

Skil Cas9-CKO Strategy

Designer:Xiaojing Li
Design Date:2019-11-18
Reviewer:Jia Yu

Project Overview

Project Name

Skil

Project type

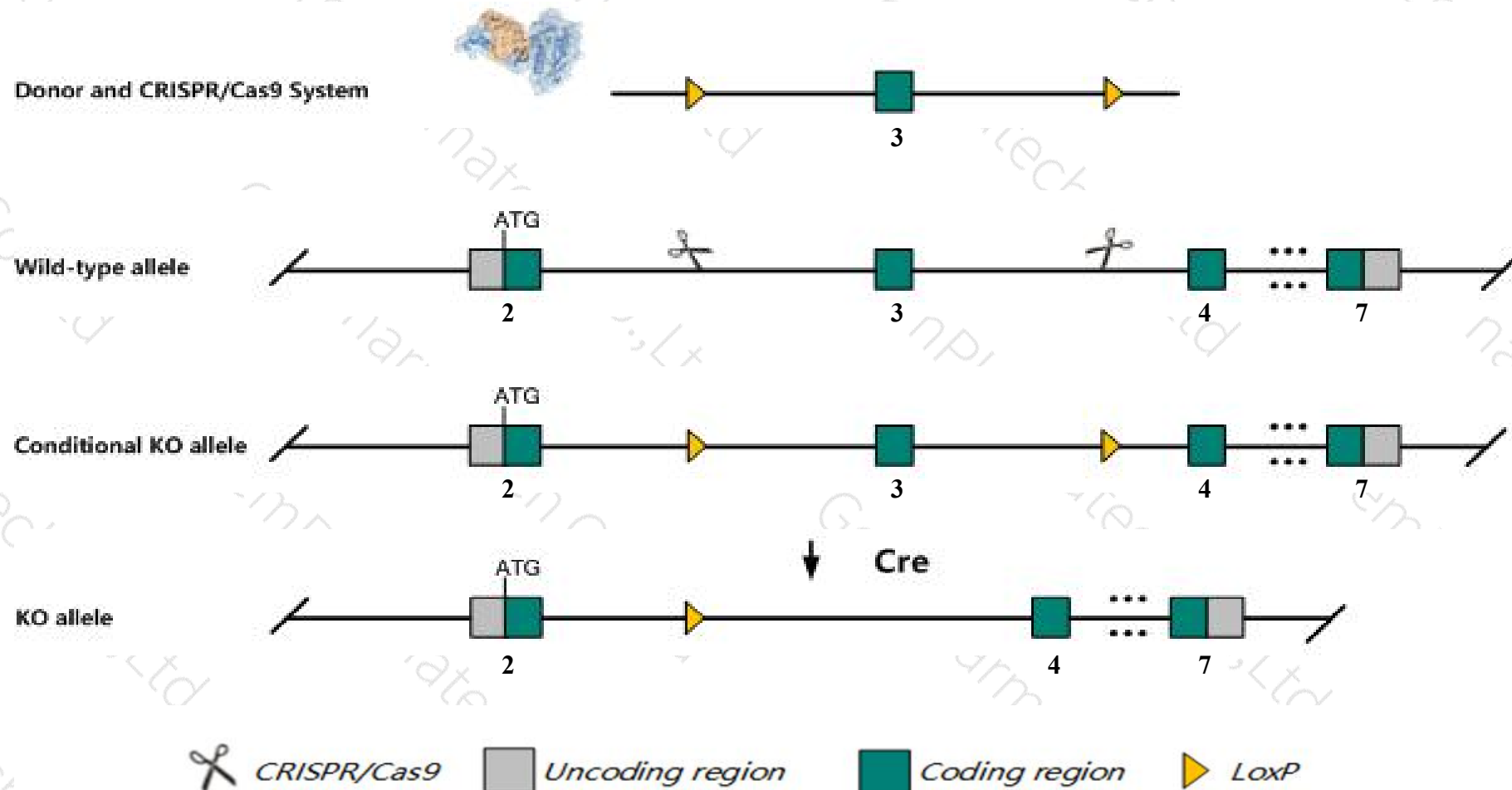
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Skil* gene has 6 transcripts. According to the structure of *Skil* gene, exon3 of *Skil*-201 (ENSMUST00000029194.11) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Skil* 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.

- According to the existing MGI data, Heterozygotes for a null allele develop lymphomas and show increased incidence of chemically-induced tumors while homozygotes die before implantation. Homozygotes for a different null allele are viable but show defective T cell activation and impaired mammary gland alveologenesis and lactogenesis.
- The *Skil* gene is located on the Chr3. 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)

Skil SKI-like [*Mus musculus* (house mouse)]

Gene ID: 20482, updated on 19-Oct-2019

Summary



| | |
|--------------------|---|
| Official Symbol | Skil provided by MGI |
| Official Full Name | SKI-like provided by MGI |
| Primary source | MGI:MGI:106203 |
| See related | Ensembl:ENSMUSG000000027660 |
| 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 | sno; Skir; SnoN |
| Summary | This gene encodes a member of a small family of proteins that play a key role in the response of cells to extracellular growth signals. The encoded protein regulates members of the transforming growth factor beta signaling pathway. It is highly expressed in certain cancer cells, where it may have both tumor-suppressing and tumor-promoting roles. Alternatively spliced transcript variants encoding multiple isoforms have been observed for this gene. [provided by RefSeq, Nov 2012] |
| Expression | Ubiquitous expression in CNS E11.5 (RPKM 8.0), CNS E18 (RPKM 5.8) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

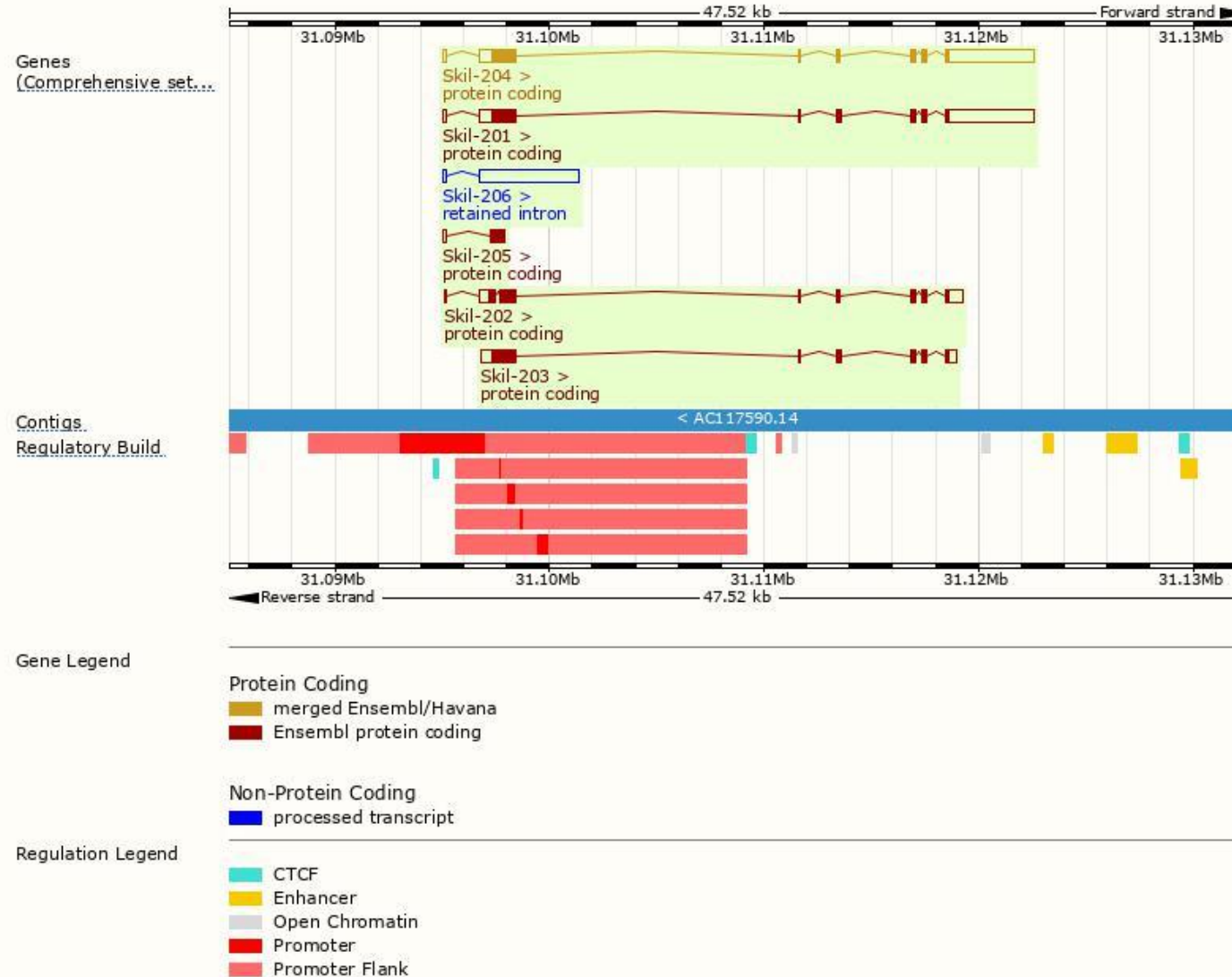
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|-------------------------------|---------------------------------|
| Skil-201 | ENSMUST00000029194.11 | 6717 | 675aa | Protein coding | CCDS38408 | Q60665 | TSL:5 GENCODE basic APPRIS P3 |
| Skil-204 | ENSMUST00000118470.7 | 6578 | 629aa | Protein coding | CCDS50886 | Q3TB81 Q60665 | TSL:1 GENCODE basic APPRIS ALT2 |
| Skil-203 | ENSMUST00000118204.1 | 2904 | 675aa | Protein coding | CCDS38408 | Q60665 | TSL:1 GENCODE basic APPRIS P3 |
| Skil-202 | ENSMUST00000117728.7 | 2899 | 549aa | Protein coding | CCDS71230 | D3Z7C5 | TSL:1 GENCODE basic APPRIS ALT2 |
| Skil-205 | ENSMUST00000123532.1 | 716 | 187aa | Protein coding | - | D3YYG2 | CDS 3' incomplete TSL:2 |
| Skil-206 | ENSMUST00000144756.7 | 4788 | No protein | Retained intron | - | - | TSL:1 |

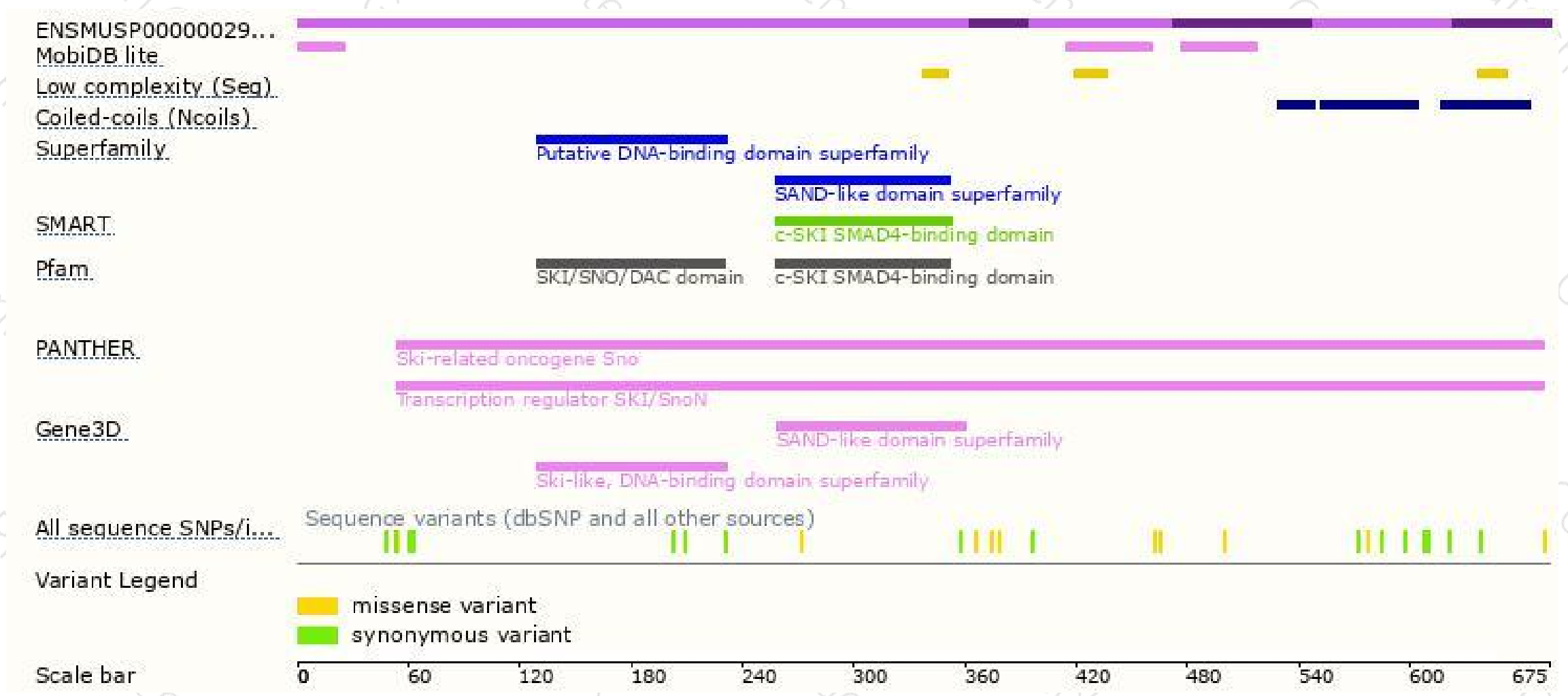
The strategy is based on the design of *Skil-201* transcript,The transcription is shown below



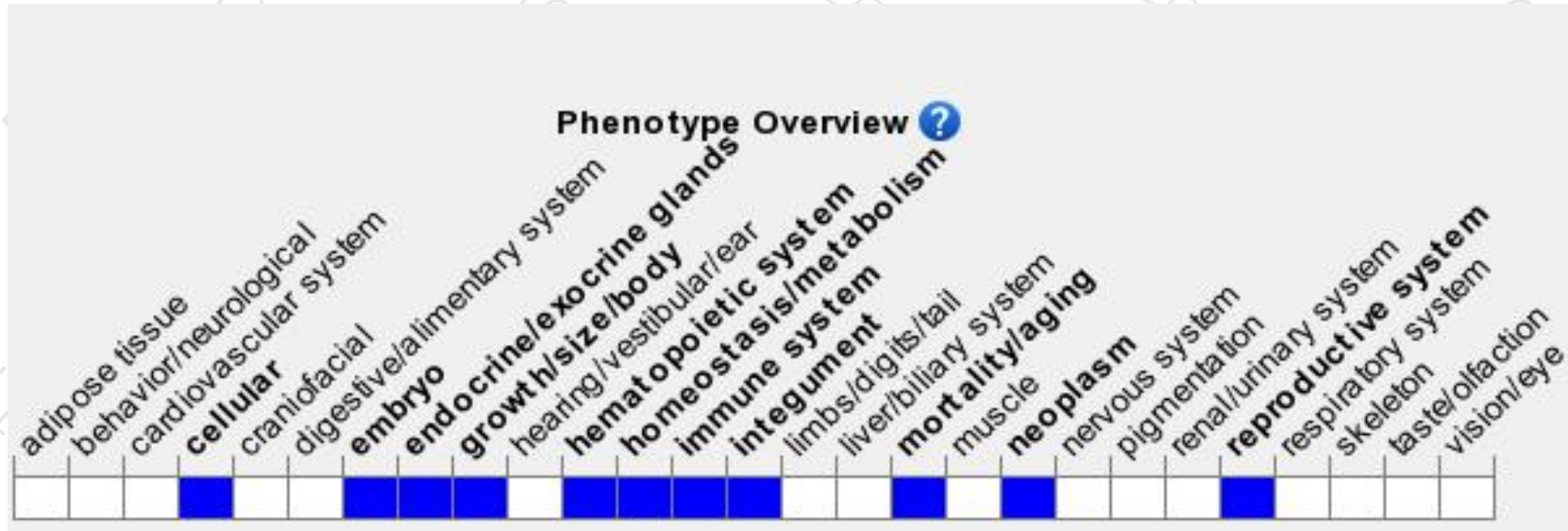
Genomic location distribution



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, Heterozygotes for a null allele develop lymphomas and show increased incidence of chemically-induced tumors while homozygotes die before implantation. Homozygotes for a different null allele are viable but show defective T cell activation and impaired mammary gland alveologenesis and lactogenesis.

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

