Plce1 Cas9-KO Strategy

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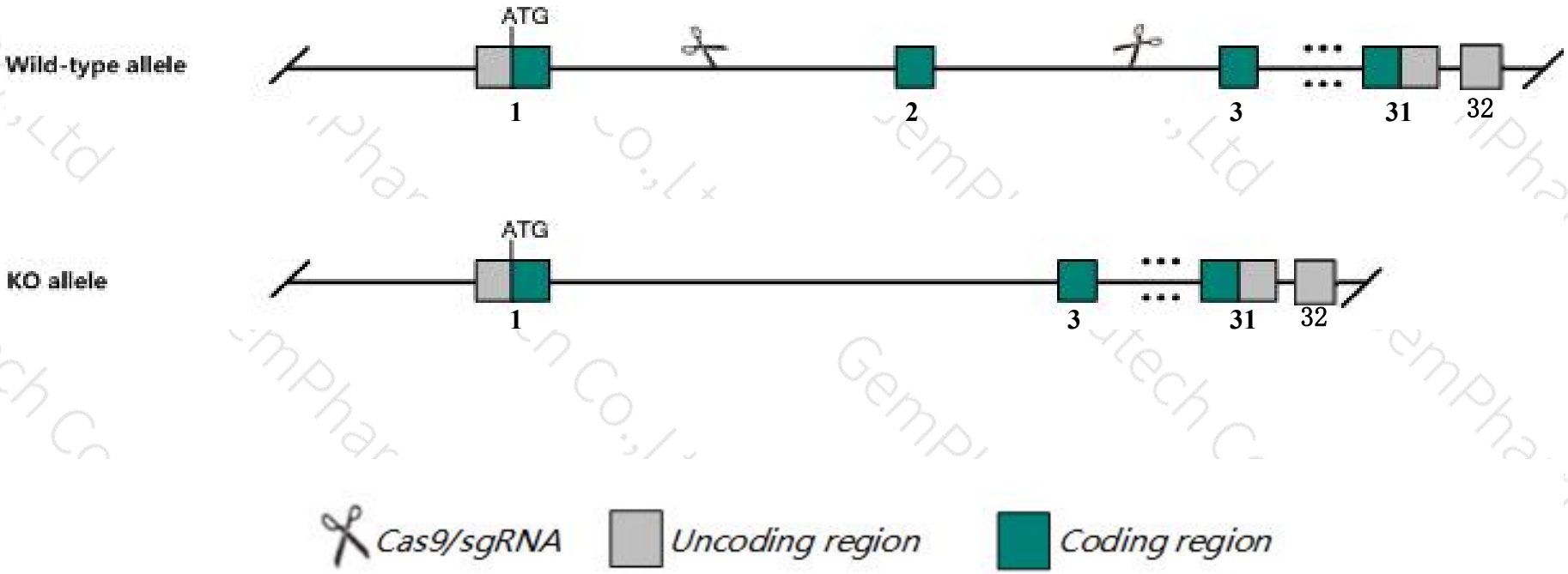
Project Overview

Project Name	***Plce1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plce1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Plce1* gene has 7 transcripts. According to the structure of *Plce1* gene, exon2 of *Plce1-201* (ENSMUST00000169713.8) transcript is recommended as the knockout region.The region contains 289bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Plce1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,homozygous mutation of this gene results in a congenital semilunar valvulogenesis defect which causes regurgitation and stenosis, and decreased incidence of induced skin tumors. Another mutant exhibits decreased cardiac contraction and increased hypertrophy in response to chronic stress.

- The *Plce1* gene is located on the Chr19. 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）

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Plce1 phospholipase C, epsilon 1 [*Mus musculus* (house mouse)]

Gene ID: 74055, updated on 10-Oct-2019

Summary

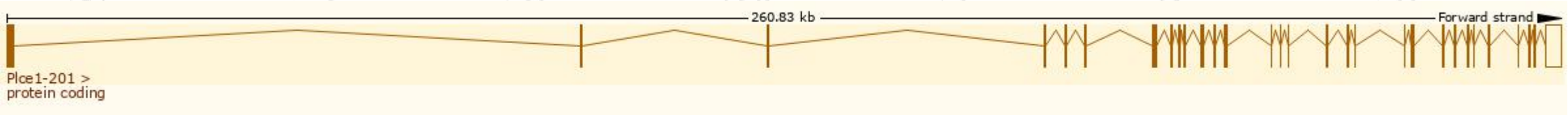
Official Symbol	Plce1 provided by MGI
Official Full Name	phospholipase C, epsilon 1 provided by MGI
Primary source	MGI:MGI:1921305
See related	Ensembl:ENSMUSG00000024998
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Plce; mKIAA1516; PLCepsilon; 4933403A21Rik
Expression	Ubiquitous expression in bladder adult (RPKM 5.0), limb E14.5 (RPKM 3.2) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

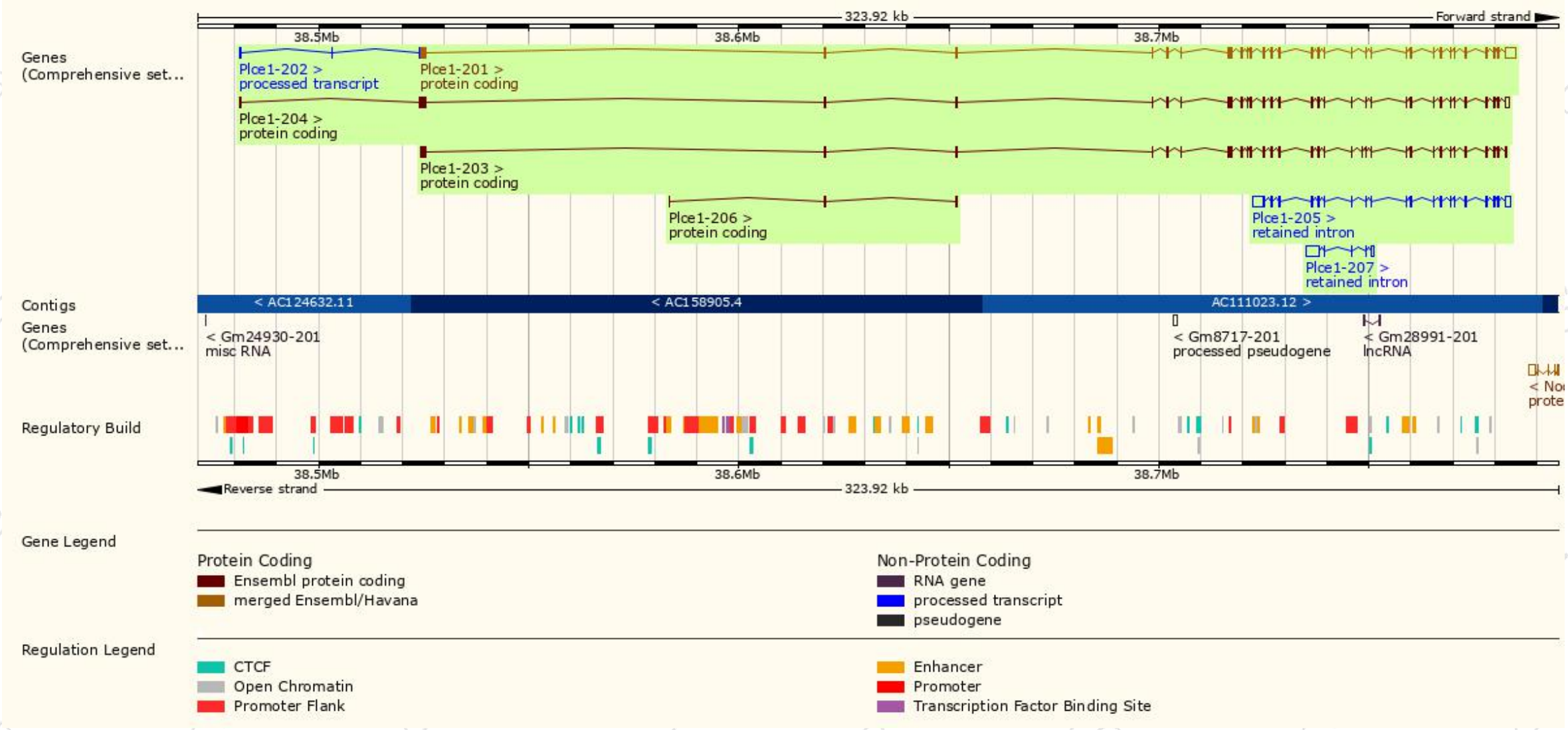
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plce1-201	ENSMUST00000169713.8	9439	2282aa	Protein coding	CCDS37973	Q8K4S1	TSL:1 GENCODE basic APPRIS P2
Plce1-204	ENSMUST00000182481.7	8357	2282aa	Protein coding	CCDS37973	Q8K4S1	TSL:5 GENCODE basic APPRIS P2
Plce1-203	ENSMUST00000182267.1	7234	2296aa	Protein coding	-	S4R1Q8	TSL:1 GENCODE basic APPRIS ALT2
Plce1-206	ENSMUST00000182999.1	619	74aa	Protein coding	-	S4R168	CDS 3' incomplete TSL:3
Plce1-202	ENSMUST00000181994.1	473	No protein	Processed transcript	-	-	TSL:2
Plce1-205	ENSMUST00000182589.7	6769	No protein	Retained intron	-	-	TSL:2
Plce1-207	ENSMUST00000183131.1	4220	No protein	Retained intron	-	-	TSL:2

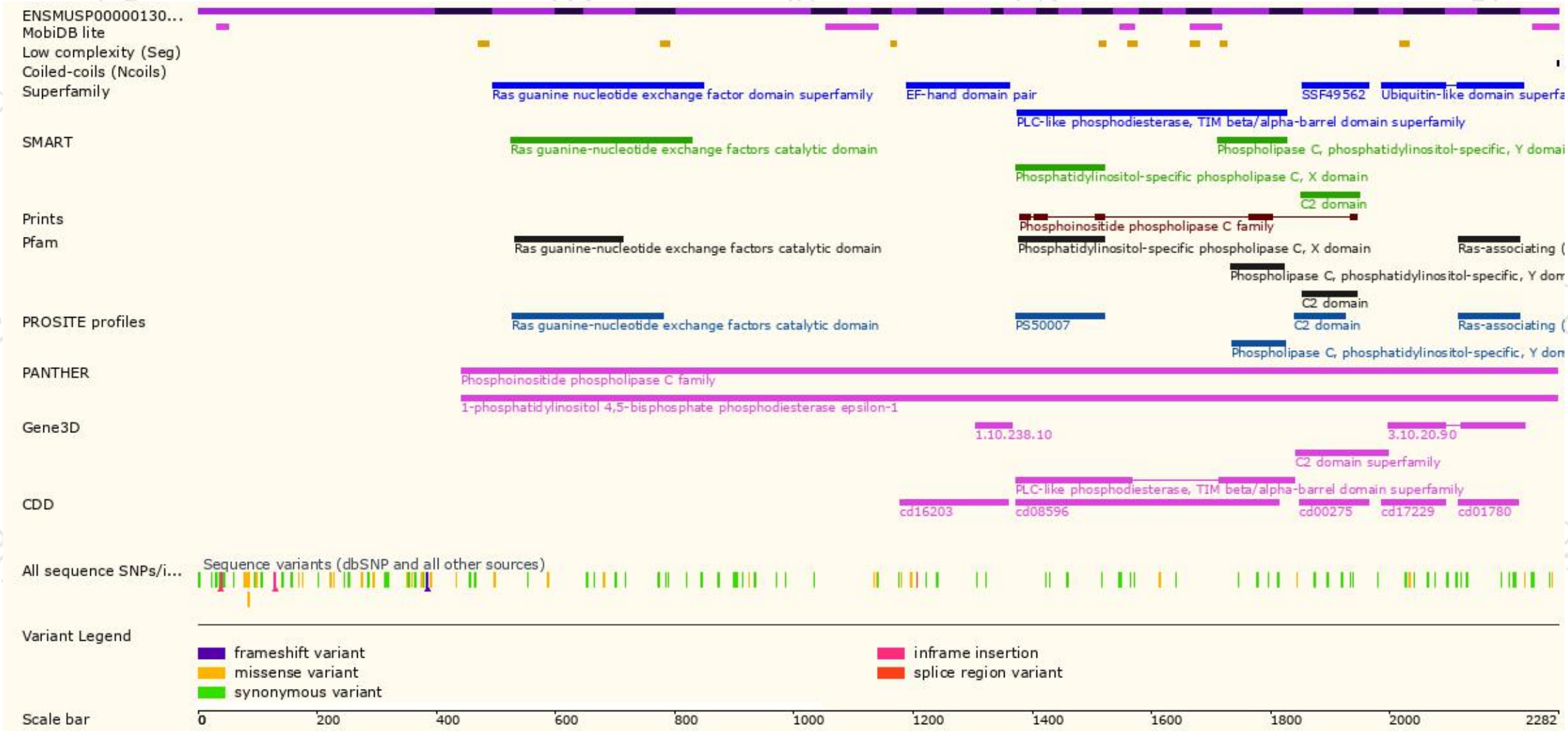
The strategy is based on the design of *Plce1-201* transcript, the transcription is shown below:



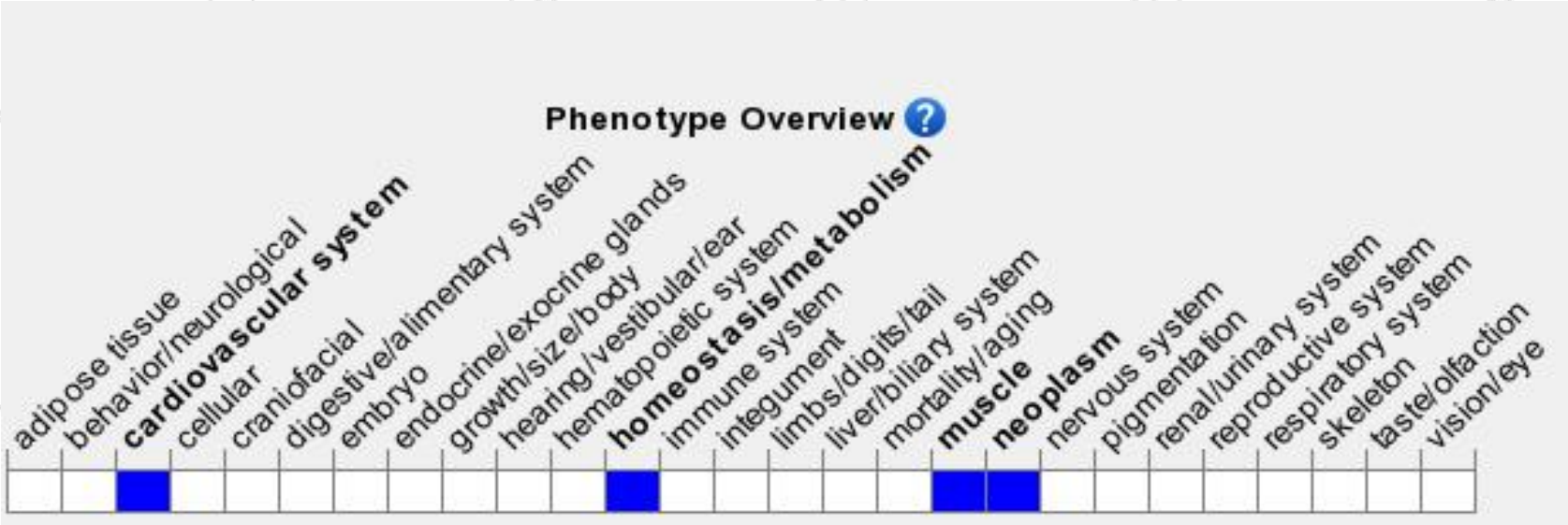
Genomic location distribution



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,homozygous mutation of this gene results in a congenital semilunar valvulogenesis defect which causes regurgitation and stenosis, and decreased incidence of induced skin tumors. Another mutant exhibits decreased cardiac contraction and increased hypertrophy in response to chronic stress.

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

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