Odc1 Cas9-CKO Strategy

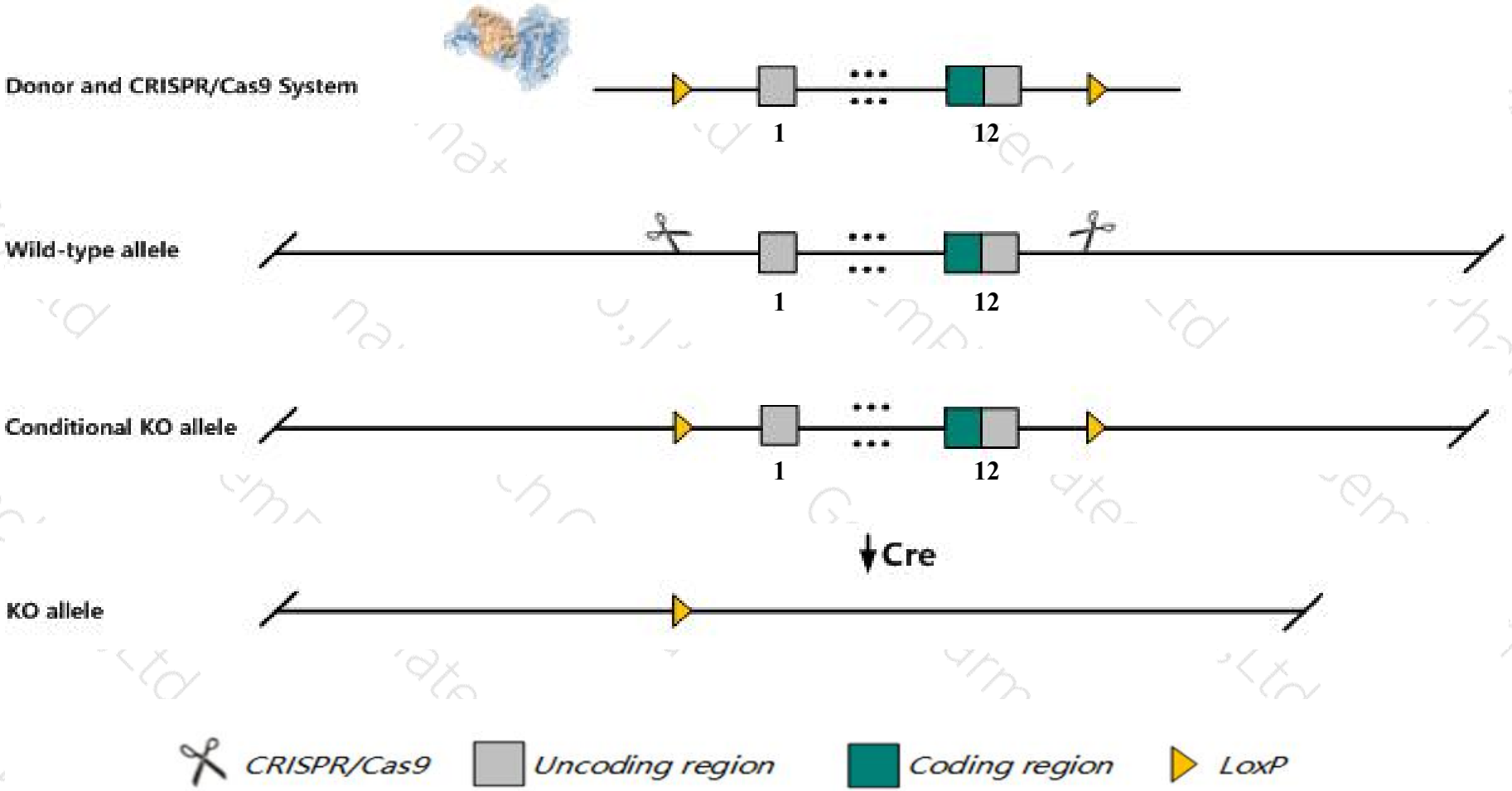
Designer: QiongZhou

Project Overview

Project Name	***Odc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Odc1* gene. The schematic diagram is as follows:



Technical routes

- The *Odc1* gene has 8 transcripts. According to the structure of *Odc1* gene, exon1-exon12 of *Odc1-201* (ENSMUST00000171737.2) 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 *Odc1* 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 null embryos die prior to gastrulation.
- The *Odc1* gene is located on the Chr12. 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）

集萃药康 GemPharmatech

Odc1 ornithine decarboxylase, structural 1 [Mus musculus (house mouse)]

Gene ID: 18263, updated on 13-Mar-2020

Summary

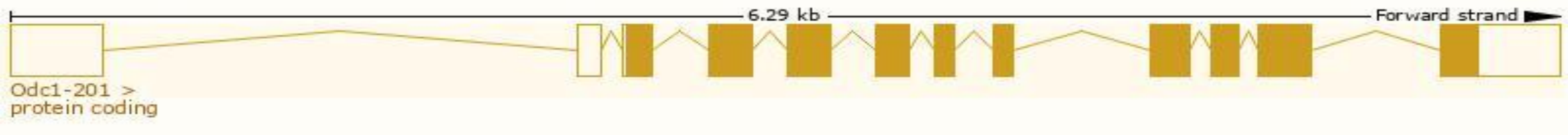
Official Symbol	Odc1 provided by MGI
Official Full Name	ornithine decarboxylase, structural 1 provided by MGI
Primary source	MGI:MGI:97402
See related	Ensembl:ENSMUSG00000011179
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ODC
Expression	Broad expression in liver E14 (RPKM 226.2), liver E14.5 (RPKM 221.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

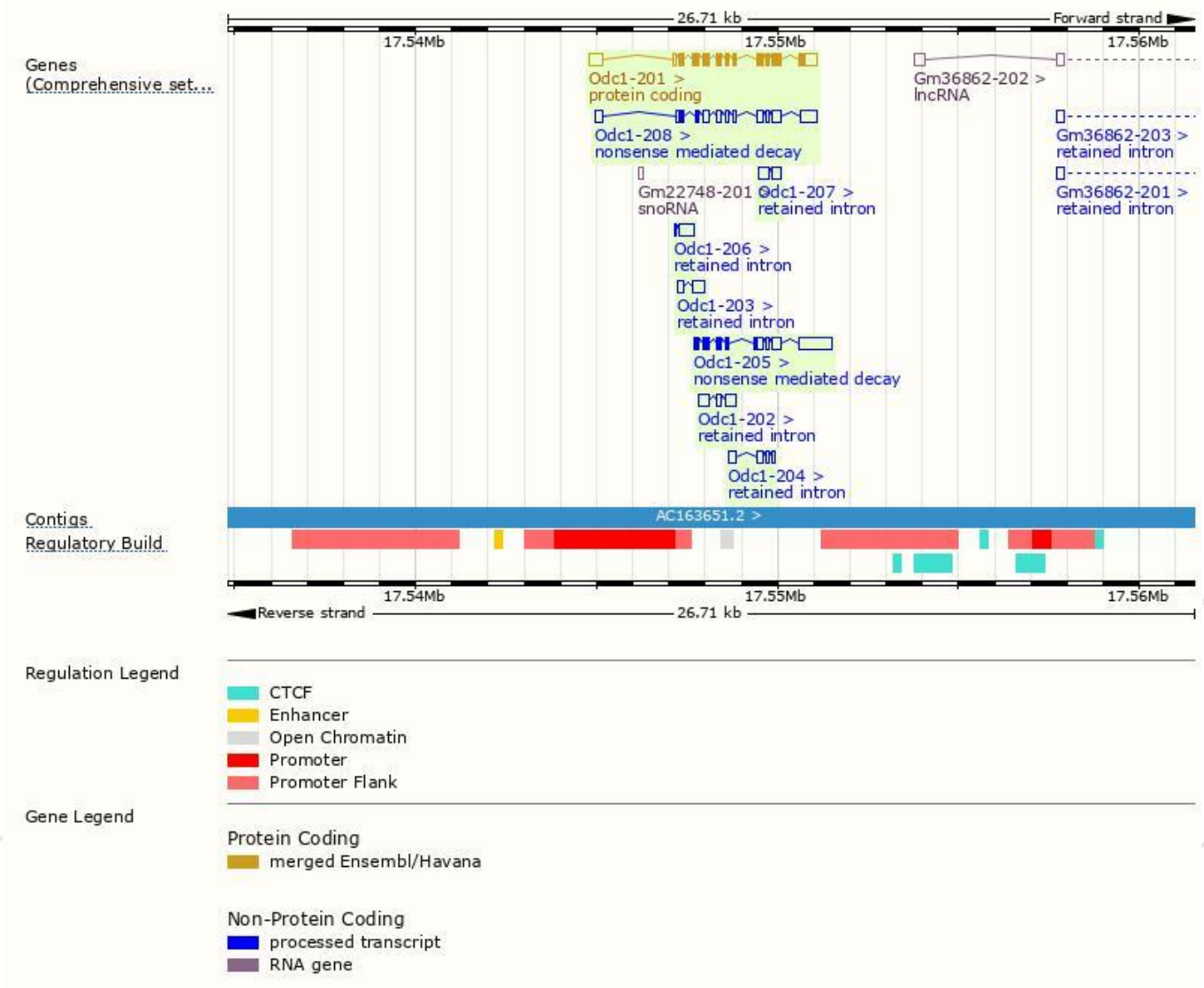
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Odc1-201	ENSMUST00000171737.2	2208	461aa	Protein coding	CCDS25829	P00860	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
Odc1-205	ENSMUST00000221613.1	1982	197aa	Nonsense mediated decay	-	A0A1Y7VJC5	CDS 5' incomplete TSL:5
Odc1-208	ENSMUST00000222617.1	1884	42aa	Nonsense mediated decay	-	A0A1Y7VMF9	TSL:5
Odc1-202	ENSMUST00000220849.1	764	No protein	Retained intron	-	-	TSL:3
Odc1-204	ENSMUST00000221354.1	561	No protein	Retained intron	-	-	TSL:2
Odc1-207	ENSMUST00000222250.1	538	No protein	Retained intron	-	-	TSL:2
Odc1-203	ENSMUST00000220947.1	504	No protein	Retained intron	-	-	TSL:2
Odc1-206	ENSMUST00000221701.1	472	No protein	Retained intron	-	-	TSL:2

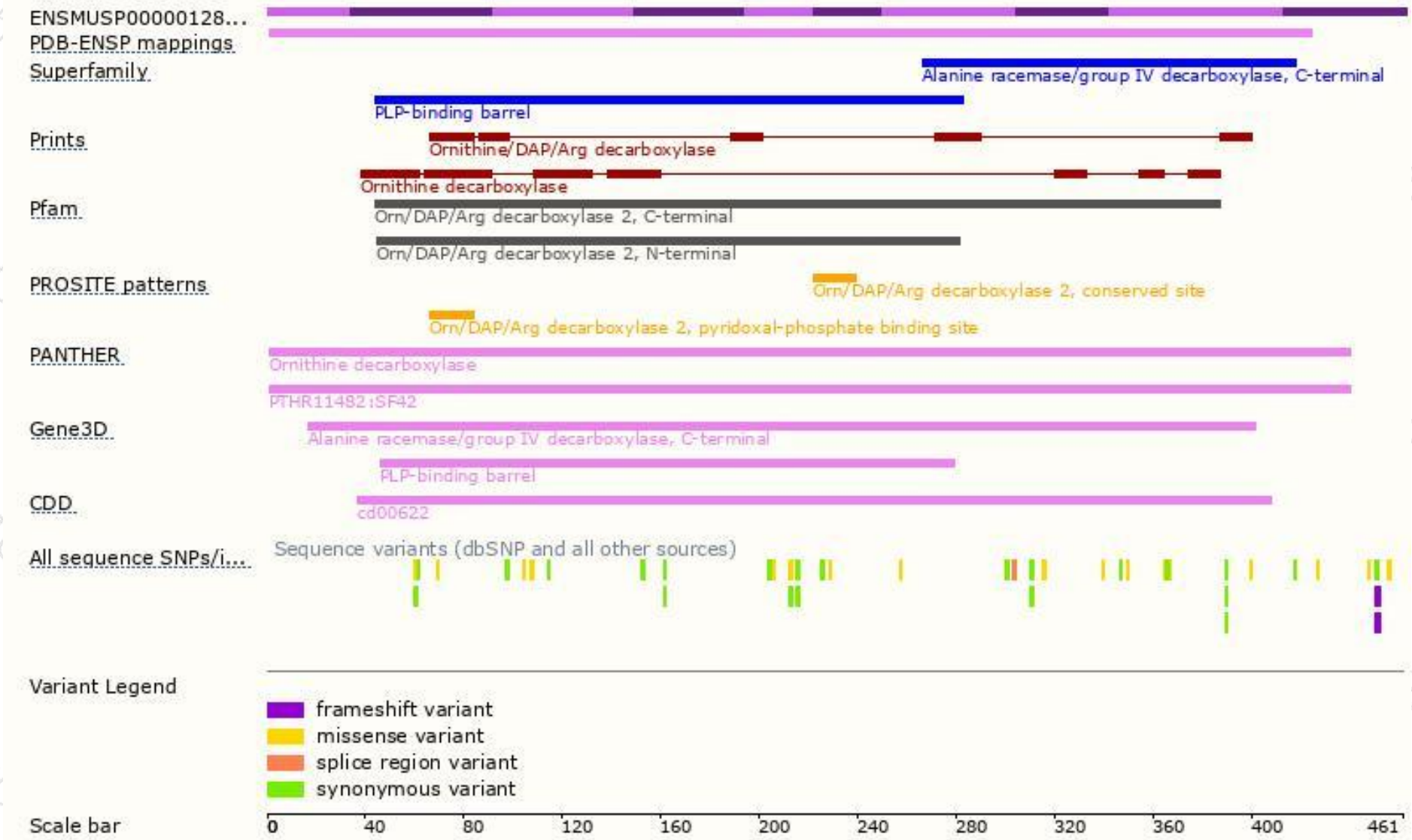
The strategy is based on the design of *Odc1-201* transcript,the transcription is shown below:



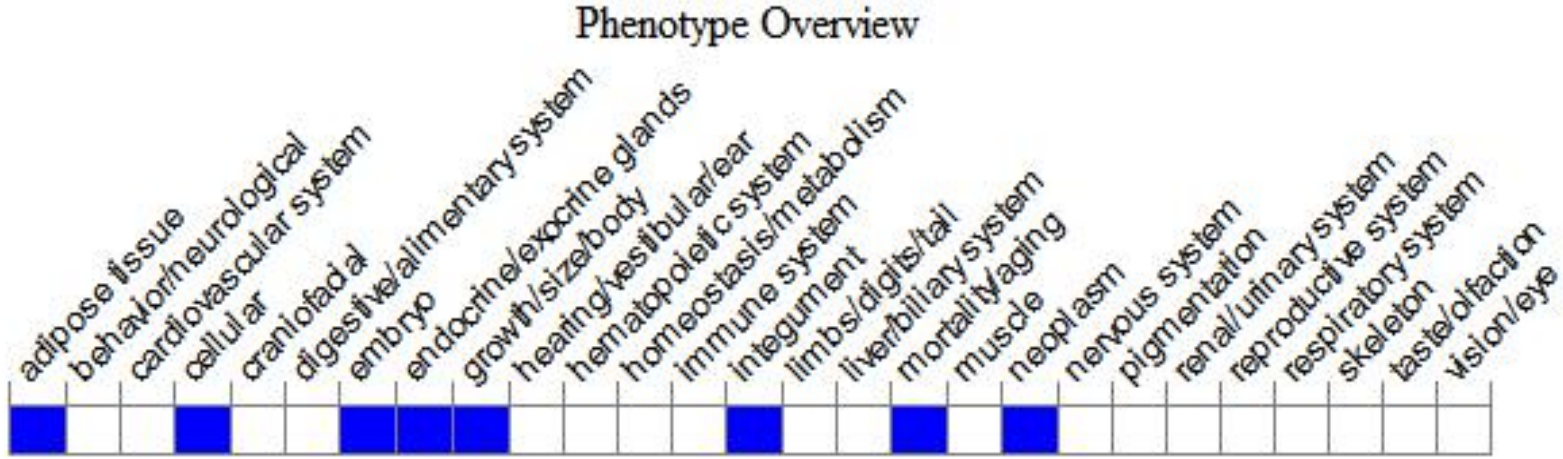
Genomic location distribution



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/).

According to the existing MGI data,homozygous null embryos die prior to gastrulation.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd