

# *Ltbp3* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Ltbp3*

**Project type**

**Cas9-CKO**

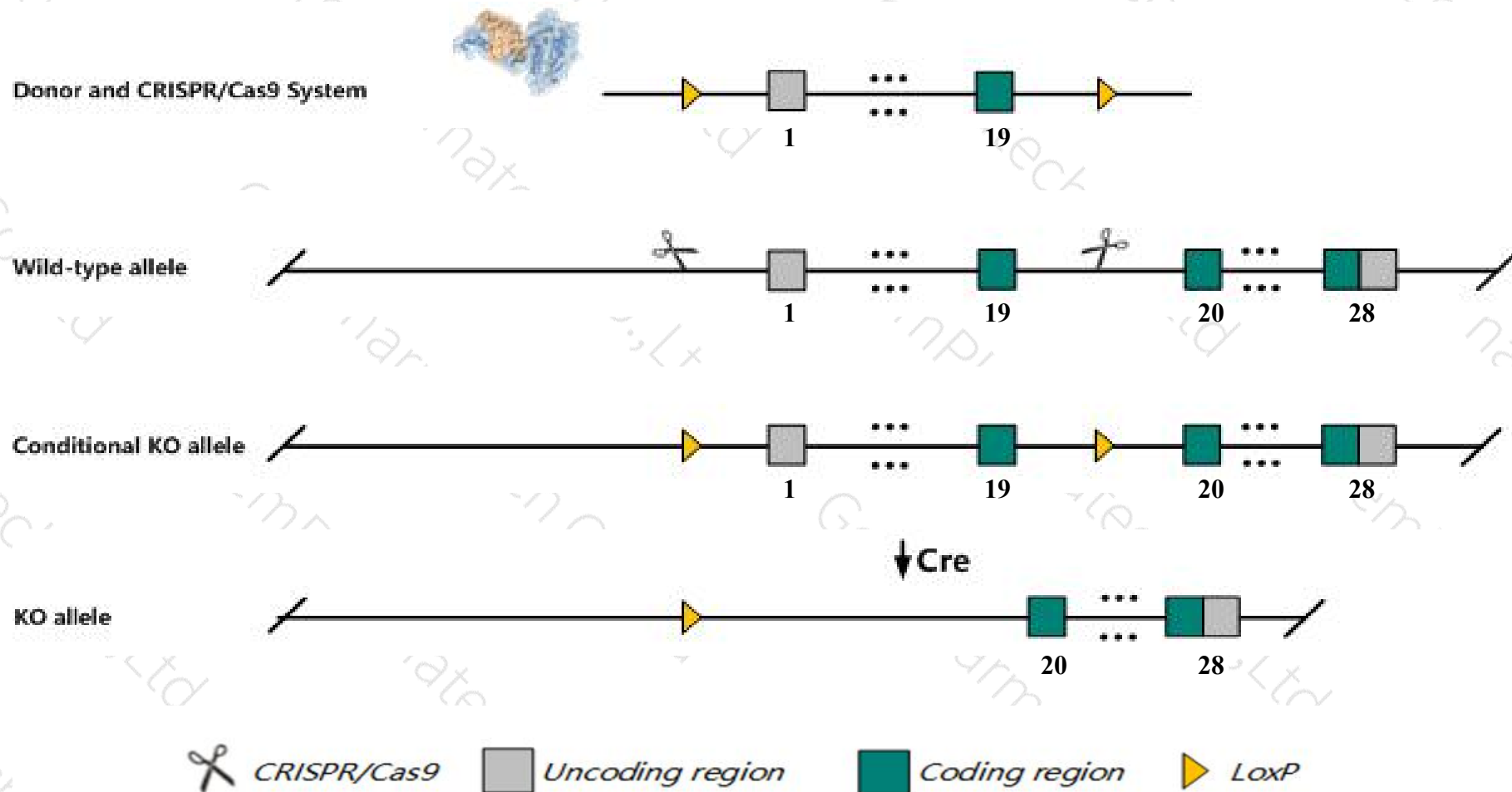
**Strain background**

**C57BL/6JGpt**



# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ltbp3* gene. The schematic diagram is as follows:





- The *Ltbp3* gene has 12 transcripts. According to the structure of *Ltbp3* gene, exon1-exon19 of *Ltbp3-201* (ENSMUST00000081496.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ltbp3* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be 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, Homozygotes for a targeted null mutation exhibit craniofacial malformations including an overshoot mandible and ossification of synchondroses. Mutants develop osteosclerosis of long bones and osteoarthritis, and, in some cases, high corticosterone levels.
- Transcript *Ltbp3* may not be affected.
- This strategy may affect the 5-terminal regulation of the target gene and the *Znrd2* gene.
- The *Ltbp3* gene is located on the Chr19. 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)

## Ltbp3 latent transforming growth factor beta binding protein 3 [Mus musculus (house mouse)]

Gene ID: 16998, updated on 31-Jan-2019

### Summary



|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Ltbp3 provided by <a href="#">MGI</a>   |
| <b>Official Full Name</b> | latent transforming growth factor beta binding protein 3 provided by <a href="#">MGI</a>  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1101355</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000024940</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>      | Ltbp2, mFLJ00070  |
| <b>Expression</b>         | Biased expression in adrenal adult (RPKM 141.5), ovary adult (RPKM 97.4) and 14 other tissues <a href="#">See more</a>  |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>   |

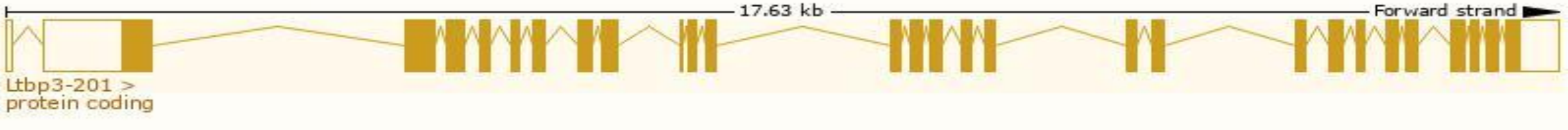


# Transcript information (Ensembl)

The gene has 12 transcripts,all transcripts are shown below:

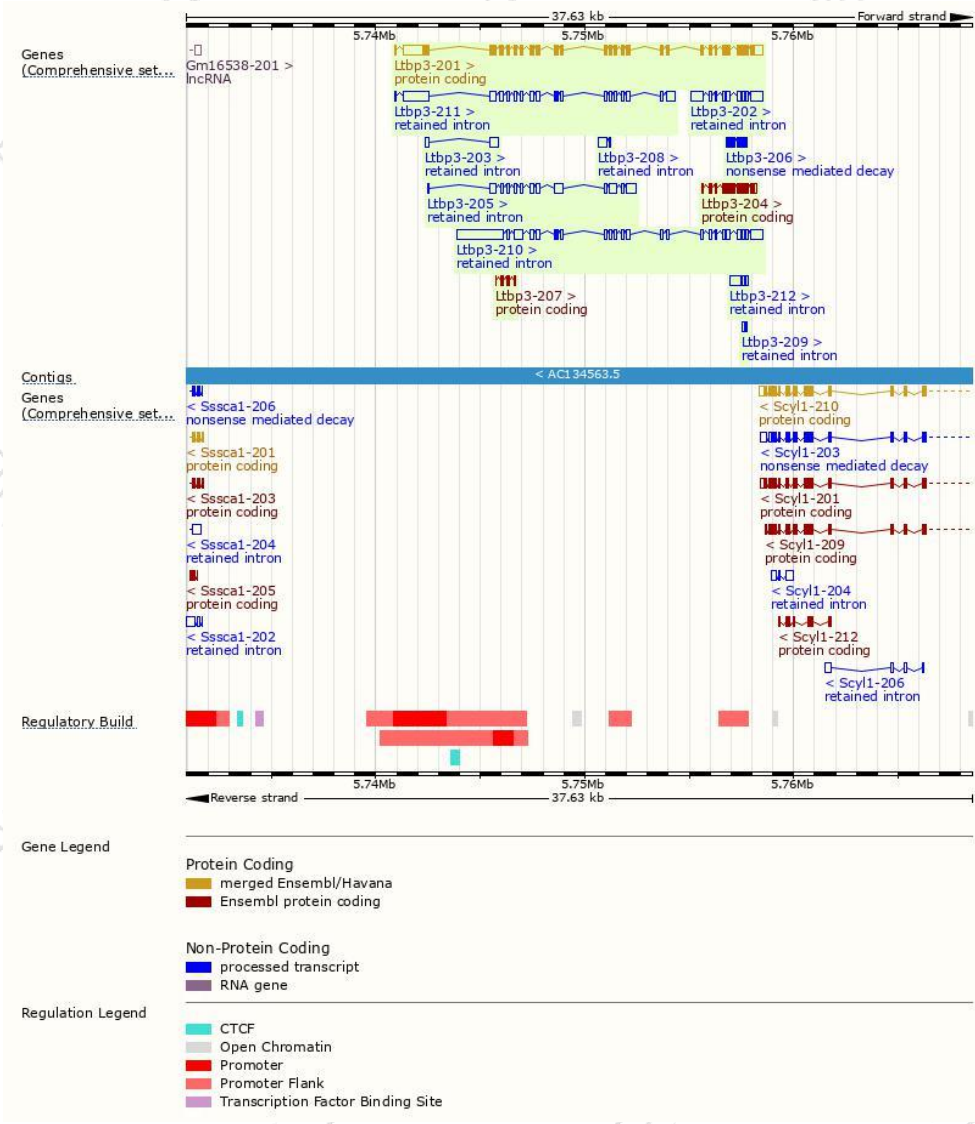
| Name      | Transcript ID                        | bp   | Protein                | Biotype                 | CCDS                      | UniProt                | Flags   |
|-----------|--------------------------------------|------|------------------------|-------------------------|---------------------------|------------------------|---|
| Ltbp3-201 | <a href="#">ENSMUST00000081496.5</a> | 5190 | <a href="#">1253aa</a> | Protein coding          | <a href="#">CCDS37891</a> | <a href="#">Q61810</a> | TSL:5 GENCODE basic APPRIS P1   |
| Ltbp3-204 | <a href="#">ENSMUST00000236130.1</a> | 1387 | <a href="#">415aa</a>  | Protein coding          | -                         | -                      | CDS 5' incomplete   |
| Ltbp3-207 | <a href="#">ENSMUST00000236617.1</a> | 356  | <a href="#">118aa</a>  | Protein coding          | -                         | -                      | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete |
| Ltbp3-206 | <a href="#">ENSMUST00000236529.1</a> | 580  | <a href="#">153aa</a>  | Nonsense mediated decay | -                         | -                      | CDS 5' incomplete   |
| Ltbp3-210 | <a href="#">ENSMUST00000237280.1</a> | 5729 | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-211 | <a href="#">ENSMUST00000237317.1</a> | 3857 | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-205 | <a href="#">ENSMUST00000236258.1</a> | 2673 | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-202 | <a href="#">ENSMUST00000235336.1</a> | 2099 | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-212 | <a href="#">ENSMUST00000237327.1</a> | 704  | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-203 | <a href="#">ENSMUST00000235898.1</a> | 650  | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-208 | <a href="#">ENSMUST00000237128.1</a> | 498  | No protein             | Retained intron         | -                         | -                      |   |
| Ltbp3-209 | <a href="#">ENSMUST00000237180.1</a> | 156  | No protein             | Retained intron         | -                         | -                      |   |

The strategy is based on the design of *Ltbp3-201* transcript,The transcription is shown below



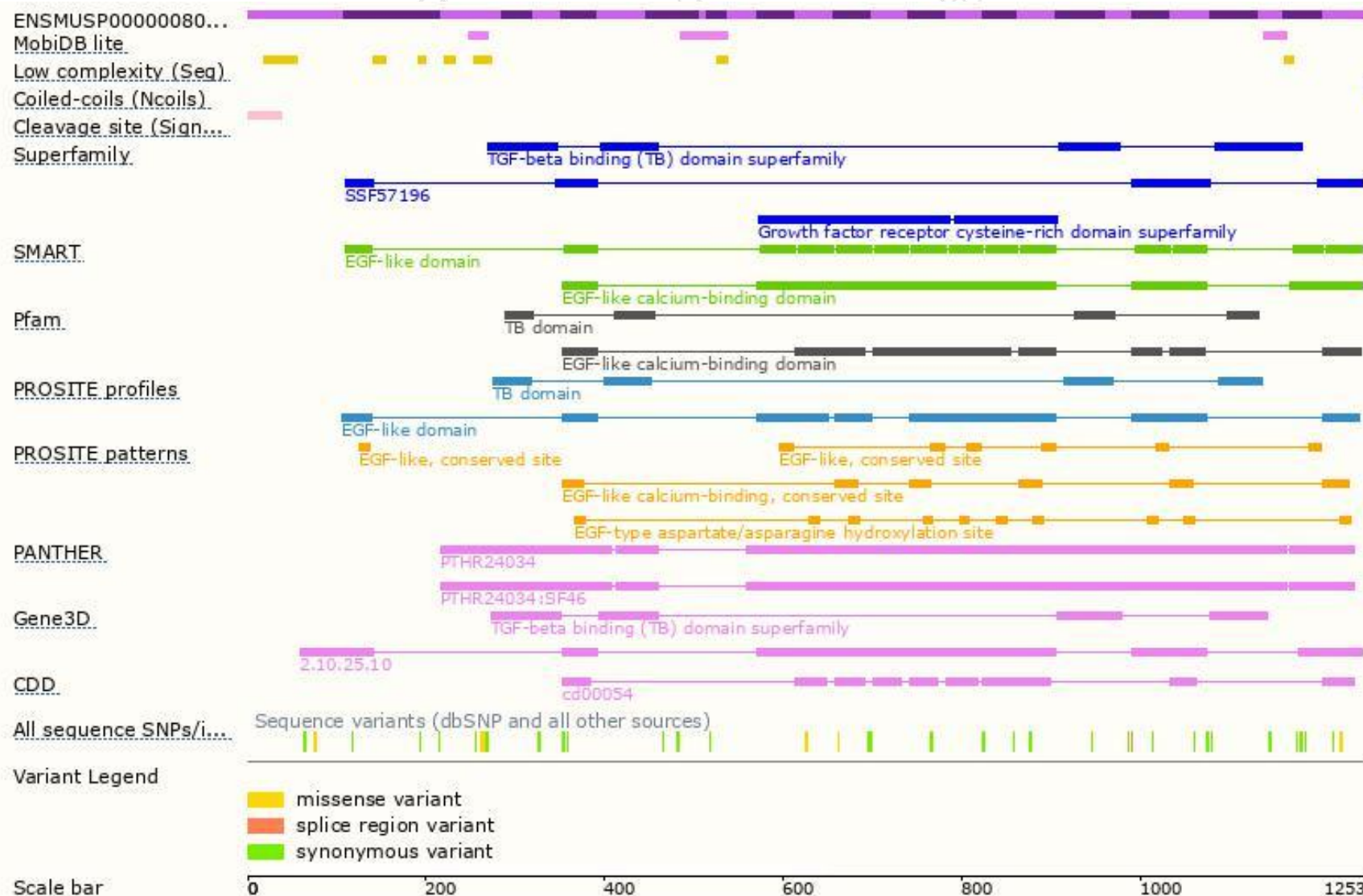


# Genomic location distribution



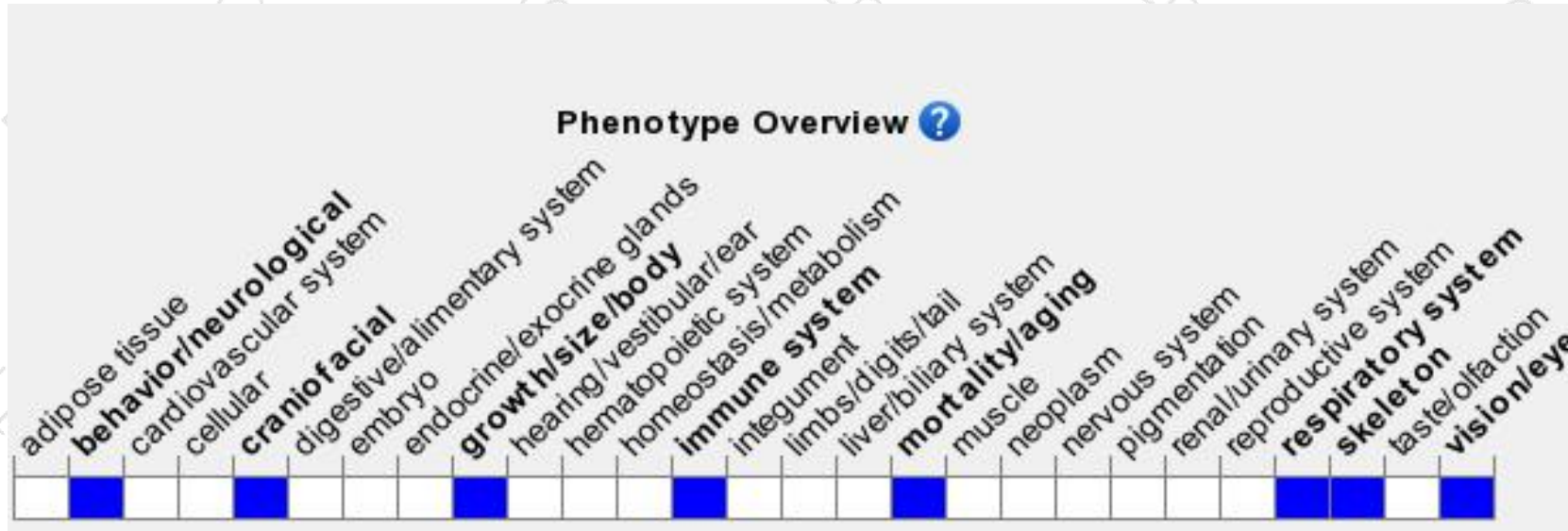


# Protein domain





# 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, Homozygotes for a targeted null mutation exhibit craniofacial malformations including an overshot mandible and ossification of synchondroses. Mutants develop osteosclerosis of long bones and osteoarthritis, and, in some cases, high corticosterone levels.



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

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