

# *Cwc25* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Cwc25***

**Project type**

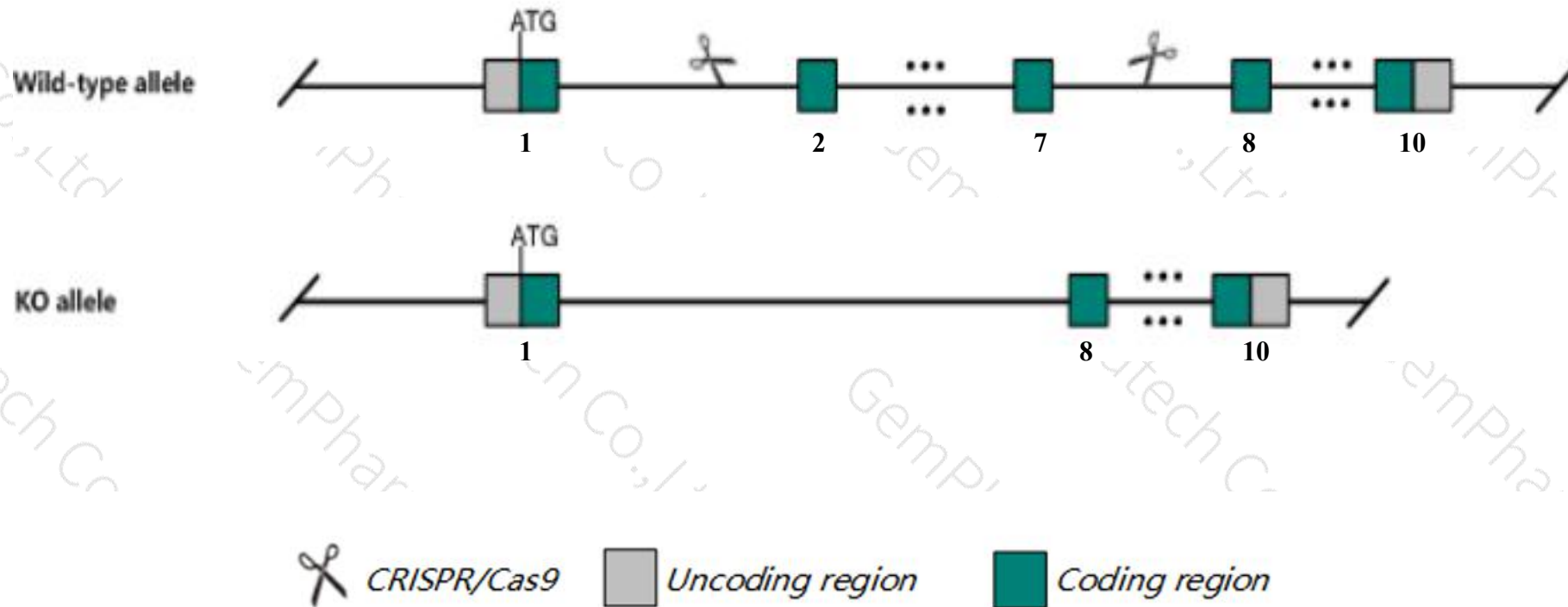
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cwc25* gene. The schematic diagram is as follows:



- The *Cwc25* gene has 4 transcripts. According to the structure of *Cwc25* gene, exon2-exon7 of *Cwc25-201* (ENSMUST00000018685.8) transcript is recommended as the knockout region. The region contains 866bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cwc25* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Cwc25-203* may not be affected.
- The effect on transcript *Cwc25-204* is unknown.
- The knockout region is near to the N-terminal of *Pip4k2b* gene and *Atp5l2* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Cwc25* gene is located on the Chr11. 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)

## Cwc25 CWC25 spliceosome-associated protein [Mus musculus (house mouse)]

Gene ID: 67480, updated on 13-Mar-2020

### Summary



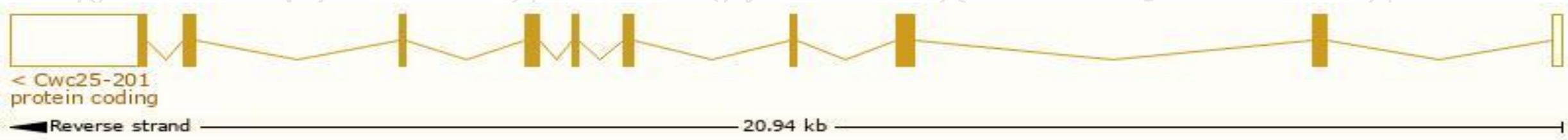
|                           |                                                                                                                                                                           |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Official Symbol</b>    | Cwc25 provided by <a href="#">MGI</a>                                                                                                                                     |
| <b>Official Full Name</b> | CWC25 spliceosome-associated protein provided by <a href="#">MGI</a>                                                                                                      |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1914730</a>                                                                                                                                           |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000018541</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>      | 1300013D05Rik, AA473636, Ccdc49, R75228                                                                                                                                   |
| <b>Expression</b>         | Ubiquitous expression in CNS E11.5 (RPKM 7.3), limb E14.5 (RPKM 5.5) and 28 other tissues <a href="#">See more</a>                                                        |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

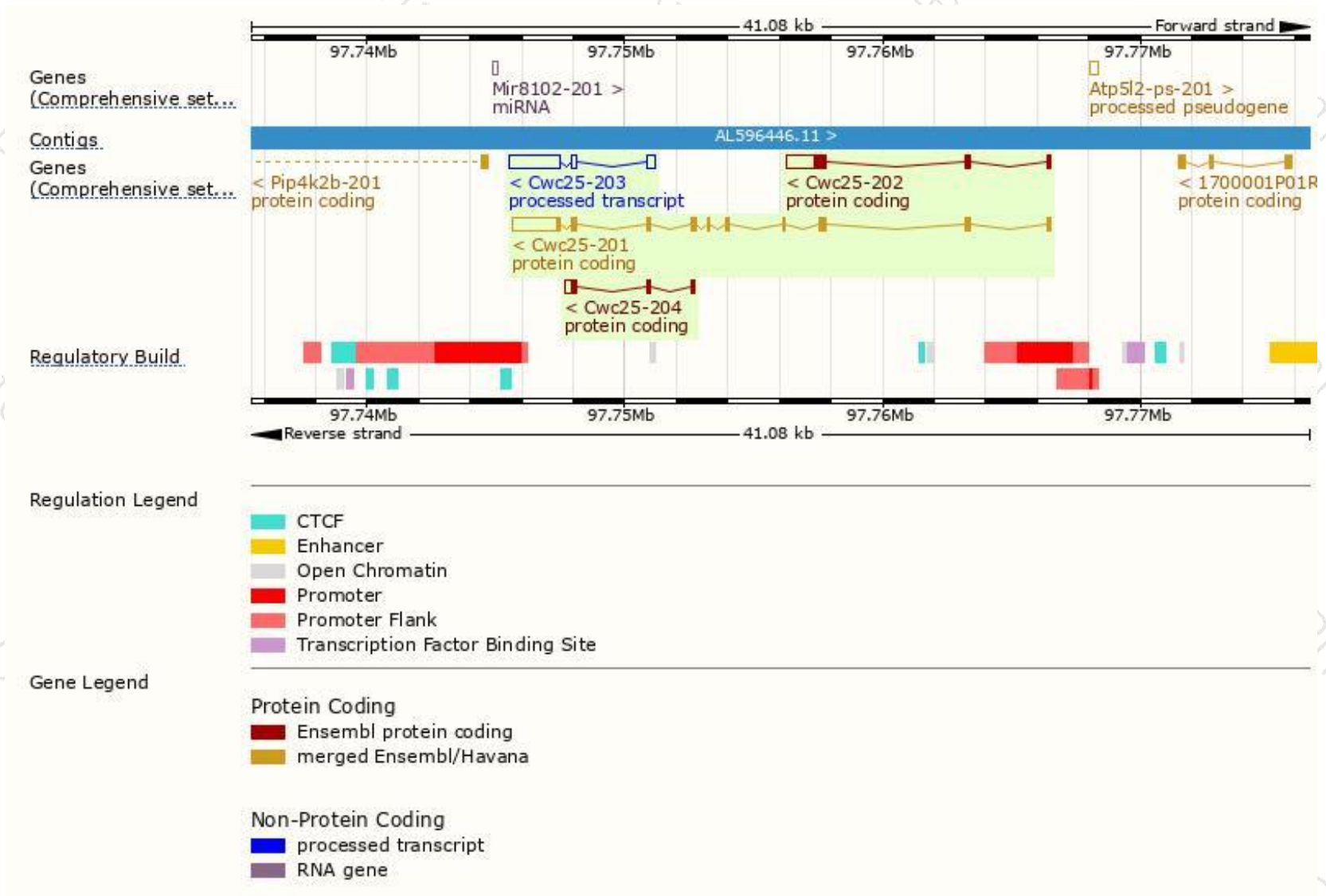
The gene has 4 transcripts,all transcripts are shown below:

| Name      | Transcript ID                        | bp   | Protein               | Biotype              | CCDS                      | UniProt                | Flags                                                                                                                                                                                                           |
|-----------|--------------------------------------|------|-----------------------|----------------------|---------------------------|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Cwc25-201 | <a href="#">ENSMUST00000018685.8</a> | 3105 | <a href="#">416aa</a> | Protein coding       | <a href="#">CCDS25330</a> | <a href="#">Q9DBF7</a> | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2   |
| Cwc25-202 | <a href="#">ENSMUST00000107579.1</a> | 1838 | <a href="#">206aa</a> | Protein coding       | -                         | <a href="#">A2A6F5</a> | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2 |
| Cwc25-204 | <a href="#">ENSMUST00000152395.1</a> | 686  | <a href="#">132aa</a> | Protein coding       | -                         | <a href="#">E7BY36</a> | CDS 5' incomplete TSL:2                                                                                                                                                                                         |
| Cwc25-203 | <a href="#">ENSMUST00000124356.1</a> | 2450 | No protein            | Processed transcript | -                         | -                      | TSL:1                                                                                                                                                                                                           |

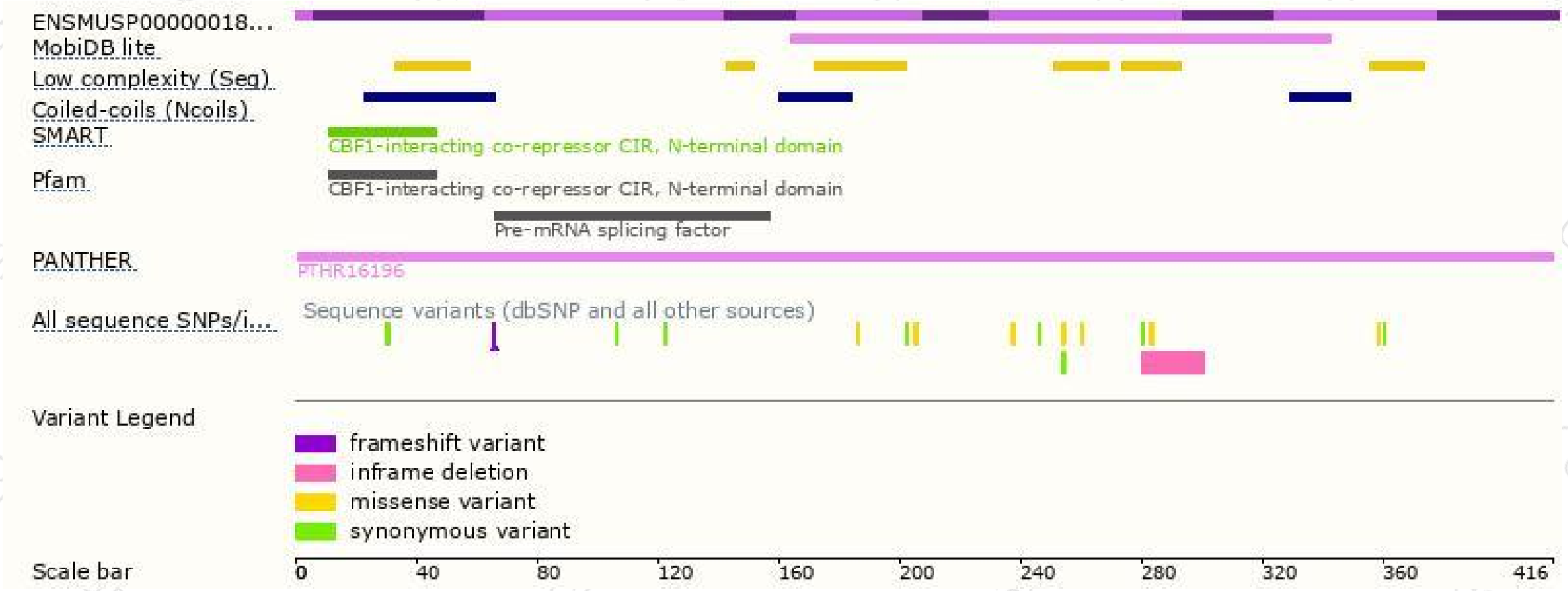
The strategy is based on the design of *Cwc25-201* transcript,the transcription is shown below



# Genomic location distribution



# Protein domain



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

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