

# *Agfg1* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Agfg1*

**Project type**

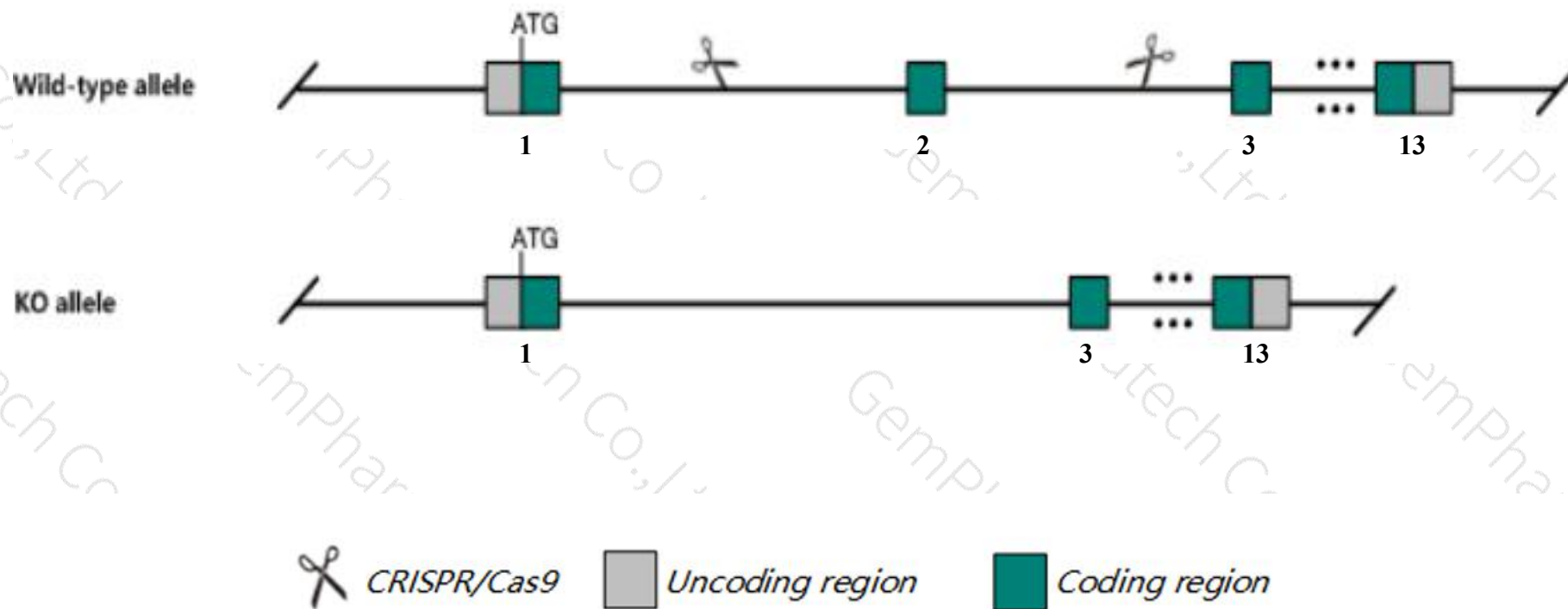
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Agfg1* gene. The schematic diagram is as follows:



- The *Agfg1* gene has 8 transcripts. According to the structure of *Agfg1* gene, exon2 of *Agfg1-206* (ENSMUST00000189220.6) transcript is recommended as the knockout region. The region contains 94bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Agfg1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, male mice homozygous for disruptions in this gene are infertile as a result of abnormalities in spermatogenesis. otherwise, males and females are normal and live a normal life span.
- The *Agfg1* gene is located on the Chr1. 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)

## Agfg1 ArfGAP with FG repeats 1 [Mus musculus (house mouse)]

Gene ID: 15463, updated on 13-Mar-2020

### Summary

**Official Symbol** Agfg1 provided by [MGI](#)

**Official Full Name** ArfGAP with FG repeats 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1333754](#)

**See related** [Ensembl:ENSMUSG00000026159](#)

**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** AU045498, C130049H11Rik, C85612, D730048C23Rik, Hrb, RAB, Rip

**Expression** Ubiquitous expression in testis adult (RPKM 19.1), liver E14.5 (RPKM 13.1) and 28 other tissues [See more](#)

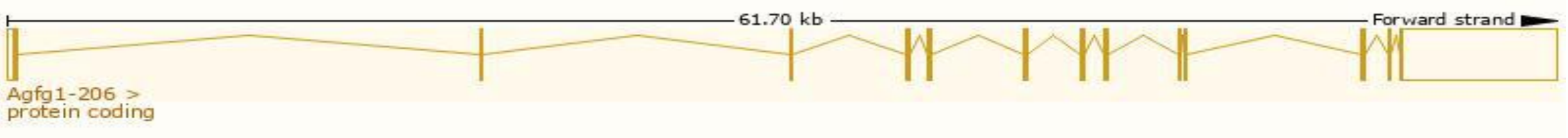
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

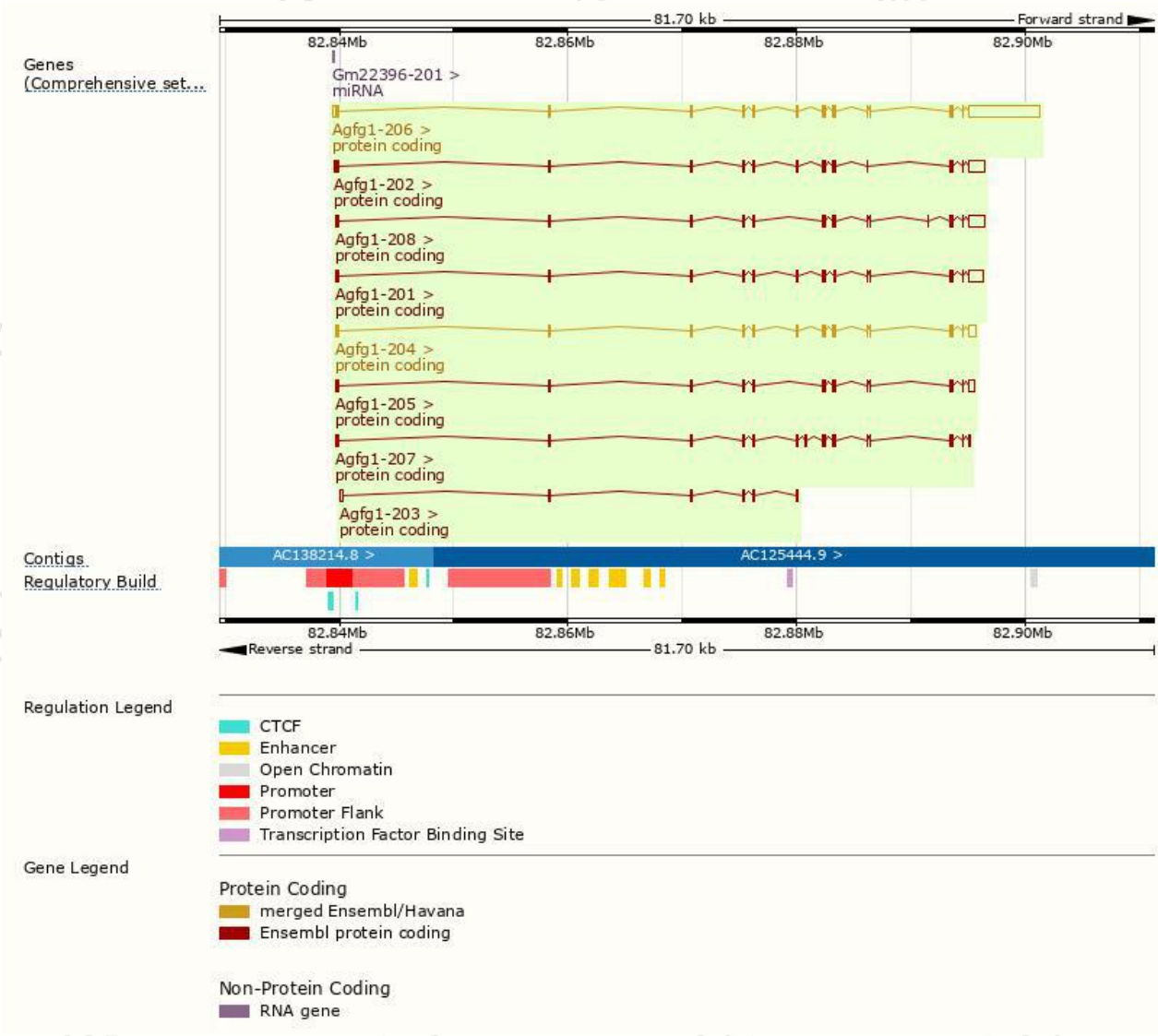
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Agfg1-206	<a href="#">ENSMUST00000189220.6</a>	8044	<a href="#">559aa</a>	Protein coding	<a href="#">CCDS15100</a>	<a href="#">Q8K2K6</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
Agfg1-202	<a href="#">ENSMUST00000113444.7</a>	3142	<a href="#">530aa</a>	Protein coding	<a href="#">CCDS78634</a>	<a href="#">Q8K2K6</a>	TSL:1 GENCODE basic
Agfg1-208	<a href="#">ENSMUST00000190052.6</a>	2991	<a href="#">537aa</a>	Protein coding	<a href="#">CCDS83564</a>	<a href="#">A0A087WSR7</a>	TSL:5 GENCODE basic
Agfg1-201	<a href="#">ENSMUST00000063380.10</a>	2896	<a href="#">540aa</a>	Protein coding	-	<a href="#">Q8K2K6</a>	TSL:1 GENCODE basic
Agfg1-204	<a href="#">ENSMUST00000186302.6</a>	2352	<a href="#">561aa</a>	Protein coding	-	<a href="#">Q8K2K6</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 ALT1
Agfg1-205	<a href="#">ENSMUST00000187899.6</a>	2078	<a href="#">521aa</a>	Protein coding	-	<a href="#">A0A087WNV1</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 ALT1
Agfg1-207	<a href="#">ENSMUST00000190046.6</a>	1805	<a href="#">580aa</a>	Protein coding	-	<a href="#">A0A087WR52</a>	CDS 5' incomplete TSL:5
Agfg1-203	<a href="#">ENSMUST00000186043.1</a>	856	<a href="#">200aa</a>	Protein coding	-	<a href="#">A0A087WRL1</a>	CDS 3' incomplete TSL:5

The strategy is based on the design of *Agfg1-206* transcript,the transcription is shown below:

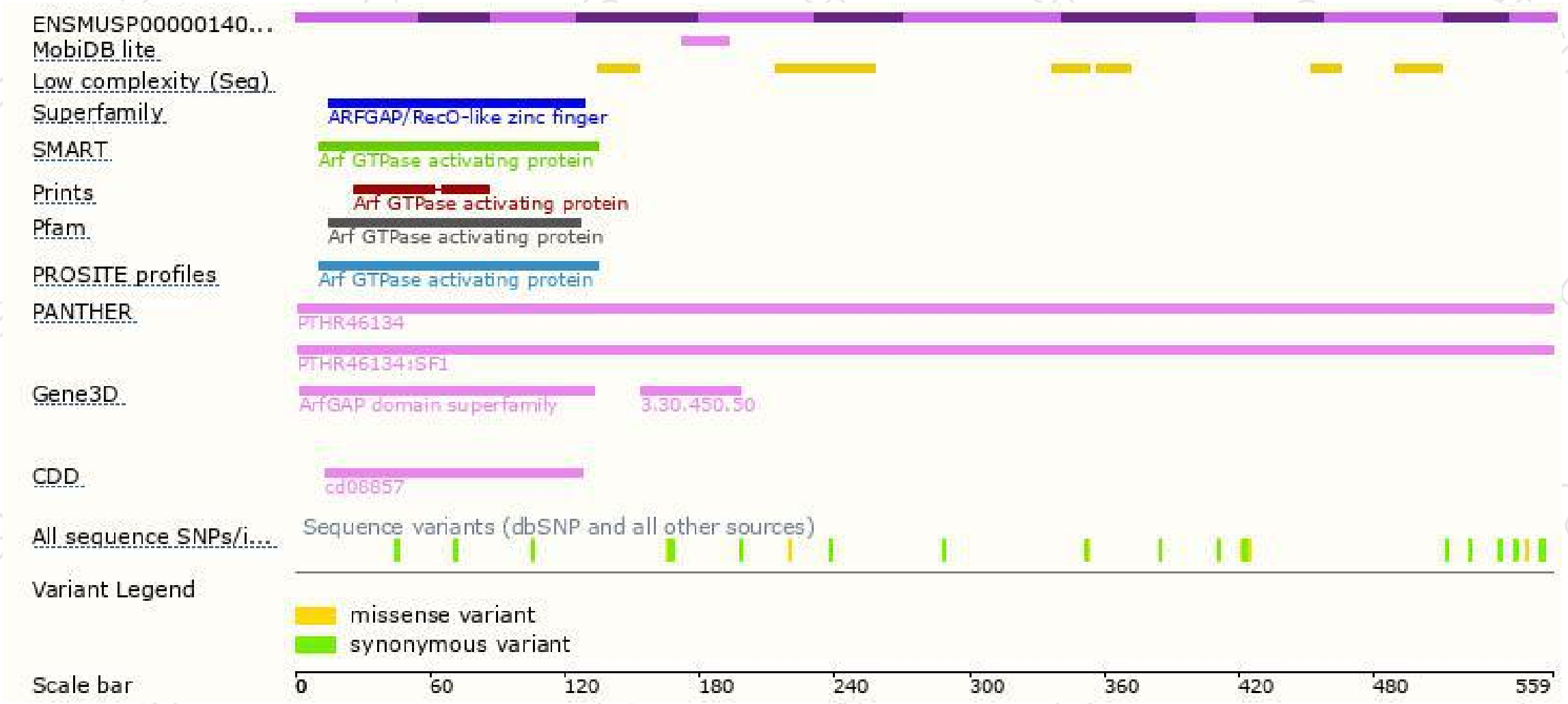


# Genomic location distribution

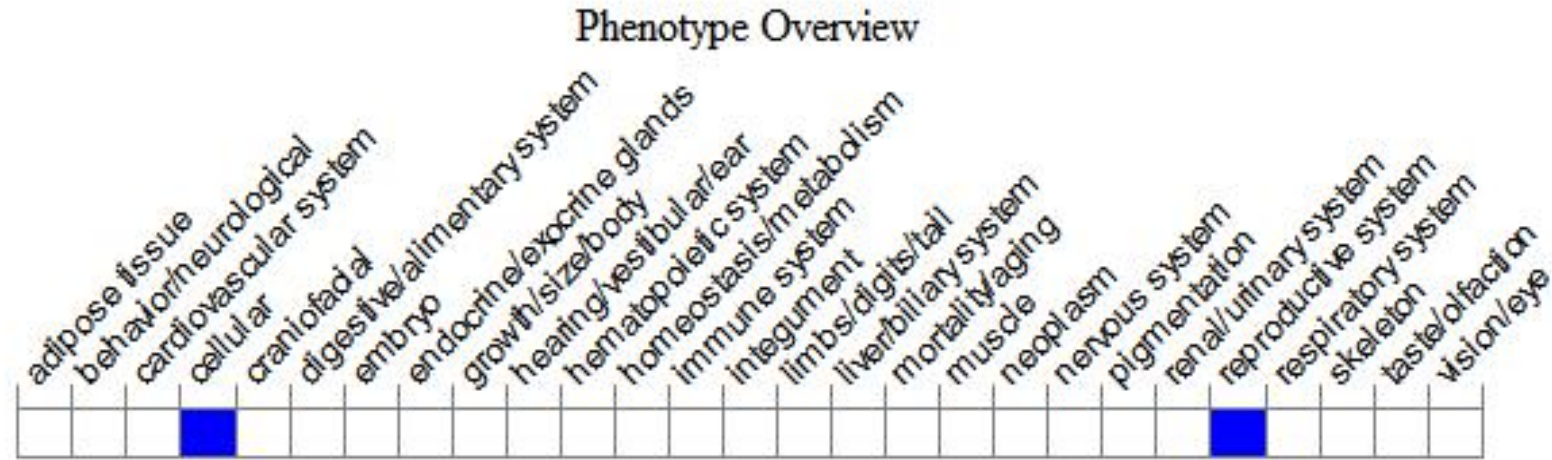




# Protein domain



# 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, male mice homozygous for disruptions in this gene are infertile as a result of abnormalities in spermatogenesis. Otherwise, males and females are normal and live a normal life span.

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

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