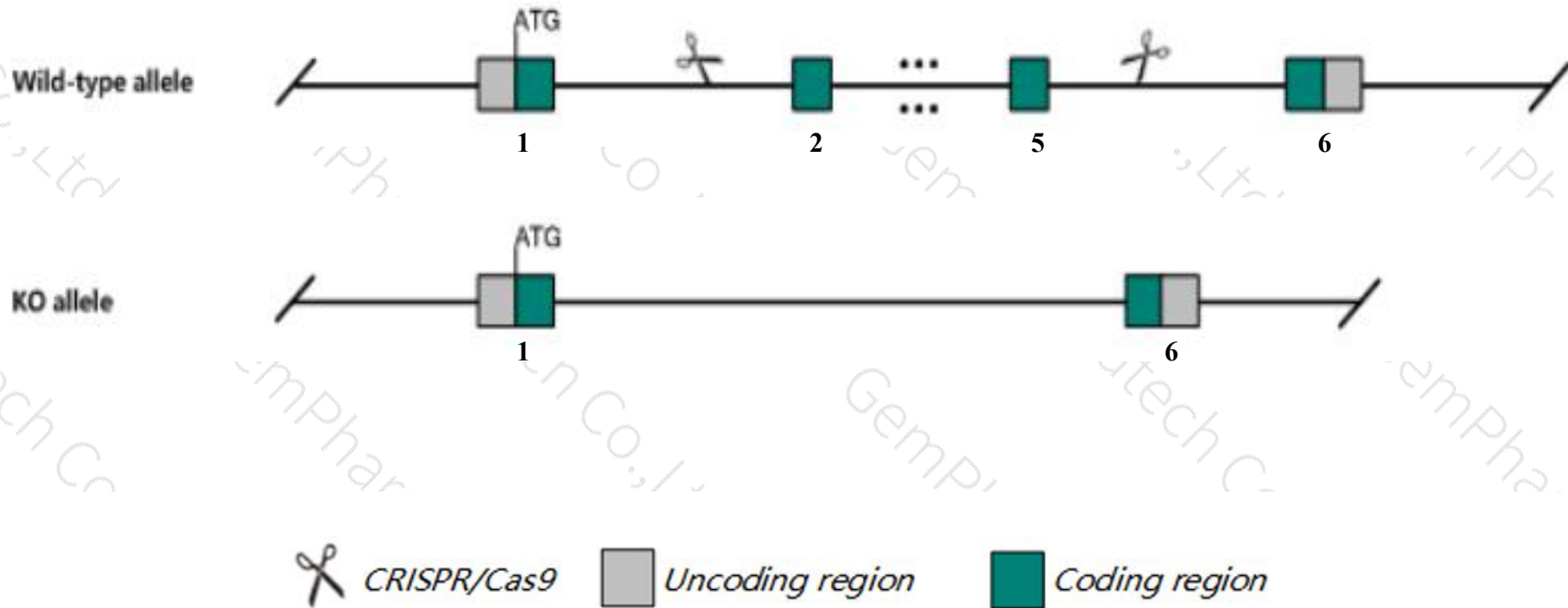
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cbll1* gene. The schematic diagram is as follows:



- The *Cbll1* gene has 5 transcripts. According to the structure of *Cbll1* gene, exon2-exon5 of *Cbll1*-203 (ENSMUST00000101499.9) transcript is recommended as the knockout region. The region contains 427bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cbll1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Cbll1* gene is located on the Chr12. 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)

Cbl1 Casitas B-lineage lymphoma-like 1 [Mus musculus (house mouse)]

Gene ID: 104836, updated on 13-Mar-2020

Summary



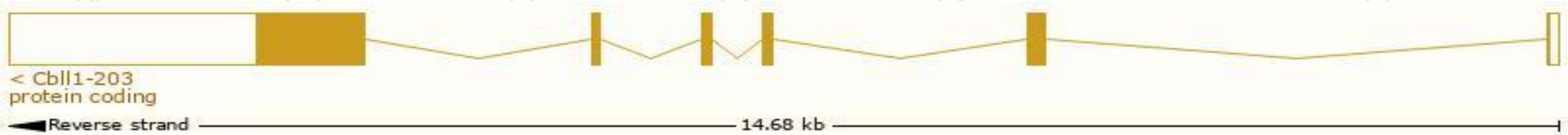
Official Symbol	Cbl1 provided by MGI
Official Full Name	Casitas B-lineage lymphoma-like 1 provided by MGI
Primary source	MGI:MGI:2144842
See related	Ensembl:ENSMUSG00000020659
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI467391, Hakai, c-Cbl-like
Expression	Ubiquitous expression in testis adult (RPKM 6.4), whole brain E14.5 (RPKM 3.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

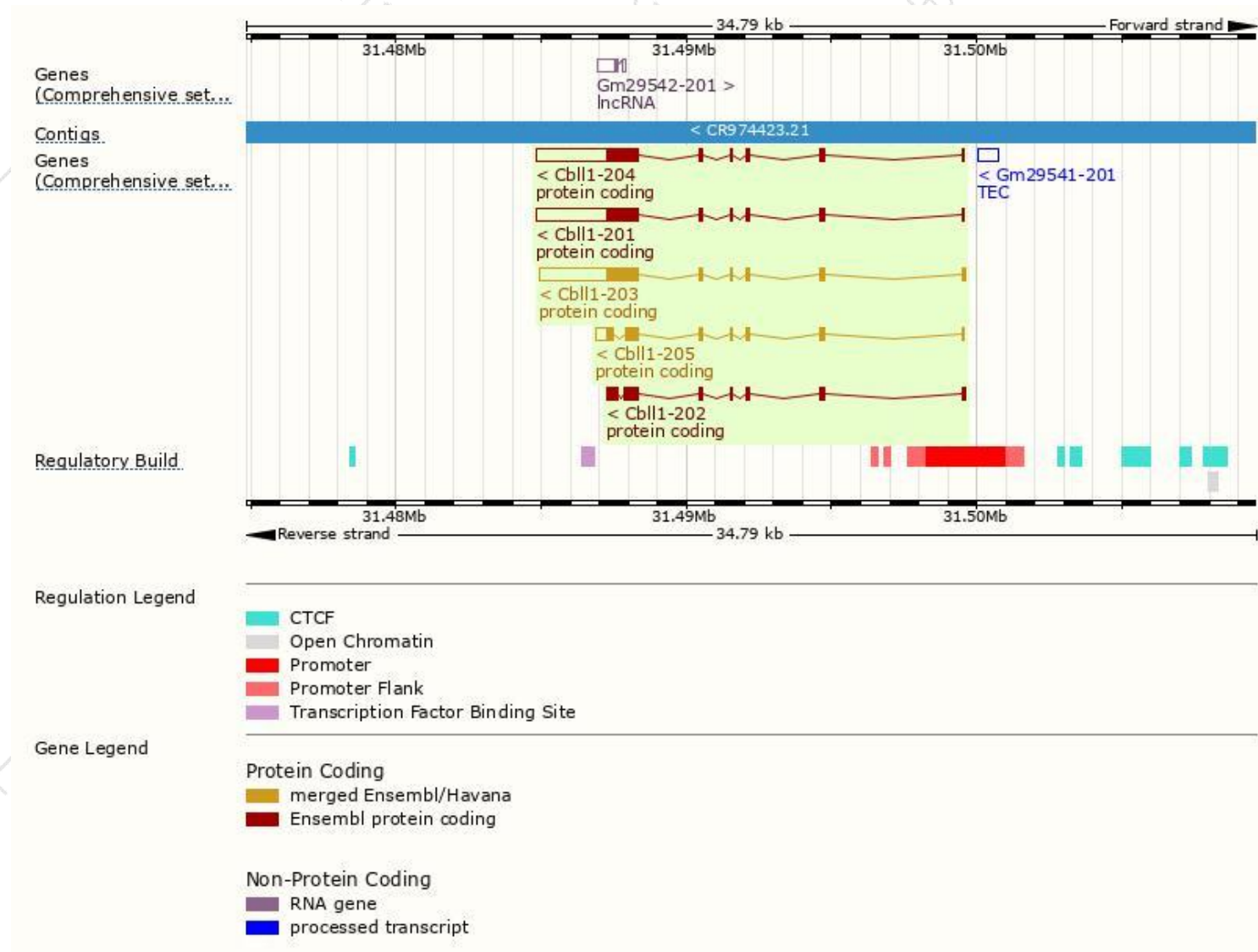
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cbll1-203	ENSMUST00000101499.9	3900	491aa	Protein coding	CCDS56834	Q9JIY2	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 P2
Cbll1-205	ENSMUST00000188326.2	1399	332aa	Protein coding	CCDS56835	A0A087WPK1_Q9JIY2	TSL:2 GENCODE basic
Cbll1-204	ENSMUST00000185739.7	3945	490aa	Protein coding	-	A0A087WSE1_Q9JIY2	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 ALT 1
Cbll1-201	ENSMUST00000064240.13	3937	488aa	Protein coding	-	A0A1X7SB71	TSL:5 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 ALT 1
Cbll1-202	ENSMUST00000085487.11	1332	416aa	Protein coding	-	E9QM14	TSL:5 GENCODE basic

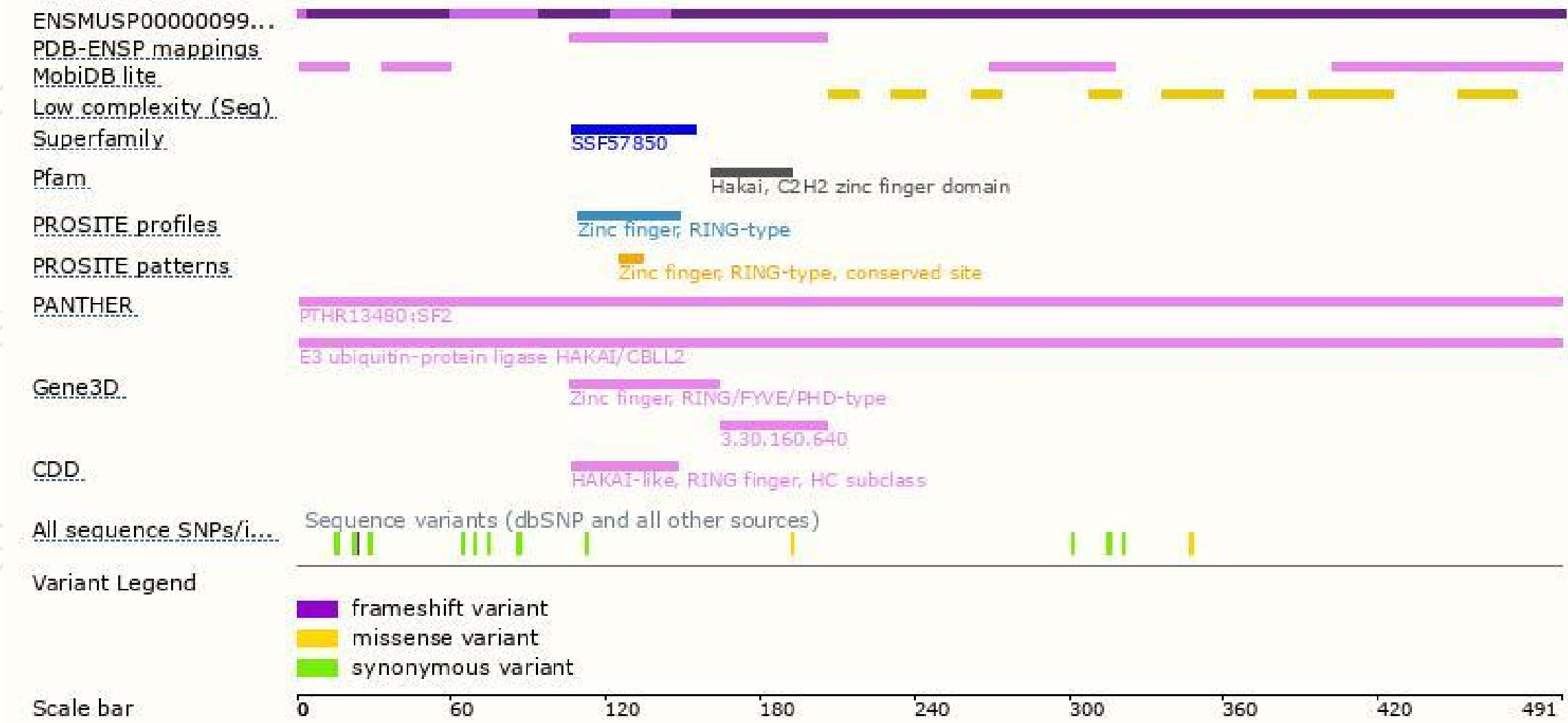
The strategy is based on the design of *Cbll1-203* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

