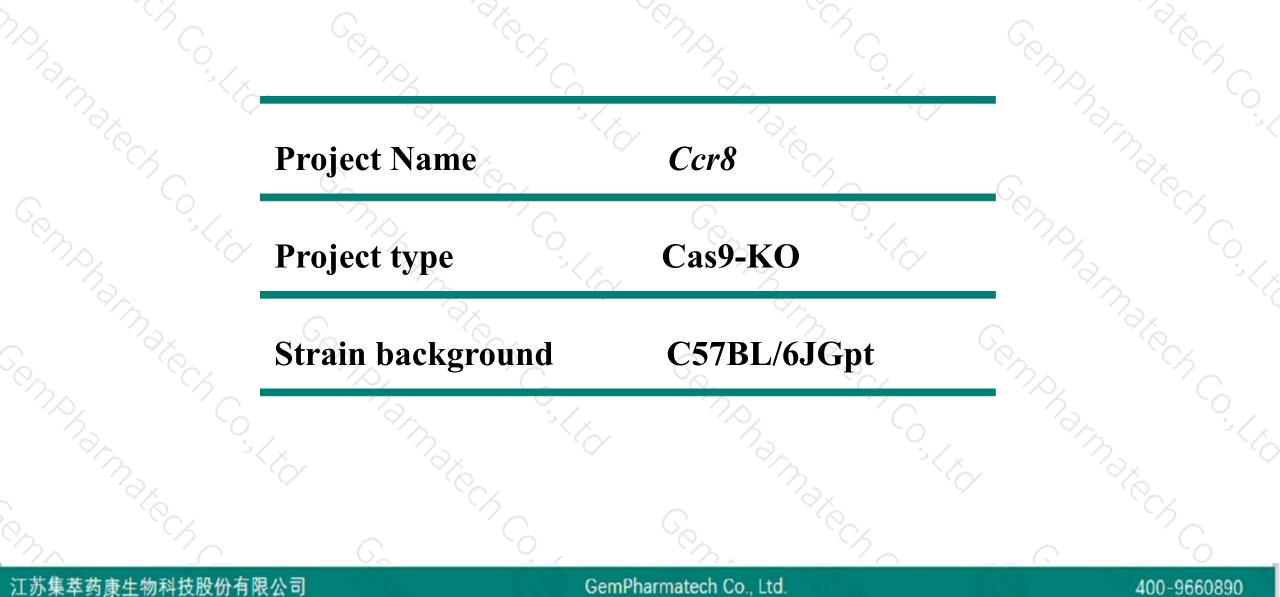


Ccr8 Cas9-KO Strategy

Designer: Reviewer: Design Date: Min Guan Yang Zeng 2018-6-28

Project Overview

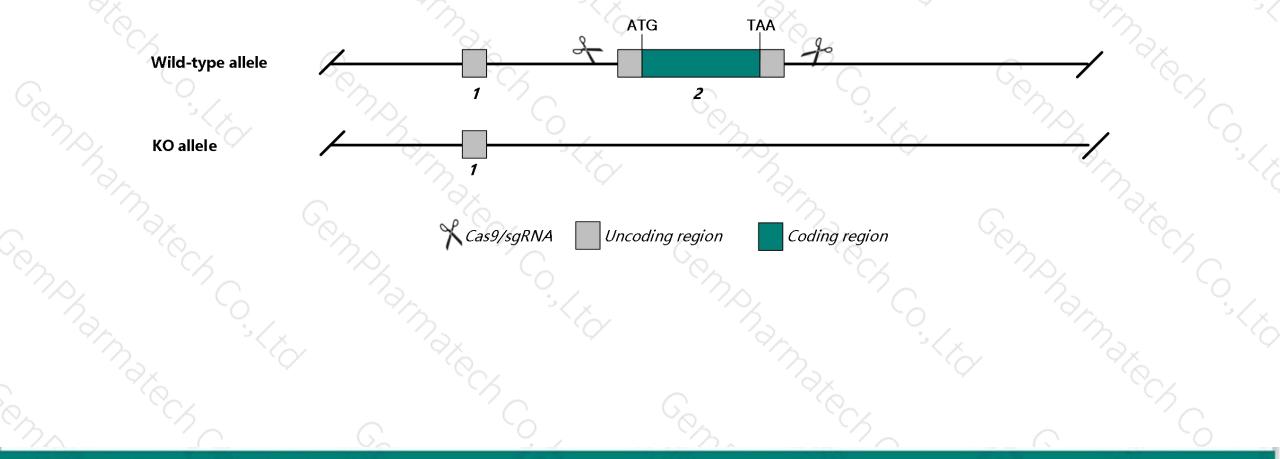




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Ccr8 gene. The schematic diagram is as follows:





- The Ccr8 gene has 1 transcript. According to the structure of Ccr8 gene, exon2 of Ccr8-201 (ENSMUST00000048777.3) transcript is recommended as the knockout region. The region contains all 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 *Ccr8* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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 either of two independently generated knock-out alleles show normal lung eosinophilia and Th2 cytokine responses in OVA-elicited asthma models. Mice homozygous for a third knock-out allele show a delay in onset of clinical signs of experimental autoimmune encephalomyelitis.
- The KO region is close to 5'UTR region of the *Gm47050* gene.Knockout the region may affect the regulatory function of *Gm47050* gene.
- The Ccr8 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.

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Gene information (NCBI)



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Ccr8 chemokine (C-C motif) receptor 8 [Mus musculus (house mouse)]

Gene ID: 12776, updated on 12-Aug-2019

Summary

Official Symbol Ccr8 provided by MGI **Official Full Name** chemokine (C-C motif) receptor 8 provided by MGI MGI:MGI:1201402 Primary source Ensembl:ENSMUSG0000042262 See related protein coding Gene type **RefSeq status** VALIDATED Organism Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Lineage Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus Also known as C-C; CCR-8; CKR-8; mCCR8; Cmkbr8; CC-CKR-8; C-C CKR-8 Biased expression in thymus adult (RPKM 6.3), mammary gland adult (RPKM 1.1) and 3 other tissues See more Expression Orthologs human all

Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

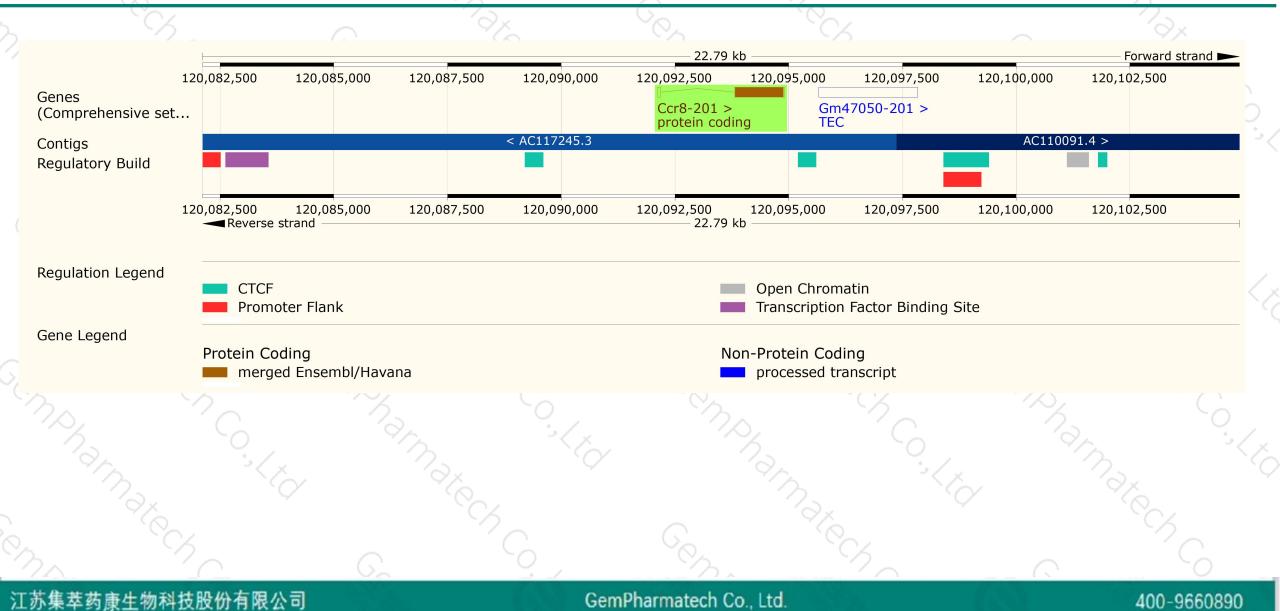
Name 🔺	Transcript ID	bp 🍦	Protein 🖕	Translation ID	Biotype 🍦	CCDS	UniProt 🝦		Flags	\$
Ccr8-201	ENSMUST0000048777.3	1175	<u>353aa</u>	ENSMUSP0000038473.2	Protein coding	<u>CCDS23621</u> &	<u>P56484</u> & <u>Q3ZB17</u> &	TSL:1	GENCODE basic	APPRIS P1

The strategy is based on the design of Ccr8-201 transcript, The transcription is shown below

	2.79 kb		Forward strand
Ccr8-201 >			
Ccr8-201 > protein coding			
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			C. YA
	$\gamma_{\alpha} \sim \gamma_{\alpha}$		
$\gamma_{\rm O} = \gamma_{\rm O}$	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Sha Sha	
		K. Co	
			x ns i
			Ch _a
γ_{\wedge}	G O		

Genomic location distribution



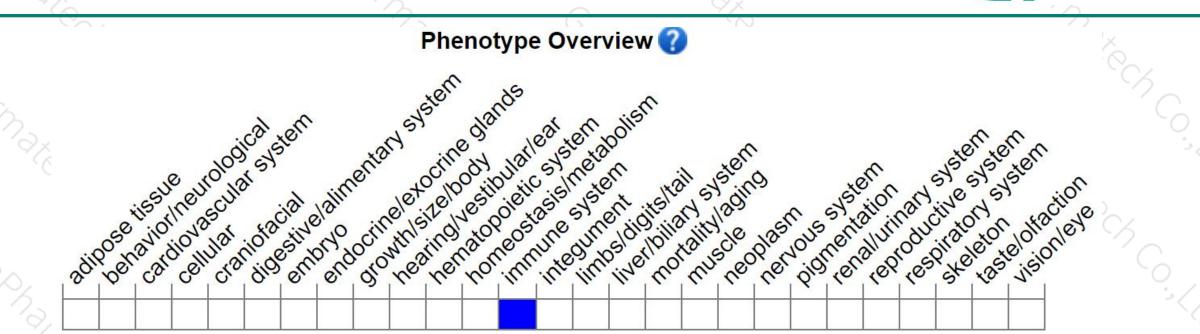


Protein domain



	~ 2									
	ENSMUSP00000038 Transmembrane heli Low complexity (Seg)								_	
	Superfamily	SSF81321								
	Prints						CC cher	mokine receptor 8	3	- 3
			Chemokine receptor family							
	Pfam		oupled receptor, rhodopsin-like						-	
	PROSITE profiles		protein-coupled receptor, rhodo CR, rhodopsin-like, 7TM	opsin-like						
	PROSITE patterns	Gr.		G protein-co	upled receptor, rhodopsin-li	ke				
	PANTHER	PTHR10489								
		PTHR10489:SF627								
	Gene3D	1.20.1070.10								
	CDD	cd15187							_	
	All sequence SNPs/i	Sequence variants (dbSNP	and all other sources)	10	n qu	$\mathbf{u} = \mathbf{u}$	1	1	0	
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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 either of two independently generated knock-out alleles show normal lung eosinophilia and Th2 cytokine responses in OVA-elicited asthma models. Mice homozygous for a third knock-out allele show a delay in onset of clinical signs of experimental autoimmune encephalomyelitis.

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



