

***Kbtbd13* Cas9-CKO Strategy**

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Design Date: 2021-3-8

Project Overview

Project Name

Kbtbd13

Project type

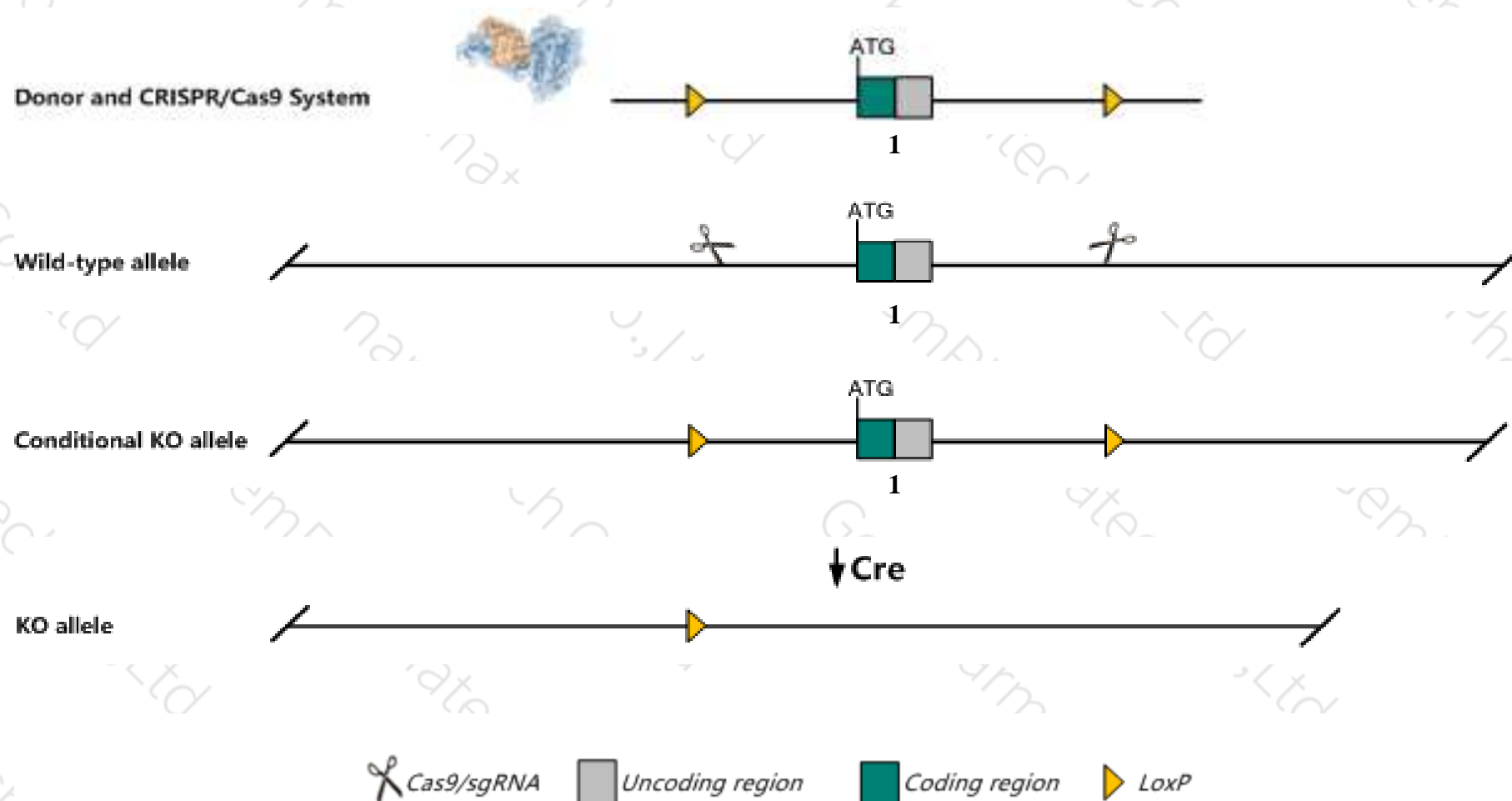
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kbtbd13* gene. The schematic diagram is as follows:



Technical routes

- The *Kbtbd13* gene has 1 transcript. According to the structure of *Kbtbd13* gene, exon1 of *Kbtbd13*-201(ENSMUST00000068307.3) 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 *Kbtbd13* 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.

- The *Kbtbd13* 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)

Kbtbd13 kelch repeat and BTB (POZ) domain containing 13 [*Mus musculus* (house mouse)]

Gene ID: 74492, updated on 22-Nov-2020

Summary



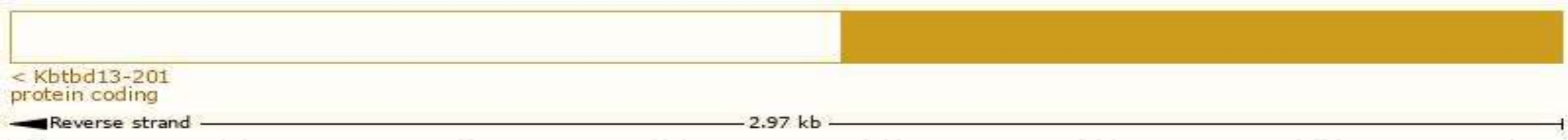
| | |
|--------------------|---|
| Official Symbol | Kbtbd13 provided by MGI |
| Official Full Name | kelch repeat and BTB (POZ) domain containing 13 provided by MGI |
| Primary source | MGI:MGI:1921742 |
| See related | Ensembl:ENSMUSG00000054978 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 5430433E21Rik |
| Orthologs | human all |

Transcript information (Ensembl)

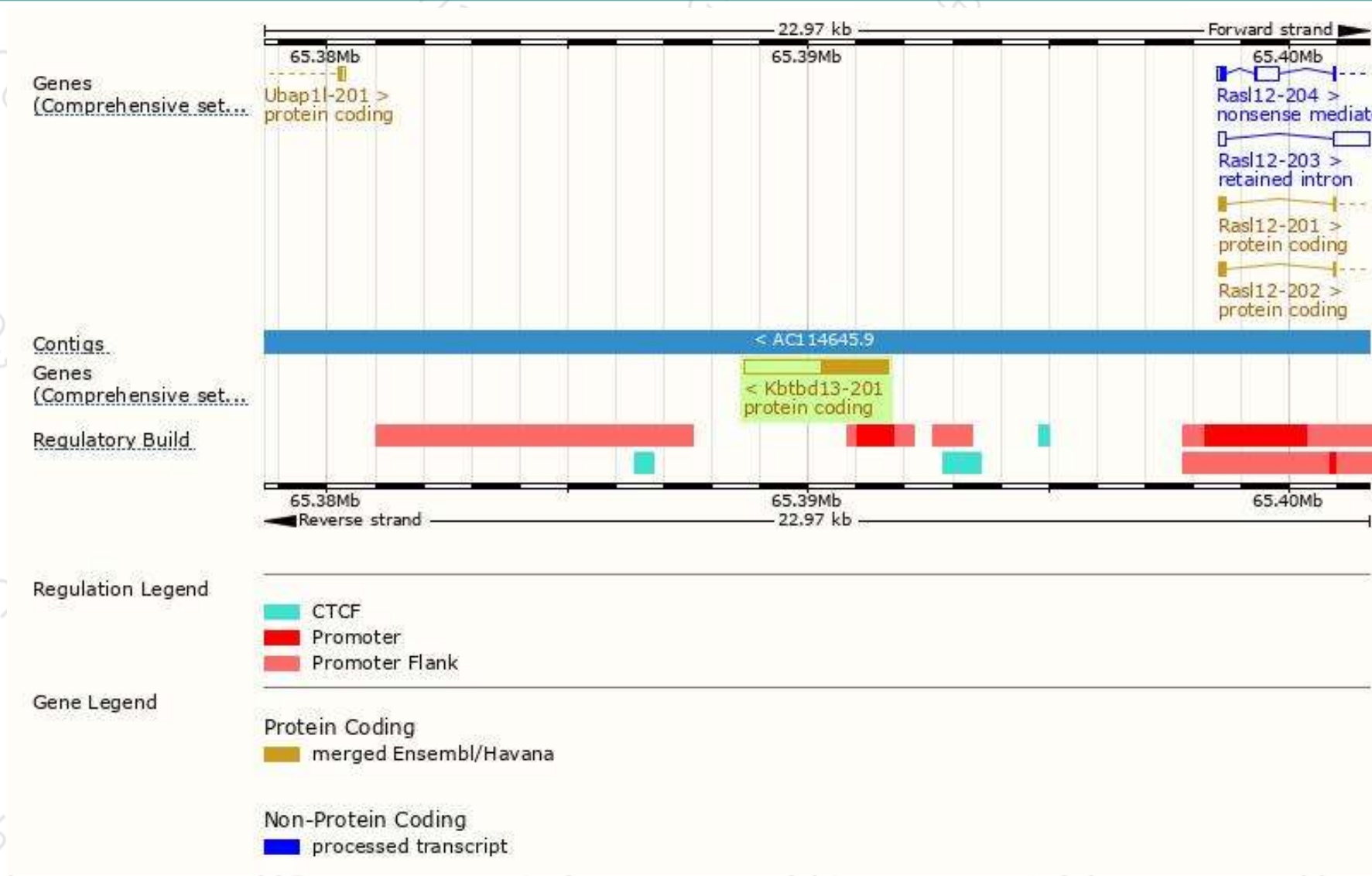
The gene has 1 transcript, and the transcript is shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|--------------------------------------|------|-----------------------|----------------|----------------------------|------------------------|--------------------------------|
| Kbtbd13-201 | ENSMUST00000068307.3 | 2969 | 458aa | Protein coding | CCDS557682 | Q8C828 | TSL:NA GENCODE basic APPRIS P1 |

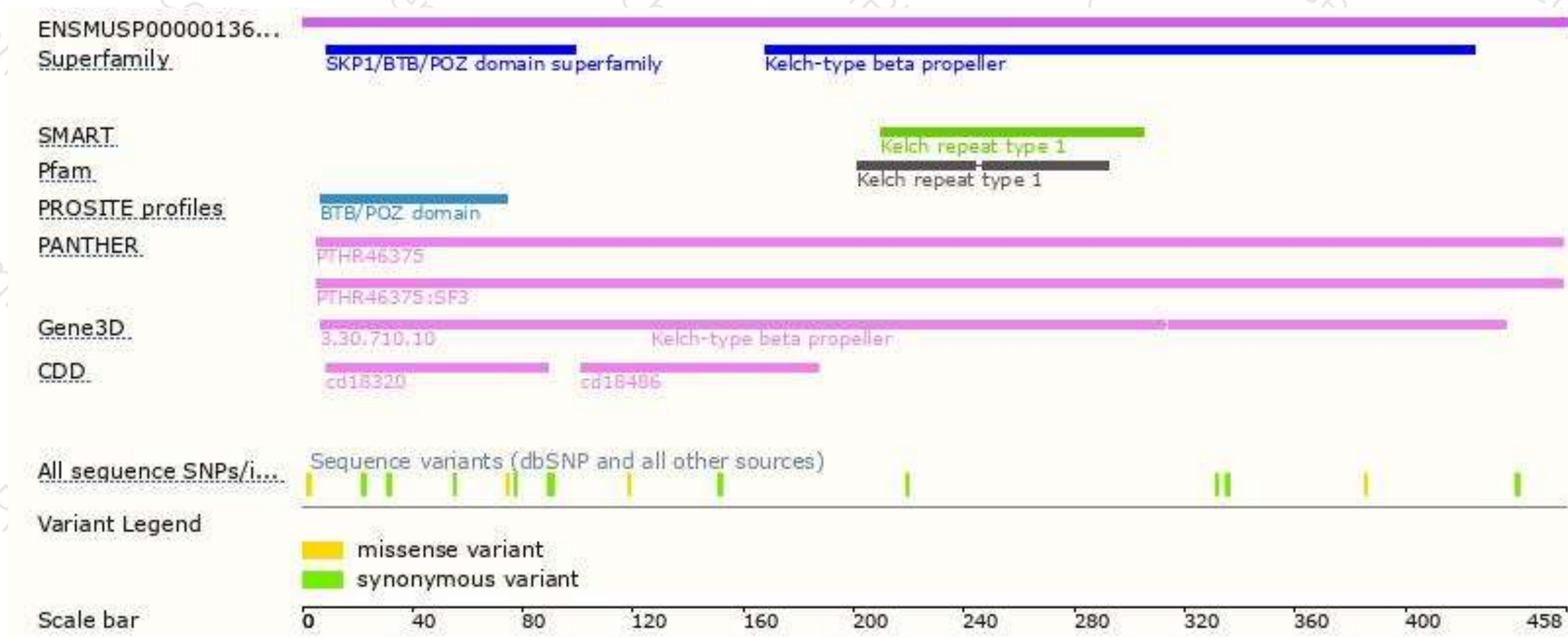
The strategy is based on the design of *Kbtbd13-201* transcript, the transcription is shown below:



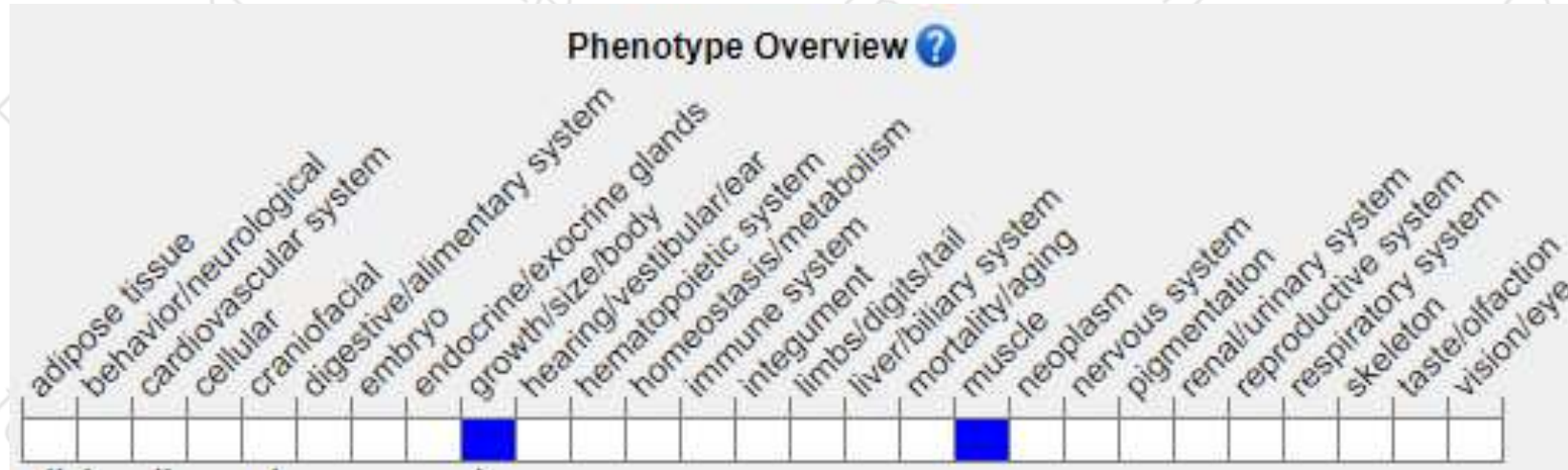
Genomic location distribution



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/>).

Homozygosity for a specific point mutation increases muscle weight and slows muscle relaxation kinetics.

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

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