

Cxcr5 Cas9-KO Strategy

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Project Overview

Project Name

Cxcr5

Project type

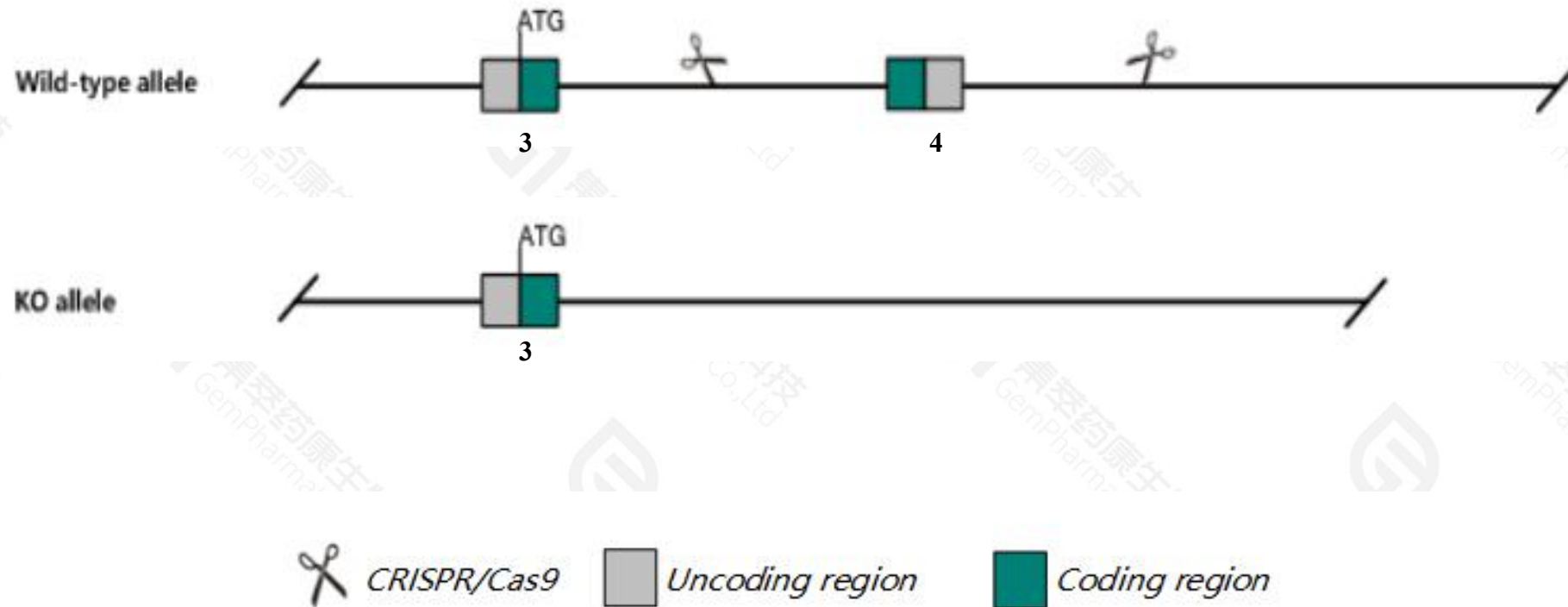
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cxcr5* gene. The schematic diagram is as follows:



- The *Cxcr5* gene has 5 transcripts. According to the structure of *Cxcr5* gene, exon4 of *Cxcr5*-204(ENSMUST00000215293.2) 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 *Cxcr5* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mutants lack inguinal lymph nodes, have a few abnormal or no Peyer's patches, morphologically altered primary lymphoid follicles and no functional germinal centers in their spleen.
- The KO region contains functional region of the *Bcl9l* gene. Knockout the region may affect the function of *Bcl9l* gene.
- The *Cxcr5* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Cxcr5 chemokine (C-X-C motif) receptor 5 [Mus musculus (house mouse)]

Gene ID: 12145, updated on 13-Dec-2020

Summary



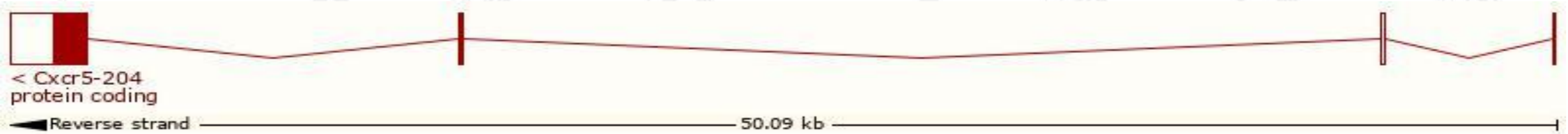
Official Symbol	Cxcr5 provided by MGI
Official Full Name	chemokine (C-X-C motif) receptor 5 provided by MGI
Primary source	MGI:MGI:103567
See related	Ensembl:ENSMUSG00000047880
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bl, Blr1, CXC-R5, CXCR-, CXCR-5, Gpc, Gpcr6, MDR15
Expression	Biased expression in spleen adult (RPKM 61.9), mammary gland adult (RPKM 12.5) and 1 other tissue See more
Orthologs	human all

Transcript information (Ensembl)

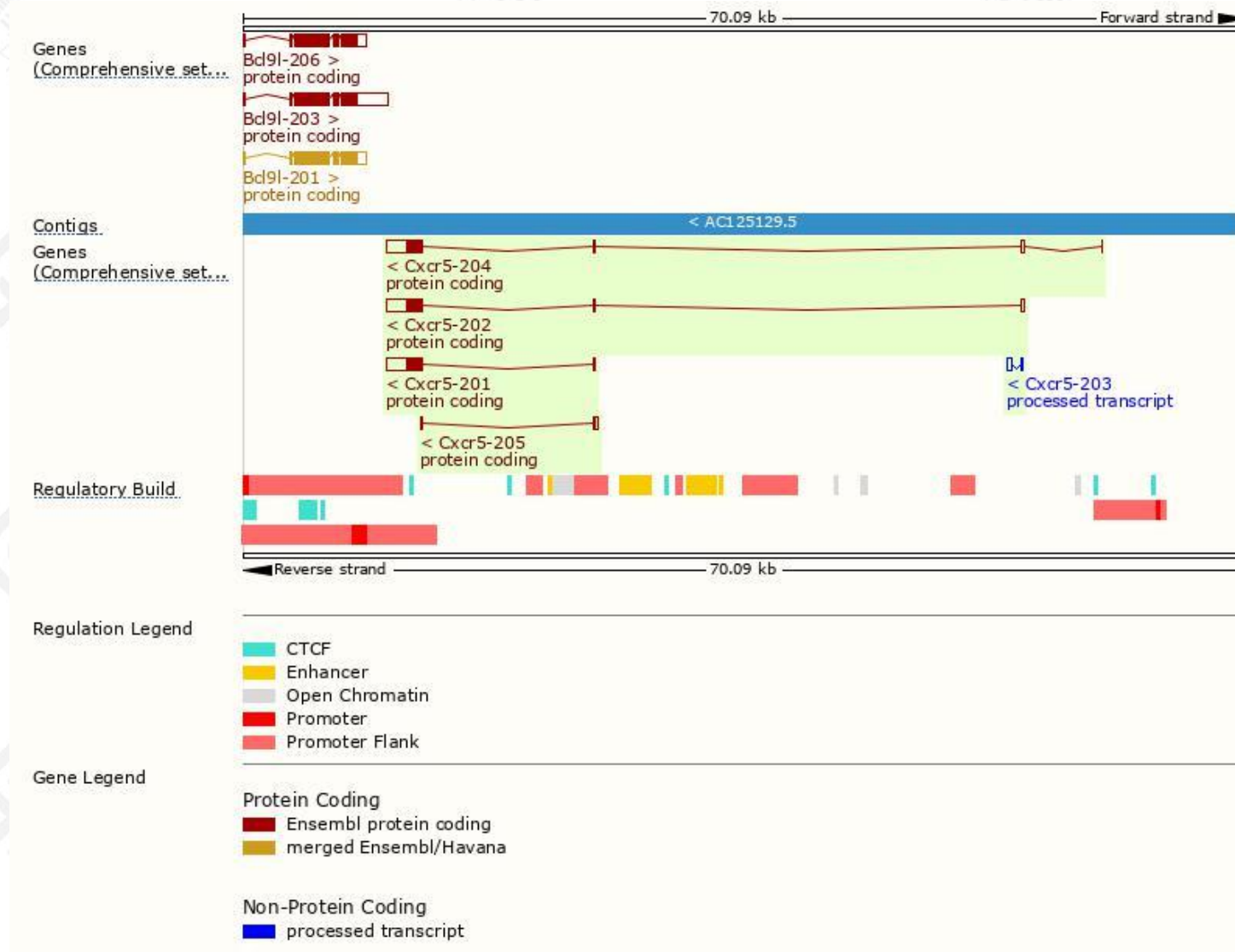
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cxcr5-204	ENSMUST00000215293.2	2846	374aa	Protein coding	CCDS23115		TSL:1 , GENCODE basic , APPRIS P1 ,
Cxcr5-202	ENSMUST00000179828.8	2824	374aa	Protein coding	CCDS23115		TSL:5 , GENCODE basic , APPRIS P1 ,
Cxcr5-201	ENSMUST00000062215.8	2614	374aa	Protein coding	CCDS23115		TSL:1 , GENCODE basic , APPRIS P1 ,
Cxcr5-205	ENSMUST00000215661.2	358	51aa	Protein coding	-		CDS 3' incomplete , TSL:1 ,
Cxcr5-203	ENSMUST00000213357.2	377	No protein	Processed transcript	-		TSL:3 ,

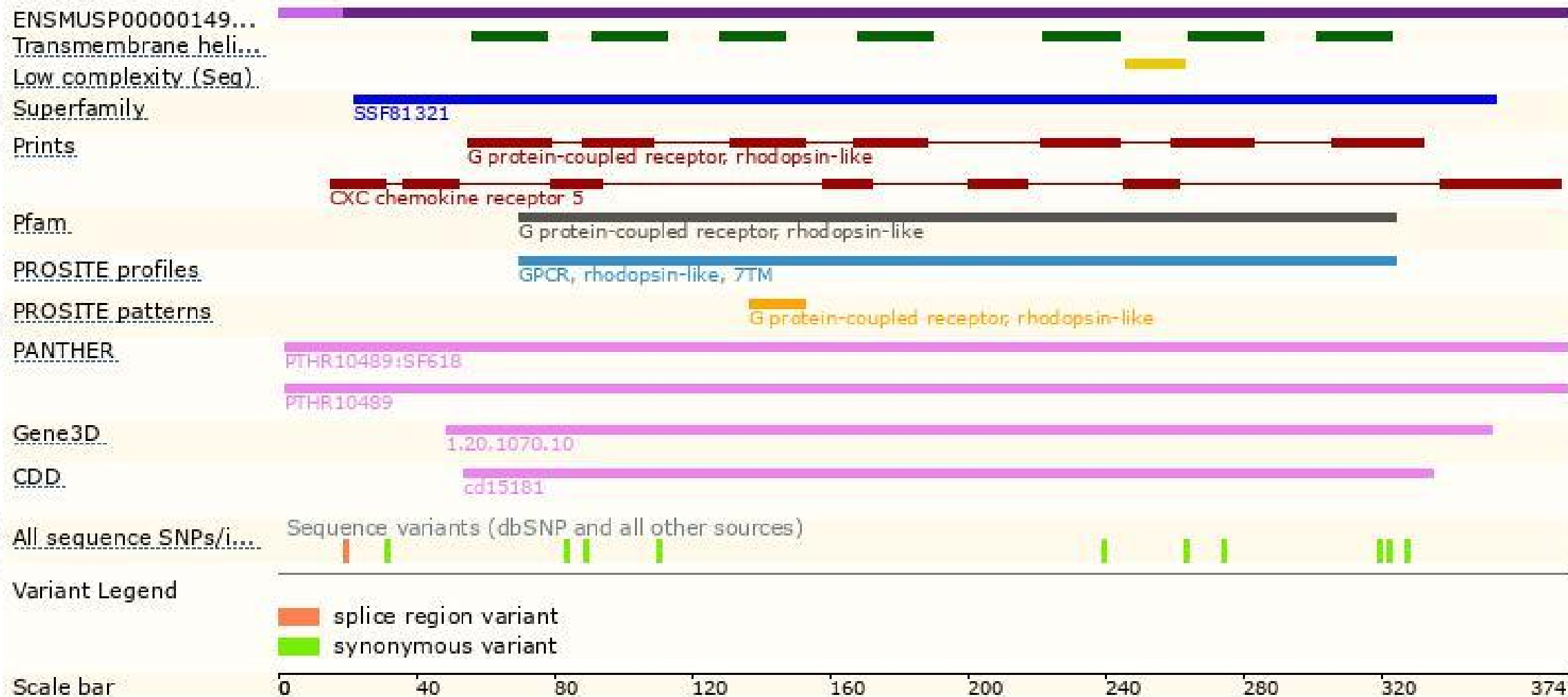
The strategy is based on the design of *Cxcr5-204* transcript,the transcription is shown below:



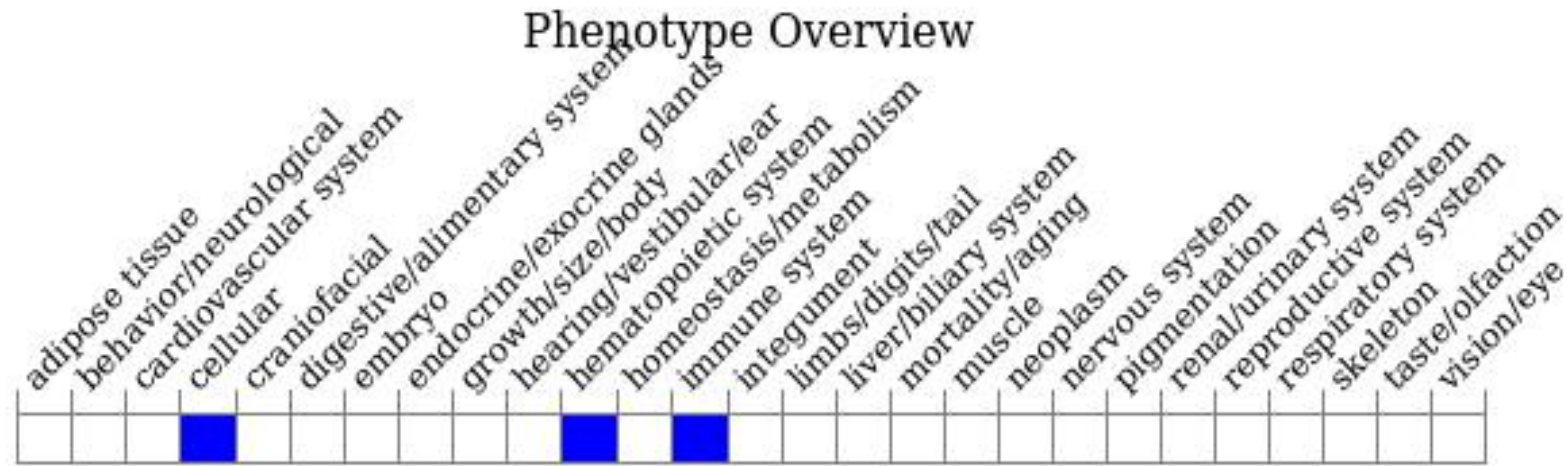
Genomic location distribution



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 mutants lack inguinal lymph nodes, have a few abnormal or no Peyer's patches, morphologically altered primary lymphoid follicles and no functional germinal centers in their spleen.

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

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