# *Relb* Cas9-KO Strategy

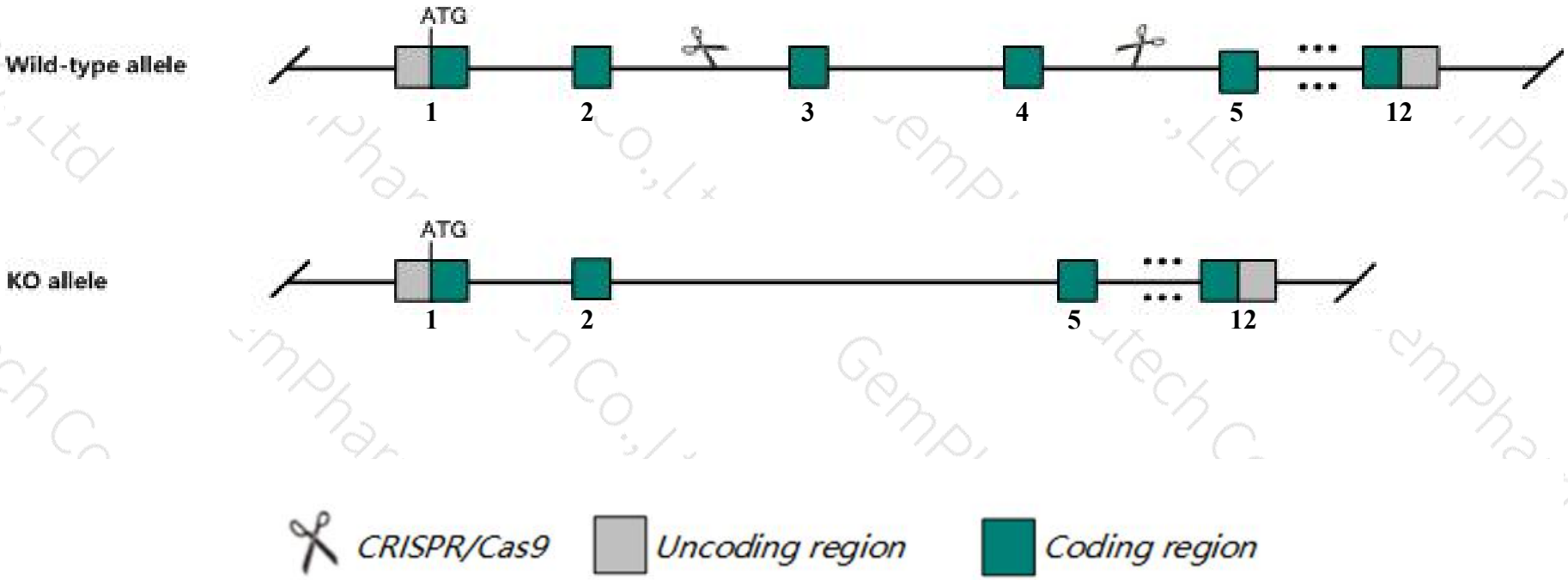
Designer: Xiaojing Li
Design Date: 2019-8-15

# Project Overview

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

# Knockout strategy

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



# Technical routes

➢ The *Relb* gene has 10 transcripts. According to the structure of *Relb* gene, exon3-exon4 of *Relb-202* (ENSMUST00000094762.9) transcript is recommended as the knockout region.The region contains 338bp coding sequence. Knock out the region will result in disruption of protein function.

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

# Notice

- According to the existing MGI data,Mutant homozygotes die prematurely with phenotypes including inflammatory cell infiltration of organs, myeloid hyperplasia, splenomegaly, reduction in thymic dendritic cells, impaired cellular immunity, hyperkeratosis, epidermal hyperplasia, or hepatitiswith mononuclear infiltration.

- The *Relb* gene is located on the Chr7. 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.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Relb avian reticuloendotheliosis viral (v-rel) oncogene related B [Mus musculus (house mouse)]

Gene ID: 19698, updated on 9-Apr-2019

### Summary

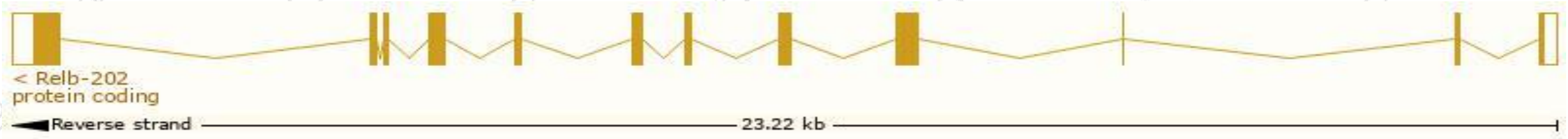
| | |
|---|---|
| **Official Symbol** | Relb provided by MGI |
| **Official Full Name** | avian reticuloendotheliosis viral (v-rel) oncogene related B provided by MGI |
| **Primary source** | MGI:MGI:103289 |
| **See related** | Ensembl:ENSMUSG00000002983 |
| **Gene type** | protein coding |
| **RefSeq 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** | shep |
| **Expression** | Broad expression in spleen adult (RPKM 33.2), adrenal adult (RPKM 28.7) and 15 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

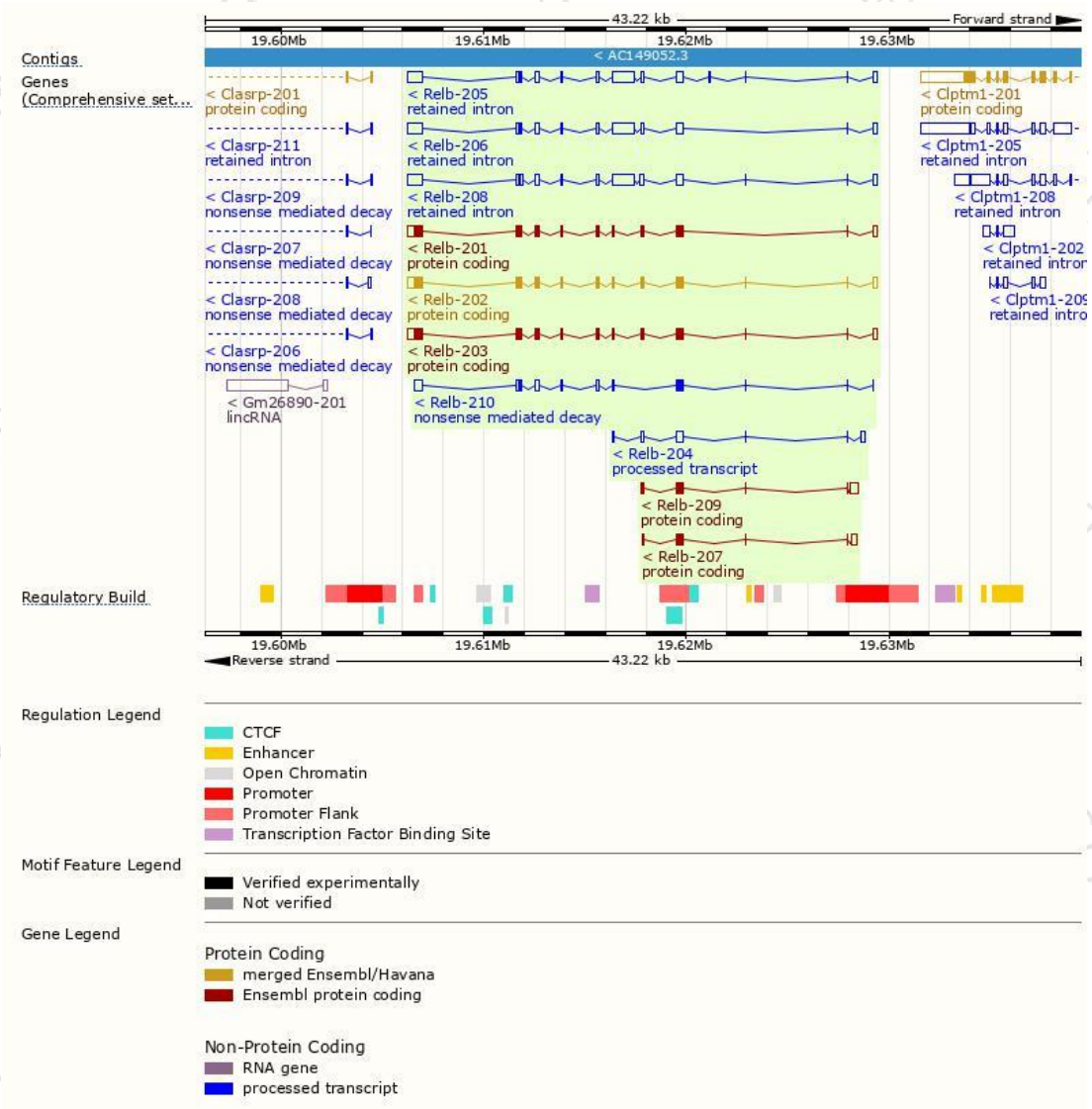
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Relb-202 | ENSMUST00000094762.9 | 2209 | 558aa | Protein coding | CCDS39799 | Q04863 | TSL:1 GENCODE basic APPRIS P3 |
| Relb-201 | ENSMUST00000049912.14 | 2200 | 555aa | Protein coding | CCDS71896 | Q8K220 | TSL:1 GENCODE basic APPRIS ALT2 |
| Relb-203 | ENSMUST00000098754.4 | 2203 | 558aa | Protein coding | - | Q04863 | TSL:5 GENCODE basic APPRIS ALT2 |
| Relb-209 | ENSMUST00000153309.7 | 931 | 138aa | Protein coding | - | A0A140LI46 | CDS 3' incomplete TSL:3 |
| Relb-207 | ENSMUST00000141586.1 | 727 | 116aa | Protein coding | - | A0A140LI24 | CDS 3' incomplete TSL:5 |
| Relb-210 | ENSMUST00000208087.1 | 1525 | 147aa | Nonsense mediated decay | - | A0A140LJD6 | TSL:1 |
| Relb-204 | ENSMUST00000130543.7 | 784 | No protein | Processed transcript | - | - | TSL:5 |
| Relb-208 | ENSMUST00000148040.7 | 3273 | No protein | Retained intron | - | - | TSL:1 |
| Relb-205 | ENSMUST00000131759.7 | 3210 | No protein | Retained intron | - | - | TSL:1 |
| Relb-206 | ENSMUST00000137615.7 | 3166 | No protein | Retained intron | - | - | TSL:1 |

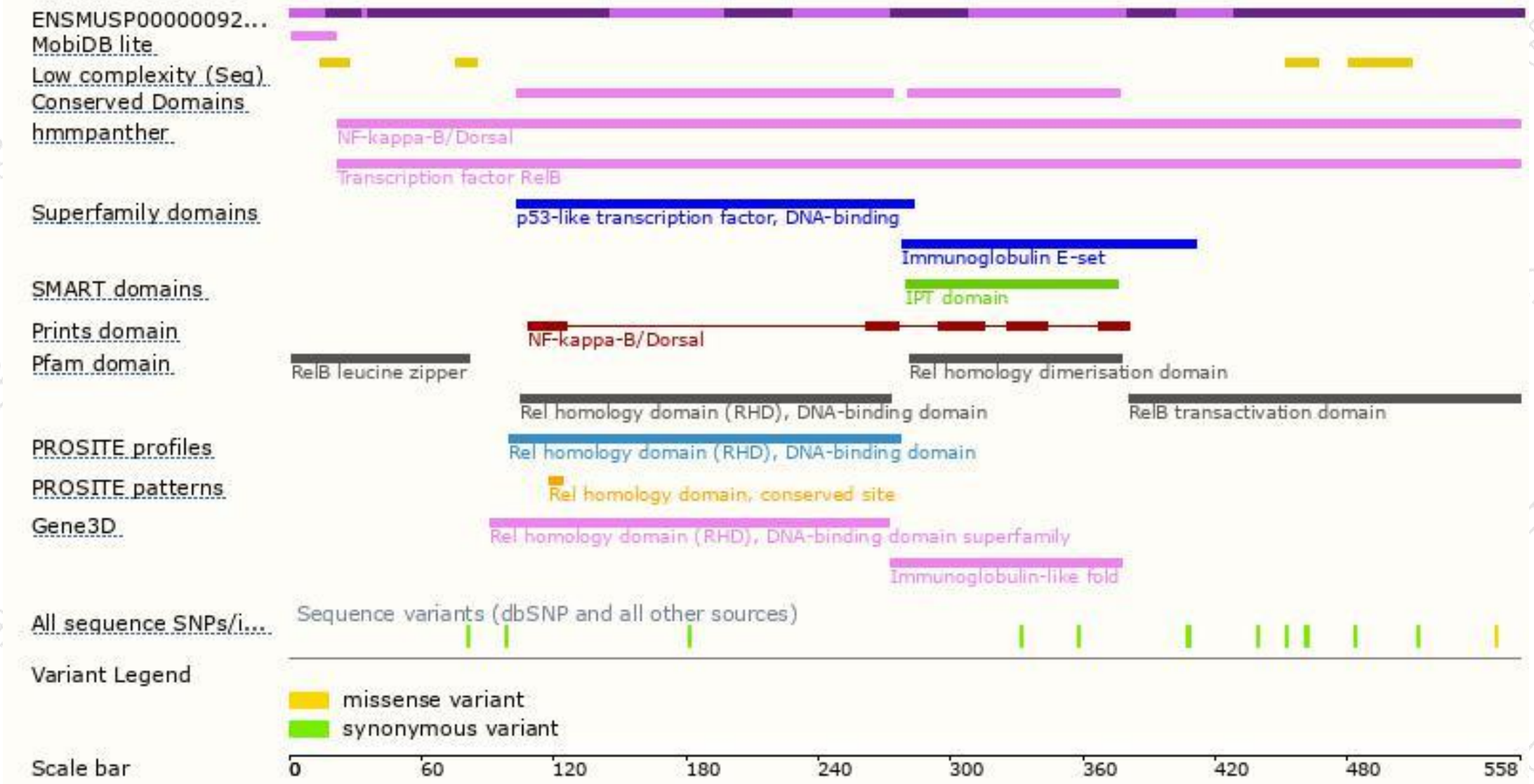
The strategy is based on the design of *Relb-202* transcript,The transcription is shown below



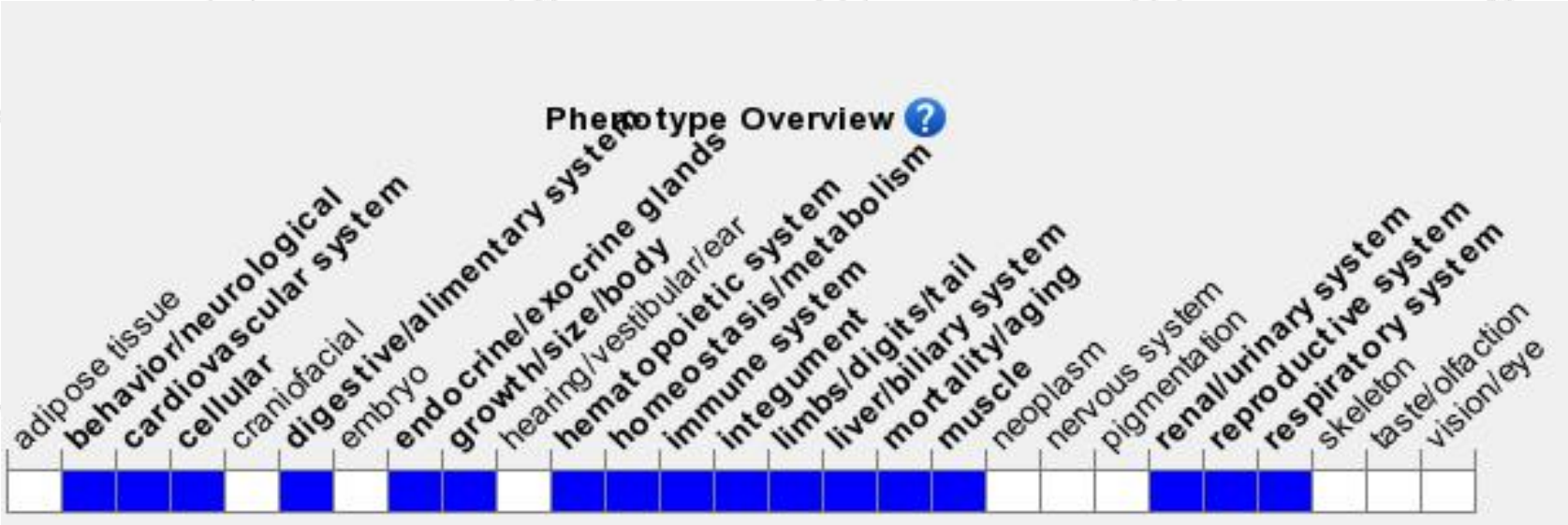
# Genomic location distribution



# 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,Mutant homozygotes die prematurely with phenotypes including inflammatory cell infiltration of organs, myeloid hyperplasia, splenomegaly, reduction in thymic dendritic cells, impaired cellular immunity, hyperkeratosis, epidermal hyperplasia, or hepatitiswith mononuclear infiltration.

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