# *Efnb1* Cas9-KO Strategy

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**Reviewer: Daohua Xu**

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# Project Overview

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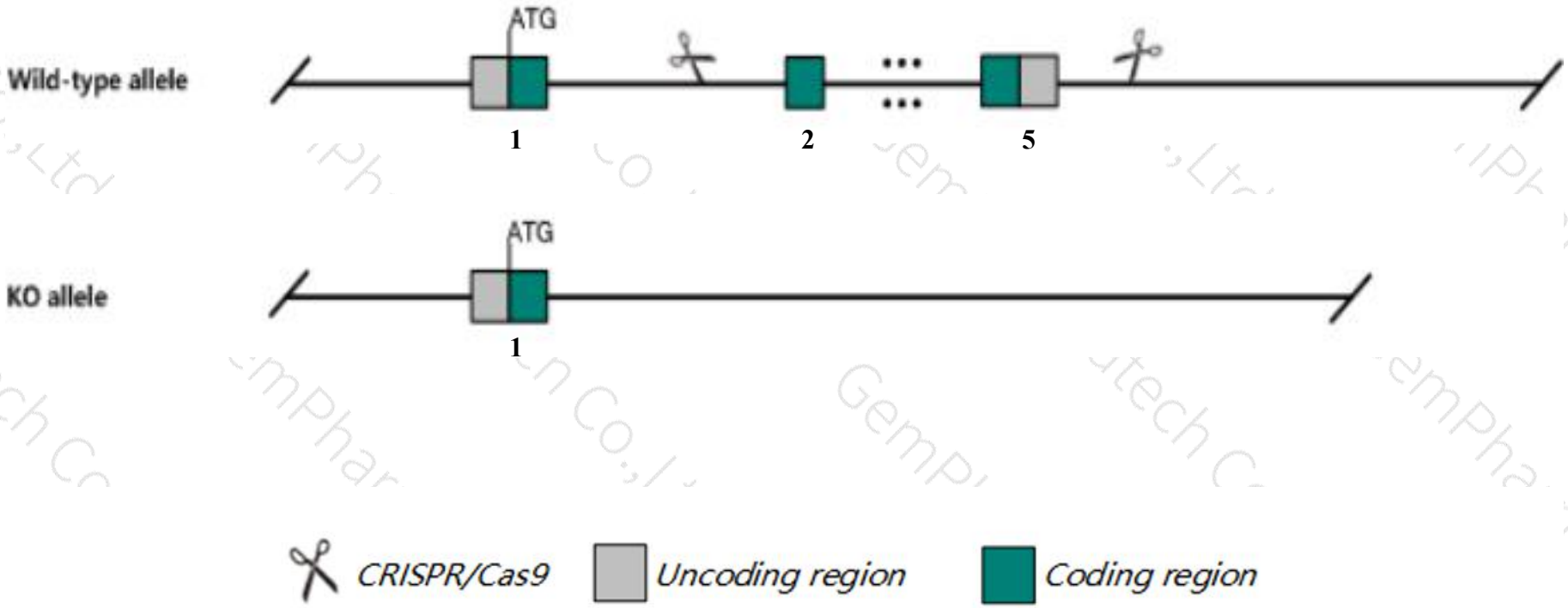
|---|---|
| **Project Name** | ***Efnb1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Efnb1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Efnb1* gene has 2 transcripts. According to the structure of *Efnb1* gene, exon2-exon5 of *Efnb1-201* (ENSMUST00000052839.6) transcript is recommended as the knockout region.The region contains most 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 *Efnb1* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- According to the existing MGI data,engineered alleles of this gene produce cranialfacial defects resulting in neonatal lethality.
- The *Efnb1* gene is located on the ChrX. 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）

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## Efnb1 ephrin B1 [Mus musculus (house mouse)]

Gene ID: 13641, updated on 13-Mar-2020

### Summary

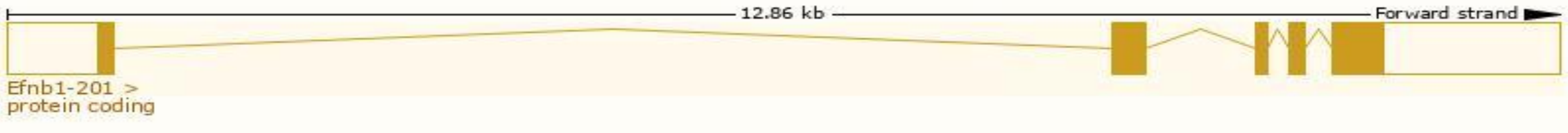
| | |
|---|---|
| **Official Symbol** | Efnb1 provided by MGI |
| **Official Full Name** | ephrin B1 provided by MGI |
| **Primary source** | MGI:MGI:102708 |
| **See related** | Ensembl:ENSMUSG00000031217 |
| **Gene type** | protein coding |
| **RefSeq status** | REVIEWED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | Cek5-L, EFL-3, Elk-L, Epl2, Eplg2, LERK-2, Lerk2, Stra1 |
| **Summary** | This gene encodes a membrane protein that acts as a ligand for Eph family receptors. Signalling occurs bidirectionally in both the cell containing the receptor and the cell expressing this protein. Activity of this protein is important in neuronal axon growth and other developmental processes. [provided by RefSeq, May 2015] |
| **Expression** | Ubiquitous expression in lung adult (RPKM 47.3), colon adult (RPKM 44.5) and 26 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

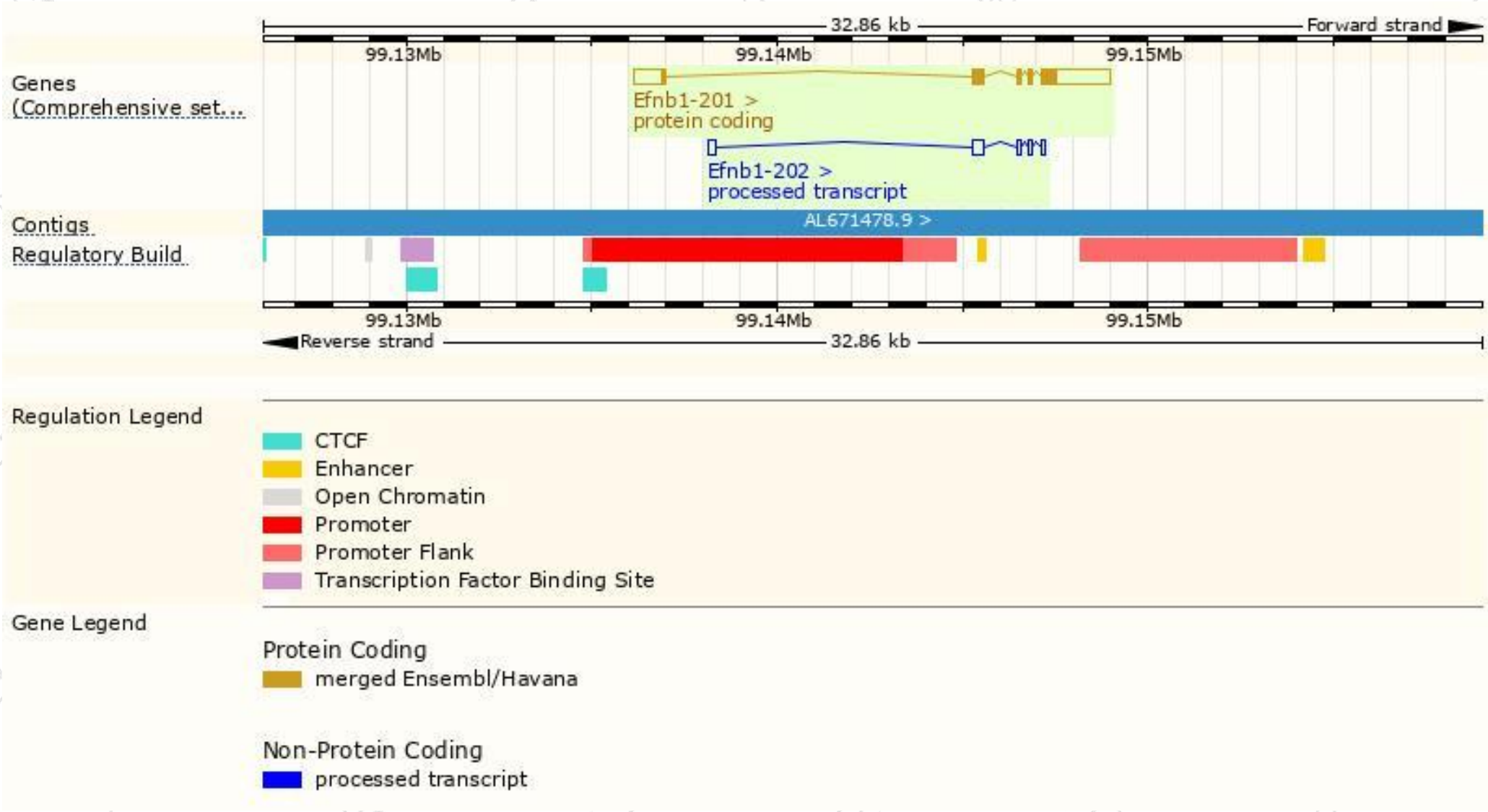
The gene has 2 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Efnb1-201 | ENSMUST00000052839.6 | 3258 | 345aa | Protein coding | CCDS30298 | P52795 Q544L9 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Efnb1-202 | ENSMUST00000151750.1 | 807 | No protein | Processed transcript | - | - | TSL:3 |

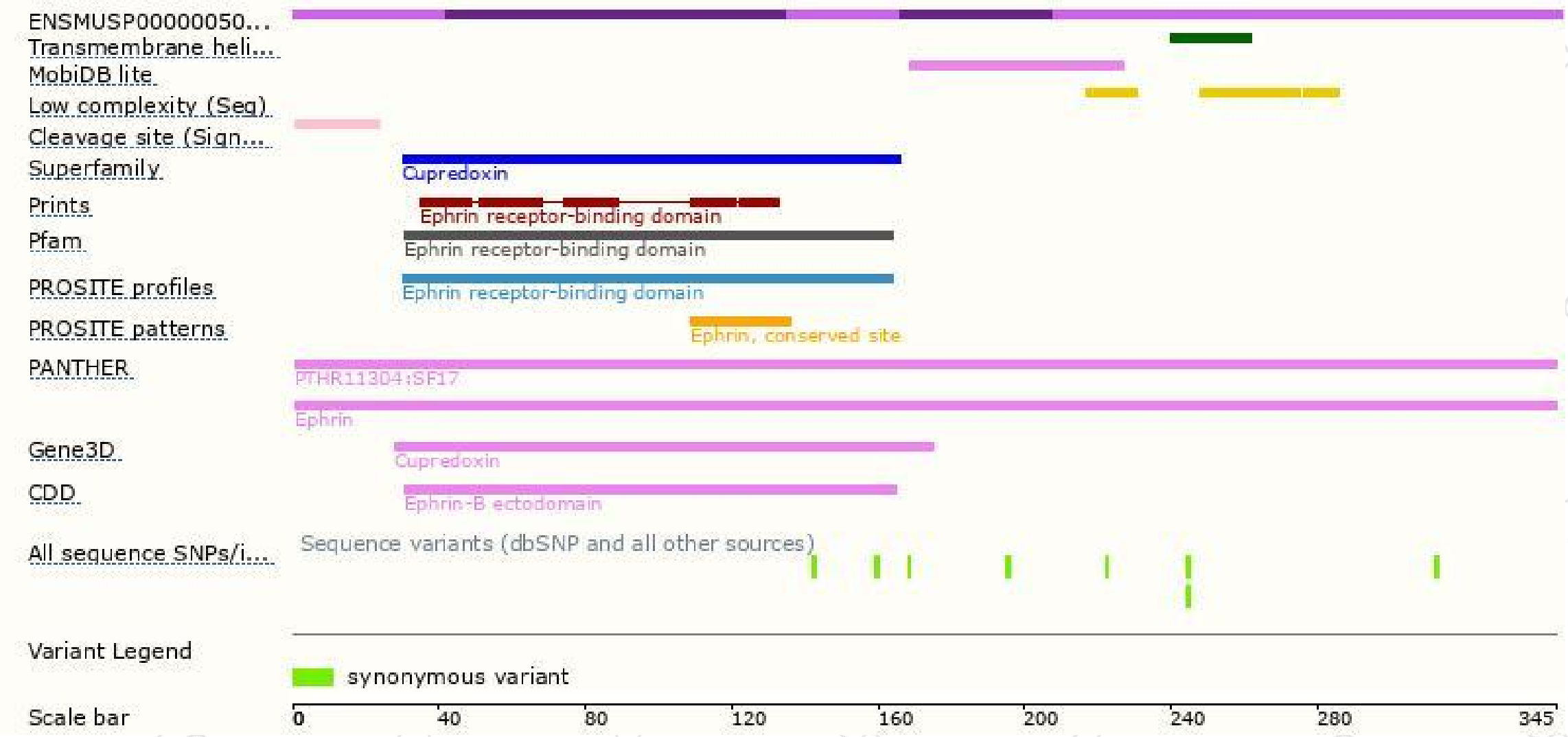
The strategy is based on the design of *Efnb1-201* transcript,the transcription is shown below:



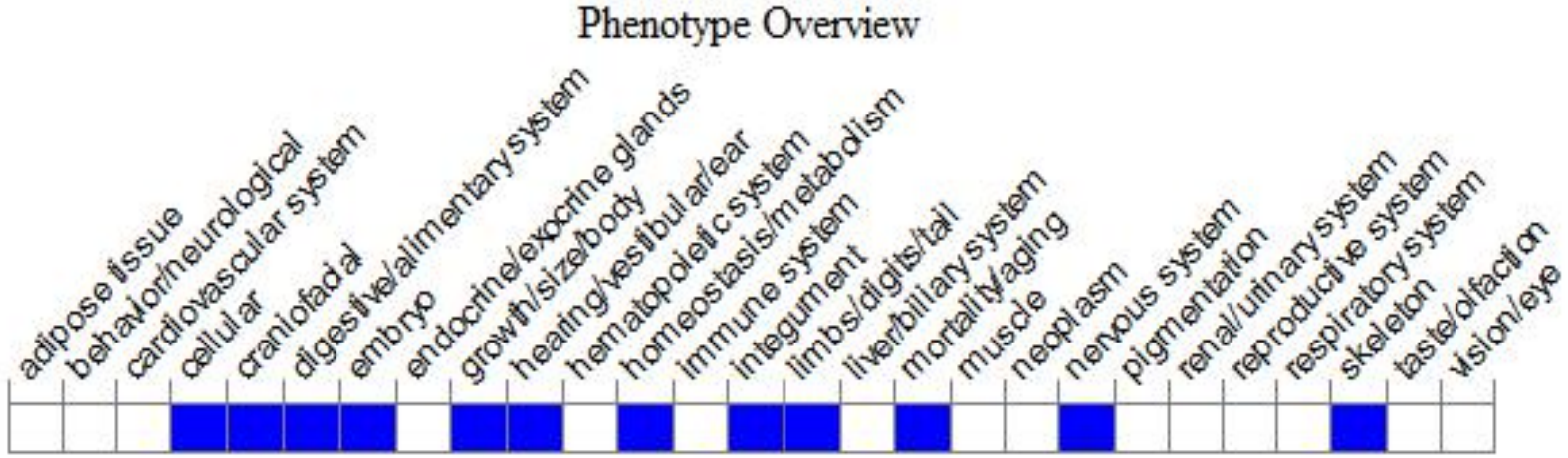
# Genomic location distribution



# 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/).*

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

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