

# ***Galnt17* Cas9-KO Strategy**

**Designer:** Daohua Xu

**Reviewer:** Huimin Su

**Design Date:** 2020-4-15

# Project Overview

**Project Name**

***Galnt17***

**Project type**

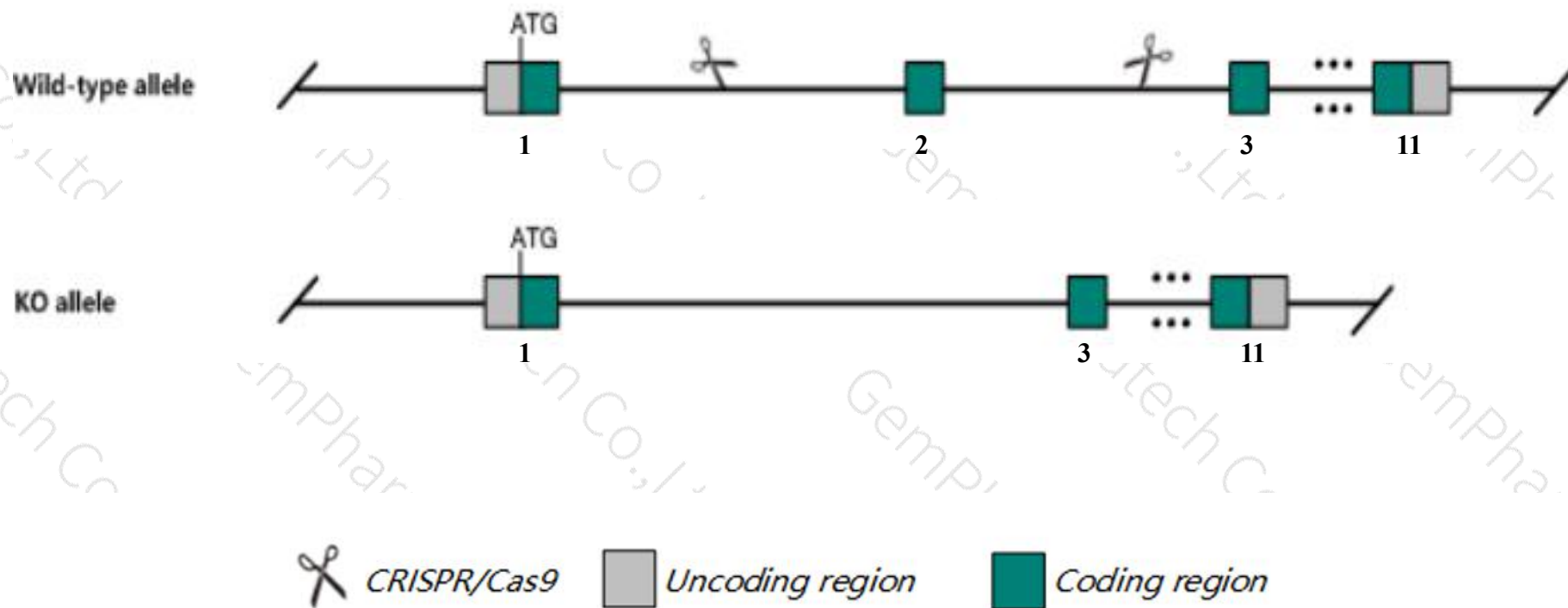
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Galnt17* gene. The schematic diagram is as follows:



- The *Galnt17* gene has 5 transcripts. According to the structure of *Galnt17* gene, exon2 of *Galnt17-201* (ENSMUST00000086023.11) transcript is recommended as the knockout region. The region contains 184bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Galnt17* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Galnt17* 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)

## Galnt17 polypeptide N-acetylgalactosaminyltransferase 17 [Mus musculus (house mouse)]

Gene ID: 212996, updated on 13-Mar-2020

### Summary



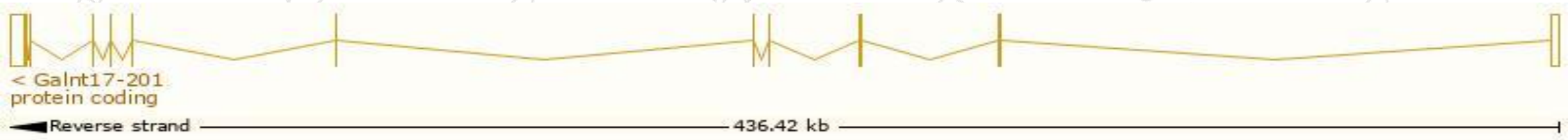
<b>Official Symbol</b>	Galnt17 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	polypeptide N-acetylgalactosaminyltransferase 17 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2137594</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000034040</a>
<b>Gene type</b>	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>	AA388321, E330012B09Rik, Galnt19, Gcap8, Wbscr17
<b>Expression</b>	Broad expression in cerebellum adult (RPKM 7.1), cortex adult (RPKM 6.3) and 18 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

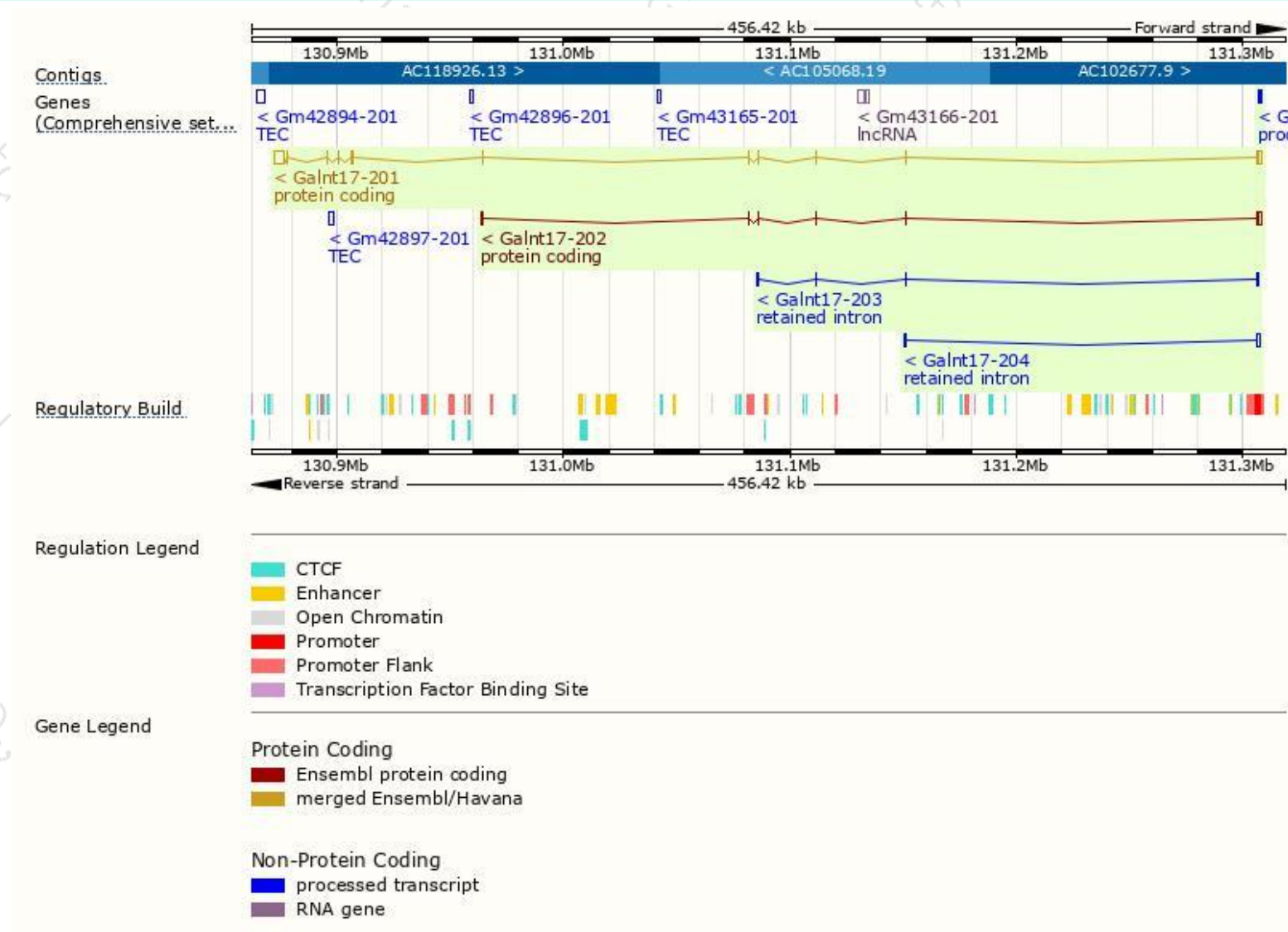
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Galnt17-201	<a href="#">ENSMUST00000086023.11</a>	8040	<a href="#">598aa</a>	Protein coding	<a href="#">CCDS39296</a>	<a href="#">Q59J92 Q7TT15</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
Galnt17-202	<a href="#">ENSMUST00000160609.1</a>	2875	<a href="#">371aa</a>	Protein coding	-	<a href="#">E9Q714</a>	TSL:5 GENCODE basic
Galnt17-205	<a href="#">ENSMUST00000162966.1</a>	731	No protein	Processed transcript	-	-	TSL:3
Galnt17-204	<a href="#">ENSMUST00000161228.1</a>	2119	No protein	Retained intron	-	-	TSL:1
Galnt17-203	<a href="#">ENSMUST00000160807.1</a>	1704	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Galnt17-201* transcript,the transcription is shown below:

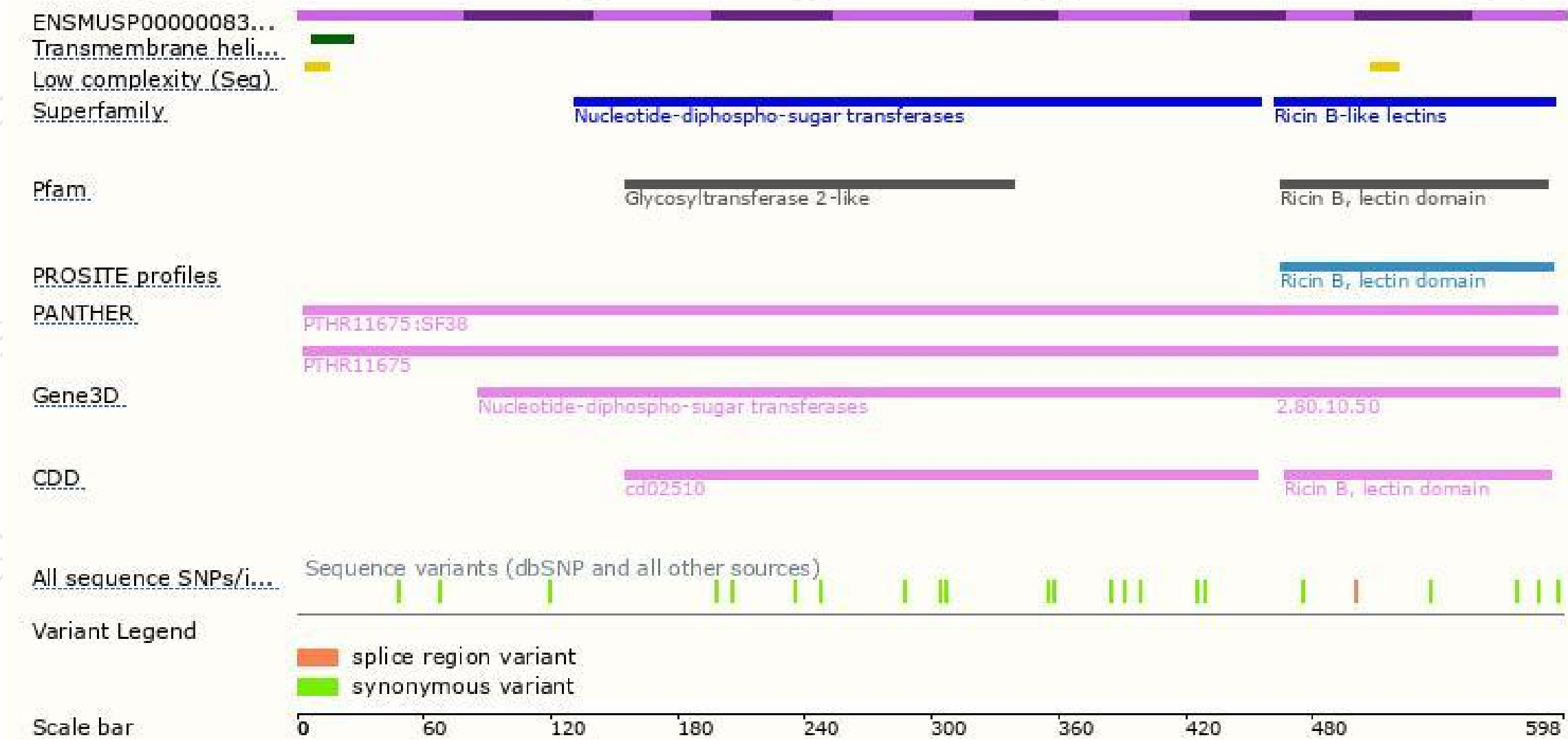


# Genomic location distribution

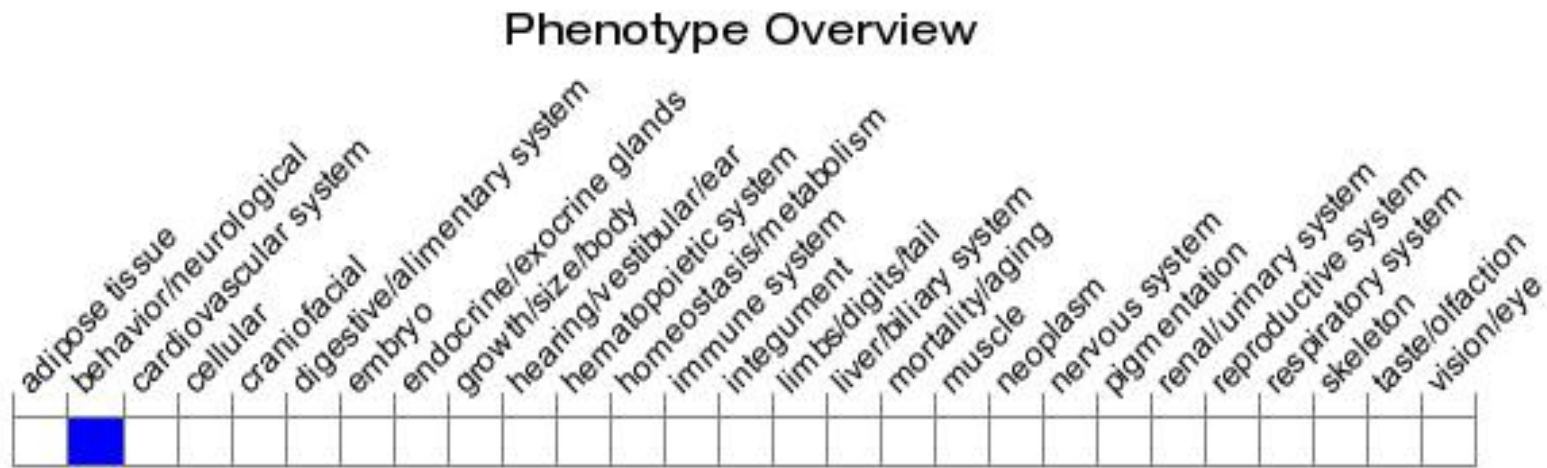




# Protein domain



# 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.

Tel: 400-9660890

