

Pex2 Cas9-CKO Strategy

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Project Overview

Project Name

Pex2

Project type

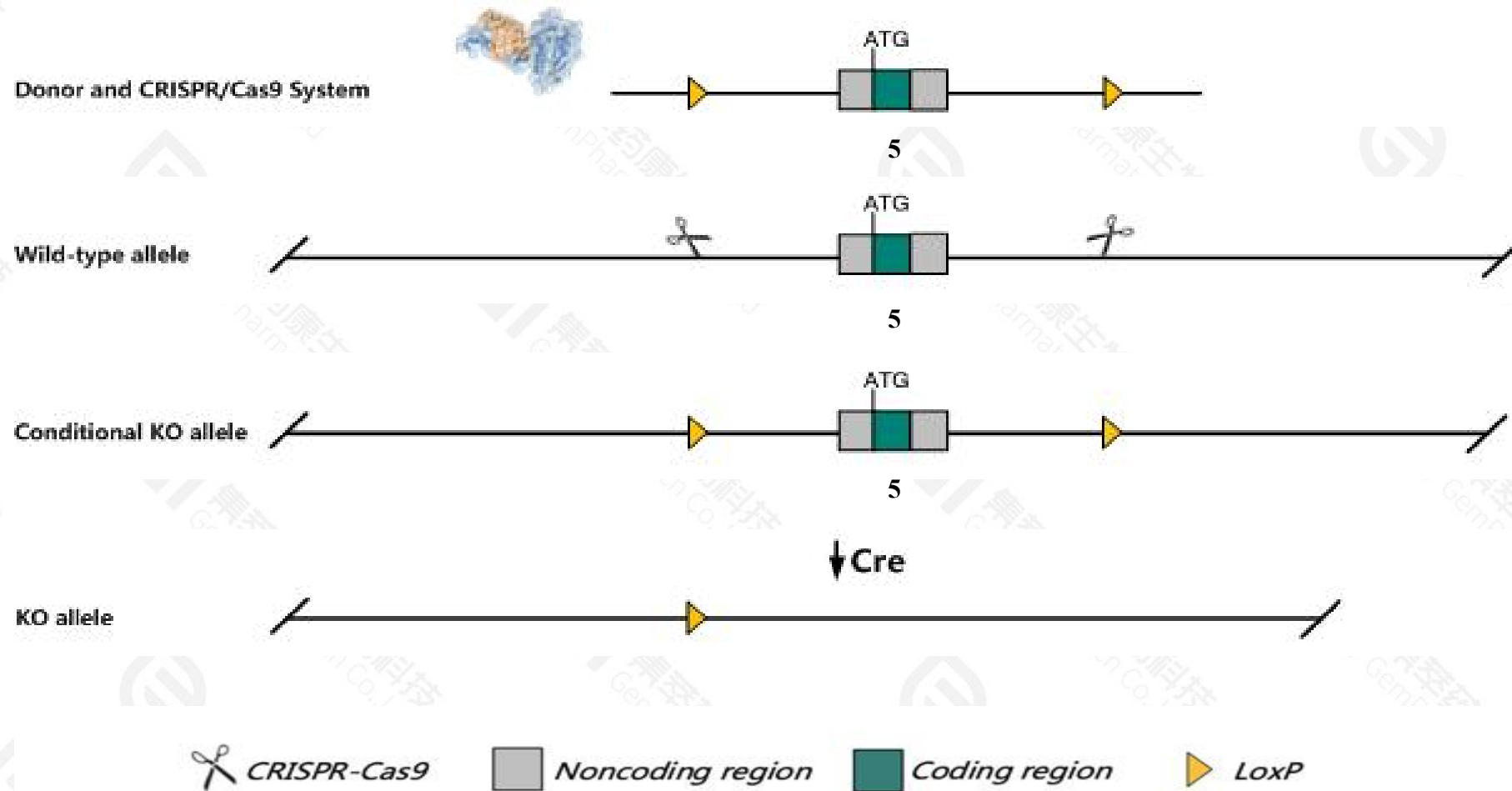
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Pex2* gene. The schematic diagram is as follows:



- The *Pex2* gene has 6 transcripts. According to the structure of *Pex2* gene, exon5 of *Pex2*-203(ENSMUST00000164828.8) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Pex2* 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 die sometime before weaning. Various abnormalities are seen in the central nervous system depending on the genetic background.
- The *Pex2* 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)

Pex2 peroxisomal biogenesis factor 2 [Mus musculus (house mouse)]

Gene ID: 19302, updated on 13-Mar-2020

Summary

Official Symbol Pex2 provided by [MGI](#)

Official Full Name peroxisomal biogenesis factor 2 provided by [MGI](#)

Primary source [MGI:MGI:107486](#)

See related [Ensembl:ENSMUSG00000040374](#)

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 D3Ert138e, PAF-1, PMP35, Pxmp3

Expression Ubiquitous expression in bladder adult (RPKM 7.6), CNS E11.5 (RPKM 7.2) and 28 other tissues [See more](#)

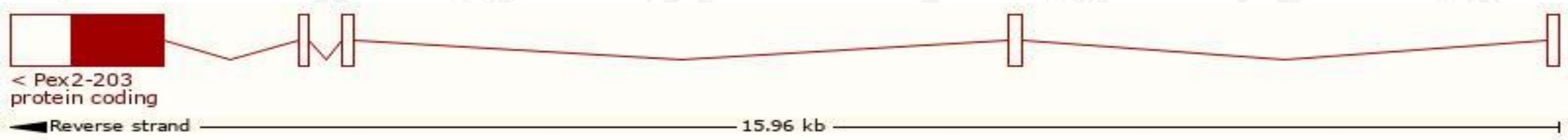
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

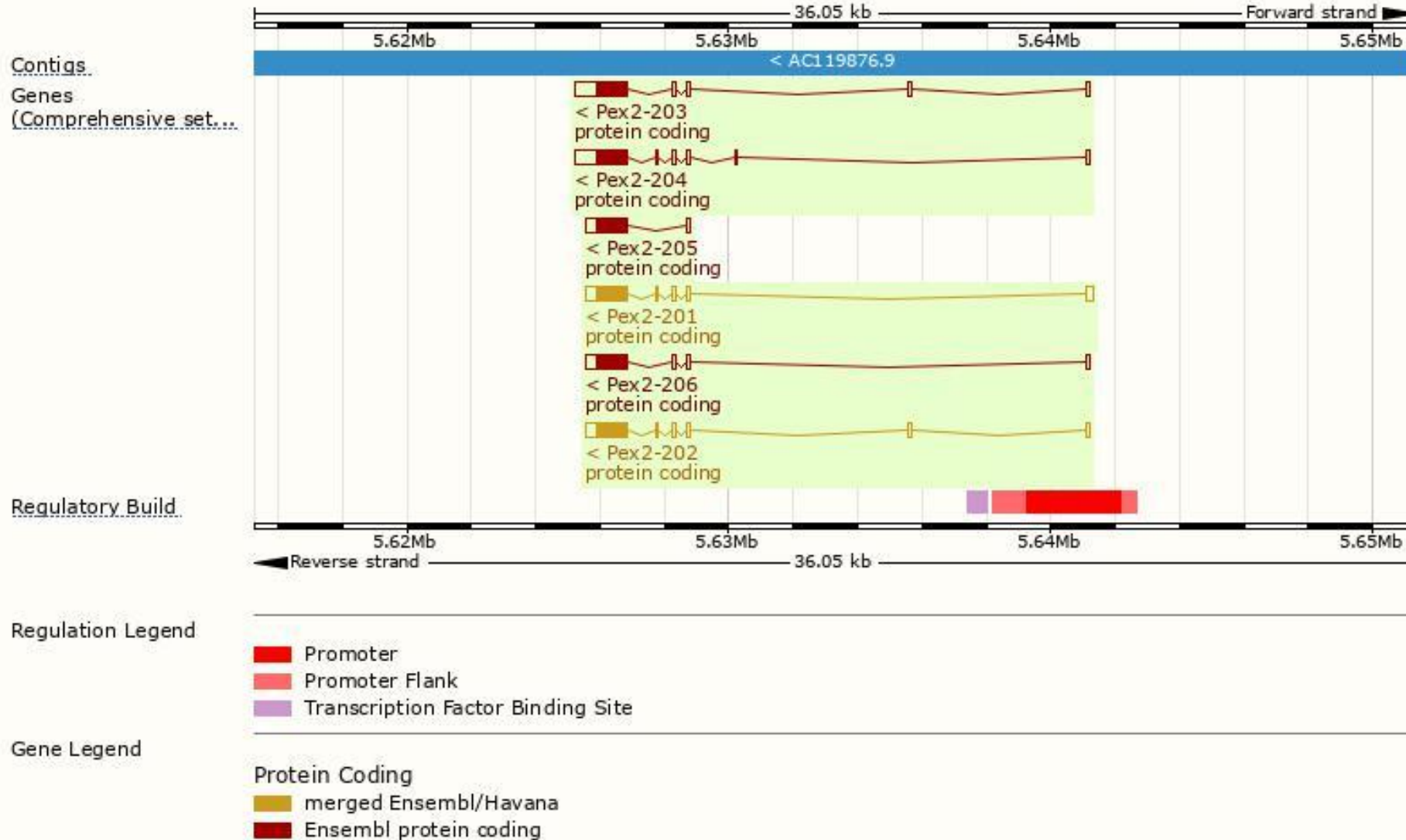
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pex2-203	ENSMUST00000164828.7	2051	305aa	Protein coding	CCDS17228	Q91YZ5	TSL:2 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
Pex2-204	ENSMUST00000165309.7	2038	305aa	Protein coding	CCDS17228	Q91YZ5	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 P1
Pex2-202	ENSMUST00000071280.7	1777	305aa	Protein coding	CCDS17228	Q91YZ5	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
Pex2-201	ENSMUST00000059021.9	1749	305aa	Protein coding	CCDS17228	Q91YZ5	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
Pex2-206	ENSMUST00000195855.5	1587	305aa	Protein coding	CCDS17228	Q91YZ5	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
Pex2-205	ENSMUST00000191916.5	1376	305aa	Protein coding	CCDS17228	Q91YZ5	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 P1

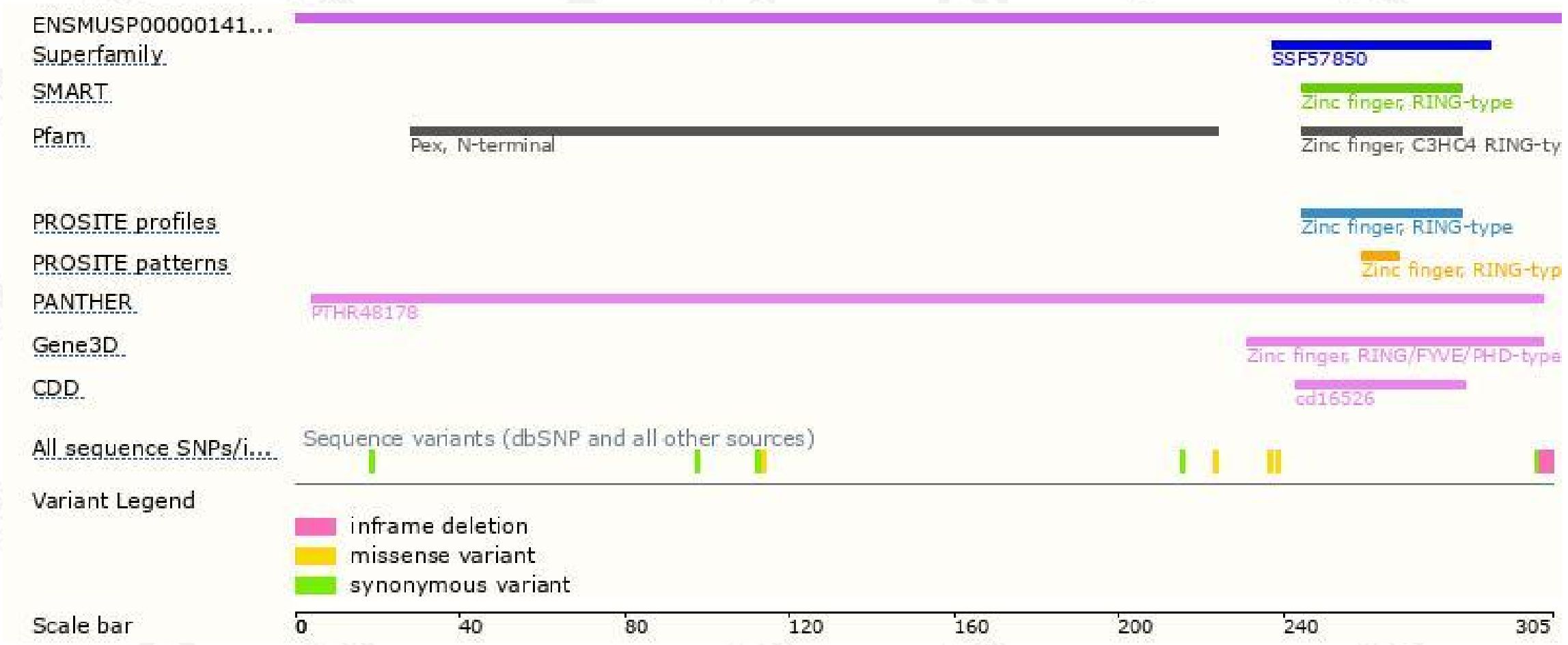
The strategy is based on the design of *Pex2-203* transcript,the transcription is shown below:



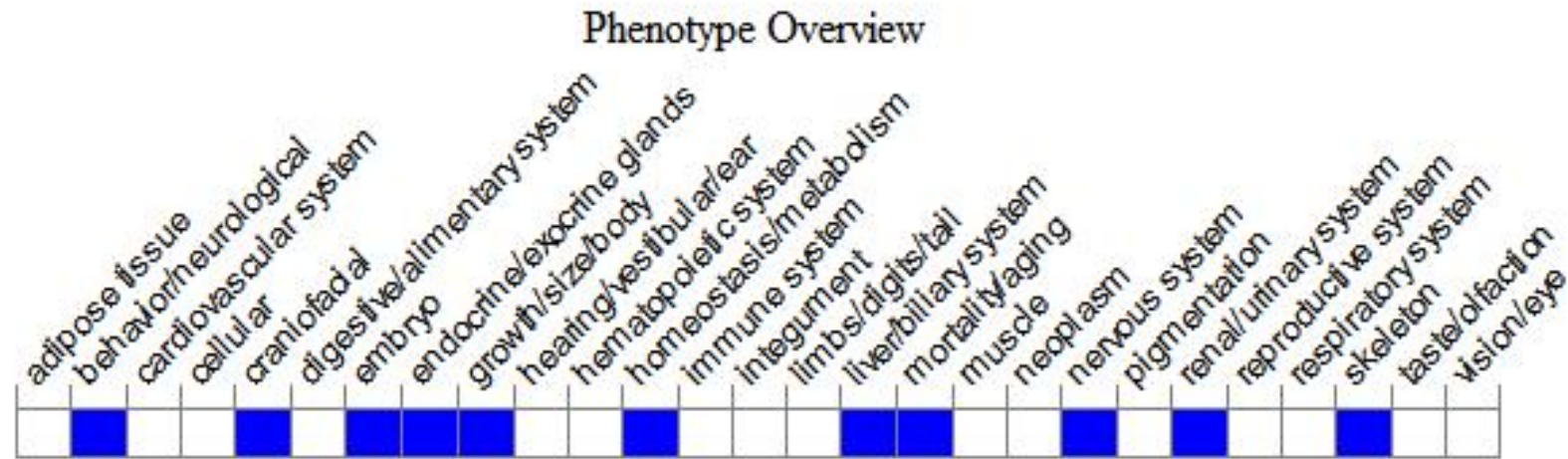
Genomic location distribution



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 die sometime before weaning.

Various abnormalities are seen in the central nervous system depending on the genetic background.

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