

# *Grin3b* Cas9-KO Strategy

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**Design Date:** 2020-4-9

# Project Overview

**Project Name**

***Grin3b***

**Project type**

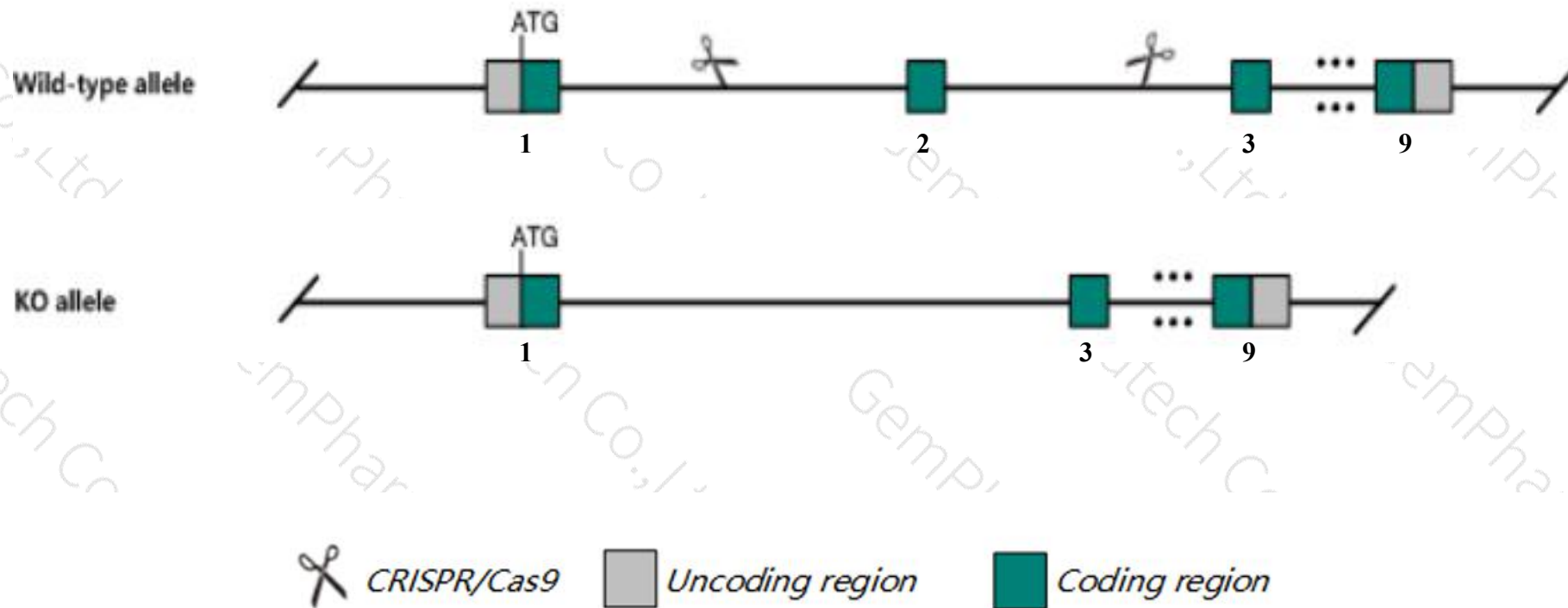
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Grin3b* gene. The schematic diagram is as follows:



- The *Grin3b* gene has 3 transcripts. According to the structure of *Grin3b* gene, exon2 of *Grin3b-201* (ENSMUST00000045085.7) transcript is recommended as the knockout region. The region contains 593bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Grin3b* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele show a mild impairment in motor learning or coordination, reduced home cage activity, a highly increased social interaction with familiar cagemates in their home cage but moderately increased anxiety-like behavior and reduced social interaction in a new environment.
- The effect on transcript *Grin3b*-202&203 is unknown.
- The knockout region is near to the C-terminal of *Tmem259* gene, this strategy may influence the regulatory function of the C-terminal of *Tmem259* gene.
- The *Grin3b* gene is located on the Chr10. 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)

## Grin3b glutamate receptor, ionotropic, NMDA3B [Mus musculus (house mouse)]

Gene ID: 170483, updated on 13-Mar-2020

### Summary



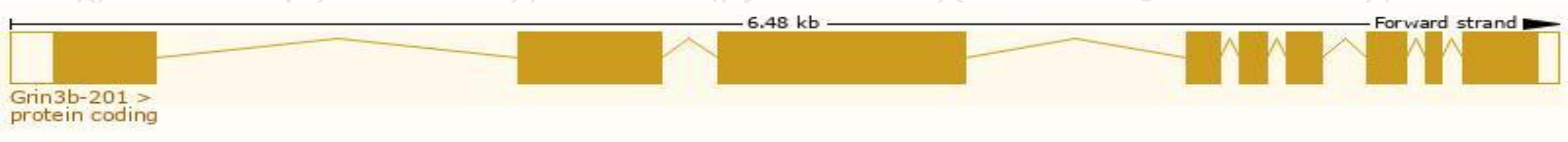
<b>Official Symbol</b>	Grin3b provided by <a href="#">MGI</a>
<b>Official Full Name</b>	glutamate receptor, ionotropic, NMDA3B provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2150393</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000035745</a>
<b>Gene type</b>	protein 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>	GluN3B, NR3B
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 4.1), ovary adult (RPKM 2.3) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

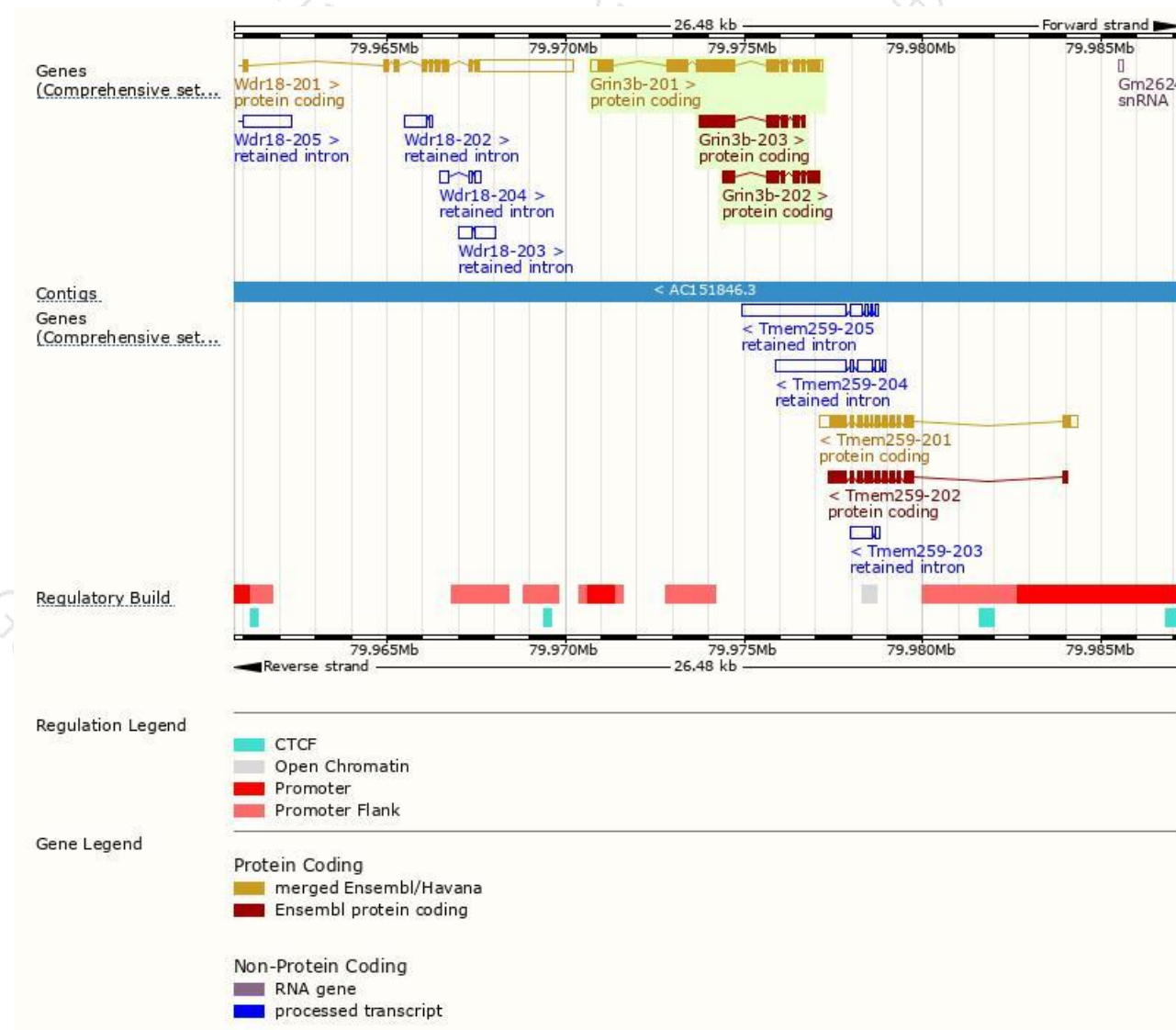
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Grin3b-201	<a href="#">ENSMUST00000045085.7</a>	3283	<a href="#">1003aa</a>	Protein coding	<a href="#">CCDS24001</a>	<a href="#">Q91ZU9</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
Grin3b-203	<a href="#">ENSMUST00000149148.7</a>	1637	<a href="#">542aa</a>	Protein coding	-	<a href="#">F7BA29</a>	CDS 5' incomplete TSL:1
Grin3b-202	<a href="#">ENSMUST00000131816.2</a>	1197	<a href="#">399aa</a>	Protein coding	-	<a href="#">F7ARC5</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1

The strategy is based on the design of *Grin3b-201* transcript,The transcription is shown below

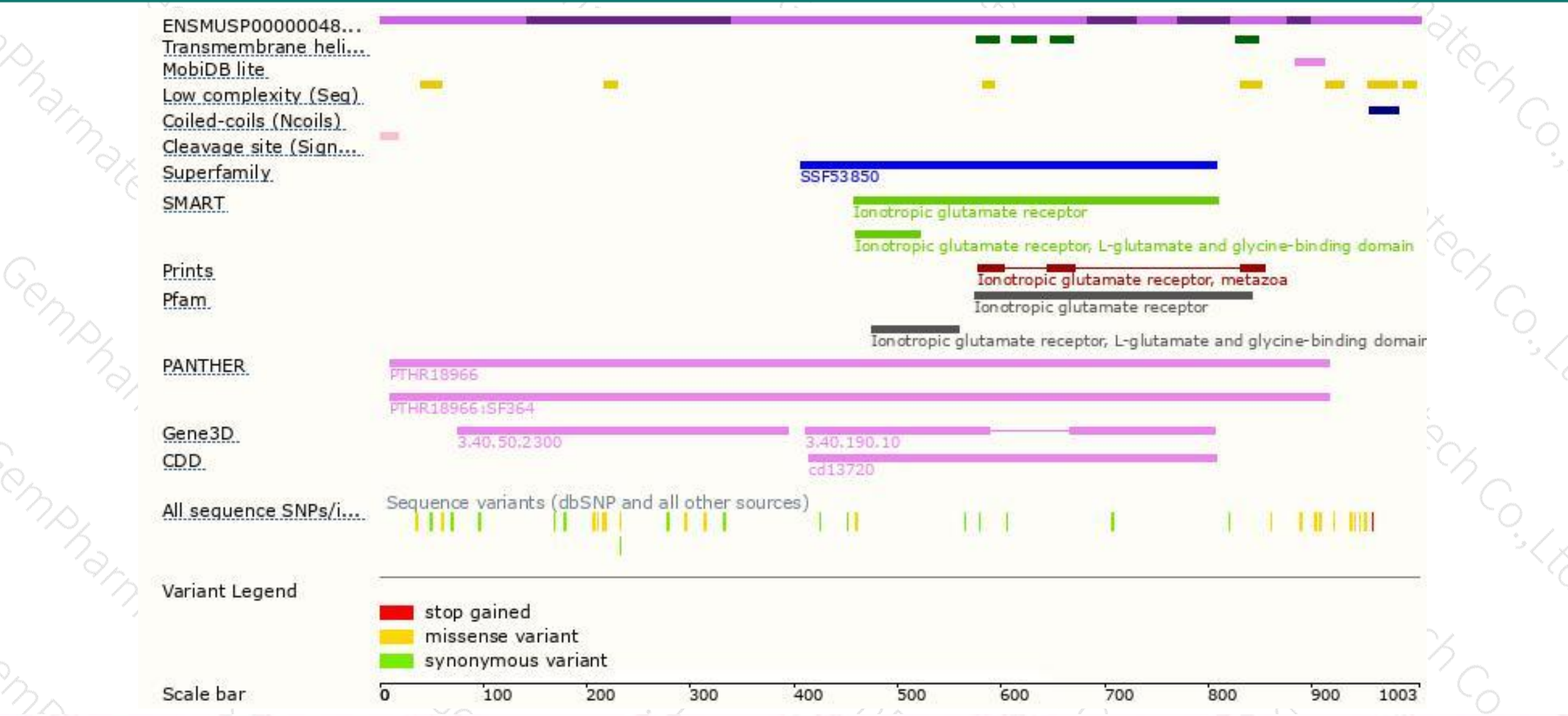


# Genomic location distribution

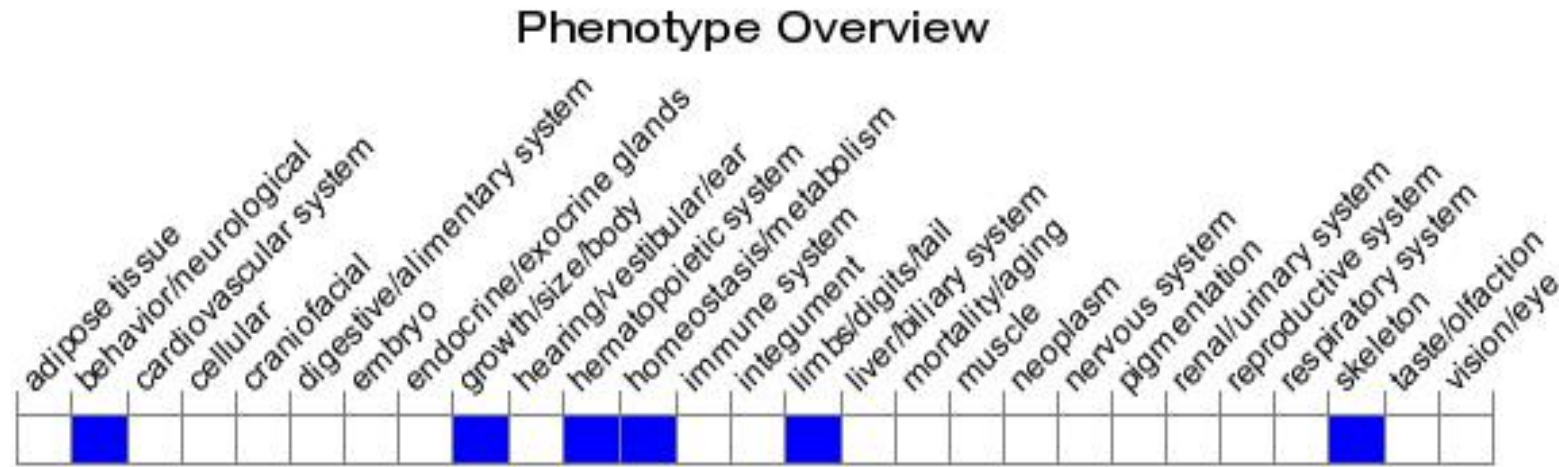




# Protein domain



# 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, mice homozygous for a null allele show a mild impairment in motor learning or coordination, reduced home cage activity, a highly increased social interaction with familiar cagemates in their home cage but moderately increased anxiety-like behavior and reduced social interaction in a new environment.

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

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