Acp2 Cas9-CKO Strategy

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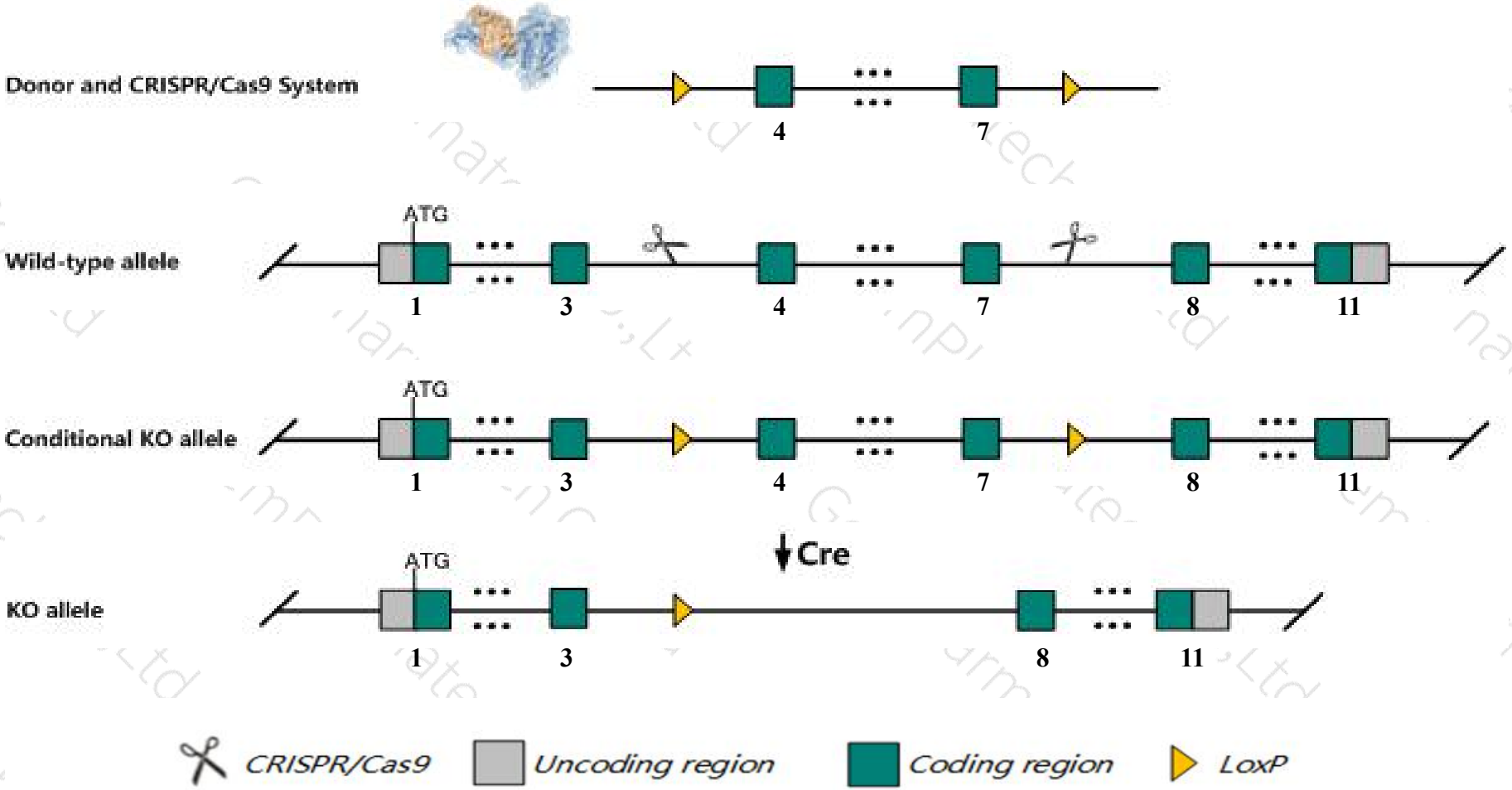
Design Date:2020-2-11

Project Overview

Project Name	***Acp2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acp2* gene. The schematic diagram is as follows:



Technical routes

- The *Acp2* gene has 5 transcripts. According to the structure of *Acp2* gene, exon4-exon7 of *Acp2-201* (ENSMUST00000002172.13) transcript is recommended as the knockout region.The region contains 475bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Acp2* 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.

Notice

- According to the existing MGI data,Homozygous mutation of this gene result in skeletal defects and a small percentage of mutant animals exhibit tonic-clonic seizures. Mice with a missense mutation (Gly244Glu) are growth retarded and exhibit a disrupted cerebellum cytoarchitecture, an abnormal hair shaft, and skin malformations.

- The *Acp2* gene is located on the Chr2. 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）

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Acp2 acid phosphatase 2, lysosomal [*Mus musculus* (house mouse)]

Gene ID: 11432, updated on 24-Oct-2019

Summary

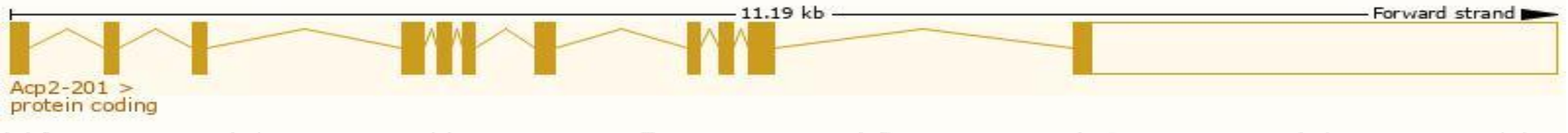
Official Symbol	Acp2 provided by MGI
Official Full Name	acid phosphatase 2, lysosomal provided by MGI
Primary source	MGI:MGI:87882
See related	Ensembl:ENSMUSG00000002103
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	LAP; Acp-2
Summary	The protein encoded by this gene belongs to the histidine acid phosphatase family, which hydrolyze orthophosphoric monoesters to alcohol and phosphate. This protein is localized to the lysosomal membrane, and is chemically and genetically distinct from the red cell acid phosphatase. Mice lacking this gene showed multiple defects, including bone structure alterations, lysosomal storage defects, and an increased tendency towards seizures. An enzymatically-inactive allele of this gene showed severe growth retardation, hair-follicle abnormalities, and an ataxia-like phenotype. Two isoforms are predicted to be produced from the same mRNA by the use of alternative in-frame translation termination codons via a stop codon readthrough mechanism. [provided by RefSeq, Oct 2017]
Expression	Ubiquitous expression in mammary gland adult (RPKM 14.6), ovary adult (RPKM 12.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

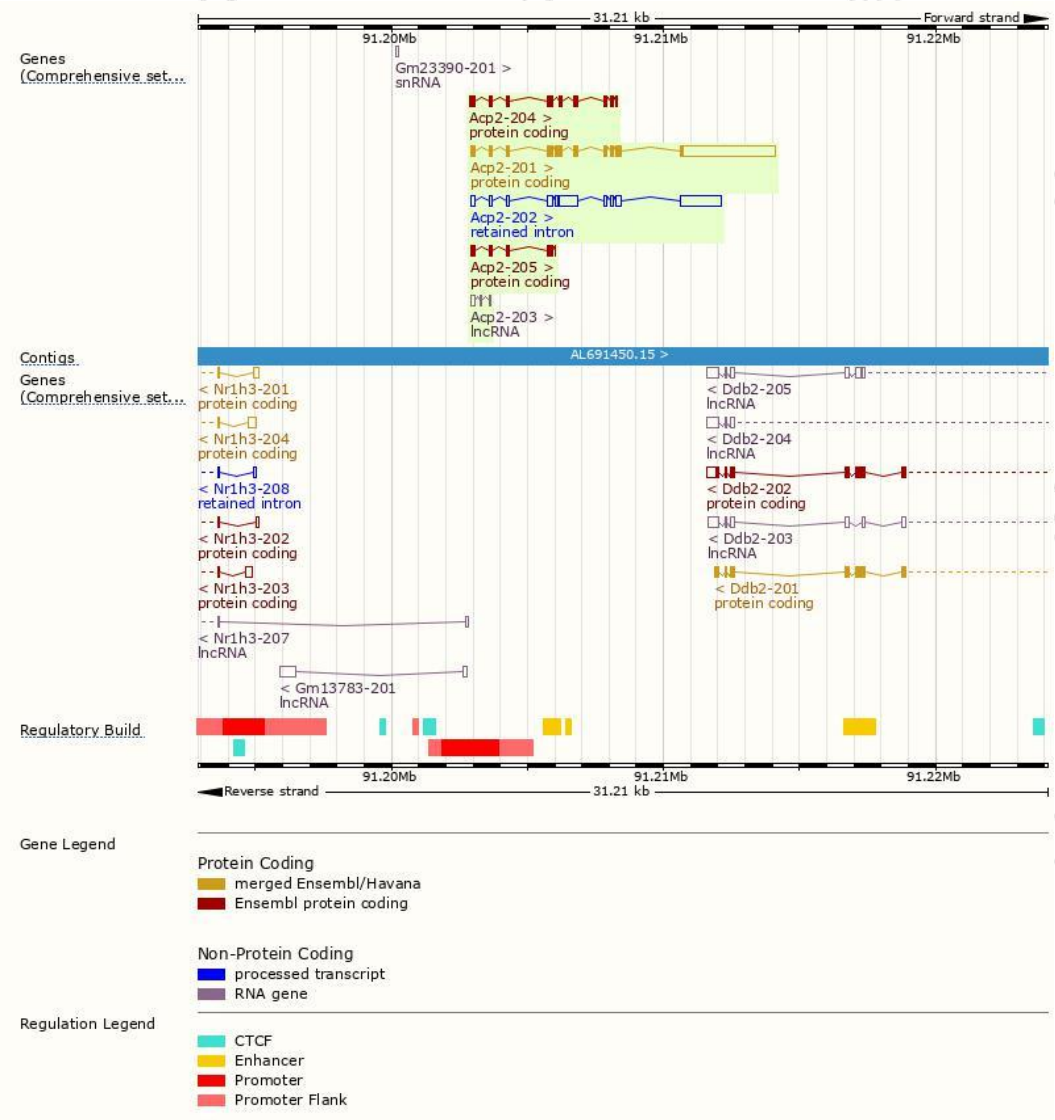
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acp2-201	ENSMUST00000002172.13	4656	423aa	Protein coding	CCDS16427	P24638	TSL:1 GENCODE basic APPRIS P1
Acp2-204	ENSMUST00000150403.7	966	305aa	Protein coding	-	B7ZCF5	CDS 3' incomplete TSL:5
Acp2-205	ENSMUST00000155418.1	510	166aa	Protein coding	-	B7ZCF4	CDS 3' incomplete TSL:3
Acp2-202	ENSMUST00000124131.1	3124	No protein	Retained intron	-	-	TSL:2
Acp2-203	ENSMUST00000127643.1	233	No protein	lncRNA	-	-	TSL:3

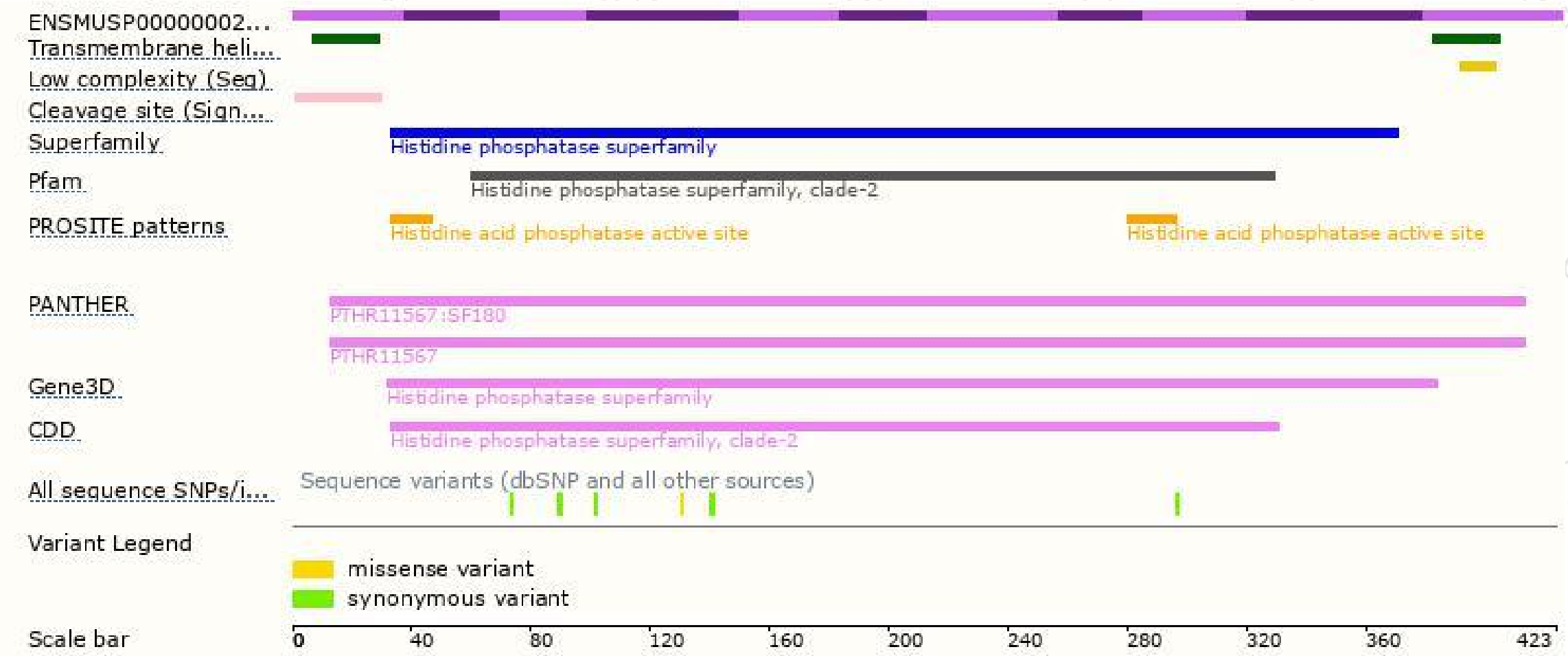
The strategy is based on the design of *Acp2-201* transcript,The transcription is shown below



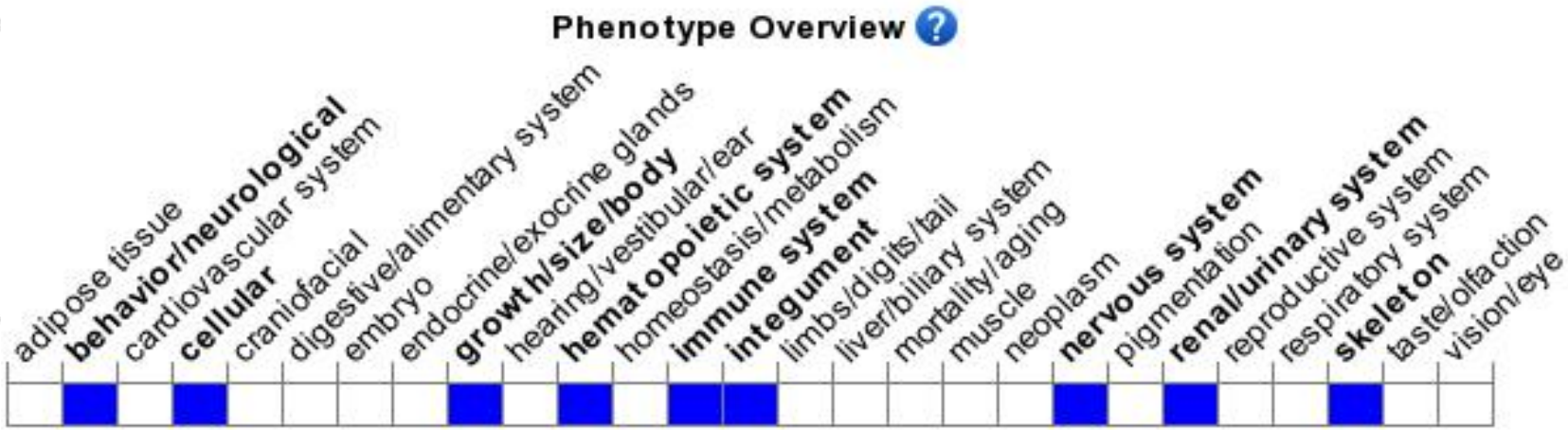
Genomic location distribution



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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