

Usp9x Cas9-KO Strategy

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Project Overview

Project Name

Usp9x

Project type

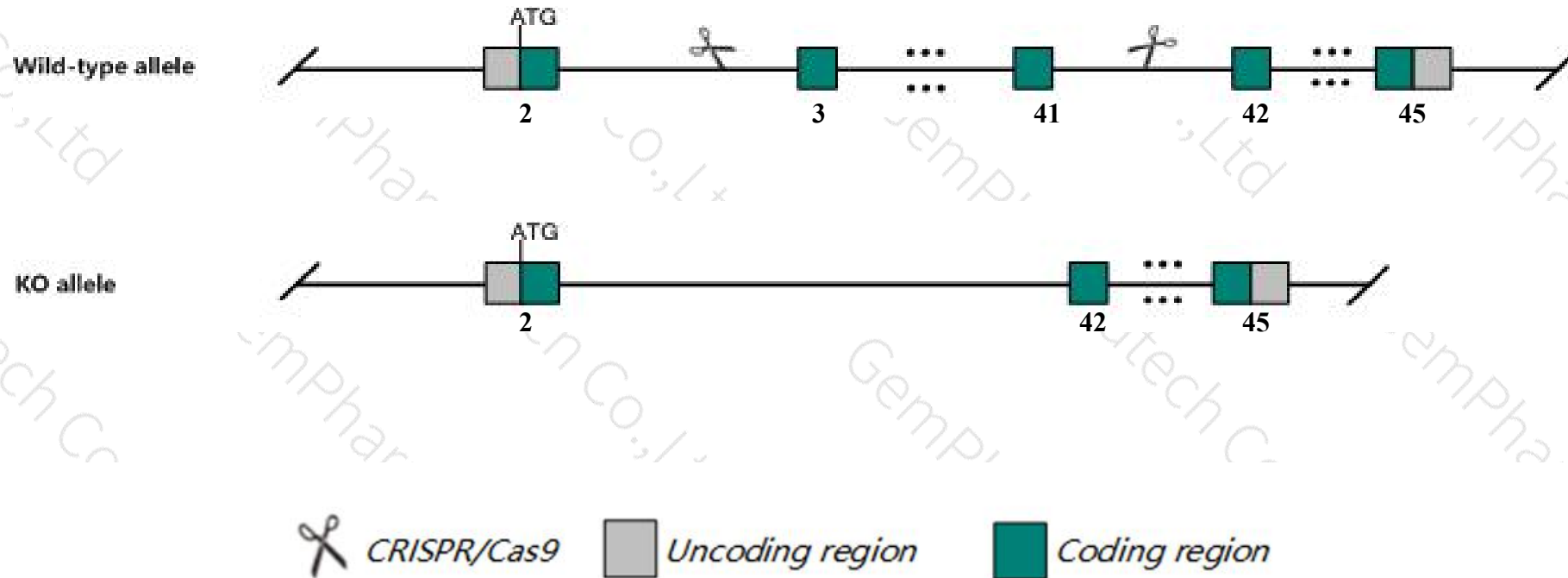
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp9x* gene. The schematic diagram is as follows:



- The *Usp9x* gene has 7 transcripts. According to the structure of *Usp9x* gene, exon3-exon41 of *Usp9x-201* (ENSMUST00000089302.10) transcript is recommended as the knockout region. The region contains 6965bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp9x* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, In a conditional model of pancreatic ductal carcinoma, hemizygous males and heterozygous females with a conditional allele exhibit accelerated tumorigenesis.
- The *Usp9x* gene is located on the ChrX. 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)

Usp9x ubiquitin specific peptidase 9, X chromosome [Mus musculus (house mouse)]

Gene ID: 22284, updated on 7-Apr-2019

Summary



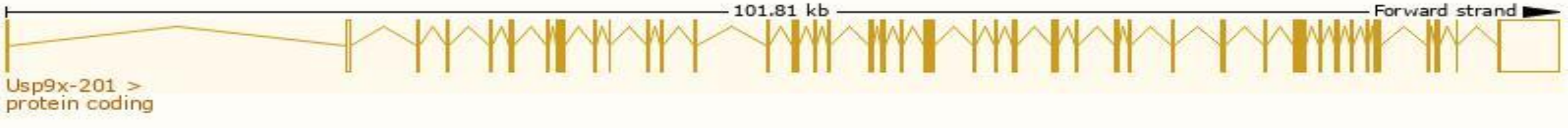
Official Symbol	Usp9x provided by MGI
Official Full Name	ubiquitin specific peptidase 9, X chromosome provided by MGI
Primary source	MGI:MGI:894681
See related	Ensembl:ENSMUSG00000031010
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730589N07Rik, AA407302, AA407699, AL022658, AL022749, Dffrx, FAF-X, Fafl
Expression	Ubiquitous expression in placenta adult (RPKM 19.5), CNS E18 (RPKM 11.9) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

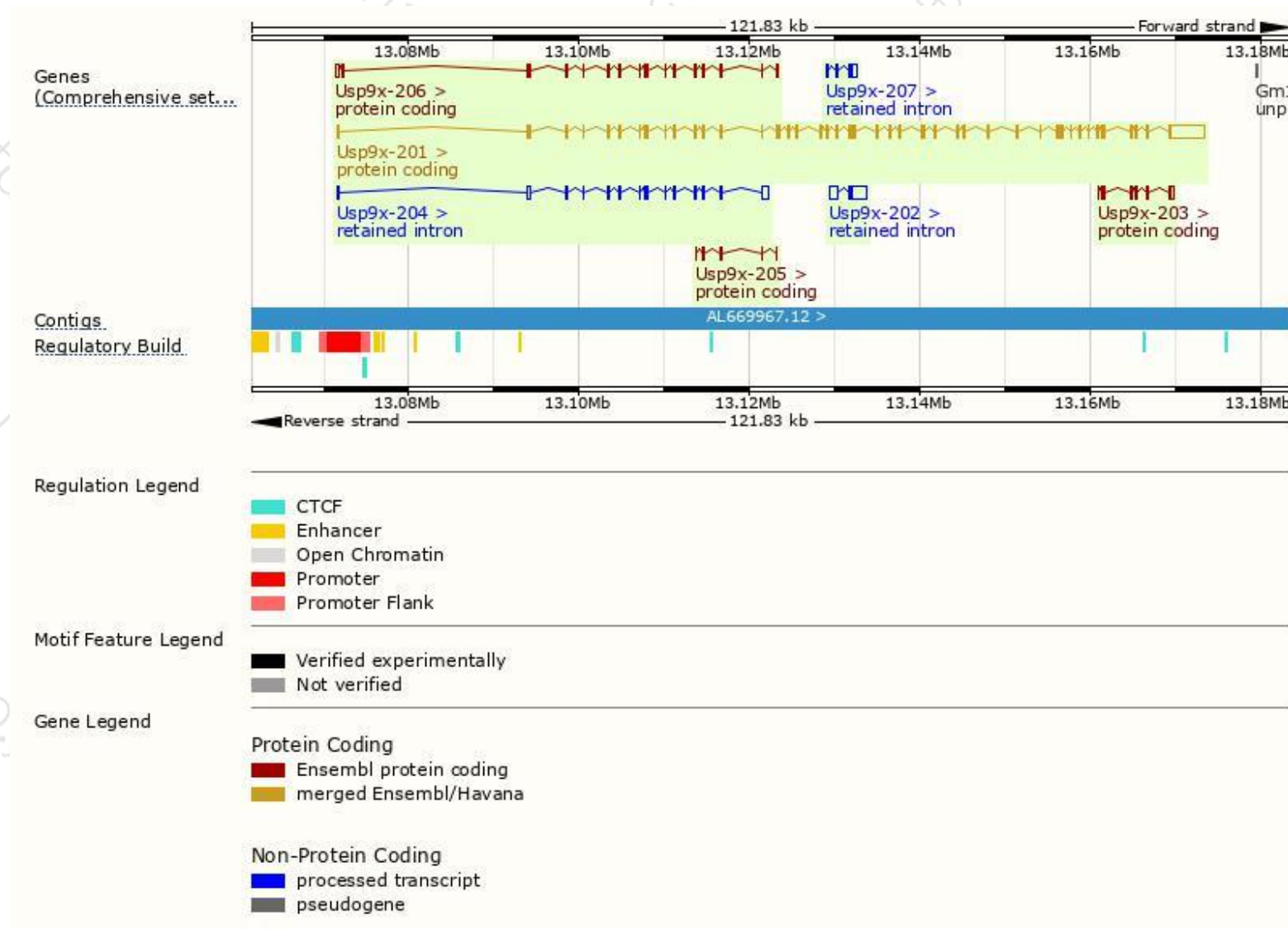
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp9x-201	ENSMUST00000089302.10	11887	2554aa	Protein coding	CCDS40875.4	Q4FE56.4	TSL:1 GENCODE basic APPRIS P1
Usp9x-202	ENSMUST00000124097.1	2864	No protein	Retained intron	-	-	TSL:3
Usp9x-203	ENSMUST00000133997.3	1452	345aa	Protein coding	-	G3UZS3.4	CDS 5' incomplete TSL:5
Usp9x-204	ENSMUST00000139764.8	3019	No protein	Retained intron	-	-	TSL:1
Usp9x-205	ENSMUST00000149021.2	523	174aa	Protein coding	-	G3UY52.4	CDS 5' and 3' incomplete TSL:3
Usp9x-206	ENSMUST00000169594.8	2772	755aa	Protein coding	-	E9PWA9.4	CDS 3' incomplete TSL:1
Usp9x-207	ENSMUST00000174762.7	820	No protein	Retained intron	-	-	TSL:5

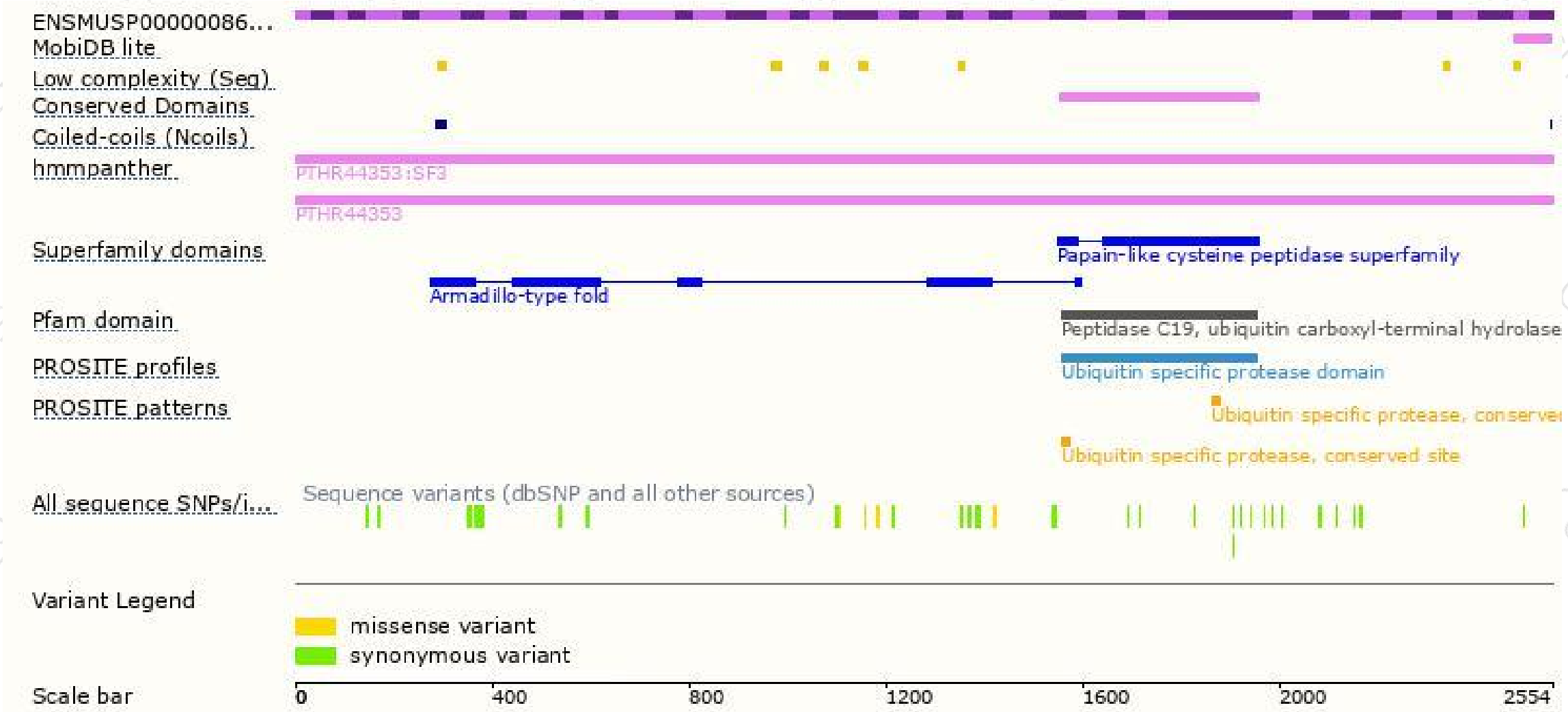
The strategy is based on the design of *Usp9x-201* transcript,The transcription is shown below



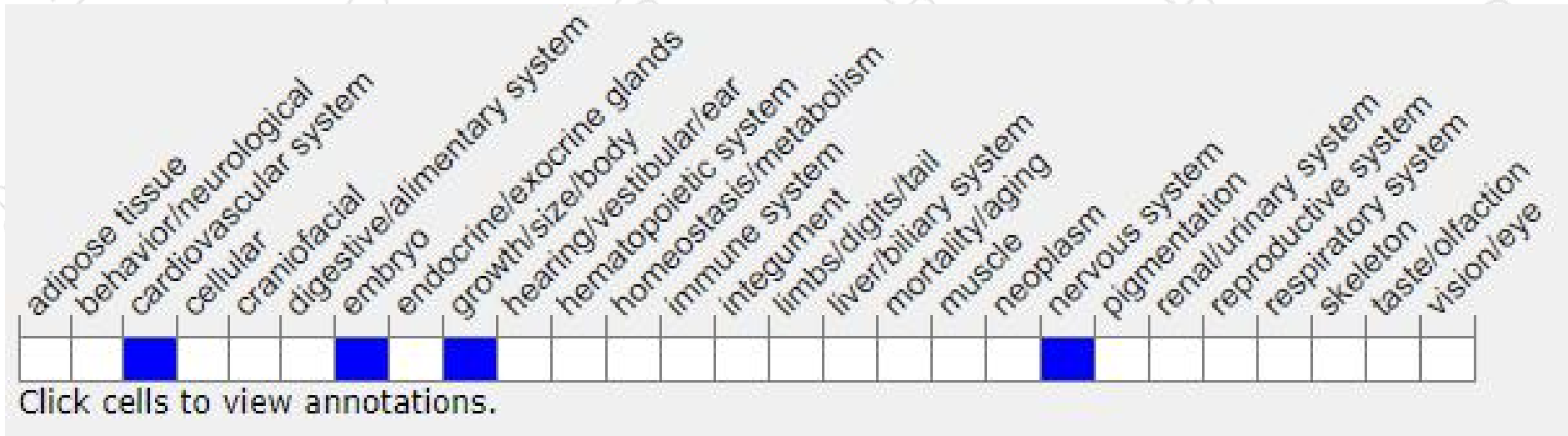
Genomic location distribution



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, In a conditional model of pancreatic ductal carcinoma, hemizygous males and heterozygous females with a conditional allele exhibit accelerated tumorigenesis.

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

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