

# *Ccrl2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Ccrl2*

**Project type**

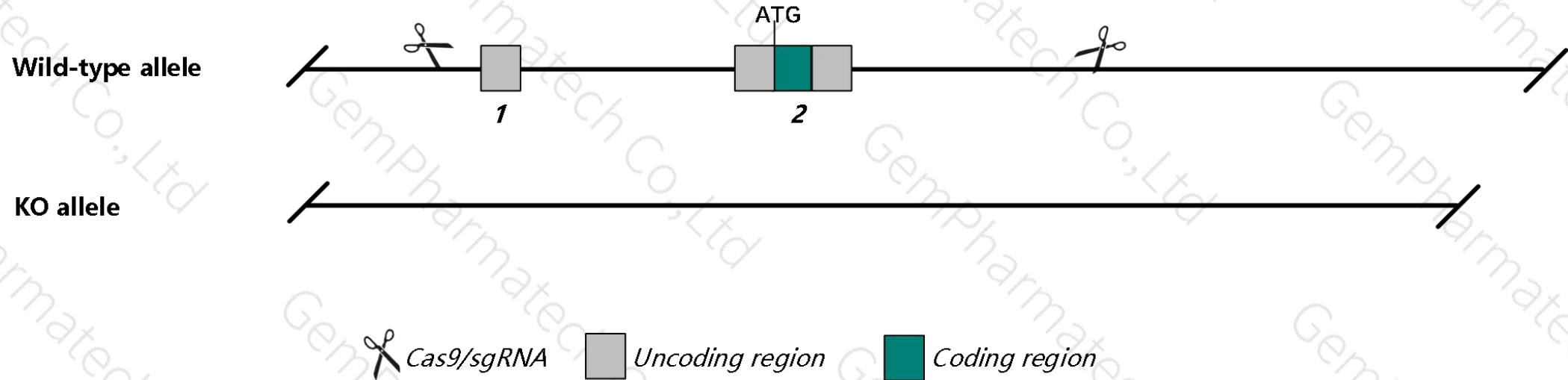
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccrl2* gene. The schematic diagram is as follows:



- The *Ccrl2* gene has 3 transcripts. According to the structure of *Ccrl2* gene, exon1-exon2 of *Ccrl2-201* (ENSMUST00000111888.2) 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 *Ccrl2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a targeted null mutation do not exhibit any significant abnormalities compared to controls.
- The KO region contains functional region of the *Gm43814* gene. Knockout the region may affect the function of *Gm43814* gene.
- The *Ccrl2* 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)

## Ccr12 chemokine (C-C motif) receptor-like 2 [Mus musculus (house mouse)]

Gene ID: 54199, updated on 31-Jan-2019

### Summary



<b>Official Symbol</b>	Ccr12 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	chemokine (C-C motif) receptor-like 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1920904</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000043953</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1810047I05Rik, Ackr5, CCR11, Cmkbr1l2, E01, L-CCR
<b>Expression</b>	Broad expression in lung adult (RPKM 16.6), placenta adult (RPKM 10.7) and 17 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

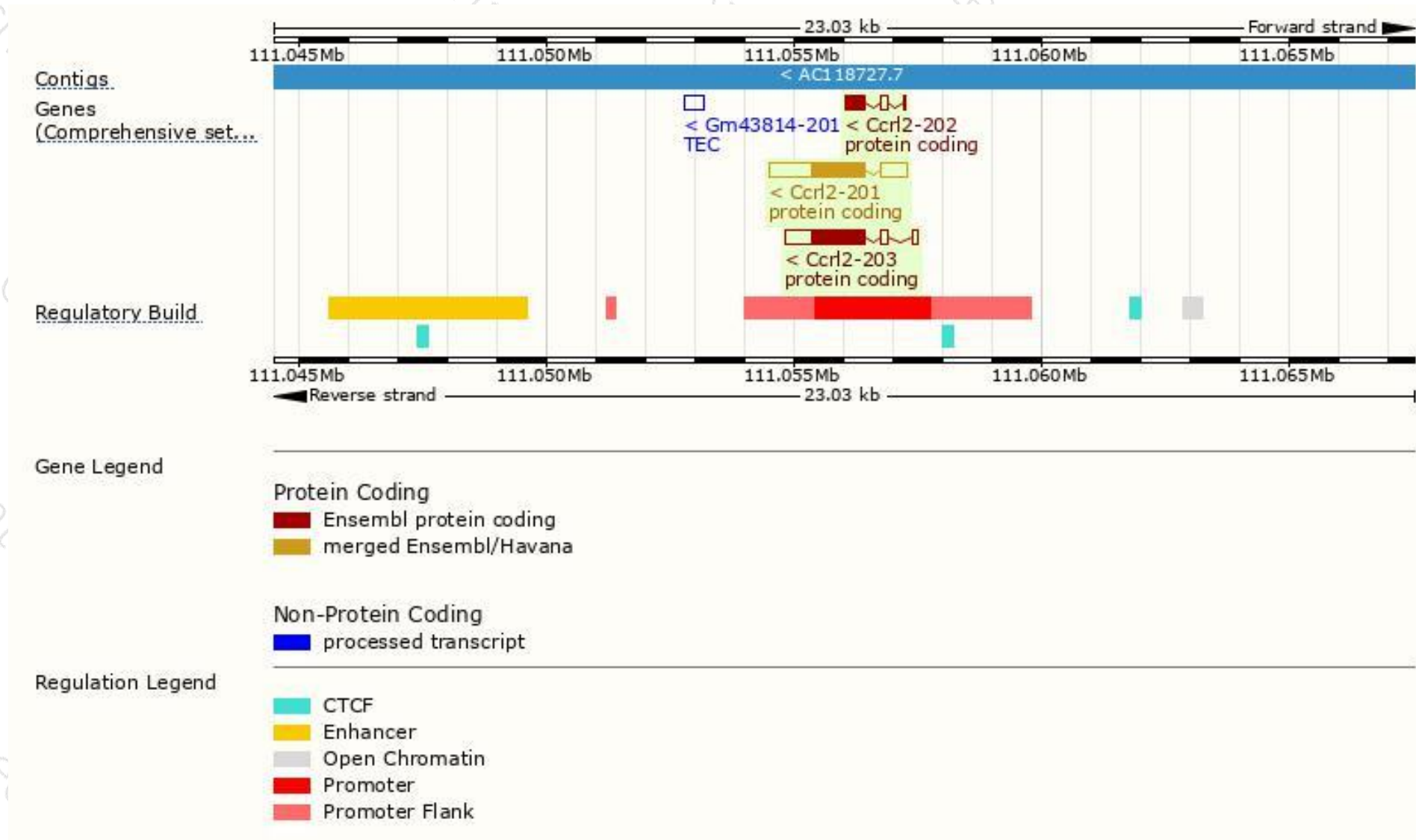
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccrl2-201	<a href="#">ENSMUST00000111888.2</a>	2459	<a href="#">360aa</a>	Protein coding	<a href="#">CCDS23582</a>	<a href="#">Q35457</a>	TSL:1 GENCODE basic APPRIS P1
Ccrl2-203	<a href="#">ENSMUST00000199839.4</a>	1864	<a href="#">360aa</a>	Protein coding	<a href="#">CCDS23582</a>	<a href="#">Q35457</a>	TSL:1 GENCODE basic APPRIS P1
Ccrl2-202	<a href="#">ENSMUST00000195968.1</a>	569	<a href="#">133aa</a>	Protein coding	-	<a href="#">A0A0G2JFB5</a>	CDS 3' incomplete TSL:2

The strategy is based on the design of *Ccrl2-201* transcript,The transcription is shown below

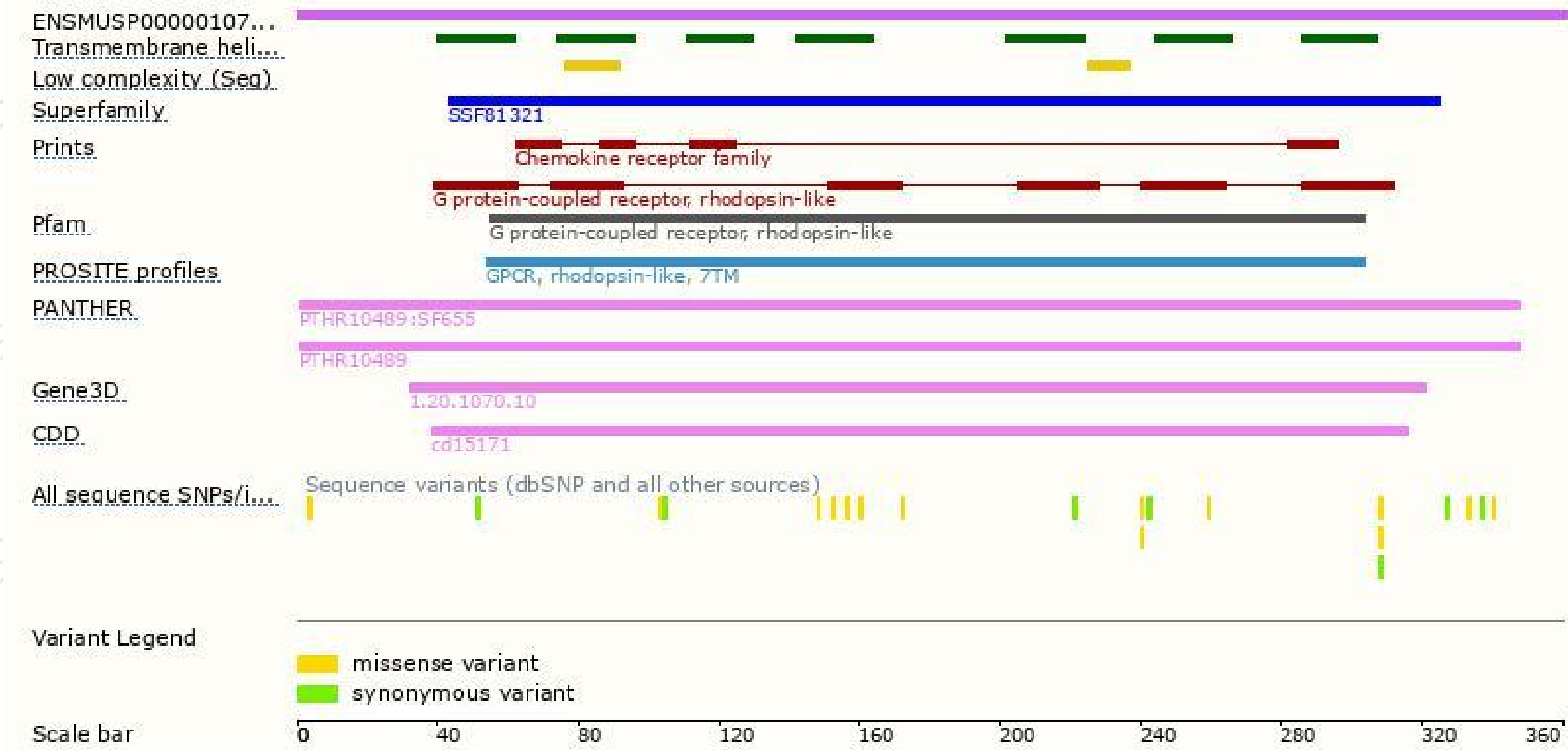


# Genomic location distribution

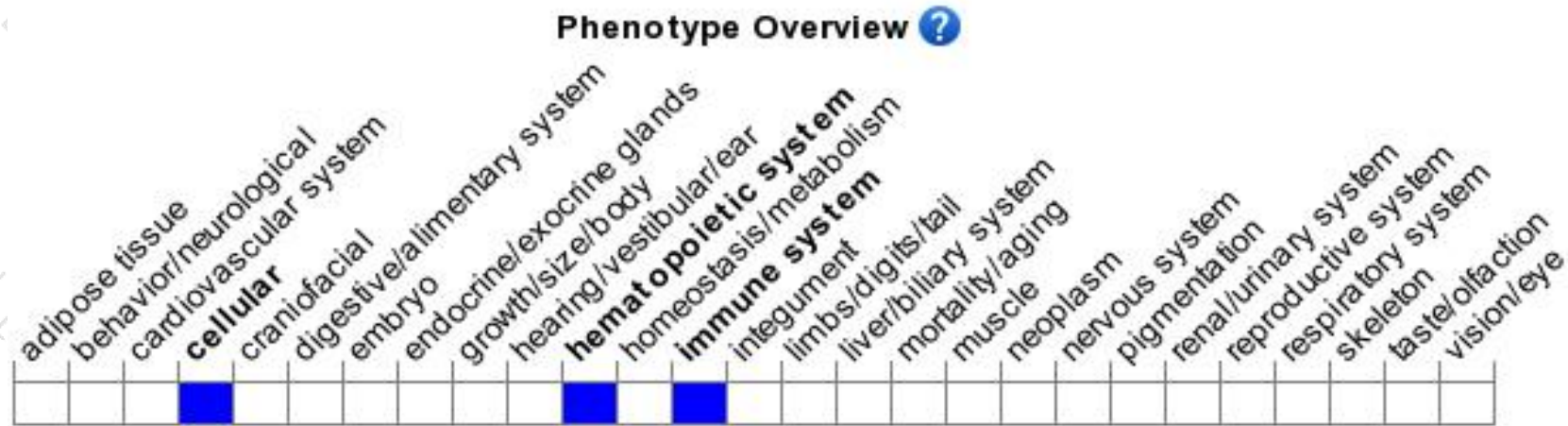




# Protein domain



# 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 targeted null mutation do not exhibit any significant abnormalities compared to controls.

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

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