# *S1pr3* Cas9-CKO Strategy

Designer: Xueting Zhang
Design Date: 2019-8-5

# Project Overview

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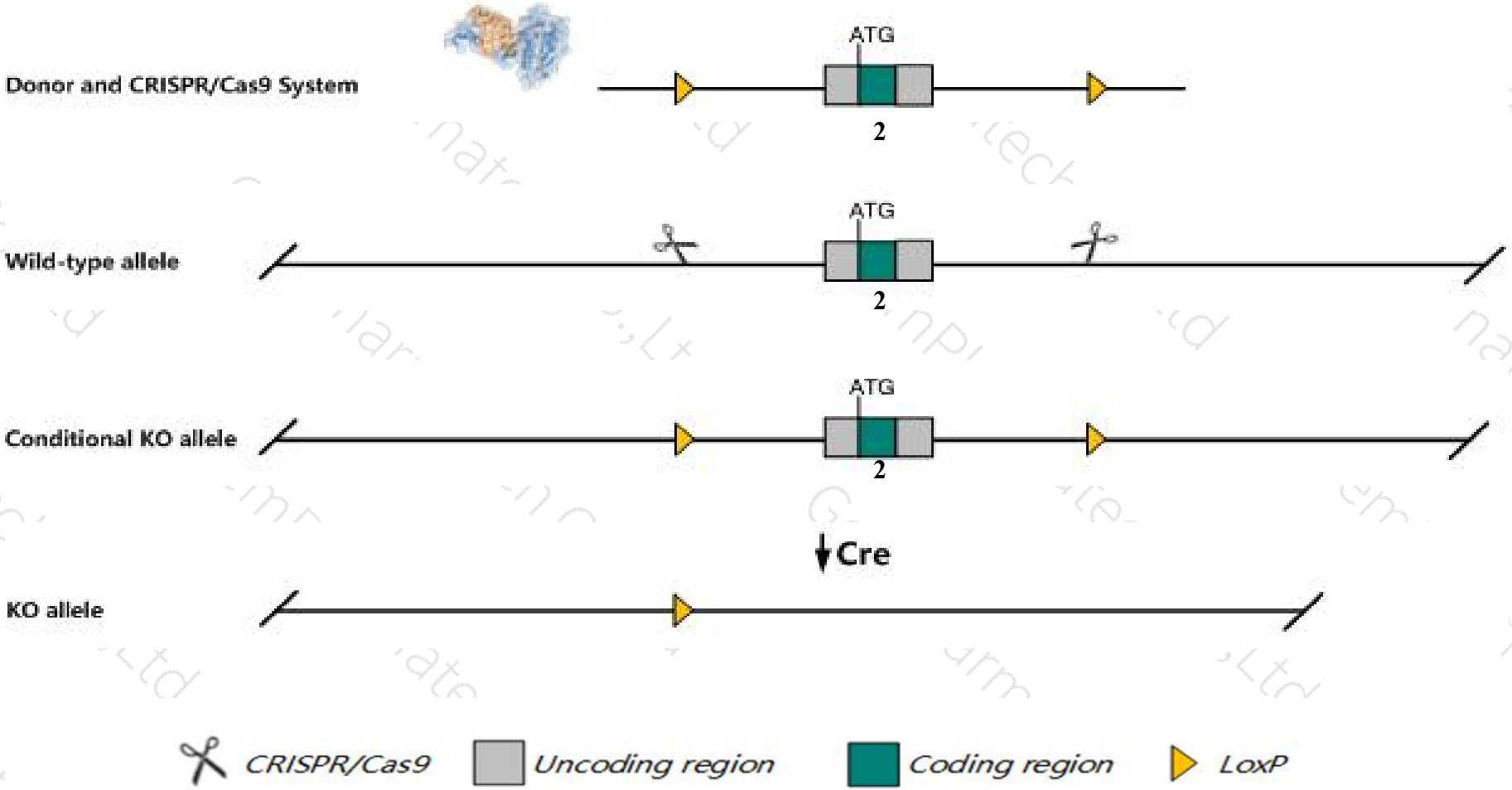
|---|---|
| **Project Name** | ***S1pr3*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *S1pr3* gene. The schematic diagram is as follows:



# Technical routes

- The *S1pr3* gene has 1 transcript. According to the structure of *S1pr3* gene, exon2 of *S1pr3-201* (ENSMUST00000087978.4) 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 *S1pr3* 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 disruptions in this gene display an essentially normal phenotype although litter sizes are reduced. Susceptibility to pulmonary edema is also reduced.

➢The partial sequence of intron of *Gm32834* gene will be deleted together in this strategy.

➢ The *S1pr3* gene is located on the Chr13. 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

## S1pr3 sphingosine-1-phosphate receptor 3 [ *Mus musculus* (house mouse) ]

Gene ID: 13610, updated on 12-Mar-2019

### Summary

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|---|---|
| **Official Symbol** | S1pr3 provided by MGI |
| **Official Full Name** | sphingosine-1-phosphate receptor 3 provided by MGI |
| **Primary source** | MGI:MGI:1339365 |
| **See related** | Ensembl:ENSMUSG00000067586 |
| **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** | Edg3; Lpb3; S1p3; AI132464 |
| **Summary** | This gene encodes a member of the G-protein coupled receptor 1 family. The encoded protein is a receptor for the lysophospholipid sphingosine 1-phosphate. The gene product functions in endothelial cells and is involved in vascular and heart development. The gene product mediates HDL and HDL-associated lysophospholipid-induced vasorelaxation, and it coordinates with other lysophospholipid receptors in the process of angiogenesis. [provided by RefSeq, Jan 2010] |
| **Expression** | Broad expression in limb E14.5 (RPKM 30.0), lung adult (RPKM 20.8) and 19 other tissues See more |
| **Orthologs** | human all |

### Genomic context

**Location:** 13; 13 A5 — See S1pr3 in Genome Data Viewer

**Exon count:** 2

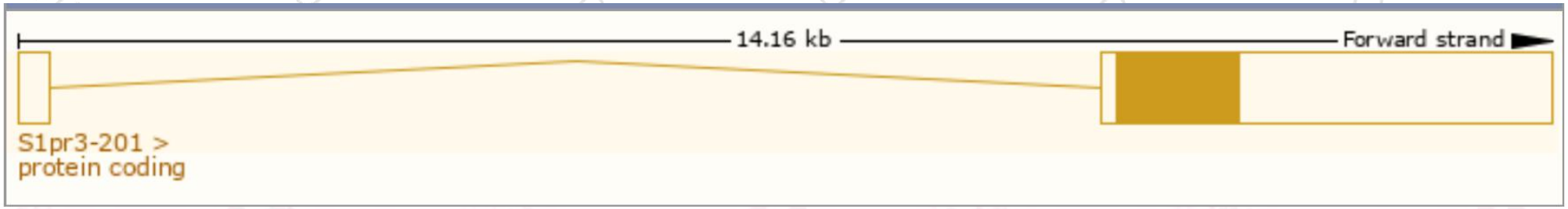
| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 106 | current | GRCm38.p4 (GCF_000001635.24) | 13 | NC_000079.6 (51408618..51422797) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 13 | NC_000079.5 (51503987..51518166) |

# Transcript information（Ensembl）

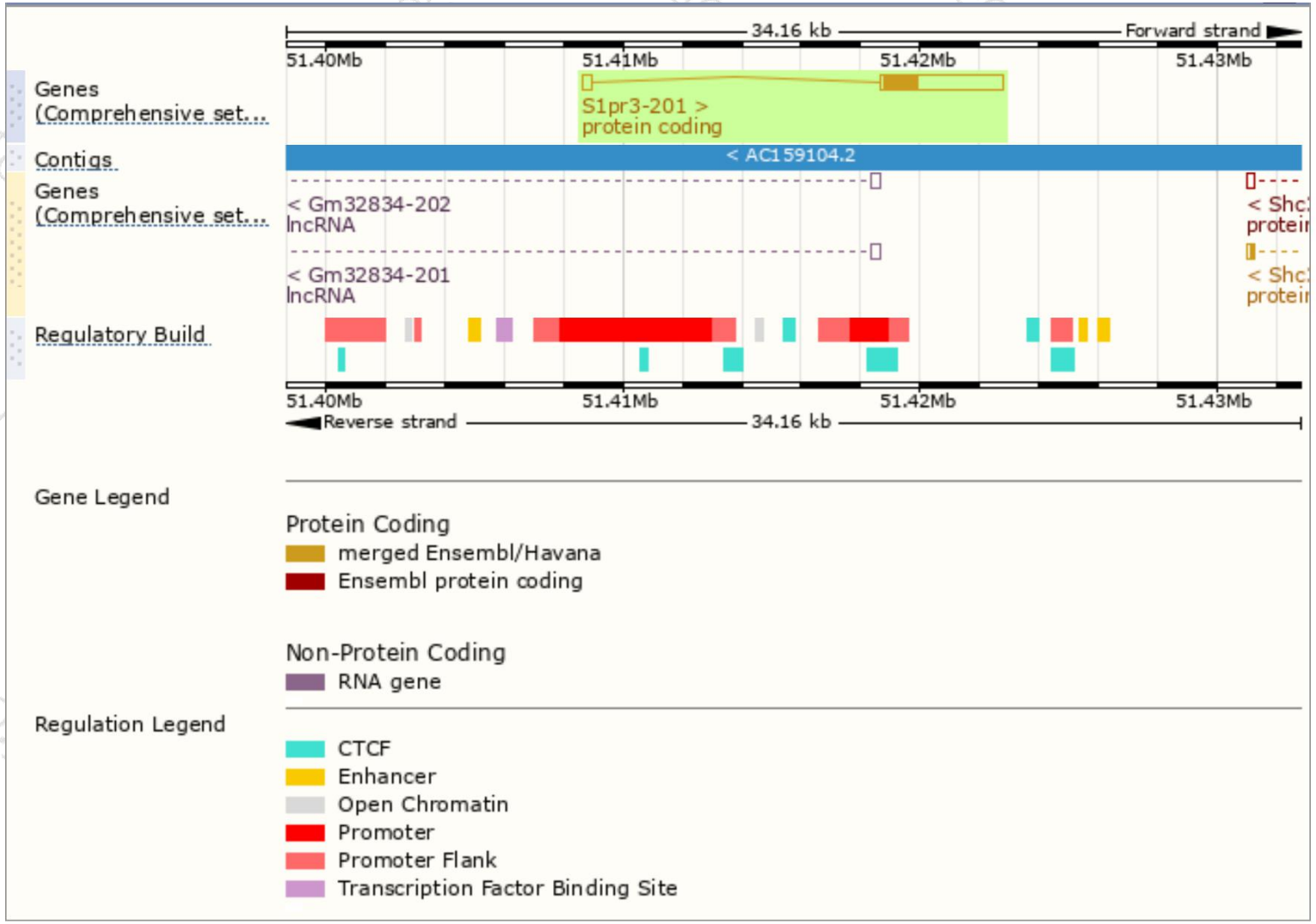
The gene has 1 transcript,and the transcript is shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| S1pr3-201 | ENSMUST00000087978.4 | 4463 | 378aa | Protein coding | CCDS26512 | Q9Z0U9 | TSL:1 GENCODE basic APPRIS P1 |

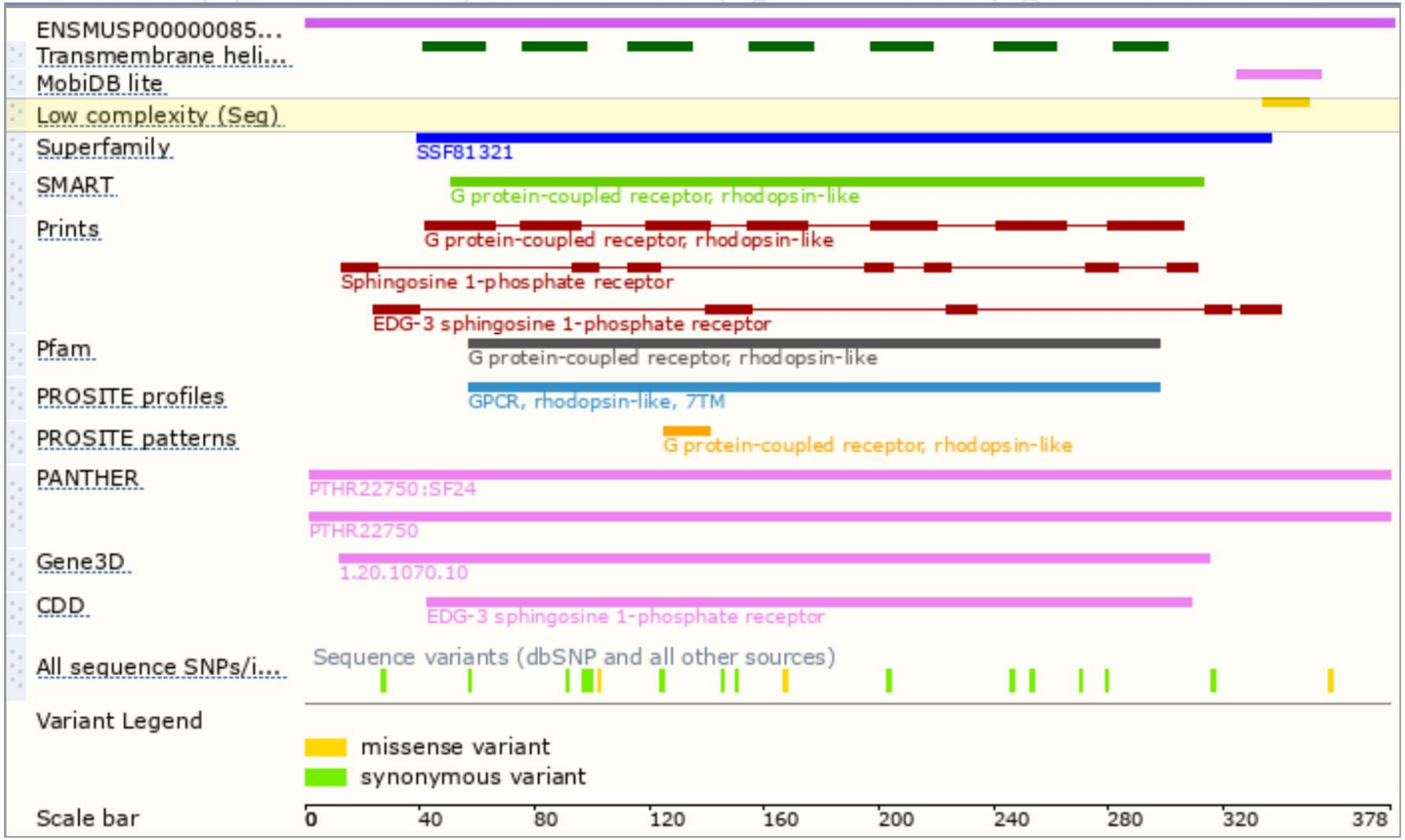
The strategy is based on the design of *S1pr3-201* transcript,The transcription is shown below



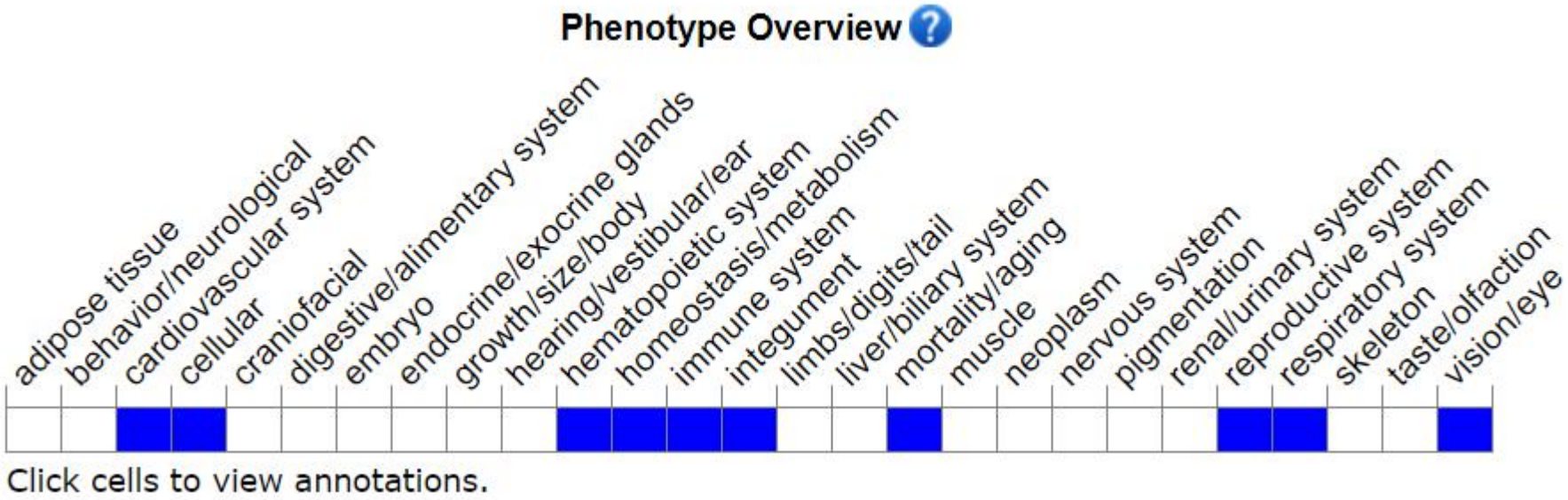
# Genomic location distribution



# 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/).*

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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