# *Scmh1* Cas9-CKO Strategy

**Designer: Shanhong Tao**

**Reviewer: Longyun Hu**

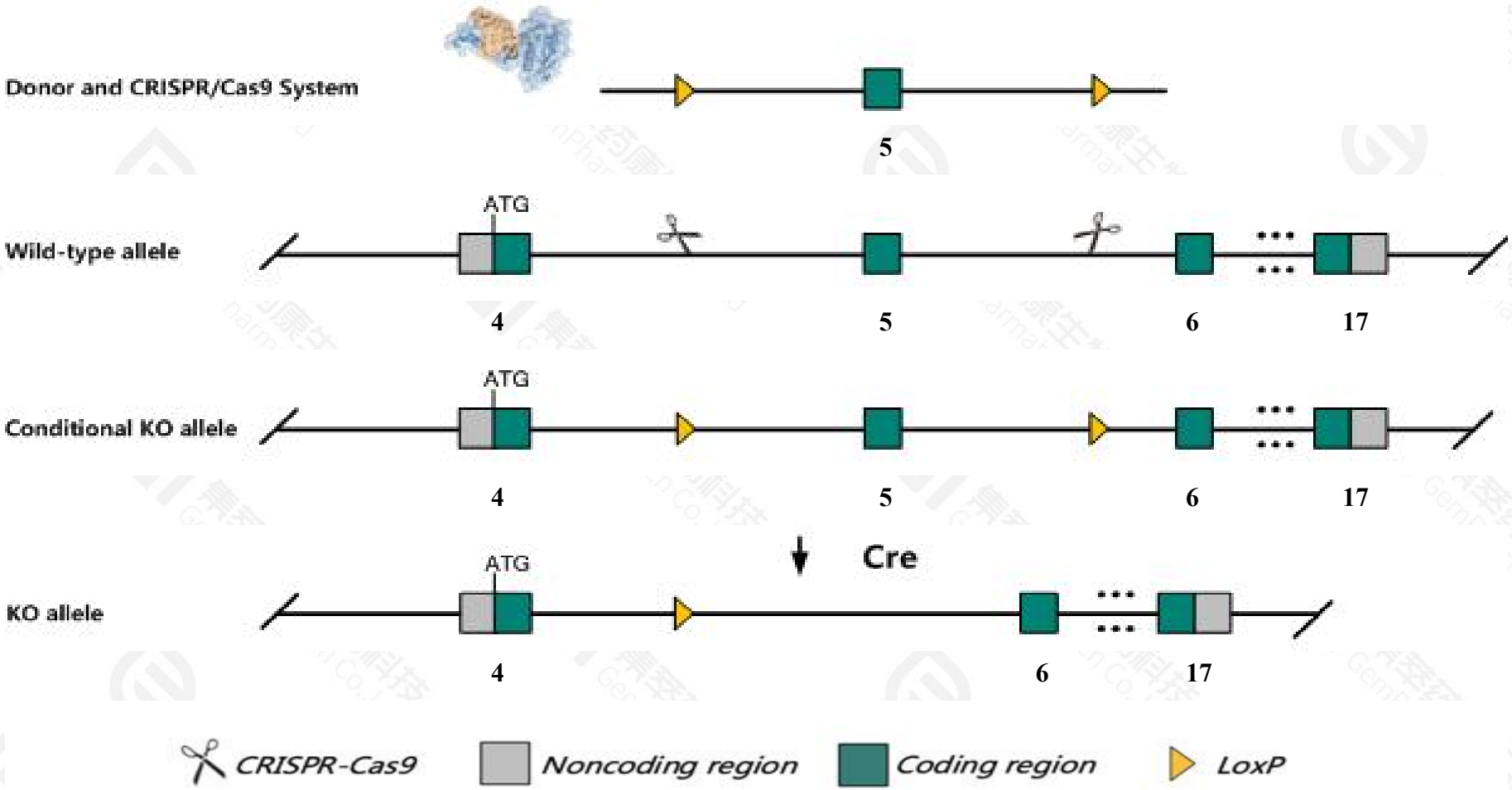
**Design Date: 2022-5-27**

# Project Overview

| | |
|---|---|
| **Project Name** | ***Scmh1*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Scmh1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Scmh1* gene has 14 transcripts. According to the structure of *Scmh1* gene, exon5 of *Scmh1-204*(ENSMUST00000106301.8) transcript is recommended as the knockout region.The region contains 71bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Scmh1* 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 an allele lacking the SPM domain exhibit partial penetrance of posterior vertebral transformations and male infertility with azoospermia and arrest of spermatogenesis. Mice homozygous for a knock-out allele exhibit abnormal hematopoiesis but normal fertility and skeleton.

➢Transcript *Scmh1-205* may not be affected.

➢ The *Scmh1* gene is located on the Chr4. 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

## Scmh1 sex comb on midleg homolog 1 [Mus musculus (house mouse)]

Gene ID: 29871, updated on 28-Apr-2022

### Summary

| | |
|---|---|
| **Official Symbol** | Scmh1 provided by MGI |
| **Official Full Name** | sex comb on midleg homolog 1 provided byMGI |
| **Primary source** | MGI:MGI:1352762 |
| **See related** | Ensembl:ENSMUSG00000000085 |
| **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** | AI315320, AI851618, Scml1, Scml3 |
| **Expression** | Ubiquitous expression in testis adult (RPKM 9.0), bladder adult (RPKM 6.2) and 28 other tissuesSee more |
| **Orthologs** | human all |

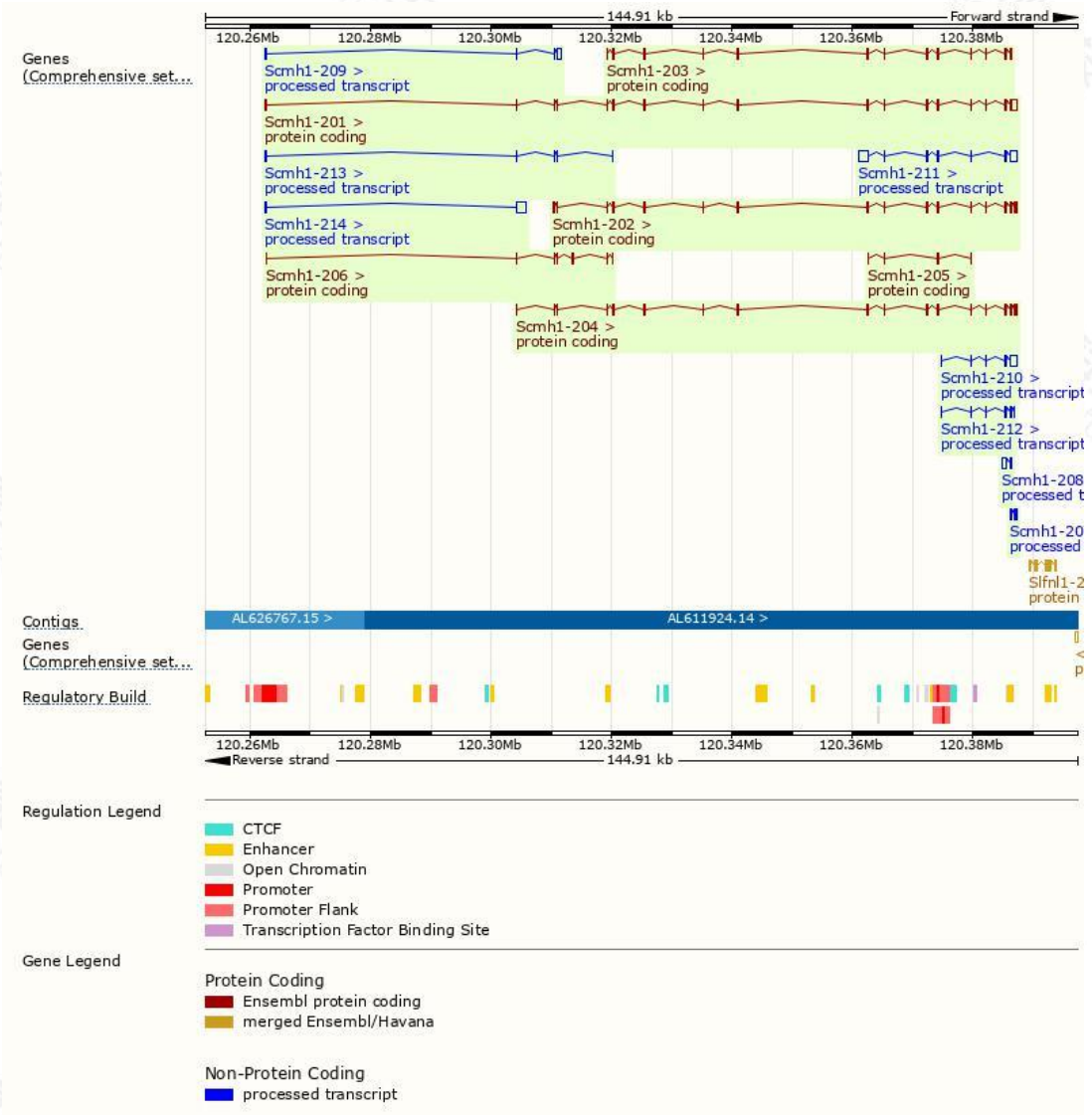
# Transcript information（Ensembl）

The gene has 14 transcripts,all transcripts are shown below:

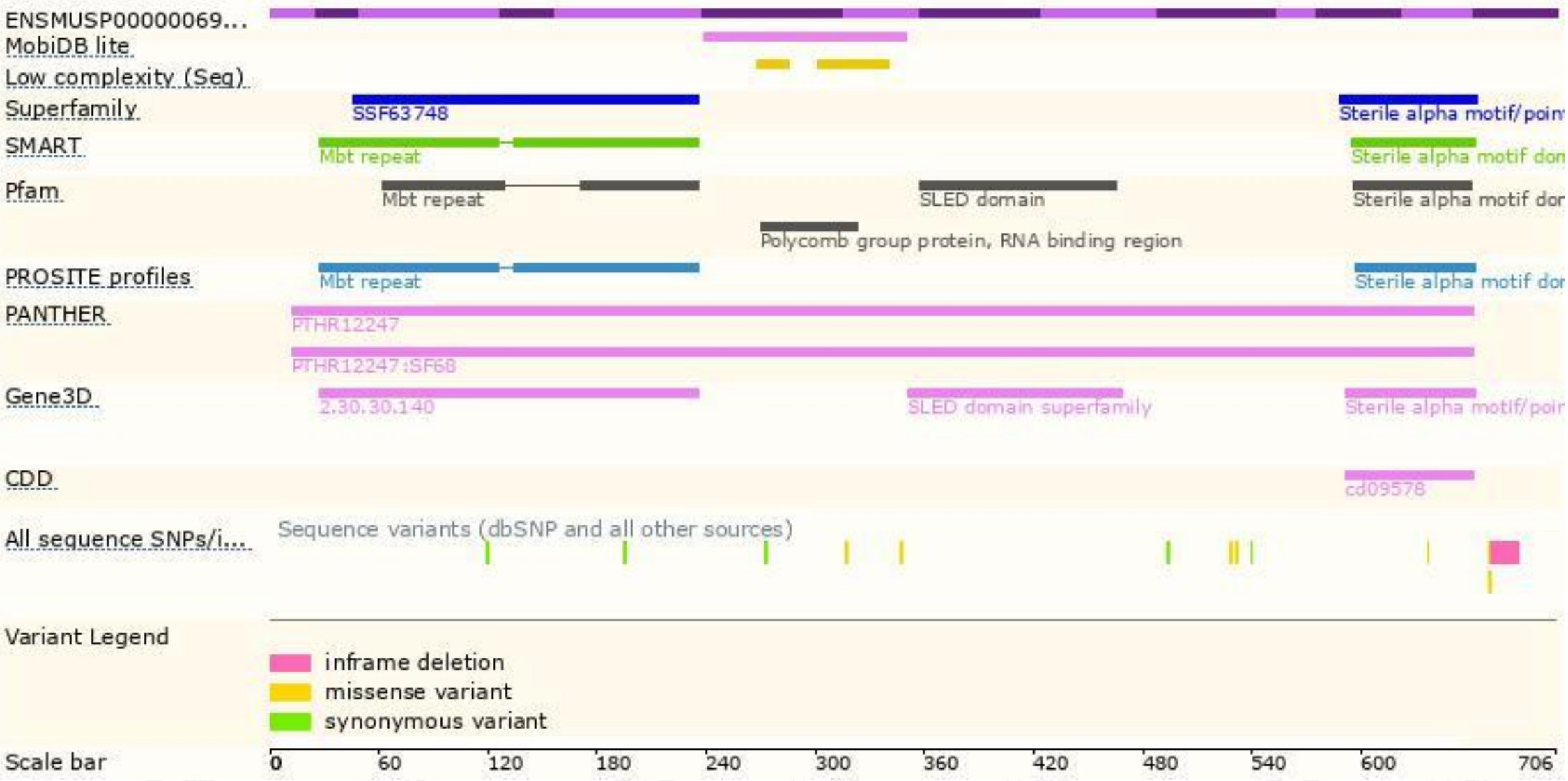
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| **Scmh1-201** | ENSMUST00000000087.13 | 3353 | 664aa | Protein coding | CCDS18589 | | TSL:1 , GENCODE basic , APPRIS P3 , |
| **Scmh1-204** | ENSMUST00000106301.8 | 2584 | 706aa | Protein coding | CCDS51292 | | TSL:1 , GENCODE basic , APPRIS ALT2 , |
| **Scmh1-202** | ENSMUST00000064991.13 | 2548 | 706aa | Protein coding | CCDS51292 | | TSL:5 , GENCODE basic , APPRIS ALT2 , |
| **Scmh1-203** | ENSMUST00000106298.10 | 1995 | 664aa | Protein coding | CCDS18589 | | TSL:1 , GENCODE basic , APPRIS P3 , |
| **Scmh1-206** | ENSMUST00000132116.8 | 623 | 28aa | Protein coding | - | | CDS 3' incomplete , TSL:5 , |
| **Scmh1-205** | ENSMUST00000122860.2 | 530 | 177aa | Protein coding | - | | CDS 5' and 3' incomplete , TSL:3 , |
| **Scmh1-211** | ENSMUST00000144555.8 | 3544 | No protein | Processed transcript | - | | TSL:1 , |
| **Scmh1-214** | ENSMUST00000153099.2 | 1776 | No protein | Processed transcript | - | | TSL:1 , |
| **Scmh1-210** | ENSMUST00000136801.8 | 1536 | No protein | Processed transcript | - | | TSL:1 , |
| **Scmh1-209** | ENSMUST00000134375.8 | 1132 | No protein | Processed transcript | - | | TSL:1 , |
| **Scmh1-212** | ENSMUST00000144862.2 | 595 | No protein | Processed transcript | - | | TSL:3 , |
| **Scmh1-208** | ENSMUST00000133290.2 | 557 | No protein | Processed transcript | - | | TSL:2 , |
| **Scmh1-207** | ENSMUST00000133169.2 | 443 | No protein | Processed transcript | - | | TSL:2 , |
| **Scmh1-213** | ENSMUST00000151345.8 | 352 | No protein | Processed transcript | - | | TSL:3 , |

The strategy is based on the design of *Scmh1-204* transcript,the transcription is shown below:

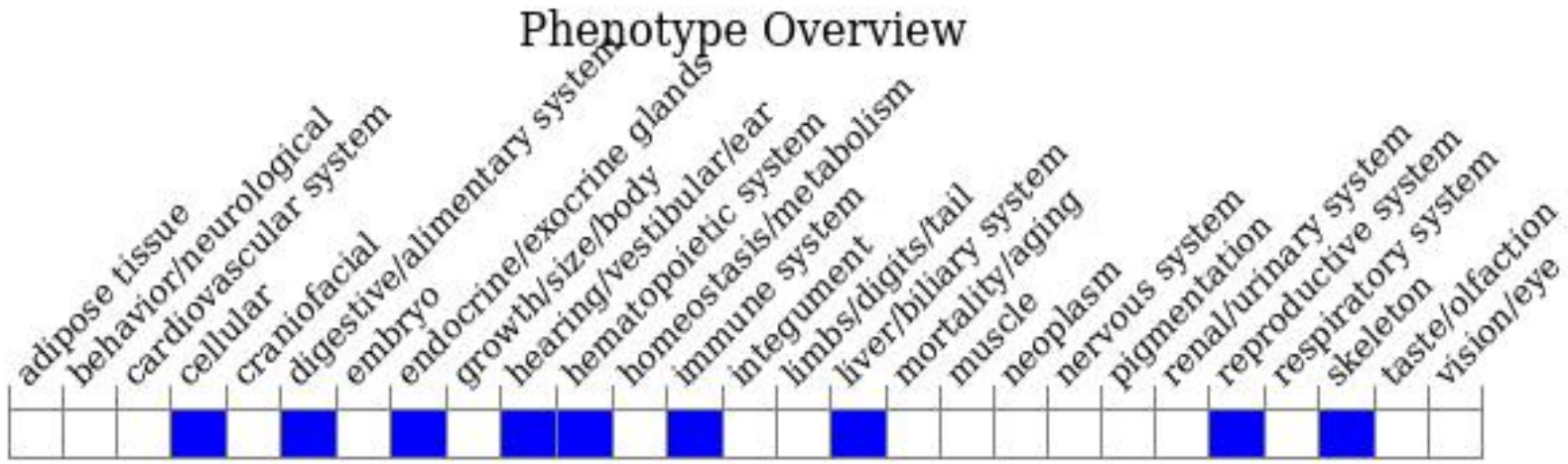
# Genomic location distribution



# 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 an allele lacking the SPM domain exhibit partial penetrance of posterior vertebral transformations and male infertility with azoospermia and arrest of spermatogenesis. Mice homozygous for a knock-out allele exhibit abnormal hematopoiesis but normal fertility and skeleton.

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