Slc30a10 Cas9-CKO Strategy

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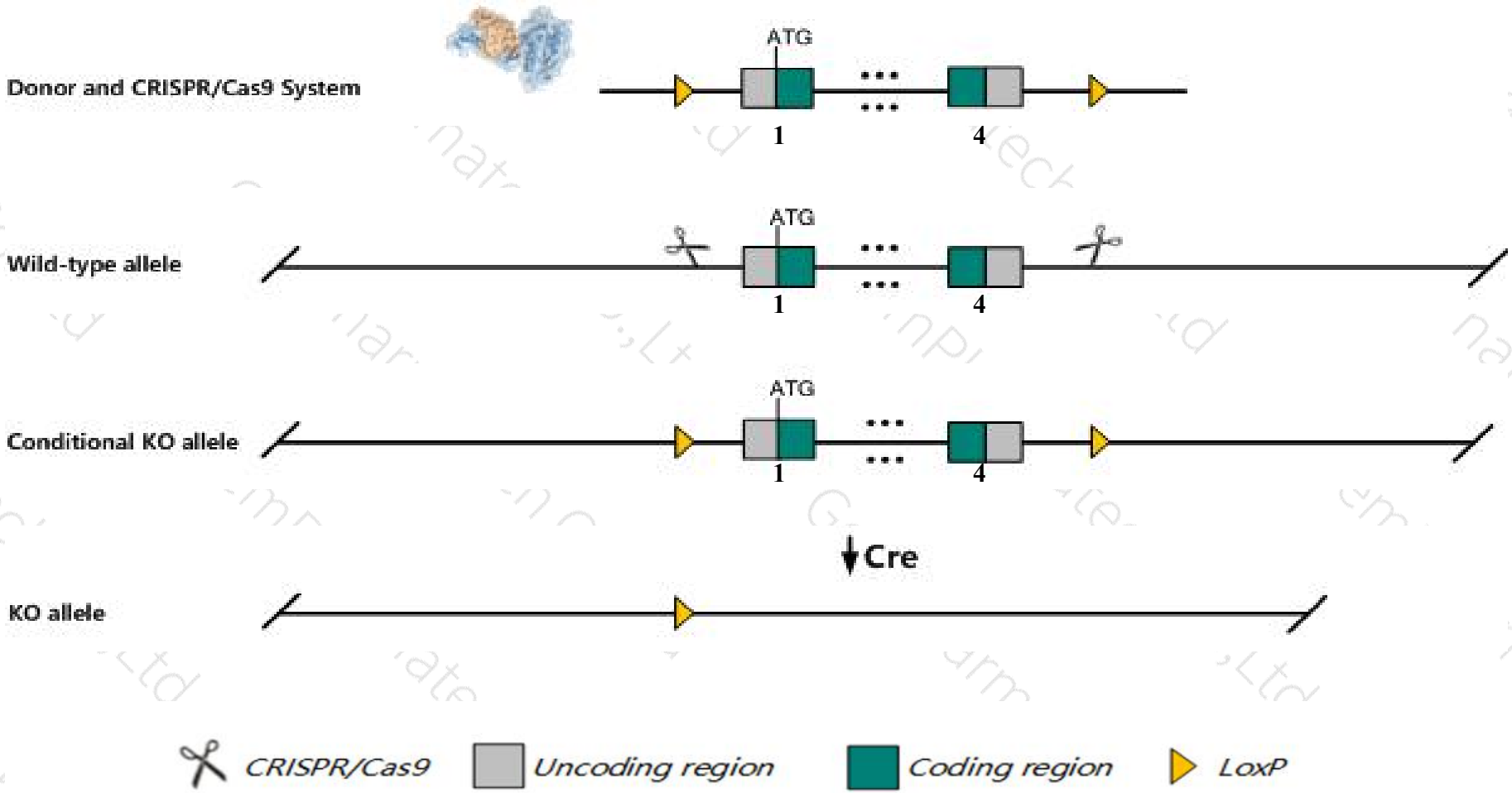
Project Overview

Project Name	***Slc30a10***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc30a10* gene. The schematic diagram is as follows:



Technical routes

- The *Slc30a10* gene has 3 transcripts. According to the structure of *Slc30a10* gene, exon1-exon4 of *Slc30a10-201* (ENSMUST00000061093.6) 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 *Slc30a10* 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,Mice homozygous for a knock-out allele exhibit post-weaning growth defects, increased manganese levels in the brain, blood, liver and thyroid gland, severe hypothyroidism and premature death.

➢The flox region overlaps with *Gm2061*-201 and destroys the gene at the same time.

➢ The *Slc30a10* 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）

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Slc30a10 solute carrier family 30, member 10 [*Mus musculus* (house mouse)]

Gene ID: 226781, updated on 12-Aug-2019

Summary

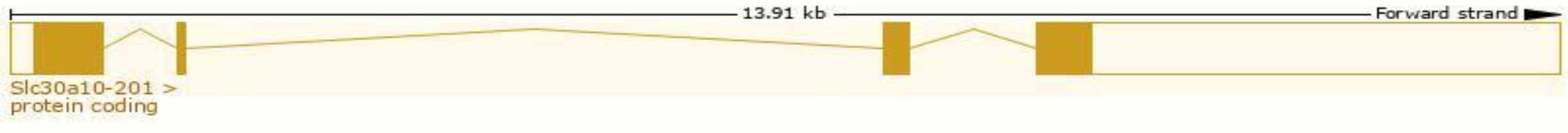
Official Symbol	Slc30a10 provided by MGI
Official Full Name	solute carrier family 30, member 10 provided by MGI
Primary source	MGI:MGI:2685058
See related	Ensembl:ENSMUSG00000026614
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm212; E130106K10Rik
Expression	Biased expression in duodenum adult (RPKM 19.5), liver E14.5 (RPKM 16.9) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

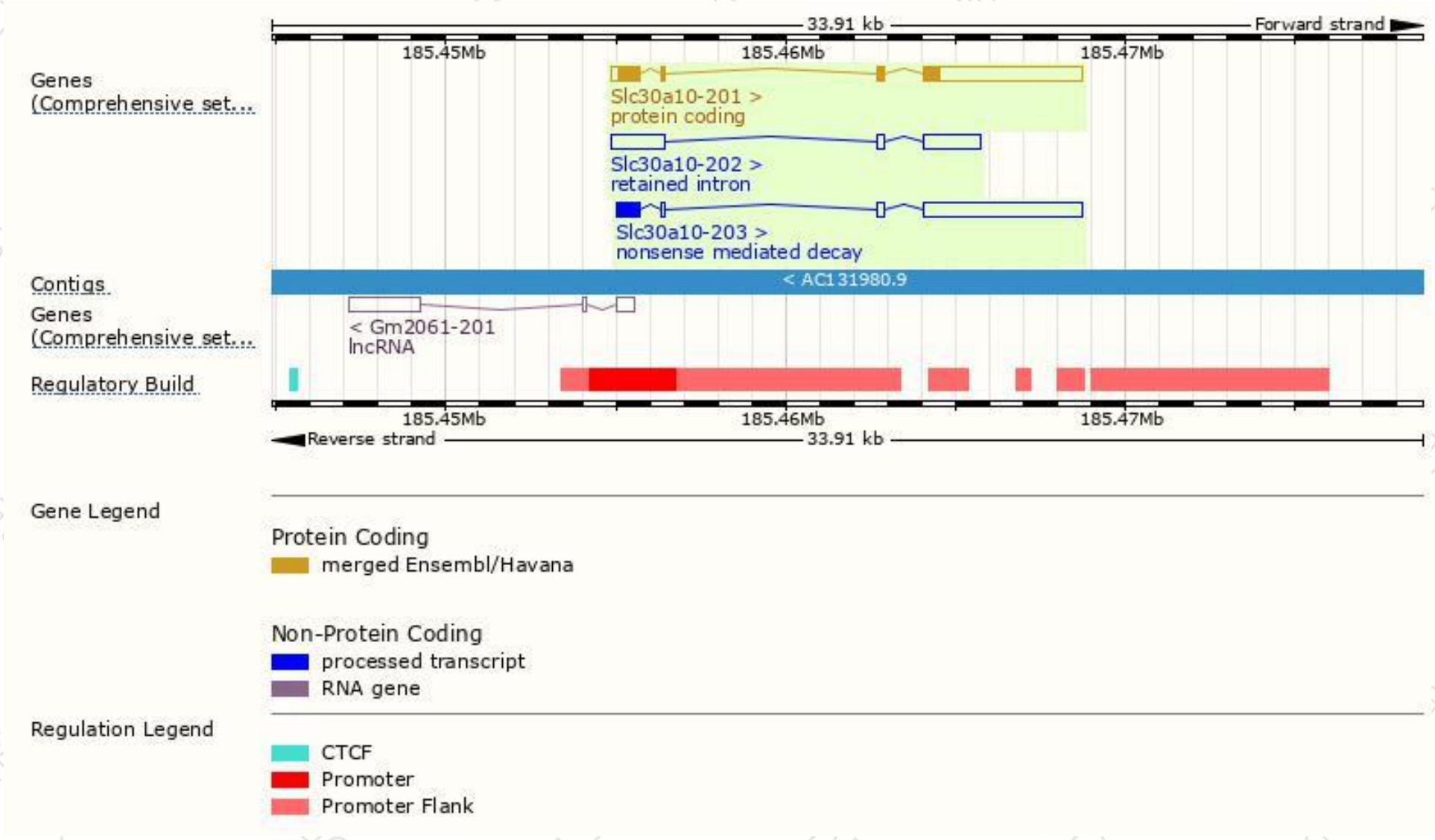
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc30a10-201	ENSMUST00000061093.6	5836	470aa	Protein coding	CCDS15599	Q3UVU3	TSL:1 GENCODE basic APPRIS P1
Slc30a10-203	ENSMUST00000238677.1	5684	215aa	Nonsense mediated decay	-	-	
Slc30a10-202	ENSMUST00000238198.1	3506	No protein	Retained intron	-	-	

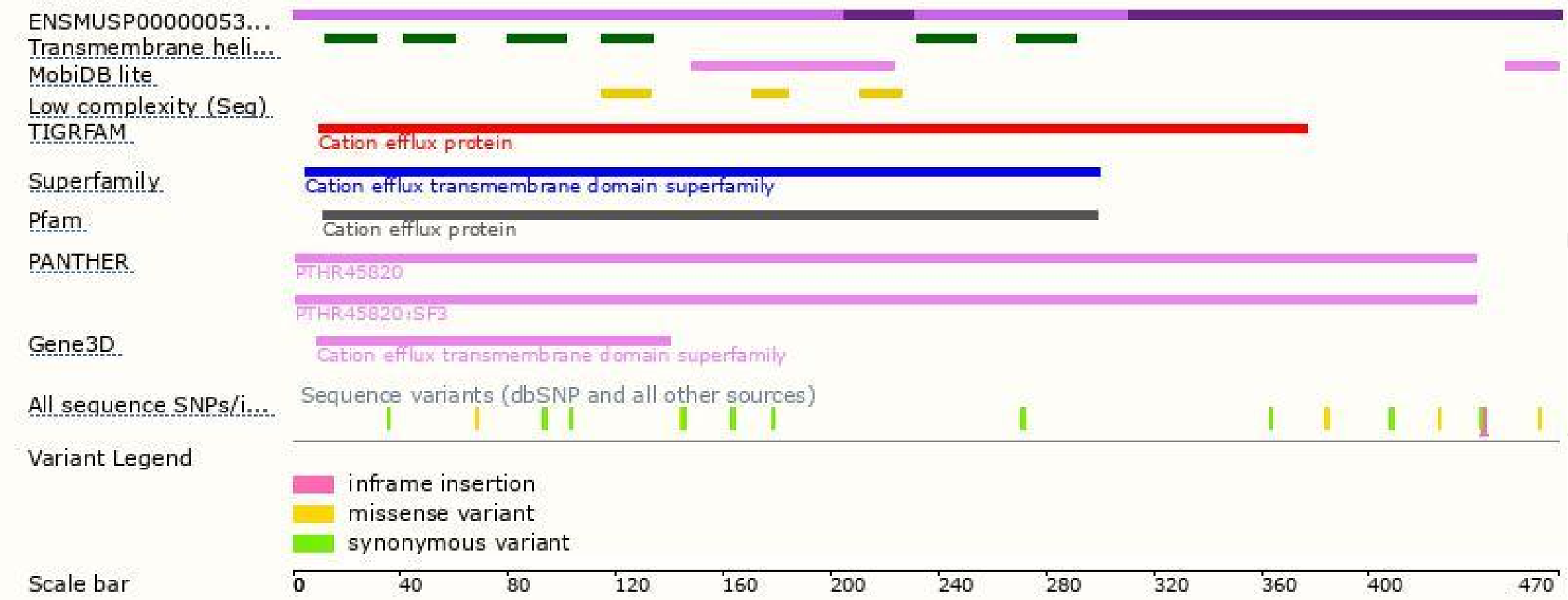
The strategy is based on the design of *Slc30a10-201* transcript,The transcription is shown below



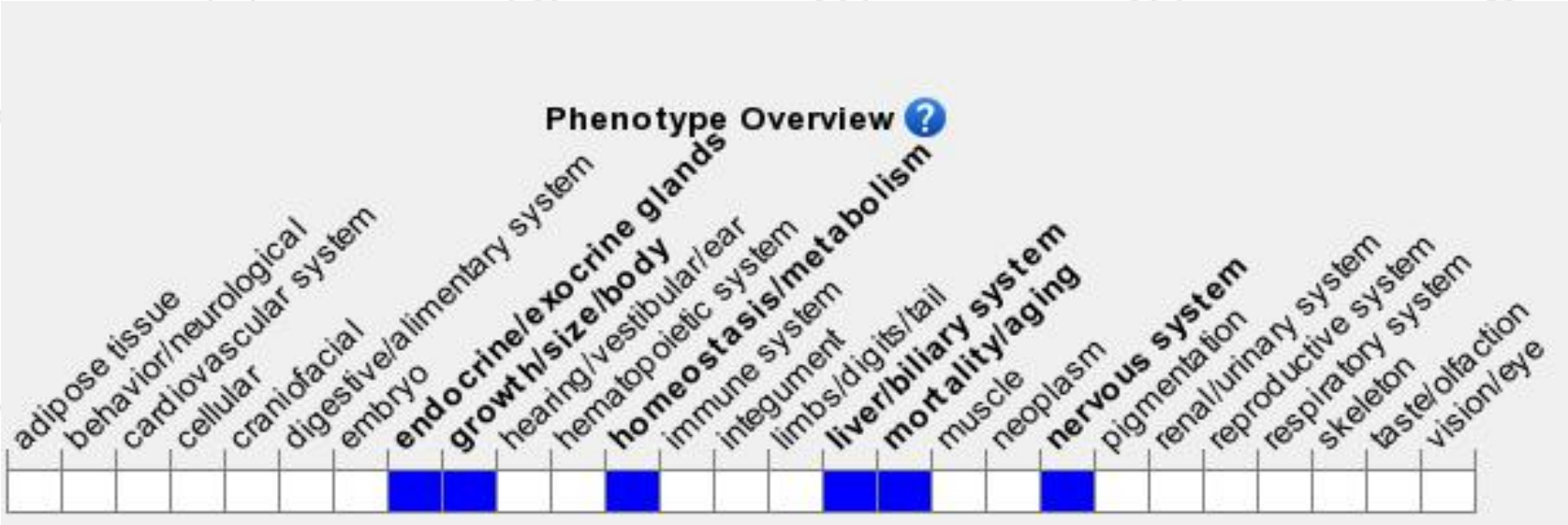
Genomic location distribution



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/).

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

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