

# ***Lzts1*** Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Lzts1*

**Project type**

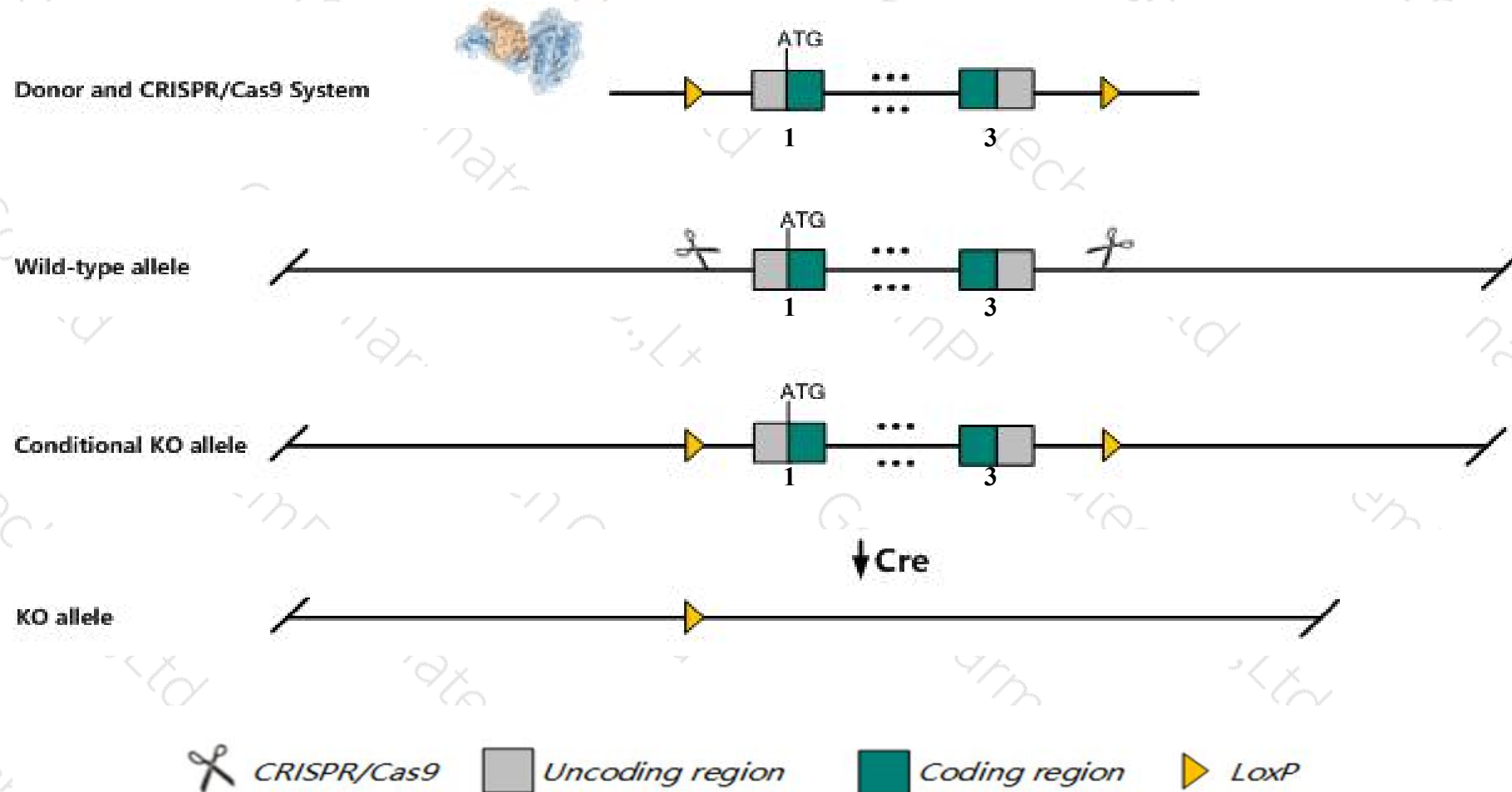
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lzts1* gene. The schematic diagram is as follows:



- The *Lzts1* gene has 5 transcripts. According to the structure of *Lzts1* gene, exon1-exon3 of *Lzts1-201* (ENSMUST00000037049.3) transcript is recommended as the knockout region. The region contains all 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 *Lzts1* 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, Heterozygous or homozygous inactivation of this gene leads to increased incidence of spontaneous and carcinogen-induced tumors. Homozygotes for a null allele show working memory and cognitive deficits, enhanced anxiety, defects in glutamatergic synaptic transmission, and impaired spine maturation.
- Transcript *Lzts1*-203&203&205 may not be affected.
- The *Lzts1* gene is located on the Chr8. 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)

## Lzts1 leucine zipper, putative tumor suppressor 1 [Mus musculus (house mouse)]

Gene ID: 211134, updated on 31-Jan-2019

### Summary



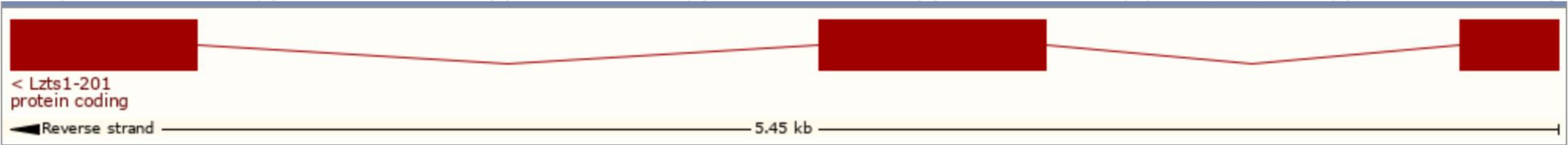
<b>Official Symbol</b>	Lzts1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	leucine zipper, putative tumor suppressor 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2684762</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000036306</a>
<b>Gene type</b>	protein 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>	F37, FEZ1, PSD-Zip70
<b>Expression</b>	Biased expression in frontal lobe adult (RPKM 14.3), cortex adult (RPKM 13.3) and 14 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

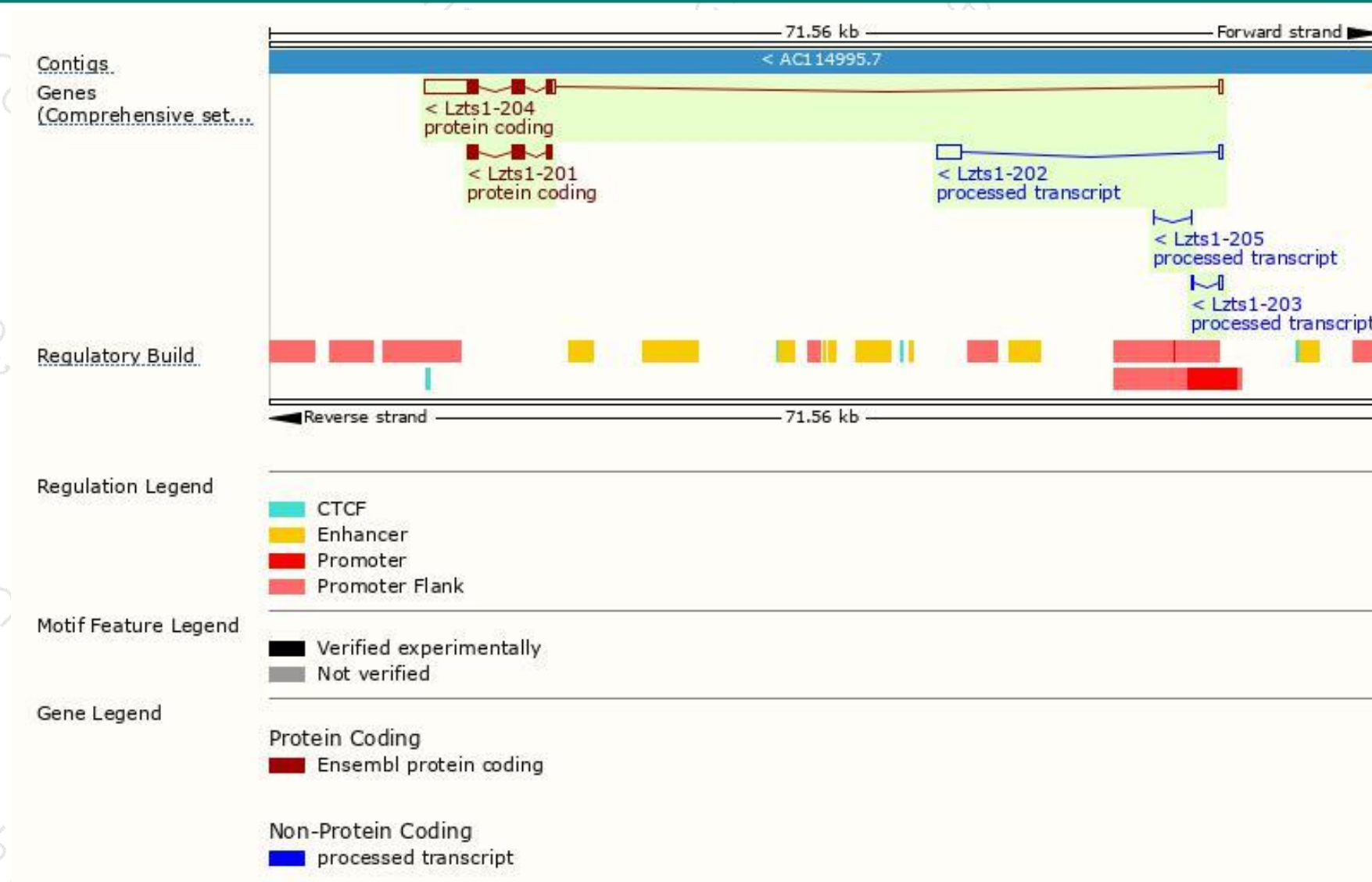
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lzts1-204	<a href="#">ENSMUST00000185176.7</a>	5019	<a href="#">599aa</a>	Protein coding	<a href="#">CCDS22345</a>	<a href="#">P60853</a>	TSL:5 GENCODE basic APPRIS P1
Lzts1-201	<a href="#">ENSMUST00000037049.3</a>	1800	<a href="#">599aa</a>	Protein coding	<a href="#">CCDS22345</a>	<a href="#">P60853</a>	TSL:1 GENCODE basic APPRIS P1
Lzts1-202	<a href="#">ENSMUST00000181890.1</a>	1784	No protein	Processed transcript	-	-	TSL:1
Lzts1-203	<a href="#">ENSMUST00000184961.1</a>	404	No protein	Processed transcript	-	-	TSL:2
Lzts1-205	<a href="#">ENSMUST00000209353.1</a>	87	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Lzts1-201* transcript,The transcription is shown below

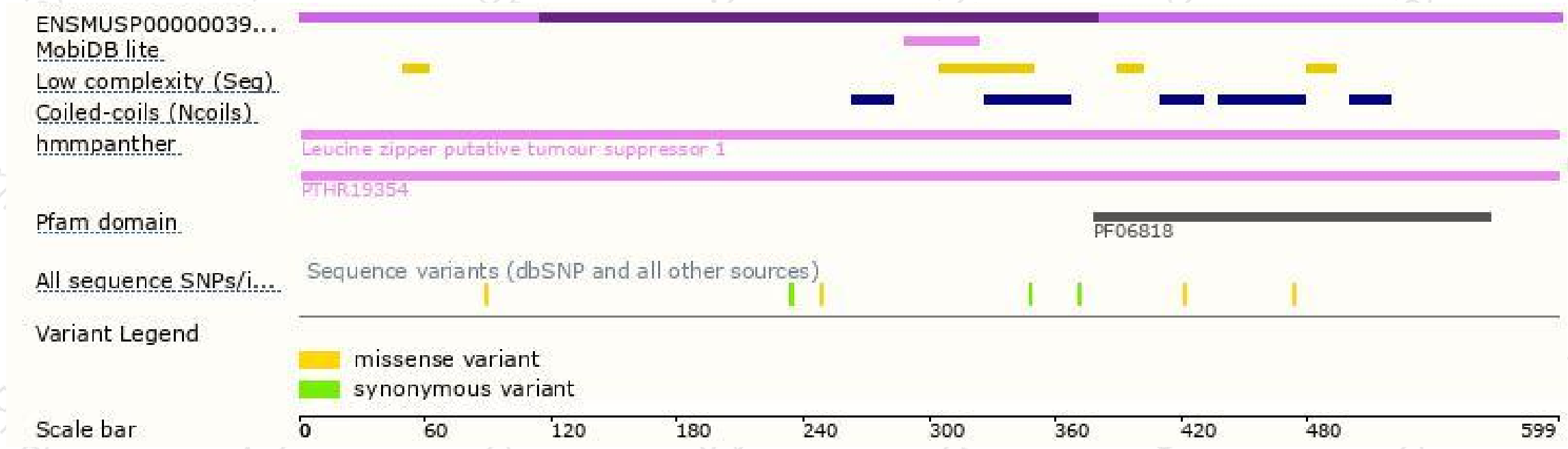


# Genomic location distribution

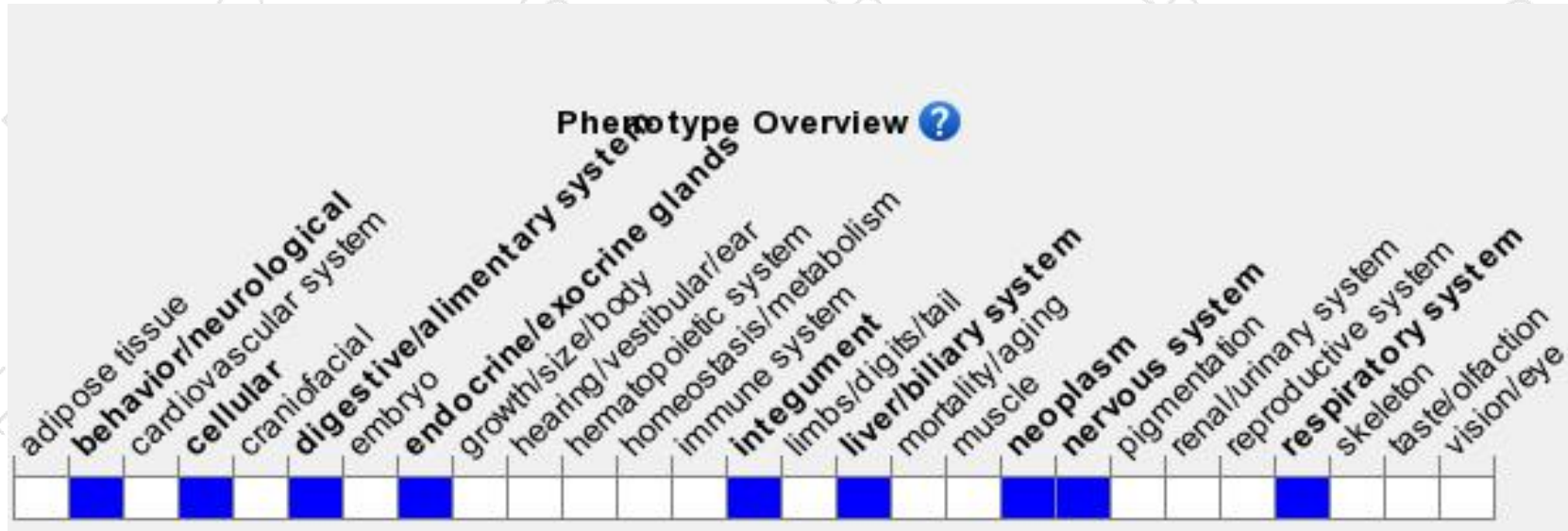




# Protein domain



# 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, Heterozygous or homozygous inactivation of this gene leads to increased incidence of spontaneous and carcinogen-induced tumors. Homozygotes for a null allele show working memory and cognitive deficits, enhanced anxiety, defects in glutamatergic synaptic transmission, and impaired spine maturation.

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

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