Pex2 Cas9-KO Strategy

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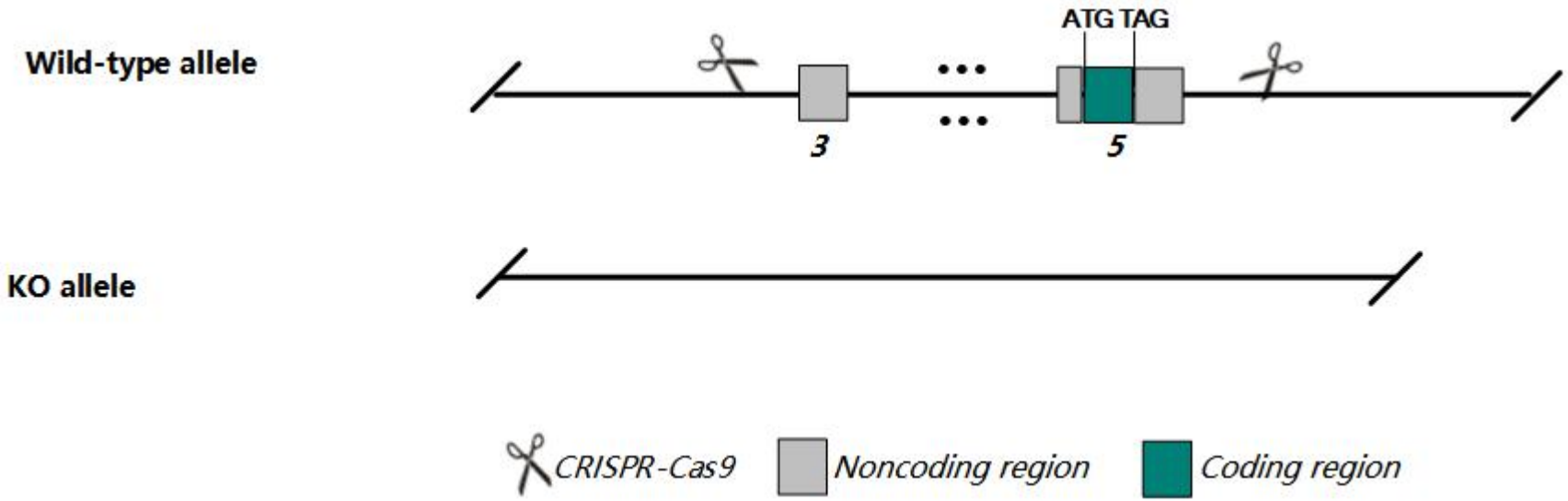
Design Date: 2020-5-6

Project Overview

Project Name	***Pex2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Pex2* gene has 6 transcripts. According to the structure of *Pex2* gene, exon3-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 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.

Notice

➢ 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

集萃药康 GemPharmatech

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

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

Summary

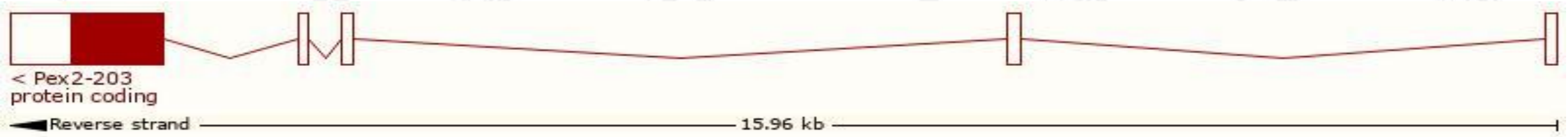
Official Symbol	Pex2 provided by MGI
Official Full Name	peroxisomal biogenesis factor 2 provided by MGI
Primary source	MGI:MGI:107486
See related	Ensembl:ENSMUSG00000040374
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D3Ertd138e, 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）

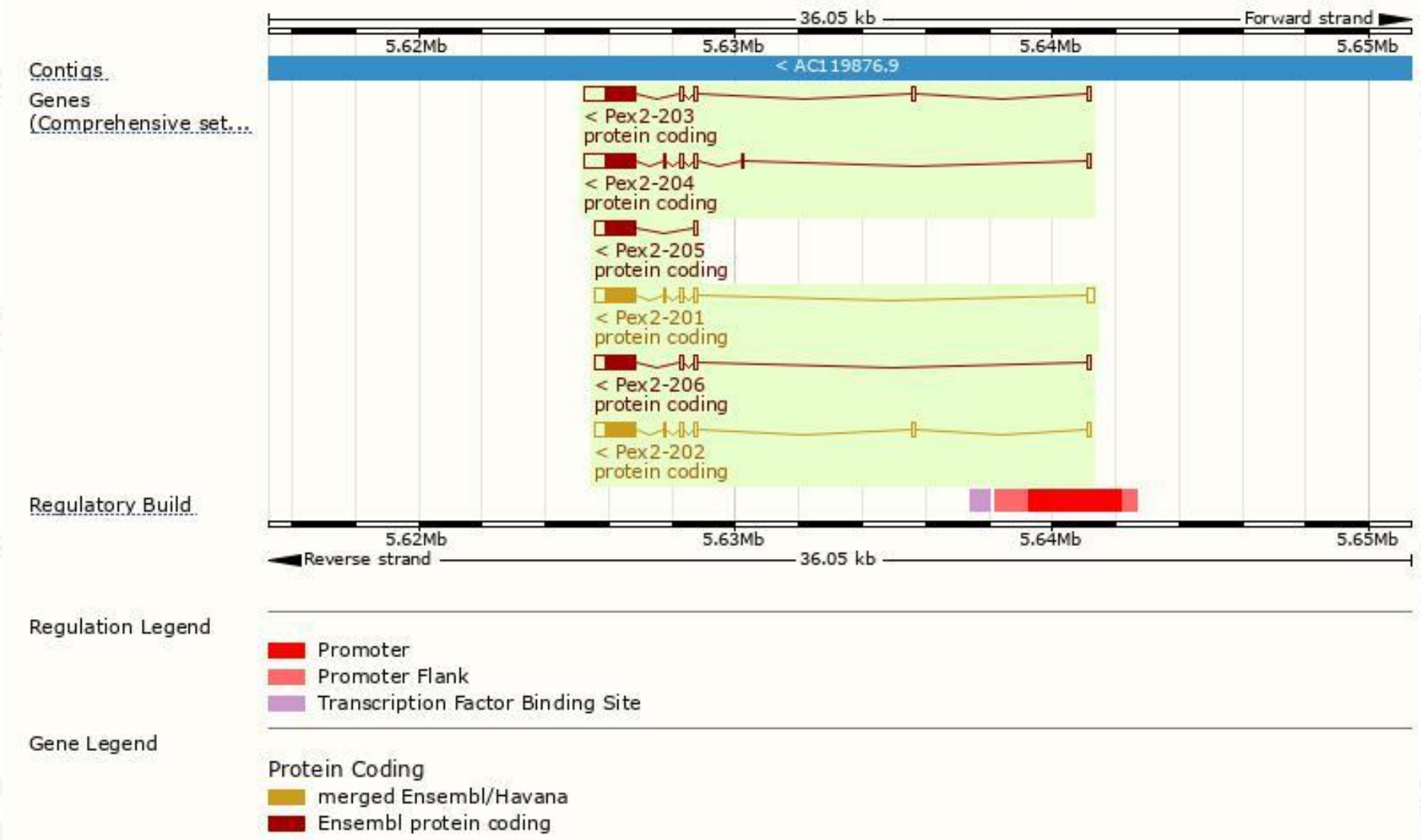
The gene has 6 transcripts,all transcripts are shown below:

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

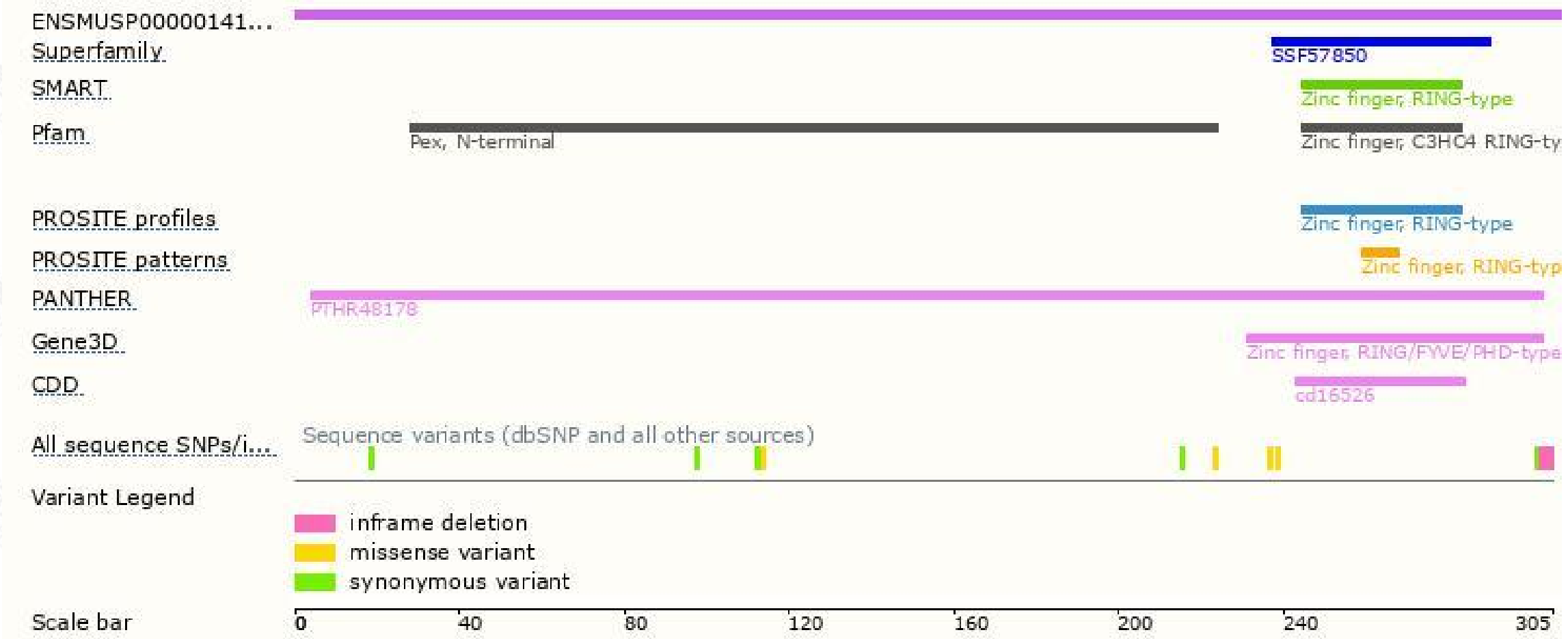
The strategy is based on the design of *Pex2-203* transcript,the transcription is shown below:



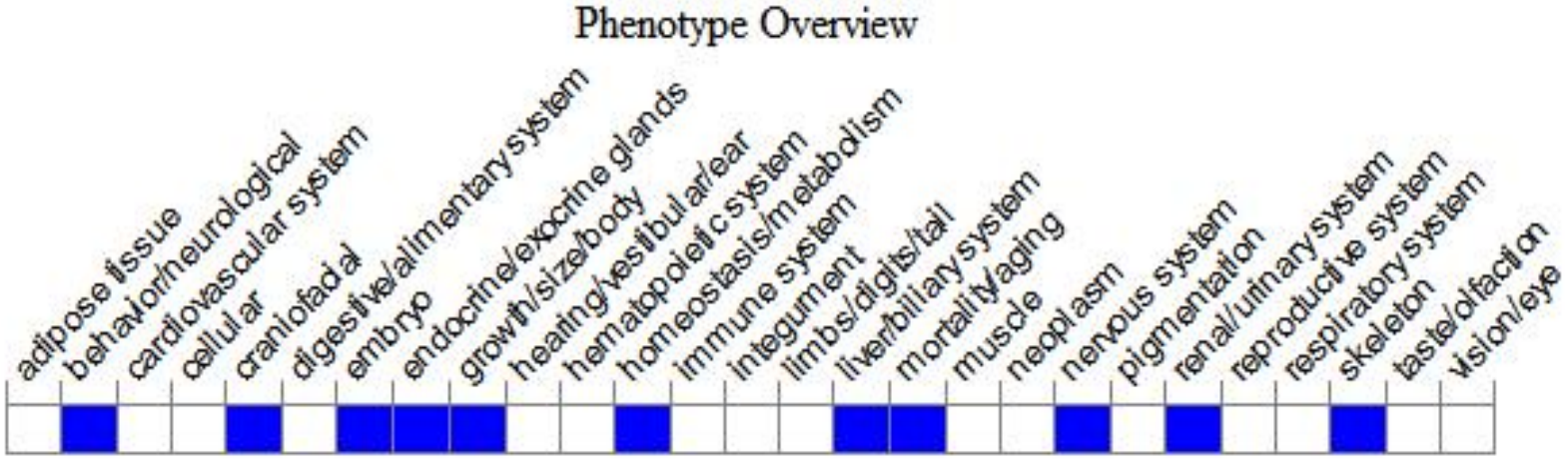
Genomic location distribution



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.

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