

Nsf Cas9-KO Strategy

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Project Overview

Project Name

Nsf

Project type

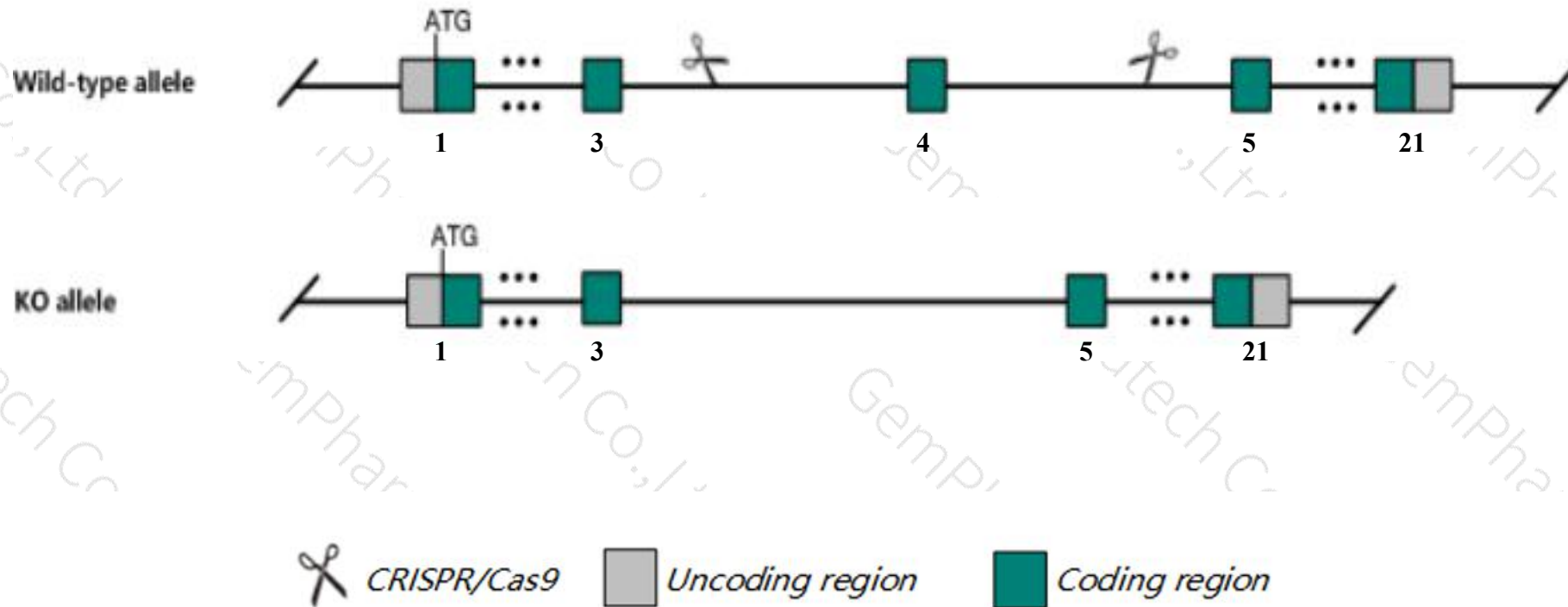
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Nsf* gene has 10 transcripts. According to the structure of *Nsf* gene, exon4 of *Nsf-202* (ENSMUST00000103075.10) transcript is recommended as the knockout region. The region contains 40bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nsf* gene. The brief process is as follows: CRISPR/Cas9 system will

- The *Nsf* gene is located on the Chr11. 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)

Nsf N-ethylmaleimide sensitive fusion protein [Mus musculus (house mouse)]

Gene ID: 18195, updated on 13-Mar-2020

Summary

Official Symbol Nsf provided by [MGI](#)

Official Full Name N-ethylmaleimide sensitive fusion protein provided by [MGI](#)

Primary source [MGI:MGI:104560](#)

See related [Ensembl:ENSMUSG00000034187](#)

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 AI316878, AU020090, AU067812, SKD2

Expression Broad expression in cerebellum adult (RPKM 105.1), frontal lobe adult (RPKM 99.1) and 21 other tissues [See more](#)

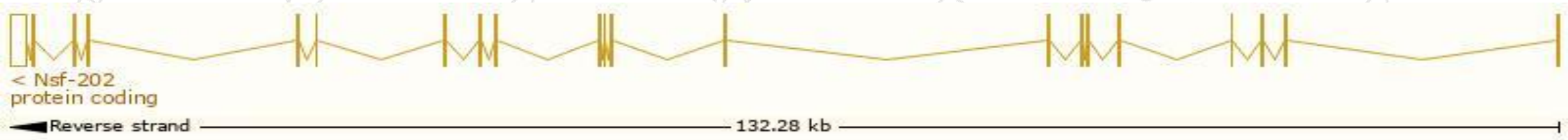
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

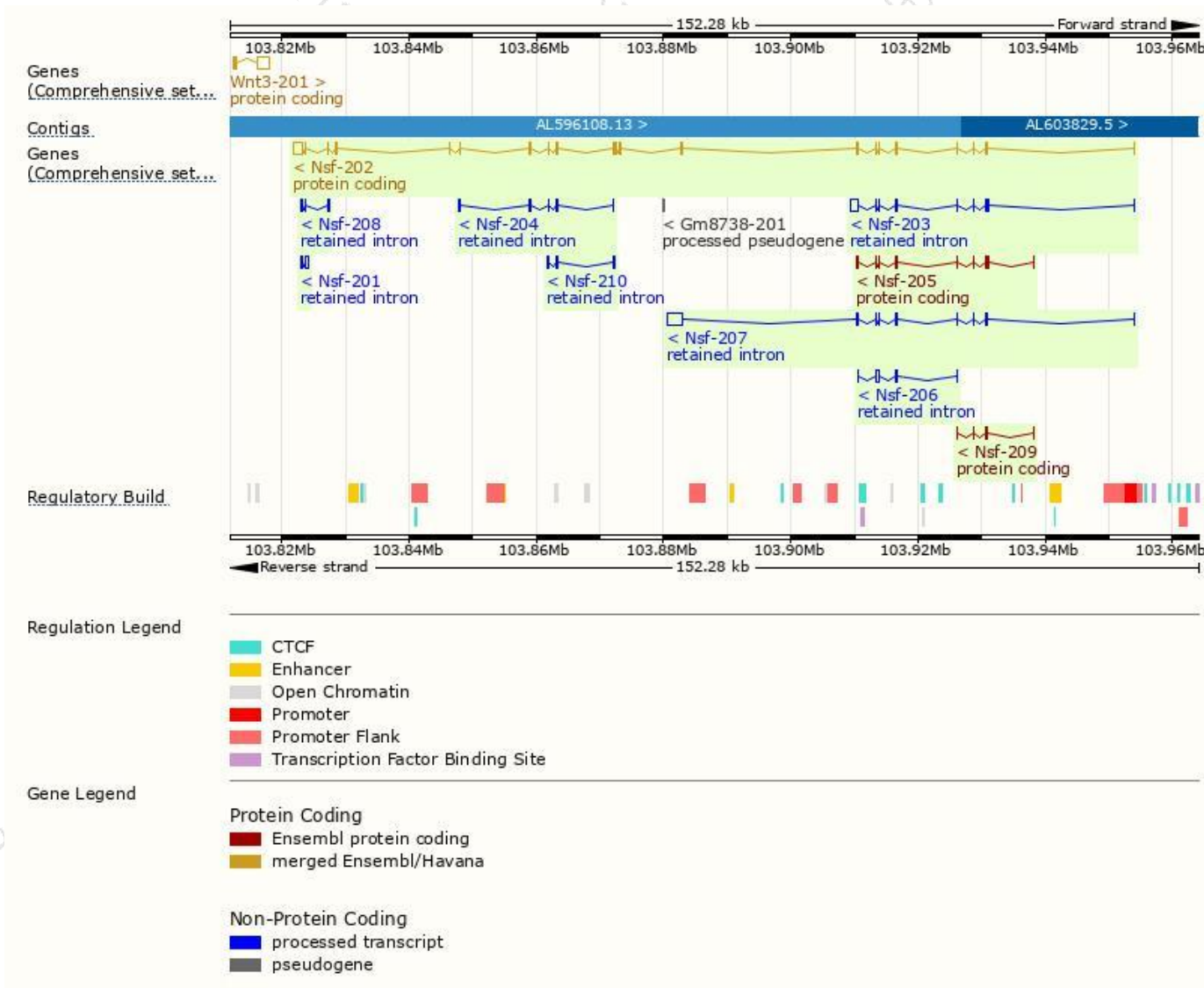
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nsf-202	ENSMUST00000103075.10	3766	744aa	Protein coding	CCDS25524	P46460	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
Nsf-205	ENSMUST00000133774.3	823	210aa	Protein coding	-	G3UX86	CDS 3' incomplete TSL:5
Nsf-209	ENSMUST00000149642.2	278	76aa	Protein coding	-	G3UX98	CDS 3' incomplete TSL:5
Nsf-207	ENSMUST00000145126.7	3212	No protein	Retained intron	-	-	TSL:1
Nsf-203	ENSMUST00000107009.7	1853	No protein	Retained intron	-	-	TSL:1
Nsf-206	ENSMUST00000140394.2	806	No protein	Retained intron	-	-	TSL:5
Nsf-201	ENSMUST00000040443.10	688	No protein	Retained intron	-	-	TSL:2
Nsf-210	ENSMUST00000150516.1	671	No protein	Retained intron	-	-	TSL:1
Nsf-204	ENSMUST00000127813.7	659	No protein	Retained intron	-	-	TSL:2
Nsf-208	ENSMUST00000146036.1	612	No protein	Retained intron	-	-	TSL:2

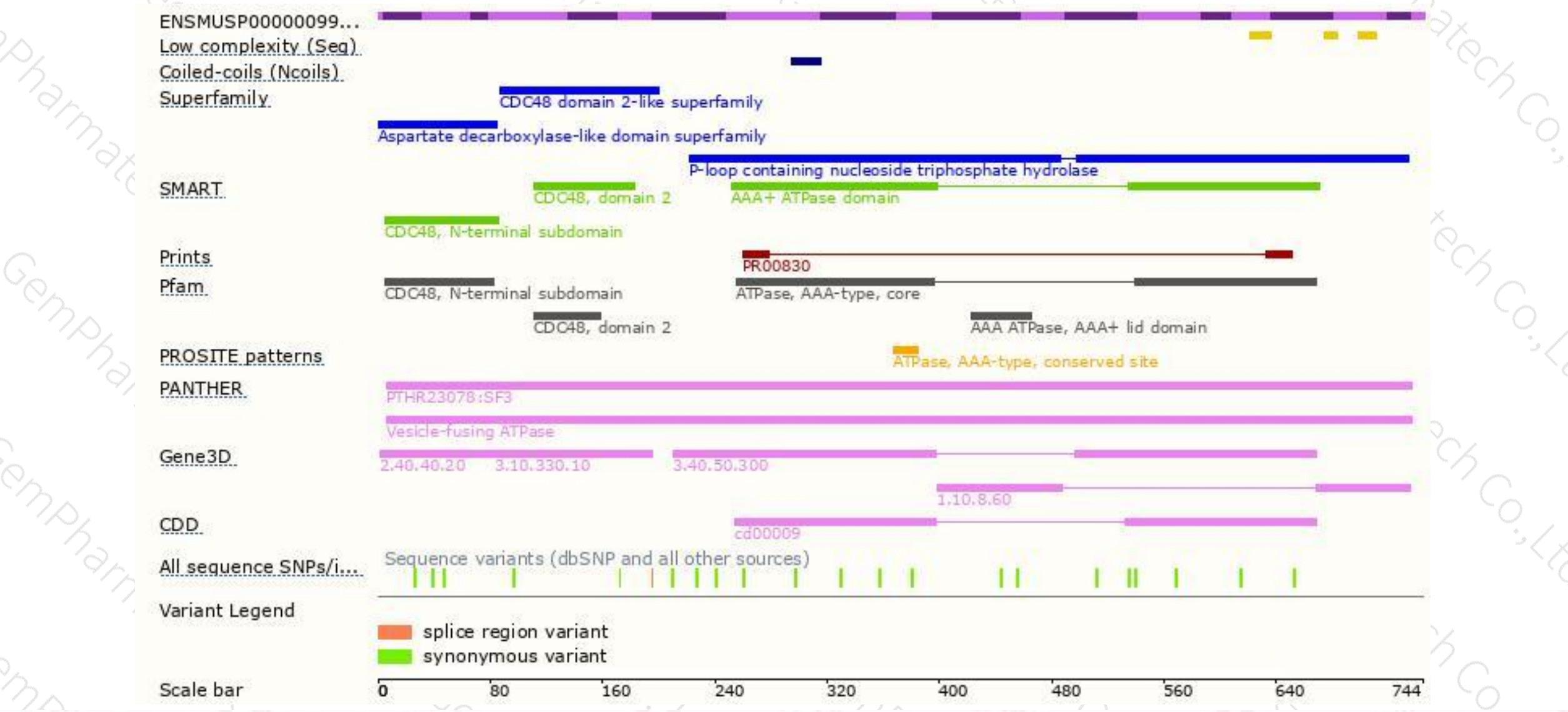
The strategy is based on the design of *Nsf-202* transcript,the transcription is shown below:



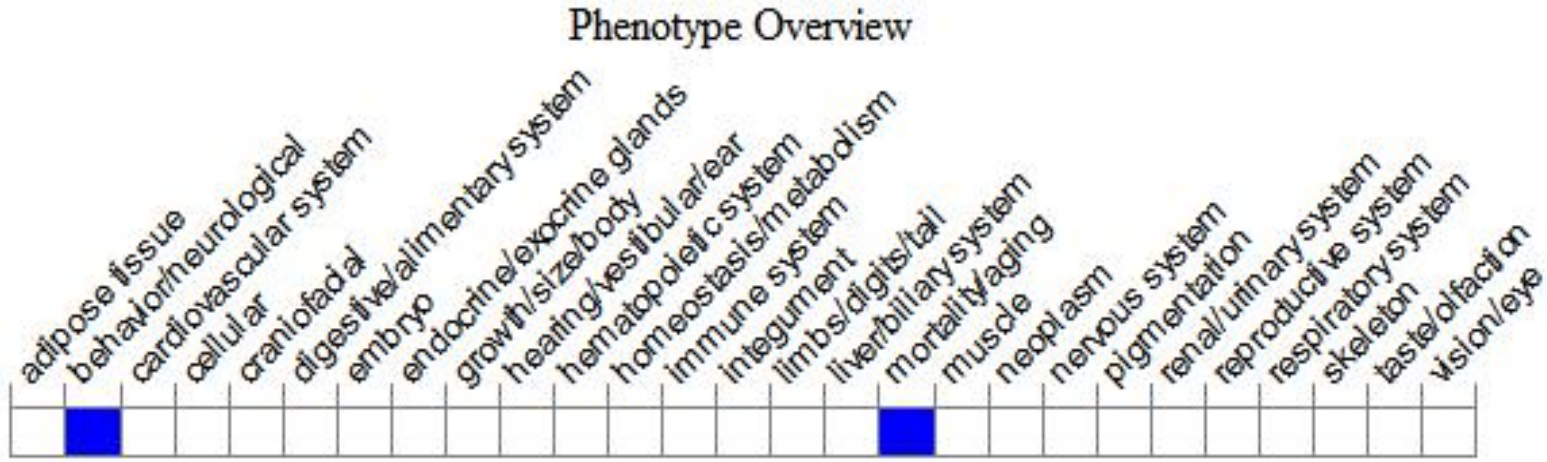
Genomic location distribution



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/>).

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

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