Aurka Cas9-KO Strategy

Designer: Shilei Zhu

Reviewer: Jinlong Zhao

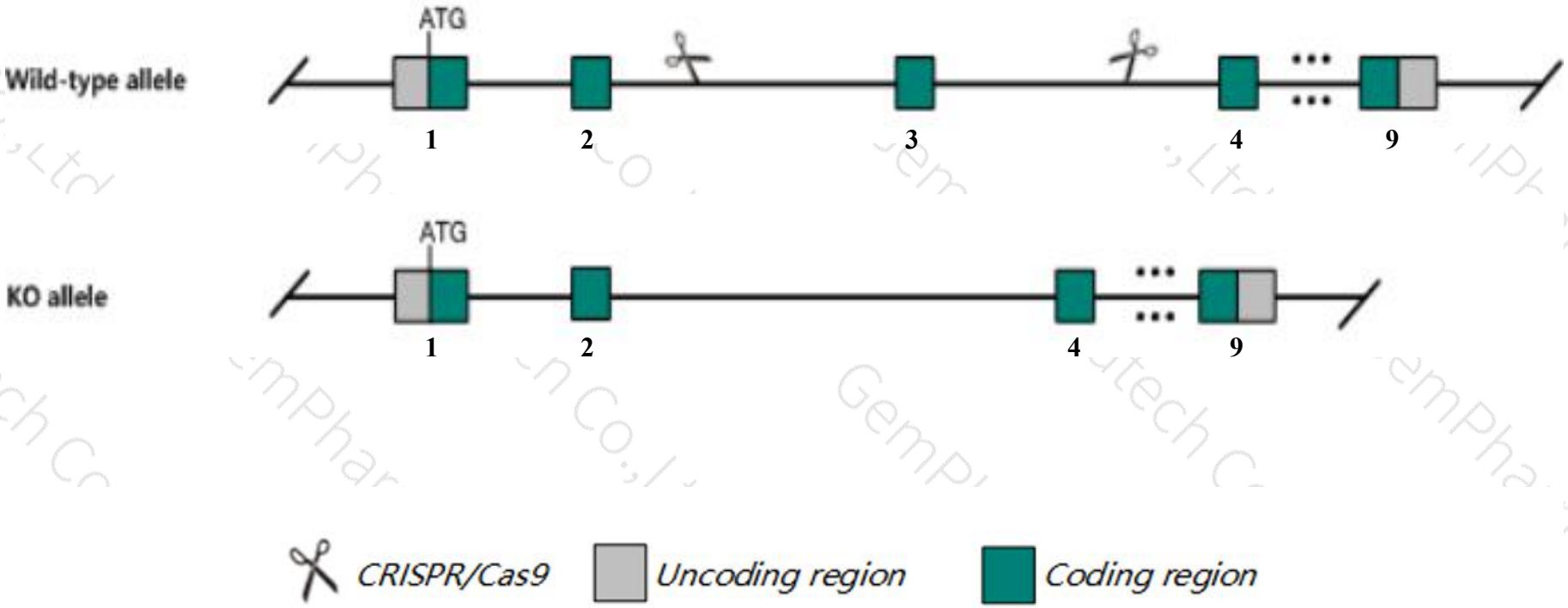
Design Date: 2020-5-29

Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Aurka* gene has 5 transcripts. According to the structure of *Aurka* gene, exon3 of *Aurka-201* (ENSMUST00000028997.7) transcript is recommended as the knockout region.The region contains 250bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,mice homozygous for a null allele display embryonic lethality before implantation, early embryonic growth arrest, and impaired mitosis. heterozygous null mice display increased incidence of tumors primarily lymphomas and chromosomal instability.
- The *Aurka* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.
- 5 'loxp was less than 5kb from gene Cstf1.

Gene information（NCBI）

集萃药康 GemPharmatech

Aurka aurora kinase A [Mus musculus (house mouse)]

Gene ID: 20878, updated on 13-Mar-2020

Summary

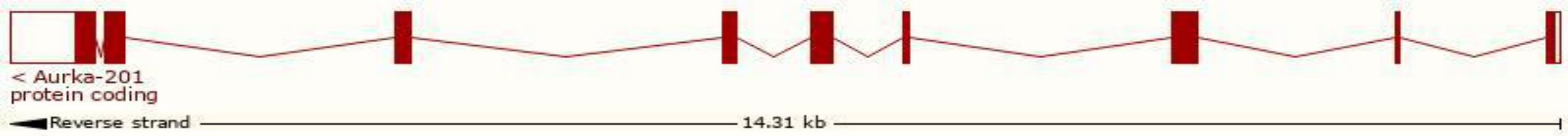
Official Symbol	Aurka provided by MGI
Official Full Name	aurora kinase A provided byMGI
Primary source	MGI:MGI:894678
See related	Ensembl:ENSMUSG00000027496
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AIRK1, ARK-1, AU019385, AW539821, Ark1, Aurora-A, Ayk1, IAK, IAK1, Stk6
Expression	Broad expression in liver E14.5 (RPKM 39.2), liver E14 (RPKM 37.7) and 15 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

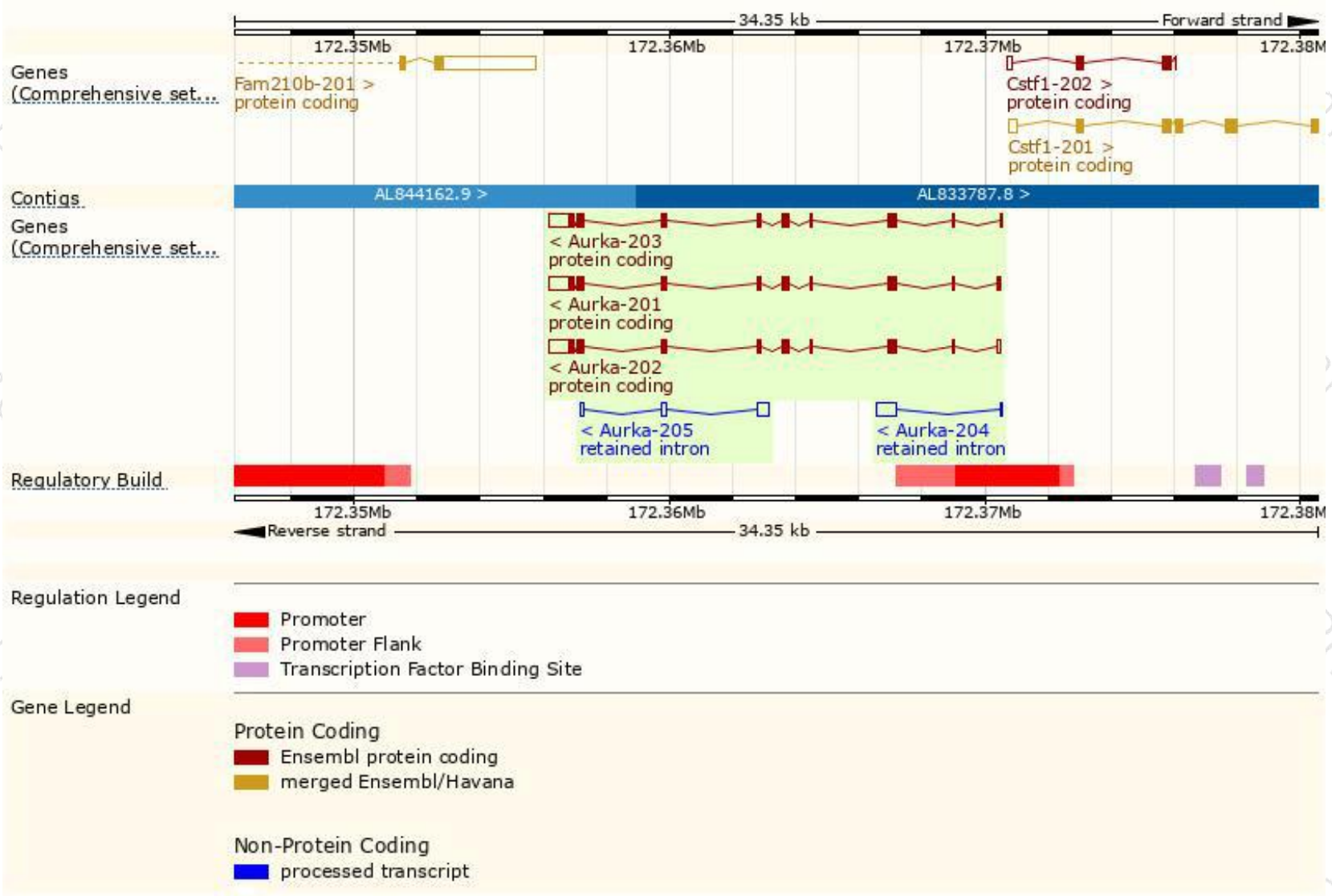
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aurka-201	ENSMUST00000028997.7	1905	417aa	Protein coding	CCDS17129	P97477	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 P3
Aurka-202	ENSMUST00000109139.7	1905	395aa	Protein coding	CCDS71204	P97477 Q3TEY6	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 ALT2
Aurka-203	ENSMUST00000109140.9	1862	395aa	Protein coding	CCDS71204	P97477 Q3TEY6	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 ALT2
Aurka-204	ENSMUST00000126107.1	672	No protein	Retained intron	-	-	TSL:3
Aurka-205	ENSMUST00000128004.1	596	No protein	Retained intron	-	-	TSL:3

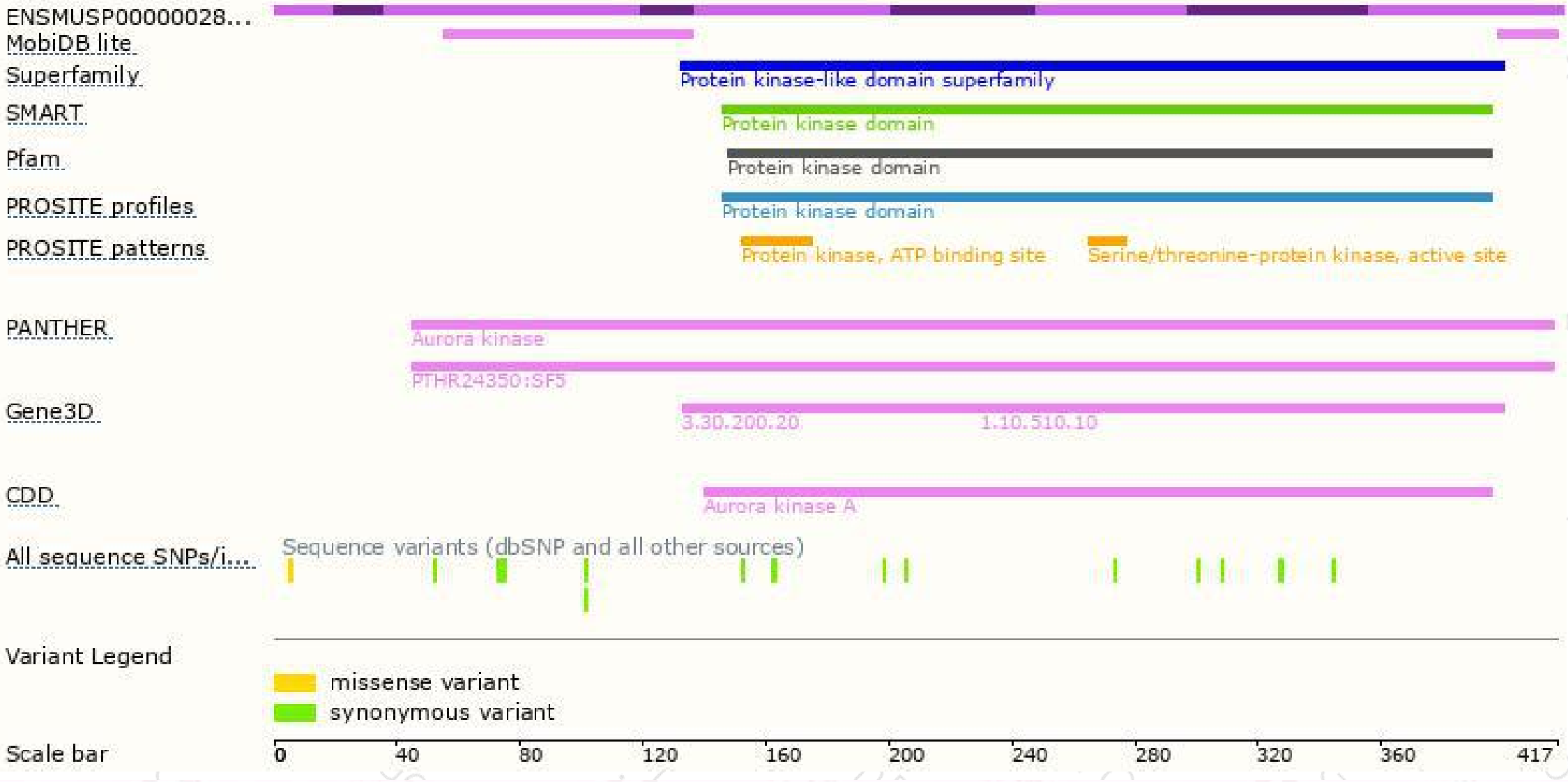
The strategy is based on the design of *Aurka-201* transcript,the transcription is shown below:



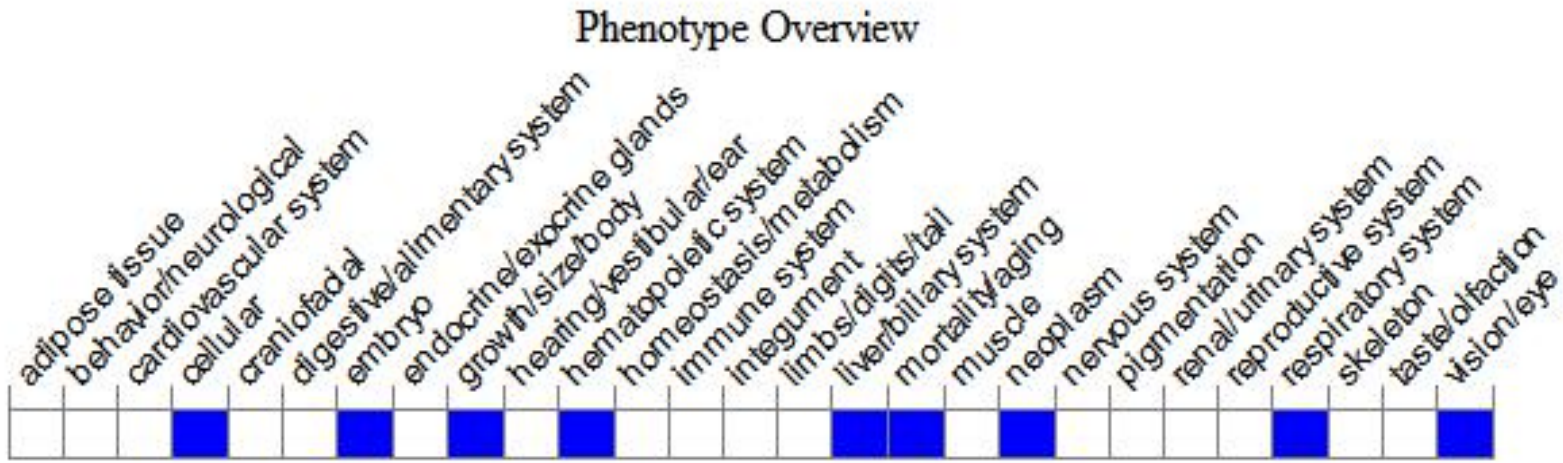
Genomic location distribution



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,mice homozygous for a null allele display embryonic lethality before implantation, early embryonic growth arrest, and impaired mitosis. Heterozygous null mice display increased incidence of tumors primarily lymphomas and chromosomal instability.

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