Pex1 Cas9-KO Strategy

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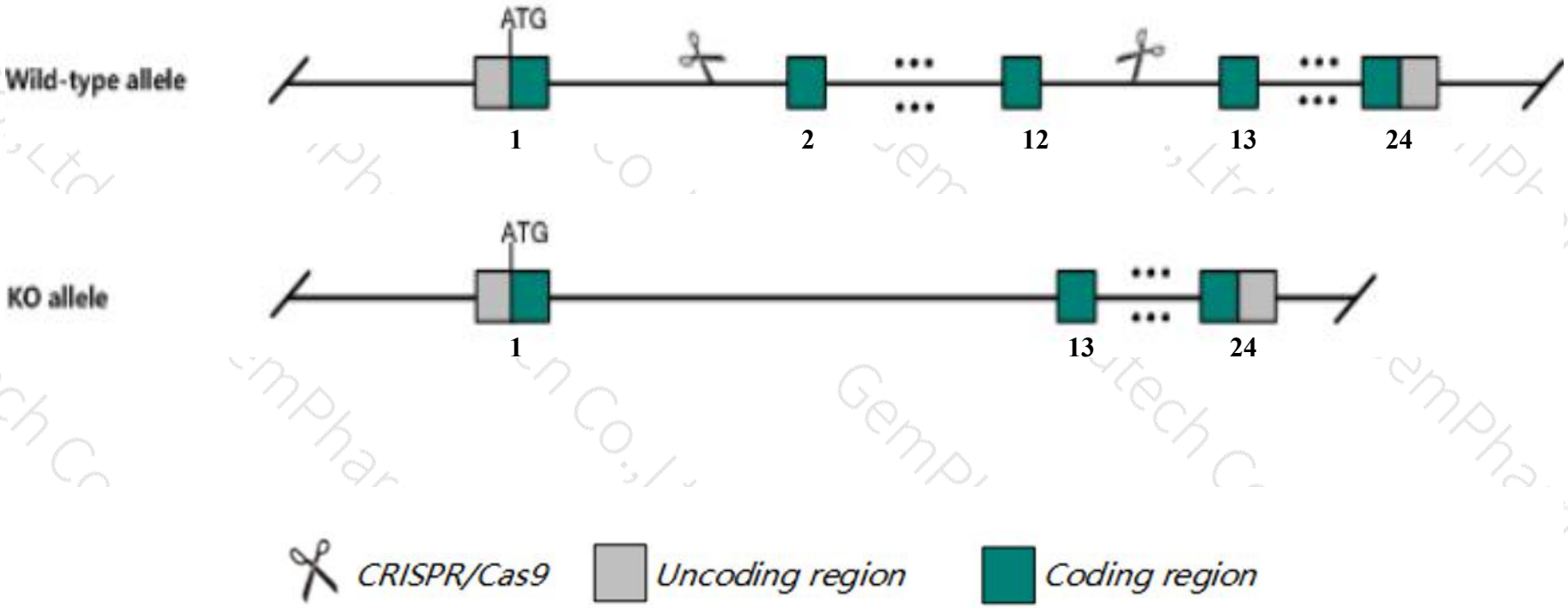
Project Overview

Project Name	***Pex1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pex1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Pex1* gene has 14 transcripts. According to the structure of *Pex1* gene, exon2-exon12 of *Pex1-202* (ENSMUST00000121291.7) transcript is recommended as the knockout region.The region contains 1945bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pex1* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Mice homozygous for a knock-in allele display premature death, postnatal growth retardation, fatty livers, a bile acid defect associated with intestinal lipid malabsorption and cholestasis, and a retinopathy associated with retinal cone cell degenerationand abnormal cone and rod electrophysiology.
- The knockout region is near to the N-terminal of *Rbm48* gene,this strategy may influence the regulatory function of the N-terminal of *Rbm48* gene.
- Transcript *Pex1*-2029&210&211&212&214 may not be affected.
- The *Pex1* gene is located on the Chr5. 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）

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Pex1 peroxisomal biogenesis factor 1 [*Mus musculus* (house mouse)]

Gene ID: 71382, updated on 25-Feb-2020

Summary

Official Symbol	Pex1 provided by MGI
Official Full Name	peroxisomal biogenesis factor 1 provided by MGI
Primary source	MGI:MGI:1918632
See related	Ensembl:ENSMUSG00000005907
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	ZWS1; 5430414H02Rik; E330005K07Rik
Expression	Ubiquitous expression in placenta adult (RPKM 4.3), CNS E14 (RPKM 3.6) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 5; 5 A1

See Pex1 in Genome Data Viewer

Exon count: 25

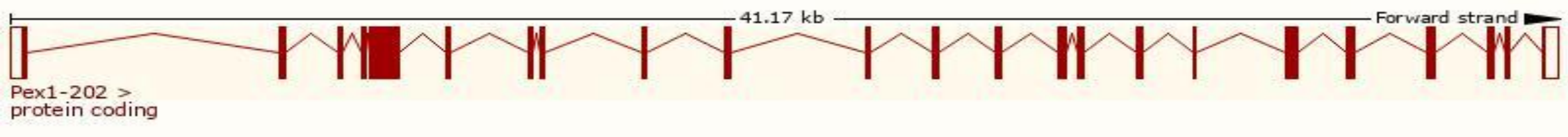
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (3596066..3637230)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (3596066..3637101)

Transcript information（Ensembl）

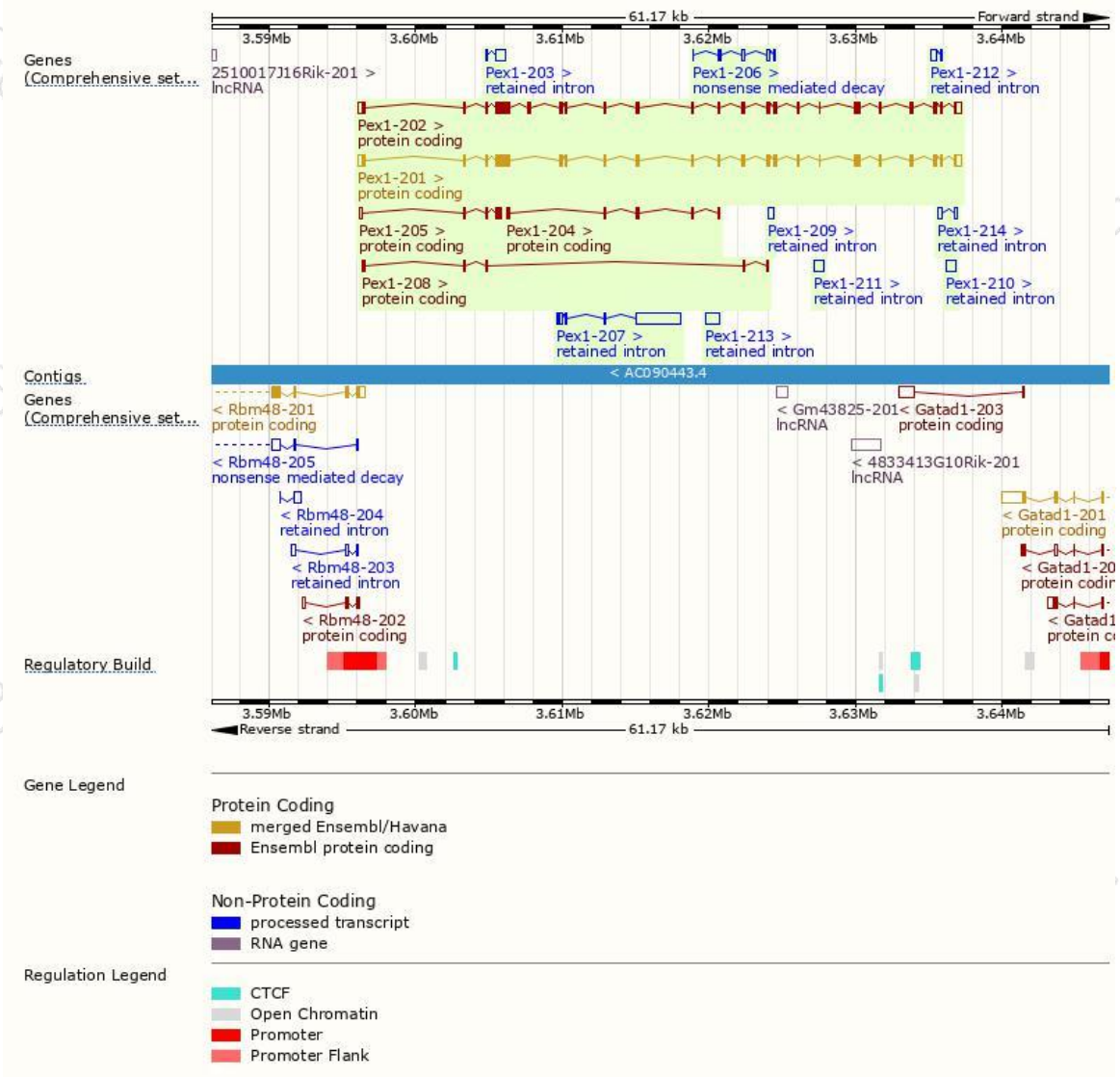
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pex1-202	ENSMUST00000121291.7	4555	1284aa	Protein coding	CCDS80201	Q5BL07	TSL:5 GENCODE basic APPRIS ALT2
Pex1-201	ENSMUST00000006061.12	4433	1244aa	Protein coding	CCDS19065	Q5BL07	TSL:1 GENCODE basic APPRIS P3
Pex1-205	ENSMUST00000142516.1	727	69aa	Protein coding	-	D3Z5A7	CDS 3' incomplete TSL:3
Pex1-204	ENSMUST00000126545.1	639	213aa	Protein coding	-	F6RUH9	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
Pex1-208	ENSMUST00000195894.1	528	143aa	Protein coding	-	A0A0G2JE39	TSL:3 GENCODE basic
Pex1-206	ENSMUST00000143132.1	664	76aa	Nonsense mediated decay	-	F7CF88	CDS 5' incomplete TSL:5
Pex1-207	ENSMUST00000143959.1	3491	No protein	Retained intron	-	-	TSL:1
Pex1-213	ENSMUST00000199035.1	987	No protein	Retained intron	-	-	TSL:NA
Pex1-203	ENSMUST00000123268.1	746	No protein	Retained intron	-	-	TSL:3
Pex1-210	ENSMUST00000196432.1	668	No protein	Retained intron	-	-	TSL:NA
Pex1-211	ENSMUST00000196692.1	638	No protein	Retained intron	-	-	TSL:NA
Pex1-214	ENSMUST00000199213.1	487	No protein	Retained intron	-	-	TSL:2
Pex1-212	ENSMUST00000197167.1	474	No protein	Retained intron	-	-	TSL:2
Pex1-209	ENSMUST00000196124.1	403	No protein	Retained intron	-	-	TSL:NA

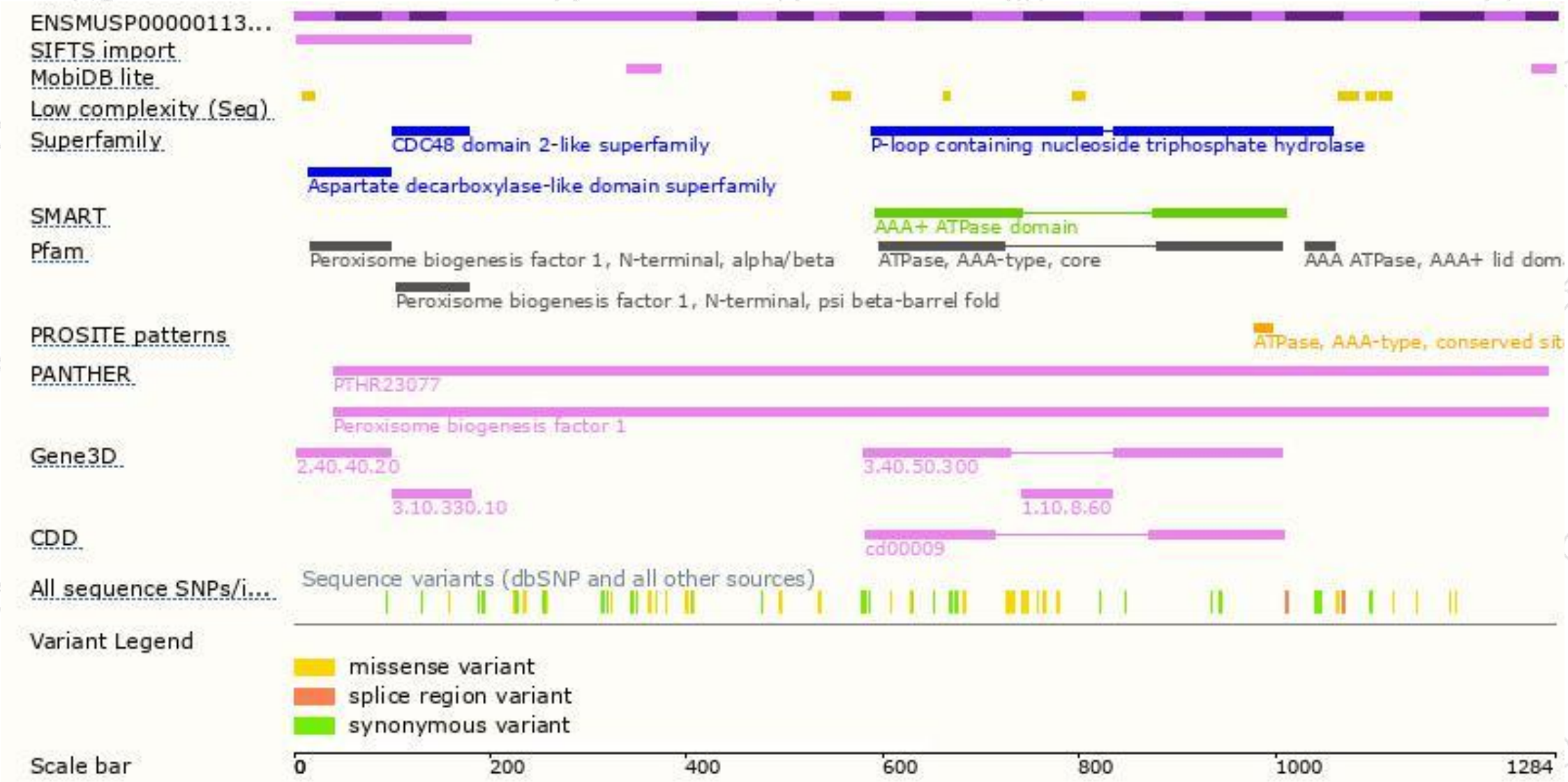
The strategy is based on the design of *Pex1-202* transcript,The transcription is shown below



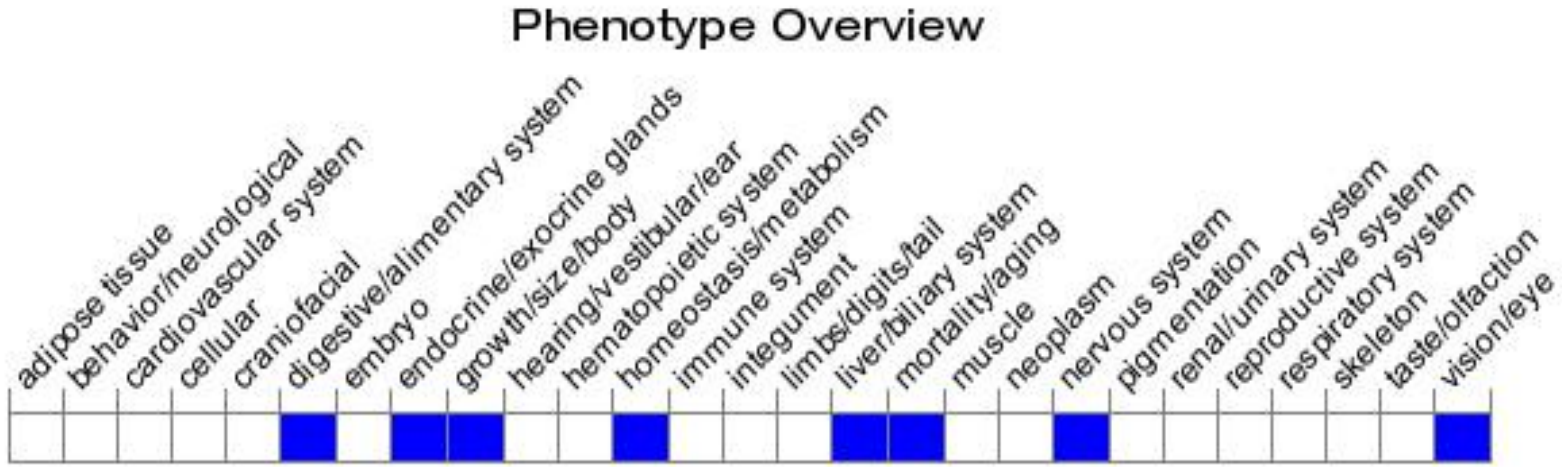
Genomic location distribution



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/).

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

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