

Ccr9 Cas9-KO Strategy

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Project Overview

Project Name

Ccr9

Project type

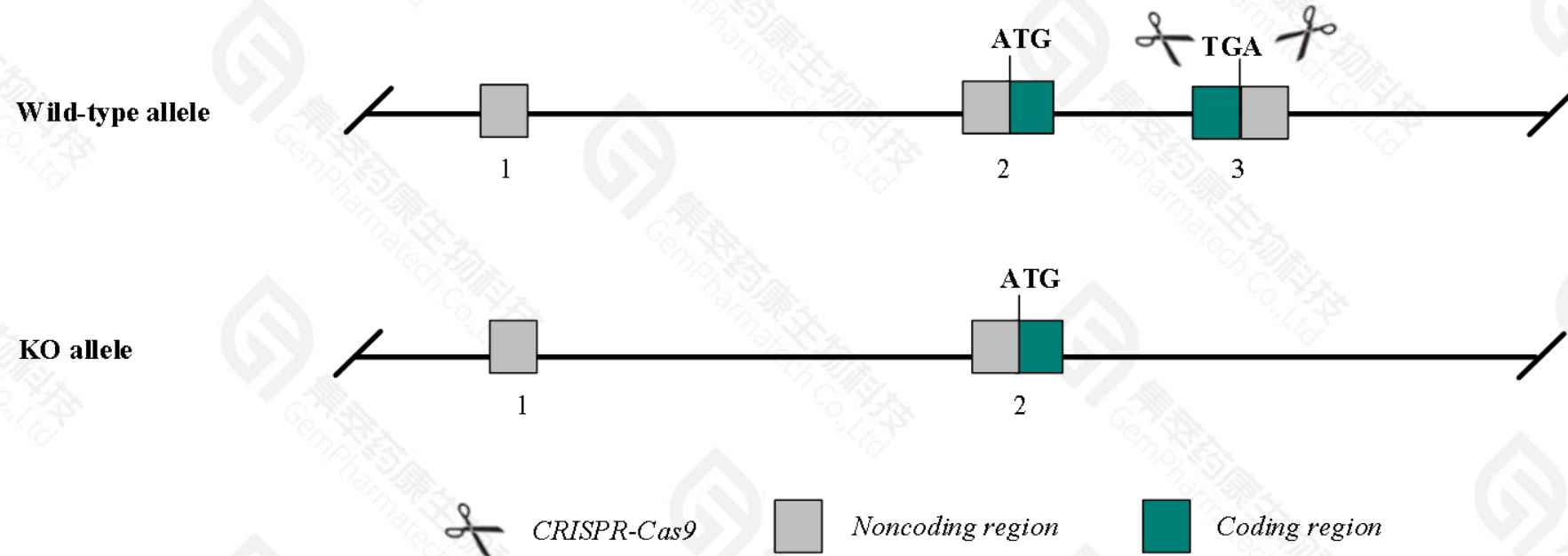
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Ccr9* gene. The schematic diagram is as follows:



- The *Ccr9* gene has 6 transcripts. According to the structure of *Ccr9* gene, exon3 of *Ccr9*-203(ENSMUST00000166236.9) 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 *Ccr9* 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 mice have altered trafficking of lymphocytes to the intestine.
- The editing site overlaps with the *Gm17021* gene, which may affect its function.
- The *Ccr9* 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.

Gene information (NCBI)

Ccr9 chemokine (C-C motif) receptor 9 [*Mus musculus* (house mouse)]

Gene ID: 12769, updated on 24-Apr-2022

[Download Datasets](#)

Summary

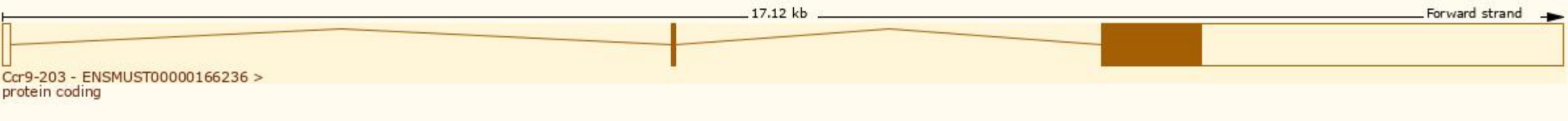
Official Symbol	Ccr9 provided by MGI
Official Full Name	chemokine (C-C motif) receptor 9 provided by MGI
Primary source	MGI:MGI:1341902
See related	Ensembl:ENSMUSG00000029530 AllianceGenome:MGI:1341902
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cmkbr10; GPR-9-6; A130091K22Rik
Summary	Enables C-C chemokine receptor activity. Acts upstream of or within CD8-positive, gamma-delta intraepithelial T cell differentiation and chemotaxis. Predicted to be located in cell surface. Predicted to be active in external side of plasma membrane. Is expressed in central nervous system; immune system; and retina. Orthologous to human CCR9 (C-C motif chemokine receptor 9). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Restricted expression toward thymus adult (RPKM 118.6) See more
Orthologs	human all
NEW	Try the new Gene table
	Try the new Transcript table

Transcript information (Ensembl)

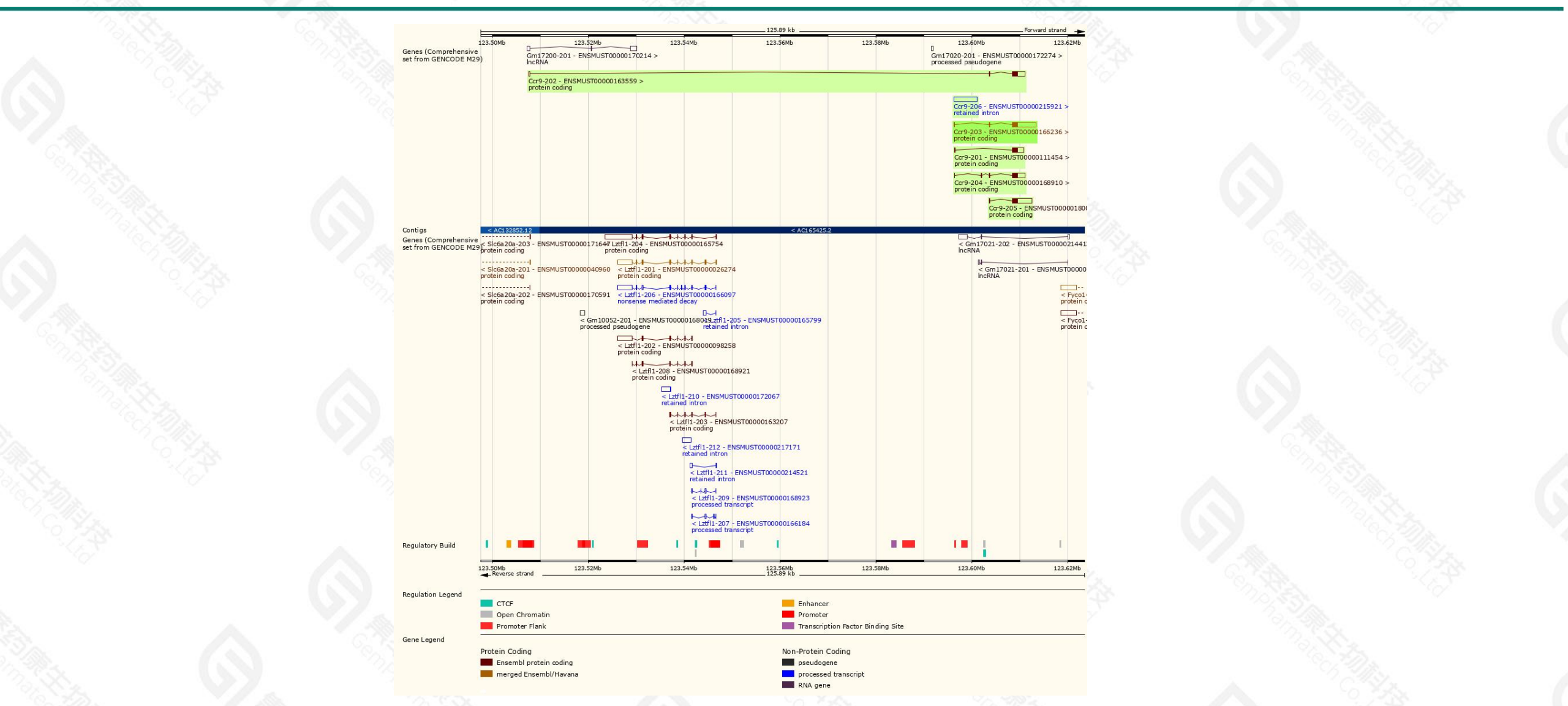
The gene has 6 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000215921.2	Ccr9-206	4811	No protein	Retained intron		-	TSL:NA	
ENSMUST00000180093.2	Ccr9-205	4239	369aa	Protein coding	CCDS23662	Q9WUT7	GENCODE basic	APPRIS P1 TSL:1
ENSMUST00000168910.2	Ccr9-204	2888	369aa	Protein coding	CCDS23662	Q9WUT7	GENCODE basic	APPRIS P1 TSL:1
ENSMUST00000166236.9	Ccr9-203	5197	369aa	Protein coding	CCDS23662	Q9WUT7	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000163559.8	Ccr9-202	3004	369aa	Protein coding	CCDS23662	Q9WUT7	GENCODE basic	APPRIS P1 TSL:1
ENSMUST00000111454.4	Ccr9-201	2620	357aa	Protein coding		F8WIS0	GENCODE basic	TSL:5

The strategy is based on the design of *Ccr9-203* transcript,the transcription is shown below:



集萃药康
GemPharmatech



Protein domain

ENSMUSP00000127024.2

Transmembrane helices

Low complexity (Seg)

AFDB-ENSP mappings

Superfamily

Prints

Chemokine receptor family

G protein-coupled receptor, rhodopsin-like

CC chemokine receptor 9

Pfam

G protein-coupled receptor, rhodopsin-like

PROSITE profiles

GPCR, rhodopsin-like, 7TM

PROSITE patterns

G protein-coupled receptor, rhodopsin-like

PANTHER

PTHR10489:SF664

PTHR10489

Gene3D

1.20.1070.10

All sequence SNPs/...

Sequence variants (dbSNP and all other sources)

Variant Legend

stop gained

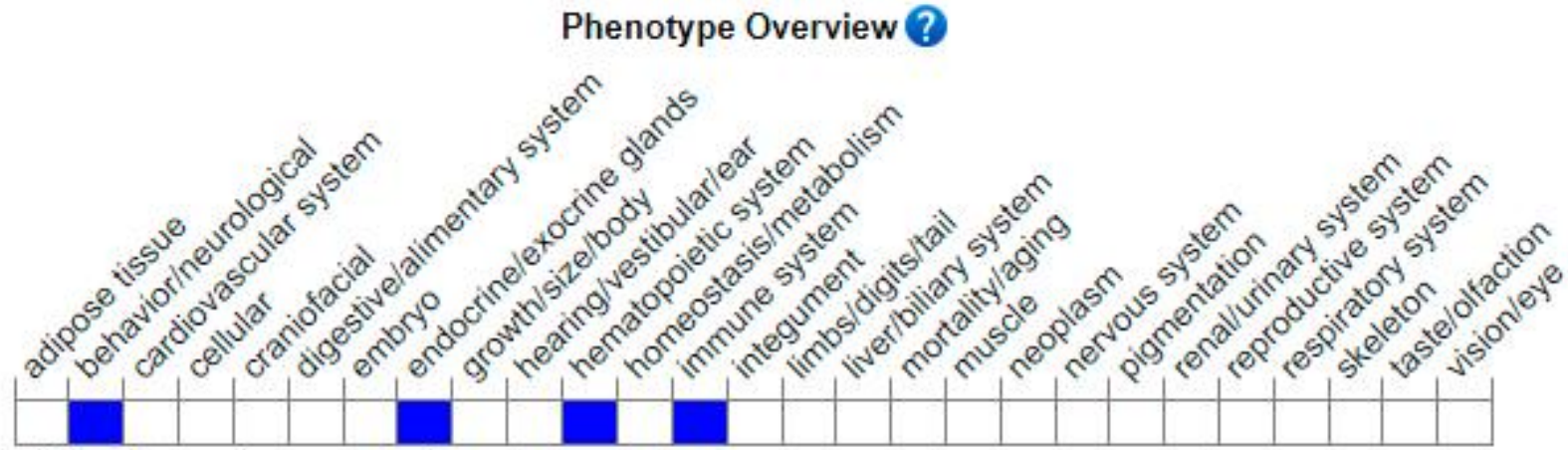
synonymous variant

missense variant

Scale bar

0 40 80 120 160 200 240 280 320 360

Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

Homozygous null mice have altered trafficking of lymphocytes to the intestine.

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

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