

# *Cfap44* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2020-5-7**

# Project Overview

**Project Name**

***Cfap44***

**Project type**

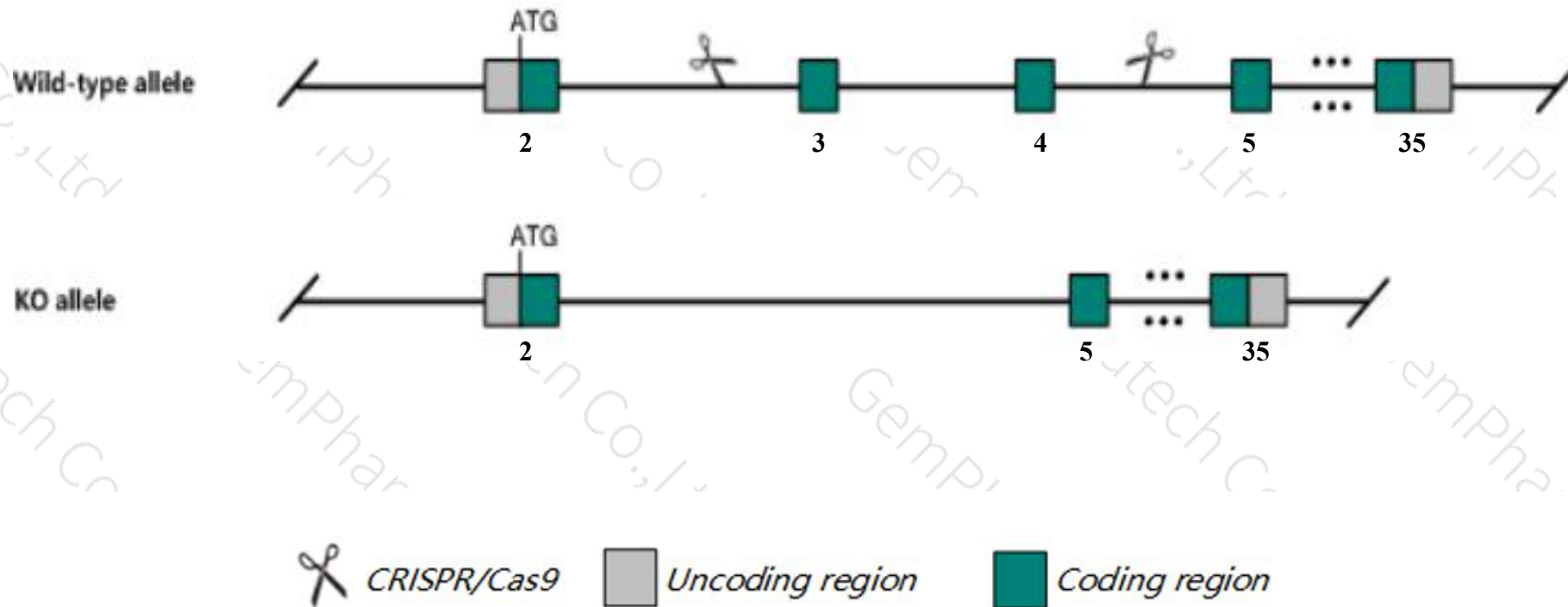
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cfap44* gene. The schematic diagram is as follows:



- The *Cfap44* gene has 7 transcripts. According to the structure of *Cfap44* gene, exon3-exon4 of *Cfap44-201* (ENSMUST00000099742.8) transcript is recommended as the knockout region. The region contains 280bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cfap44* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit complete male sterility, asthenozoospermia, and teratozoospermia characterized by multiple sperm axonemal defects.
- Transcripts 203,204,205,206 may not be affected.
- The *Cfap44* gene is located on the Chr16. 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)

## Cfap44 cilia and flagella associated protein 44 [Mus musculus (house mouse)]

Gene ID: 212517, updated on 13-Mar-2020

### Summary



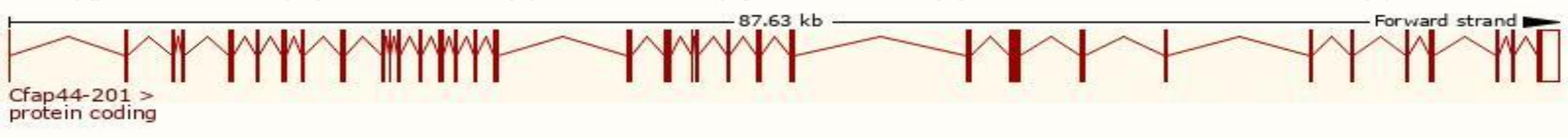
|                           |                                                                                                                                                                           |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Official Symbol</b>    | Cfap44 provided by <a href="#">MGI</a>                                                                                                                                    |
| <b>Official Full Name</b> | cilia and flagella associated protein 44 provided by <a href="#">MGI</a>                                                                                                  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1277238</a>                                                                                                                                           |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000071550</a>                                                                                                                                |
| <b>Gene type</b>          | protein coding                                                                                                                                                            |
| <b>RefSeq status</b>      | PROVISIONAL                                                                                                                                                               |
| <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>      | 6330444M21Rik, D16Etd642e, Gm1750, Wdr52                                                                                                                                  |
| <b>Expression</b>         | Biased expression in testis adult (RPKM 4.1), CNS E14 (RPKM 1.6) and 11 other tissues <a href="#">See more</a>                                                            |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information（Ensembl）

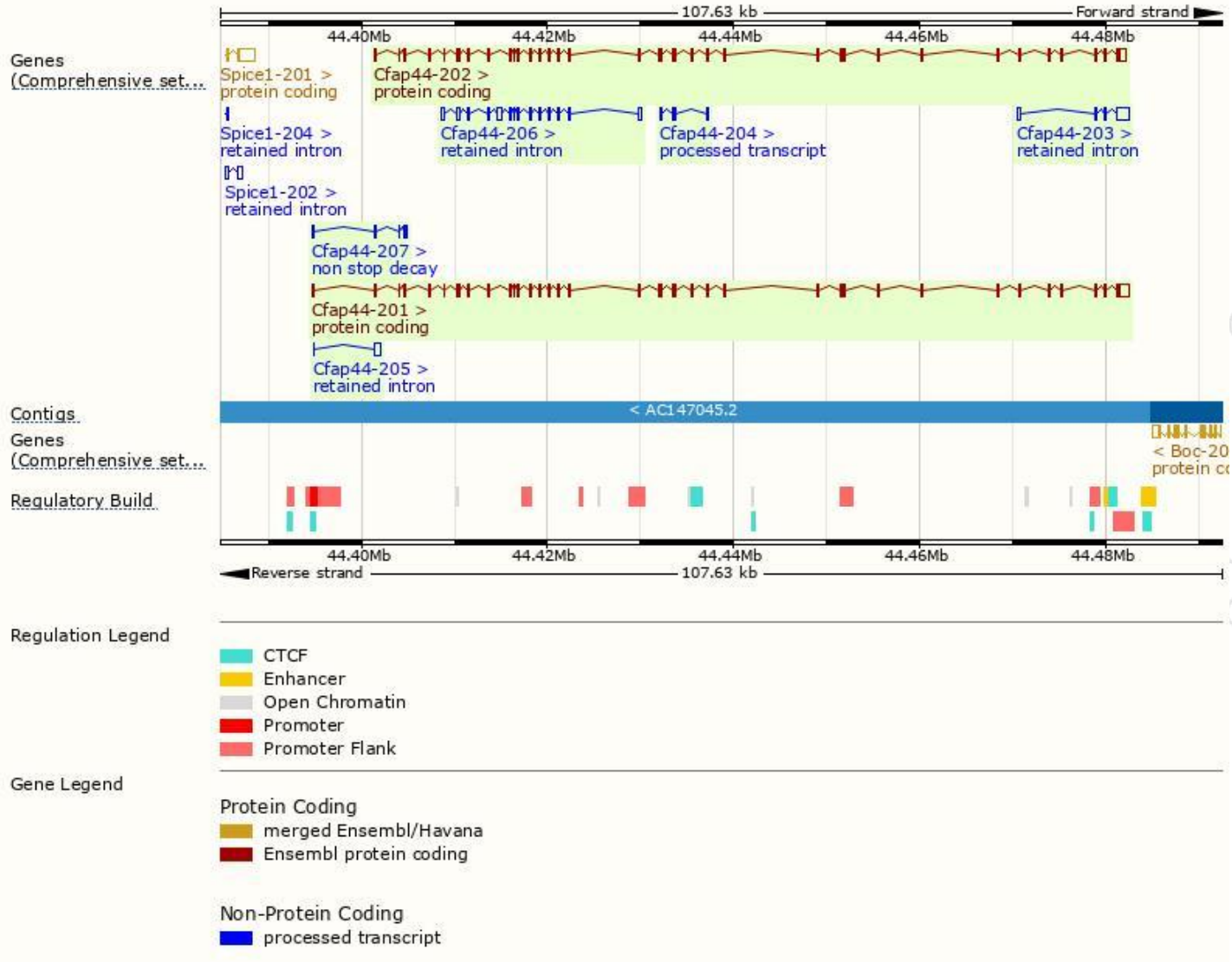
The gene has 7 transcripts,all transcripts are shown below:

| Name       | Transcript ID                        | bp   | Protein                | Biotype              | CCDS                      | UniProt                    | Flags                                                                                                                                                                                                         |
|------------|--------------------------------------|------|------------------------|----------------------|---------------------------|----------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Cfap44-201 | <a href="#">ENSMUST00000099742.8</a> | 6583 | <a href="#">1843aa</a> | Protein coding       | <a href="#">CCDS49854</a> | <a href="#">E9Q5M6</a>     | TSL:5 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 P1 |
| Cfap44-202 | <a href="#">ENSMUST00000120049.7</a> | 6199 | <a href="#">1843aa</a> | Protein coding       | <a href="#">CCDS49854</a> | <a href="#">E9Q5M6</a>     | TSL:5 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 P1 |
| Cfap44-207 | <a href="#">ENSMUST00000147988.1</a> | 593  | <a href="#">178aa</a>  | Non stop decay       | -                         | <a href="#">A0A338P712</a> | CDS 3' incomplete TSL:1                                                                                                                                                                                       |
| Cfap44-204 | <a href="#">ENSMUST00000128916.1</a> | 488  | No protein             | Processed transcript | -                         | -                          | TSL:3                                                                                                                                                                                                         |
| Cfap44-206 | <a href="#">ENSMUST00000142648.1</a> | 2756 | No protein             | Retained intron      | -                         | -                          | TSL:1                                                                                                                                                                                                         |
| Cfap44-203 | <a href="#">ENSMUST00000127303.1</a> | 1904 | No protein             | Retained intron      | -                         | -                          | TSL:1                                                                                                                                                                                                         |
| Cfap44-205 | <a href="#">ENSMUST00000136514.1</a> | 601  | No protein             | Retained intron      | -                         | -                          | TSL:3                                                                                                                                                                                                         |

The strategy is based on the design of *Cfap44-201* transcript,the transcription is shown below:

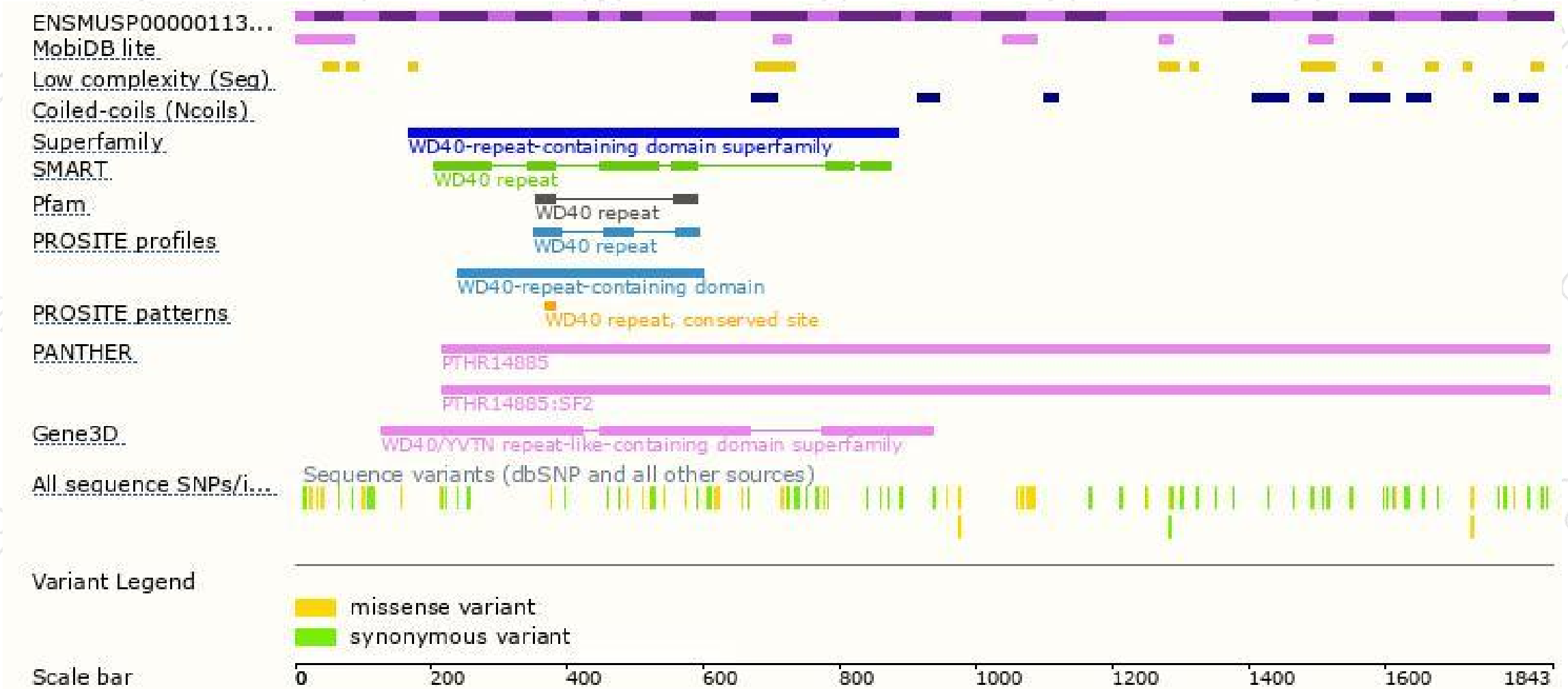


# Genomic location distribution

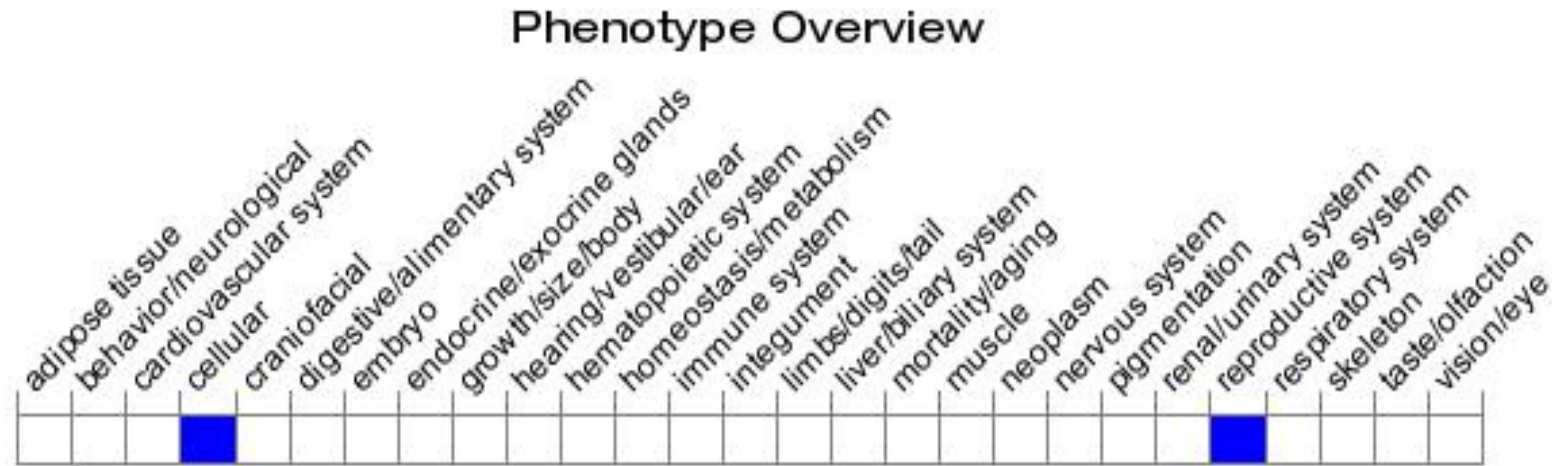




# Protein domain



# 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 complete male sterility, asthenozoospermia, and teratozoospermia characterized by multiple sperm axonemal defects.

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

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