

Sctr Cas9-CKO Strategy

Designer: JiaYu

Project Overview

Project Name

Sctr

Project type

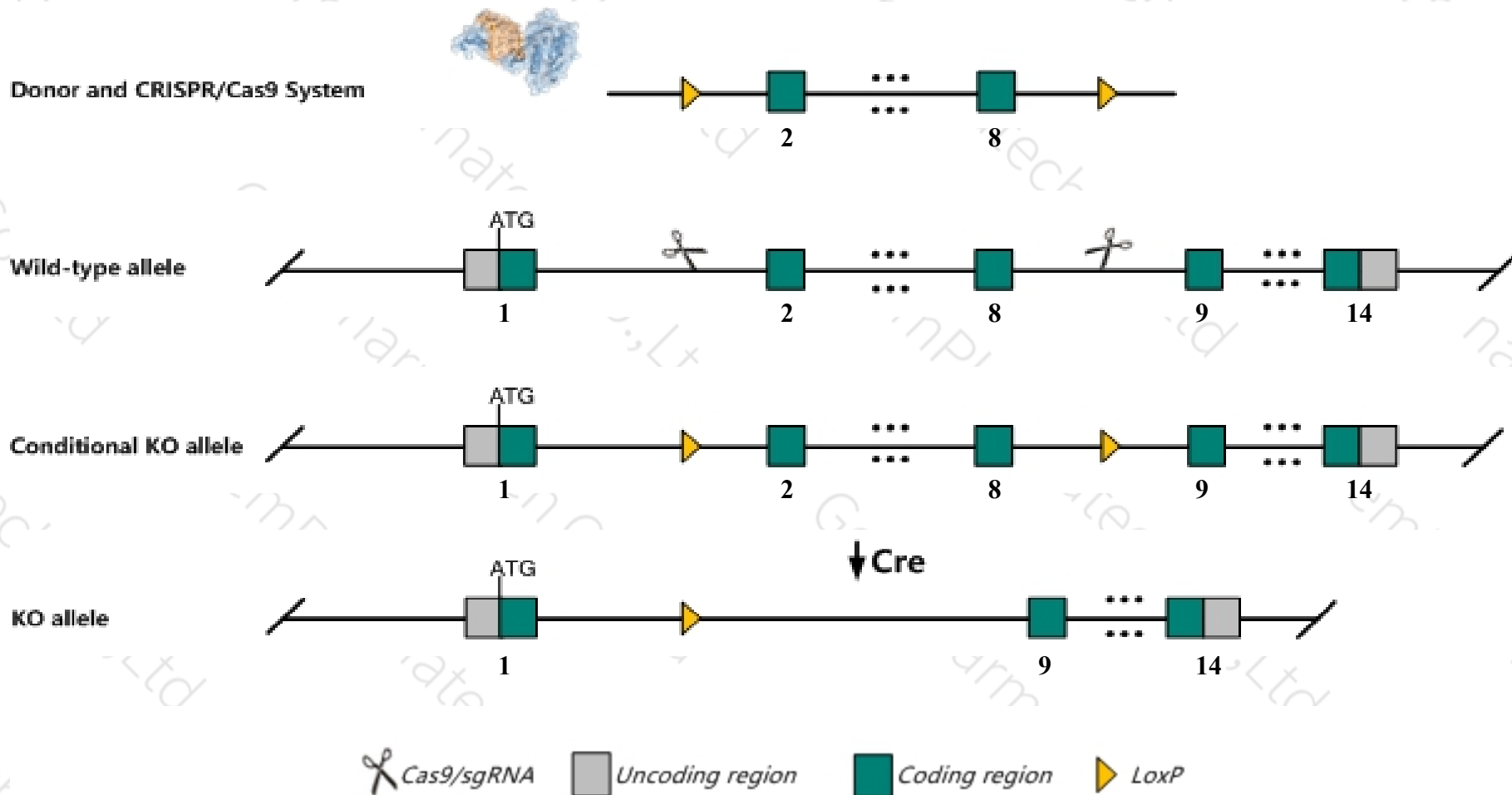
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

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



Technical routes

- The *Sctr* gene has 2 transcripts. According to the structure of *Sctr* gene, exon2-exon8 of *Sctr-201* (ENSMUST00000072886.10) transcript is recommended as the knockout region. The region contains 757bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sctr* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.
- The flox mice was 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, Homozygotes for a null allele show polydipsia, polyuria, decreased urine osmolality, higher serum glucose levels, kidney glomerular and tubular pathology, and impaired renal water reabsorption. Homozygotes for a different null allele show impaired synaptic plasticity and social behavior.
- The *Sctr* gene is located on the Chr1. 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)

Sctr secretin receptor [Mus musculus (house mouse)]

Gene ID: 319229, updated on 31-Jan-2019

Summary



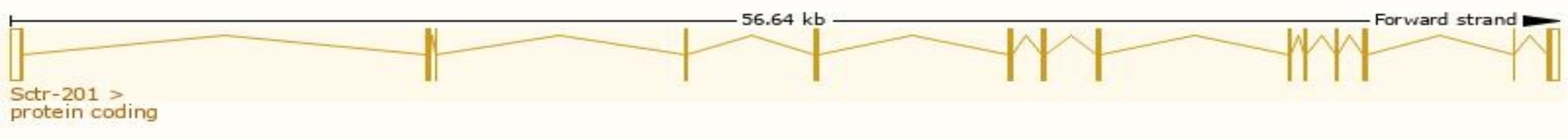
Official Symbol	Sctr provided by MGI
Official Full Name	secretin receptor provided by MGI
Primary source	MGI:MGI:2441720
See related	Ensembl:ENSMUSG00000026387
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6530402O03Rik
Expression	Biased expression in stomach adult (RPKM 11.4), adrenal adult (RPKM 3.1) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

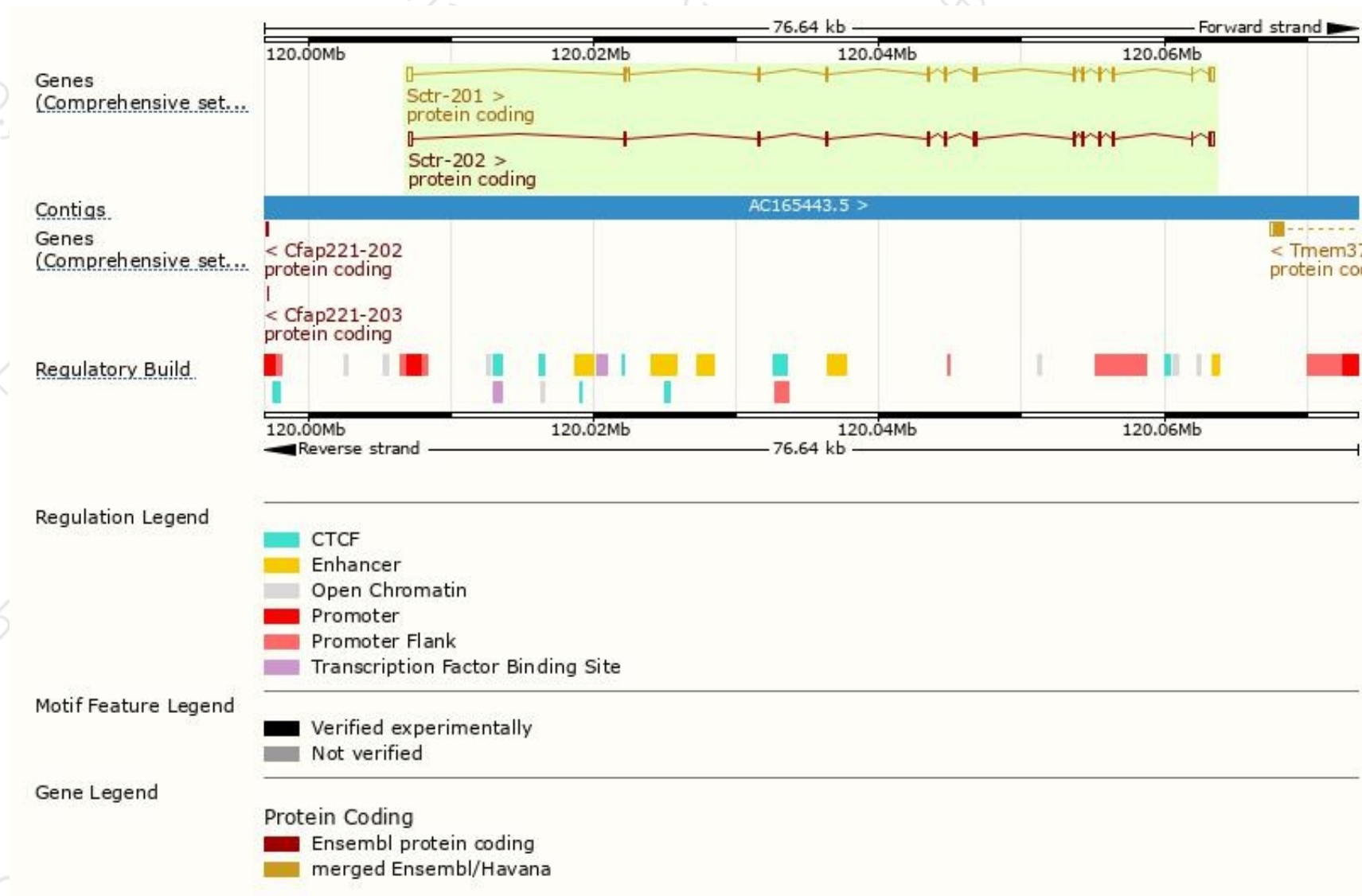
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sctr-201	ENSMUST00000072886.10	2012	464aa	Protein coding	CCDS48341	H7BX37	TSL:2 GENCODE basic APPRIS P3
Sctr-202	ENSMUST00000189037.1	1819	447aa	Protein coding	CCDS78668	Q5FWI2	TSL:1 GENCODE basic APPRIS ALT2

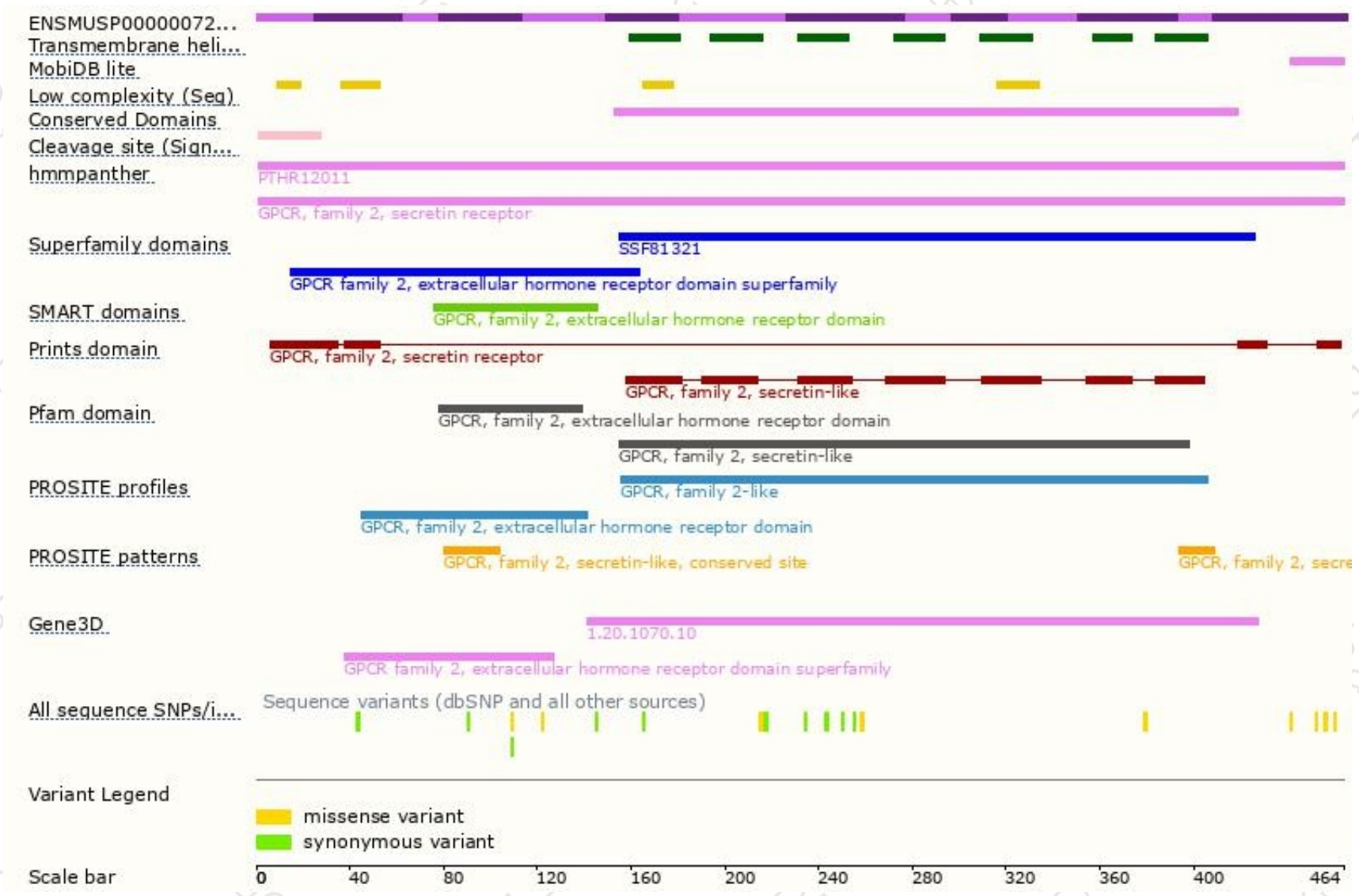
The strategy is based on the design of *Sctr-201* transcript,The transcription is shown below



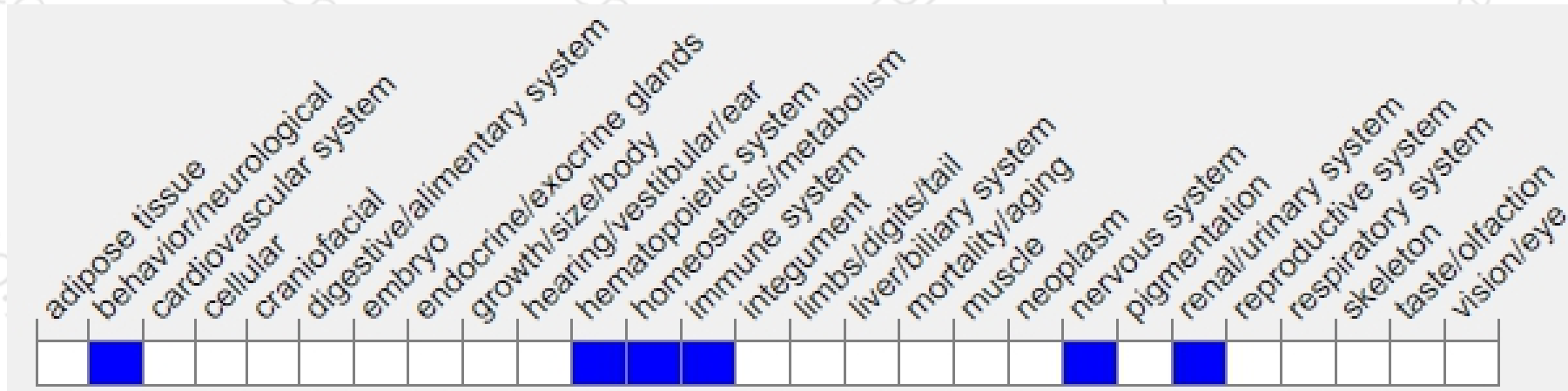
Genomic location distribution



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 null allele show polydipsia, polyuria, decreased urine osmolality, higher serum glucose levels, kidney glomerular and tubular pathology, and impaired renal water reabsorption. Homozygotes for a different null allele show impaired synaptic plasticity and social behavior.

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

Tel: 025-5864 1534

