# *Rcn3* Cas9-KO Strategy

**Designer: Xueting Zhang**

**Reviewer: Daohua Shen**

**Design Date: 2020-6-10**

# Project Overview

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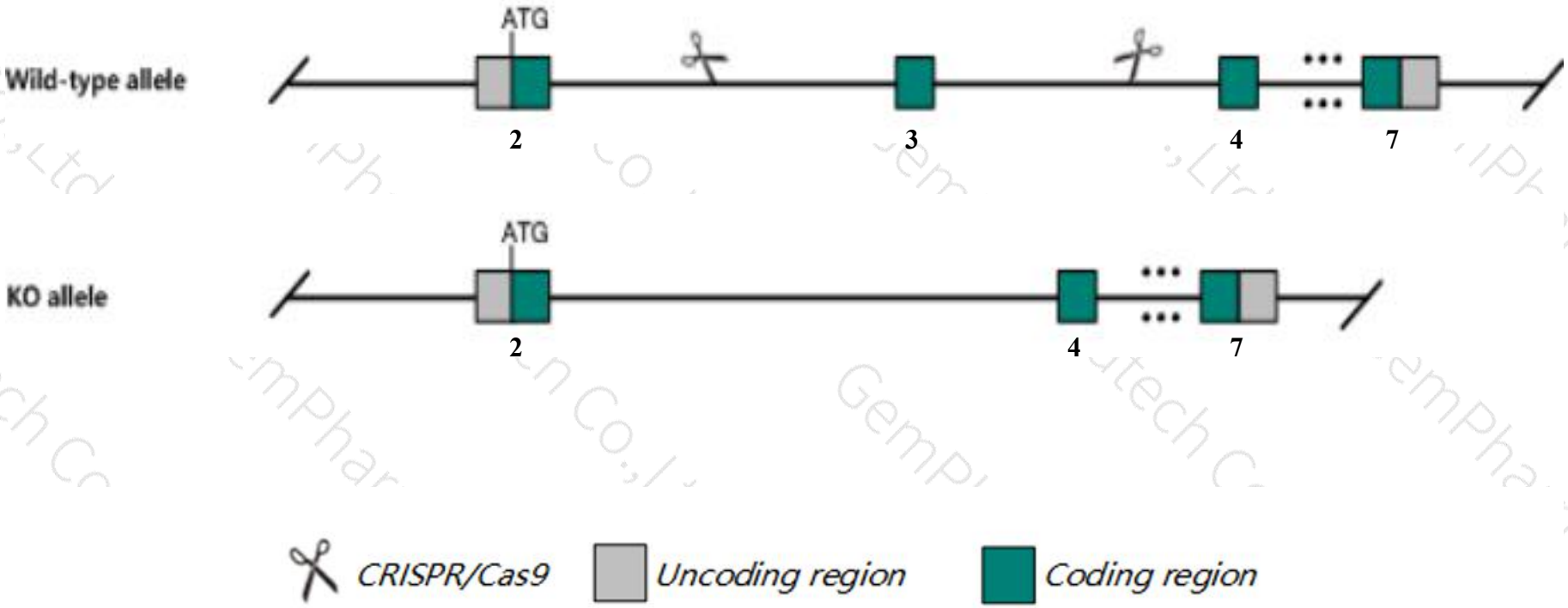
|---|---|
| **Project Name** | ***Rcn3*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rcn3* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Rcn3* gene has 9 transcripts. According to the structure of *Rcn3* gene, exon3 of *Rcn3-201* (ENSMUST00000019683.10) transcript is recommended as the knockout region.The region contains 203bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rcn3* gene. The brief process is as follows: CRISPR/Cas9 system v

# Notice

- According to the existing MGI data,mice homozygous for a knock-out allele exhibit neonatal lethality due to atelectasis-induced respiratory distress associated with failure of type ii pneumocyte maturation, decreased surfactant protein secretion, altered surfactant phospholipid homeostasis, and abnormal lamellar body formation.
- Transcript *Rcn3*-203&206 may not be affected.
- The effect on transcript *Rcn3*-205&209 is unknown.
- The knockout region is near to the N-terminal of *Gm45669* gene,this strategy may influence the regulatory function of the N-terminal of *Gm45669* gene.
- The *Rcn3* gene is located on the Chr7. 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）

集萃药康 GemPharmatech

## Rcn3 reticulocalbin 3, EF-hand calcium binding domain [Mus musculus (house mouse)]

Gene ID: 52377, updated on 13-Mar-2020

### Summary

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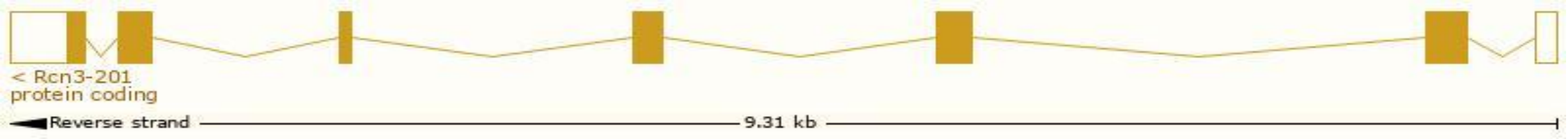
|---|---|
| **Official Symbol** | Rcn3 provided by MGI |
| **Official Full Name** | reticulocalbin 3, EF-hand calcium binding domain provided by MGI |
| **Primary source** | MGI:MGI:1277122 |
| **See related** | Ensembl:ENSMUSG00000019539 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 6030455P07Rik, D530026G20Rik, D7Ertd671e, RLP49 |
| **Expression** | Broad expression in limb E14.5 (RPKM 194.2), ovary adult (RPKM 178.1) and 21 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

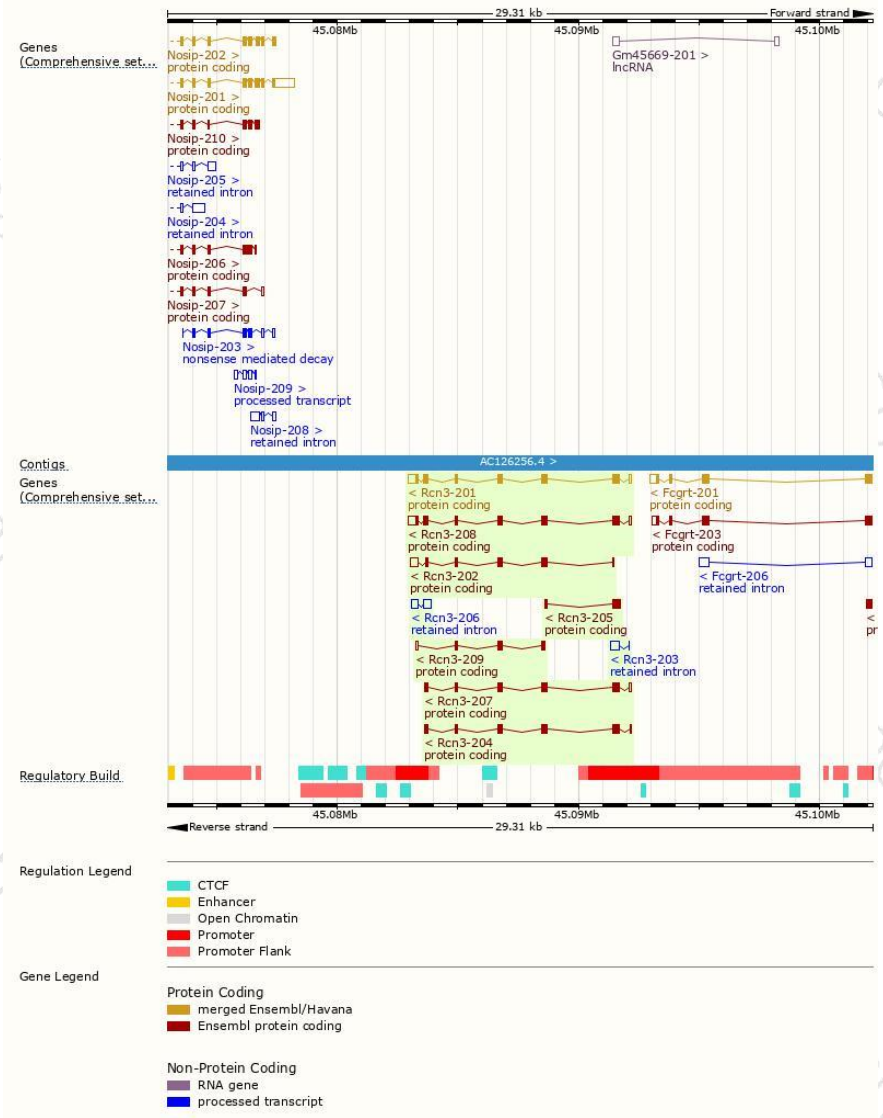
The gene has 9 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Rcn3-201 | ENSMUST00000019683.10 | 1462 | 328aa | Protein coding | CCDS21229 | Q8BH97 | TSL:1 GENCODE basic APPRIS P1 |
| Rcn3-208 | ENSMUST00000211352.1 | 1453 | 328aa | Protein coding | CCDS21229 | Q8BH97 | TSL:1 GENCODE basic APPRIS P1 |
| Rcn3-207 | ENSMUST00000210734.1 | 905 | 280aa | Protein coding | - | A0A1B0GR86 | CDS 3' incomplete TSL:5 |
| Rcn3-202 | ENSMUST00000209761.1 | 892 | 186aa | Protein coding | - | A0A1B0GSK5 | CDS 5' incomplete TSL:5 |
| Rcn3-204 | ENSMUST00000210469.1 | 884 | 274aa | Protein coding | - | A0A1B0GR19 | CDS 3' incomplete TSL:3 |
| Rcn3-209 | ENSMUST00000211760.1 | 471 | 122aa | Protein coding | - | A0A1B0GS22 | CDS 5' incomplete TSL:5 |
| Rcn3-205 | ENSMUST00000210527.1 | 389 | 115aa | Protein coding | - | A0A1B0GRI0 | CDS 3' incomplete TSL:2 |
| Rcn3-206 | ENSMUST00000210615.1 | 589 | No protein | Retained intron | - | - | TSL:2 |
| Rcn3-203 | ENSMUST00000210355.1 | 381 | No protein | Retained intron | - | - | TSL:2 |

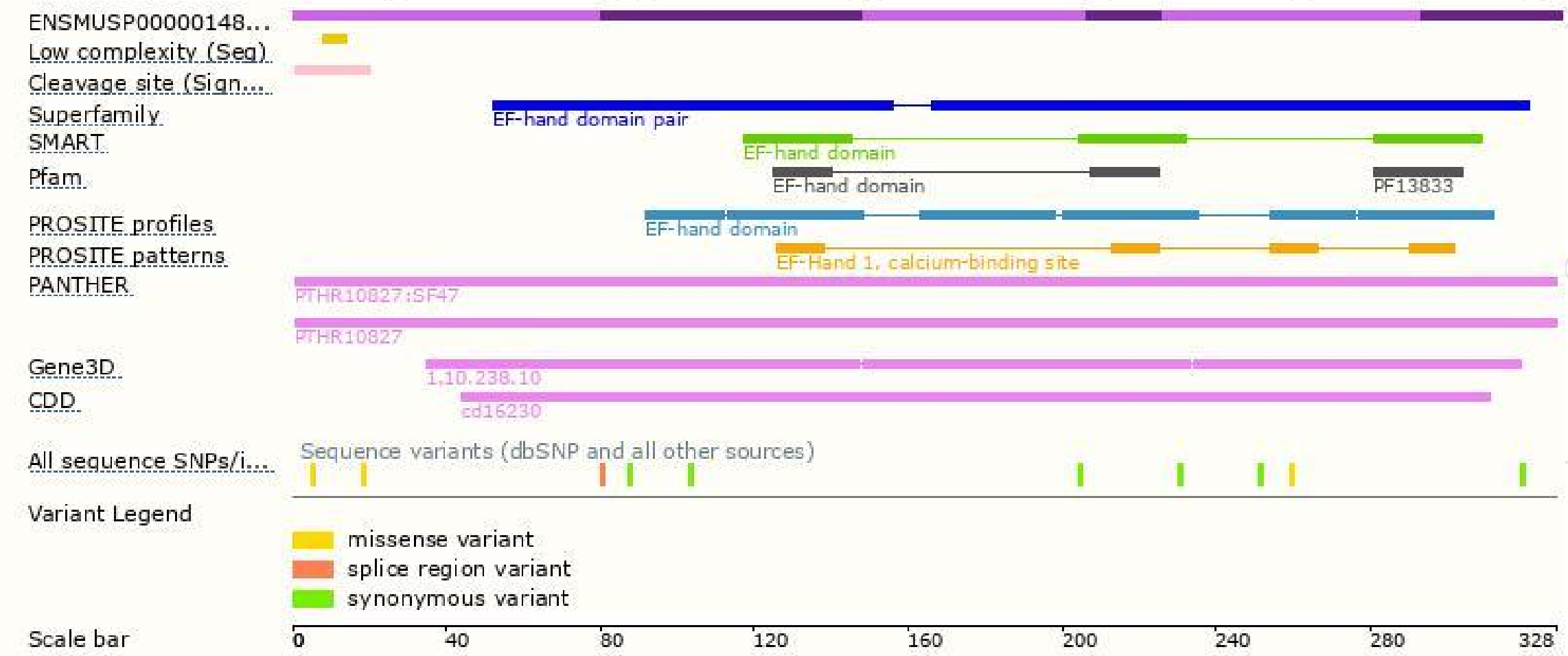
The strategy is based on the design of *Rcn3-201* transcript,the transcription is shown below:



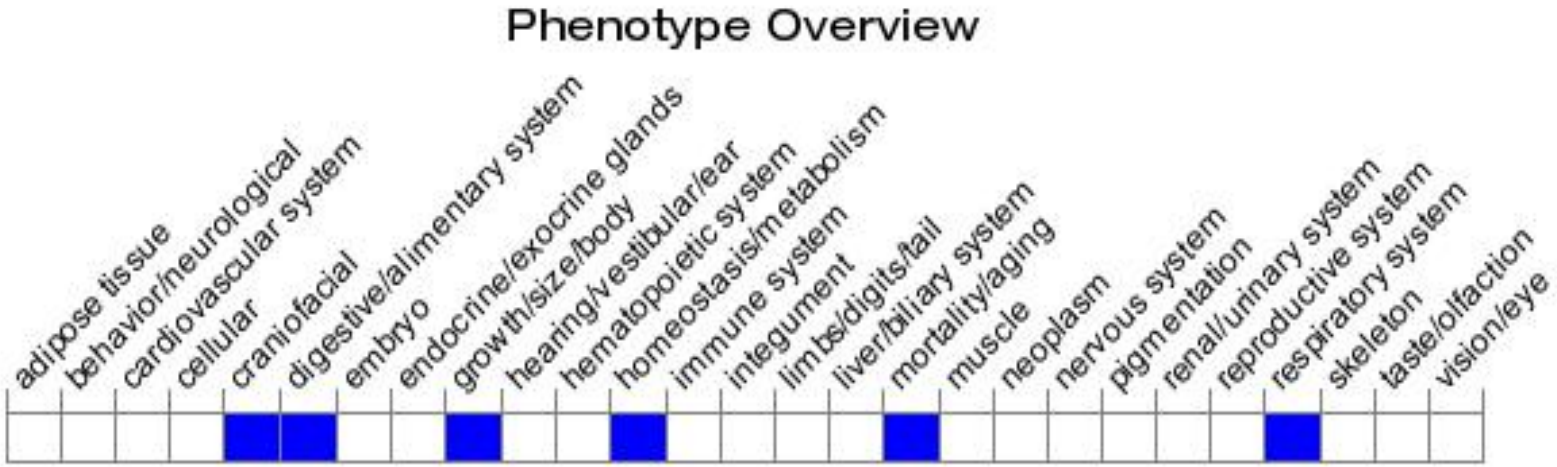
# Genomic location distribution



# 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 knock-out allele exhibit neonatal lethality due to atelectasis-induced respiratory distress associated with failure of type II pneumocyte maturation, decreased surfactant protein secretion, altered surfactant phospholipid homeostasis, and abnormal lamellar body formation.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd