Trim37 Cas9-CKO Strategy

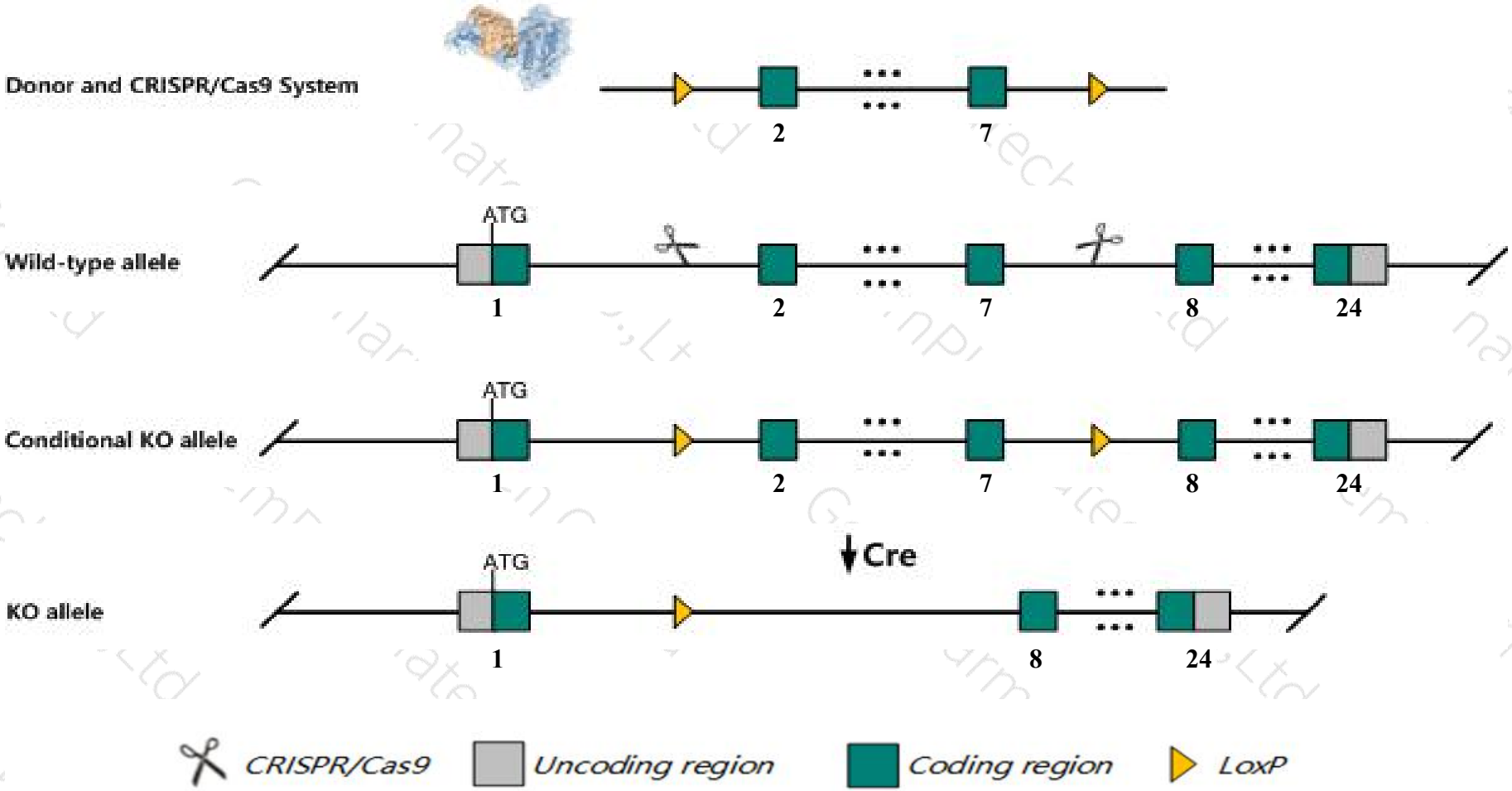
Designer: JiaYu

Project Overview

Project Name	***Trim37***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trim37* gene. The schematic diagram is as follows:



Technical routes

- The *Trim37* gene has 4 transcripts. According to the structure of *Trim37* gene, exon2-exon7 of *Trim37-201* (ENSMUST00000041282.12) transcript is recommended as the knockout region.The region contains 595bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Trim37* 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,Mice homozygous for a knock-out allele are infertile due to gonadal degeneration and exhibit late-onset weight loss, smaller skull size, non-compaction cardiomyopathy, hepatomegaly, fatty liver, altered glucose metabolism, splenomegaly, and increased tumor incidence.

➢ The *Trim37* gene is located on the Chr11. 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

Trim37 tripartite motif-containing 37 [Mus musculus (house mouse)]

Gene ID: 68729, updated on 31-Jan-2019

Summary

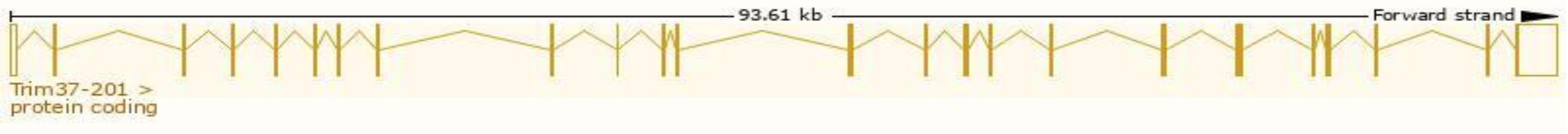
Official Symbol	Trim37 provided by MGI
Official Full Name	tripartite motif-containing 37 provided by MGI
Primary source	MGI:MGI:2153072
See related	Ensembl:ENSMUSG00000018548
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110032A10Rik, 2810004E07Rik, AI848587, AU043018, MUL, TEF3
Summary	The protein encoded by this gene is part of the tripartite-motif containing family (TRIM), which is typified by the RING, B-box type 1, B-box type 2, and coiled-coil region domains. In mouse this protein is proposed to oligomerize through its coiled coil domain and has been reported to be expressed in neural crest-derived tissues as well as in tissues whose development is regulated by mesenchymal-epithelial interactions. In humans, mutations in this gene are associated with mulibrey (muscle-liver-brain-eye) nanism, an autosomal recessive disorder characterized by prenatal onset growth failure, cardiomyopathy and dysmorphic features. [provided by RefSeq, Jan 2013]
Expression	Biased expression in cortex adult (RPKM 34.0), testis adult (RPKM 33.1) and 14 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

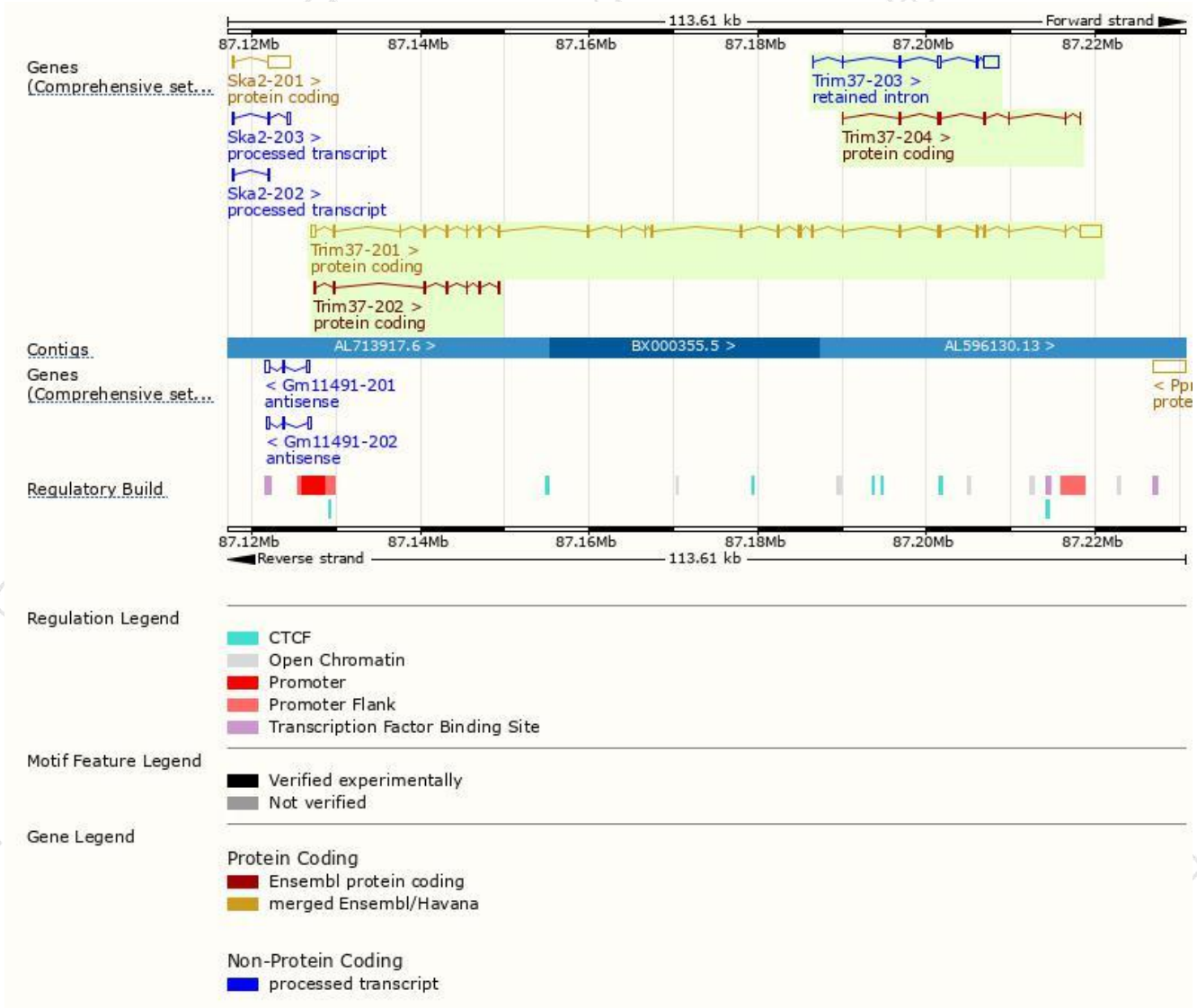
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim37-201	ENSMUST00000041282.12	5632	961aa	Protein coding	CCDS25210	Q6PCX9	TSL:1 GENCODE basic APPRIS P1
Trim37-204	ENSMUST00000154138.1	1017	339aa	Protein coding	-	F6XMH5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Trim37-202	ENSMUST00000139532.1	766	197aa	Protein coding	-	Q5SQY9	CDS 3' incomplete TSL:5
Trim37-203	ENSMUST00000152637.1	2488	No protein	Retained intron	-	-	TSL:5

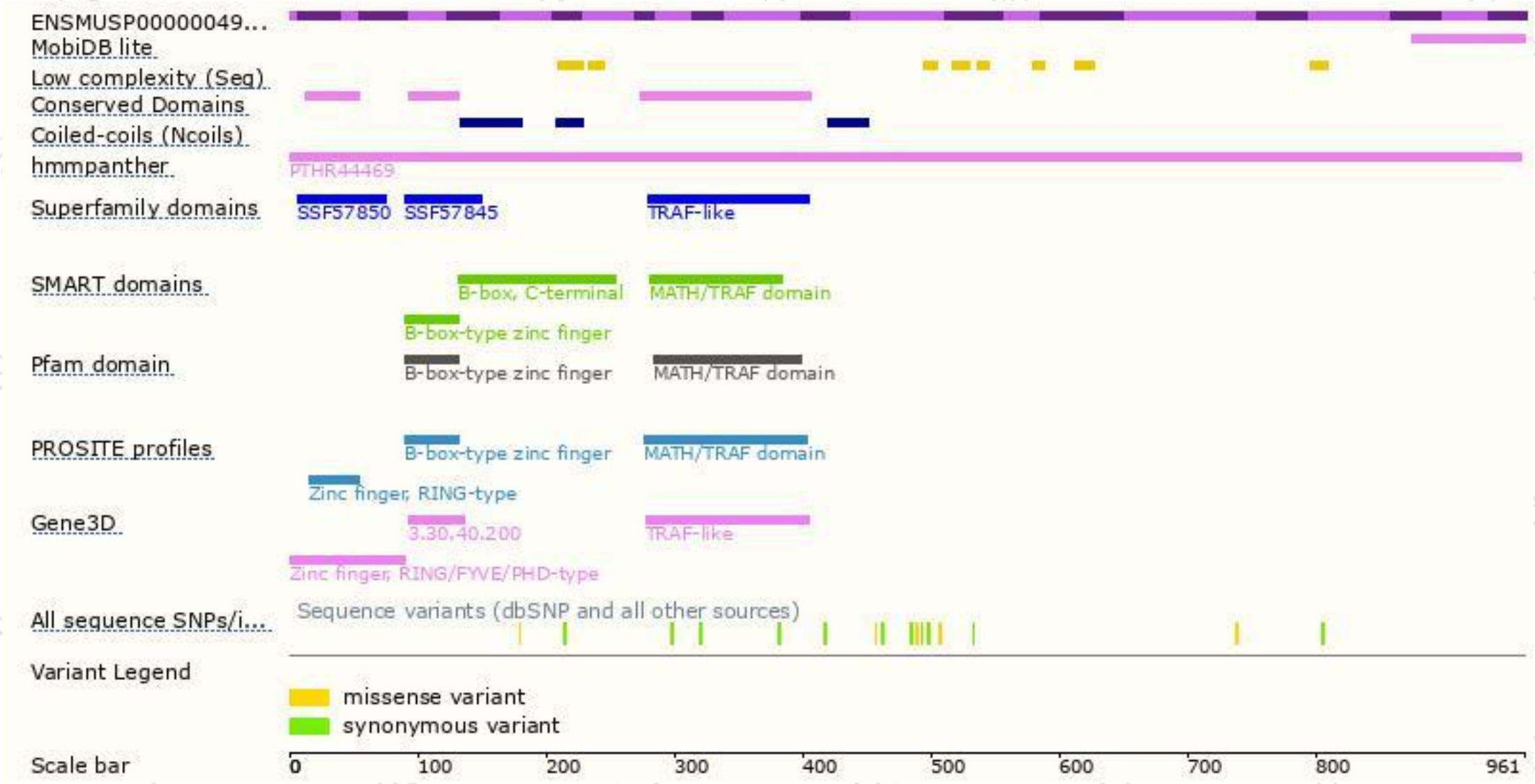
The strategy is based on the design of *Trim37-201* transcript,The transcription is shown below



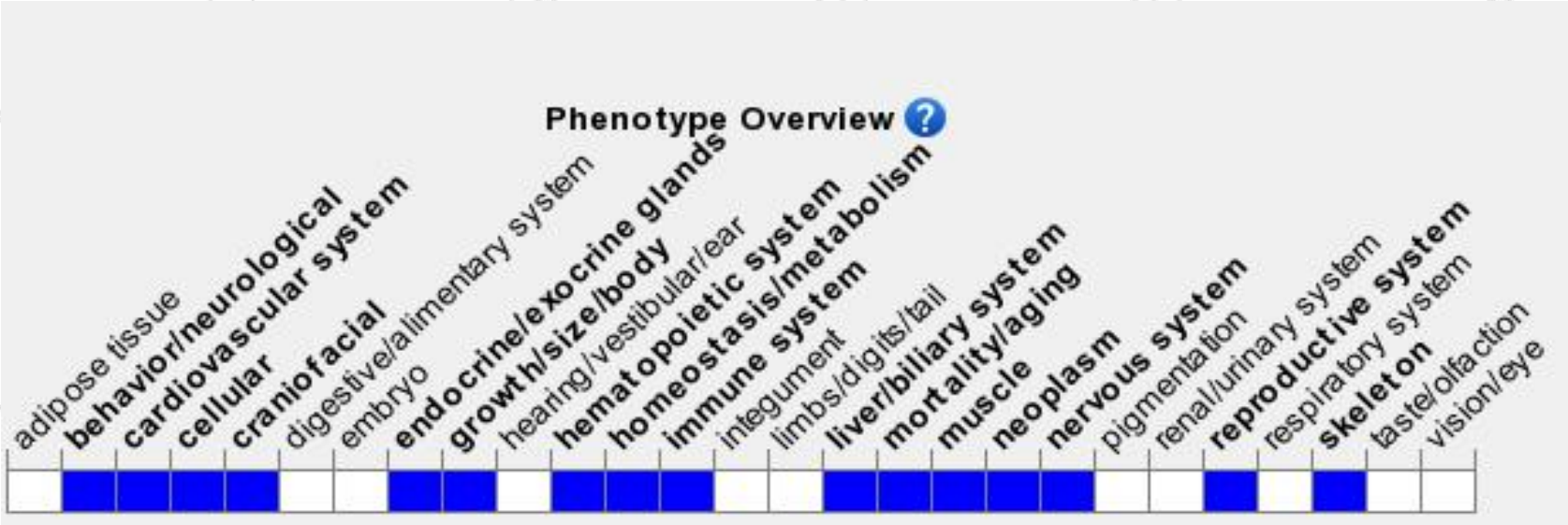
Genomic location distribution



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 knock-out allele are infertile due to gonadal degeneration and exhibit late-onset weight loss, smaller skull size, non-compaction cardiomyopathy, hepatomegaly, fatty liver, altered glucose metabolism, splenomegaly, and increased tumor incidence.

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