

Serpina6 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-2-14

Project Overview

Project Name

Serpina6

Project type

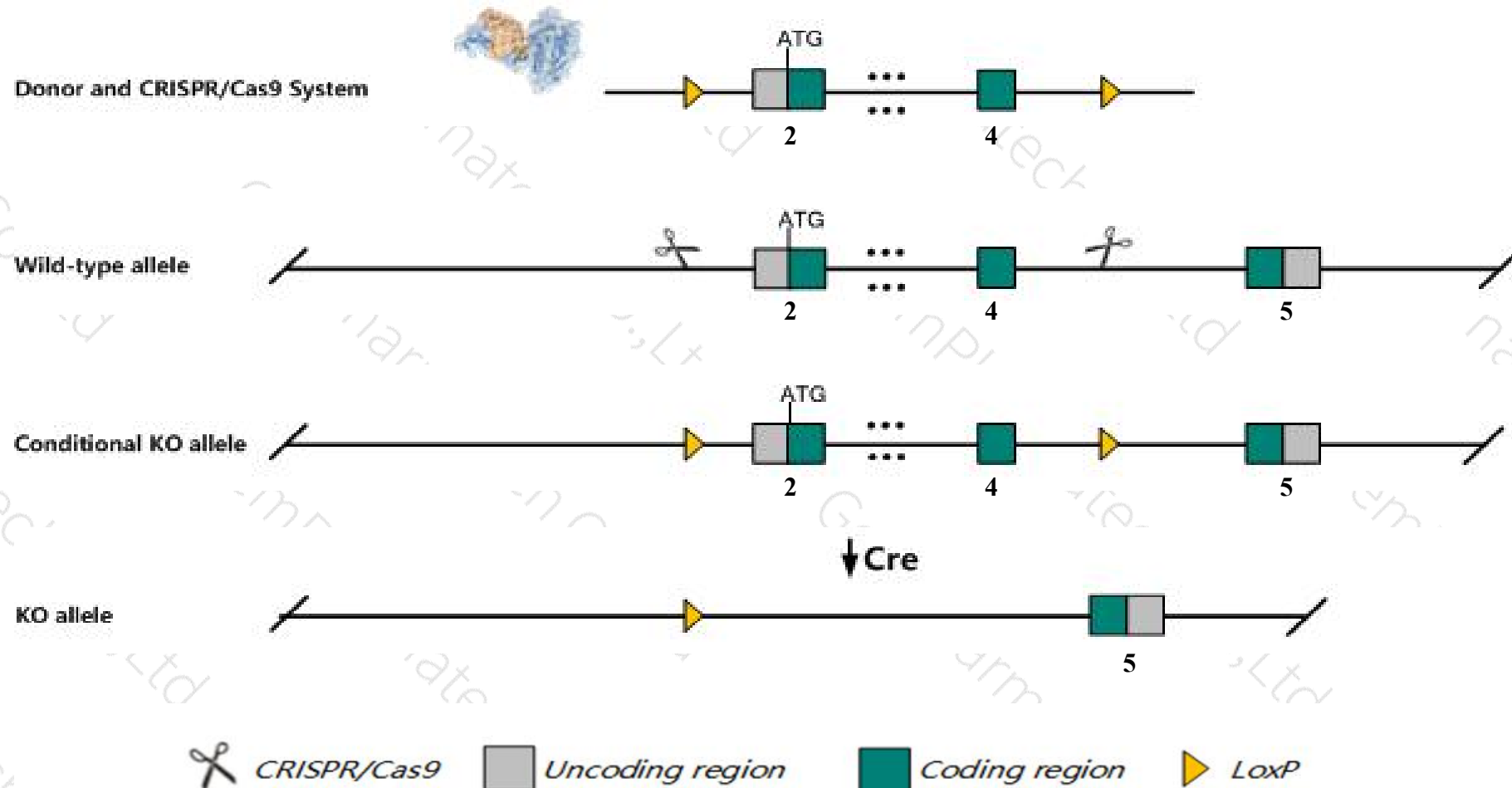
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpina6* gene. The schematic diagram is as follows:



Technical routes

- The *Serpina6* gene has 2 transcripts. According to the structure of *Serpina6* gene, exon2-exon4 of *Serpina6*-201 (ENSMUST00000044159.6) 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 *Serpina6* 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.

- According to the existing MGI data, Null homozygotes exhibit reduced total plasma corticosterone, increased susceptibility to bacterial infection, attenuation of the stress-induced surge in free corticosterone, and enhanced behavioral response to intense or uncontrollable stress. They exhibit no locomotor sensitization to cocaine.
- The *Serpina6* gene is located on the Chr12. 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)

Serpina6 serine (or cysteine) peptidase inhibitor, clade A, member 6 [Mus musculus (house mouse)]

Gene ID: 12401, updated on 31-Jan-2019

Summary



Official Symbol Serpina6 provided by [MGI](#)

Official Full Name serine (or cysteine) peptidase inhibitor, clade A, member 6 provided by [MGI](#)

Primary source [MGI:MGI:88278](#)

See related [Ensembl:ENSMUSG00000060807](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Cbg

Summary This gene encodes a protein that belongs to the serpin (serine protease inhibitor) family. The encoded protein is an alpha-globulin with corticosteroid-binding properties. This is the major transport protein for glucocorticoids and progestins in the blood of most vertebrates. The gene localizes to a chromosomal region containing several closely related serine protease inhibitors. [provided by RefSeq, Sep 2015]

Expression Biased expression in liver E14.5 (RPKM 537.1), liver E14 (RPKM 488.5) and 1 other tissue [See more](#)

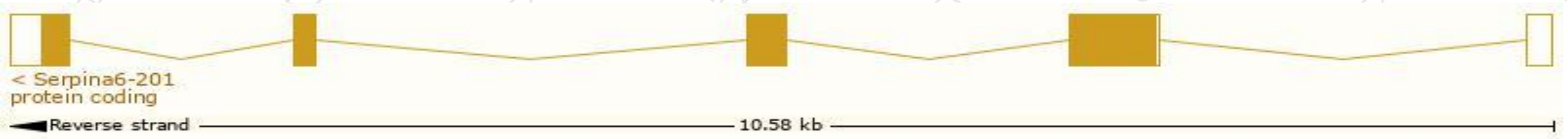
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

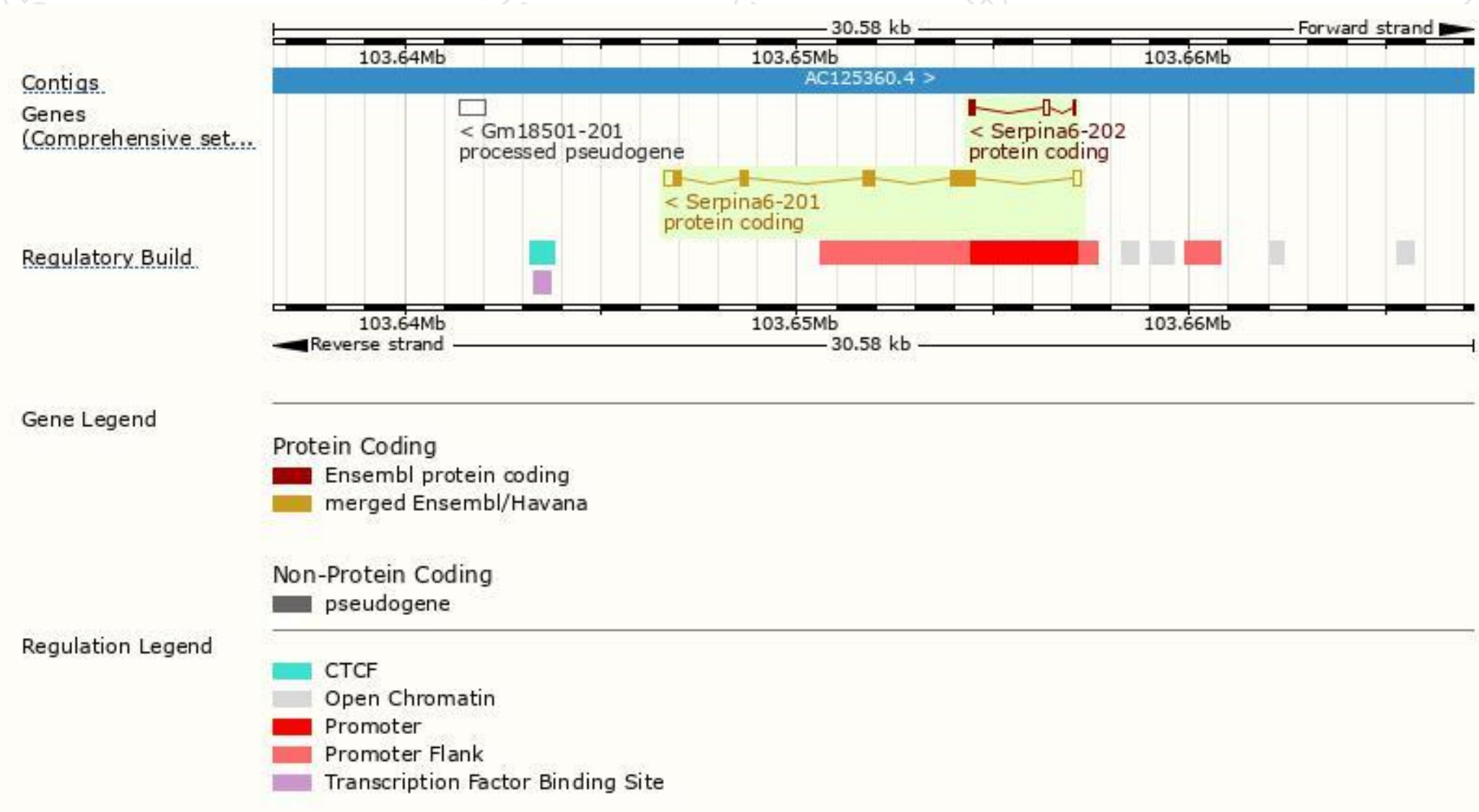
The gene has 2 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|--------------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------------------|
| Serpina6-201 | ENSMUST00000044159.6 | 1605 | 397aa | Protein coding | CCDS26135 | Q06770 | TSL:1 GENCODE basic APPRIS P1 |
| Serpina6-202 | ENSMUST00000152517.1 | 356 | 38aa | Protein coding | - | D3Z2I9 | CDS 3' incomplete TSL:3 |

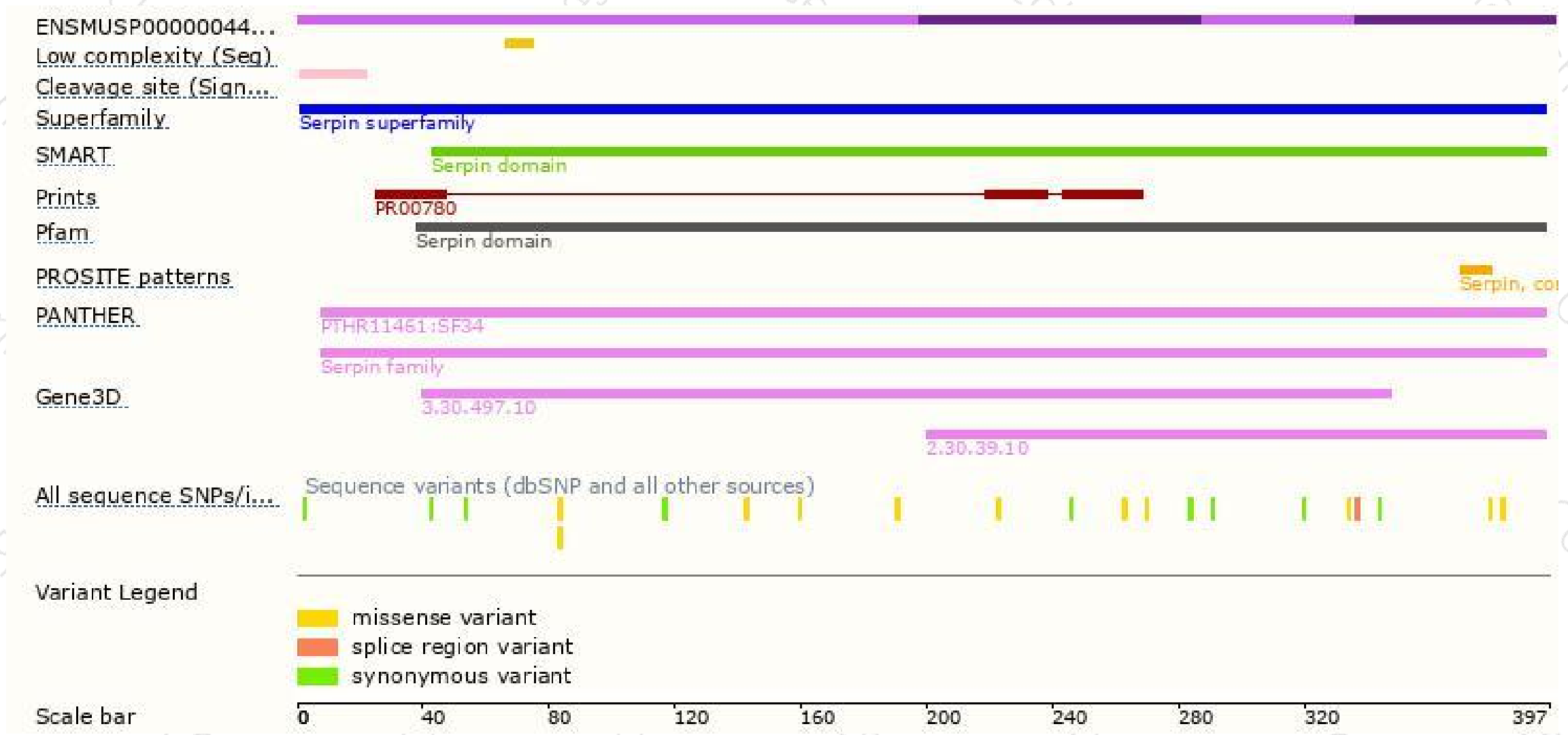
The strategy is based on the design of *Serpina6-201* transcript,The transcription is shown below



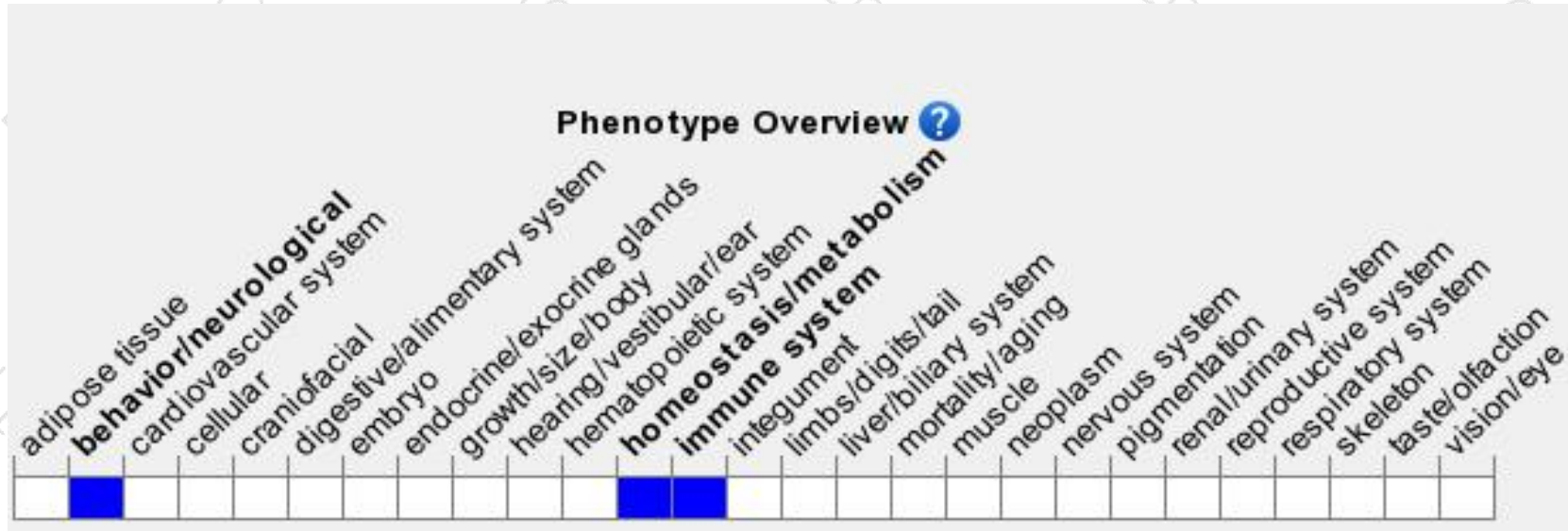
Genomic location distribution



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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