

Egflam Cas9-KO Strategy

Designer:

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Design Date:

2019-7-18

Project Overview

Project Name

Egflam

Project type

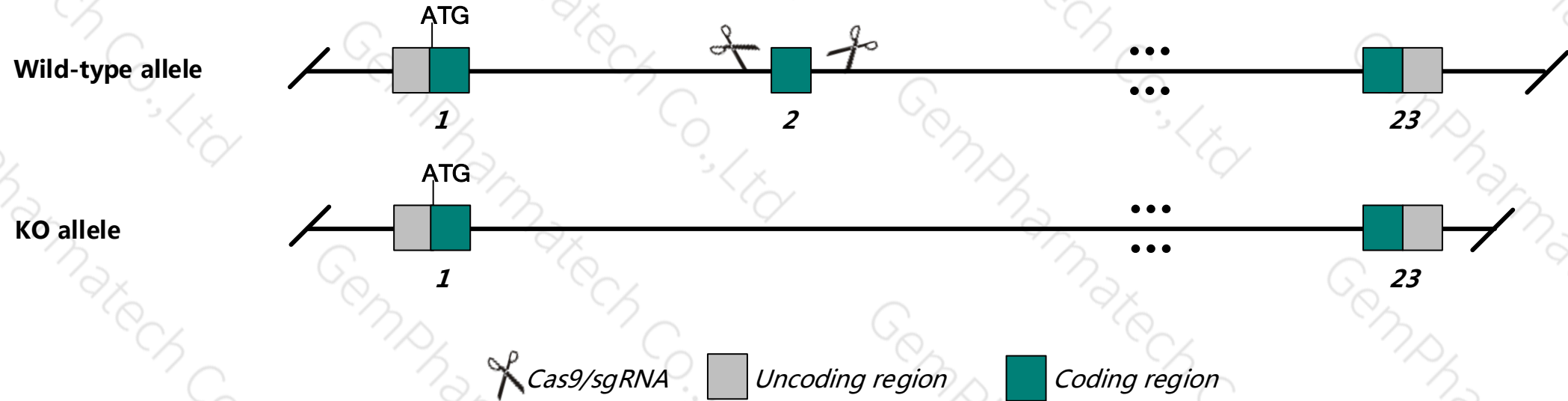
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



Technical routes

- The *Egflam* gene has 7 transcripts. According to the structure of *Egflam* gene, exon2 of *Egflam*-202 (ENSMUST00000096494.4) transcript is recommended as the knockout region. The region contains 110bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Egflam* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA 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.

- According to the existing MGI data , Homozygous null mutants are viable and fertile under normal conditions. They exhibit abnormal photoreceptor ribbon synapses, resulting in alteration in synaptic signal transmission and visual function.
- The *Egflam* gene is located on the Chr15. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Egflam EGF-like, fibronectin type III and laminin G domains [*Mus musculus* (house mouse)]

Gene ID: 268780, updated on 22-May-2018

Summary

Official Symbol Egflam provided by [MGI](#)

Official Full Name EGF-like, fibronectin type III and laminin G domains provided by [MGI](#)

Primary source [MGI:MGI:2146149](#)

See related [Ensembl:ENSMUSG000000042961](#) [Vega:OTTMUSG000000029264](#)

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 AU040377; 5930412K08

Expression Broad expression in lung adult (RPKM 9.0), ovary adult (RPKM 6.9) and 16 other tissues [See more](#)

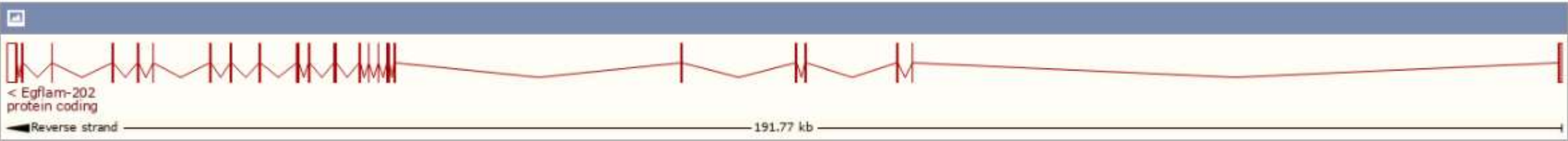
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

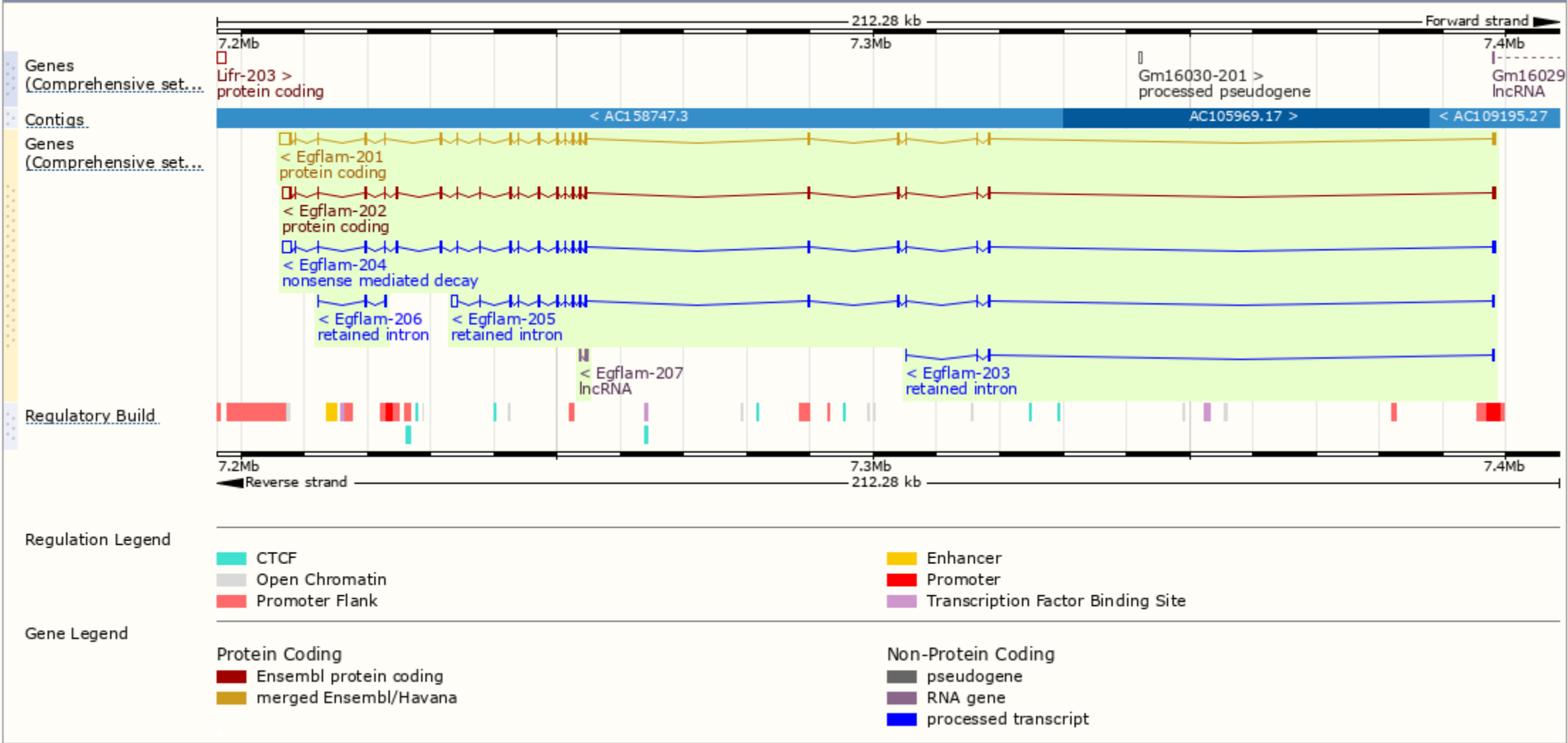
The gene has 7 transcripts, and all transcripts are shown below:

| Show/hide columns (1 hidden) | | | | | | | Filter | |
|------------------------------|--------------------------------------|------|------------------------|-------------------------|---------------------------|------------------------|--------|---------------------------|
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags | |
| Egflam-201 | ENSMUST00000058593.9 | 4778 | 1009aa | Protein coding | CCDS27370 | Q4VBE4 | TSL:1 | GENCODE basic APPRIS P3 |
| Egflam-202 | ENSMUST00000096494.4 | 4391 | 1017aa | Protein coding | CCDS79359 | Q4VBE4 | TSL:1 | GENCODE basic APPRIS ALT2 |
| Egflam-204 | ENSMUST00000160207.7 | 4420 | 37aa | Nonsense mediated decay | - | E0CXM4 | TSL:1 | |
| Egflam-205 | ENSMUST00000160273.7 | 3327 | No protein | Retained intron | - | - | TSL:1 | |
| Egflam-203 | ENSMUST00000159726.1 | 618 | No protein | Retained intron | - | - | TSL:2 | |
| Egflam-206 | ENSMUST00000160314.1 | 490 | No protein | Retained intron | - | - | TSL:5 | |
| Egflam-207 | ENSMUST00000162105.1 | 446 | No protein | lncRNA | - | - | TSL:3 | |

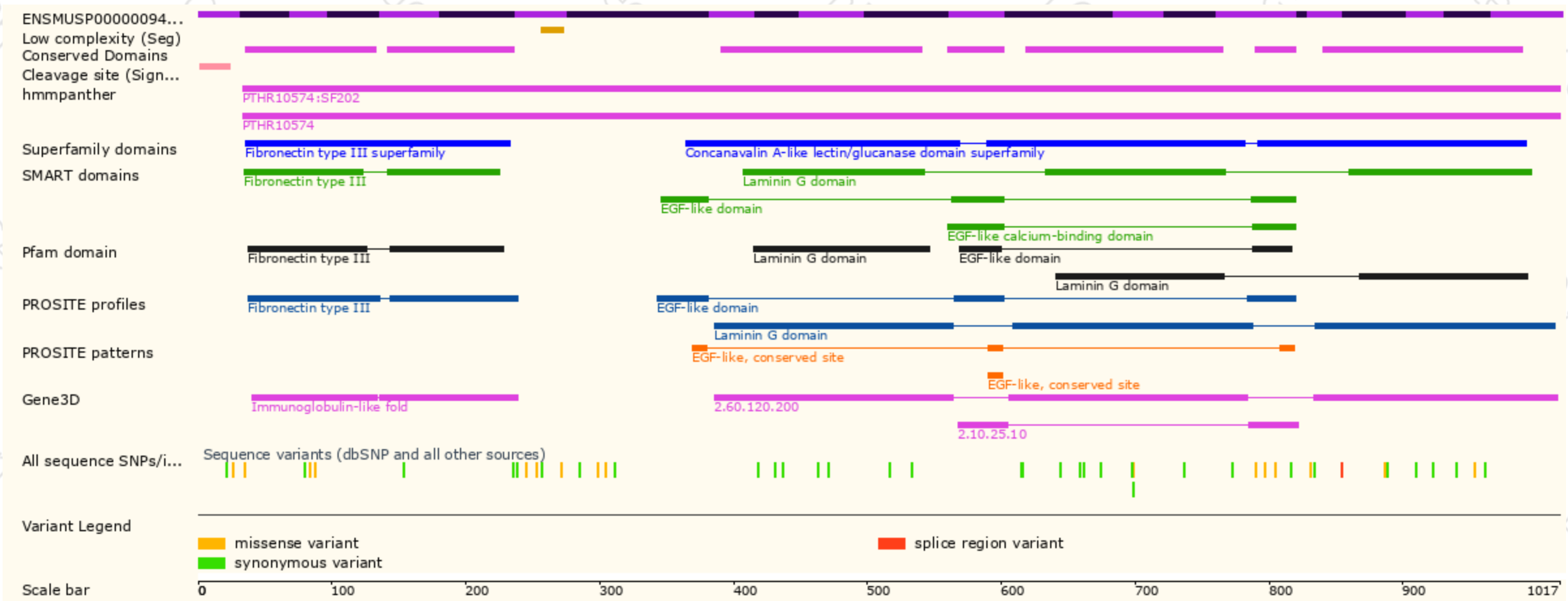
The strategy is based on the design of *Egflam-202* transcript,The transcription is shown below



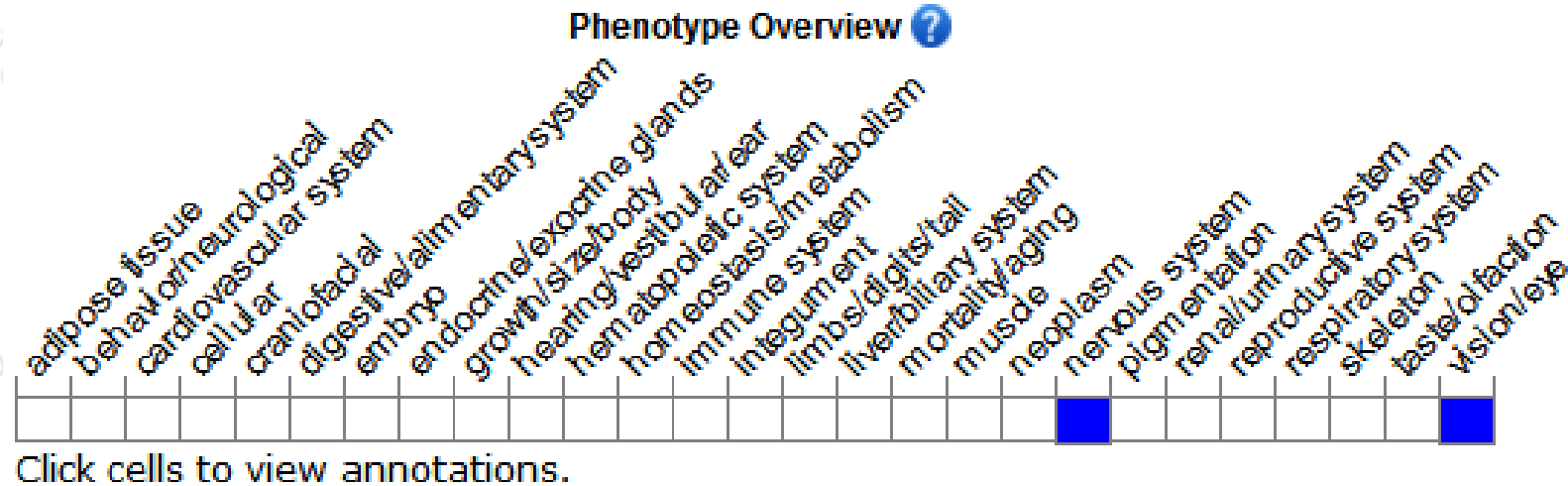
Genomic location distribution



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, Homozygous null mutants are viable and fertile under normal conditions. They exhibit abnormal photoreceptor ribbon synapses, resulting in alteration in synaptic signal transmission and visual function.

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