



# *Efr3a Cas9-CKO* Strategy

**Designer:**

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**Reviewer:**

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**Design Date:**

**2020-4-22**

# Project Overview

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**Project Name*****Efr3a***

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**Project type****Cas9-CKO**

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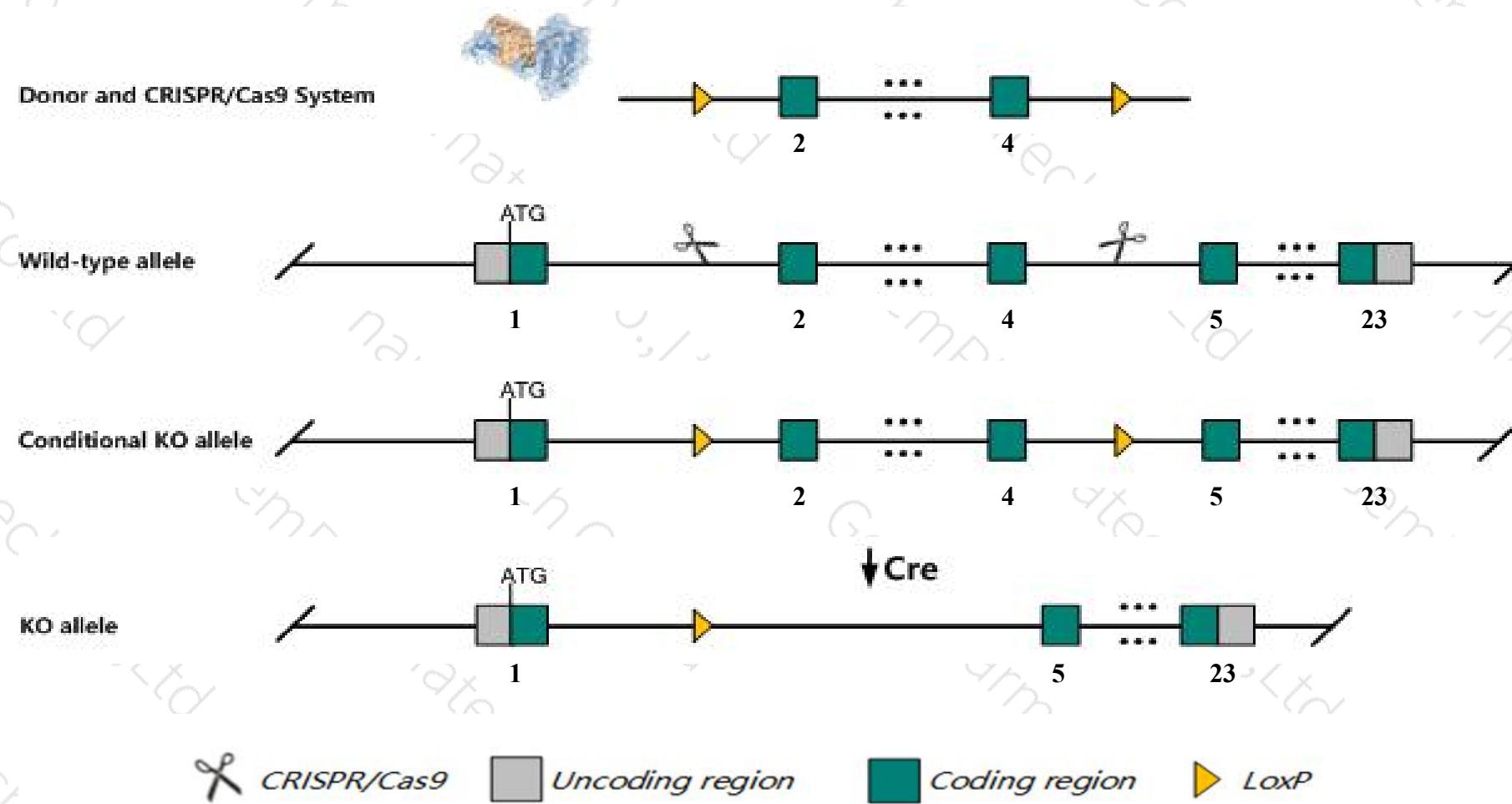
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**Strain background****C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Efr3a* gene. The schematic diagram is as follows:



# Technical routes

- The *Efr3a* gene has 14 transcripts. According to the structure of *Efr3a* gene, exon2-exon4 of *Efr3a-201* (ENSMUST00000015146.15) transcript is recommended as the knockout region. The region contains 356bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Efr3a* 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.



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# Notice

- According to the existing MGI data, mice homozygous for a conditional allele activated in the nervous system exhibit decreased neuron apoptosis in the dentate gyrus resulting in increased adult hippocampal neurogenesis.
- *Efr3a-214* may not be affected.
- The *Efr3a* gene is located on the Chr15. 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)

## Efr3a EFR3 homolog A [Mus musculus (house mouse)]

Gene ID: 76740, updated on 13-Mar-2020

### Summary



**Official Symbol** Efr3a provided by [MGI](#)

**Official Full Name** EFR3 homolog A provided by [MGI](#)

**Primary source** [MGI:MGI:1923990](#)

**See related** [Ensembl:ENSMUSG00000015002](#)

**Gene type** protein coding

**RefSeq status** VALIDATED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** A130089M23Rik, BB071175, C76891, C920006C10Rik, D030063F01Rik, mKIAA0143

**Expression** Ubiquitous expression in cerebellum adult (RPKM 23.6), cortex adult (RPKM 17.9) and 28 other tissues [See more](#)

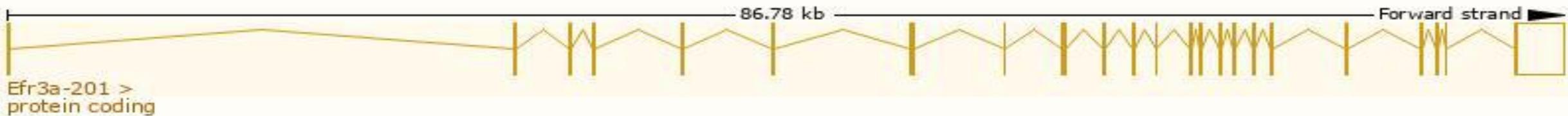
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

The gene has 14 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Efr3a-201	<a href="#">ENSMUST0000015146.15</a>	5215	819aa	Protein coding	<a href="#">CCDS27507</a>	<a href="#">Q8BG67</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
Efr3a-205	<a href="#">ENSMUST00000173858.7</a>	2848	821aa	Protein coding	-	<a href="#">Q8BG67</a>	TSL:1 GENCODE basic
Efr3a-213	<a href="#">ENSMUST00000211878.1</a>	2541	846aa	Protein coding	-	<a href="#">A0A1D5RLL3</a>	TSL:5 GENCODE basic
Efr3a-203	<a href="#">ENSMUST00000172756.1</a>	1411	174aa	Protein coding	-	<a href="#">Q8BWC5</a>	TSL:1 GENCODE basic
Efr3a-212	<a href="#">ENSMUST00000174856.6</a>	612	41aa	Protein coding	-	<a href="#">G3UX01</a>	CDS 3' incomplete TSL:2
Efr3a-214	<a href="#">ENSMUST00000227340.1</a>	518	112aa	Protein coding	-	<a href="#">A0A2I3BR57</a>	CDS 5' incomplete
Efr3a-207	<a href="#">ENSMUST00000174135.1</a>	1425	No protein	Processed transcript	-	-	TSL:1
Efr3a-202	<a href="#">ENSMUST00000096411.3</a>	981	No protein	Processed transcript	-	-	TSL:1
Efr3a-204	<a href="#">ENSMUST00000173008.1</a>	762	No protein	Processed transcript	-	-	TSL:3
Efr3a-209	<a href="#">ENSMUST00000174601.7</a>	643	No protein	Processed transcript	-	-	TSL:3
Efr3a-208	<a href="#">ENSMUST00000174591.2</a>	3225	No protein	Retained intron	-	-	TSL:1
Efr3a-210	<a href="#">ENSMUST00000174615.1</a>	866	No protein	Retained intron	-	-	TSL:3
Efr3a-211	<a href="#">ENSMUST00000174749.1</a>	691	No protein	Retained intron	-	-	TSL:3
Efr3a-206	<a href="#">ENSMUST00000173936.1</a>	387	No protein	Retained intron	-	-	TSL:2

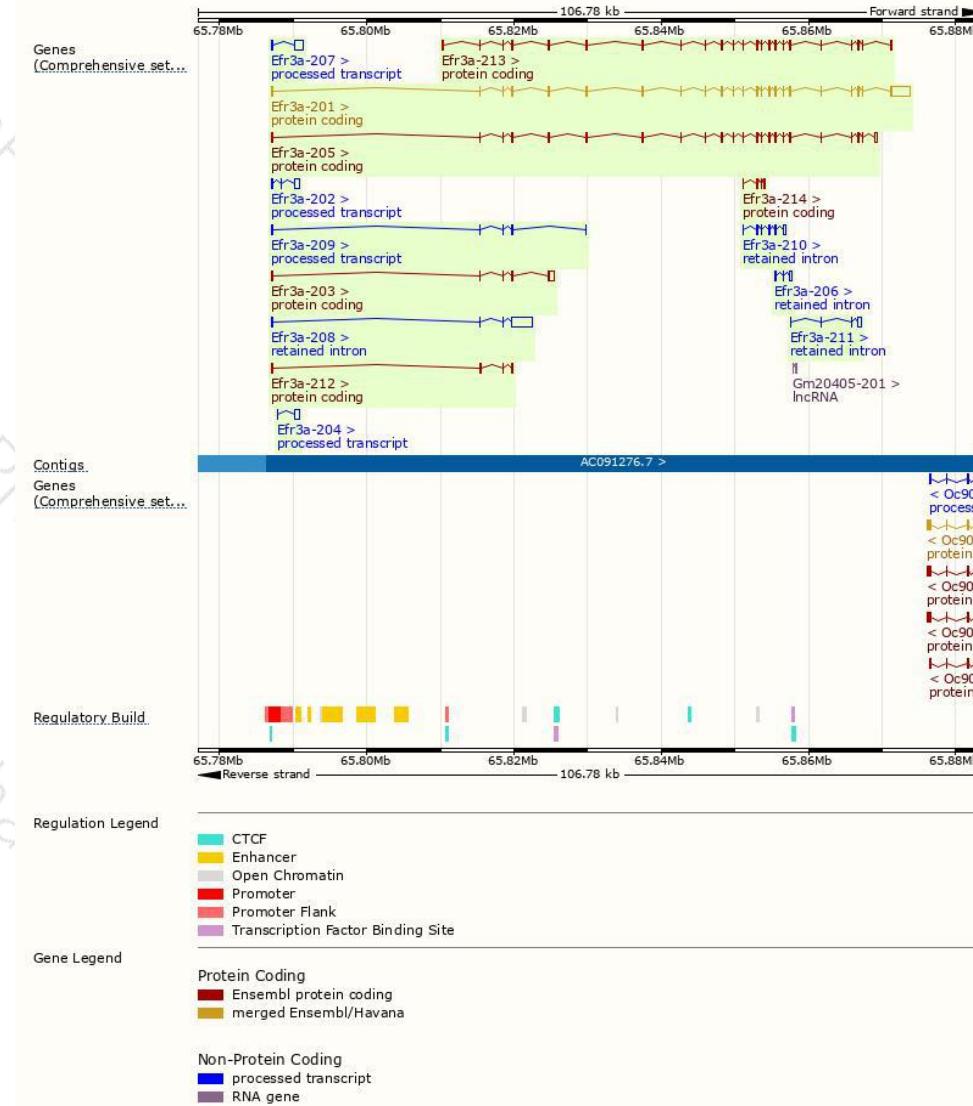
The strategy is based on the design of *Efr3a-201* transcript, the transcription is shown below:





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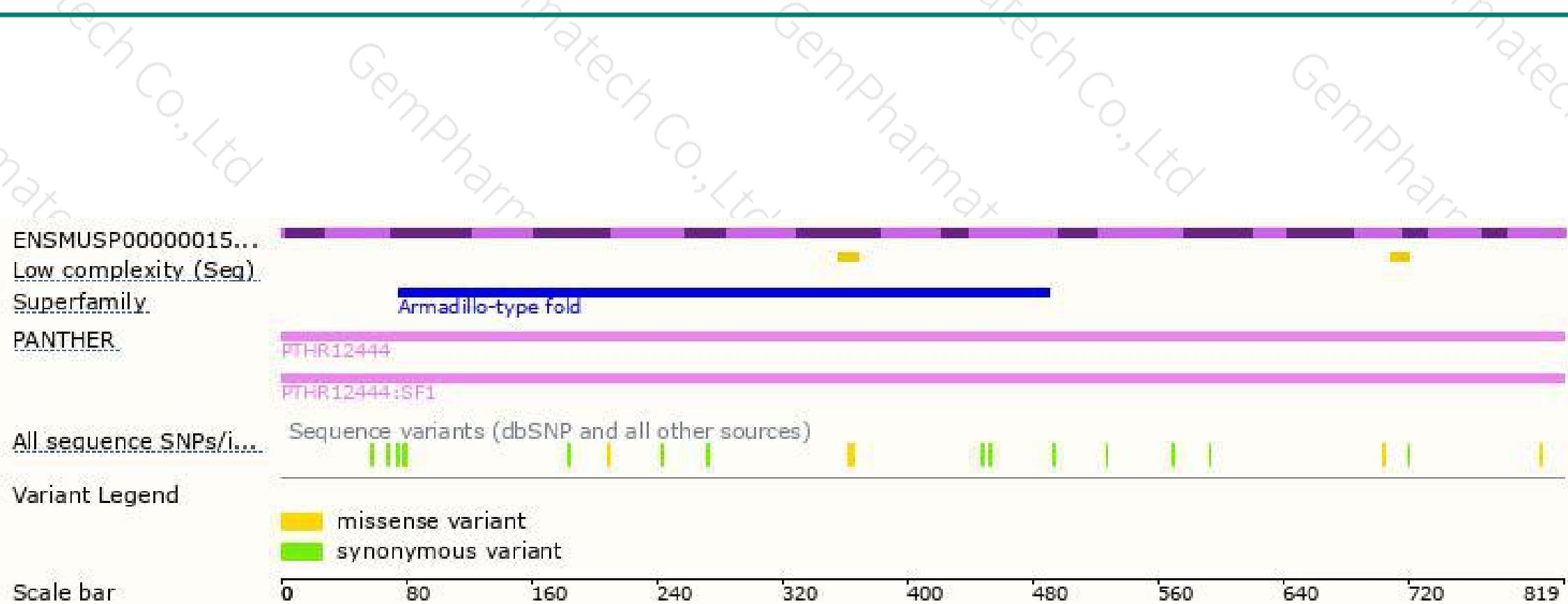
# Genomic location distribution





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# Protein domain

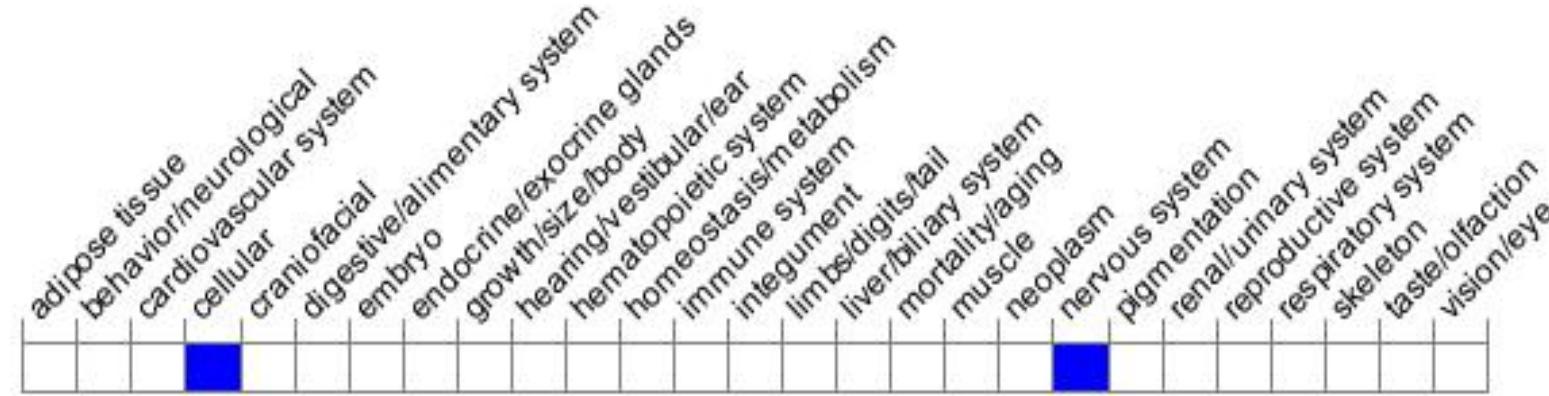




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# Mouse phenotype description(MGI)

Phenotype Overview



*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 conditional allele activated in the nervous system exhibit decreased neuron apoptosis in the dentate gyrus resulting in increased adult hippocampal neurogenesis.



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

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