Orc1 Cas9-CKO Strategy

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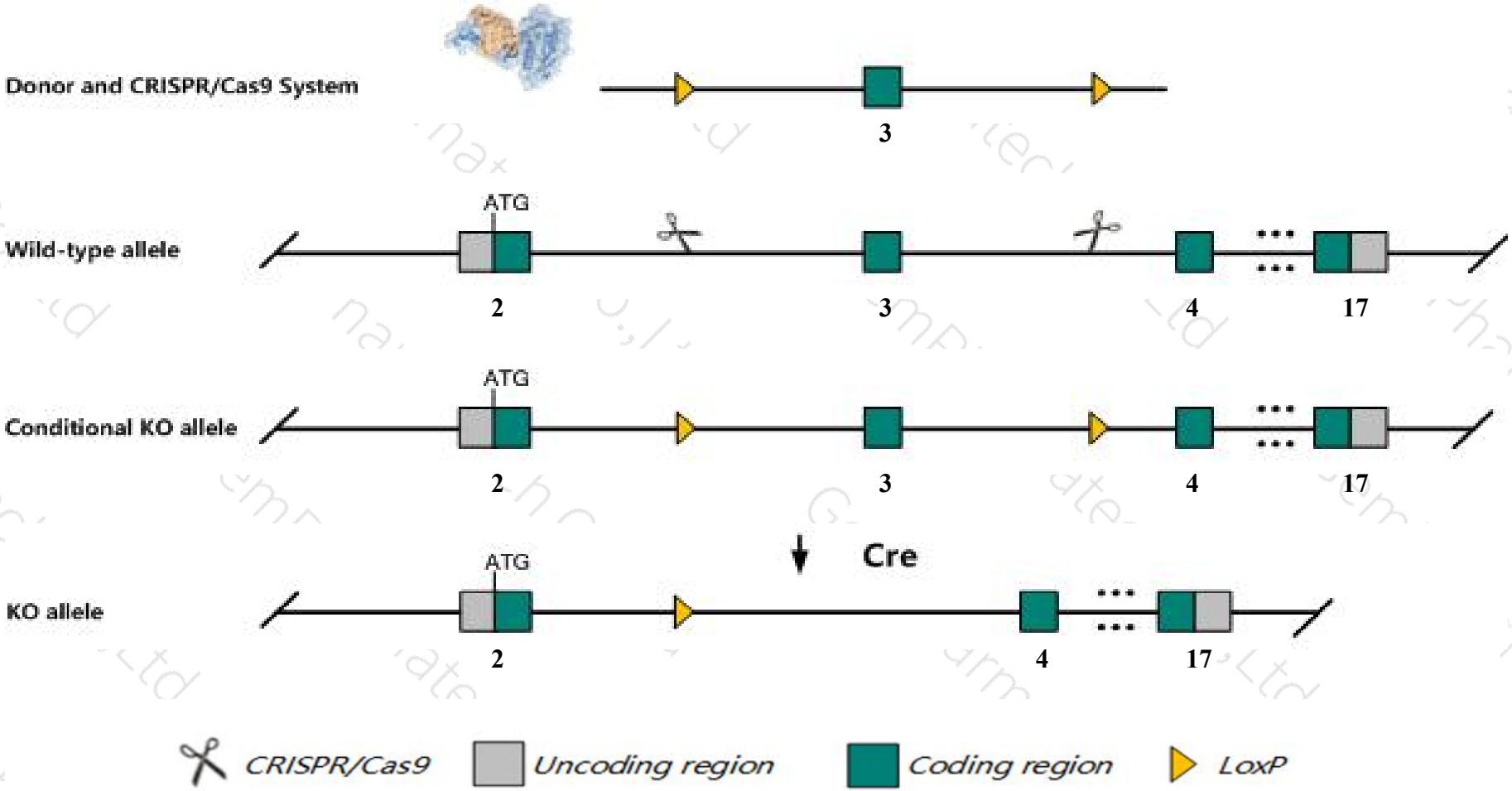
Project Overview

Project Name	***Orc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Orc1* gene. The schematic diagram is as follows:



Technical routes

- The *Orc1* gene has 5 transcripts. According to the structure of *Orc1* gene, exon3 of *Orc1-201* (ENSMUST00000102744.3) transcript is recommended as the knockout region.The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Orc1* 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

- The *Orc1* gene is located on the Chr4. 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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Orc1 origin recognition complex, subunit 1 [Mus musculus (house mouse)]

Gene ID: 18392, updated on 13-Mar-2020

Summary

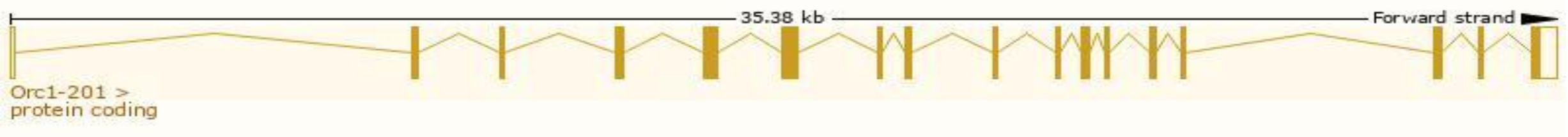
Official Symbol	Orc1 provided by MGI
Official Full Name	origin recognition complex, subunit 1 provided byMGI
Primary source	MGI:MGI:1328337
See related	Ensembl:ENSMUSG00000028587
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA545195, MmORC1, Orc1l
Expression	Broad expression in liver E14 (RPKM 4.8), liver E14.5 (RPKM 4.6) and 16 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

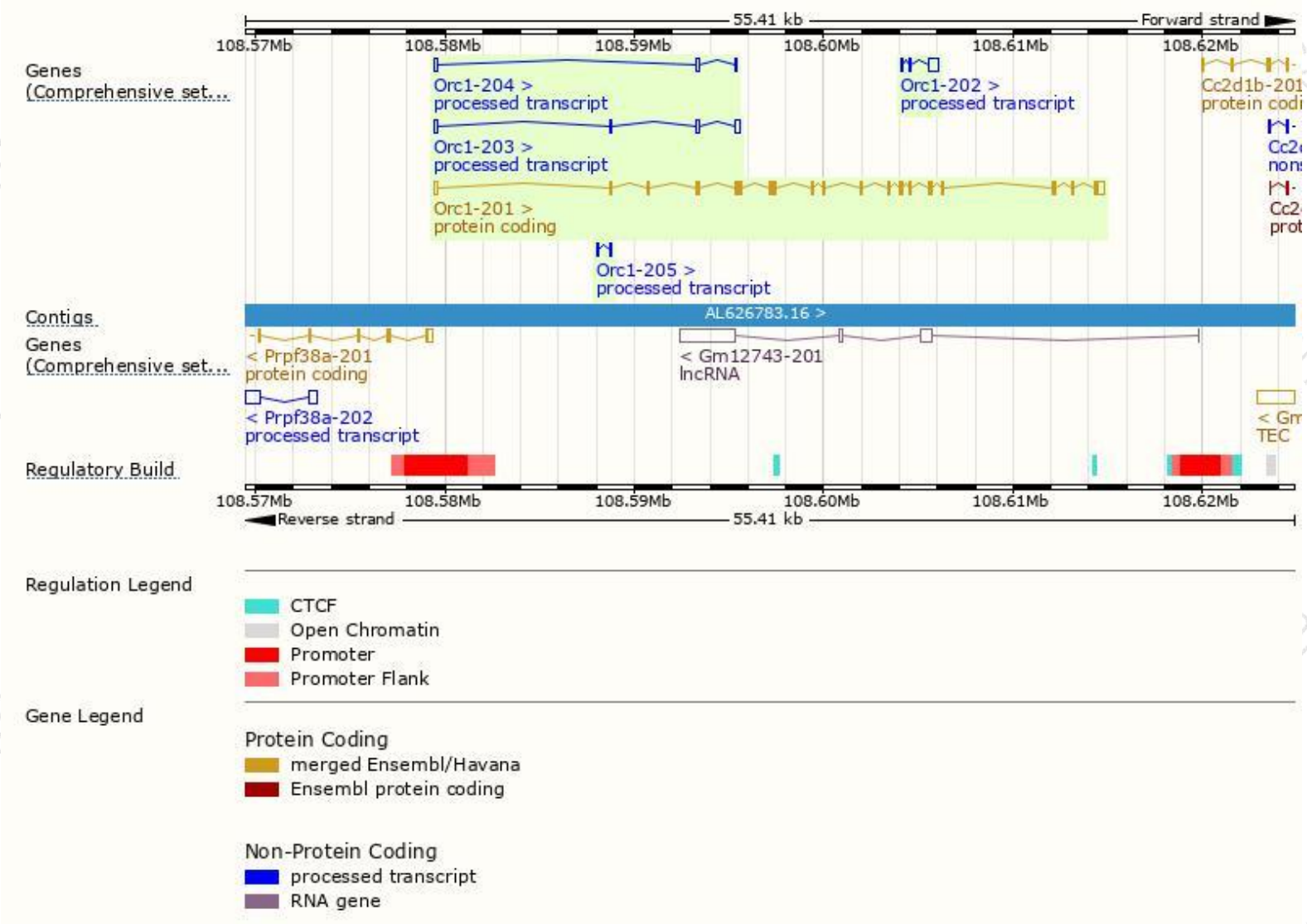
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Orc1-201	ENSMUST00000102744.3	3014	840aa	Protein coding	CCDS18453	Q9Z1N2	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
Orc1-203	ENSMUST00000130162.1	679	No protein	Processed transcript	-	-	TSL:2
Orc1-202	ENSMUST00000129931.1	670	No protein	Processed transcript	-	-	TSL:3
Orc1-204	ENSMUST00000139772.7	443	No protein	Processed transcript	-	-	TSL:3
Orc1-205	ENSMUST00000143497.1	173	No protein	Processed transcript	-	-	TSL:5

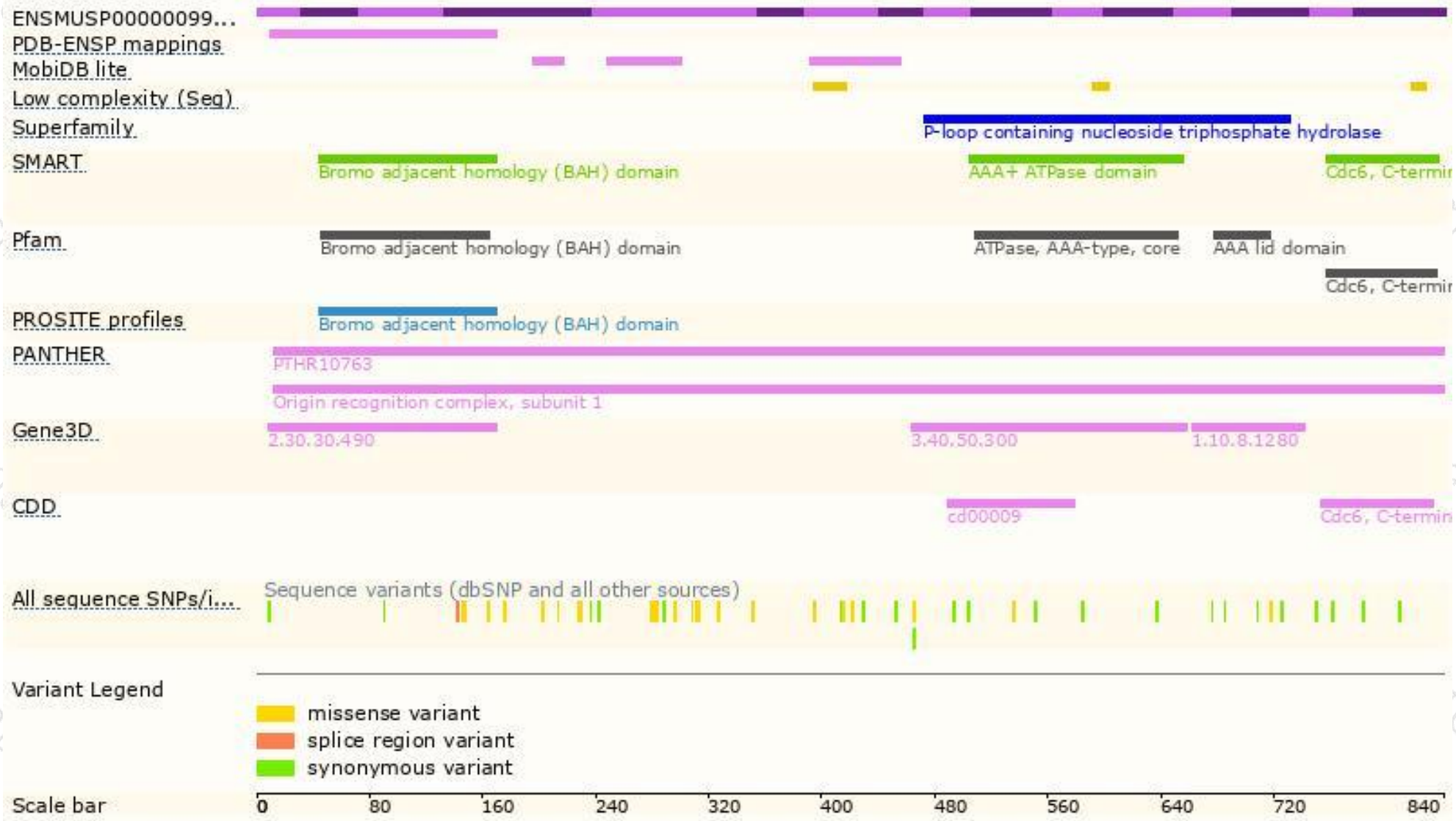
The strategy is based on the design of *Orc1-201* transcript,the transcription is shown below:



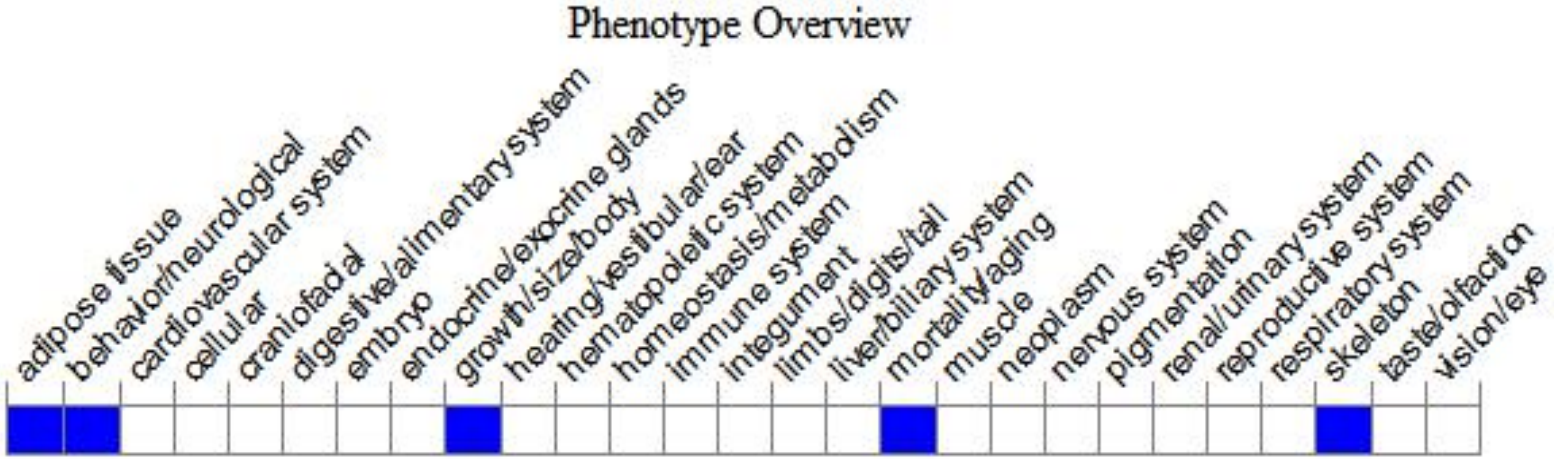
Genomic location distribution



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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