# *Fus* Cas9-CKO Strategy

Designer:Shilei Zhu

# Project Overview

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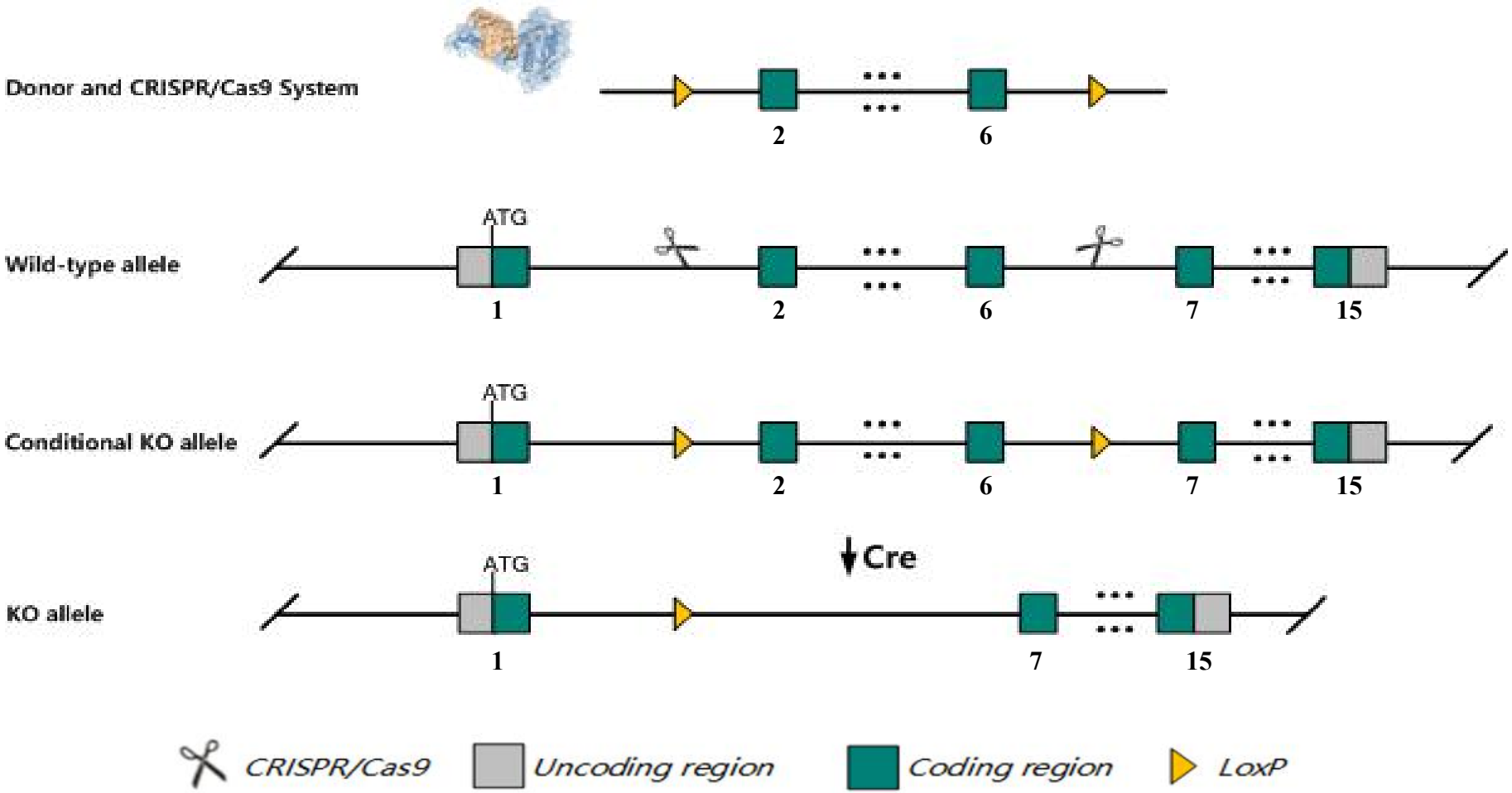
|---|---|
| **Project Name** | ***Fus*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

集萃药康 GemPharmatech

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



# Technical routes

The *Fus* gene has 16 transcripts. According to the structure of *Fus* gene, exon2-exon6 of *Fus-203* (ENSMUST00000106251.9) transcript is recommended as the knockout region.The region contains 730bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Fus* 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,Homozygotes for targeted null mutations exhibit impaired lymphocyte development, chromosomal instability, increased cellular radiation sensitivity, high neonatal mortality, and male sterility associated with lack of chromosomal pairing.

The *Fus* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Gene information NCBI

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## Fus fused in sarcoma [Mus musculus (house mouse)]

Gene ID: 233908, updated on 7-Apr-2019

### Summary

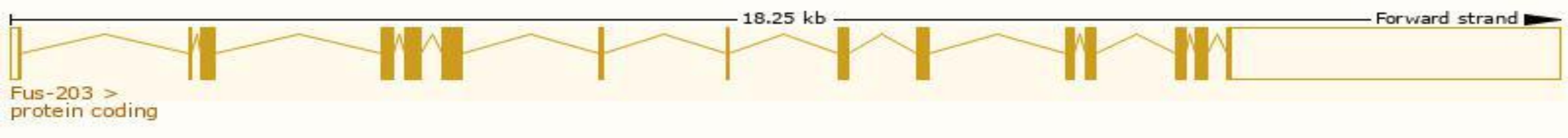
| | |
|---|---|
| **Official Symbol** | Fus provided by MGI |
| **Official Full Name** | fused in sarcoma provided by MGI |
| **Primary source** | MGI:MGI:1353633 |
| **See related** | Ensembl:ENSMUSG00000030795 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | D430004D17Rik, D930039C12Rik, Fus1, Tls |
| **Expression** | Ubiquitous expression in limb E14.5 (RPKM 160.0), CNS E11.5 (RPKM 159.5) and 28 other tissues See more |
| **Orthologs** | human all |

# Transcript information Ensembl

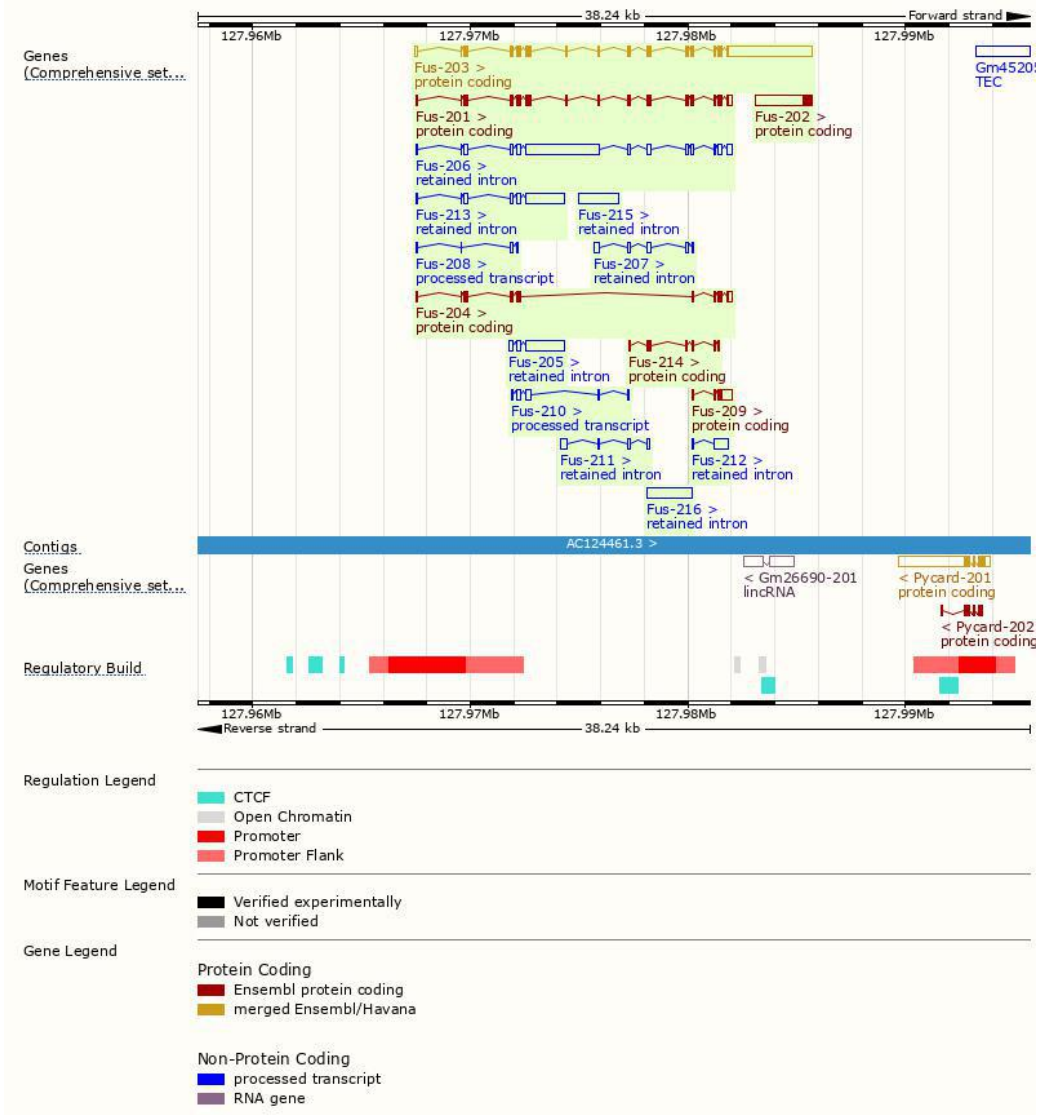
The gene has 16 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Fus-203 | ENSMUST00000106251.9 | 5536 | 518aa | Protein coding | CCDS21886 | P56959 Q564D0 | TSL:1 GENCODE basic APPRIS P3 |
| Fus-201 | ENSMUST00000077609.11 | 1831 | 517aa | Protein coding | CCDS85425 | Q8CFQ9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Fus-202 | ENSMUST00000079045.2 | 2623 | 122aa | Protein coding | - | Q8BNR3 | TSL:NA GENCODE basic |
| Fus-204 | ENSMUST00000121616.8 | 1102 | 280aa | Protein coding | - | Q91VQ2 | TSL:1 GENCODE basic |
| Fus-209 | ENSMUST00000141997.1 | 761 | 104aa | Protein coding | - | G3UZD2 | CDS 5' incomplete TSL:2 |
| Fus-214 | ENSMUST00000174632.7 | 390 | 130aa | Protein coding | - | G3UXT7 | 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 |
| Fus-210 | ENSMUST00000154843.7 | 600 | No protein | Processed transcript | - | - | TSL:3 |
| Fus-208 | ENSMUST00000137464.6 | 354 | No protein | Processed transcript | - | - | TSL:5 |
| Fus-206 | ENSMUST00000128851.7 | 4909 | No protein | Retained intron | - | - | TSL:5 |
| Fus-213 | ENSMUST00000174196.7 | 2374 | No protein | Retained intron | - | - | TSL:1 |
| Fus-205 | ENSMUST00000123151.7 | 2158 | No protein | Retained intron | - | - | TSL:1 |
| Fus-216 | ENSMUST00000205351.1 | 2055 | No protein | Retained intron | - | - | TSL:NA |
| Fus-215 | ENSMUST00000205261.1 | 1859 | No protein | Retained intron | - | - | TSL:NA |
| Fus-212 | ENSMUST00000172755.1 | 670 | No protein | Retained intron | - | - | TSL:5 |
| Fus-207 | ENSMUST00000136289.1 | 600 | No protein | Retained intron | - | - | TSL:3 |
| Fus-211 | ENSMUST00000155941.7 | 516 | No protein | Retained intron | - | - | TSL:3 |

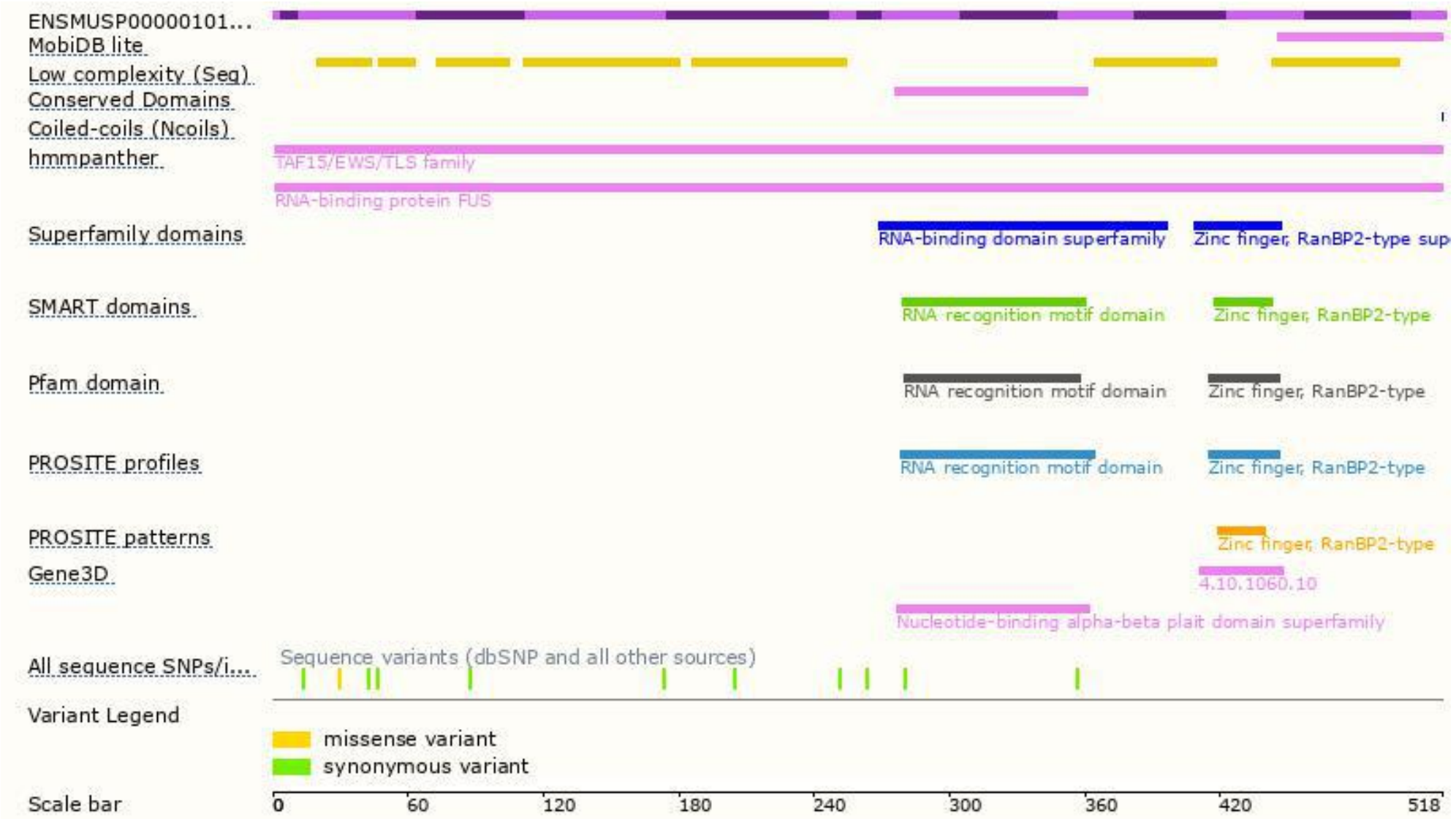
The strategy is based on the design of *Fus-203* transcript,The transcription is shown below



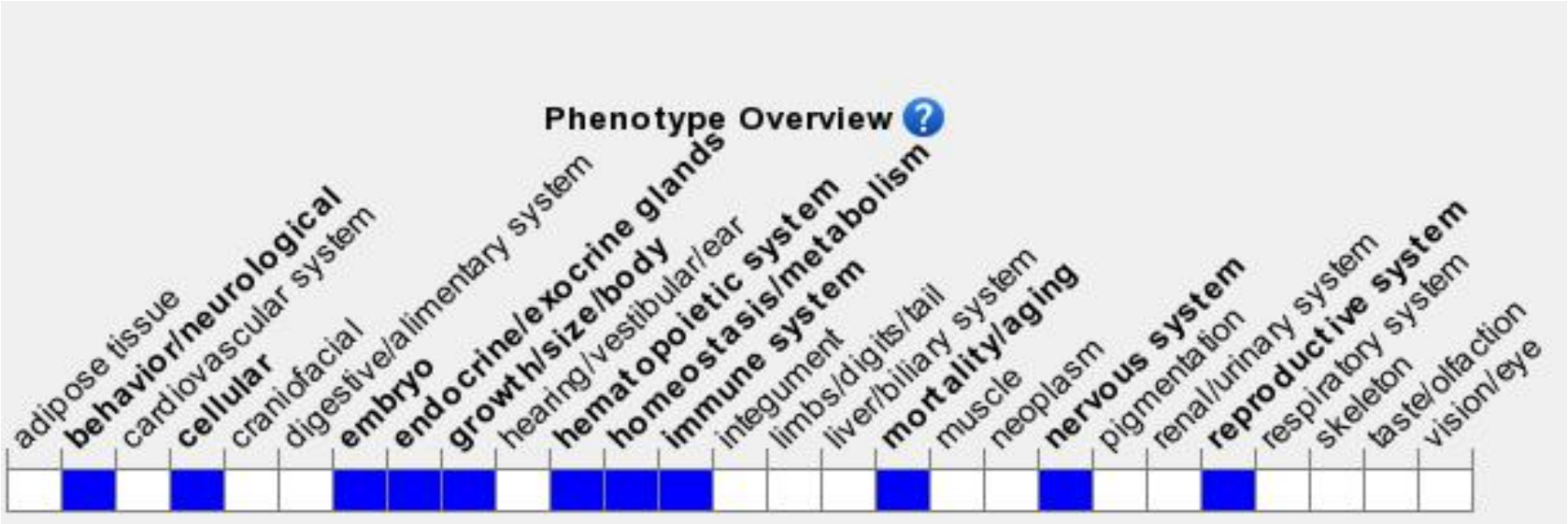
# Genomic location distribution



# 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

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