

Crtam Cas9-CKO Strategy

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Project Overview

Project Name

Crtam

Project type

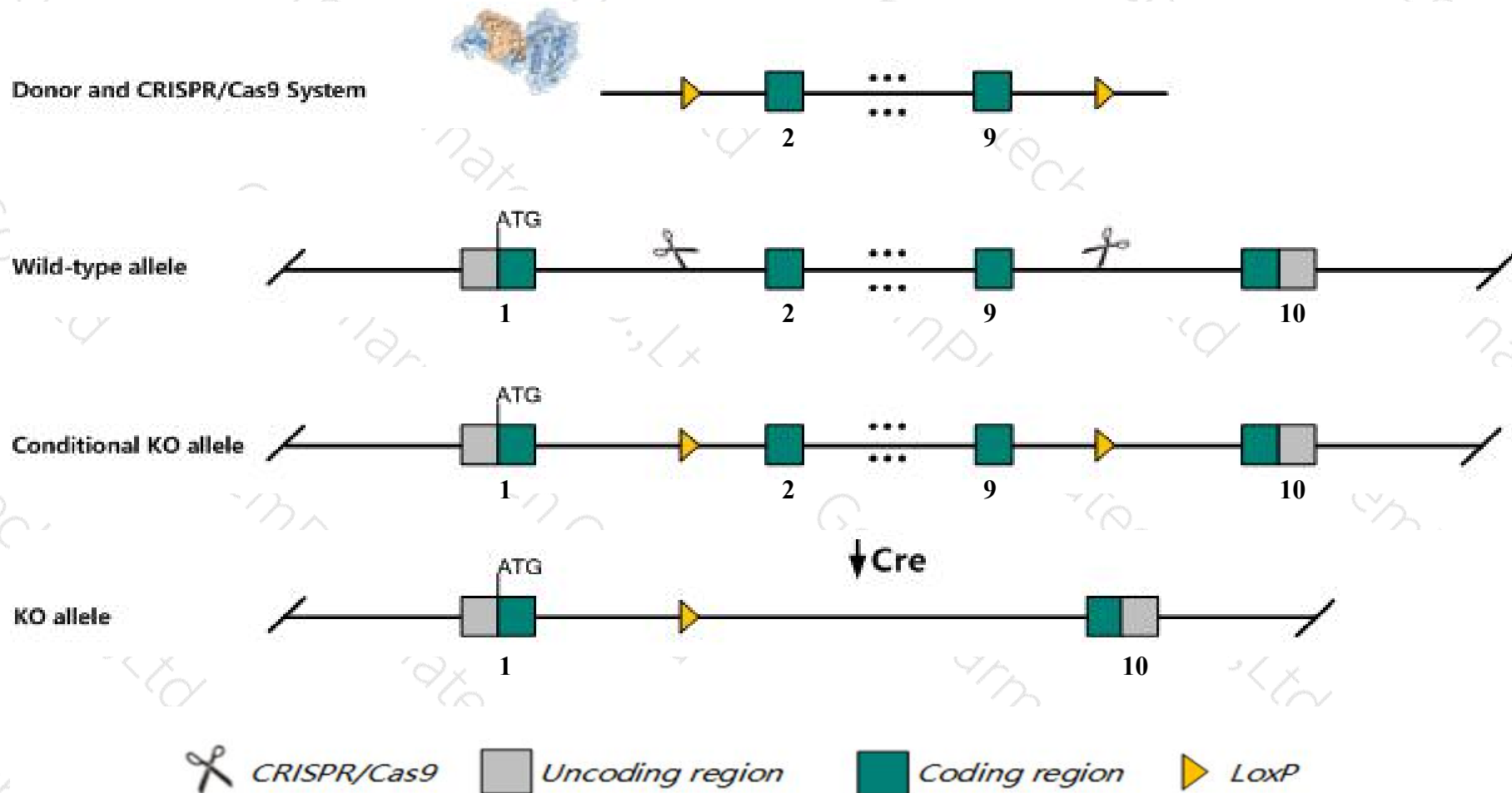
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Crtam* gene has 4 transcripts. According to the structure of *Crtam* gene, exon2-exon9 of *Crtam*-202 (ENSMUST00000180384.2) 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 *Crtam* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous null mice have defects in late stage T cell activation that leads to less production of inflammatory cytokines, higher proliferation, and an increase in T cell number with age.
- The *Crtam* gene is located on the Chr9. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Crtam cytotoxic and regulatory T cell molecule [*Mus musculus* (house mouse)]

Gene ID: 54698, updated on 17-Sep-2019

Summary

- Official Symbol** Crtam provided by [MGI](#)
- Official Full Name** cytotoxic and regulatory T cell molecule provided by [MGI](#)
- Primary source** [MGI:MGI:1859822](#)
- See related** [Ensembl:ENSMUSG00000032021](#)
- 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
- Expression** Biased expression in cerebellum adult (RPKM 7.1) and testis adult (RPKM 4.5) [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 9 A5.1; 9 21.79 cM

See Crtam in [Genome Data Viewer](#)

Exon count: 10

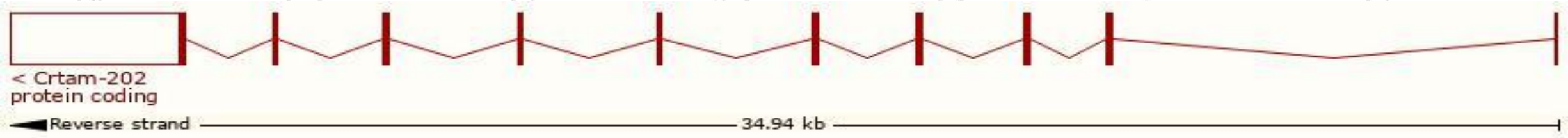
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (40972798..41004628, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (40780881..40812669, complement)

Transcript information (Ensembl)

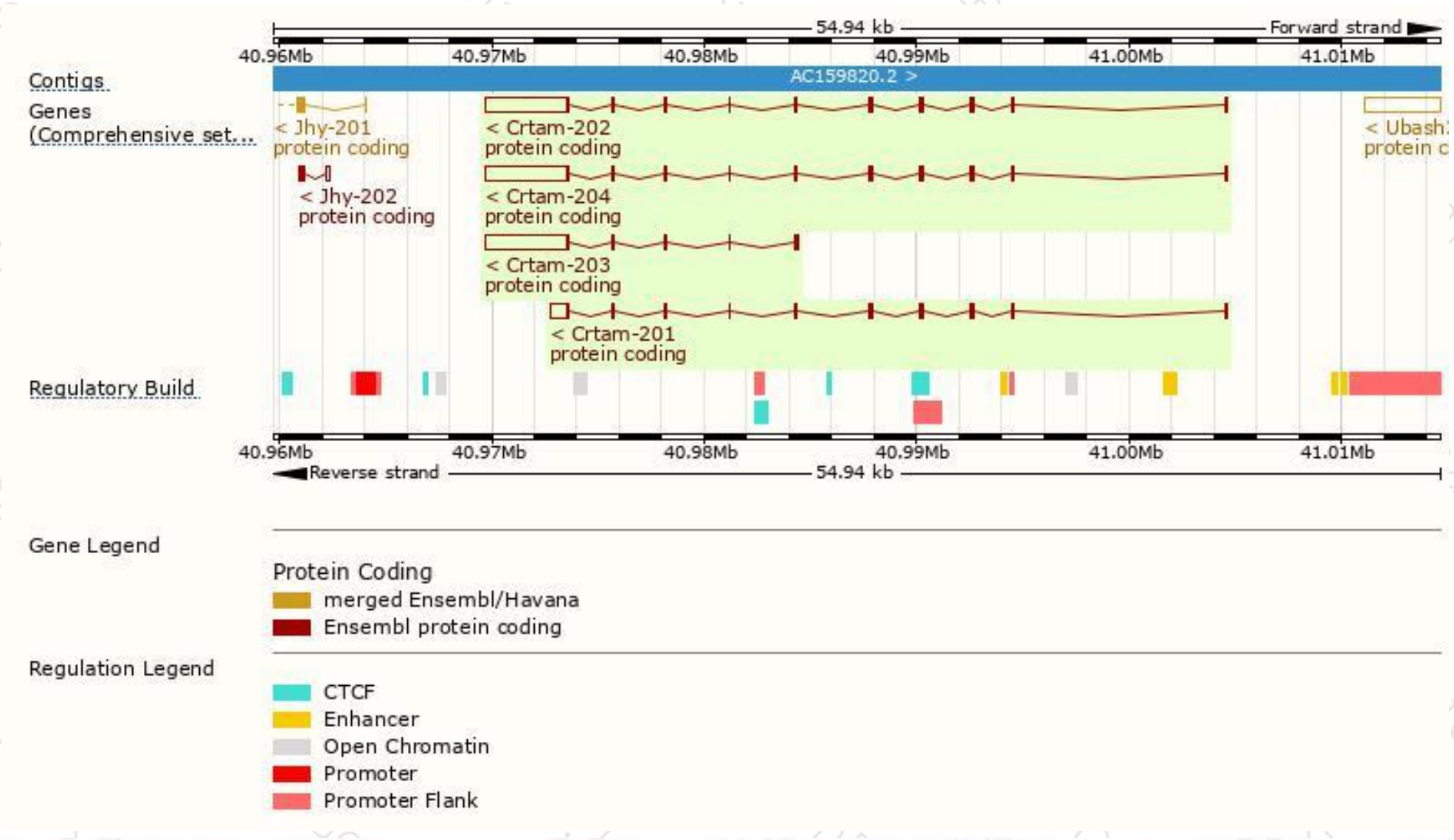
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Crtam-202	ENSMUST00000180384.2	5046	393aa	Protein coding	CCDS72216	Q149L7	TSL:1 GENCODE basic APPRIS ALT2
Crtam-204	ENSMUST00000188848.7	5001	392aa	Protein coding	CCDS40593	Q149L7	TSL:1 GENCODE basic APPRIS P3
Crtam-203	ENSMUST00000180872.8	4443	196aa	Protein coding	-	A0A0R4J297 Q149L7	TSL:1 GENCODE basic
Crtam-201	ENSMUST00000034519.12	1876	386aa	Protein coding	-	E9QPS7	TSL:5 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Crtam-202* transcript,The transcription is shown below



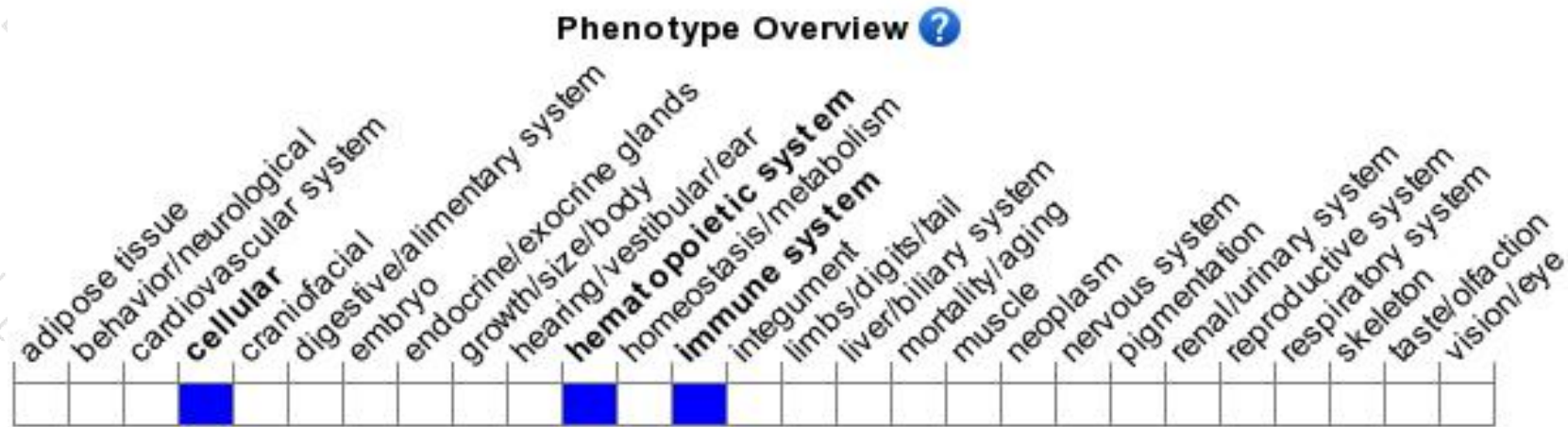
Genomic location distribution



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 have defects in late stage T cell activation that leads to less production of inflammatory cytokines, higher proliferation, and an increase in T cell number with age.

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

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