

Cxcl9 Cas9-KO Strategy

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Project Overview

Project Name

Cxcl9

Project type

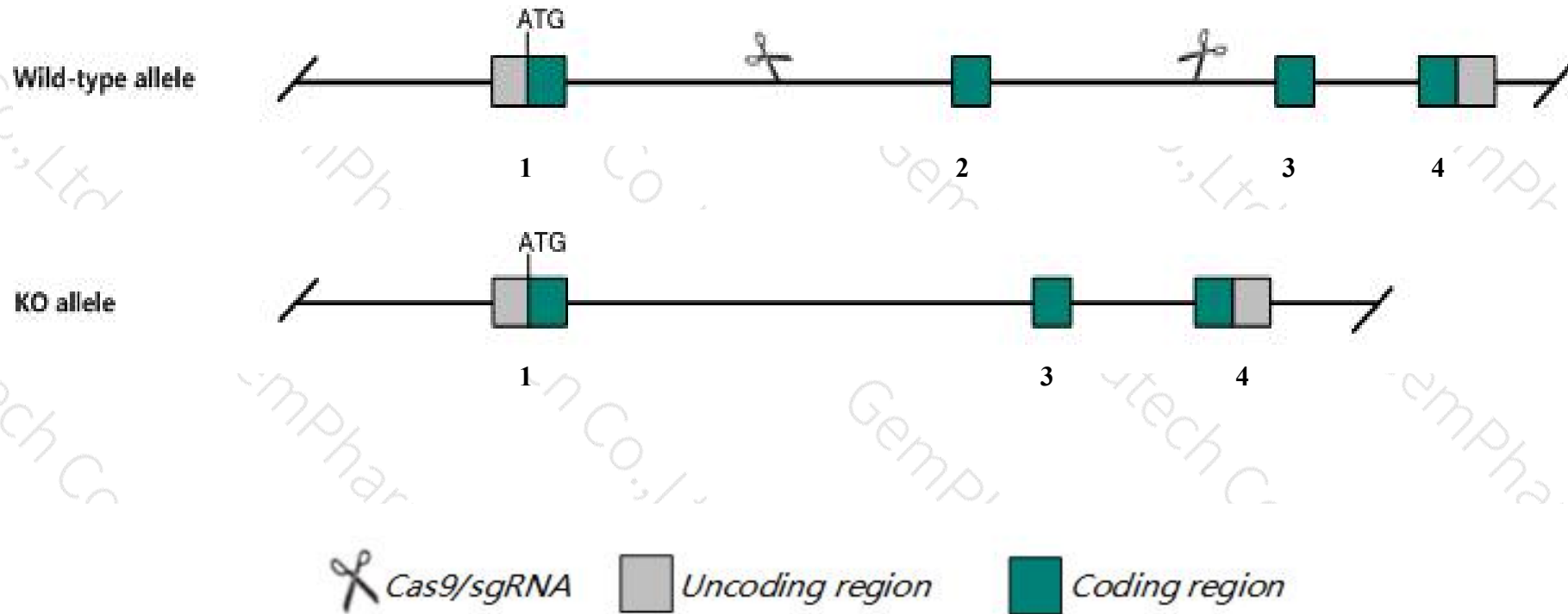
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cxcl9* gene. The schematic diagram is as follows:



- The *Cxcl9* gene has 2 transcripts. According to the structure of *Cxcl9* gene, exon2 of *Cxcl9-201* (ENSMUST00000113093.4) transcript is recommended as the knockout region. The region contains 127bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cxcl9* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a knock-out allele show a significant reduction in CD4+ T cell infiltration into the cornea in response to ocular HSV-1 infection, and produce lower titers of antibodies in response to primary infection with the intracellular bacterium *Francisella tularensis* live vaccine strain.
- The *Cxcl9* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Cxcl9 chemokine (C-X-C motif) ligand 9 [Mus musculus (house mouse)]

Gene ID: 17329, updated on 10-Feb-2019

Summary



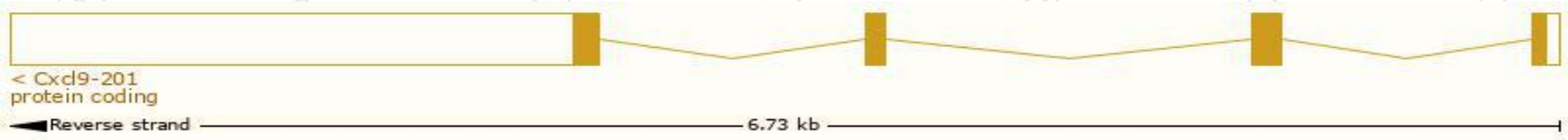
Official Symbol	Cxcl9 provided by MGI
Official Full Name	chemokine (C-X-C motif) ligand 9 provided by MGI
Primary source	MGI:MGI:1352449
See related	Ensembl:ENSMUSG00000029417
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BB139920, CMK, Mig, MuMIG, Scyb9, crg-10
Expression	Biased expression in subcutaneous fat pad adult (RPKM 7.5), mammary gland adult (RPKM 6.2) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

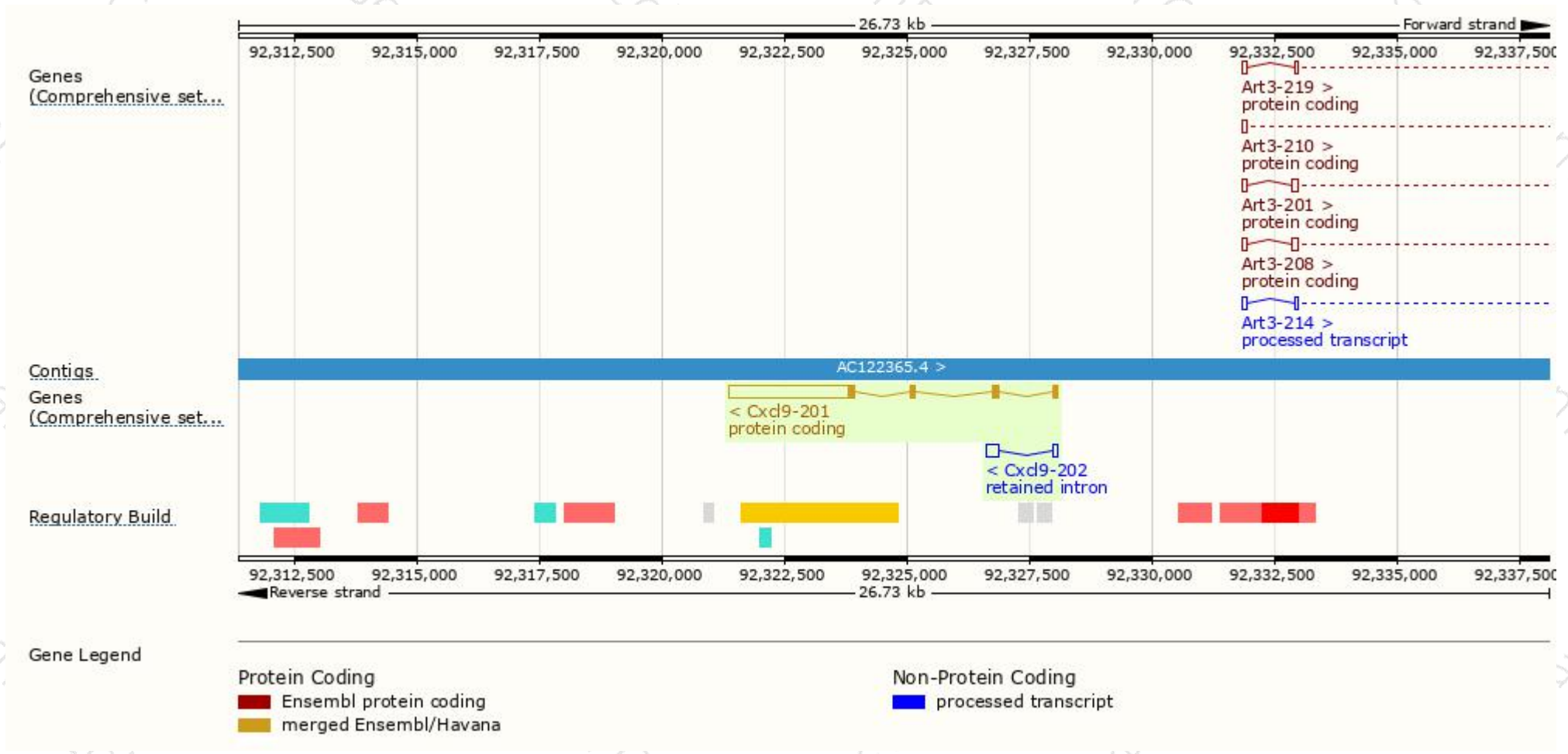
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cxcl9-201	ENSMUST00000113093.4	2889	126aa	Protein coding	CCDS39152	P18340	TSL:1 GENCODE basic APPRIS P1
Cxcl9-202	ENSMUST00000202404.1	370	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Cxcl9-201* transcript,The transcription is shown below



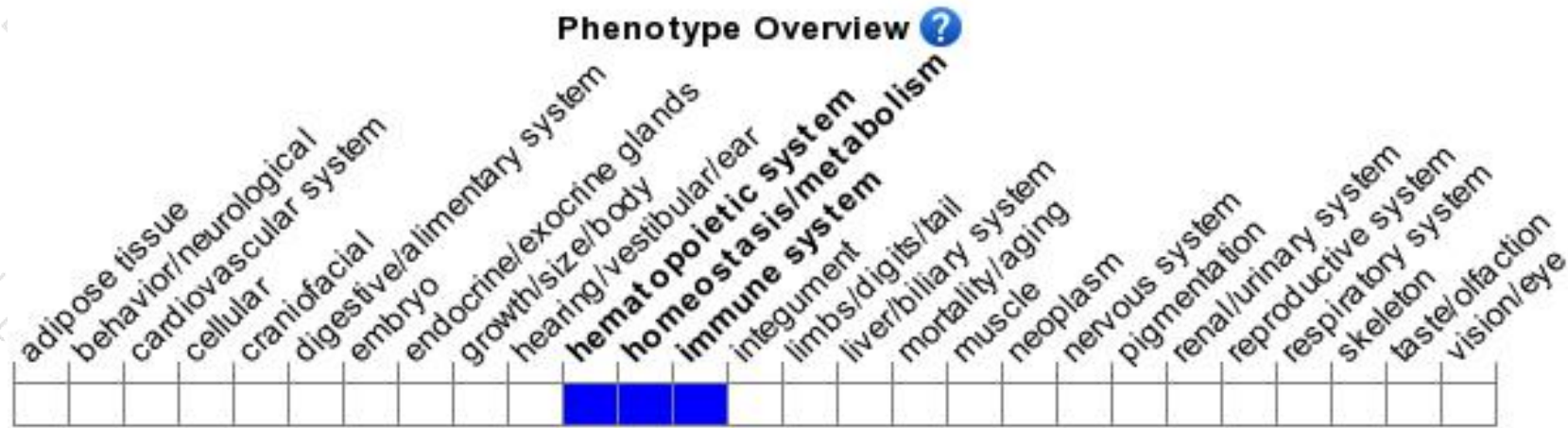
Genomic location distribution



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 knock-out allele show a significant reduction in CD4⁺ T cell infiltration into the cornea in response to ocular HSV-1 infection, and produce lower titers of antibodies in response to primary infection with the intracellular bacterium *Francisella tularensis* live vaccine strain.

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

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