

Serpind1 Cas9-KO Strategy

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Reviewer :

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Design Date:

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Project Overview

Project Name

Serpind1

Project type

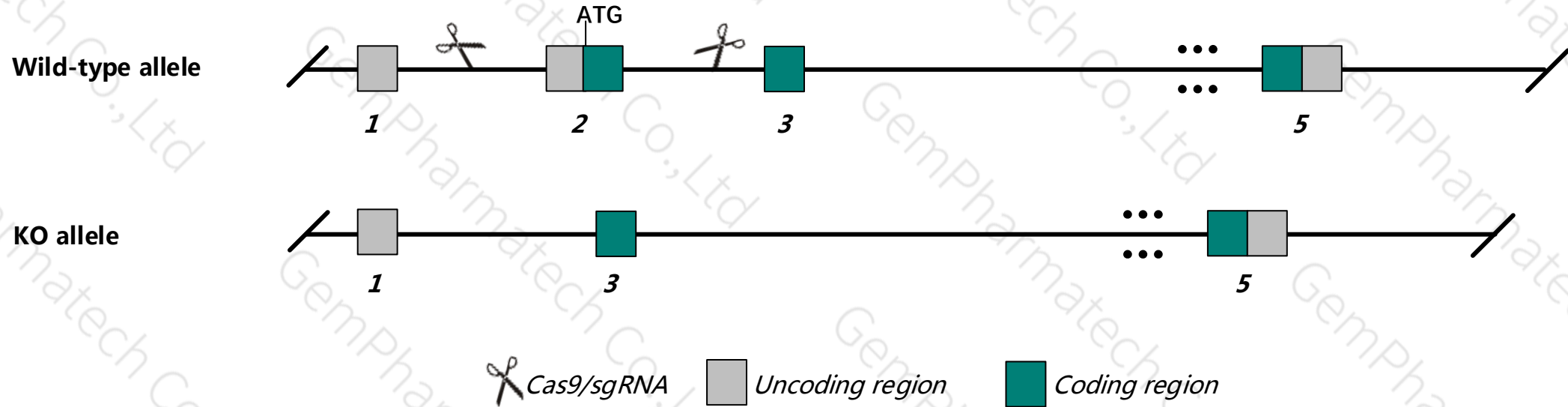
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpind1* gene. The schematic diagram is as follows:



Technical routes

- The *Serpind1* gene has 2 transcripts. According to the structure of *Serpind1* gene, exon2 of *Serpind1*-201 (ENSMUST00000023450.14) 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 *Serpind1* gene. The brief process is as follows: sgRNA was transcribed in vitro was constructed. Cas9, sgRNA 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.

- According to the existing MGI data , Mice homozygous for disruptions in this gene display a normal phenotype.
- The KO region contains partial intron of the *Pi4ka* gene. Knockout the region may affect the function of *Pi4ka* gene.
- The *Serpind1* gene is located on the Chr16. 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)

Serpind1 serine (or cysteine) peptidase inhibitor, clade D, member 1 [*Mus musculus* (house mouse)]

Gene ID: 15160, updated on 12-Aug-2019

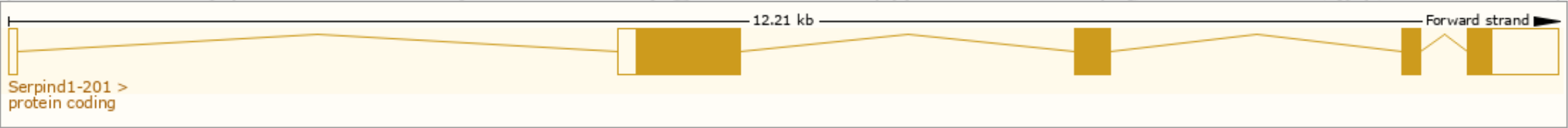
Summary	
Official Symbol	Serpind1 provided by MGI
Official Full Name	serine (or cysteine) peptidase inhibitor, clade D, member 1 provided by MGI
Primary source	MGI:MGI:96051
See related	Ensembl:ENSMUSG00000022766
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	HCII; Hcf2; HC-II; AA985900; AI303446
Expression	Biased expression in liver adult (RPKM 147.0), liver E18 (RPKM 126.4) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

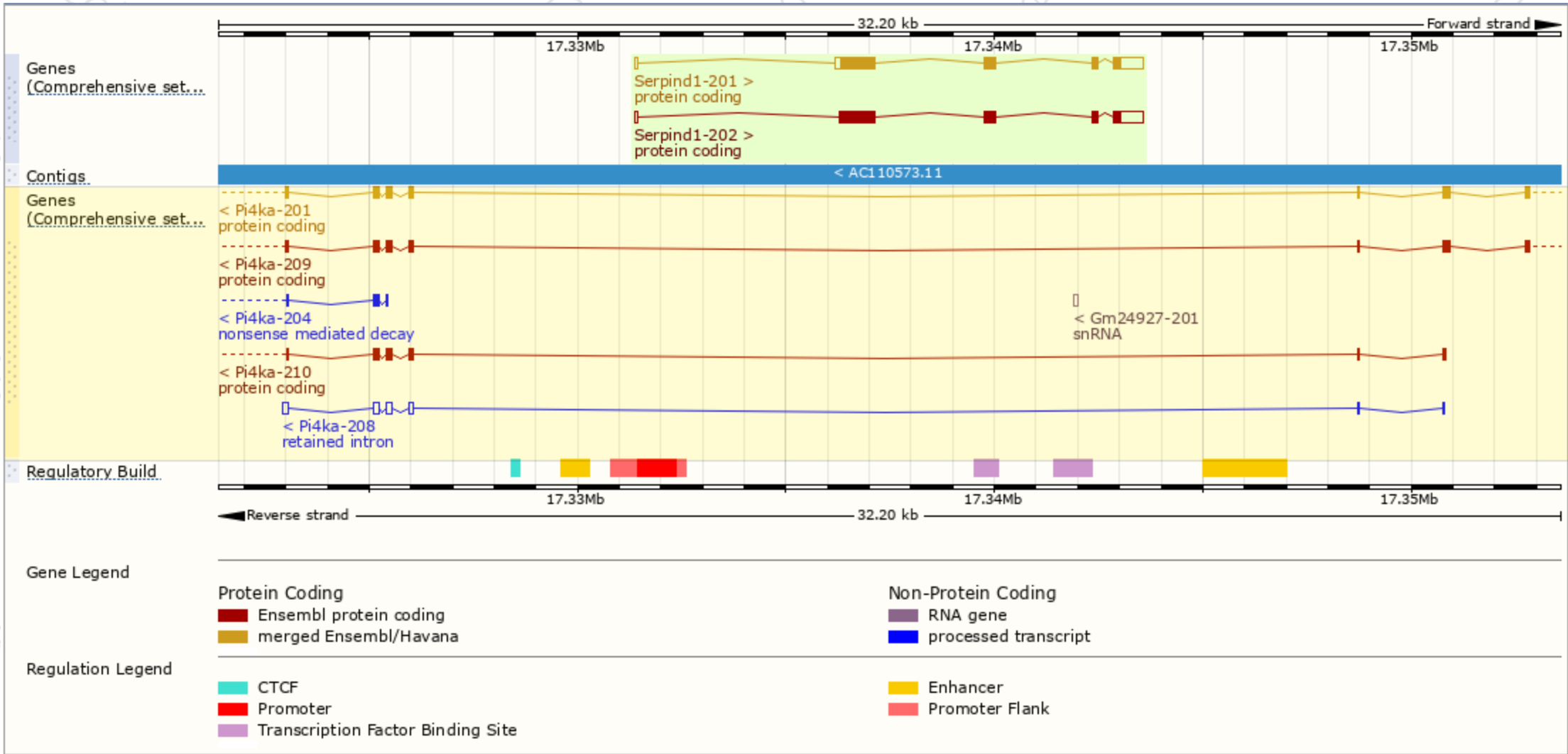
The gene has 2 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Serpind1-201	ENSMUST00000023450.14	2191	478aa	 Protein coding	CCDS28000	P49182	TSL:1 GENCODE basic APPRIS P1
Serpind1-202	ENSMUST00000231884.1	2051	478aa	 Protein coding	CCDS28000	P49182	GENCODE basic APPRIS P1

The strategy is based on the design of *Serpind1*-201 transcript, The transcription is shown below



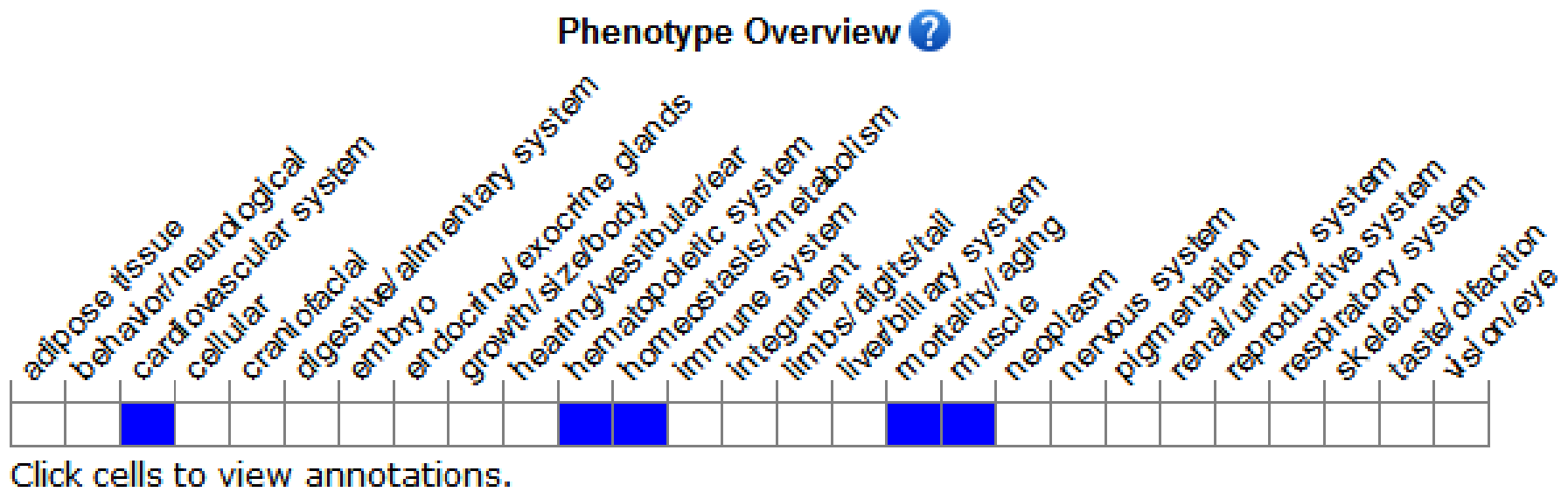
Genomic location distribution



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,Mice homozygous for disruptions in this gene display a normal phenotype.

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