

# *Vipr1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Vipr1*

**Project type**

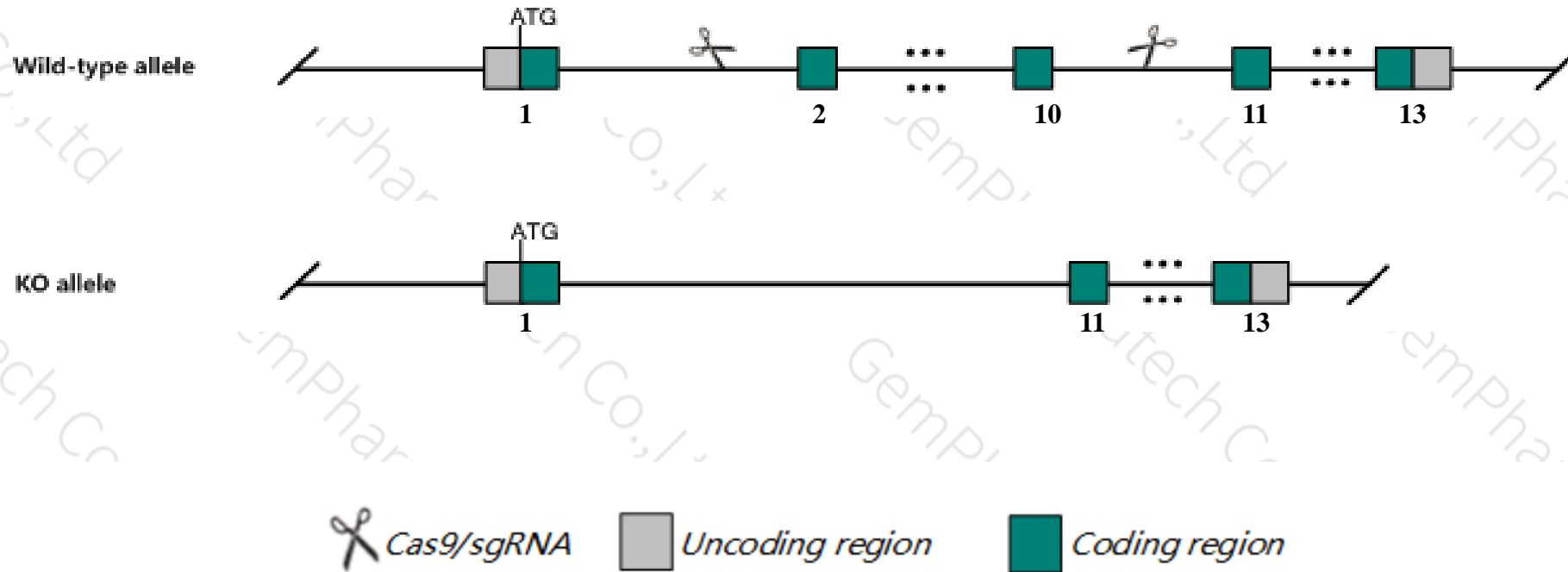
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vipr1* gene. The schematic diagram is as follows:



- The *Vipr1* gene has 5 transcripts. According to the structure of *Vipr1* gene, exon2-exon10 of *Vipr1-201* (ENSMUST00000035115.4) transcript is recommended as the knockout region. The region contains 938bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vipr1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit prenatal lethality associated with severe neonatal growth failure, enlarged cecum, intestinal hemorrhage, and enterocyte hyperproliferation in addition to disorganized islets and impaired glucose homeostasis in surviving mice.
- Transcript *Vipr1-204* may not be affected.
- The *Vipr1* gene is located on the Chr9. 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)

## Vipr1 vasoactive intestinal peptide receptor 1 [Mus musculus (house mouse)]

Gene ID: 22354, updated on 19-Mar-2019

### Summary



<b>Official Symbol</b>	Vipr1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	vasoactive intestinal peptide receptor 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:109272</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032528</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>	AV071699, VIP-R1, VPAC1
<b>Expression</b>	Biased expression in colon adult (RPKM 47.0), small intestine adult (RPKM 34.2) and 8 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

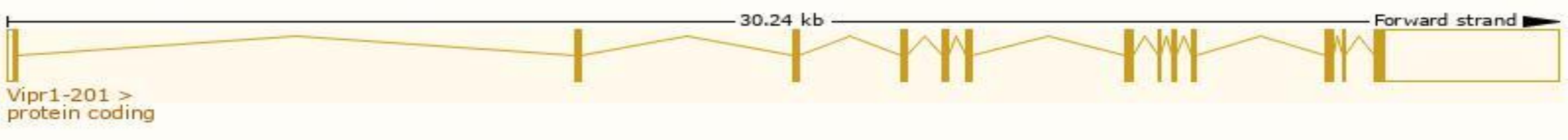


# Transcript information (Ensembl)

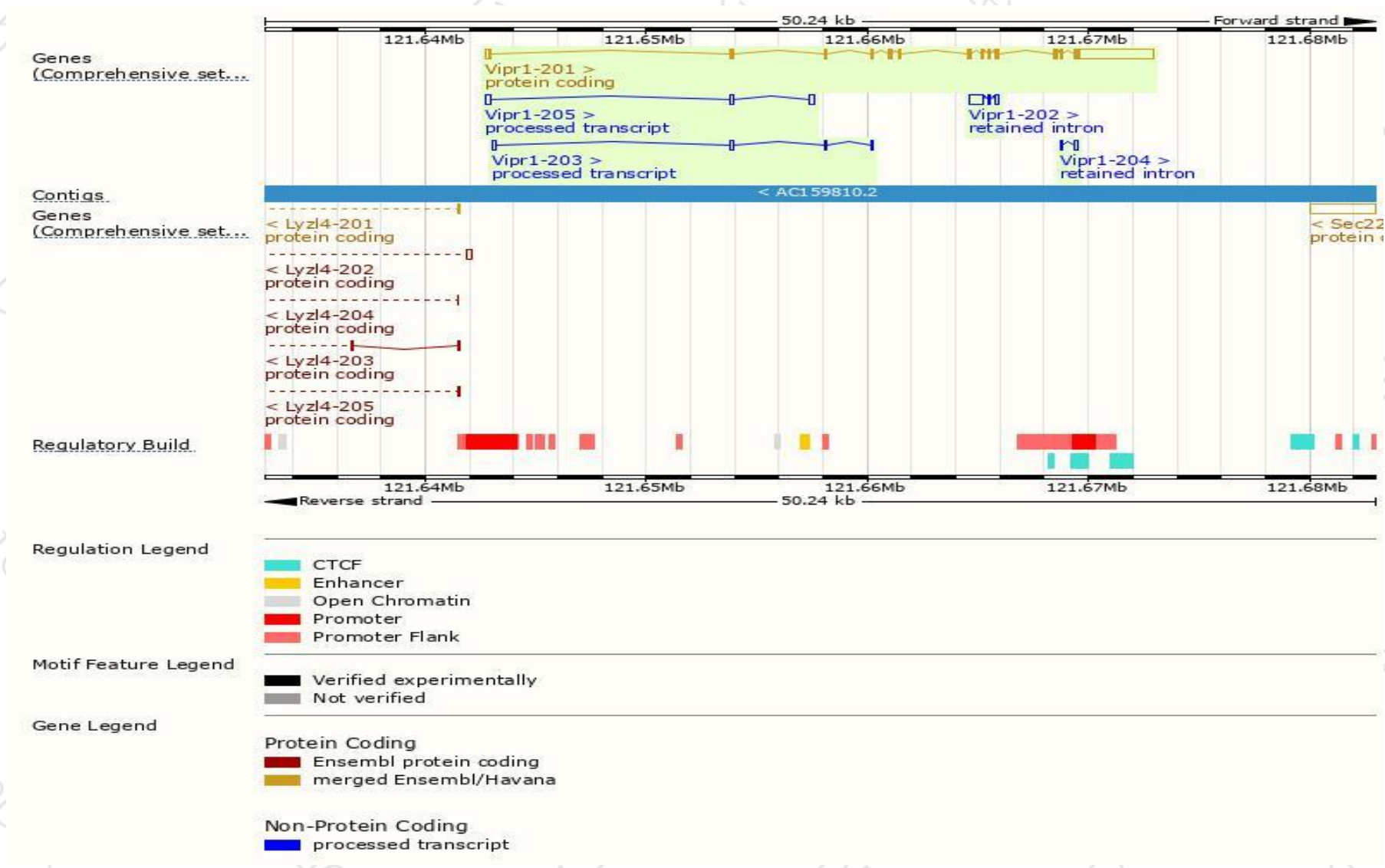
The gene has 5 transcripts,all transcripts are shown below:

Show/hide columns								Filter	
Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Translation ID ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲	
Vipr1-201	<a href="#">ENSMUST00000035115.4</a>	4902	<a href="#">459aa</a>	<a href="#">ENSMUSP00000035115.4</a>	Protein coding	<a href="#">CCDS23633</a>	<a href="#">P97751</a>	TSL:1	GENCODE basic APPRIS P1
Vipr1-202	<a href="#">ENSMUST00000129394.1</a>	763	No protein	-	Retained intron	-	-	TSL:3	
Vipr1-203	<a href="#">ENSMUST00000139189.1</a>	412	No protein	-	lncRNA	-	-	TSL:5	
Vipr1-204	<a href="#">ENSMUST00000149959.1</a>	224	No protein	-	Retained intron	-	-	TSL:5	
Vipr1-205	<a href="#">ENSMUST00000213272.1</a>	508	No protein	-	lncRNA	-	-	TSL:5	

The strategy is based on the design of *Vipr1-201* transcript,The transcription is shown below

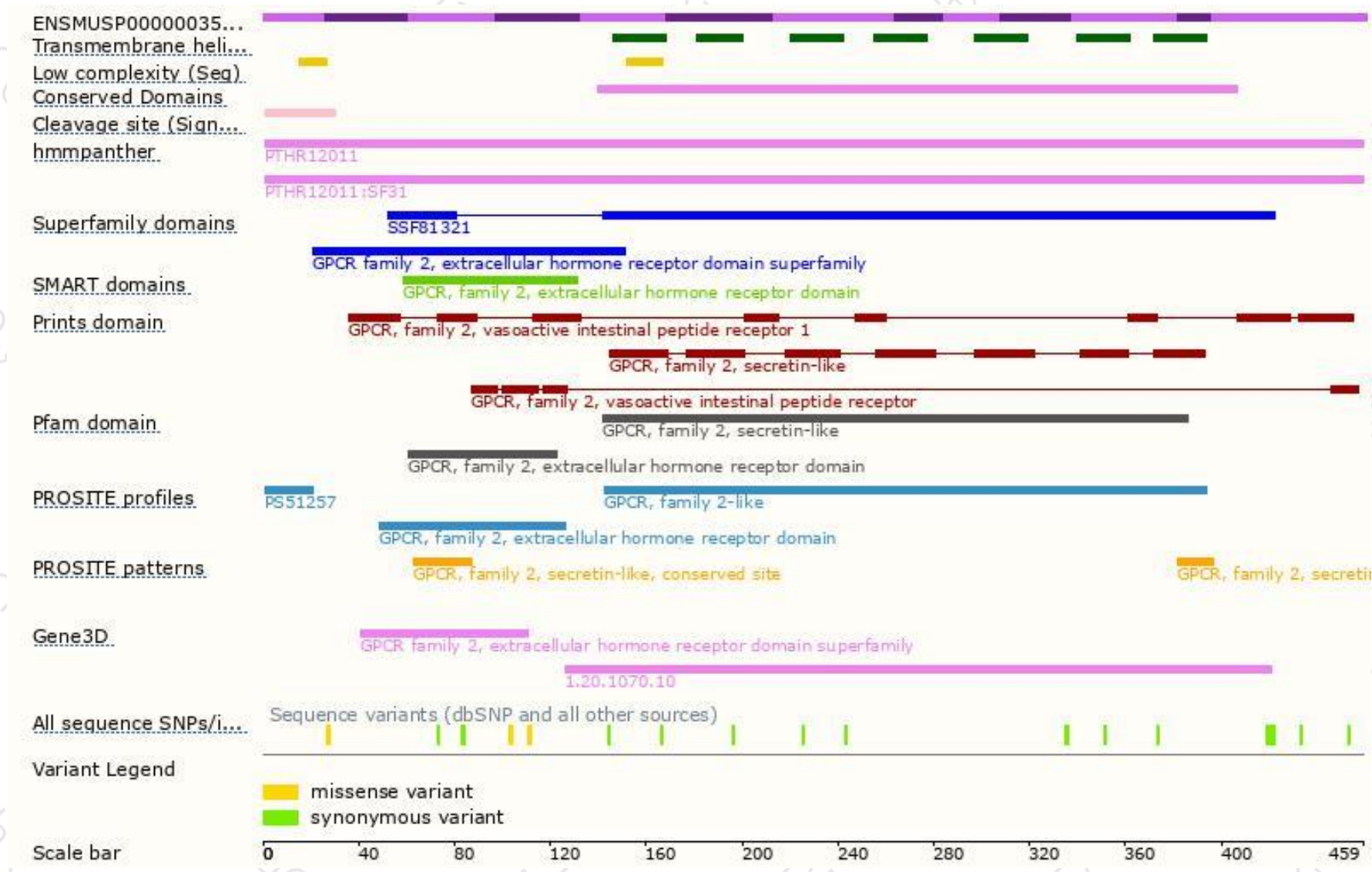


# Genomic location distribution



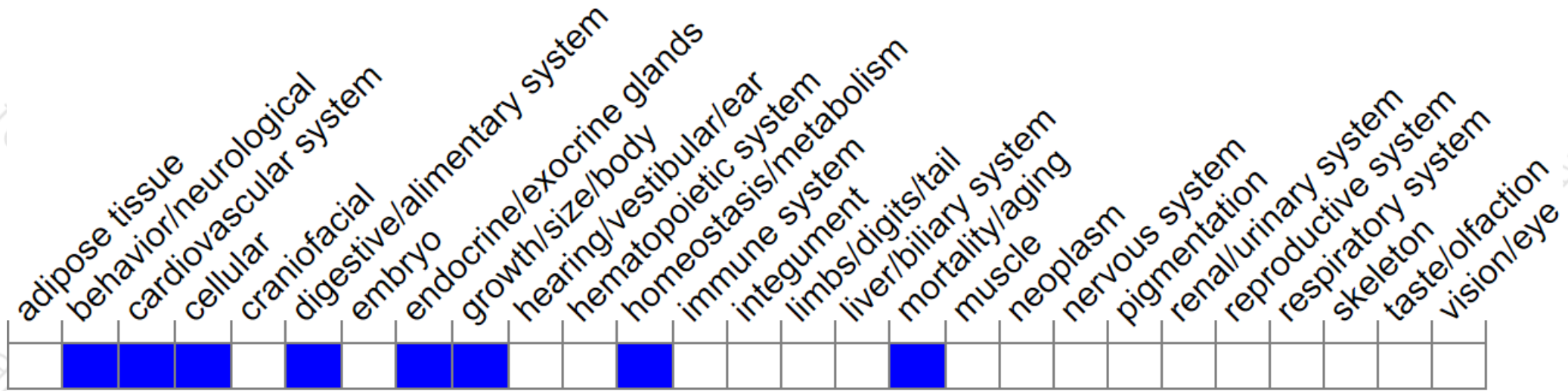


# Protein domain



# 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 knock-out allele exhibit prenatal lethality associated with severe neonatal growth failure, enlarged cecum, intestinal hemorrhage, and enterocyte hyperproliferation in addition to disorganized islets and impaired glucose homeostasis in surviving mice.

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

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