

Fcrla Cas9-KO Strategy

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Project Overview

Project Name

Fcrla

Project type

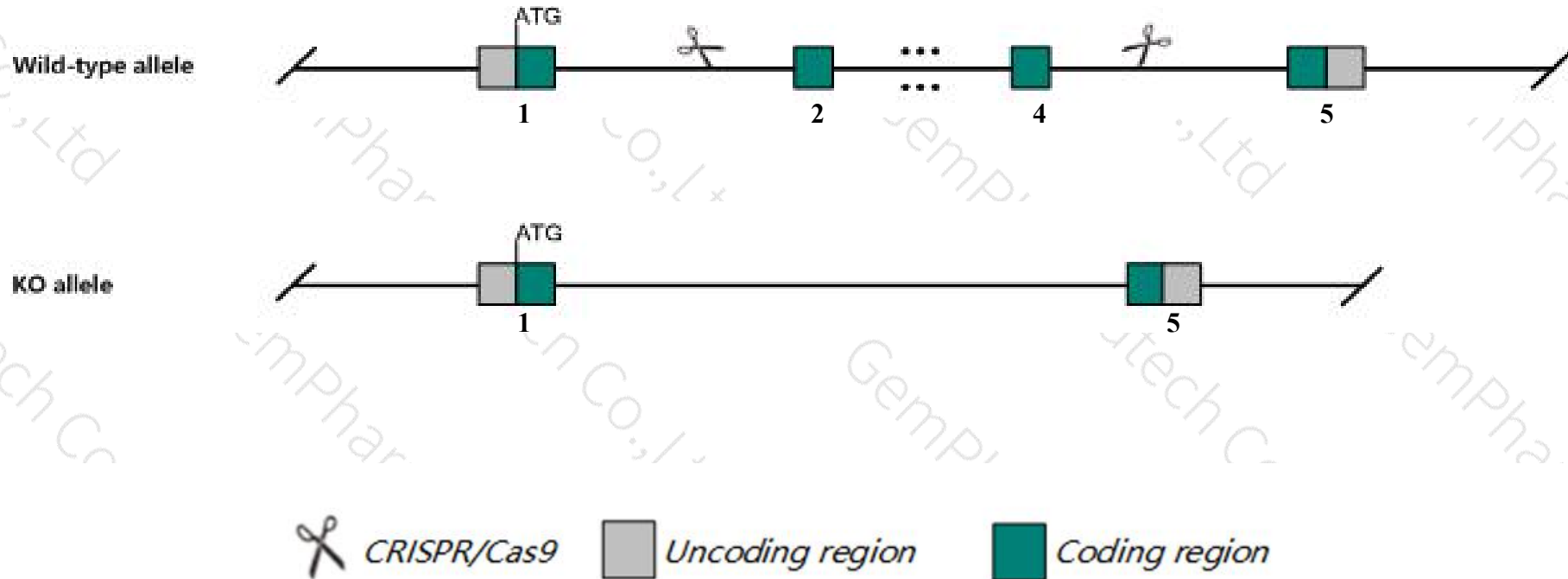
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Fcrla* gene has 6 transcripts. According to the structure of *Fcrla* gene, exon2-exon4 of *Fcrla*-201 (ENSMUST00000046322.13) 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 *Fcrla* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a targeted allele exhibit largely normal T-dependent and T-independent antibody responses with an increase in IgG1 after secondary challenge with sheep red blood cells.
- The KO region deletes most of the coding sequence, but does not result in frameshift.
- The *Fcrla* gene is located on the Chr1. 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)

Fcrla Fc receptor-like A [*Mus musculus* (house mouse)]

Gene ID: 98752, updated on 12-Aug-2019

Summary

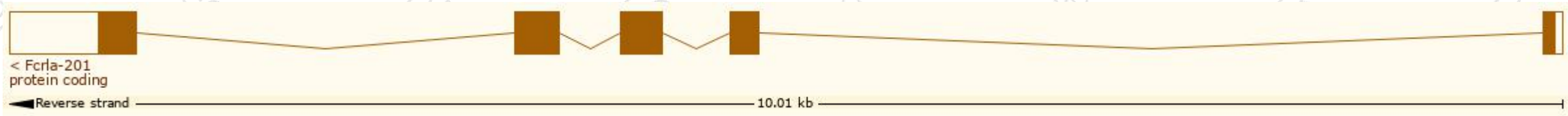
Official Symbol	Fcrla provided by MGI
Official Full Name	Fc receptor-like A provided by MGI
Primary source	MGI:MGI:2138647
See related	Ensembl:ENSMUSG000000038421
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FCRL; FREB; Fcrx; FCRL1; Freb1; mFREB; mFcrX; Fcrlm1; BB219290
Expression	Biased expression in spleen adult (RPKM 43.6), mammary gland adult (RPKM 10.0) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

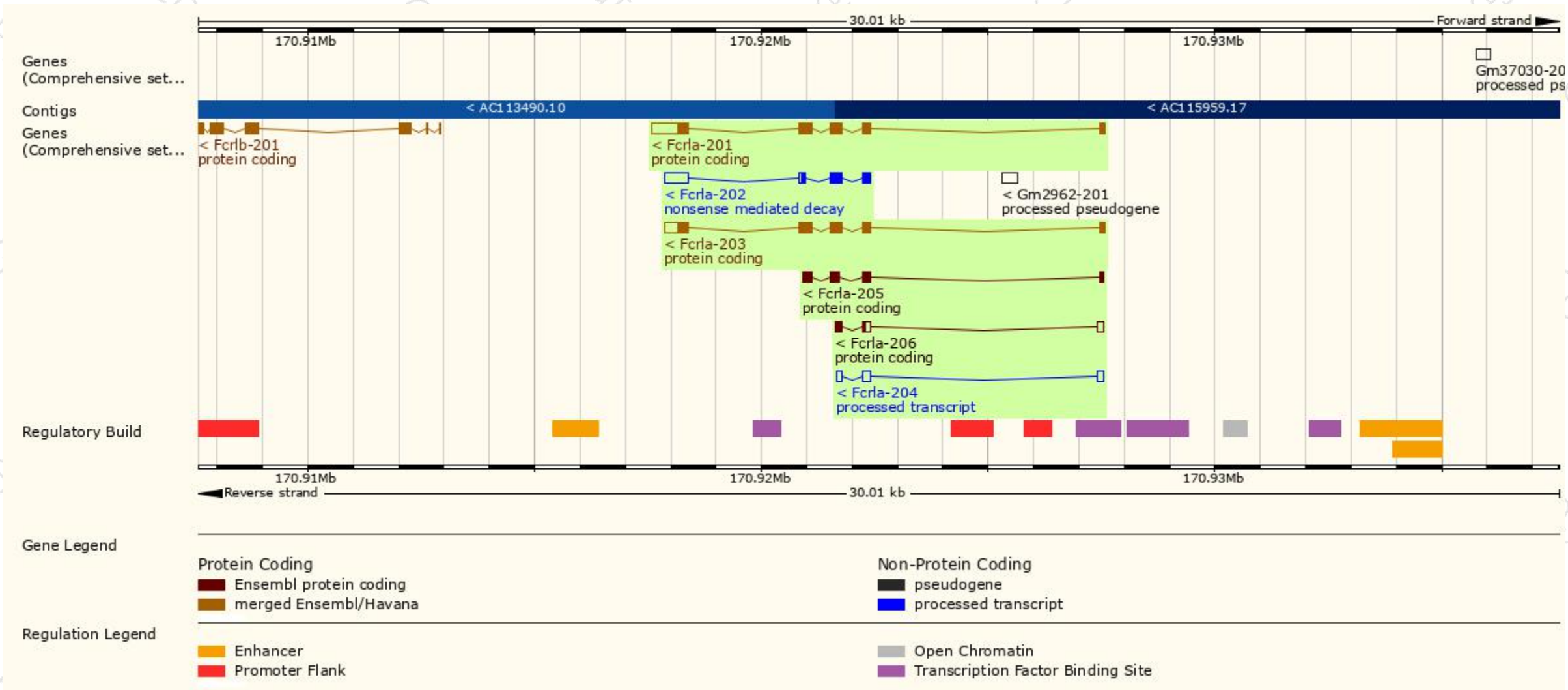
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fcrla-201	ENSMUST00000046322.13	1679	353aa	Protein coding	CCDS48440	Q920A9	TSL:1 GENCODE basic APPRIS P4
Fcrla-203	ENSMUST00000159171.1	1371	352aa	Protein coding	CCDS48439	Q920A9	TSL:1 GENCODE basic APPRIS ALT2
Fcrla-205	ENSMUST00000162136.1	663	216aa	Protein coding	-	E0CX78	CDS 3' incomplete TSL:3
Fcrla-206	ENSMUST00000162887.1	509	79aa	Protein coding	-	E0CY58	CDS 3' incomplete TSL:2
Fcrla-202	ENSMUST00000159149.7	1116	177aa	Nonsense mediated decay	-	F7DEW9	CDS 5' incomplete TSL:5
Fcrla-204	ENSMUST00000161050.1	460	No protein	Processed transcript	-	-	TSL:3

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



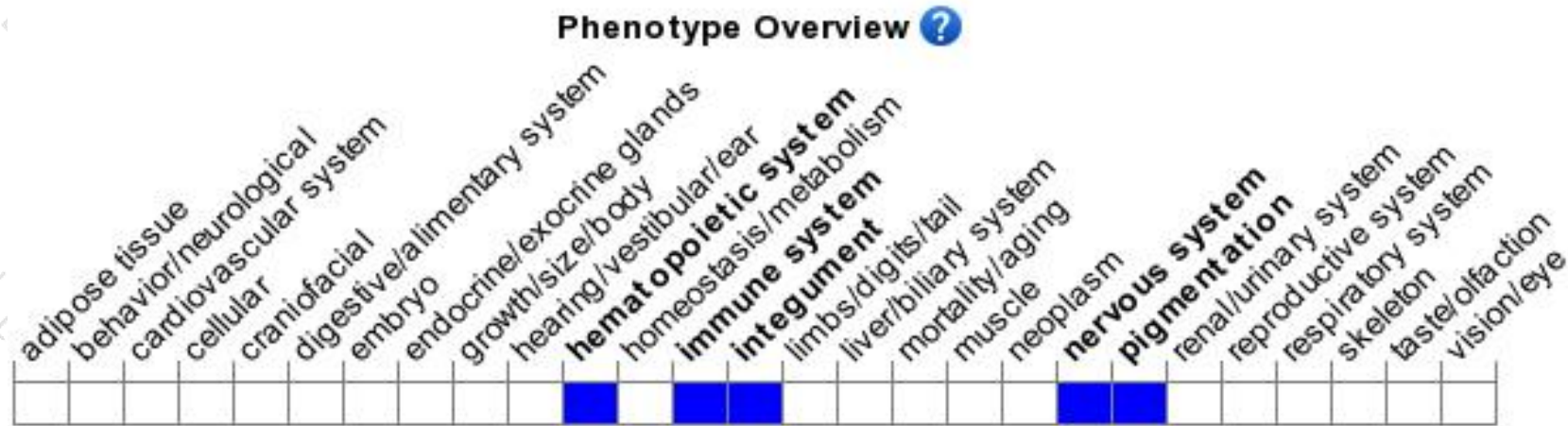
Genomic location distribution



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 targeted allele exhibit largely normal T-dependent and T-independent antibody responses with an increase in IgG1 after secondary challenge with sheep red blood cells.

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

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