# *Hrh2* Cas9-CKO Strategy

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**Design Date:** 2019-7-22

# Project Overview

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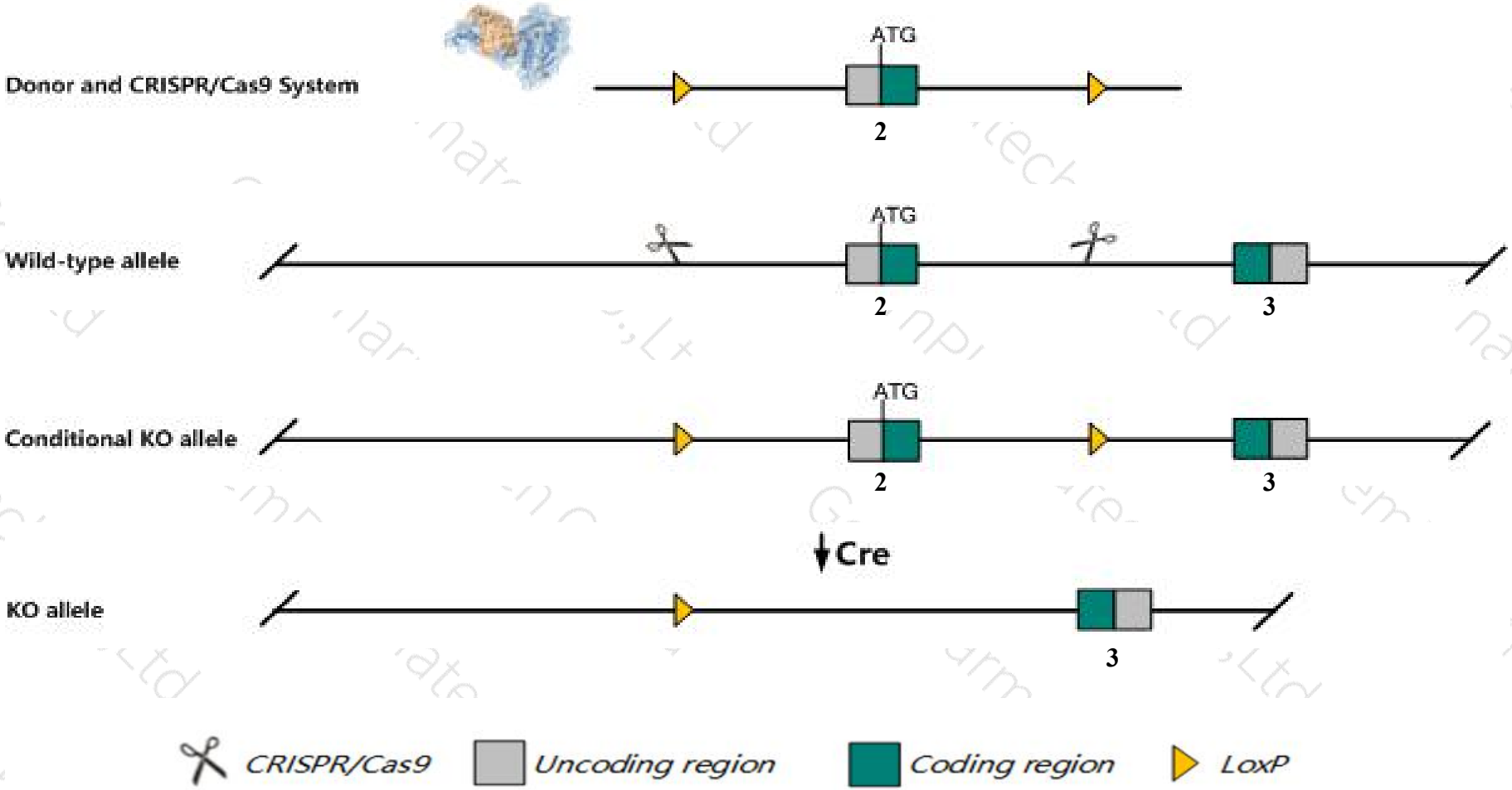
|---|---|
| **Project Name** | ***Hrh2*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hrh2* gene. The schematic diagram is as follows:



# Technical routes

- The *Hrh2* gene has 3 transcripts. According to the structure of *Hrh2* gene, exon2 of *Hrh2-201* (ENSMUST00000038101.3) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hrh2* 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.

# Notice

➢ According to the existing MGI data,Homozygotes for a targeted null mutation exhibit enlarged folds in gastric mucosa, elevated serum gastrin levels, increased numbers of parietal and enterochromaffin-like cells, and lack of secretion of gastric acid in response to histamine or gastrin.

➢ The *Hrh2* gene is located on the Chr13. 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）

集萃药康 GemPharmatech

## Hrh2 histamine receptor H2 [Mus musculus (house mouse)]

Gene ID: 15466, updated on 31-Jan-2019

### Summary

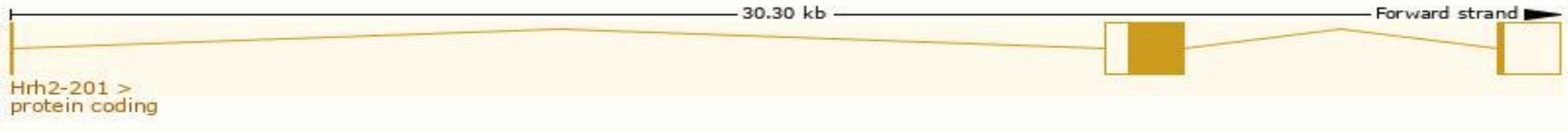
| | |
|---|---|
| **Official Symbol** | Hrh2 provided by MGI |
| **Official Full Name** | histamine receptor H2 provided by MGI |
| **Primary source** | MGI:MGI:108482 |
| **See related** | Ensembl:ENSMUSG00000034987 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | H2R, HH2R |
| **Expression** | Broad expression in frontal lobe adult (RPKM 1.9), stomach adult (RPKM 1.8) and 18 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

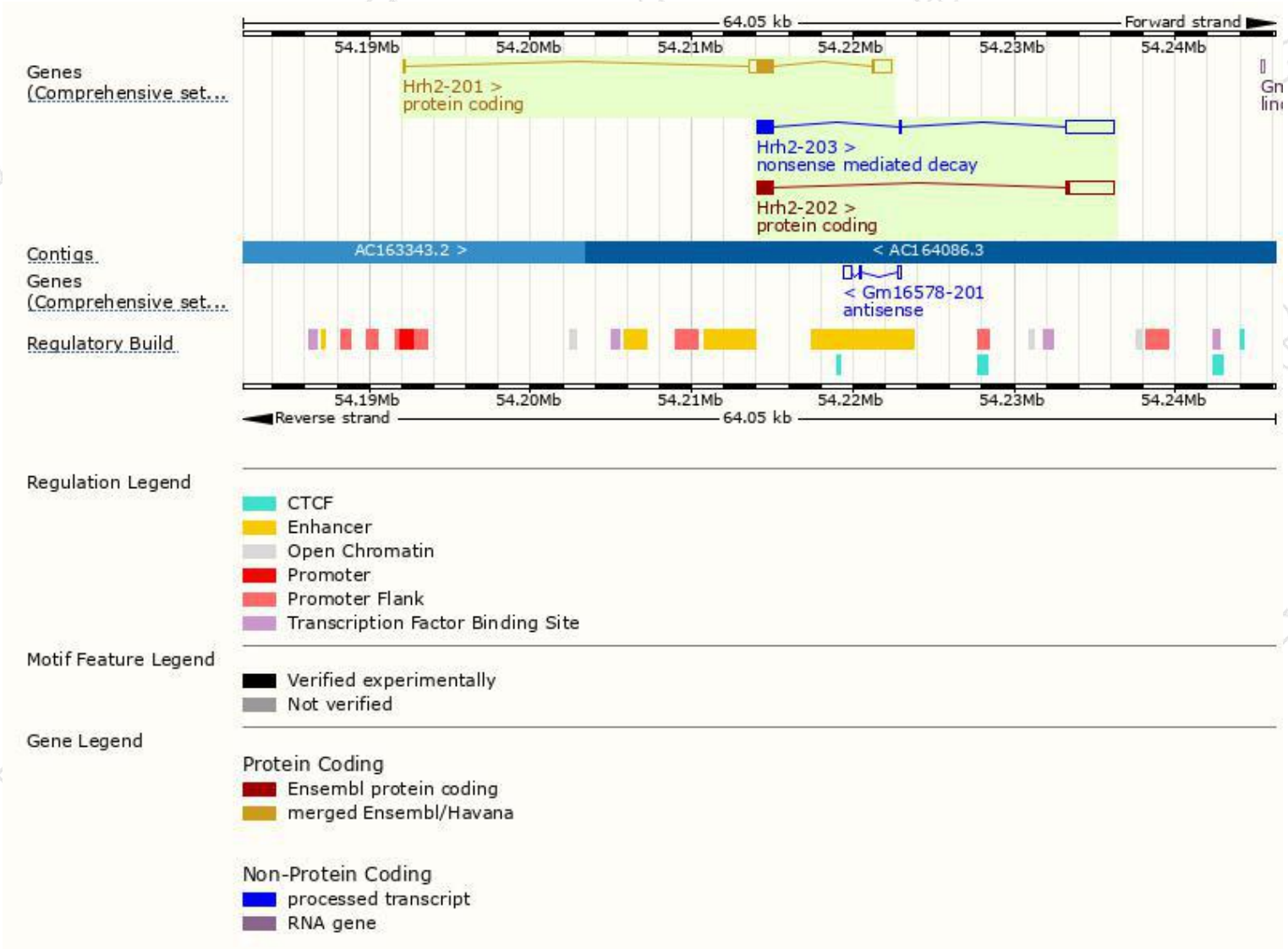
The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Hrh2-203 | ENSMUST00000211742.1 | 4219 | 371aa | Nonsense mediated decay | - | A0A1B0GR79 | TSL:5 |
| Hrh2-202 | ENSMUST00000209846.1 | 4074 | 421aa | Protein coding | - | A0A1B0GSX9 | TSL:5 GENCODE basic APPRIS ALT2 |
| Hrh2-201 | ENSMUST00000038101.3 | 2789 | 397aa | Protein coding | CCDS26526 | P97292 | TSL:1 GENCODE basic APPRIS P2 |

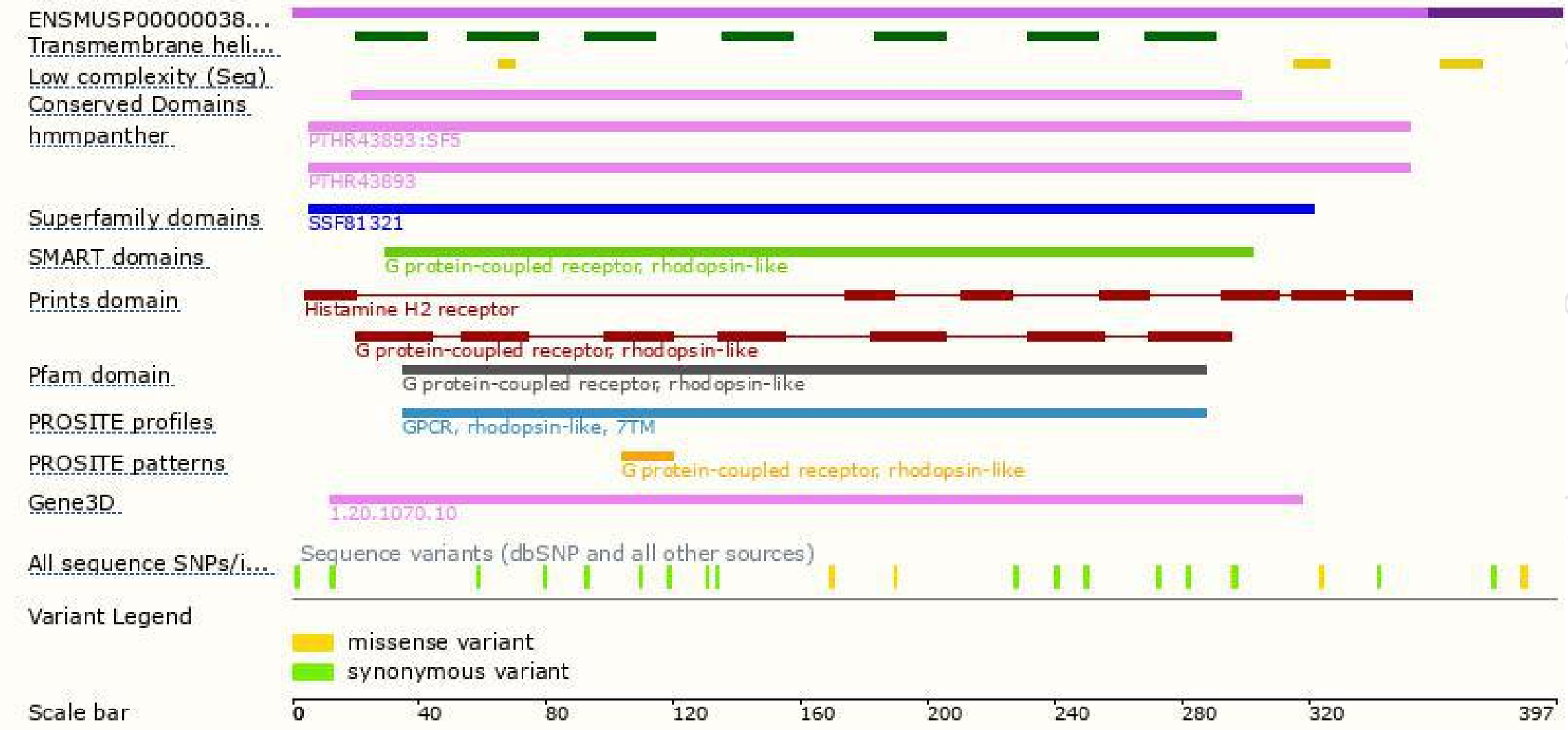
The strategy is based on the design of *Hrh2-201* transcript,The transcription is shown below



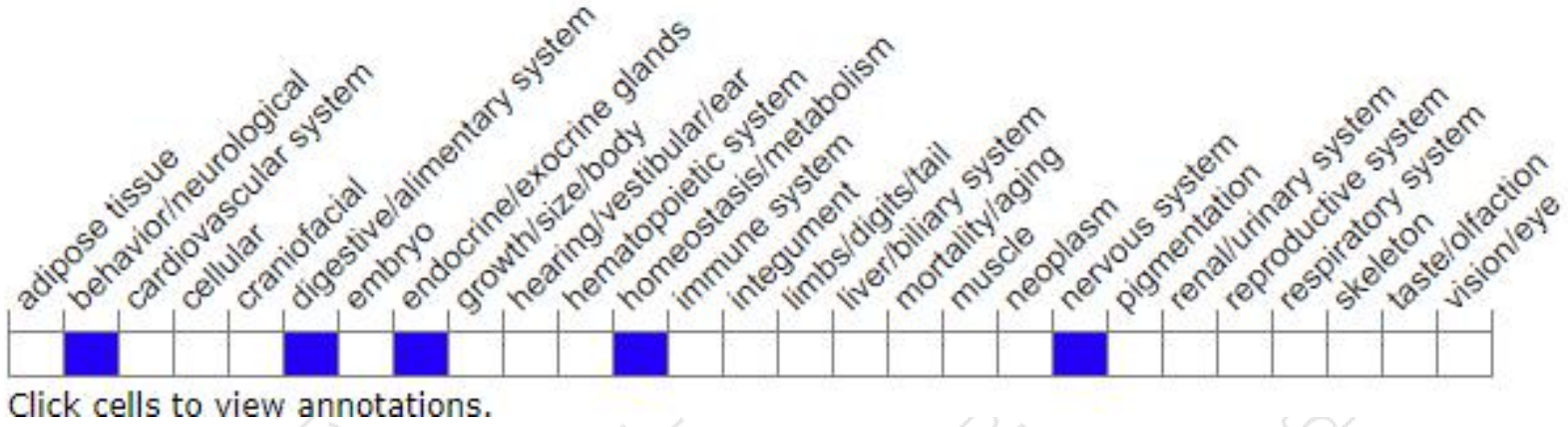
# Genomic location distribution



# 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,Homozygotes for a targeted null mutation exhibit enlarged folds in gastric mucosa, elevated serum gastrin levels, increased numbers of parietal and enterochromaffin-like cells, and lack of secretion of gastric acid in response to histamine or gastrin.

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

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