

# Hyc2 Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Hycc2

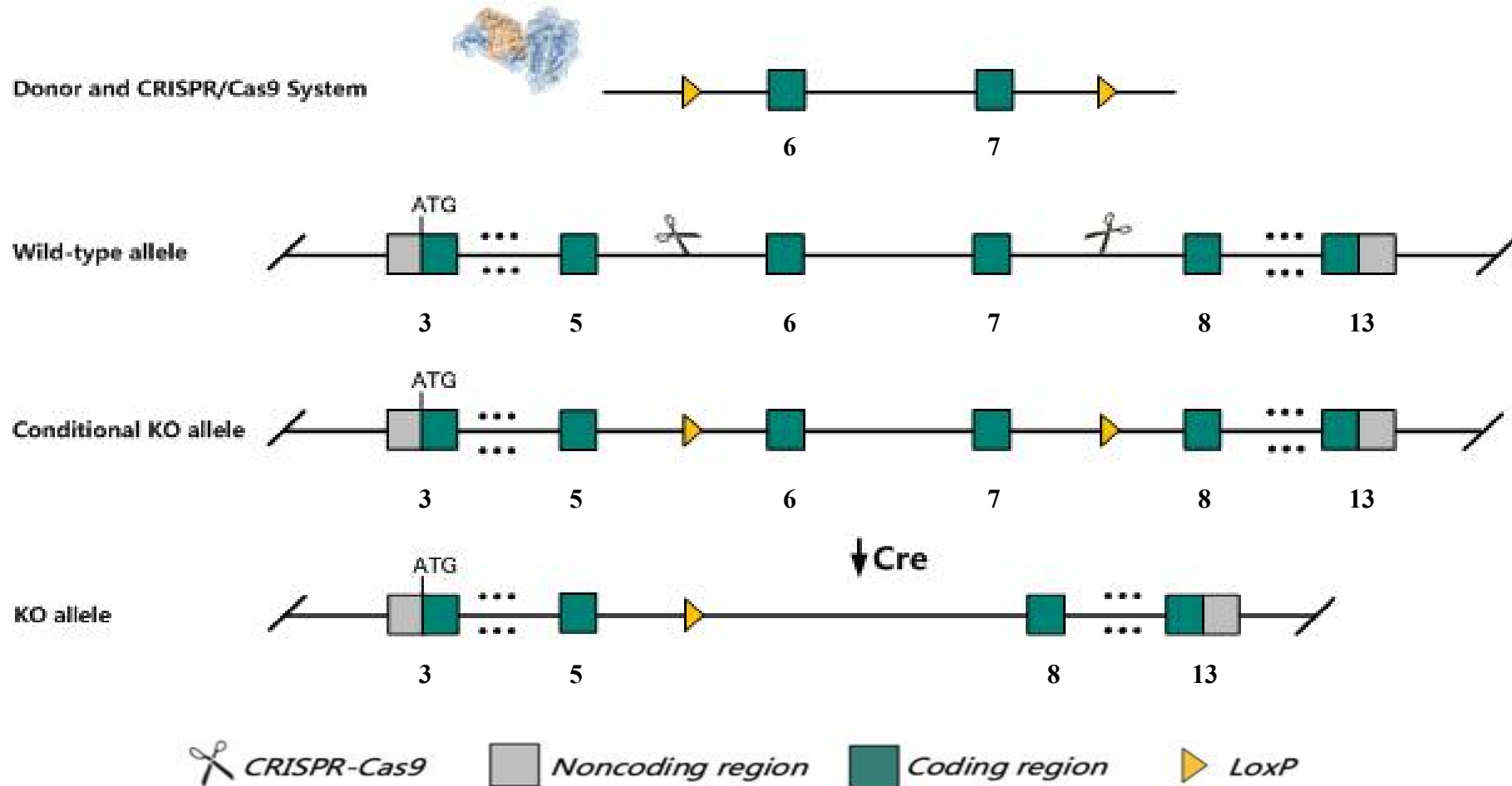
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Hycc2* gene.

# Technical Information

- The *Hycc2* gene has 9 transcripts. According to the structure of *Hycc2* gene, exon6-exon7 of *Hycc2*-202 (ENSMUST00000097724.10) transcript is recommended as the knockout region. The region contains 197bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Hycc2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Gene Information

## Hycc2 hyccin PI4KA lipid kinase complex subunit 2 [Mus musculus (house mouse)]

Gene ID: 213056, updated on 12-Apr-2023

### Summary

|                           |  |
|---------------------------|--|
| <b>Official Symbol</b>    | Hycc2 provided by <a href="#">MGI</a>  |
| <b>Official Full Name</b> | hyccin PI4KA lipid kinase complex subunit 2 provided by <a href="#">MGI</a>  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1098784</a>  |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000038174</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>      | C130065N10Rik, D1Ert53e, D630010C10, Fam126b   |
| <b>Summary</b>            | Predicted to be involved in phosphatidylinositol phosphate biosynthetic process and protein localization to plasma membrane. Predicted to be located in cytoplasm and membrane. Predicted to be active in plasma membrane. Orthologous to human FAM126B (family with sequence similarity 126 member B). [provided by Alliance of Genome Resources, Apr 2022] |
| <b>Expression</b>         | Broad expression in cortex adult (RPKM 5.3), cerebellum adult (RPKM 5.2) and 22 other tissues <a href="#">See more</a>   |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>  |

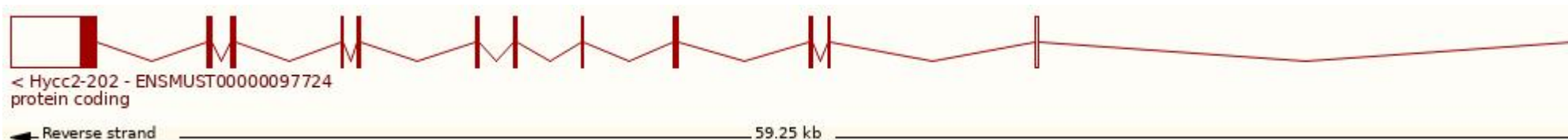
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

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

| Transcript ID                         | Name      | bp   | Protein               | Biotype                        | CCDS                      | UniProt Match              | Flags   |
|---------------------------------------|-----------|------|-----------------------|--------------------------------|---------------------------|----------------------------|---|
| <a href="#">ENSMUST00000097724.10</a> | Hycc2-202 | 4581 | <a href="#">586aa</a> | Protein coding                 | <a href="#">CCDS78588</a> | <a href="#">Q8C729-2</a>   | Ensembl Canonical Gencode basic APPRIS ALT1 TSL:1 |
| <a href="#">ENSMUST00000161600.8</a>  | Hycc2-207 | 8685 | <a href="#">530aa</a> | Protein coding                 | <a href="#">CCDS14976</a> | <a href="#">Q8C729</a>     | Gencode basic APPRIS P4 TSL:1                     |
| <a href="#">ENSMUST00000038372.14</a> | Hycc2-201 | 2385 | <a href="#">530aa</a> | Protein coding                 | <a href="#">CCDS14976</a> | <a href="#">Q8C729</a>     | Gencode basic APPRIS P4 TSL:1                     |
| <a href="#">ENSMUST00000161000.2</a>  | Hycc2-206 | 390  | <a href="#">98aa</a>  | Protein coding                 |                           | <a href="#">E0CZ67</a>     | TSL:3 CDS 3' incomplete                           |
| <a href="#">ENSMUST00000187717.7</a>  | Hycc2-208 | 3860 | <a href="#">100aa</a> | Nonsense mediated decay        |                           | <a href="#">A0A087WSI2</a> | TSL:5   |
| <a href="#">ENSMUST00000160546.8</a>  | Hycc2-205 | 421  | No protein            | Protein coding CDS not defined |                           | -                          | TSL:3   |
| <a href="#">ENSMUST00000191472.2</a>  | Hycc2-209 | 2790 | No protein            | Retained intron                |                           | -                          | TSL:NA  |
| <a href="#">ENSMUST00000159185.2</a>  | Hycc2-203 | 437  | No protein            | Retained intron                |                           | -                          | TSL:2   |
| <a href="#">ENSMUST00000159980.2</a>  | Hycc2-204 | 348  | No protein            | Retained intron                |                           | -                          | TSL:5   |

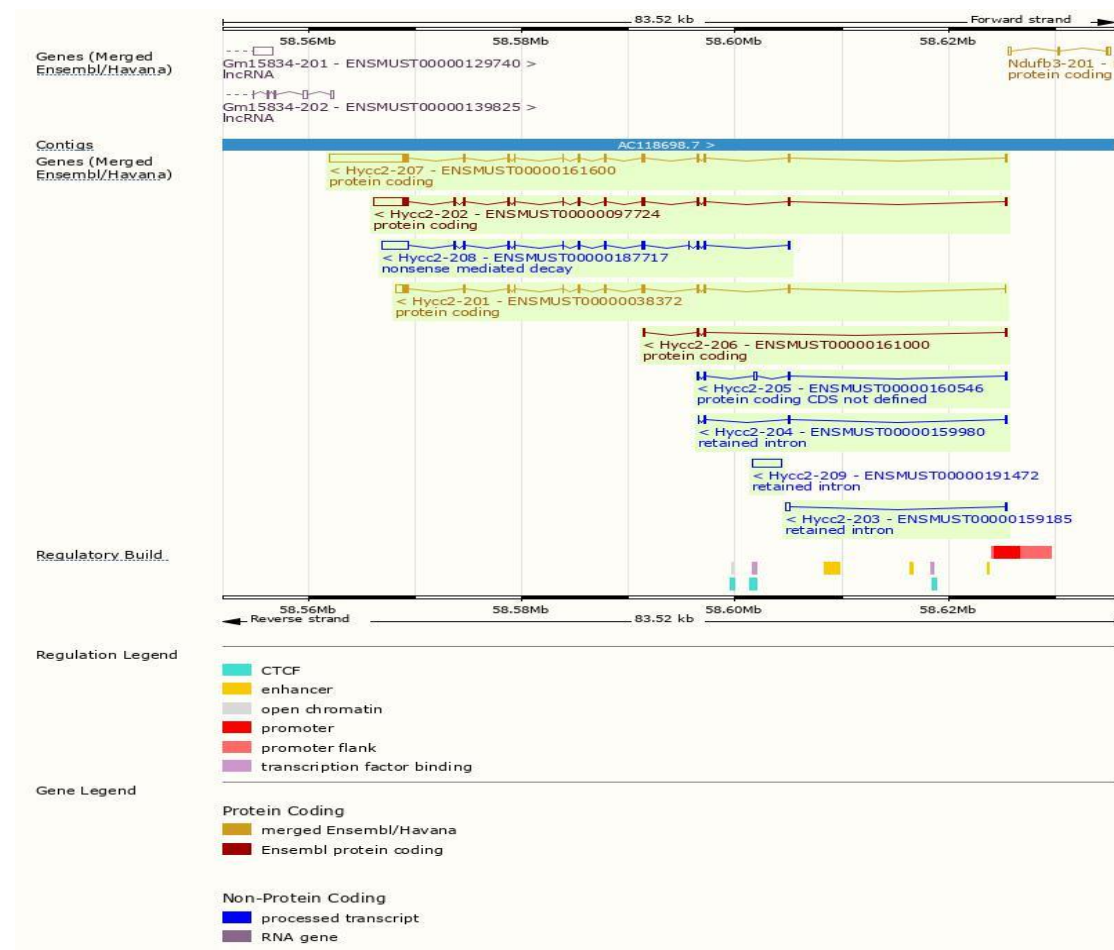
The strategy is based on the design of *Hycc2-202* transcript, the transcription is shown below:



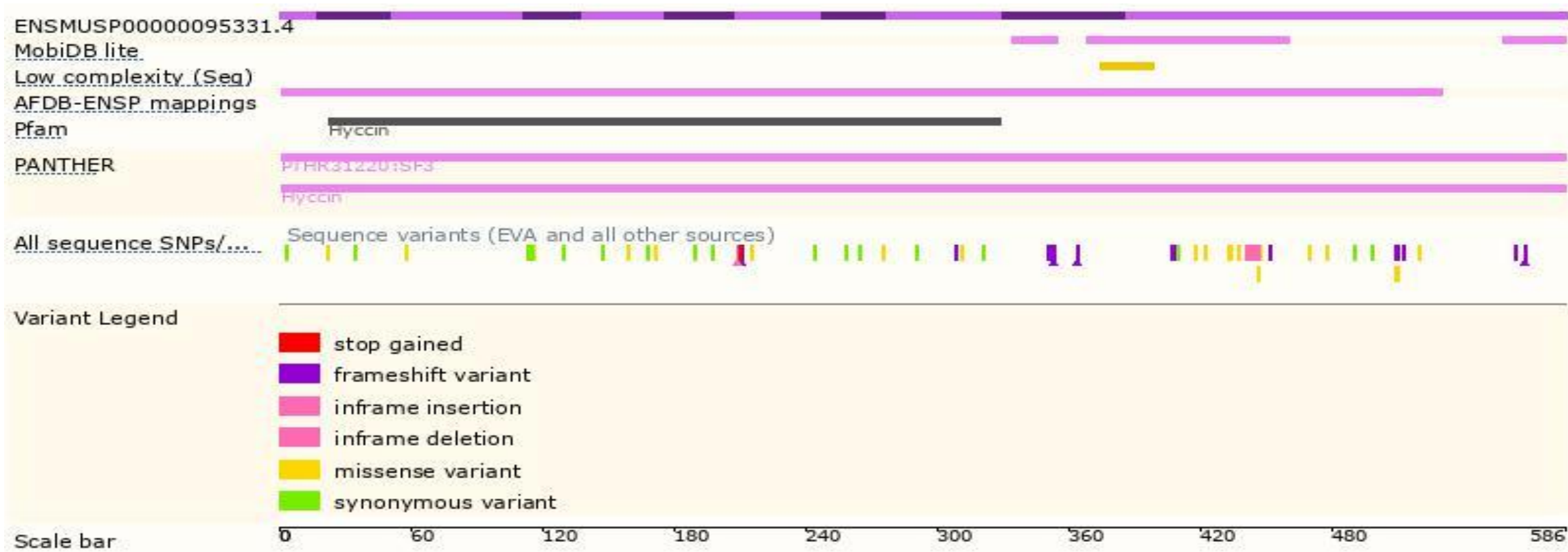
Source: <https://www.ensembl.org>



# Genomic Information



# Protein Information





# Important Information

- The lethality of *Hycc2* gene knockout is unknown.
- The effect on transcript *Hycc2*-206 is unknown.
- There will be several amino acids of the N-terminal of *Hycc2* gene remained, and the effect is unknown.
- *Hycc2* is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.