

# ***Paics*** Cas9-KO Strategy

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# Project Overview

**Project Name**

*Paics*

**Project type**

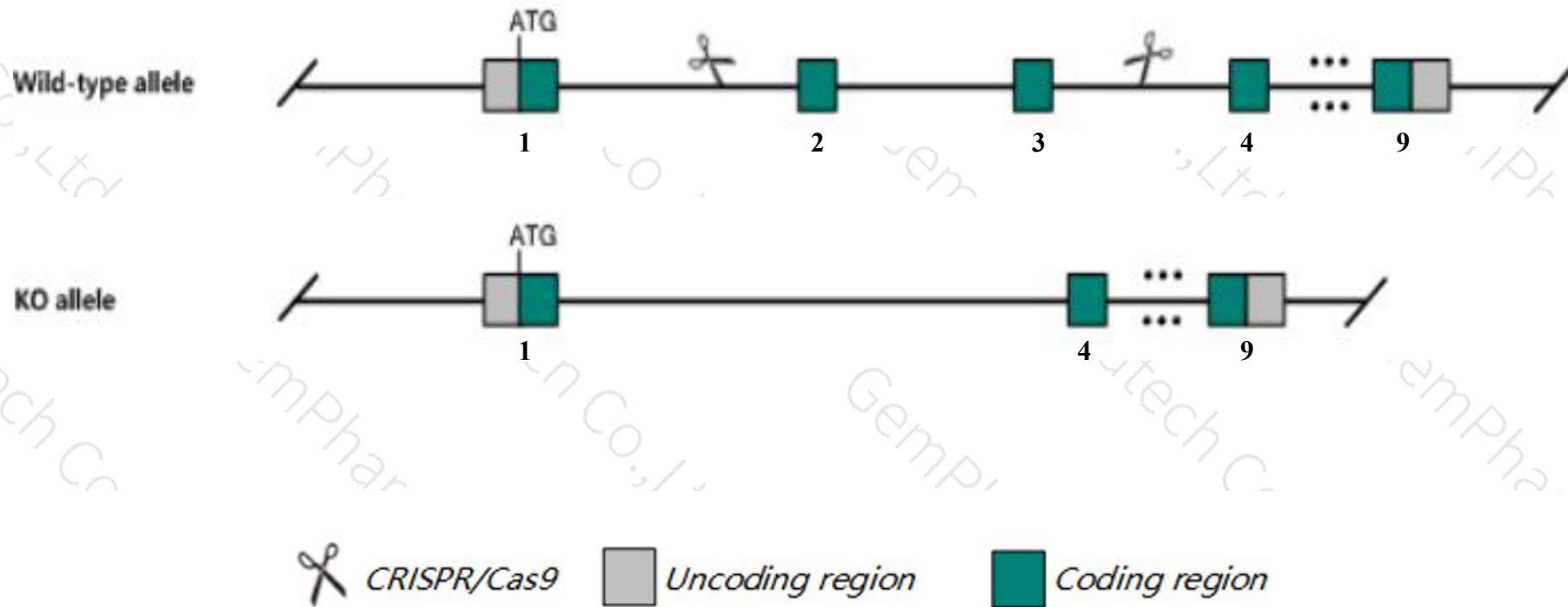
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Paics* gene has 7 transcripts. According to the structure of *Paics* gene, exon2-exon3 of *Paics*-201 (ENSMUST00000031160.15) transcript is recommended as the knockout region. The region contains 377bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Paics* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Paics* gene is located on the Chr5. 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)

## Paics phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase [Mus musculus (house mouse)]

Gene ID: 67054, updated on 13-Mar-2020

### Summary



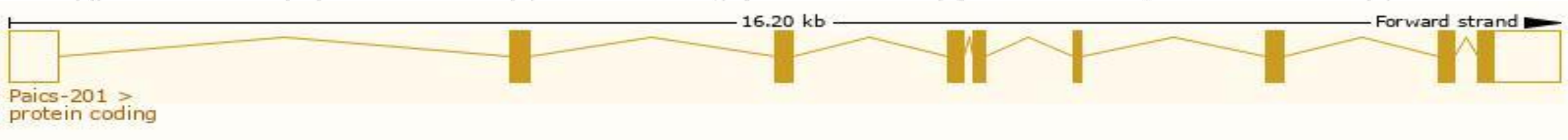
|                           |                                                                                                                                                                           |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Official Symbol</b>    | Paics provided by <a href="#">MGI</a>                                                                                                                                     |
| <b>Official Full Name</b> | phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase provided by <a href="#">MGI</a>                         |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1914304</a>                                                                                                                                           |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000029247</a>                                                                                                                                |
| <b>Gene type</b>          | protein coding                                                                                                                                                            |
| <b>RefSeq status</b>      | VALIDATED                                                                                                                                                                 |
| <b>Organism</b>           | <a href="#">Mus musculus</a>                                                                                                                                              |
| <b>Lineage</b>            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| <b>Also known as</b>      | 2610511I09Rik, ADE2H1, AIRC, PAIS                                                                                                                                         |
| <b>Expression</b>         | Ubiquitous expression in CNS E11.5 (RPKM 67.7), placenta adult (RPKM 55.6) and 26 other tissues <a href="#">See more</a>                                                  |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information（Ensembl）

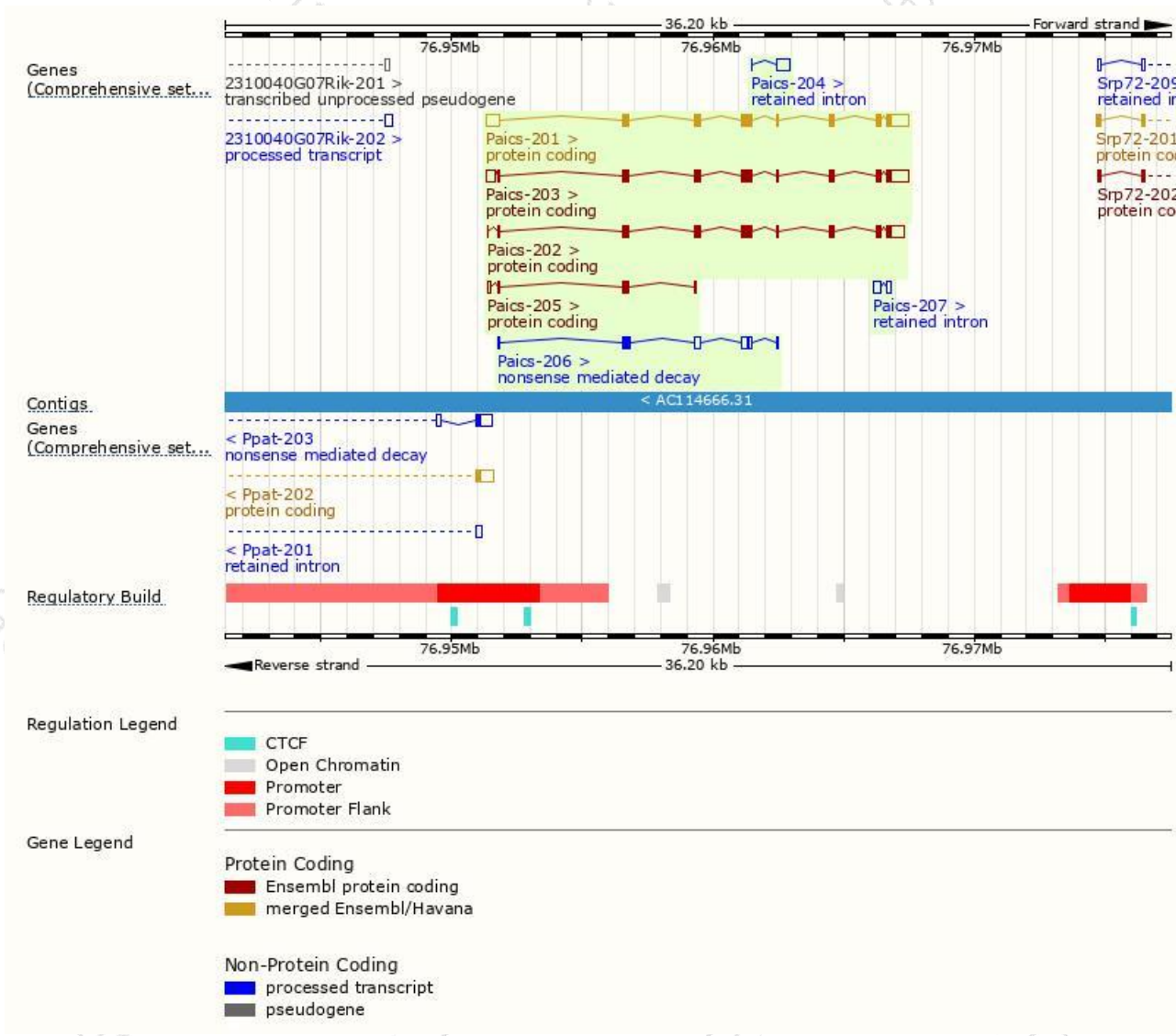
The gene has 7 transcripts,all transcripts are shown below:

| Name      | Transcript ID                         | bp   | Protein               | Biotype                 | CCDS                      | UniProt                | Flags                                                                                                                                                                                                         |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Paics-201 | <a href="#">ENSMUST00000031160.15</a> | 2482 | <a href="#">425aa</a> | Protein coding          | <a href="#">CCDS19367</a> | <a href="#">Q9DCL9</a> | 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 |
| Paics-203 | <a href="#">ENSMUST00000120912.7</a>  | 2345 | <a href="#">425aa</a> | Protein coding          | <a href="#">CCDS19367</a> | <a href="#">Q9DCL9</a> | 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 |
| Paics-202 | <a href="#">ENSMUST00000117536.7</a>  | 1862 | <a href="#">425aa</a> | Protein coding          | <a href="#">CCDS19367</a> | <a href="#">Q9DCL9</a> | TSL:5 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 |
| Paics-205 | <a href="#">ENSMUST00000141687.1</a>  | 422  | <a href="#">83aa</a>  | Protein coding          | -                         | <a href="#">D3Z6P1</a> | CDS 3' incomplete TSL:5                                                                                                                                                                                       |
| Paics-206 | <a href="#">ENSMUST00000153648.1</a>  | 886  | <a href="#">103aa</a> | Nonsense mediated decay | -                         | <a href="#">D6RCU8</a> | TSL:5                                                                                                                                                                                                         |
| Paics-204 | <a href="#">ENSMUST00000140051.1</a>  | 575  | No protein            | Retained intron         | -                         | -                      | TSL:5                                                                                                                                                                                                         |
| Paics-207 | <a href="#">ENSMUST00000154688.1</a>  | 443  | No protein            | Retained intron         | -                         | -                      | TSL:2                                                                                                                                                                                                         |

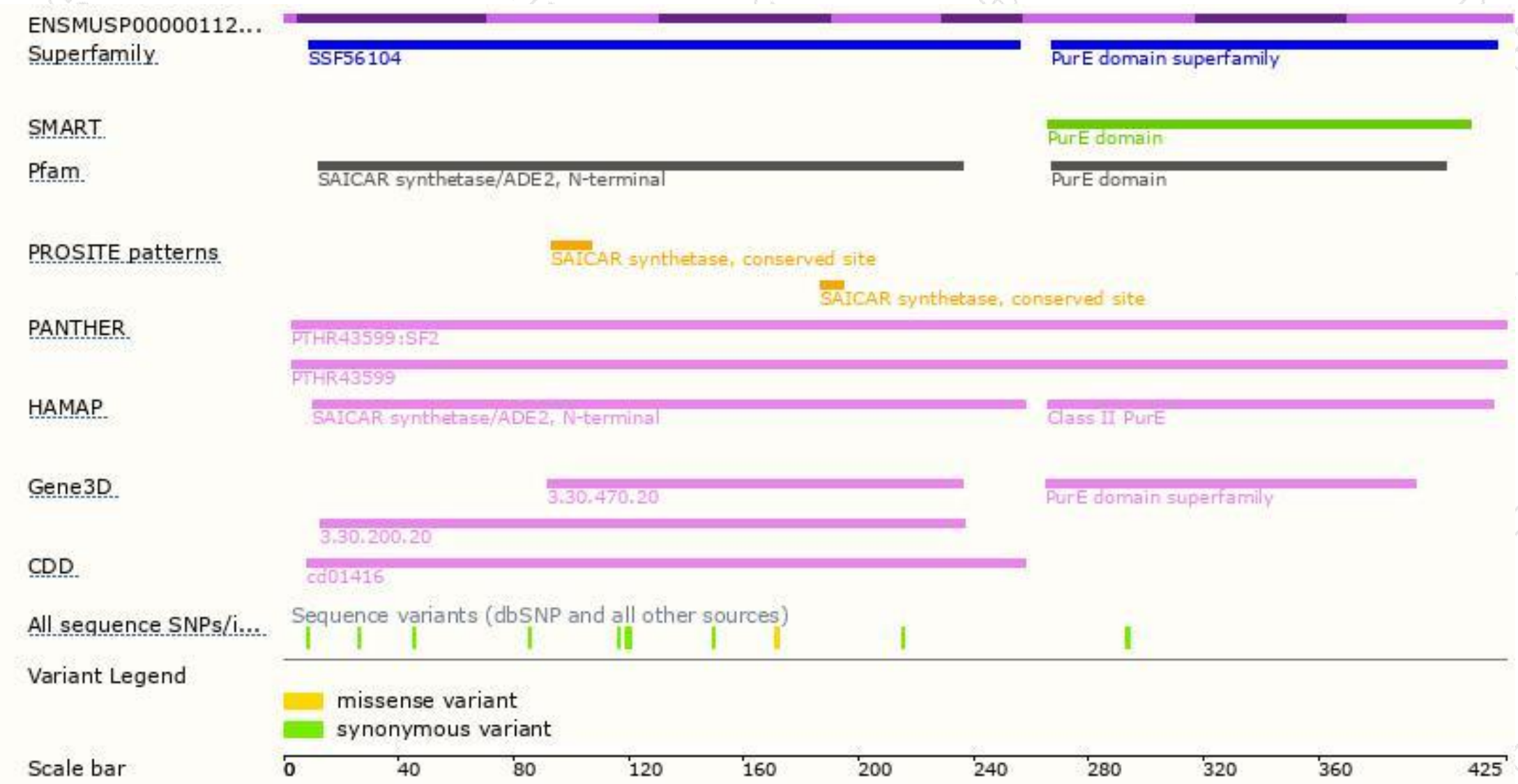
The strategy is based on the design of *Paics-201* transcript,the transcription is shown below:



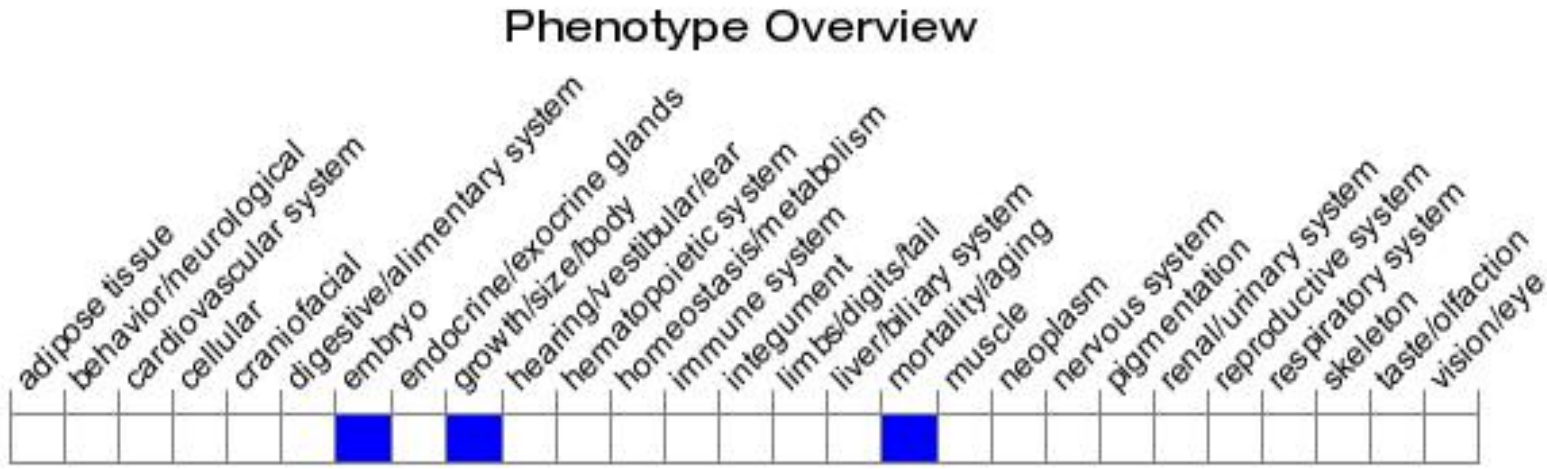
# Genomic location distribution



# 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/>).*

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

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