

Crlf2 Cas9-KO Strategy

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Design Date:

2019-11-22

Project Overview

Project Name

Crlf2

Project type

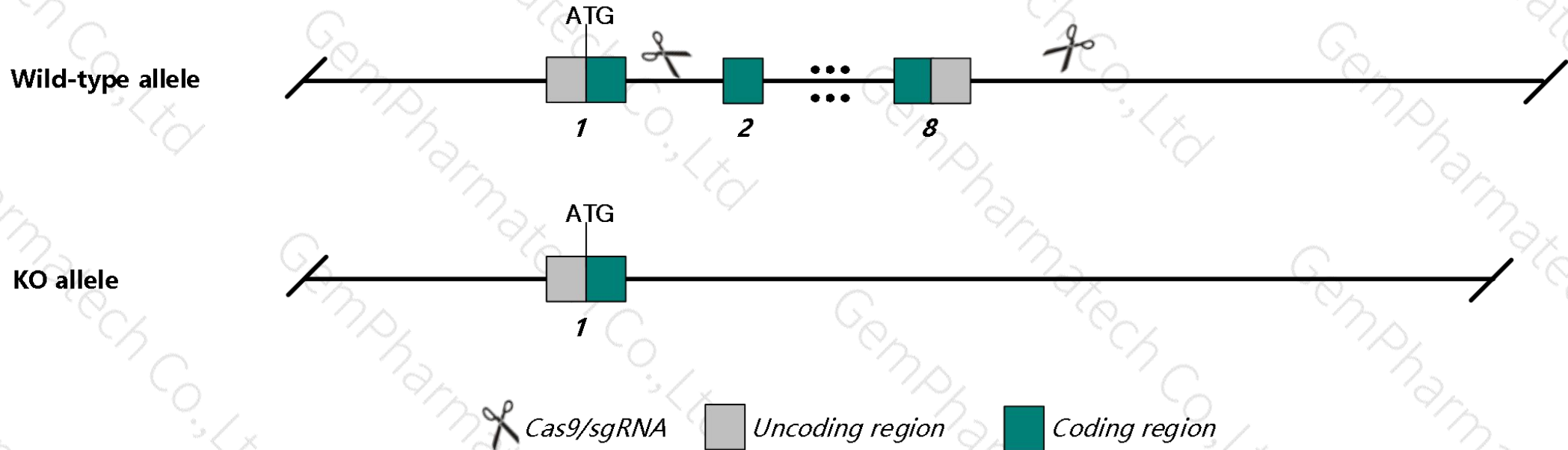
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Crlf2* gene. The schematic diagram is as follows:



- The *Crlf2* gene has 3 transcripts. According to the structure of *Crlf2* gene, exon2-exon8 of *Crlf2-201* (ENSMUST00000044579.11) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Crlf2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous null mice are overtly normal and maintain normal lymphopoiesis.
- The *Crlf2* gene is located on the Chr5. 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)

Crlf2 cytokine receptor-like factor 2 [Mus musculus (house mouse)]

Gene ID: 57914, updated on 19-Feb-2019

Summary



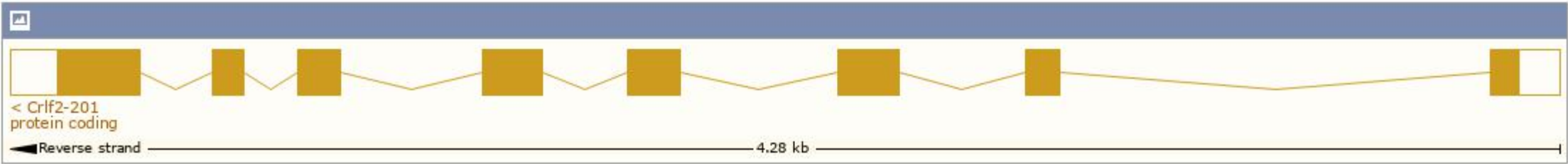
Official Symbol	Crlf2 provided by MGI
Official Full Name	cytokine receptor-like factor 2 provided by MGI
Primary source	MGI:MGI:1889506
See related	Ensembl:ENSMUSG00000033467
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CRLM2, Ly114, Tpte2, Tslpr
Expression	Ubiquitous expression in adrenal adult (RPKM 40.0), spleen adult (RPKM 35.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

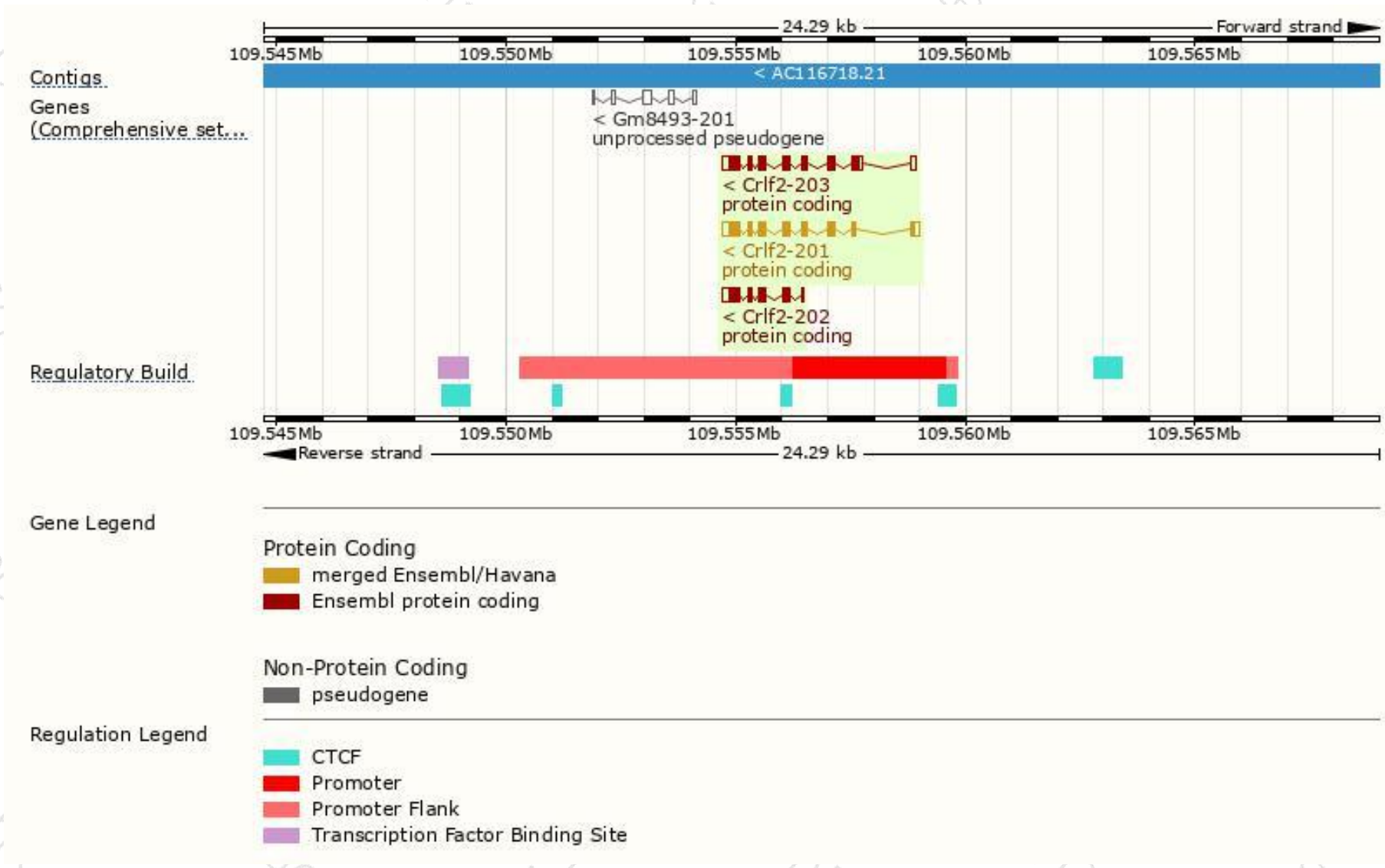
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
CrIf2-203	ENSMUST00000200284.4	1405	357aa	Protein coding	CCDS80356	A0A0G2JGP1	TSL:1 GENCODE basic APPRIS ALT2
CrIf2-201	ENSMUST00000044579.11	1323	359aa	Protein coding	CCDS19521	A0A0R4J0F5	TSL:1 GENCODE basic APPRIS P3
CrIf2-202	ENSMUST00000198960.1	812	226aa	Protein coding	-	A0A0G2JF13	CDS 5' incomplete TSL:3

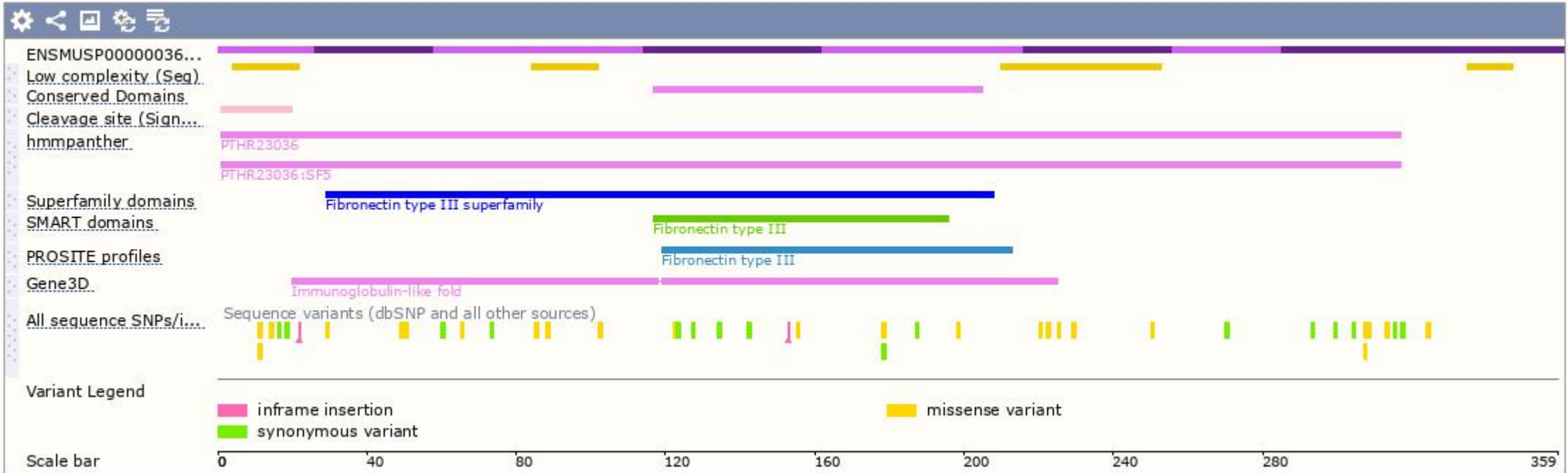
The strategy is based on the design of *CrIf2-201* transcript,The transcription is shown below



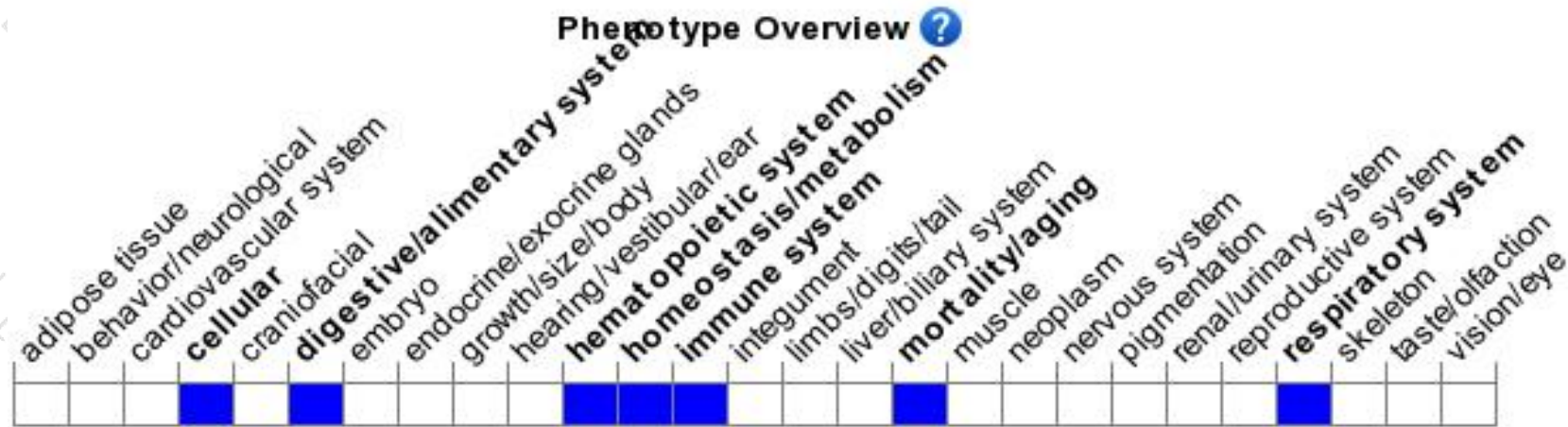
Genomic location distribution



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 null mice are overtly normal and maintain normal lymphopoiesis.

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

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