

Cxcl16 Cas9-KO Strategy

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Project Overview

Project Name

Cxcl16

Project type

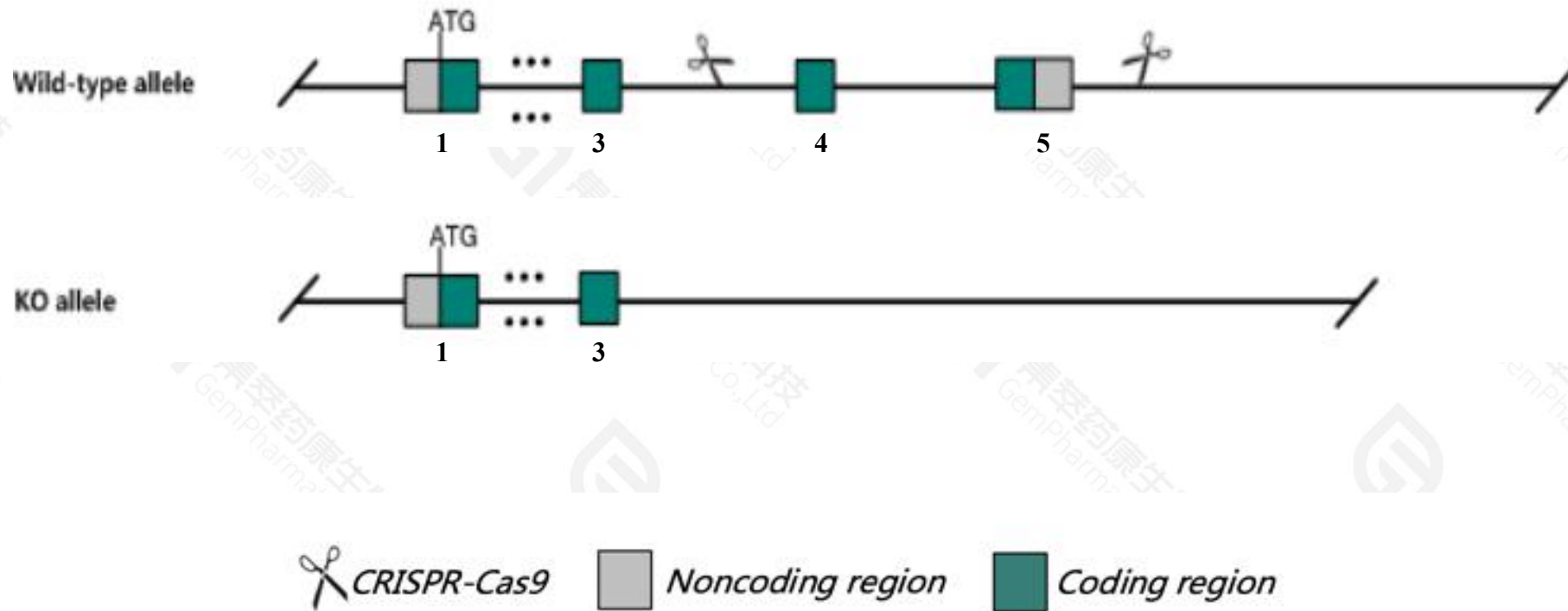
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Cxcl16* gene. The schematic diagram is as follows:



- The *Cxcl16* gene has 3 transcripts. According to the structure of *Cxcl16* gene, exon4-exon5 of *Cxcl16*-201(ENSMUST00000019064.9) 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 *Cxcl16* 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, mice homozygous for a null allele exhibit decreased NK T cells, decreased secretion and serum levels of IL4 and IFN-gamma, and decreased inhibition of B16 melanoma cell growth by alpha-galactosylceramide treatment.
- The knockout region is about 3 kb away from the 5-terminal of *Zmynd15* gene, which may affect the regulation of the 5-terminal of *Zmynd15* gene.
- The knockout region is about 200 bp away from the C-terminal of *Med11* gene, which may affect the regulation of the 3-terminal of *Med11* gene.
- The *Cxcl16* gene is located on the Chr11. 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.

Cxcl16 chemokine (C-X-C motif) ligand 16 [Mus musculus (house mouse)]

Gene ID: 66102, updated on 24-Apr-2022

Summary



Official Symbol Cxcl16 provided by [MGI](#)

Official Full Name chemokine (C-X-C motif) ligand 16 provided by [MGI](#)

Primary source [MGI:MGI:1932682](#)

See related [Ensembl:ENSMUSG00000018920](#)

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 0910001K24Rik, AV290116, BB024863, CXCL16v1, CXCL16v2, SR-PSOX, Zmynd15, b2b498Clo

Expression Broad expression in kidney adult (RPKM 38.8), lung adult (RPKM 36.7) and 18 other tissues [See more](#)

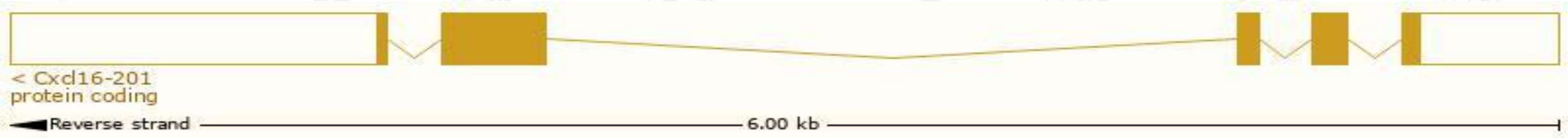
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

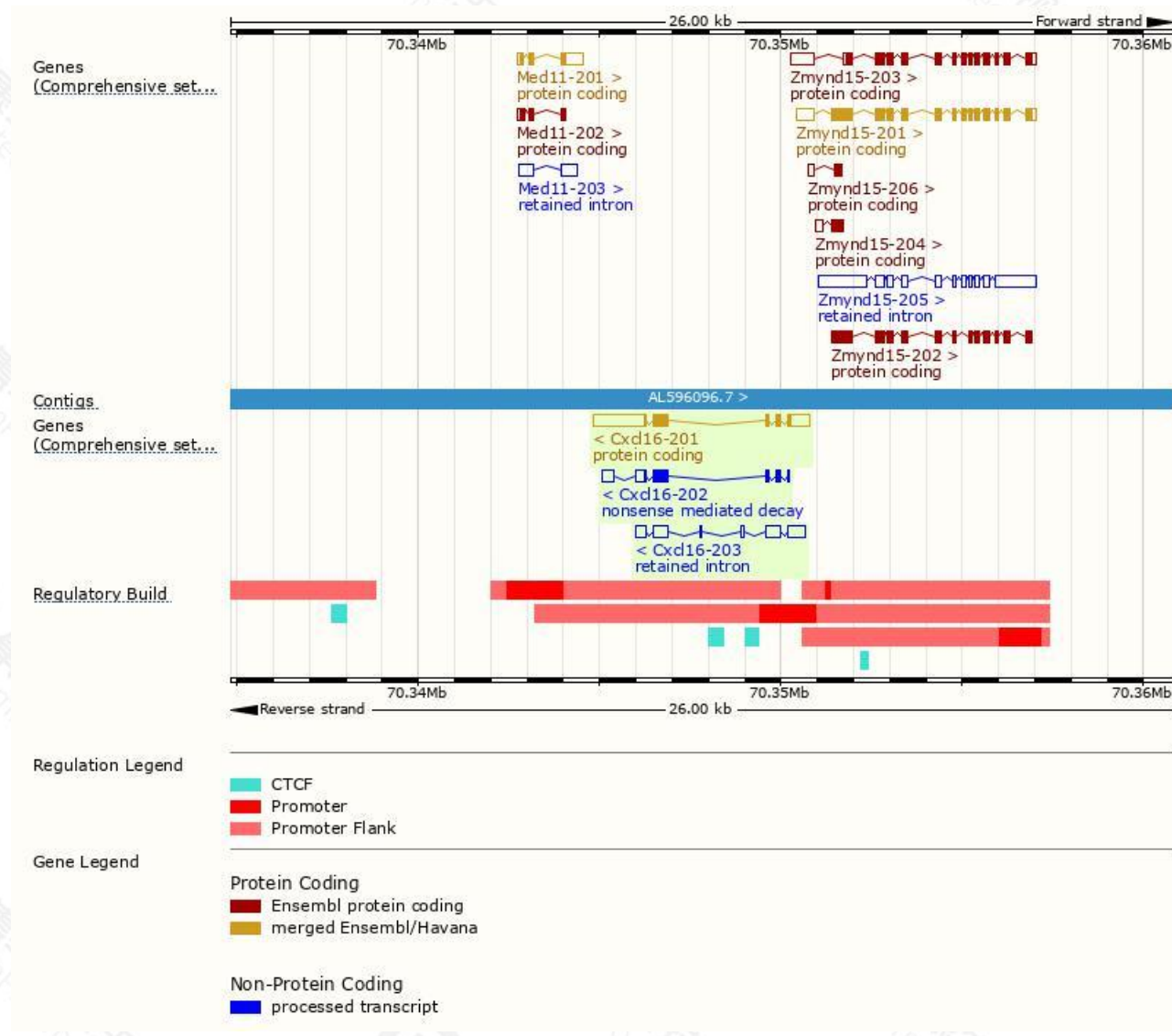
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cxcl16-201	ENSMUST00000019064.9	2699	246aa	Protein coding	CCDS24948		TSL:1 , GENCODE basic , APPRIS P1 ,
Cxcl16-202	ENSMUST00000126391.2	1267	233aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:1 ,
Cxcl16-203	ENSMUST00000154475.2	1662	No protein	Retained intron	-		TSL:2 ,

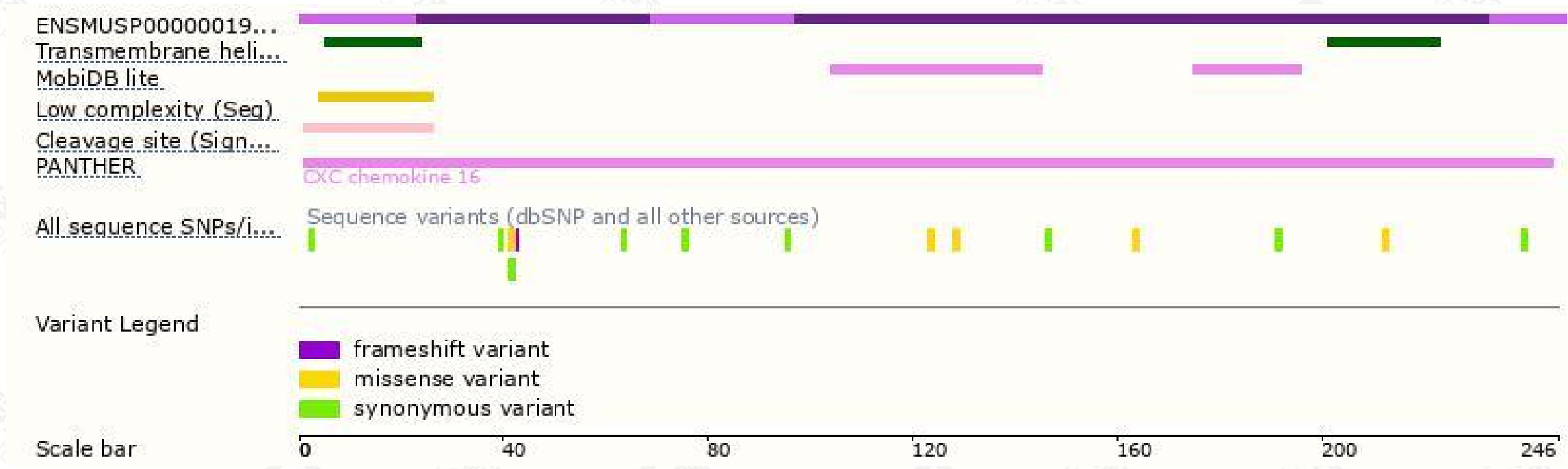
The strategy is based on the design of *Cxcl16-201* transcript,the transcription is shown below:



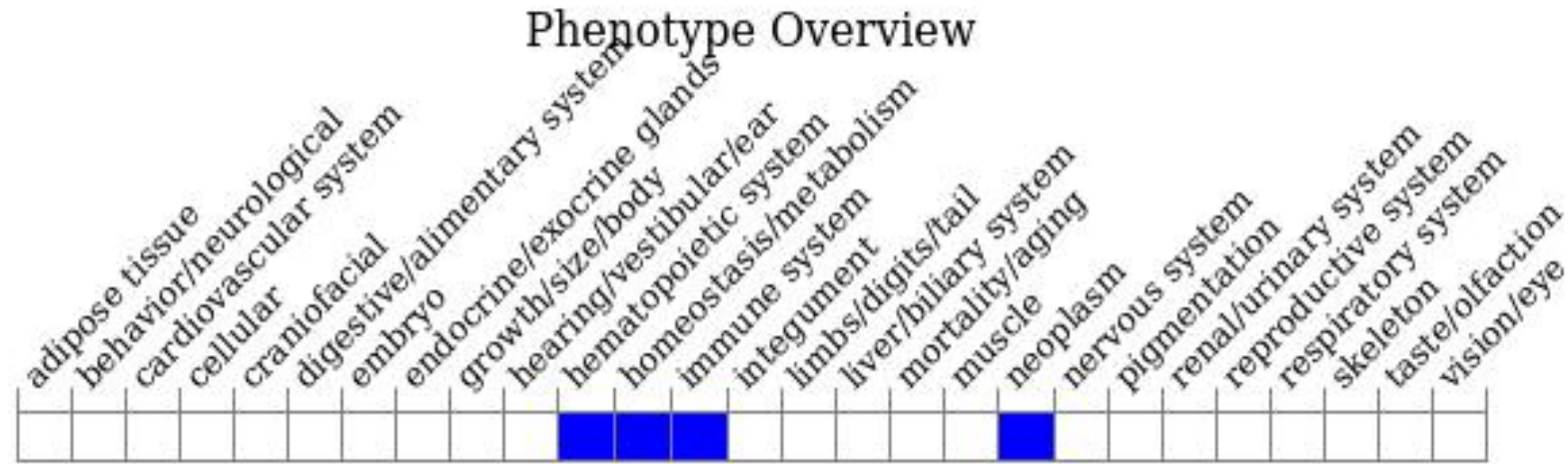
Genomic location distribution



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 null allele exhibit decreased NK T cells, decreased secretion and serum levels of IL4 and IFN-gamma, and decreased inhibition of B16 melanoma cell growth by alpha-galactosylceramide treatment.

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