

Cr2 Cas9-CKO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

Design Date:

2019/10/12

Project Overview

Project Name

Cr2

Project type

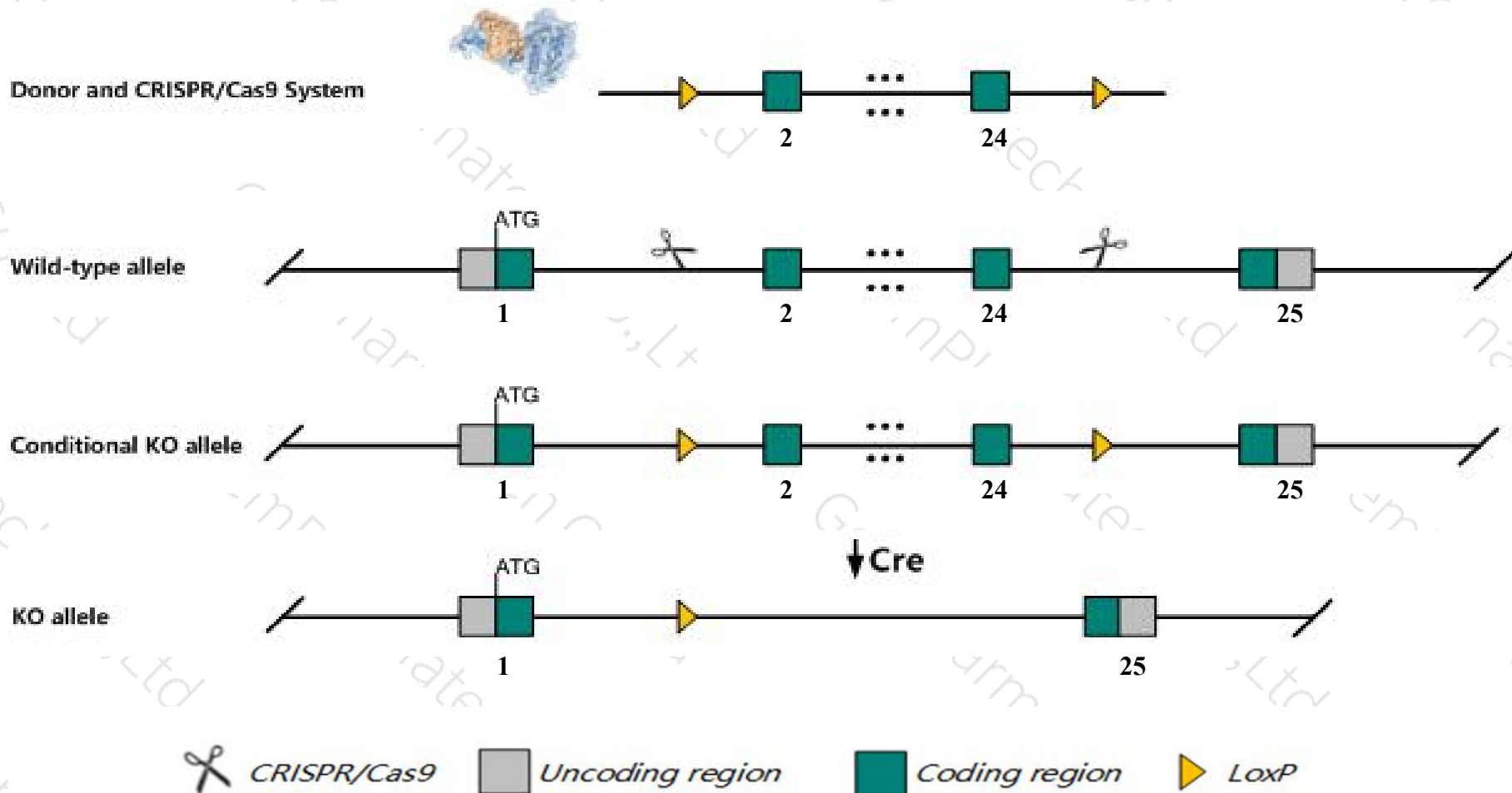
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cr2* gene. The schematic diagram is as follows:



- The *Cr2* gene has 12 transcripts. According to the structure of *Cr2* gene, exon2-exon24 of *Cr2-212* (ENSMUST00000210219.1) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cr2* 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, Homozygotes for targeted null mutations exhibit impaired humoral immune responses to T cell-dependent antigens, with limited affinity maturation, and reduced memory B cell and germinal center formation.
- The *Cr2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Cr2 complement receptor 2 [*Mus musculus* (house mouse)]

Gene ID: 12902, updated on 21-Aug-2019

Summary

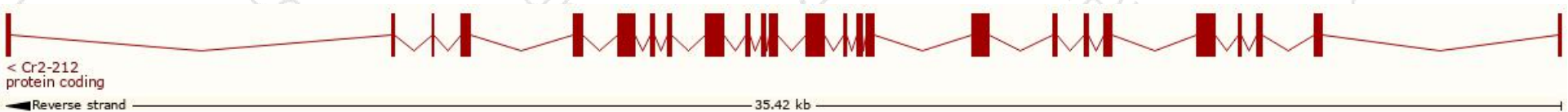
Official Symbol	Cr2 provided by MGI
Official Full Name	complement receptor 2 provided by MGI
Primary source	MGI:MGI:88489
See related	Ensembl:ENSMUSG00000026616
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cr1; C3DR; CD21; CD35; Cr-1; Cr-2
Expression	Biased expression in spleen adult (RPKM 7.1), mammary gland adult (RPKM 1.4) and 1 other tissue See more
Orthologs	human all

Transcript information (Ensembl)

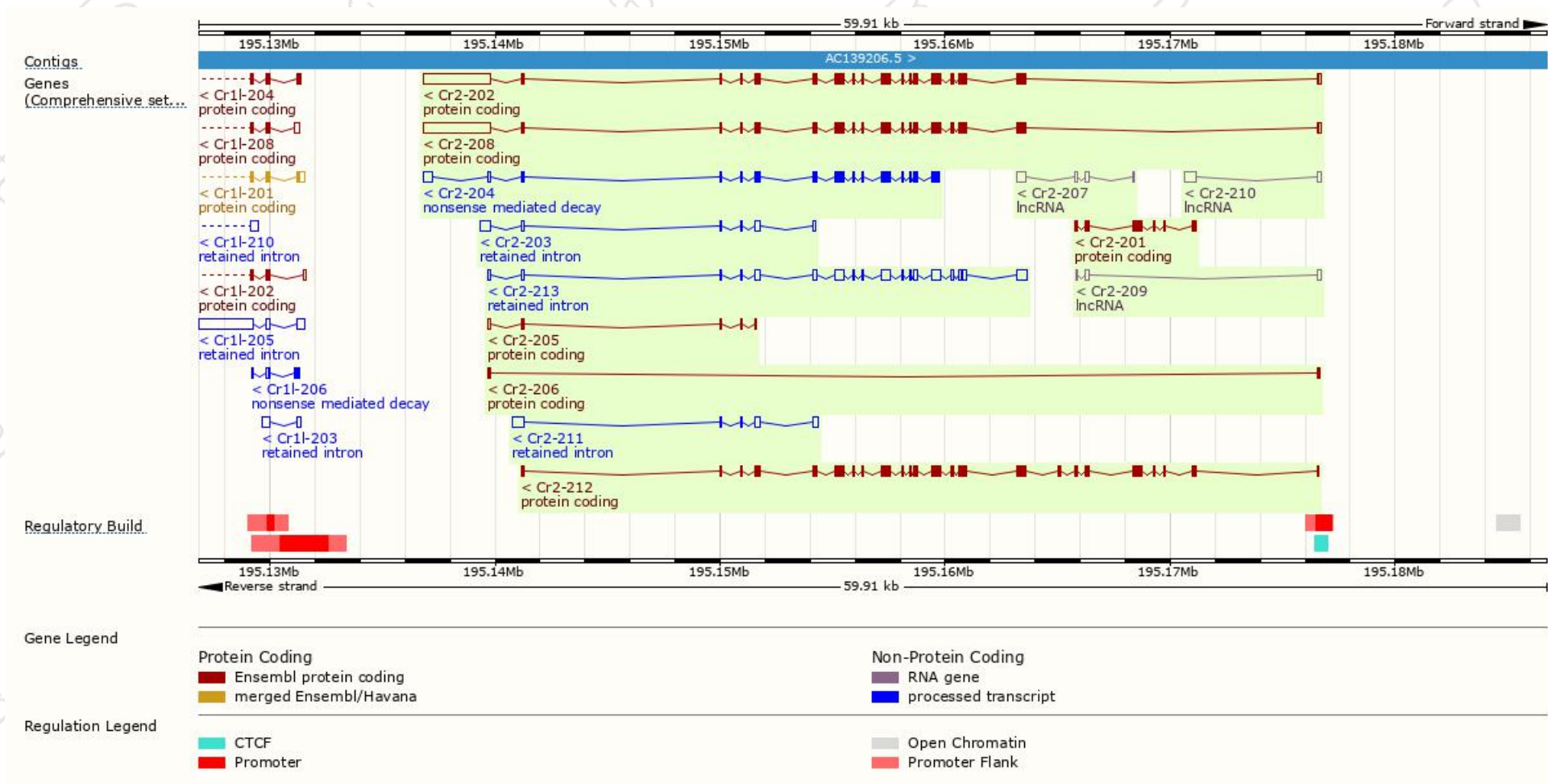
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cr2-202	ENSMUST00000082321.8	6207	1032aa	Protein coding	CCDS15642	Q9DC83	TSL:1 GENCODE basic
Cr2-208	ENSMUST00000195120.5	6212	1026aa	Protein coding	-	A0A0A6YWG3	TSL:5 GENCODE basic
Cr2-212	ENSMUST00000210219.1	4227	1408aa	Protein coding	-	A0A1B0GS59	TSL:5 GENCODE basic APPRIS P1
Cr2-201	ENSMUST00000043104.8	1044	347aa	Protein coding	-	E9Q3S5	TSL:5 GENCODE basic
Cr2-205	ENSMUST00000193436.1	355	62aa	Protein coding	-	A0A0A6YXU7	CDS 5' incomplete TSL:5
Cr2-206	ENSMUST00000193801.1	206	50aa	Protein coding	-	Q32M14	TSL:1 GENCODE basic
Cr2-204	ENSMUST00000193356.1	2736	735aa	Nonsense mediated decay	-	A0A0A6YWU7	CDS 5' incomplete TSL:1
Cr2-213	ENSMUST00000238929.1	3220	No protein	Retained intron	-	-	-
Cr2-211	ENSMUST00000195737.1	1000	No protein	Retained intron	-	-	TSL:3
Cr2-203	ENSMUST00000192604.5	974	No protein	Retained intron	-	-	TSL:3
Cr2-207	ENSMUST00000194149.5	751	No protein	lncRNA	-	-	TSL:3
Cr2-210	ENSMUST00000195722.1	689	No protein	lncRNA	-	-	TSL:2
Cr2-209	ENSMUST00000195347.5	357	No protein	lncRNA	-	-	TSL:3

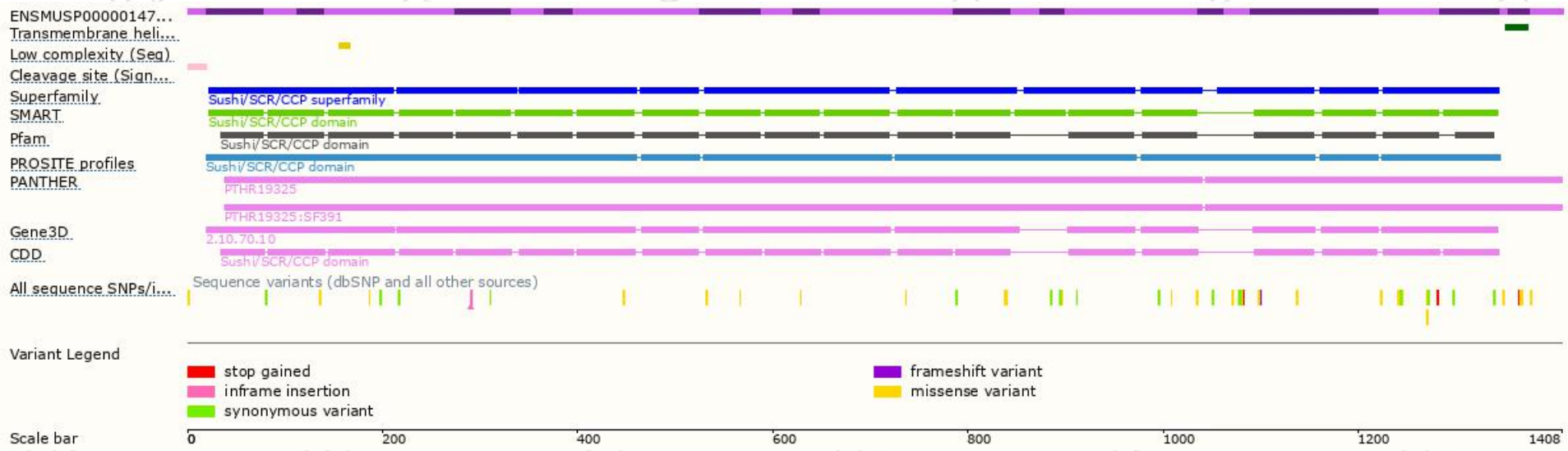
The strategy is based on the design of *Cr2-212* transcript,The transcription is shown below



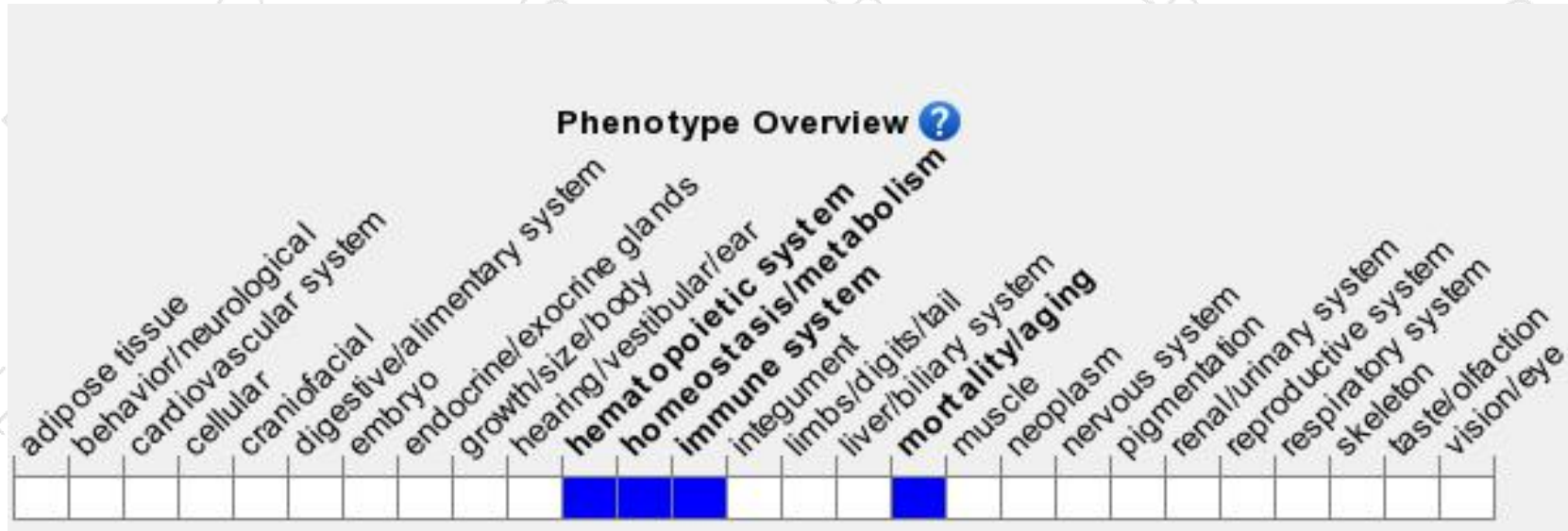
Genomic location distribution



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, Homozygotes for targeted null mutations exhibit impaired humoral immune responses to T cell-dependent antigens, with limited affinity maturation, and reduced memory B cell and germinal center formation.

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

Tel: 400-9660890

