

Agfg1 Cas9-CKO Strategy

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Project Overview

Project Name

Agfg1

Project type

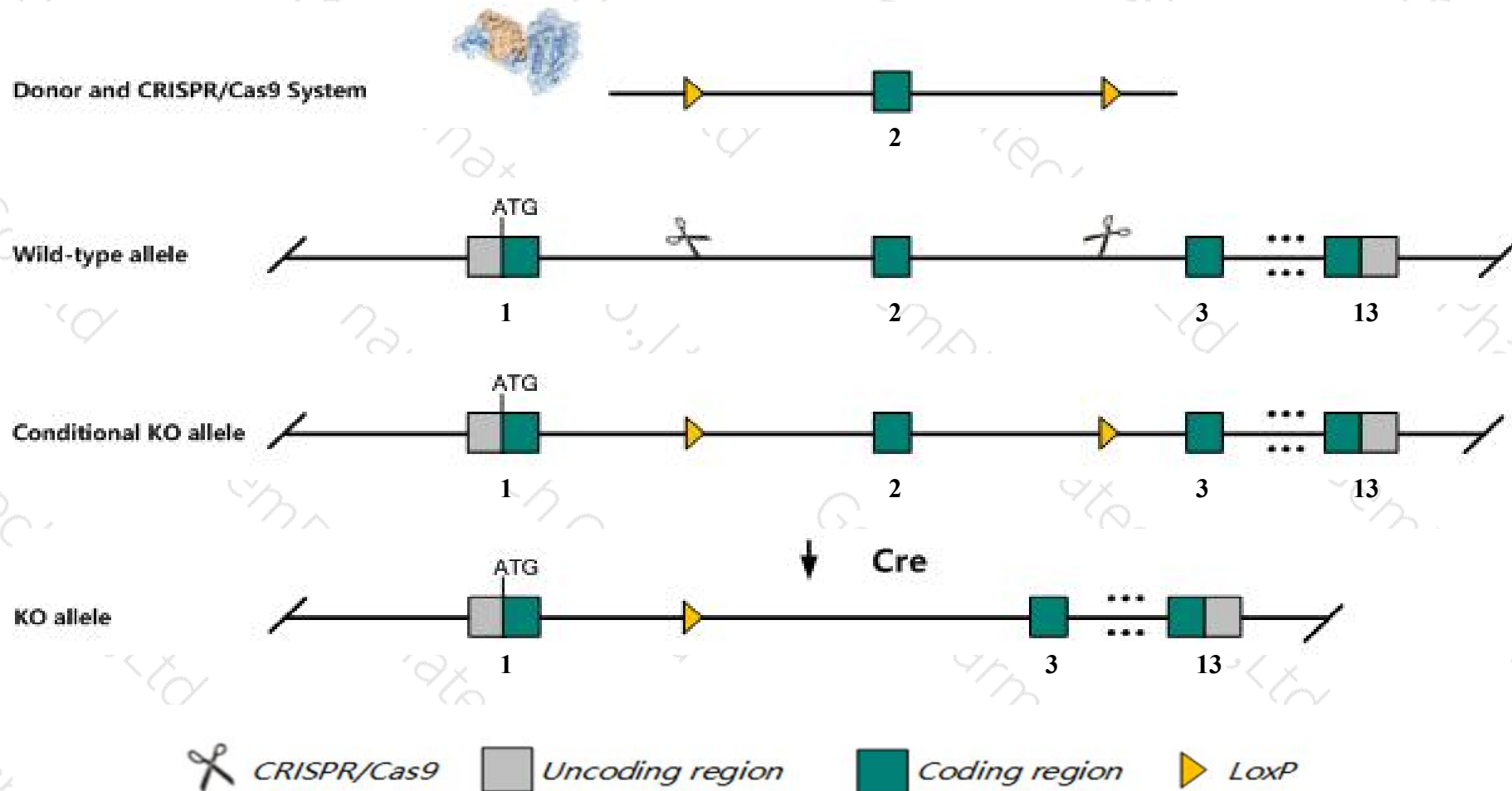
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional 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 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

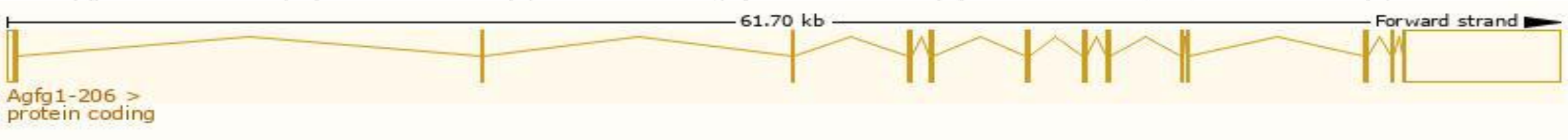
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

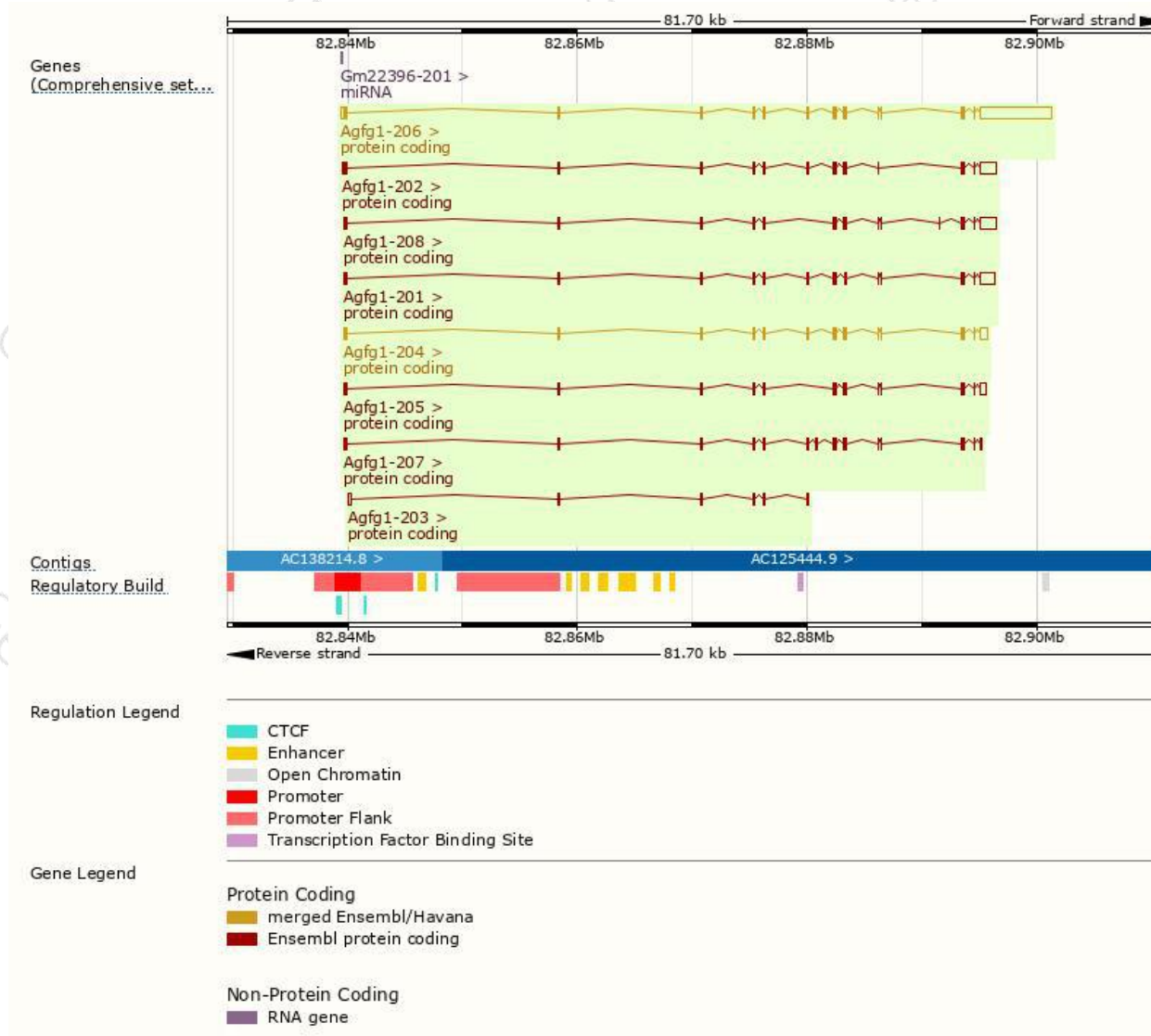
The gene has 8 transcripts,all transcripts are shown below:

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

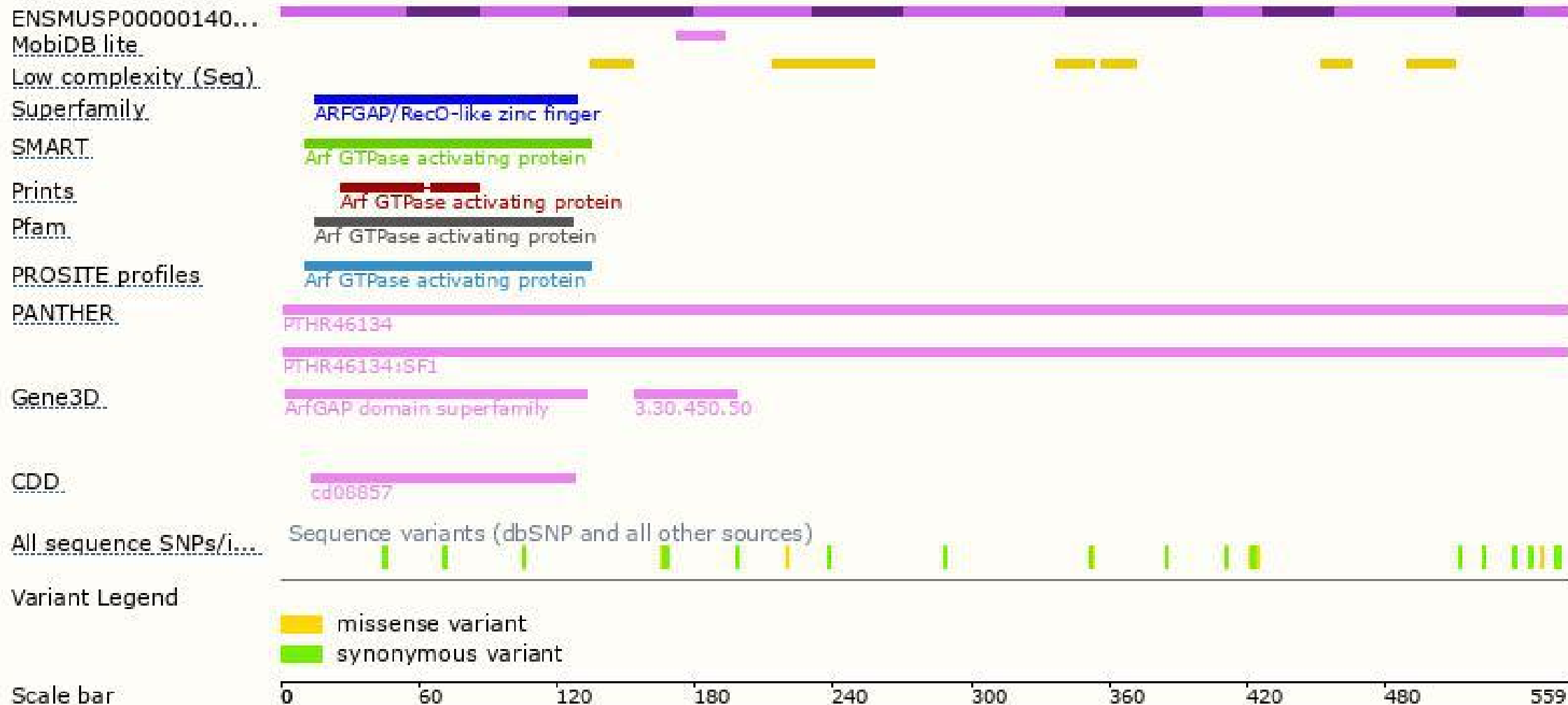
The strategy is based on the design of *Agfg1-206* transcript,the transcription is shown below:



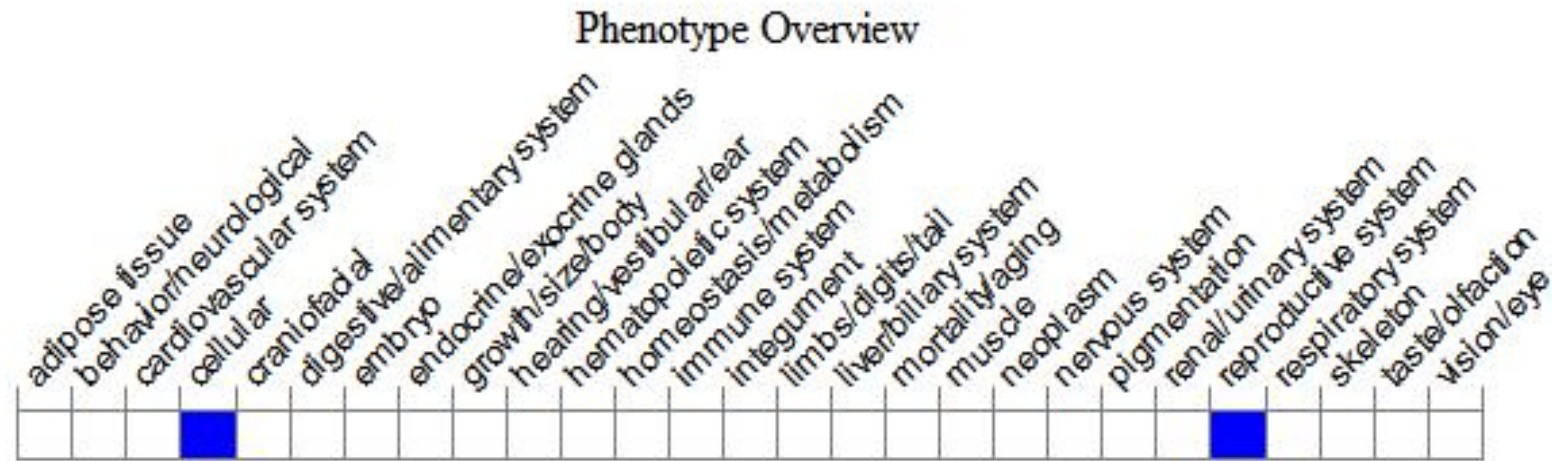
Genomic location distribution



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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