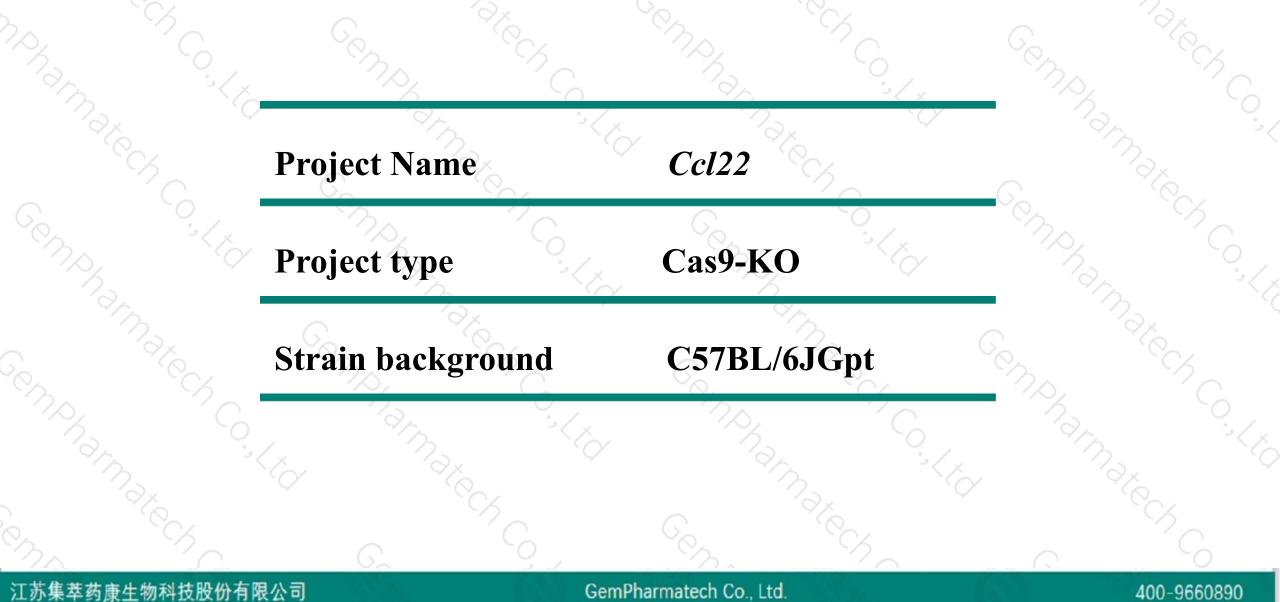


Ccl22 Cas9-KO Strategy

Designer: Reviewer: Design Date: Yang Zeng Xiaojing Li 2019-11-26

Project Overview

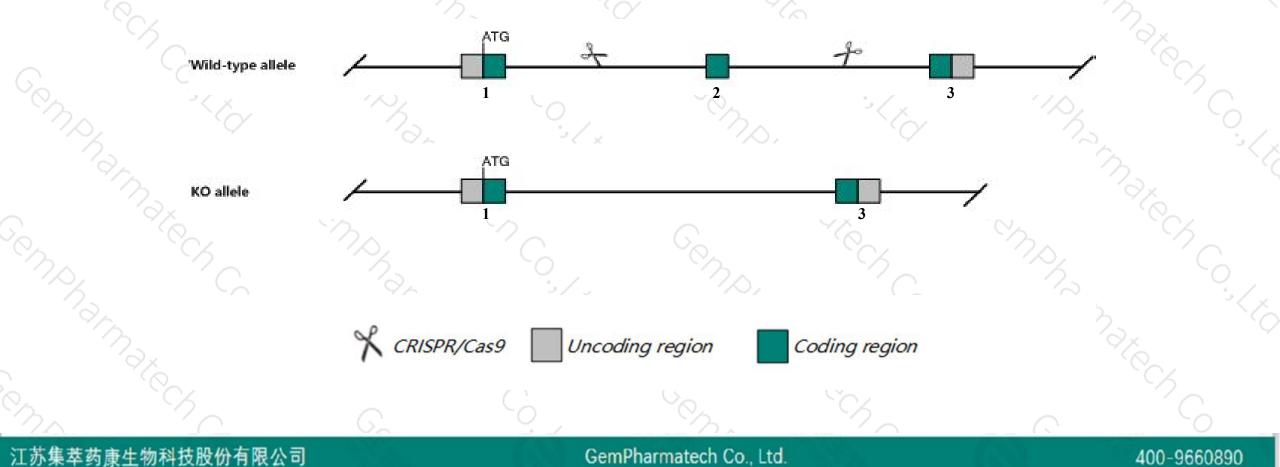




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Ccl22 gene. The schematic diagram is as follows:





- The Ccl22 gene has 2 transcripts. According to the structure of Ccl22 gene, exon2 of Ccl22-201 (ENSMUST00000034231.3) transcript is recommended as the knockout region. The region contains 124bp coding sequence.
 Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Ccl22 gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock out allele exhibit dendritic cell physiology relating to CCR4-mediated cell contacts between dendritic cells and cytotoxic T cells.
 - > The Ccl22 gene is located on the Chr8. 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.

Notice

Gene information (NCBI)



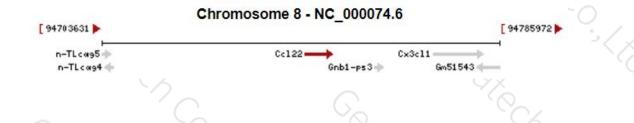
Ccl22 chemokine (C-C motif) ligand 22 [Mus musculus (house mouse)]

Gene ID: 20299, updated on 10-Oct-2019

Summary

*? 🗘

Official Symbol	Ccl22 provided by MGI							
Official Full Name	chemokine (C-C motif) ligand 22 provided by MGI							
Primary source	MGI:MGI:1306779							
See related	Ensembl:ENSMUSG0000031779							
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	MDC; DCBCK; ABCD-1; Scya22							
Expression	Biased expression in thymus adult (RPKM 44.5), mammary gland adult (RPKM 25.2) and 5 other tissues See more							
Orthologs	human all							
Second Second	Chromosome 8 - NC 000074.6							



Transcript information (Ensembl)



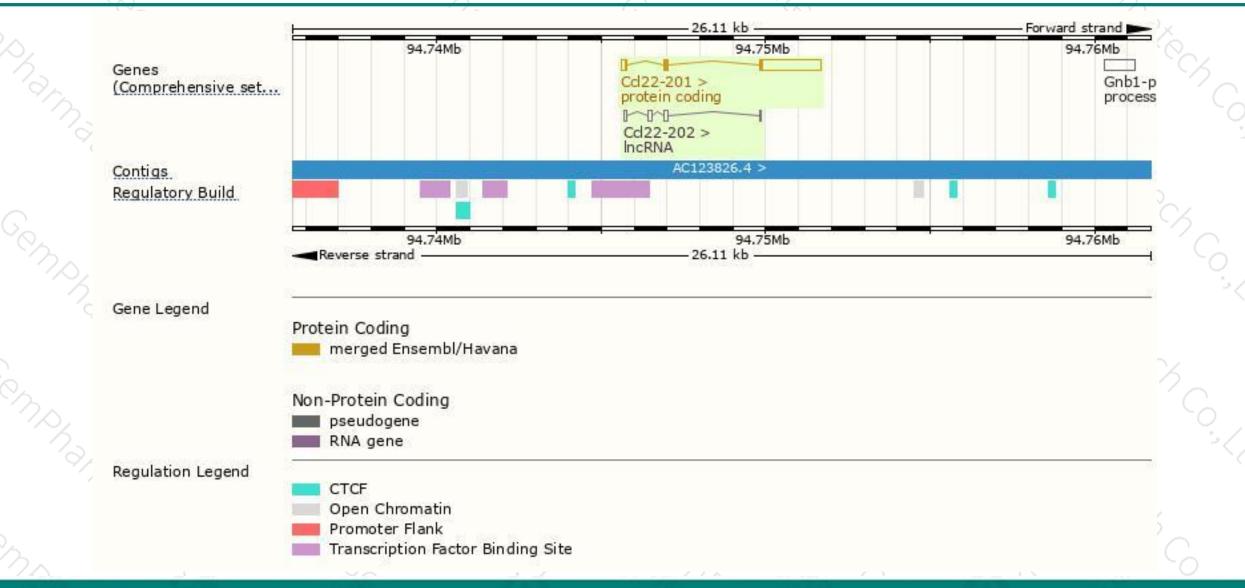
The gene has 2 transcripts, all transcripts are shown below:

Name 🖕	Transcript ID 🖕	bp 🍦	Protein 🖕	Translation ID	Biotype 🖕	CCDS 🖕	UniProt 🝦		Flags	\$
Ccl22-201	ENSMUST0000034231.3	2216	<u>92aa</u>	ENSMUSP0000034231.3	Protein coding	<u>CCDS40441</u> &	<u>088430</u> & <u>Q546S6</u> &	TSL:1	GENCODE basic	APPRIS P1
Ccl22-202	ENSMUST00000156137.1	409	No protein		IncRNA	-		TSL:3		

The strategy is based on the design of Ccl22-201 transcript, The transcription is shown below

6.11 kb Forward strand Cd22-201 > protein coding

Genomic location distribution



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400-9660890

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Protein domain



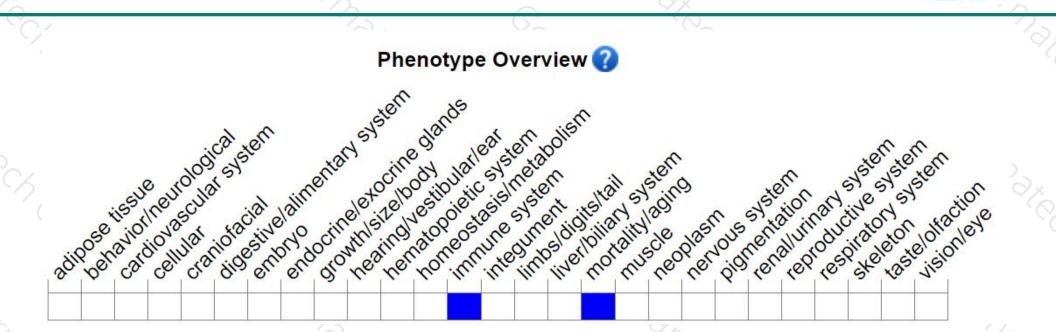
° C	G _e	19×		N ²	G	
ENSMUSP00000034 Low complexity (Seg)						20
Cleavage site (Sign Superfamily			Chemokine interleu	kin-8-like superfamily		
SMART			And the second second second	leukin-8-like domain	-	
Prints Pfam	PR00436		Chemokine i	nterleukin-8-like domai	n	
PROSITE patterns			CC chemoki	ne, conserved site		•
PANTHER	Chemokine beta	/gamma/delta				
Gene3D	C-C-motif cheme		2.40.50.40			
CDD			cd00272			
All sequence SNPs/i	Sequence varia	nts (dbSNP and all o	ther sources) <mark>Y</mark>			
Variant Legend	synonymo	us variant				
Scale bar	0 8	16 24	32 40	48 56	64 72	80 92
~~~	G_	í G	Gen Solo	i Solo	(	S 16

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# 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 exhibit dendritic cell physiology relating to CCR4-mediated cell contacts between dendritic cells and cytotoxic T cells.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



