

***Rnf7* Cas9-CKO Strategy**

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Design Date: 2019-08-05

Project Overview

Project Name

Rnf7

Project type

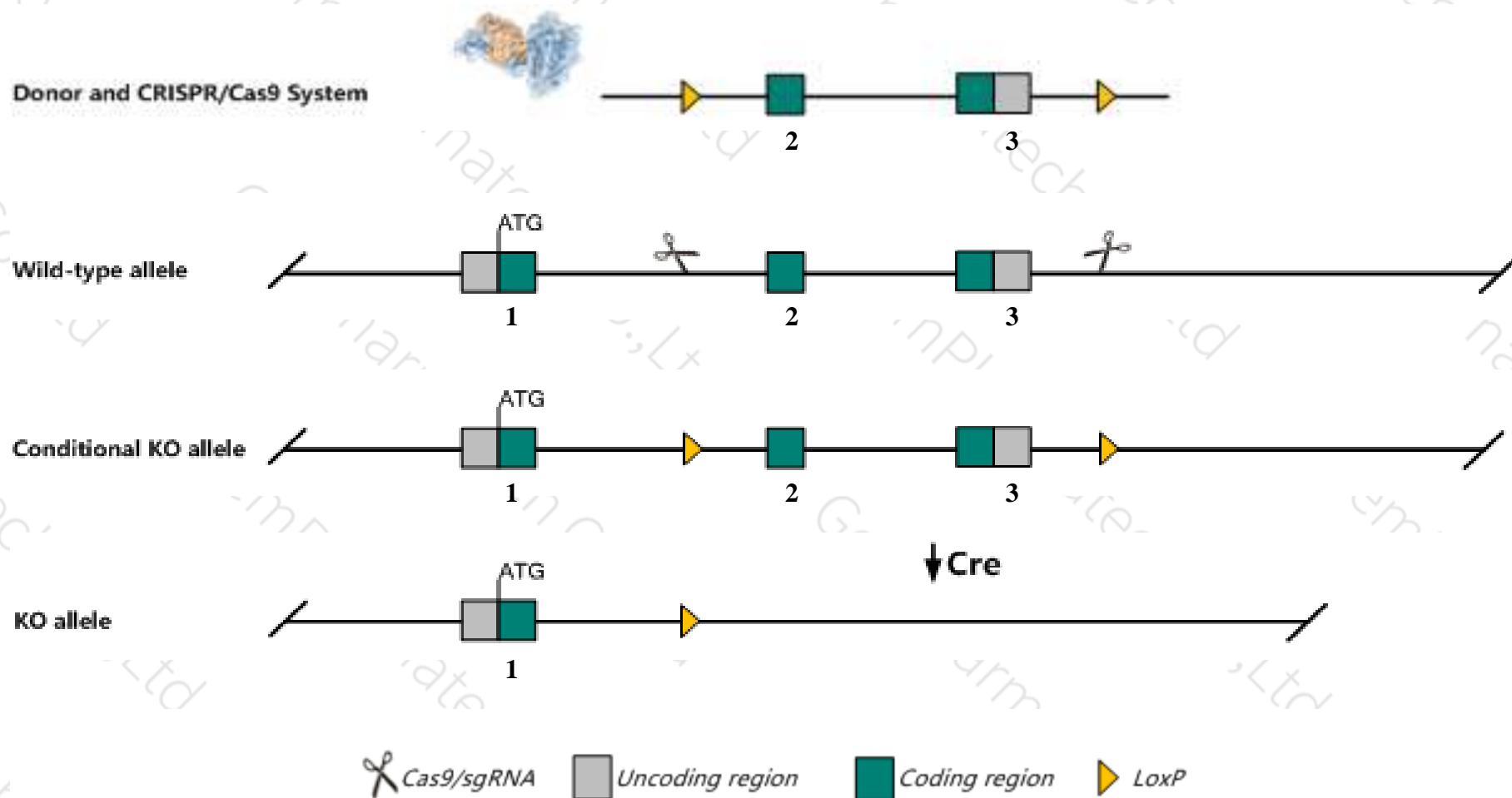
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf7* gene. The schematic diagram is as follows:



- The *Rnf7* gene has 3 transcripts. According to the structure of *Rnf7* gene, exon2-exon3 of *Rnf7*-201 (ENSMUST00000057500.5) transcript is recommended as the knockout region. The region contains 167bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnf7* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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, Mice homozygous for a null mutation display complete embryonic lethality during organogenesis with defects in angiogenesis, widespread apoptosis, impaired cell cycle progression of neuronal precursors and embryonic growth retardation.
- The *Rnf7* gene is located on the Chr9. 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)

Rnf7 ring finger protein 7 [Mus musculus (house mouse)]

Gene ID: 19823, updated on 31-Jan-2019

Summary



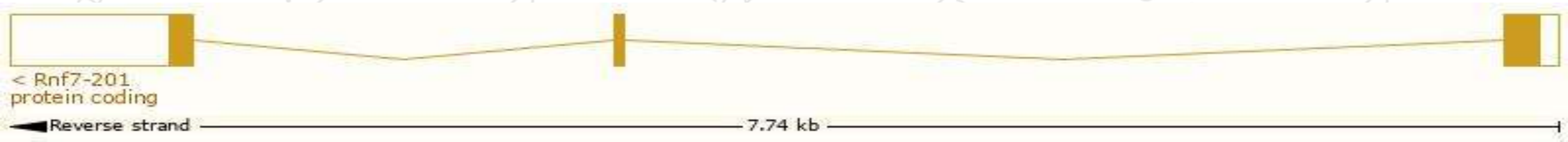
| | |
|---------------------------|---|
| Official Symbol | Rnf7 provided by MGI |
| Official Full Name | ring finger protein 7 provided by MGI |
| Primary source | MGI:MGI:1337096 |
| See related | Ensembl:ENSMUSG00000051234 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | Rbx2, SAG |
| Expression | Ubiquitous expression in CNS E11.5 (RPKM 73.0), CNS E14 (RPKM 56.6) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

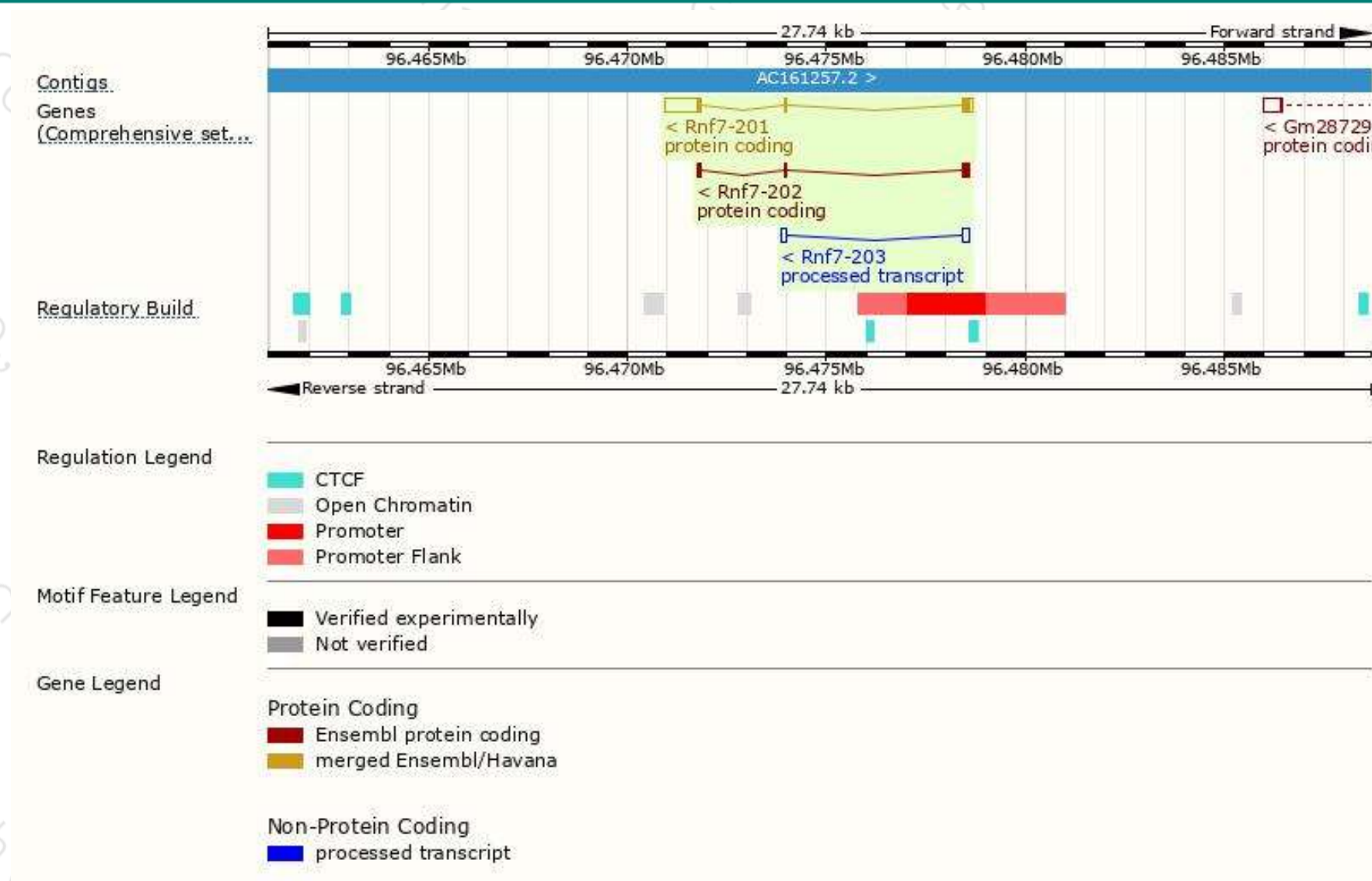
The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|-----------------------|----------------------|---------------------------|------------------------|-------------------------------|
| Rnf7-201 | ENSMUST00000057500.5 | 1232 | 113aa | Protein coding | CCDS40730 | Q9WTZ1 | TSL:1 GENCODE basic APPRIS P1 |
| Rnf7-202 | ENSMUST00000071301.4 | 334 | 90aa | Protein coding | CCDS81056 | D3Z392 | TSL:2 GENCODE basic |
| Rnf7-203 | ENSMUST00000128955.1 | 325 | No protein | Processed transcript | - | - | TSL:2 |

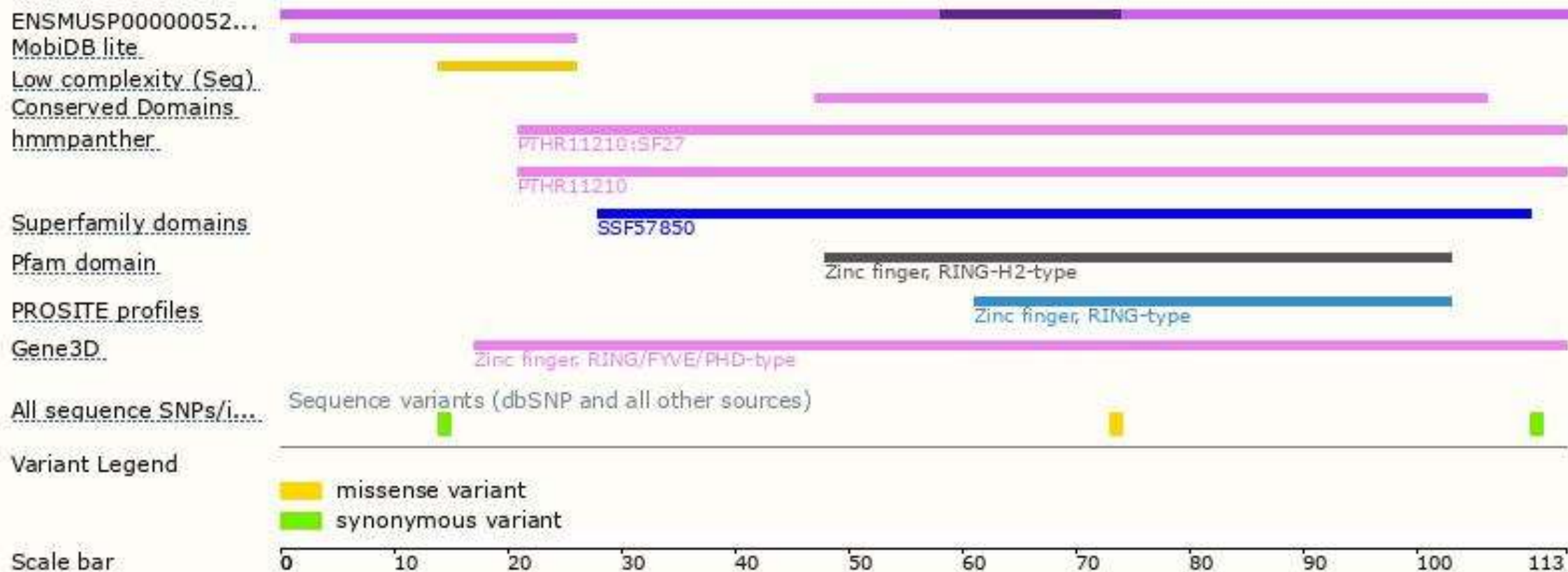
The strategy is based on the design of *Rnf7-201* transcript,The transcription is shown below



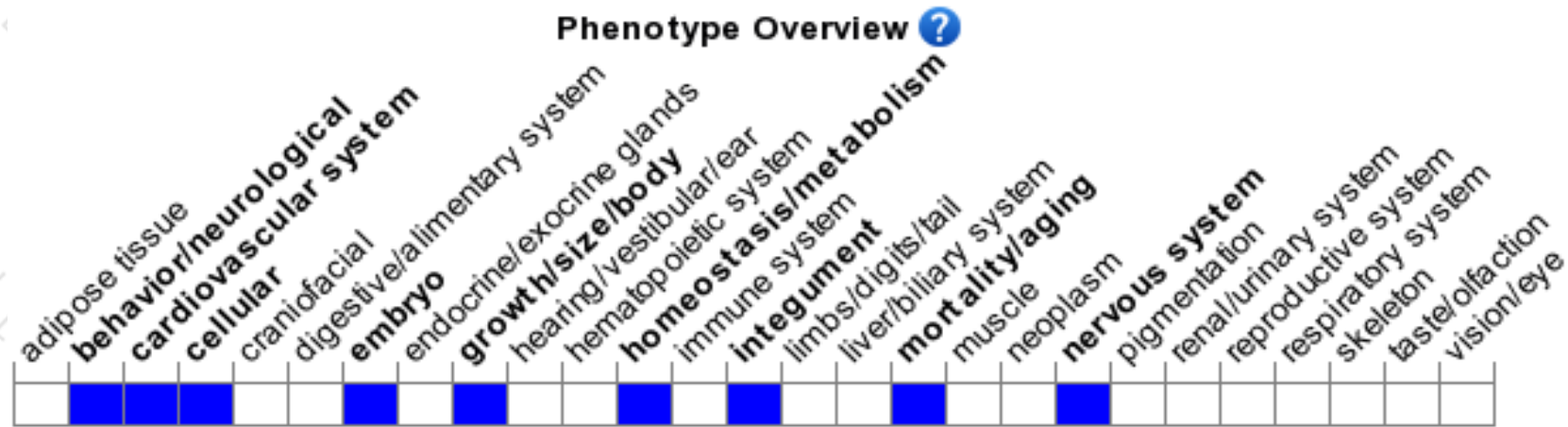
Genomic location distribution



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, Mice homozygous for a null mutation display complete embryonic lethality during organogenesis with defects in angiogenesis, widespread apoptosis, impaired cell cycle progression of neuronal precursors and embryonic growth retardation.

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

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