

***C8b* Cas9-KO Strategy**

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Design Date: 2020-5-14

Project Overview

Project Name

C8b

Project type

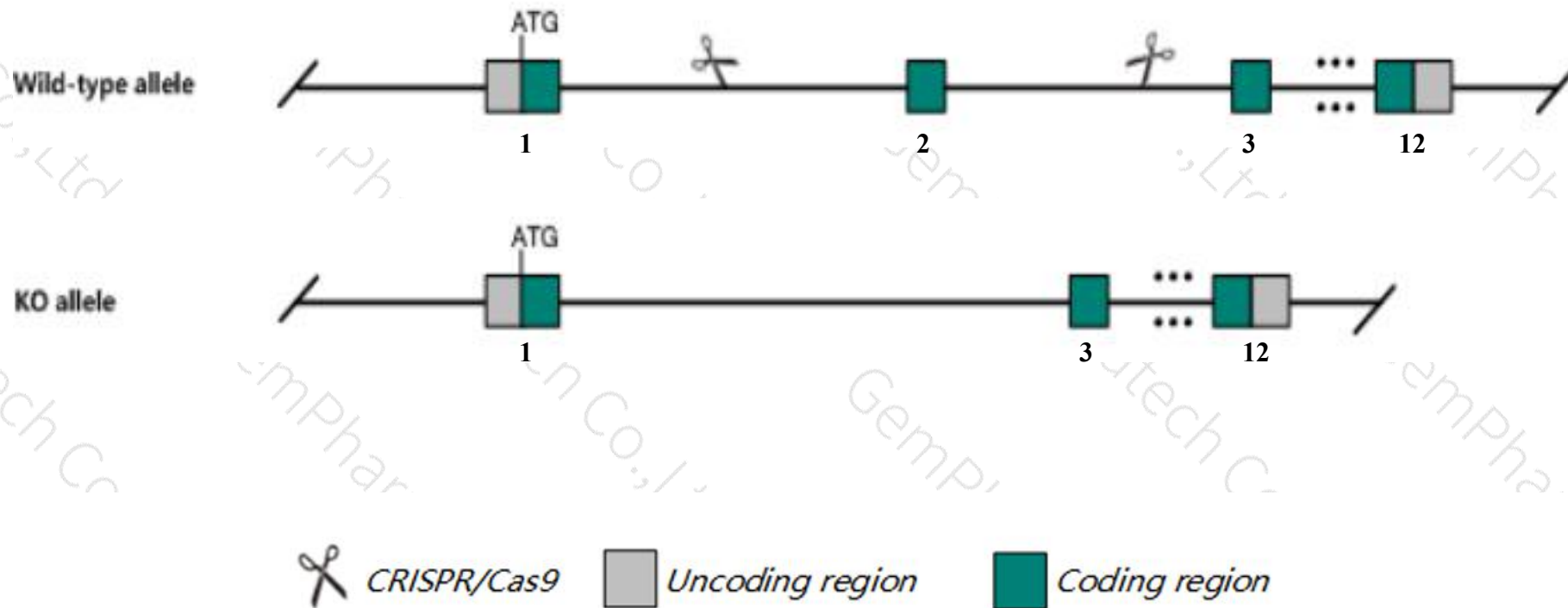
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *C8b* gene. The schematic diagram is as follows:



- The *C8b* gene has 3 transcripts. According to the structure of *C8b* gene, exon2 of *C8b-201* (ENSMUST00000031663.9) transcript is recommended as the knockout region. The region contains 157bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *C8b* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, in a controlled microbial environment ("clean") laboratory, mice homozygous for an inactivating mutation of this gene are viable and fertile and exhibit no apparent abnormal phenotype.
- Transcript *C8b*-203 may not be affected.
- The *C8b* gene is located on the Chr4. 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)

C8b complement component 8, beta polypeptide [Mus musculus (house mouse)]

Gene ID: 110382, updated on 13-Mar-2020

Summary



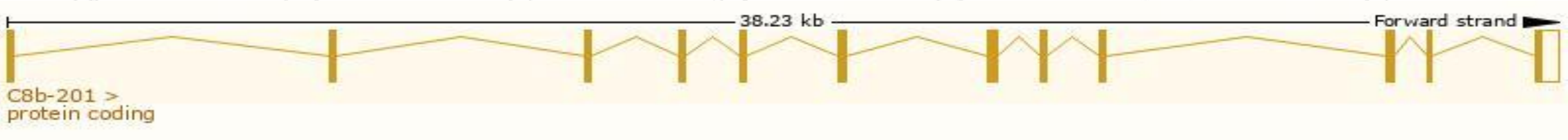
Official Symbol	C8b provided by MGI
Official Full Name	complement component 8, beta polypeptide provided by MGI
Primary source	MGI:MGI:88236
See related	Ensembl:ENSMUSG00000029656
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930439B20Rik, A1595927
Summary	This gene encodes the beta subunit of complement component C8 that participates in the assembly of the complement membrane attack complex. The encoded preproprotein undergoes proteolytic processing to generate the beta subunit, which associates with the alpha and gamma subunits to form a trimeric complement component, C8. Alternative splicing results in multiple transcript variants encoding different isoforms that may undergo similar proteolytic processing. This gene is located adjacent to the gene encoding the alpha subunit. [provided by RefSeq, Oct 2015]
Expression	Biased expression in liver E18 (RPKM 92.7), liver adult (RPKM 25.5) and 2 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

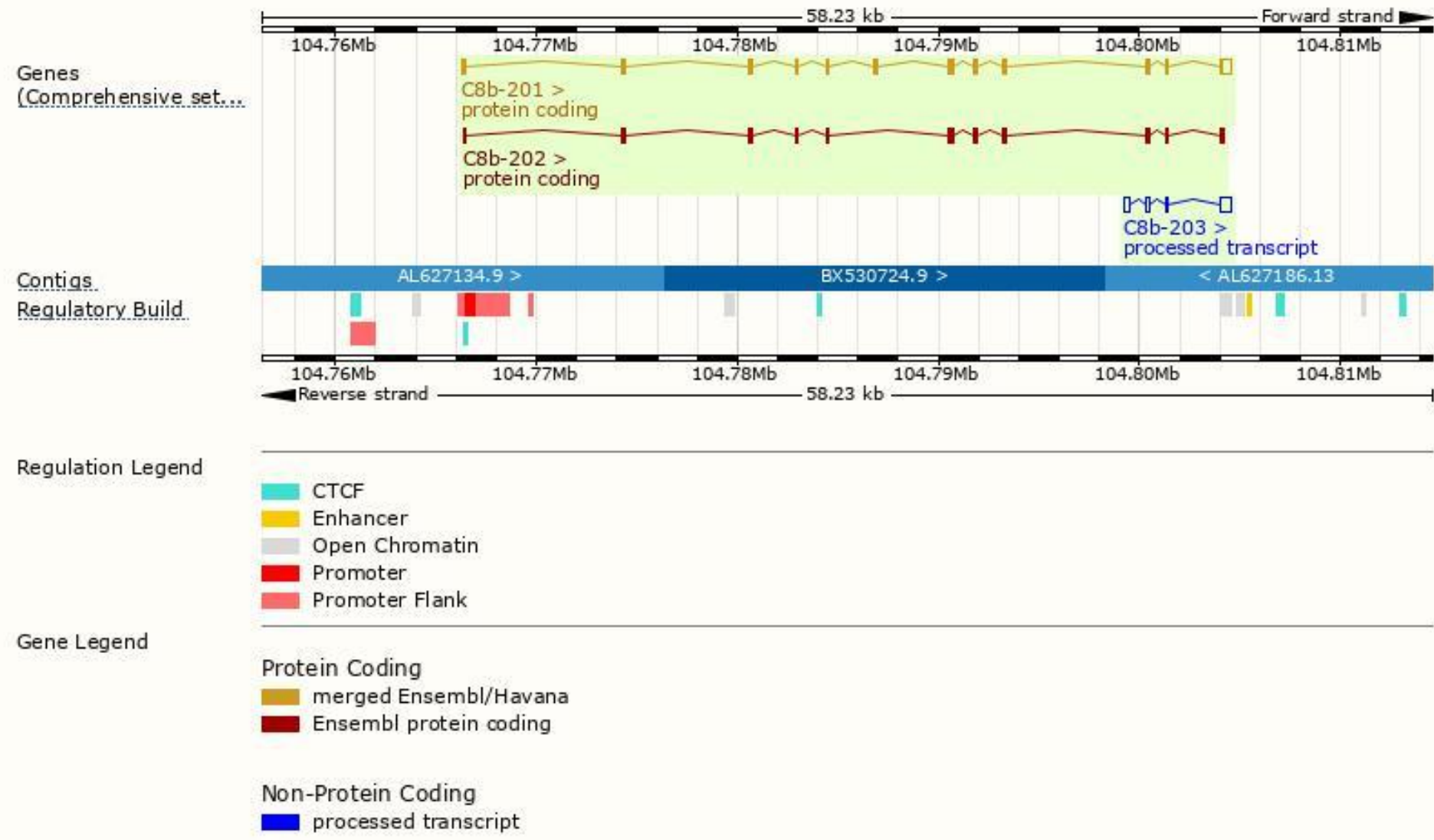
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C8b-201	ENSMUST00000031663.9	2239	589aa	Protein coding	CCDS18414	Q8BH35	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 P3
C8b-202	ENSMUST00000065072.6	1586	523aa	Protein coding	CCDS84762	Q8BH35	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 ALT2
C8b-203	ENSMUST00000123892.1	1061	No protein	Processed transcript	-	-	TSL:1

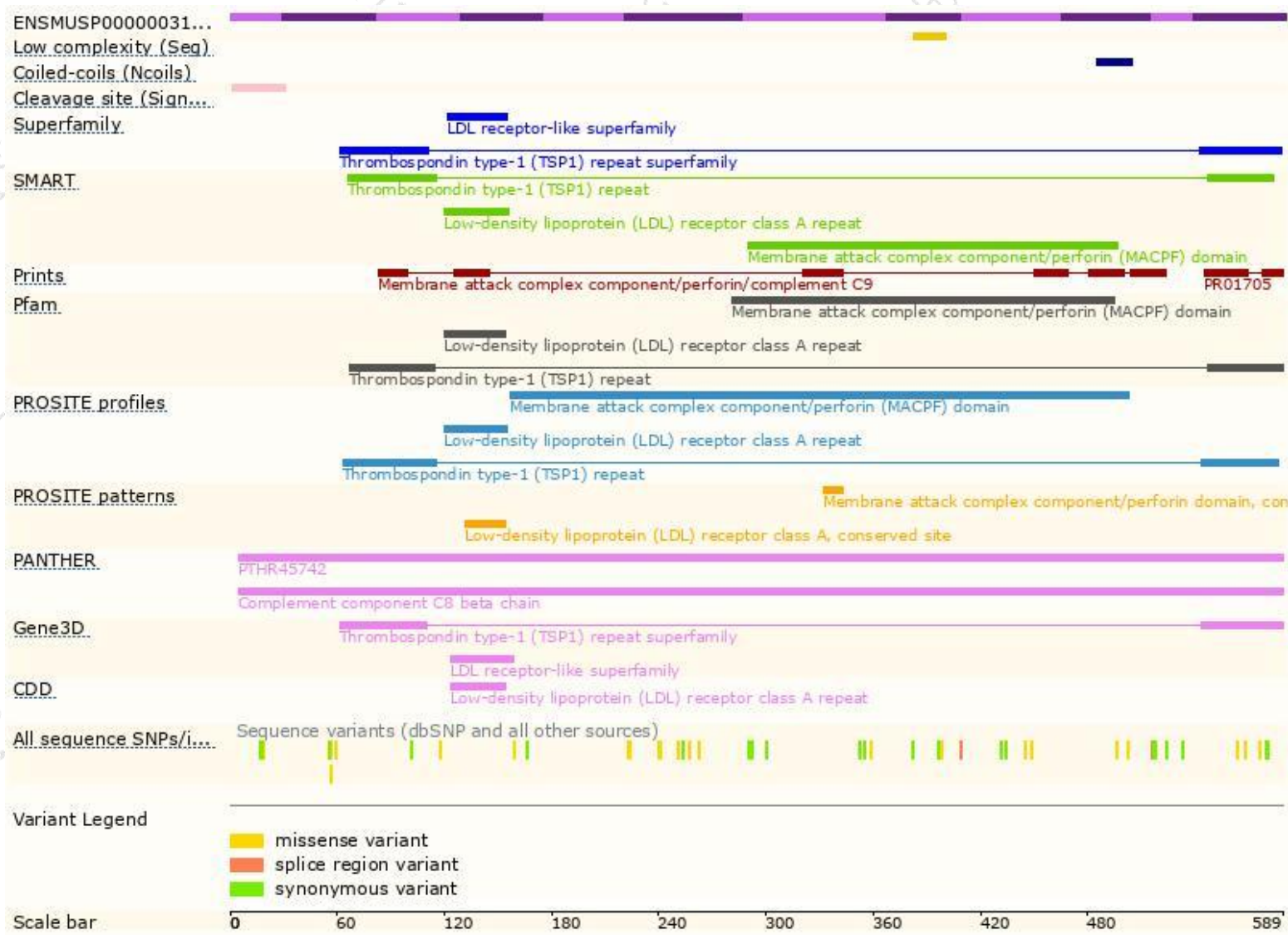
The strategy is based on the design of *C8b-201* transcript,the transcription is shown below:



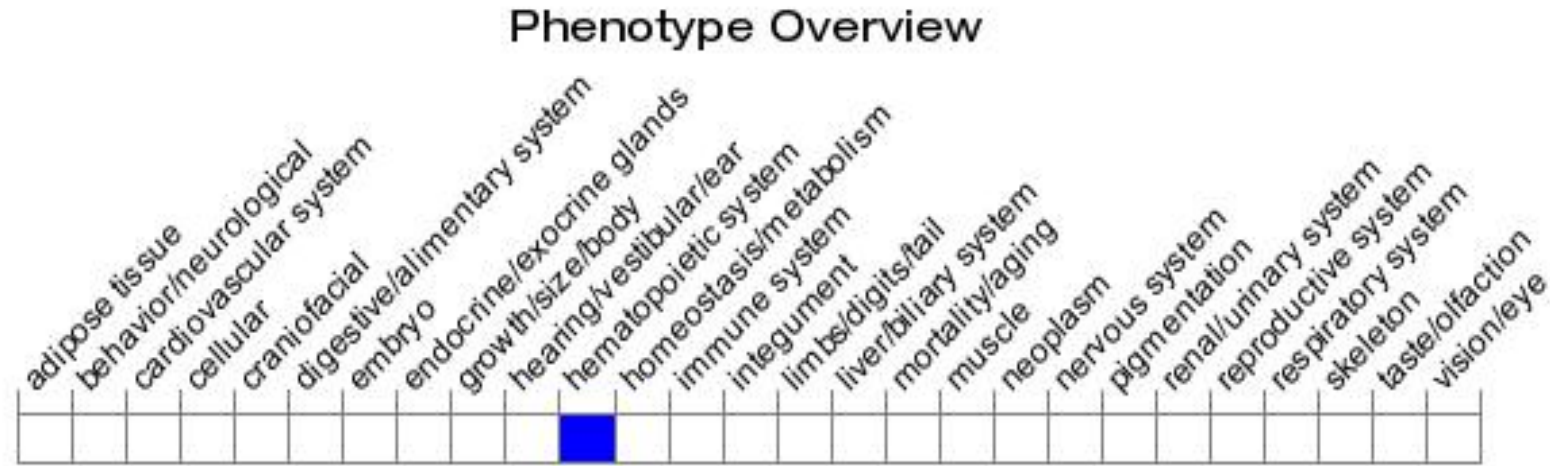
Genomic location distribution



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, in a controlled microbial environment ("clean") laboratory, mice homozygous for an inactivating mutation of this gene are viable and fertile and exhibit no apparent abnormal phenotype.

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

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