

Hspa4l Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Hspa4l

Project type

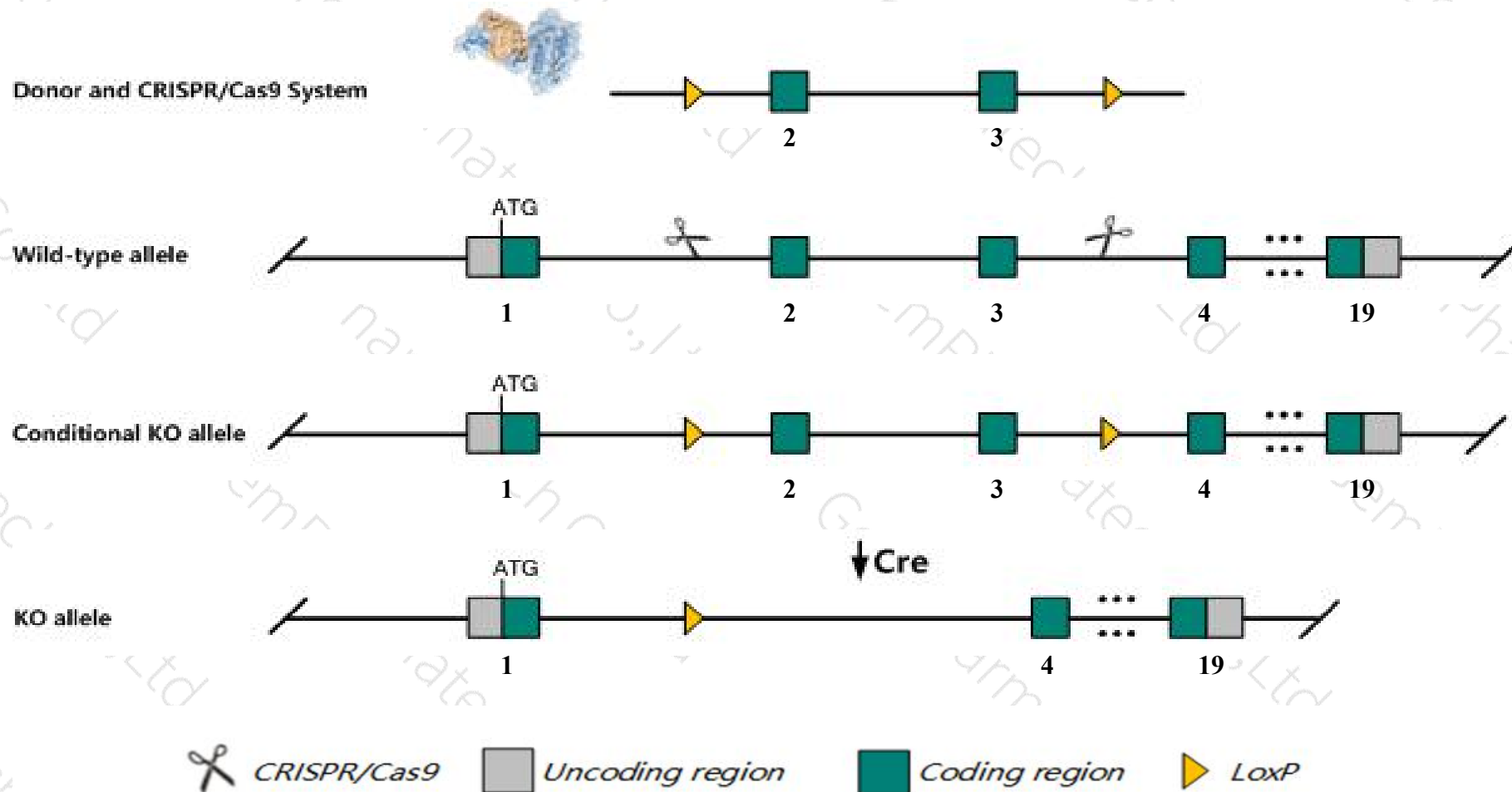
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- 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 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, 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

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](#)

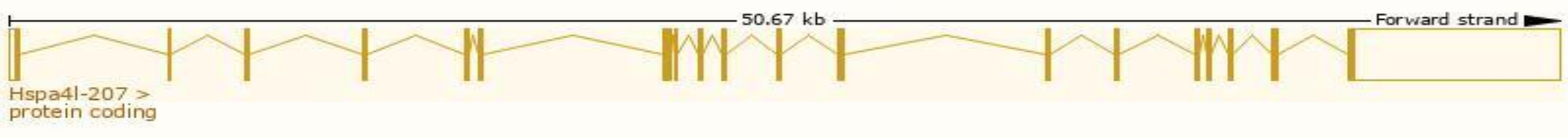
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

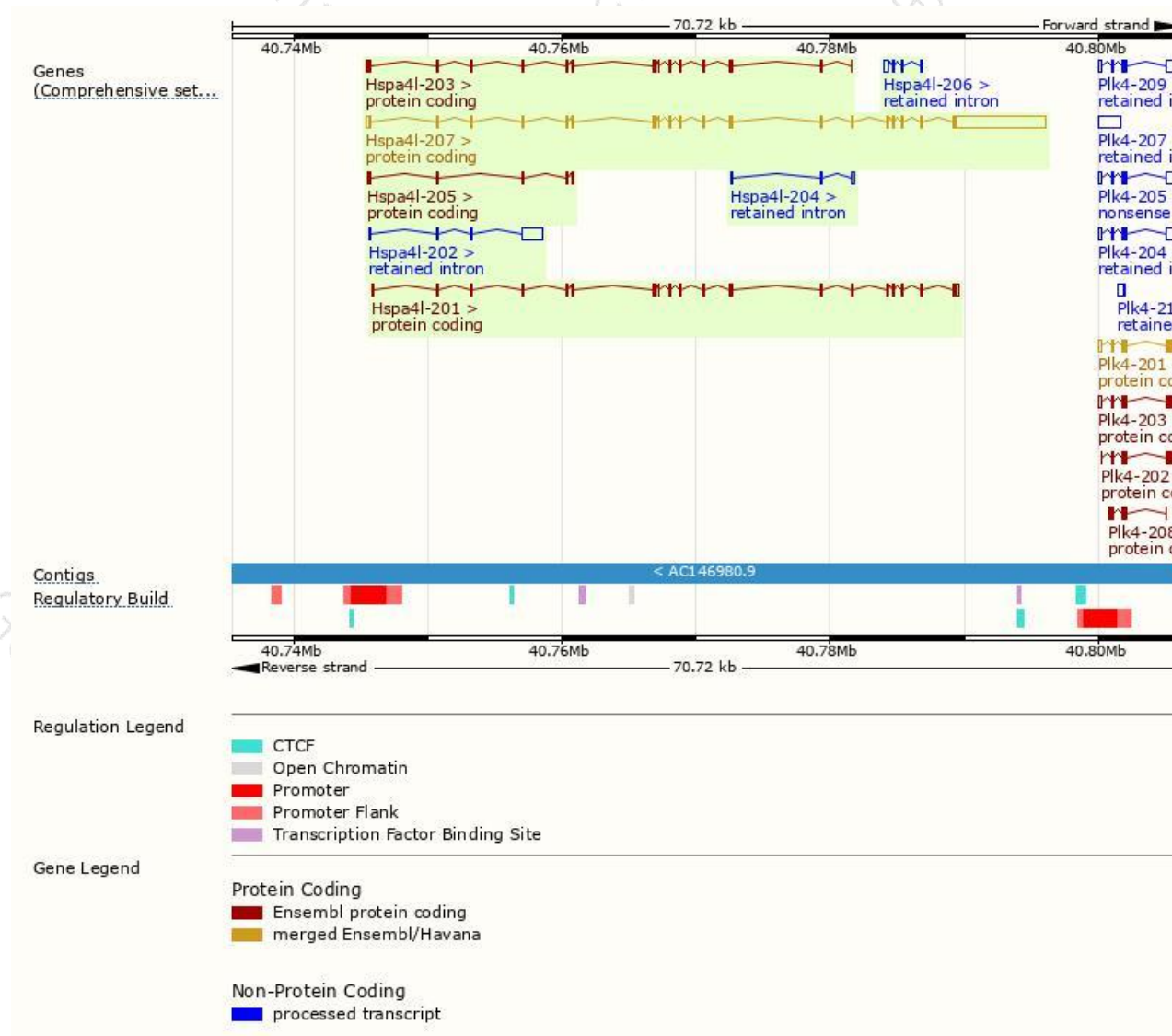
The gene has 7 transcripts,all transcripts are shown below:

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

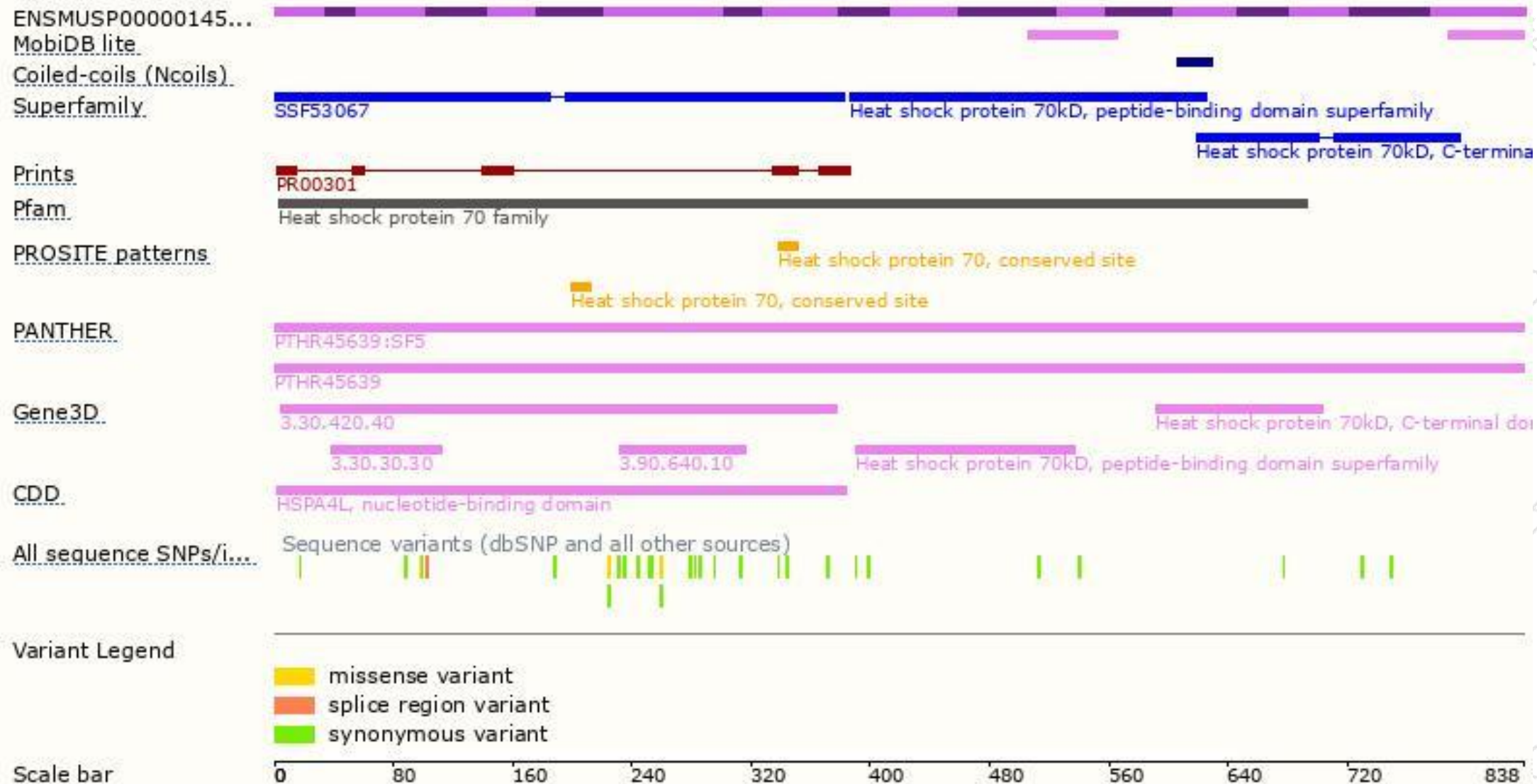
The strategy is based on the design of *Hspa4l-207* transcript,the transcription is shown below:



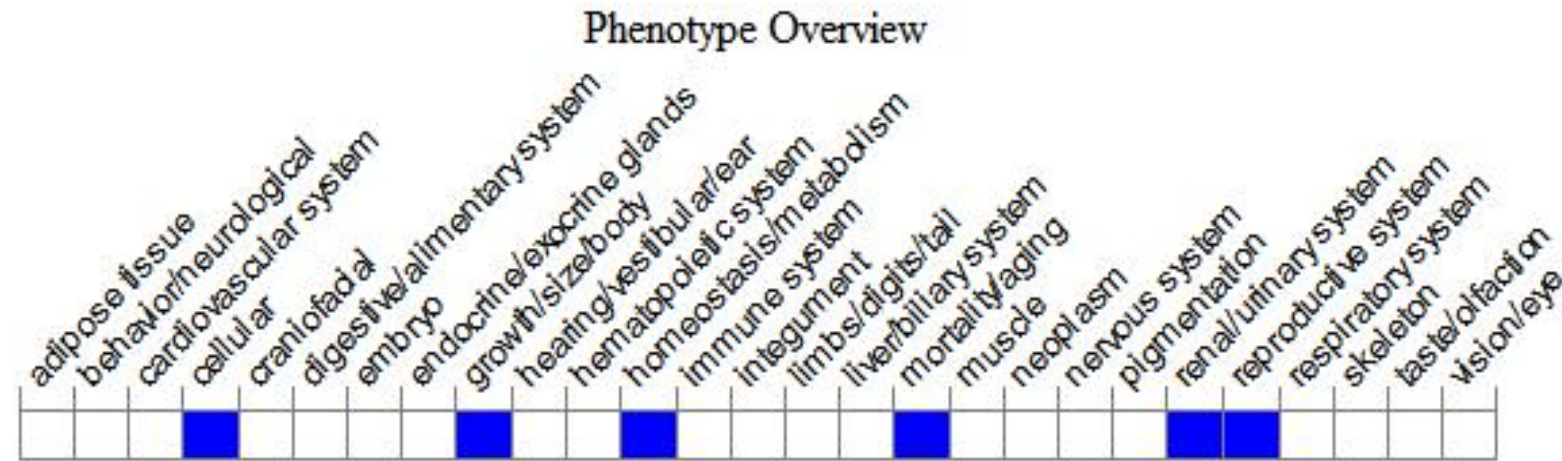
Genomic location distribution



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.

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

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