Nipbl Cas9-CKO Strategy

Designer: Jinling Wang

Reviewer: Miaomiao Cui

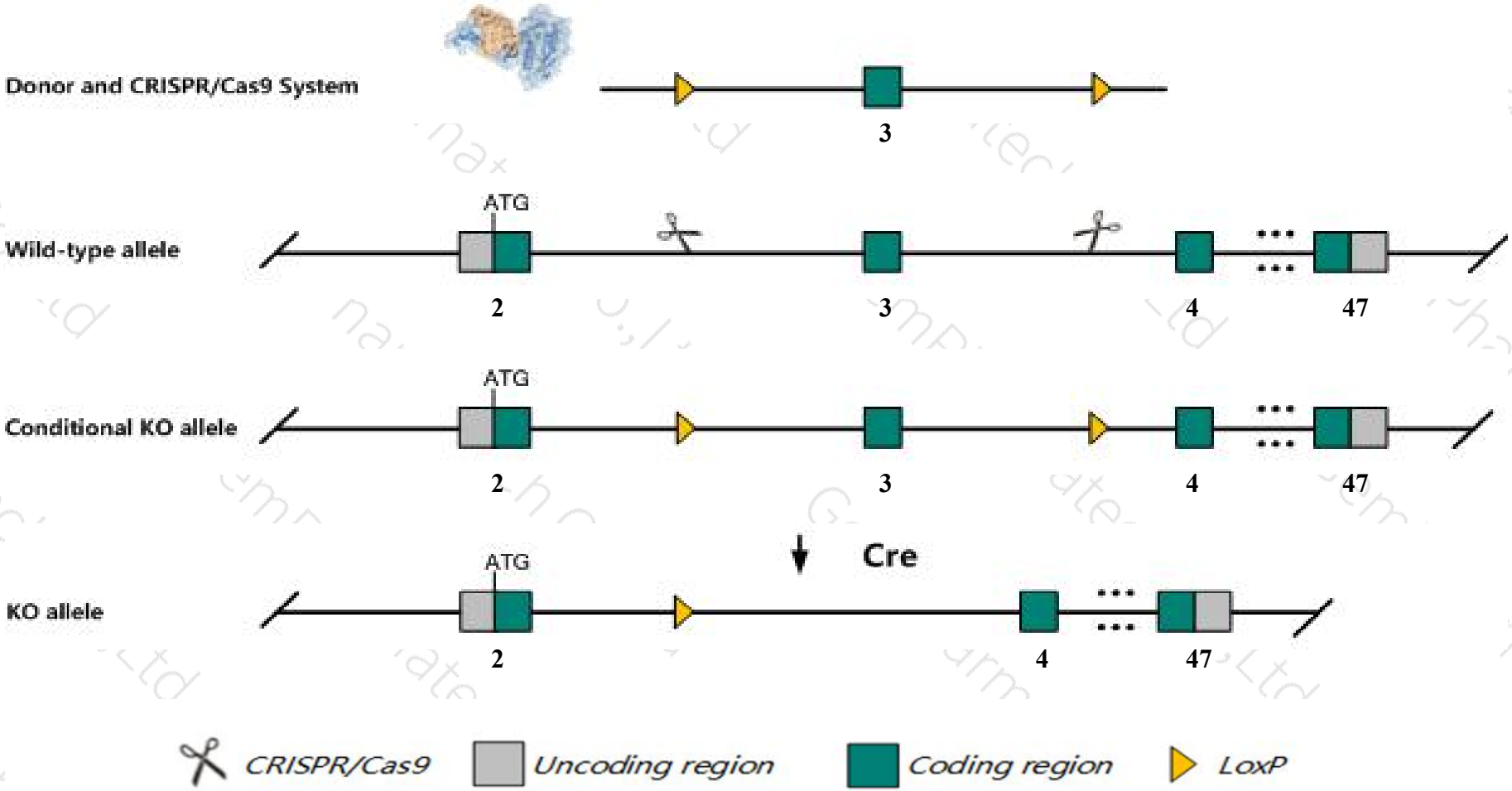
Design Date: 2019-1-21

Project Overview

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

Conditional Knockout strategy

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



Technical routes

➢ The *Nipbl* gene has 1 transcript. According to the structure of *Nipbl* gene, exon3 of *Nipbl-201*(ENSMUST00000052965.7) transcript is recommended as the knockout region.The region contains 166bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nipbl* 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,nullizygous mice are embryonic lethal. Heterozygous null mice are growth-retarded and show various skeletal anomalies. Heterozygotes for a gene-trap allele are small and show craniofacial, heart, eye, hearing and behavioral defects, delayed bone maturation, reduced body fat, and postnatal mortality.

➢ The *Nipbl* gene is located on the Chr15. 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

Nipbl NIPBL cohesin loading factor [Mus musculus (house mouse)]

Gene ID: 71175, updated on 13-Mar-2020

Summary

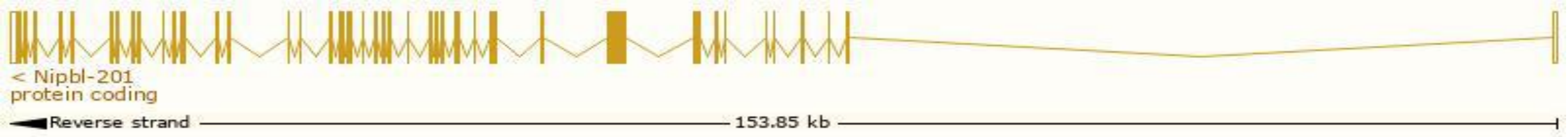
Official Symbol	Nipbl provided by MGI
Official Full Name	NIPBL cohesin loading factor provided byMGI
Primary source	MGI:MGI:1913976
See related	Ensembl:ENSMUSG00000022141
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Idn3
Expression	Ubiquitous expression in testis adult (RPKM 9.6), CNS E11.5 (RPKM 8.2) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

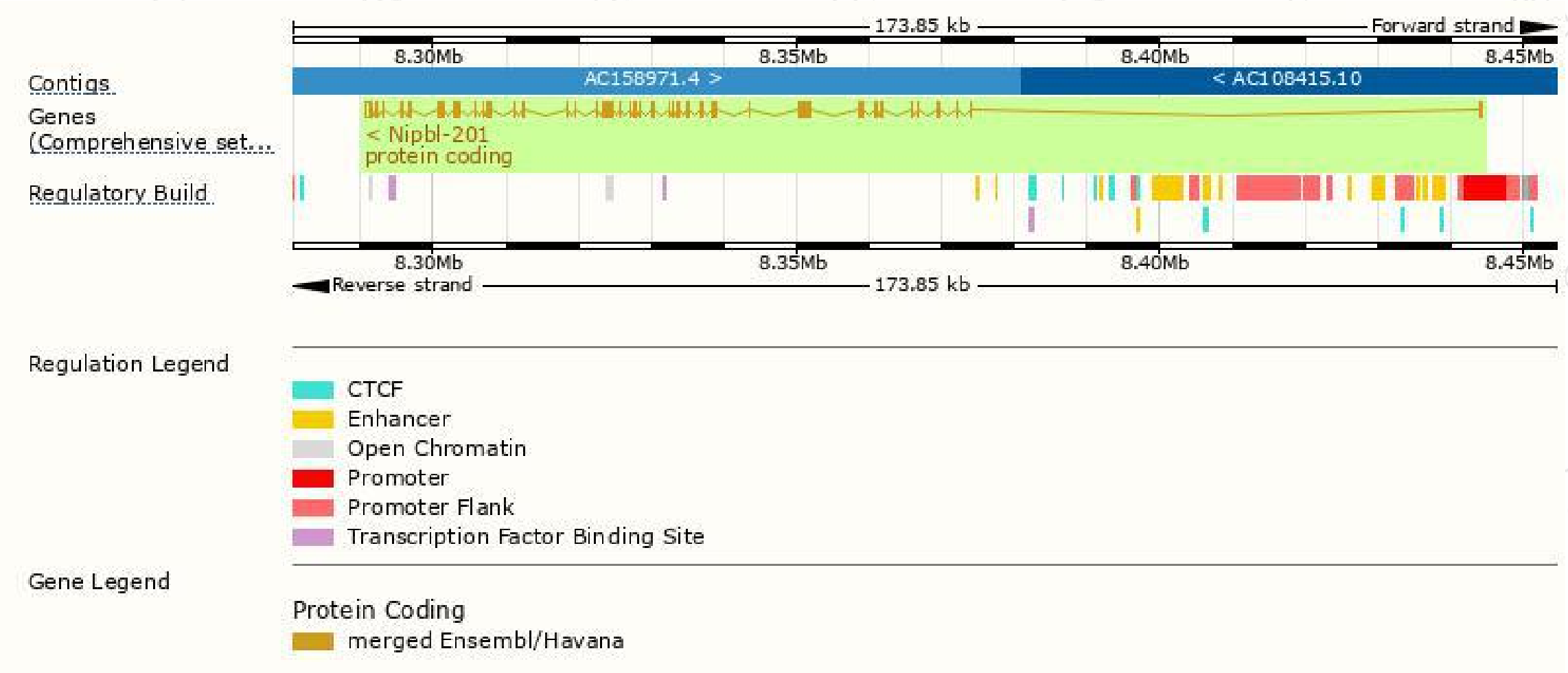
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nipbl-201	ENSMUST00000052965.7	9423	2798aa	Protein coding	CCDS37035	Q6KCD5	TSL:1 GENCODE basic APPRIS P1

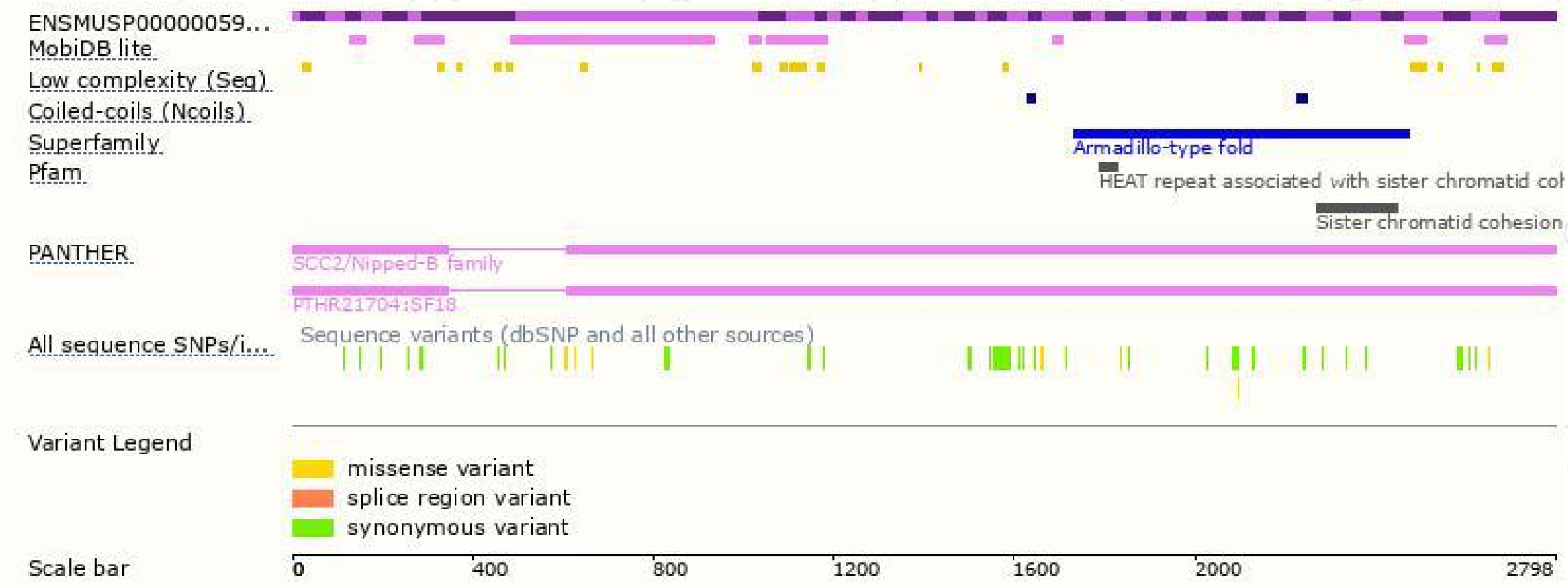
The strategy is based on the design of *Nipbl-201* transcript,the transcription is shown below:



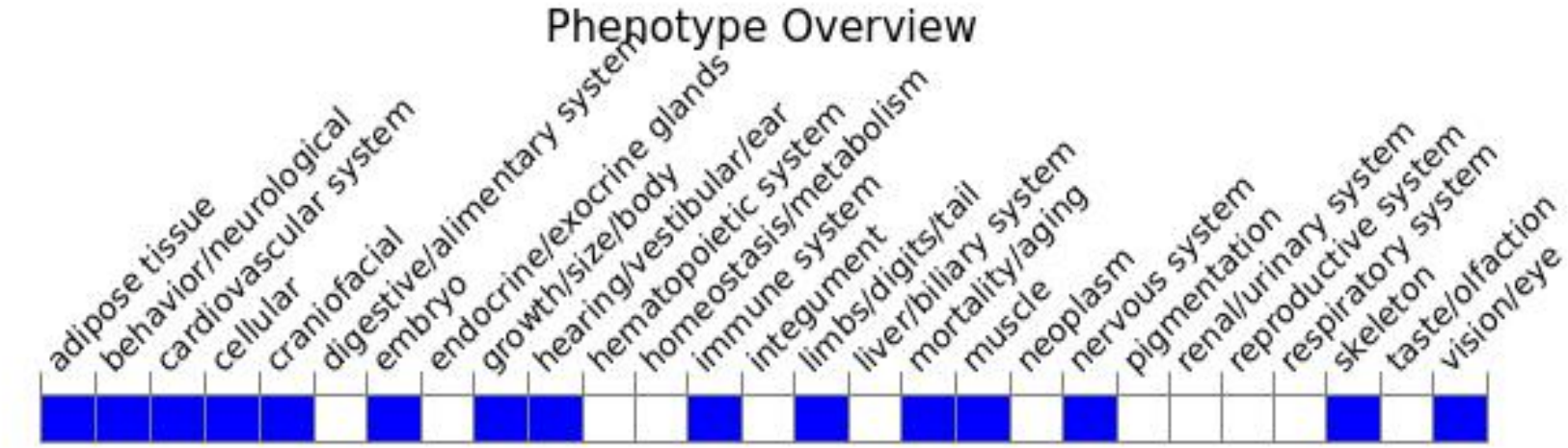
Genomic location distribution



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,nullizygous mice are embryonic lethal. Heterozygous null mice are growth-retarded and show various skeletal anomalies. Heterozygotes for a gene-trap allele are small and show craniofacial, heart, eye, hearing and behavioral defects, delayed bone maturation, reduced body fat, and postnatal mortality.

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd