# *Ccl20* Cas9-KO Strategy

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# Project Overview

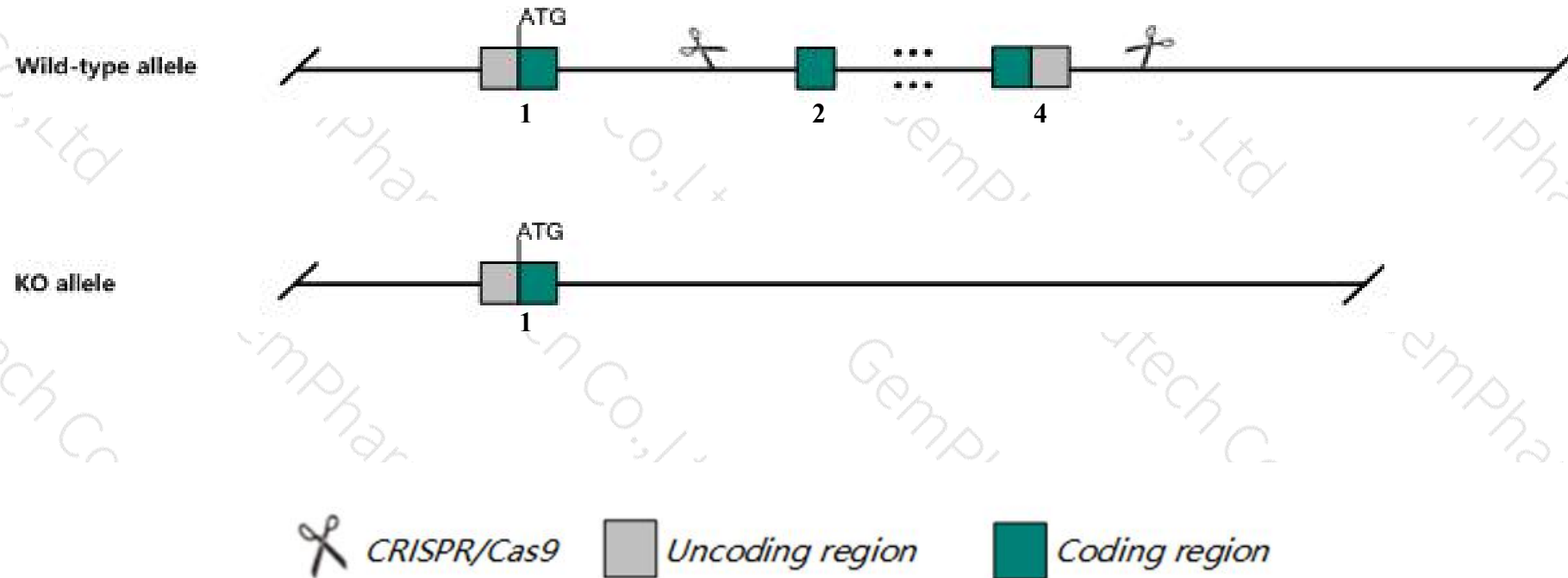| | |
|---|---|
| **Project Name** | *Ccl20* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccl20* gene. The schematic diagram is as follows:

# Technical routes

➢ The *Ccl20* gene has 3 transcripts. According to the structure of *Ccl20* gene, exon2-exon4 of *Ccl20-202* (ENSMUST00000113437.8) transcript is recommended as the knockout region.The region contains 215bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ccl20* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

➢ The *Ccl20* gene is located on the Chr1. 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）

## Ccl20 chemokine (C-C motif) ligand 20 [Mus musculus (house mouse)]

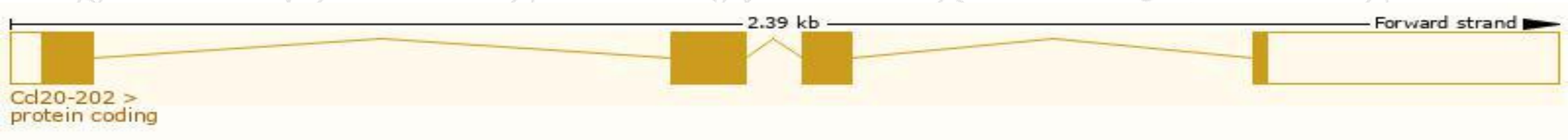Gene ID: 20297, updated on 12-Mar-2019

### ▲ Summary

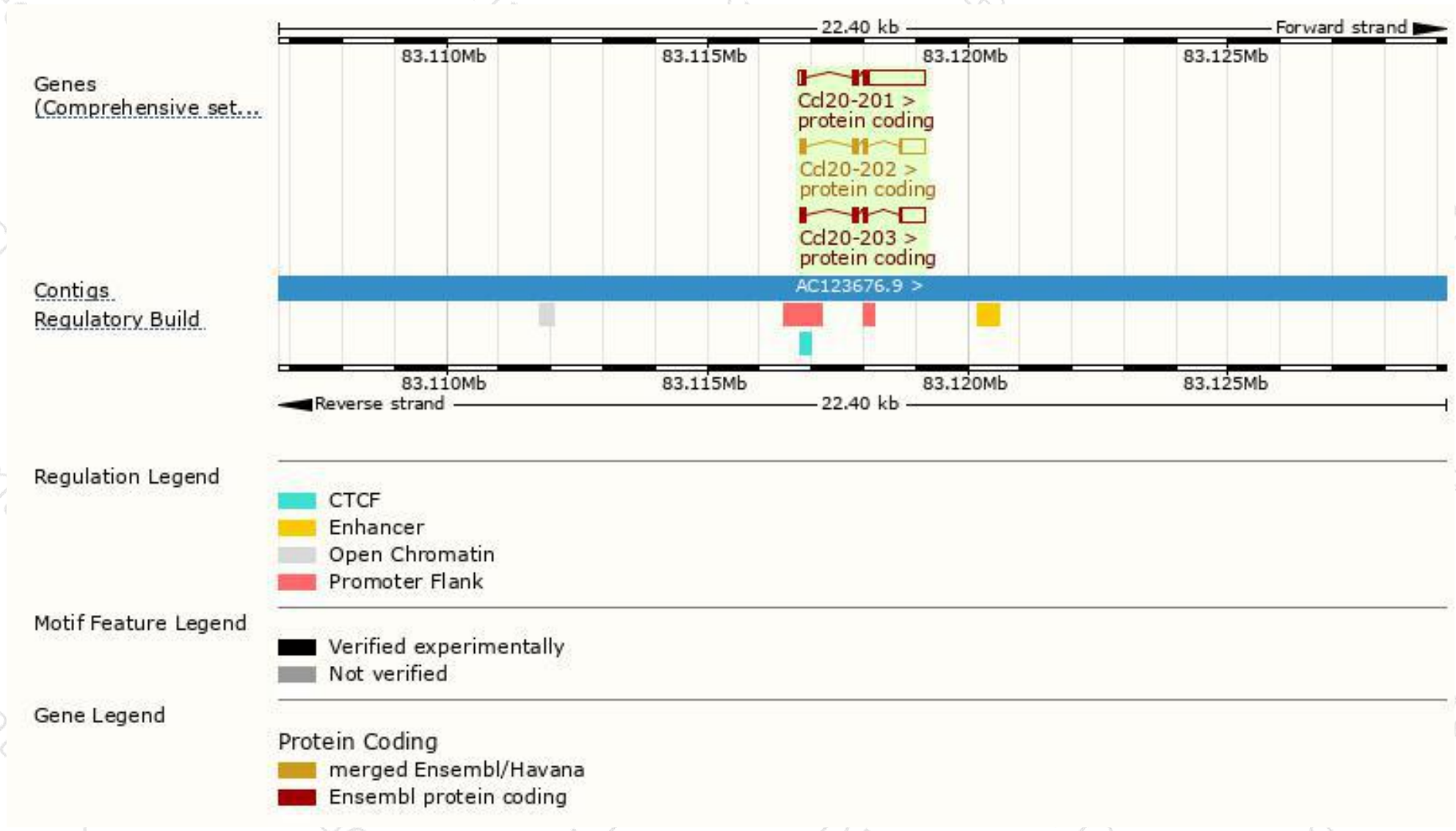| | |
|---|---|
| **Official Symbol** | Ccl20 provided by MGI |
| **Official Full Name** | chemokine (C-C motif) ligand 20 provided by MGI |
| **Primary source** | MGI:MGI:1329031 |
| **See related** | Ensembl:ENSMUSG00000026166 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | CKb4, LARC, MIP-3A, MIP-3[a], MIP3A, ST38, Scya20, exodus-1 |
| **Expression** | Biased expression in duodenum adult (RPKM 6.4), small intestine adult (RPKM 4.1) and 3 other tissuesSee 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 |
|------|--------------|-----|---------|---------|------|---------|-------|
| Ccl20-202 | ENSMUST00000113437.8 | 794 | 97aa | Protein coding | CCDS35632 | O89093 Q54AI7 | TSL:1 GENCODE basic APPRIS P3 |
| Ccl20-203 | ENSMUST00000186832.1 | 772 | 96aa | Protein coding | CCDS78638 | O89093 Q642U4 | TSL:1 GENCODE basic APPRIS ALT2 |
| Ccl20-201 | ENSMUST00000027351.12 | 1417 | 102aa | Protein coding | - | F8WHA7 | TSL:1 GENCODE basic |

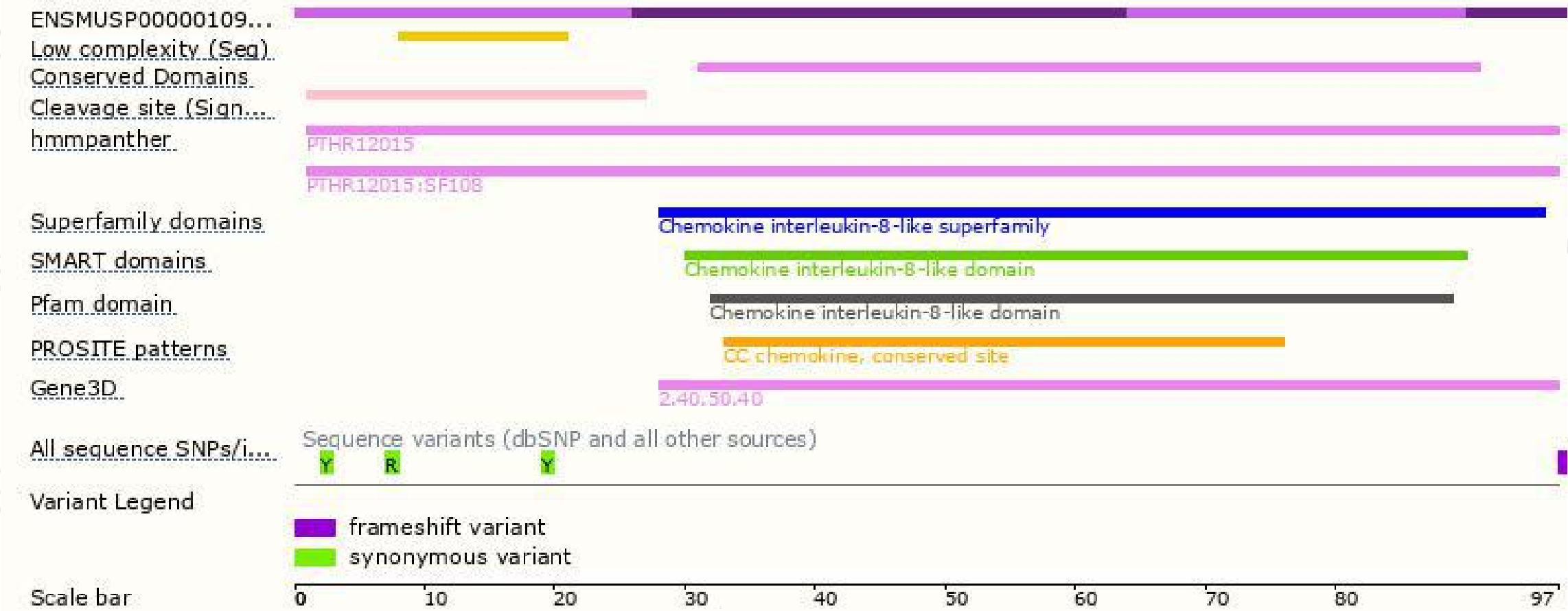The strategy is based on the design of *Ccl20-202* transcript,The transcription is shown below

# Genomic location distribution

# Protein domain



ENSMUSP00000109...
Low complexity (Seg)
Conserved Domains
Cleavage site (Sign...
hmmpanther
PTHR12015
PTHR12015:SF108

Superfamily domains
Chemokine interleukin-8-like superfamily

SMART domains
Chemokine interleukin-8-like domain

Pfam domain
Chemokine interleukin-8-like domain

PROSITE patterns
CC chemokine, conserved site

Gene3D
2.40.50.40

All sequence SNPs/i...
Sequence variants (dbSNP and all other sources)
Y    R         Y

Variant Legend

■ frameshift variant
■ synonymous variant

Scale bar
0    10    20    30    40    50    60    70    80    97

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