Serpinf1 Cas9-CKO Strategy

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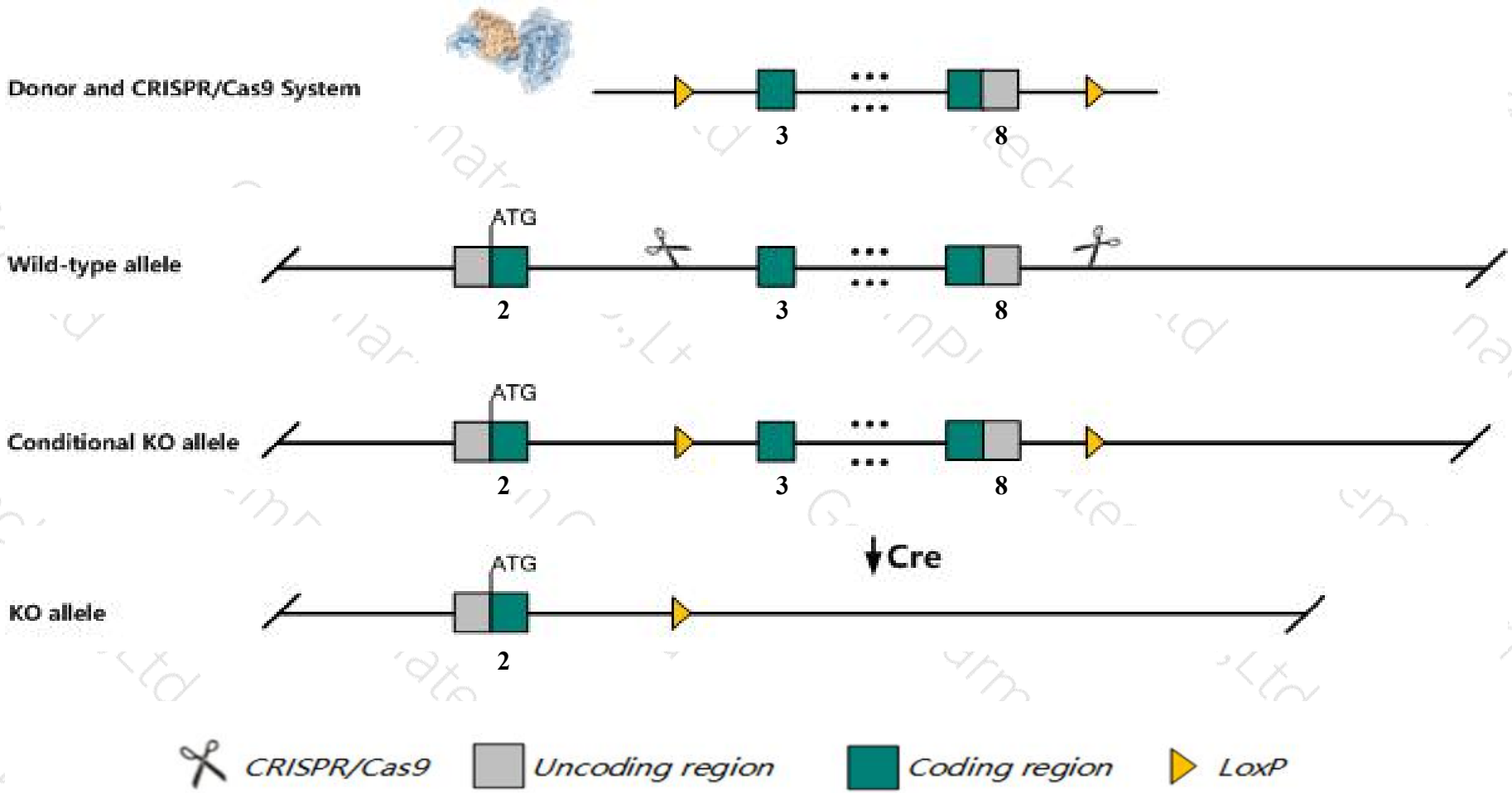
Project Overview

Project Name	***Serpinf1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpinf1* gene. The schematic diagram is as follows:



Technical routes

- The *Serpinf1* gene has 8 transcripts. According to the structure of *Serpinf1* gene, exon3-exon8 of *Serpinf1-201* (ENSMUST00000000769.13) transcript is recommended as the knockout region.The region contains most 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 *Serpinf1* 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,Loss of function results in increased microvasculature, pancreatic enlargement, and prostatic hyperplasia.

- The *Serpinf1* gene is located on the Chr11. 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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Serpinf1 serine (or cysteine) peptidase inhibitor, clade F, member 1 [Mus musculus (house mouse)]

Gene ID: 20317, updated on 5-Mar-2019

Summary

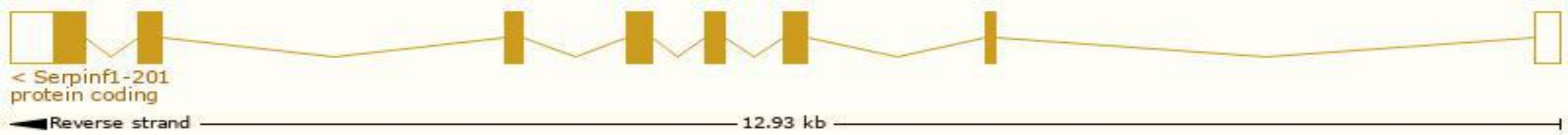
Official Symbol	Serpinf1 provided by MGI
Official Full Name	serine (or cysteine) peptidase inhibitor, clade F, member 1 provided by MGI
Primary source	MGI:MGI:108080
See related	Ensembl:ENSMUSG00000000753
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI195227, EPC-1, Pedf, Pedfl, Sdf3
Expression	Biased expression in liver adult (RPKM 193.9), mammary gland adult (RPKM 118.2) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

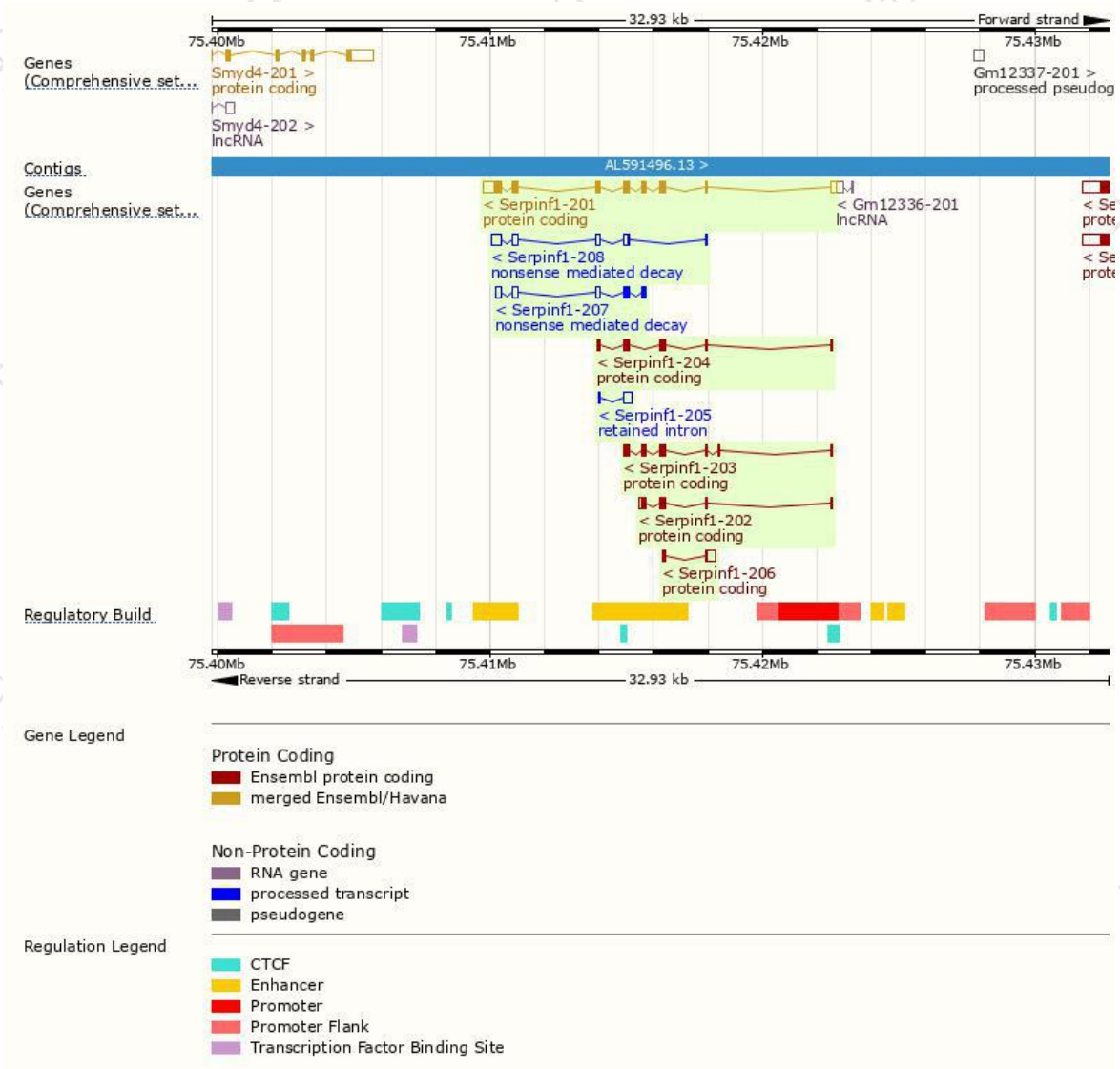
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Serpinf1-201	ENSMUST00000000769.13	1832	417aa	Protein coding	CCDS25045	P97298	TSL:1 GENCODE basic APPRIS P1
Serpinf1-203	ENSMUST00000137103.7	757	213aa	Protein coding	-	B7ZC25	CDS 3' incomplete TSL:3
Serpinf1-204	ENSMUST00000138661.7	718	206aa	Protein coding	-	Q5ND37	CDS 3' incomplete TSL:3
Serpinf1-202	ENSMUST00000125982.1	605	147aa	Protein coding	-	E9PWS2	TSL:1 GENCODE basic
Serpinf1-206	ENSMUST00000155009.1	502	64aa	Protein coding	-	E9PZX2	CDS 3' incomplete TSL:2
Serpinf1-208	ENSMUST00000168902.7	976	55aa	Nonsense mediated decay	-	E9PXR9	TSL:5
Serpinf1-207	ENSMUST00000167281.7	882	125aa	Nonsense mediated decay	-	F6S1M4	CDS 5' incomplete TSL:3
Serpinf1-205	ENSMUST00000139403.1	352	No protein	Retained intron	-	-	TSL:3

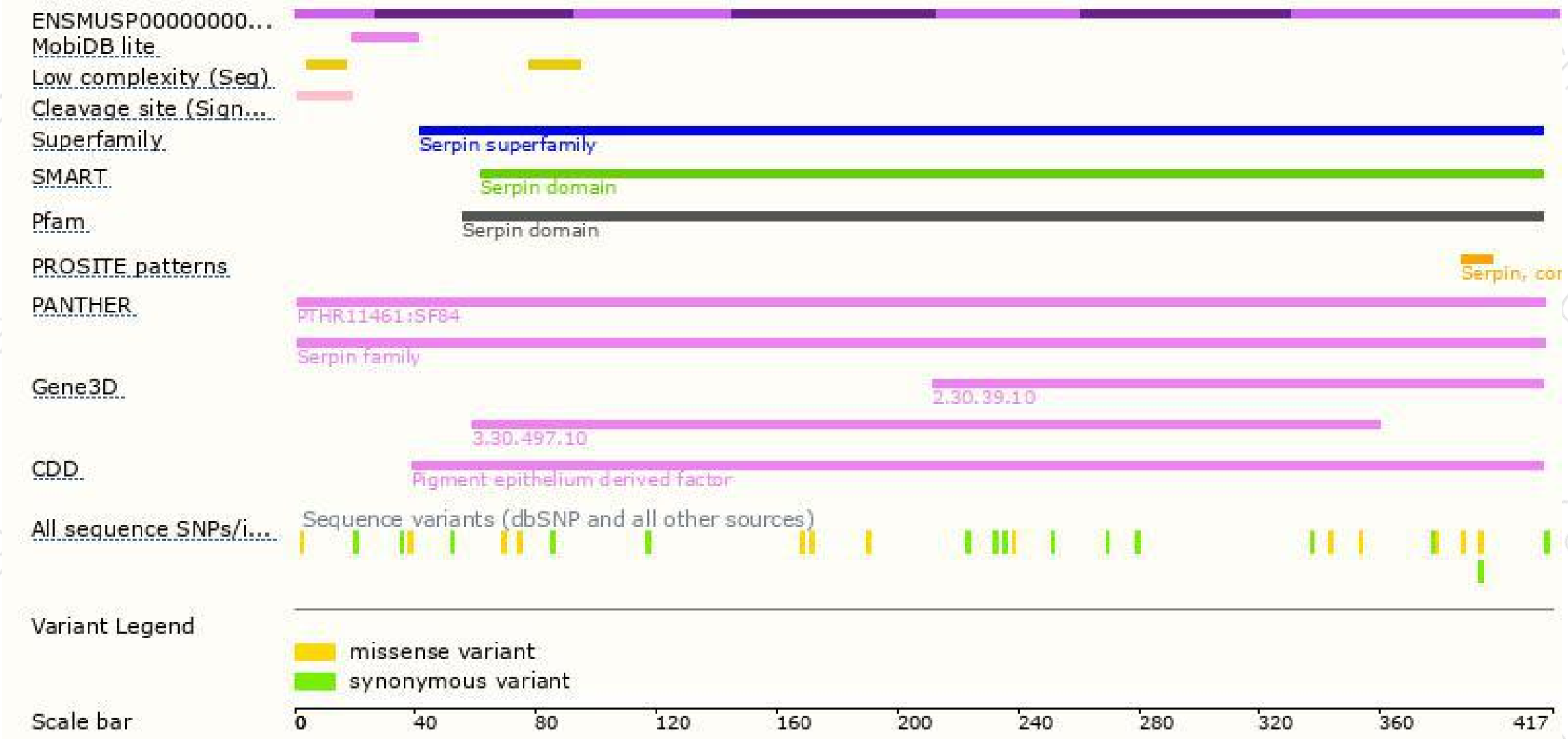
The strategy is based on the design of *Serpinf1-201* transcript,The transcription is shown below



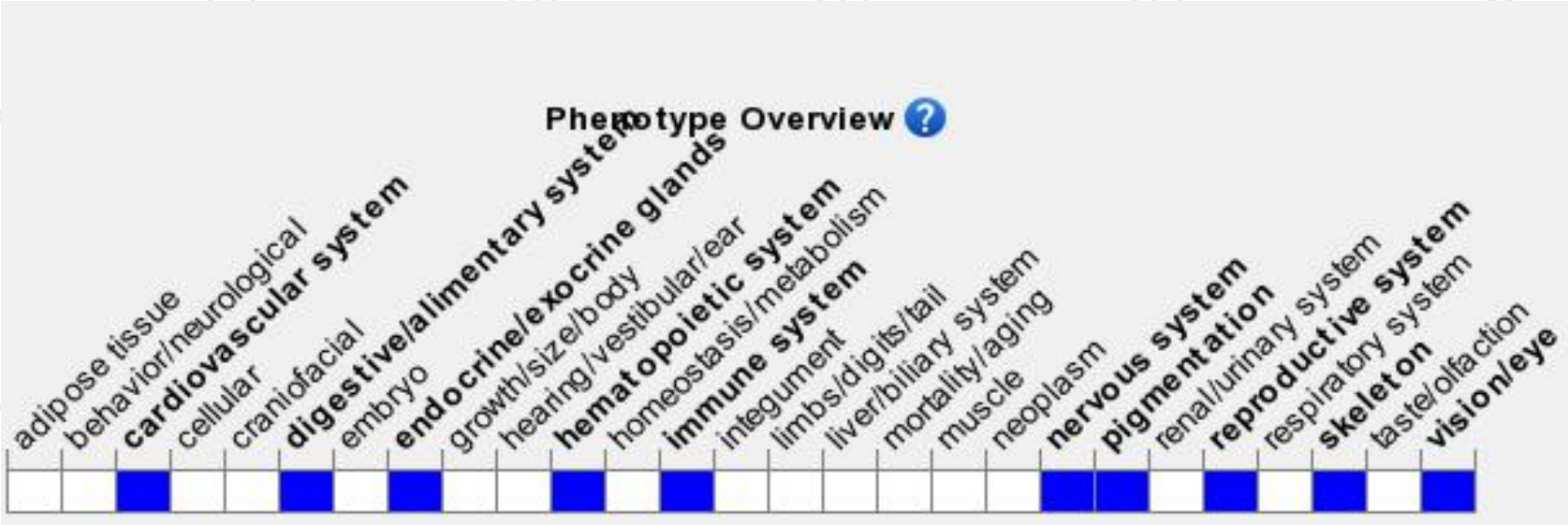
Genomic location distribution



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,Loss of function results in increased microvasculature, pancreatic enlargement, and prostatic hyperplasia.

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

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