# *Hspa4l* Cas9-KO Strategy

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**Reviewer:** Xueting Zhang

**Design Date:** 2020-4-17

# Project Overview

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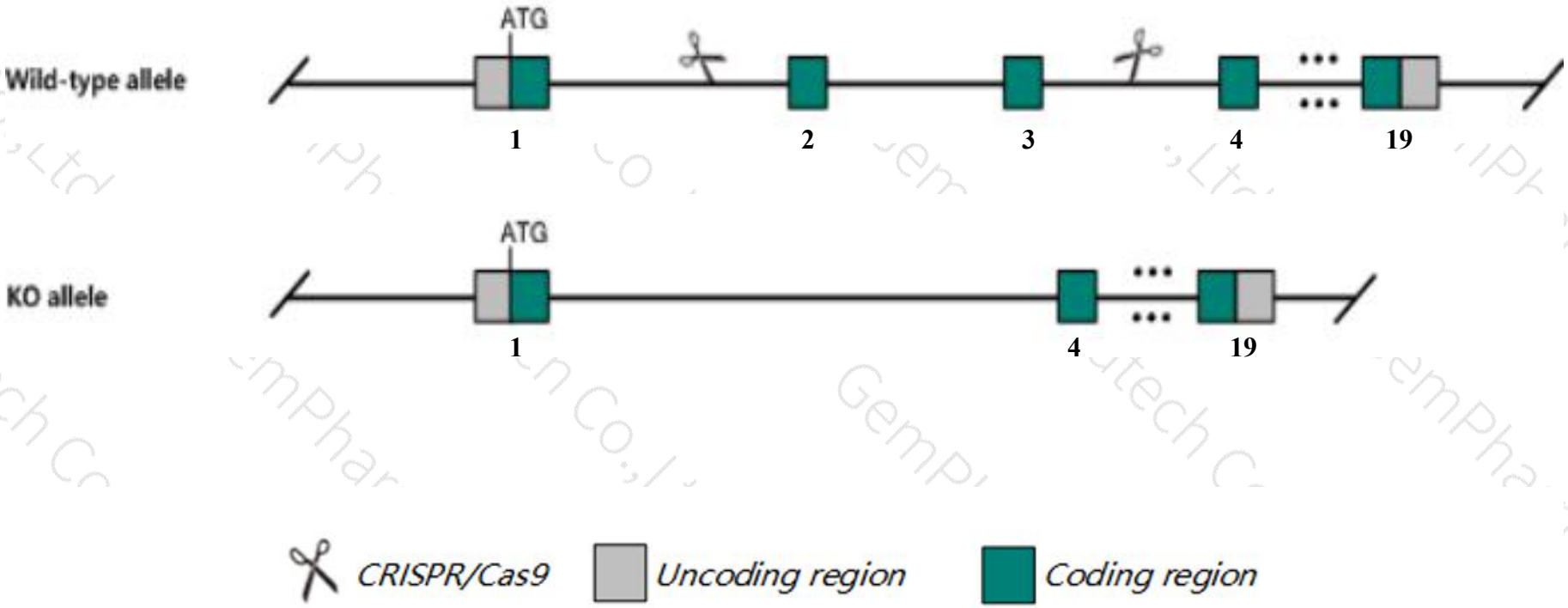
|---|---|
| **Project Name** | ***Hspa4l*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hspa4l* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Hspa4l* gene has 7 transcripts. According to the structure of *Hspa4l* gene, exon2-exon3 of *Hspa4l-207* (ENSMUST00000204702.2) transcript is recommended as the knockout region.The region contains 199bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hspa4l* gene. The brief process is as follows: CRISPR/Cas9 systen

# Notice

- According to the existing MGI data,mice homozygous for disruptions in this gene display increased incidence of male infertility, due to reduced number of mature sperm and reduced sperm motility, and hydronephrosis development.
- Transcripts 204,206 may not be affected. The effect of transcript 203 is unknown.
- The *Hspa4l* gene is located on the Chr3. 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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## Hspa4l heat shock protein 4 like [Mus musculus (house mouse)]

Gene ID: 18415, updated on 13-Mar-2020

### Summary

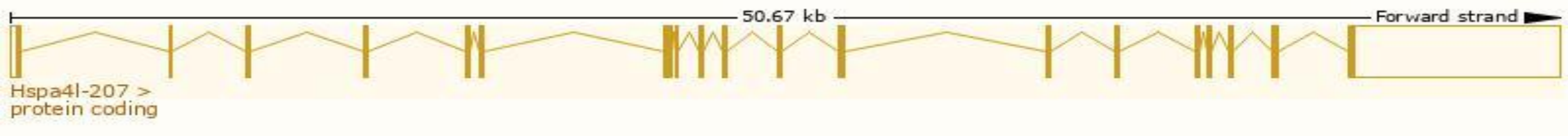
| | |
|---|---|
| **Official Symbol** | Hspa4l provided by MGI |
| **Official Full Name** | heat shock protein 4 like provided by MGI |
| **Primary source** | MGI:MGI:107422 |
| **See related** | Ensembl:ENSMUSG00000025757 |
| **Gene type** | protein coding |
| **RefSeq status** | PROVISIONAL |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 94kDa, AI461691, APG-1, Osp94 |
| **Expression** | Broad expression in testis adult (RPKM 20.6), cerebellum adult (RPKM 14.3) and 16 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

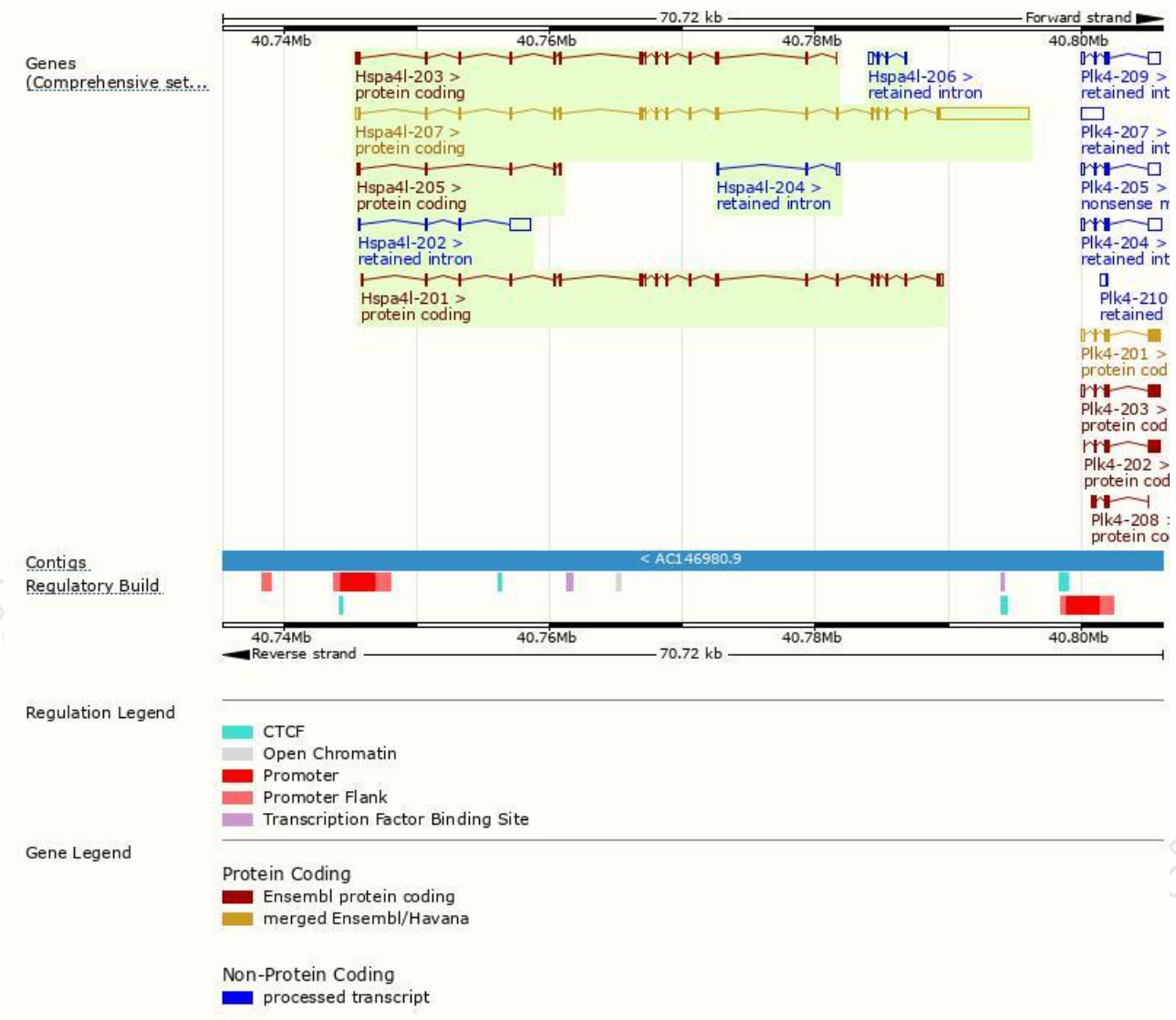
The gene has 7 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Hspa4l-207 | ENSMUST00000204702.2 | 9479 | 838aa | Protein coding | CCDS17327 | P48722 | 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 P1 |
| Hspa4l-201 | ENSMUST00000108086.6 | 2744 | 817aa | Protein coding | - | P48722 | TSL:1 GENCODE basic |
| Hspa4l-203 | ENSMUST00000203353.2 | 1949 | 571aa | Protein coding | - | E0CY23 | CDS 3' incomplete TSL:5 |
| Hspa4l-205 | ENSMUST00000203496.2 | 669 | 158aa | Protein coding | - | A0A0N4SVU2 | CDS 3' incomplete TSL:2 |
| Hspa4l-202 | ENSMUST00000203267.1 | 1997 | No protein | Retained intron | - | - | TSL:1 |
| Hspa4l-206 | ENSMUST00000204174.1 | 670 | No protein | Retained intron | - | - | TSL:2 |
| Hspa4l-204 | ENSMUST00000203425.1 | 480 | No protein | Retained intron | - | - | TSL:2 |

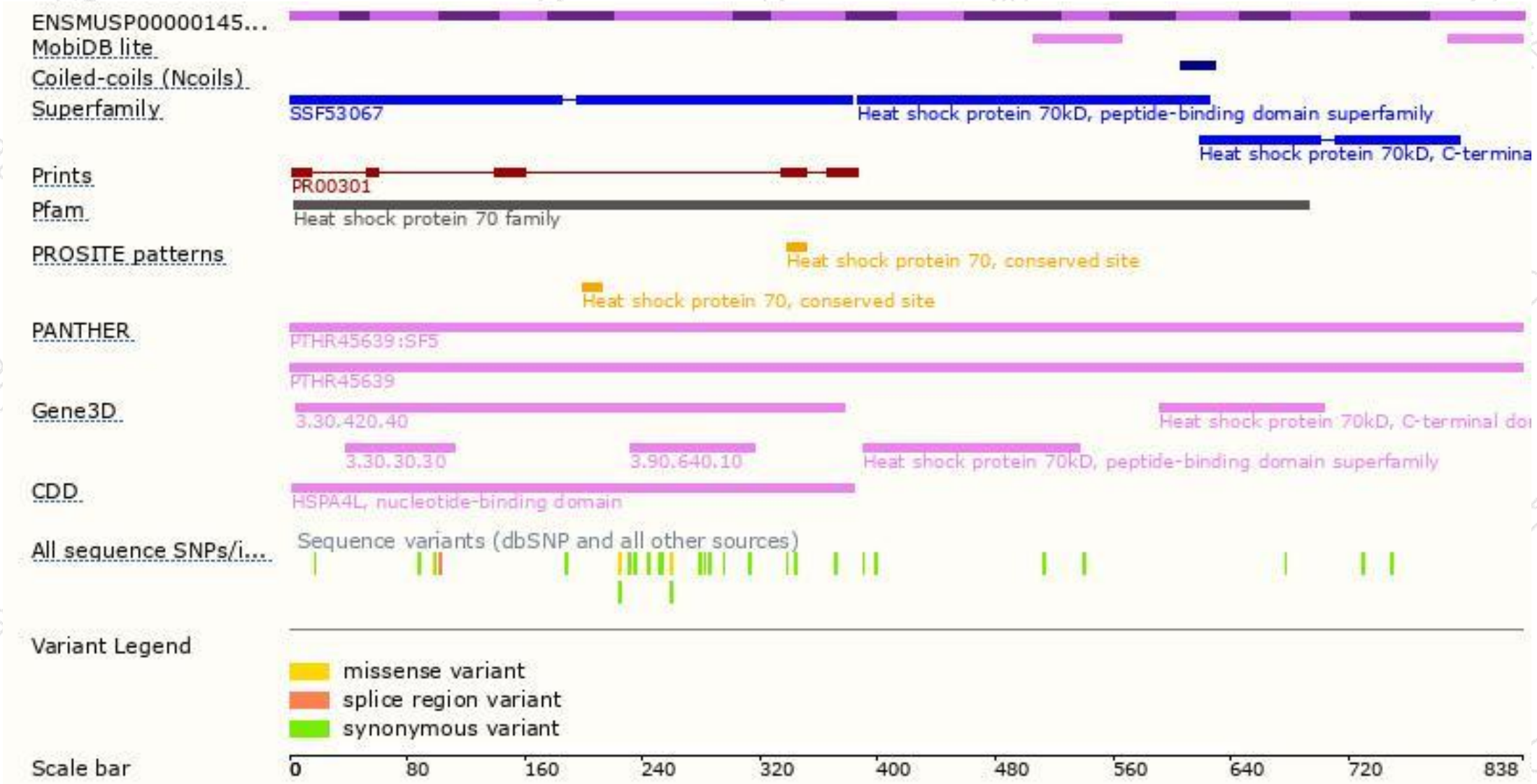
The strategy is based on the design of *Hspa4l-207* transcript,the transcription is shown below:



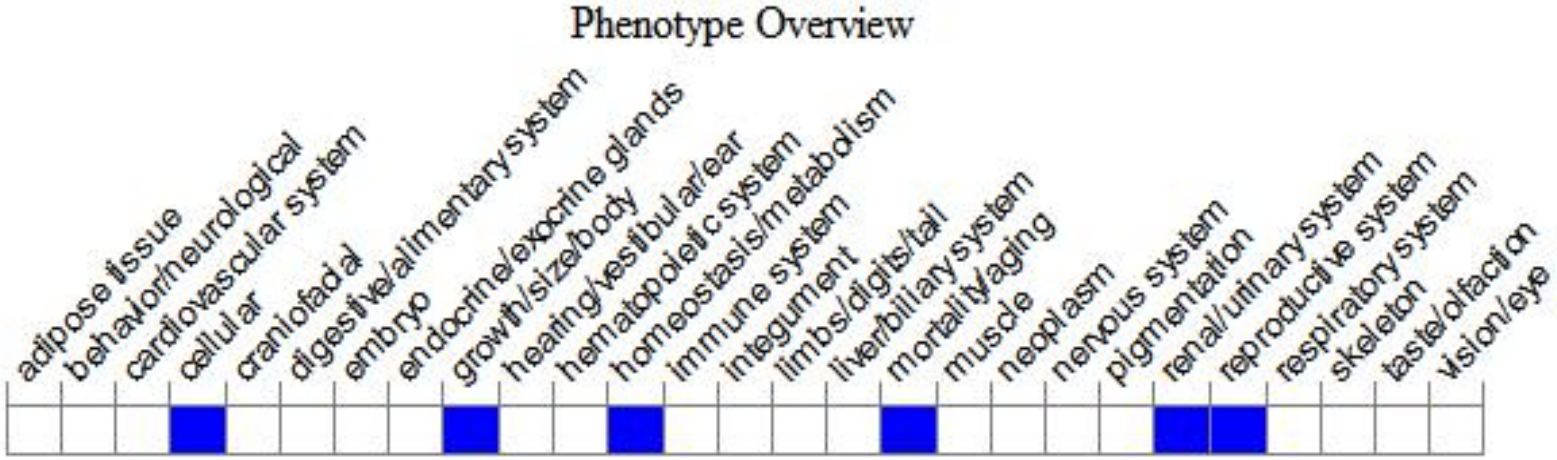
# Genomic location distribution



# 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 display increased incidence of male infertility, due to reduced number of mature sperm and reduced sperm motility, and hydronephrosis development.

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

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