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GemPharmatech

# *Ciapin1* Cas9-KO Strategy

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Reviewer: Ruiuri Zhang

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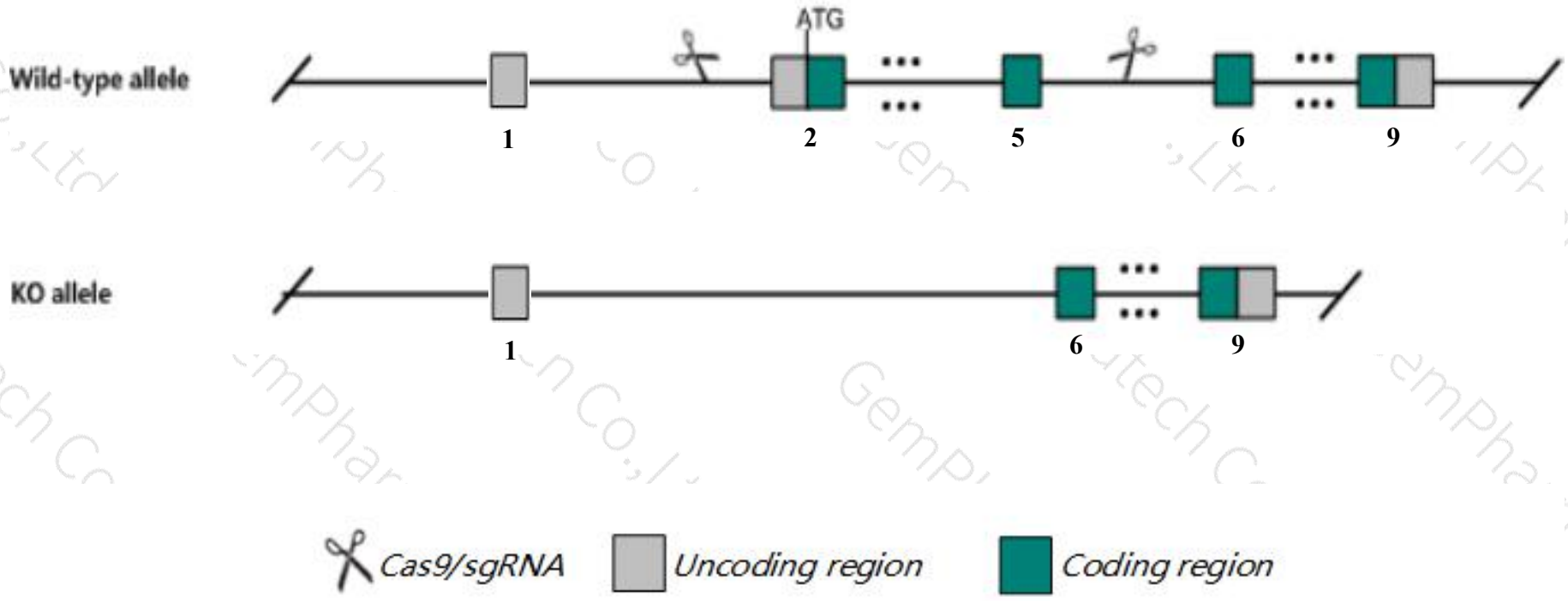
# Project Overview

| | |
|---|---|
| **Project Name** | ***Ciapin1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ciapin1* gene. The schematic diagram is as follows:



# Technical routes

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- The *Ciapin1* gene has 10 transcripts. According to the structure of *Ciapin1* gene, exon2-exon5 of *Ciapin1-209* (ENSMUST00000162538.8) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ciapin1* gene. The brief process is as follows: CRISPR/Cas9 syste

# Notice

- According to the existing MGI data,mice homozygous for disruptions in this gene die as embryos with erythropoietic abnormalities.
- The 5-terminal regulation of *Gm7418* may be affect.
- The *Ciapin1* gene is located on the Chr8. 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）

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**Ciapin1 cytokine induced apoptosis inhibitor 1 [ *Mus musculus* (house mouse) ]**

Gene ID: 109006, updated on 13-Mar-2020

**Summary**

| | |
|---|---|
| **Official Symbol** | Ciapin1 provided by MGI |
| **Official Full Name** | cytokine induced apoptosis inhibitor 1 provided by MGI |
| **Primary source** | MGI:MGI:1922083 |
| **See related** | Ensembl:ENSMUSG00000031781 |
| **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** | AA617265; AU021794; anamorsin; 2810413N20Rik |
| **Expression** | Ubiquitous expression in whole brain E14.5 (RPKM 7.5), CNS E14 (RPKM 7.3) and 28 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

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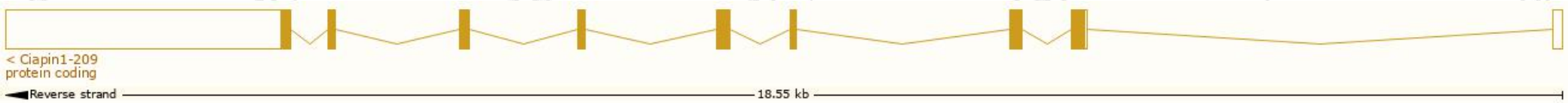
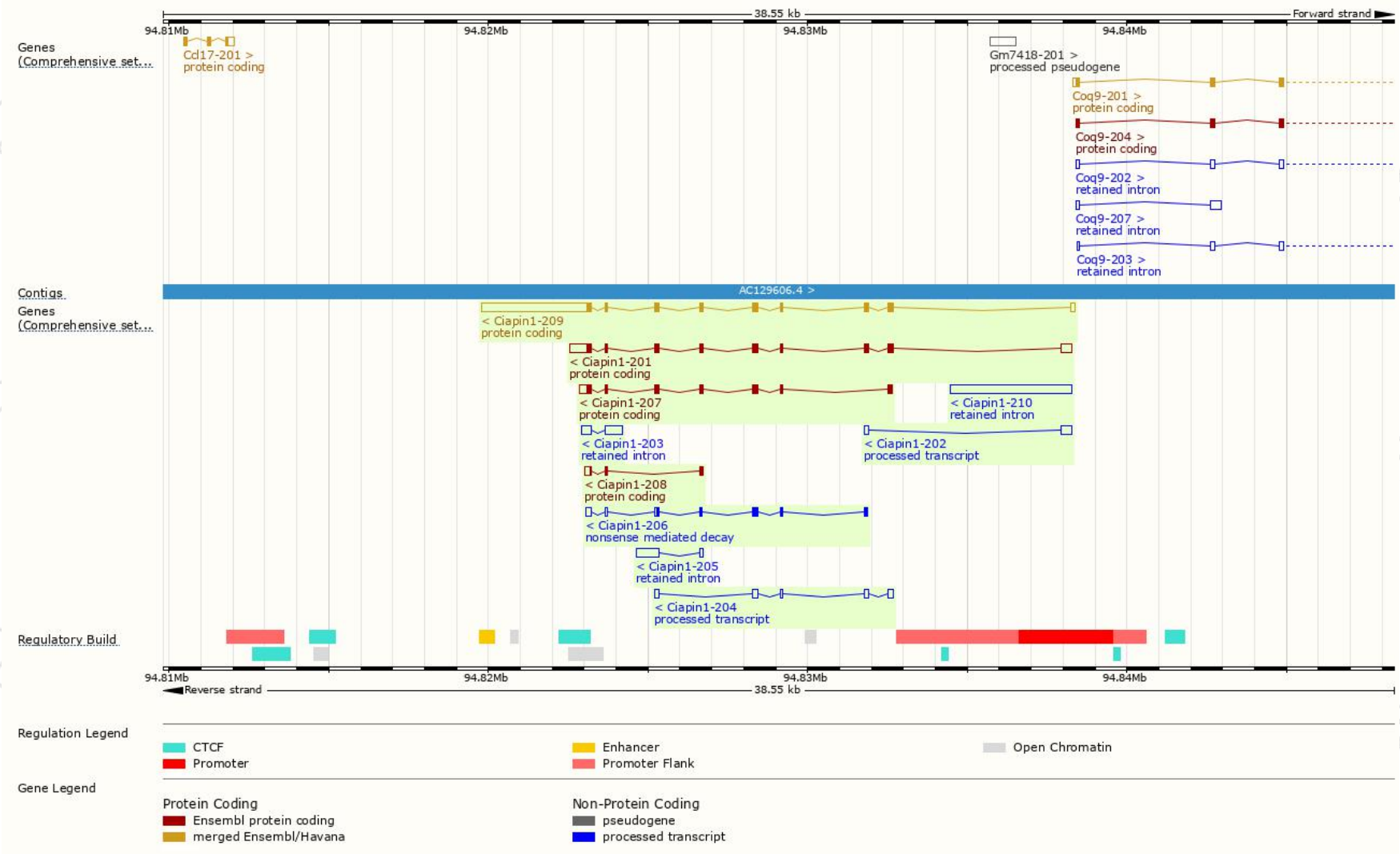
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Ciapin1-209 | ENSMUST00000162538.8 | 4359 | 309aa | Protein coding | CCDS22549 | Q8WTY4 | TSL:1 GENCODE basic APPRIS P1 |
| Ciapin1-201 | ENSMUST00000034233.14 | 1807 | 309aa | Protein coding | CCDS22549 | F8WIK0 Q8WTY4 | TSL:5 GENCODE basic APPRIS P1 |
| Ciapin1-207 | ENSMUST00000161792.8 | 1008 | 254aa | Protein coding | - | F7BWP1 | CDS 5' incomplete TSL:5 |
| Ciapin1-208 | ENSMUST00000162357.1 | 346 | 57aa | Protein coding | - | A0A1D5RLF8 | CDS 5' incomplete TSL:5 |
| Ciapin1-206 | ENSMUST00000161762.3 | 775 | 152aa | Nonsense mediated decay | - | E0CYY1 | CDS 5' incomplete TSL:5 |
| Ciapin1-204 | ENSMUST00000160301.2 | 690 | No protein | Processed transcript | - | - | TSL:3 |
| Ciapin1-202 | ENSMUST00000159377.1 | 461 | No protein | Processed transcript | - | - | TSL:2 |
| Ciapin1-210 | ENSMUST00000162589.2 | 3803 | No protein | Retained intron | - | - | TSL:NA |
| Ciapin1-203 | ENSMUST00000160245.1 | 814 | No protein | Retained intron | - | - | TSL:2 |
| Ciapin1-205 | ENSMUST00000160898.1 | 774 | No protein | Retained intron | - | - | TSL:3 |

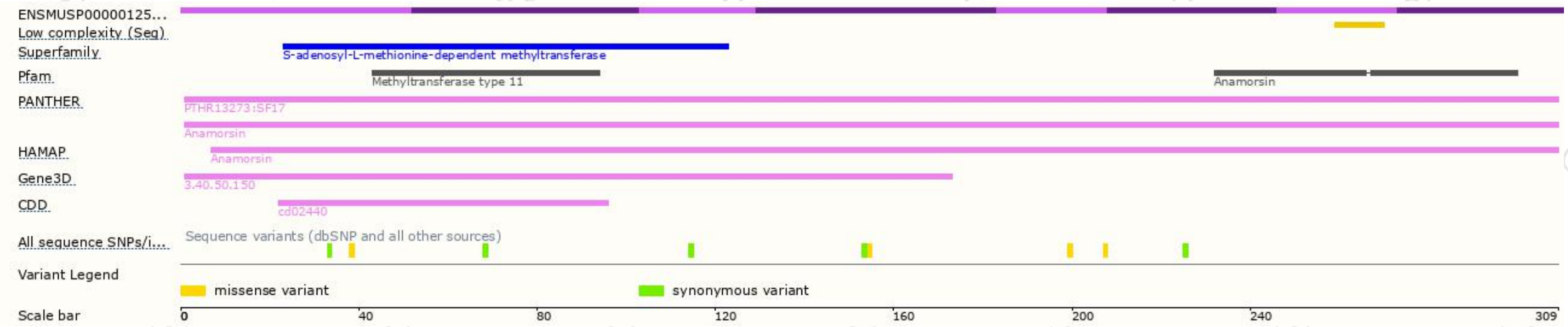
The strategy is based on the design of *Ciapin1-209* transcript, the transcription is shown below



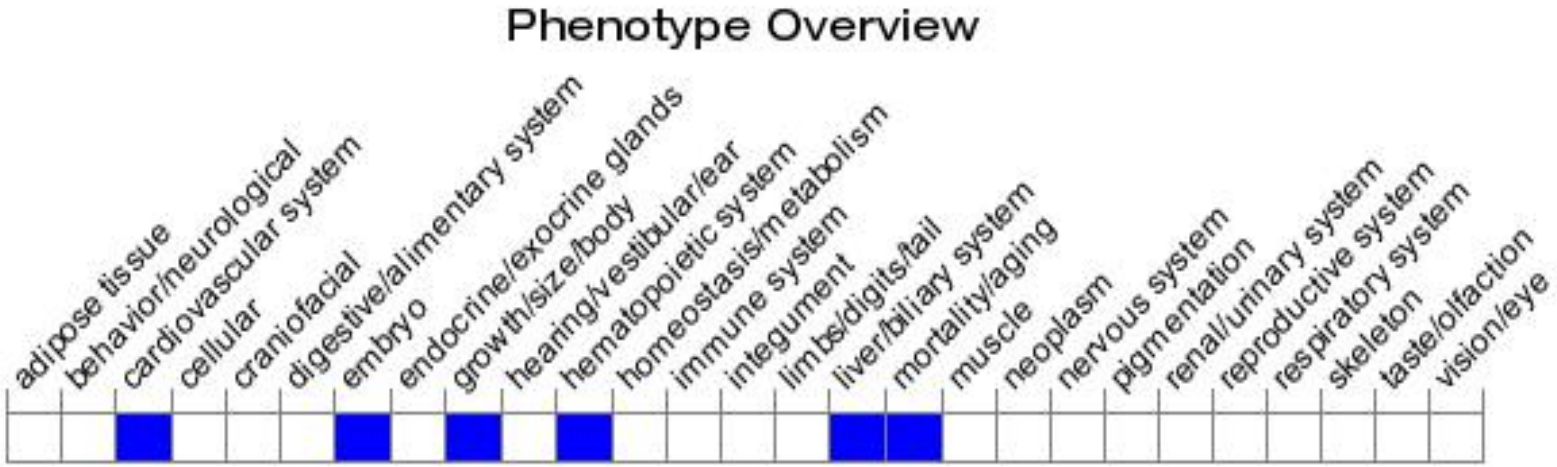
# Genomic location distribution



# 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 disruptions in this gene die as embryos with erythropoietic abnormalities.

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