

Spata13 Cas9-CKO Strategy

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Project Overview

Project Name

Spata13

Project type

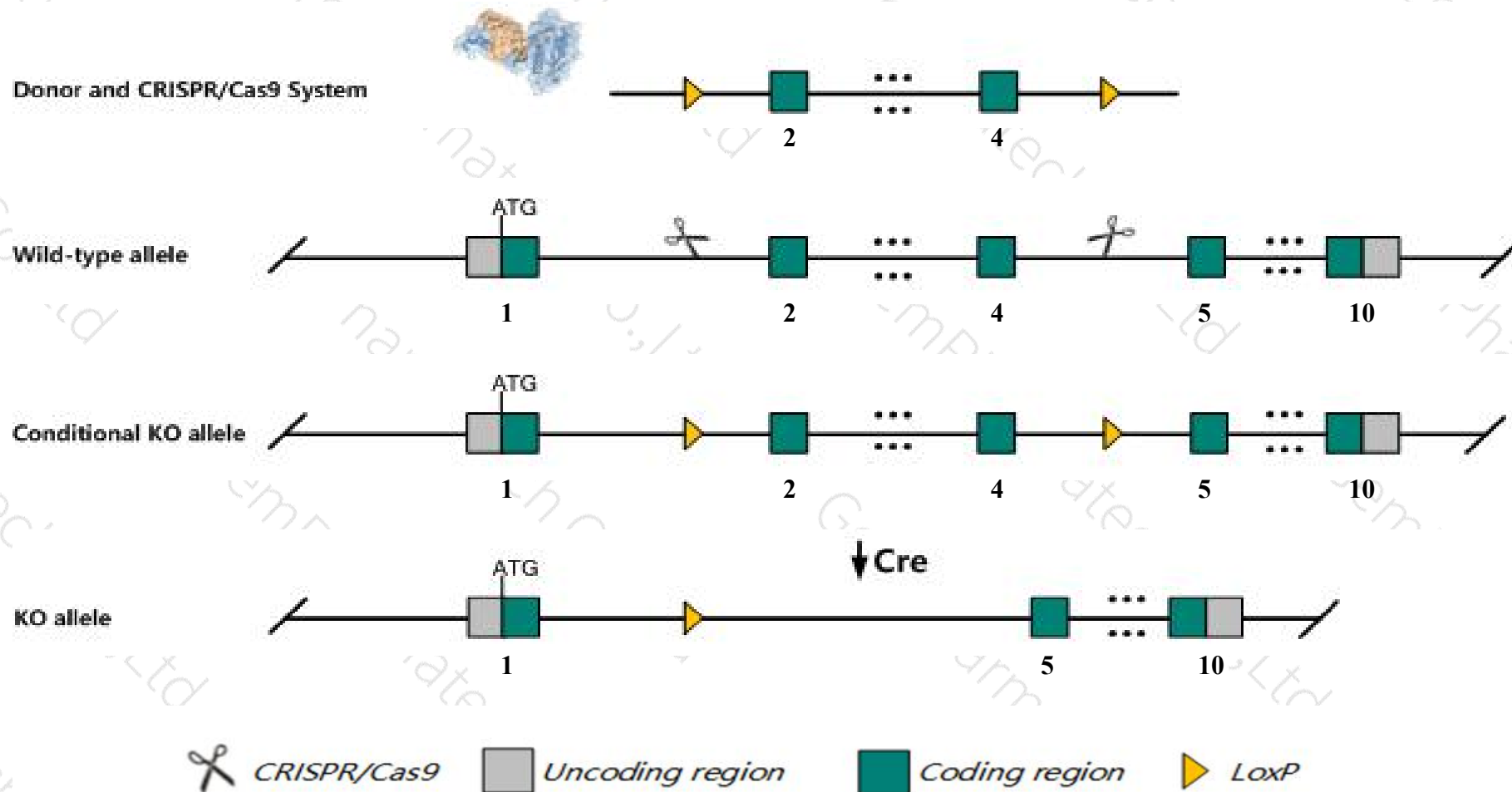
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Spata13* gene. The schematic diagram is as follows:



Technical routes

- The *Spata13* gene has 9 transcripts. According to the structure of *Spata13* gene, exon2-exon4 of *Spata13*-209 (ENSMUST00000162945.1) transcript is recommended as the knockout region. The region contains 503bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Spata13* 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 a knock-out allele are viable, fertile and overtly normal. behavioral tests indicate that mutant mice exhibit submissive social hierarchy behavior and females exhibit increased voluntary activity in the dark phase of the light-dark cycle.
- Transcript *Spata13-203*, *Spata13-204* and *Spata13-205* may not be affected.
- The *Spata13* gene is located on the Chr14. 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)

Spata13 spermatogenesis associated 13 [Mus musculus (house mouse)]

Gene ID: 219140, updated on 13-Mar-2020

Summary



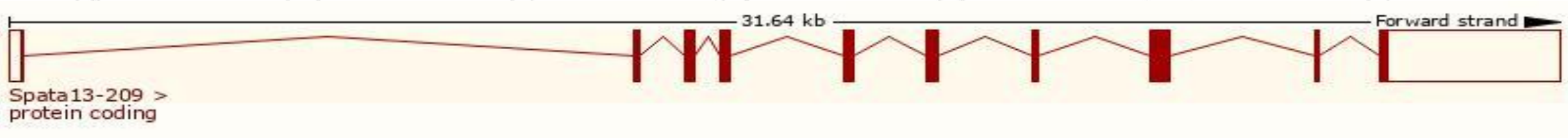
Official Symbol	Spata13 provided by MGI
Official Full Name	spermatogenesis associated 13 provided by MGI
Primary source	MGI:MGI:104838
See related	Ensembl:ENSMUSG000000021990
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C79050, ESTM11, X83327, mFLJ00298
Expression	Ubiquitous expression in thymus adult (RPKM 11.9), adrenal adult (RPKM 5.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

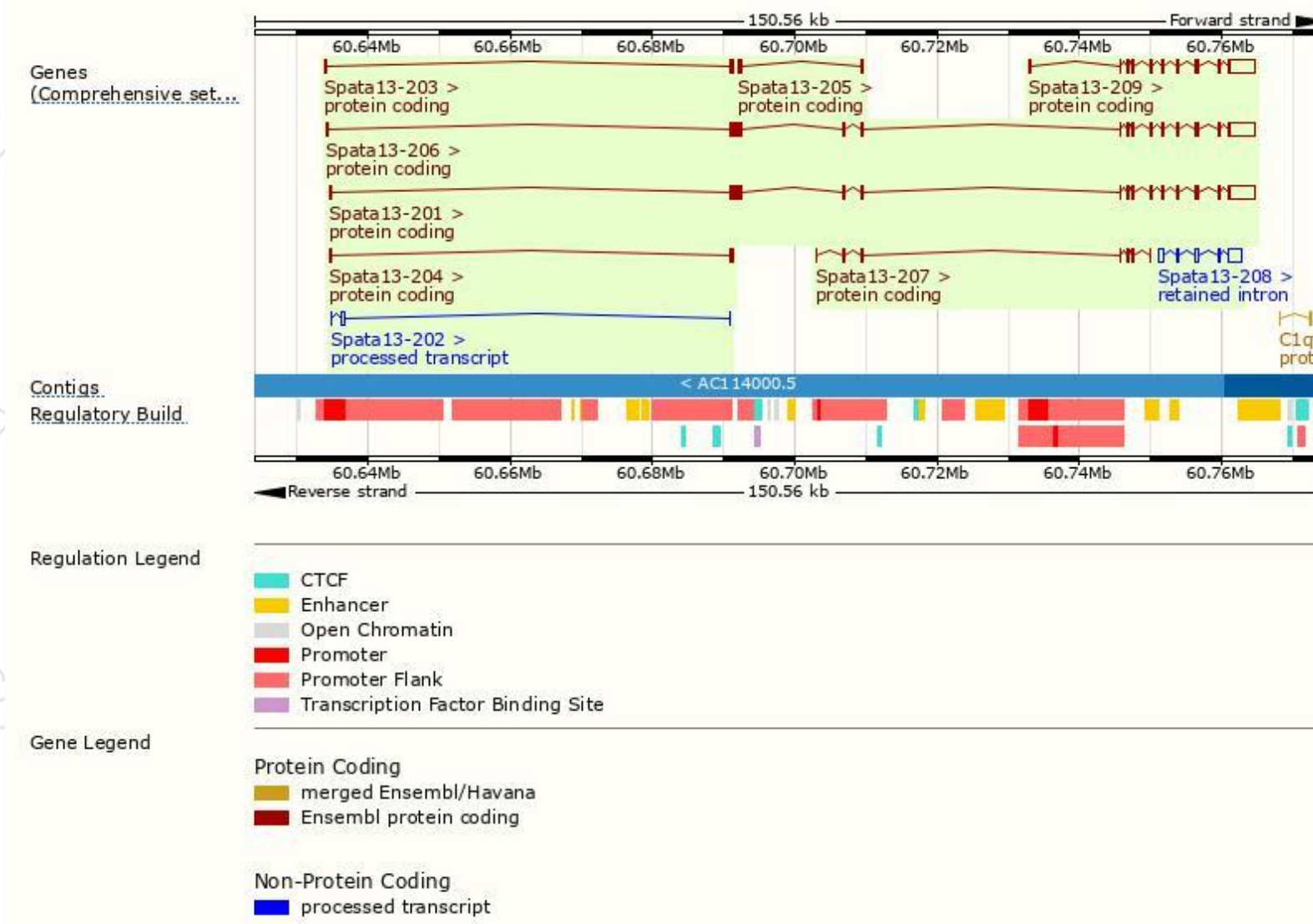
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spata13-201	ENSMUST00000022566.13	7517	1244aa	Protein coding	CCDS49516	E9Q3I3	TSL:5 GENCODE basic
Spata13-206	ENSMUST00000160973.7	7467	1244aa	Protein coding	CCDS49516	E9Q3I3	TSL:1 GENCODE basic
Spata13-209	ENSMUST00000162945.1	5469	574aa	Protein coding	CCDS79328	E0CYU0	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
Spata13-207	ENSMUST00000162131.8	1208	369aa	Protein coding	-	F6SRZ4	CDS 3' incomplete TSL:2
Spata13-205	ENSMUST00000160095.2	719	240aa	Protein coding	-	F6V9S1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Spata13-203	ENSMUST00000159169.1	697	124aa	Protein coding	-	E0CXN6	CDS 3' incomplete TSL:2
Spata13-204	ENSMUST00000159729.1	686	138aa	Protein coding	-	E0CZ51	CDS 3' incomplete TSL:2
Spata13-202	ENSMUST00000159135.1	429	No protein	Processed transcript	-	-	TSL:3
Spata13-208	ENSMUST00000162939.1	3161	No protein	Retained intron	-	-	TSL:5

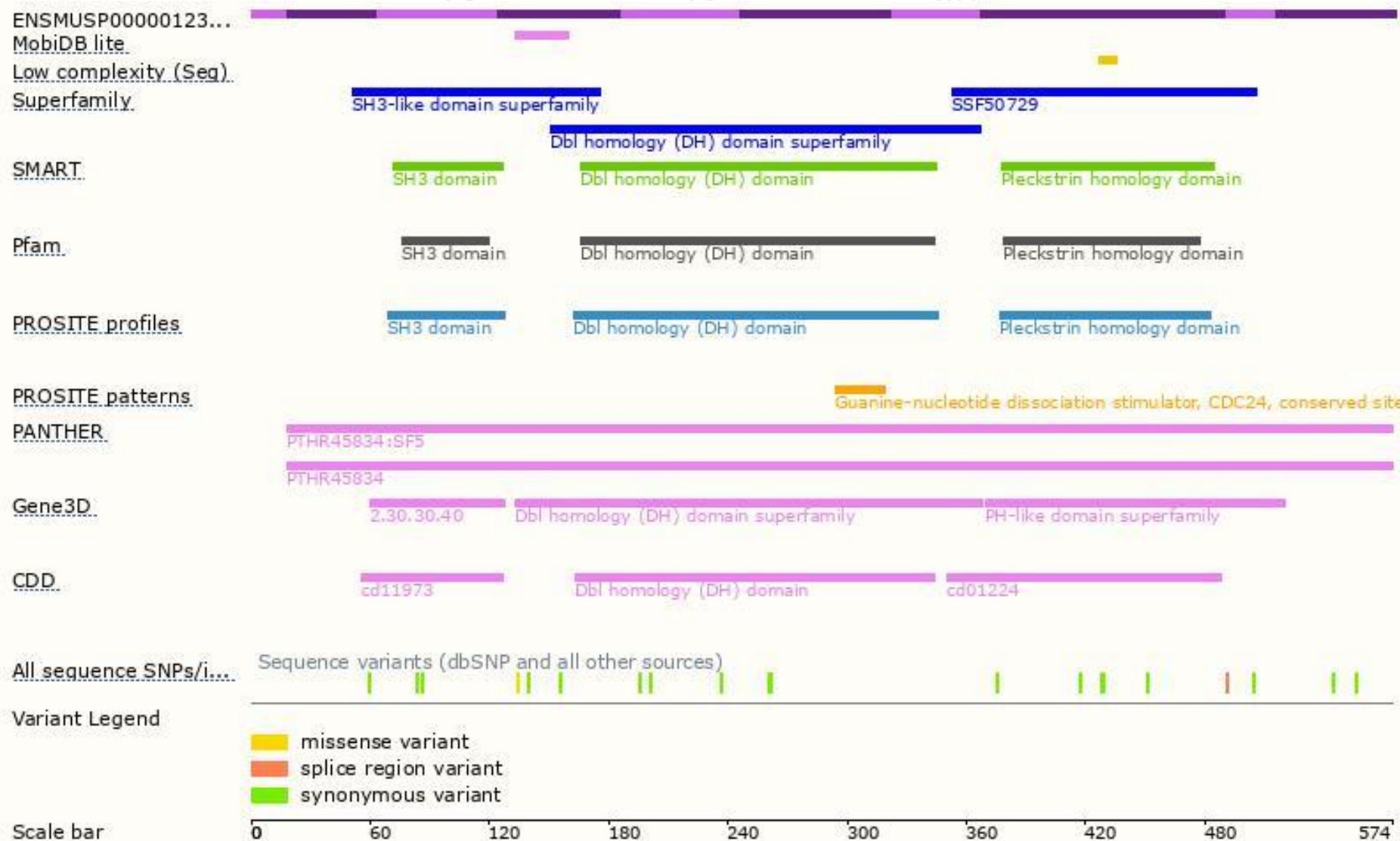
The strategy is based on the design of *Spata13-209* transcript,the transcription is shown below:



Genomic location distribution

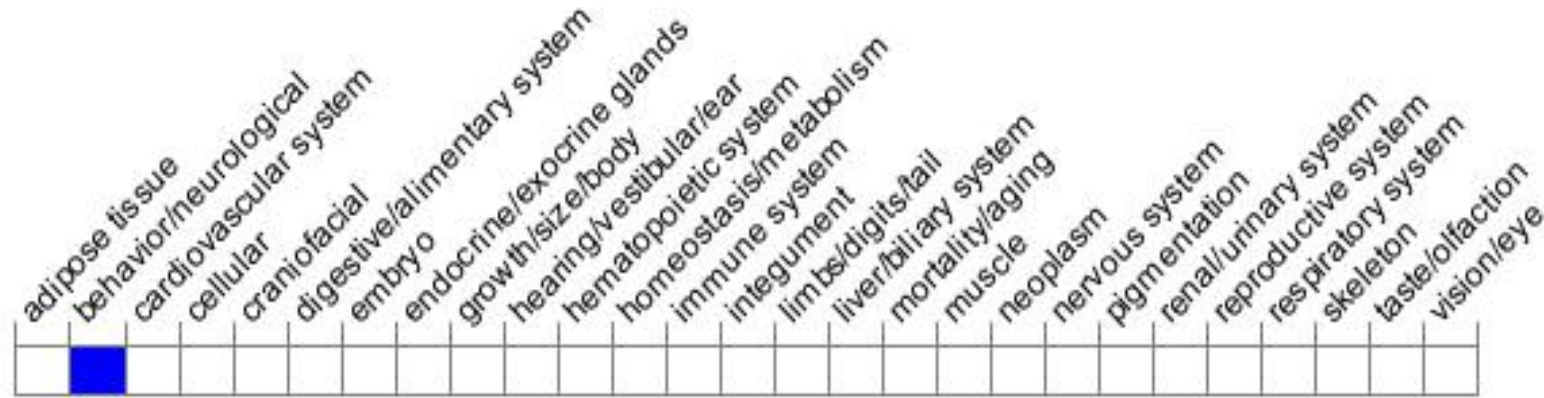


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 are viable, fertile and overtly normal.

Behavioral tests indicate that mutant mice exhibit submissive social hierarchy behavior and females exhibit increased voluntary activity in the dark phase of the light-dark cycle.

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

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