Sephs2 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

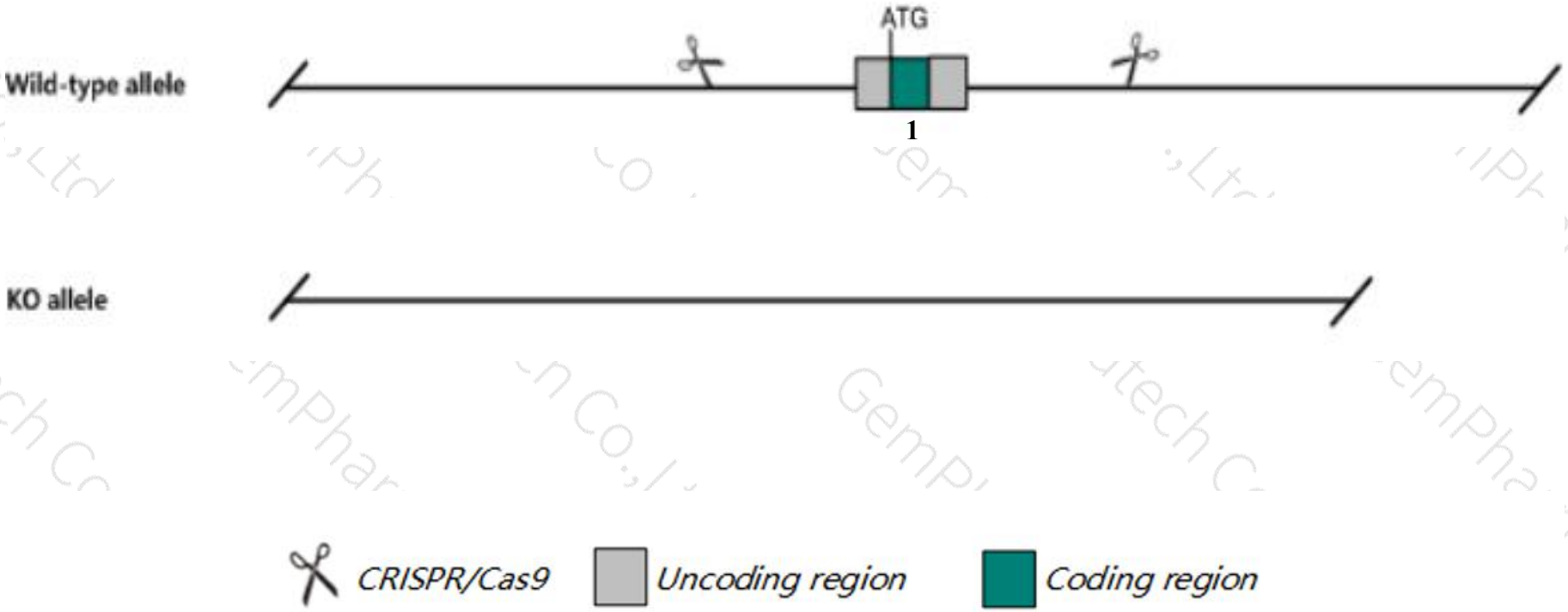
Design Date: 2020-8-26

Project Overview

Project Name	***Sephs2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sephs2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sephs2* gene has 1 transcript. According to the structure of *Sephs2* gene, exon1 of *Sephs2-201*(ENSMUST00000082428.4) transcript is recommended as the knockout region.The region contains all 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 *Sephs2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ *Gm44729-201* will be deleted.

➢ The *Sephs2* gene is located on the Chr7. 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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Sephs2 selenophosphate synthetase 2 [Mus musculus (house mouse)]

Gene ID: 20768, updated on 13-Mar-2020

Summary

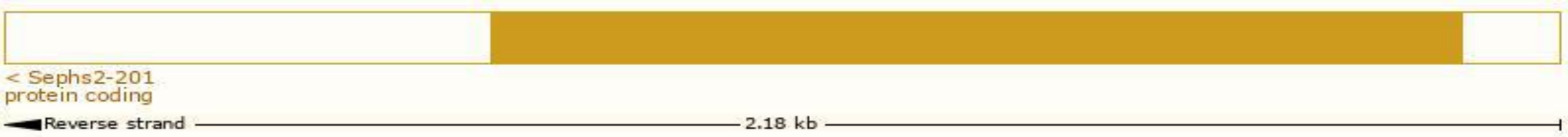
Official Symbol	Sephs2 provided by MGI
Official Full Name	selenophosphate synthetase 2 provided byMGI
Primary source	MGI:MGI:108388
See related	Ensembl:ENSMUSG00000049091
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Sps2, Ysg3
Summary	This gene encodes an enzyme that catalyzes the production of monoselenophosphate (MSP) from selenide and ATP. MSP is the selenium donor required for synthesis of selenocysteine (Sec), which is co-translationally incorporated into selenoproteins at in-frame UGA codons that normally signal translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, the Sec insertion sequence (SECIS) element, which is necessary for the recognition of UGA as a Sec codon rather than as a stop signal. This protein is itself a selenoprotein containing a Sec residue at its active site, suggesting the existence of an autoregulatory mechanism. It is preferentially expressed in tissues implicated in the synthesis of selenoproteins and in sites of blood cell development. [provided by RefSeq, May 2017]
Orthologs	human all

Transcript information（Ensembl）

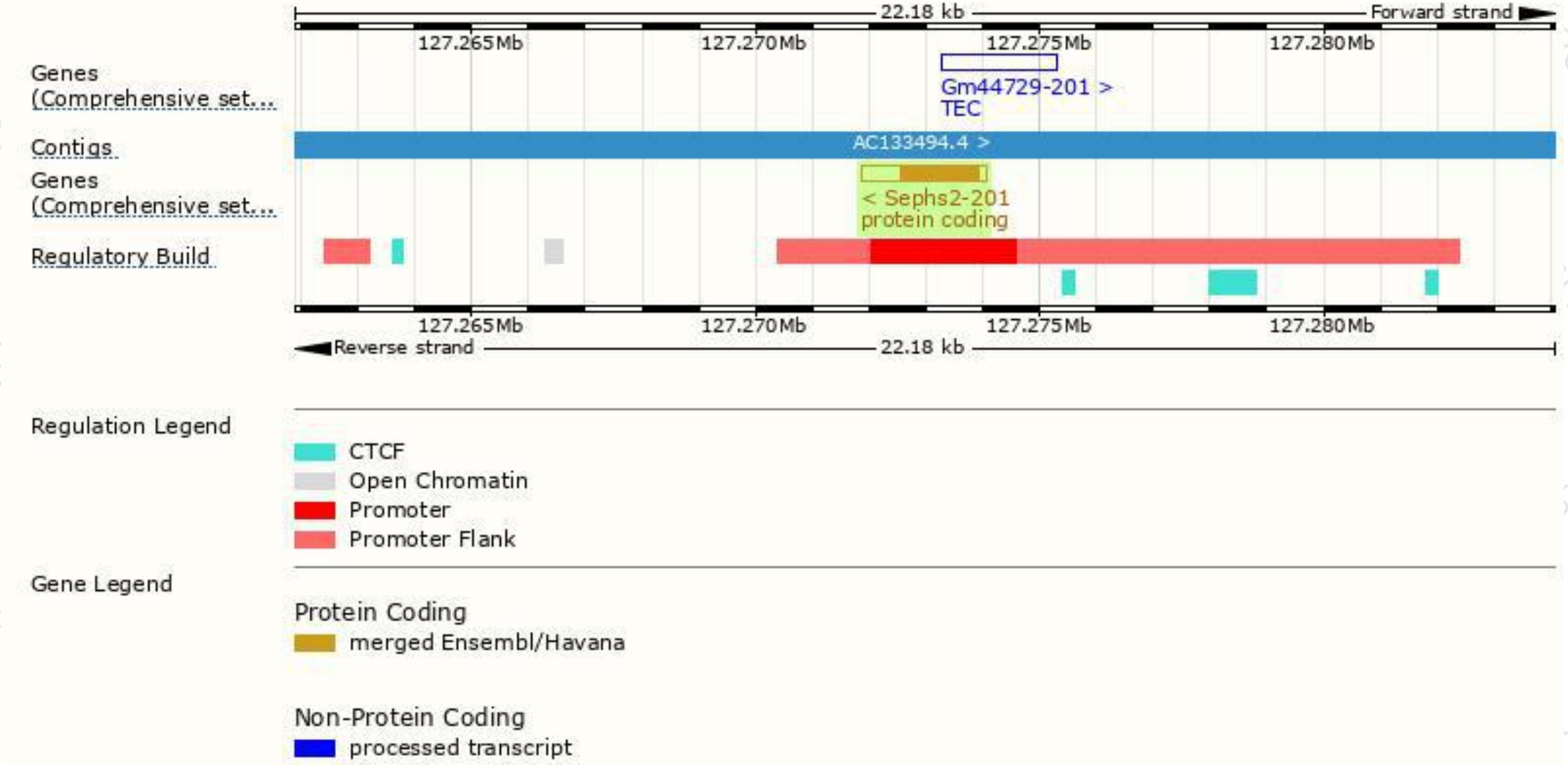
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sephs2-201	ENSMUST00000082428.4	2177	452aa	Protein coding	CCDS21863	P97364	TSL:NA GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

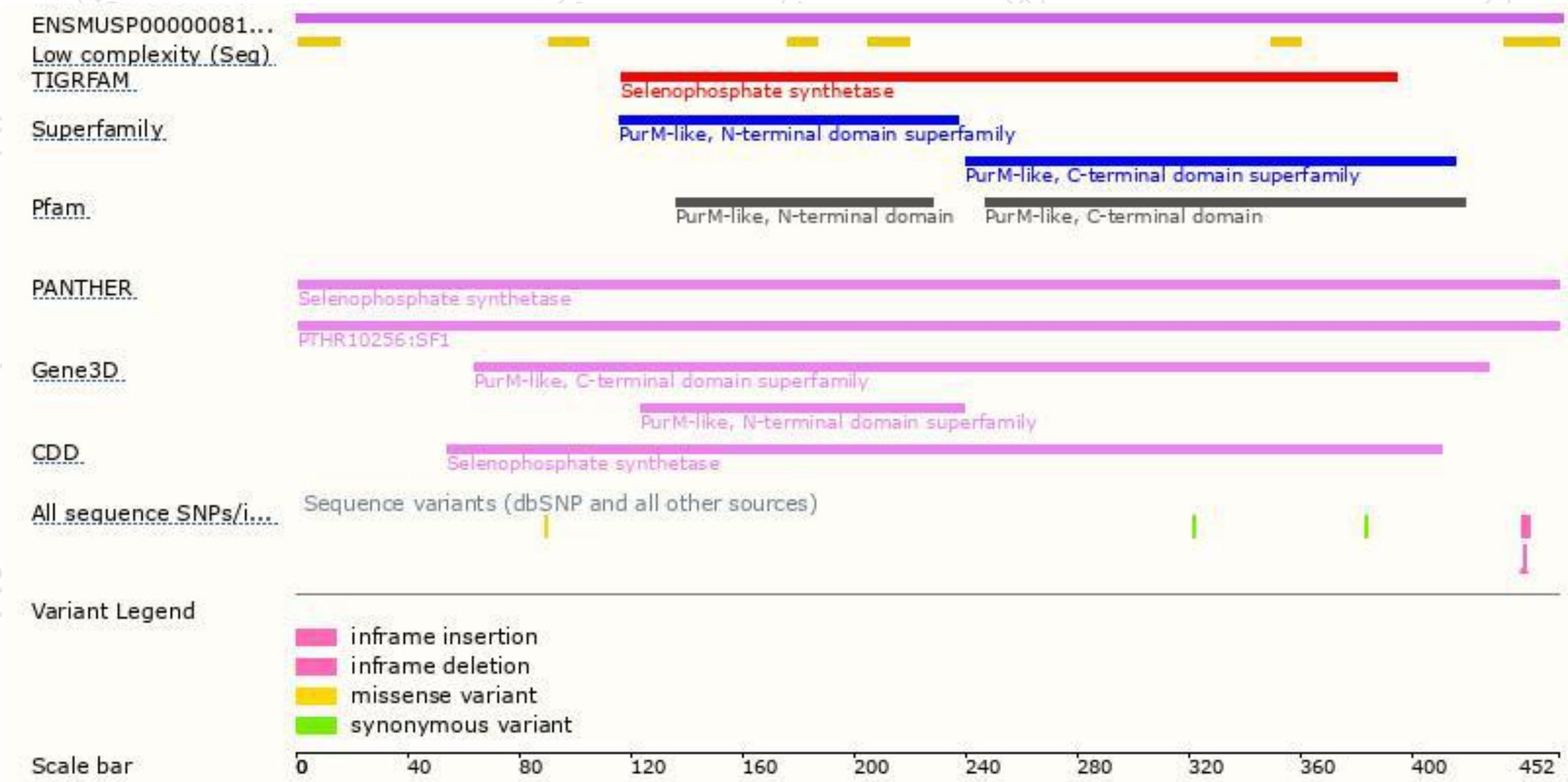
The strategy is based on the design of *Sephs2-201* transcript,the transcription is shown below:



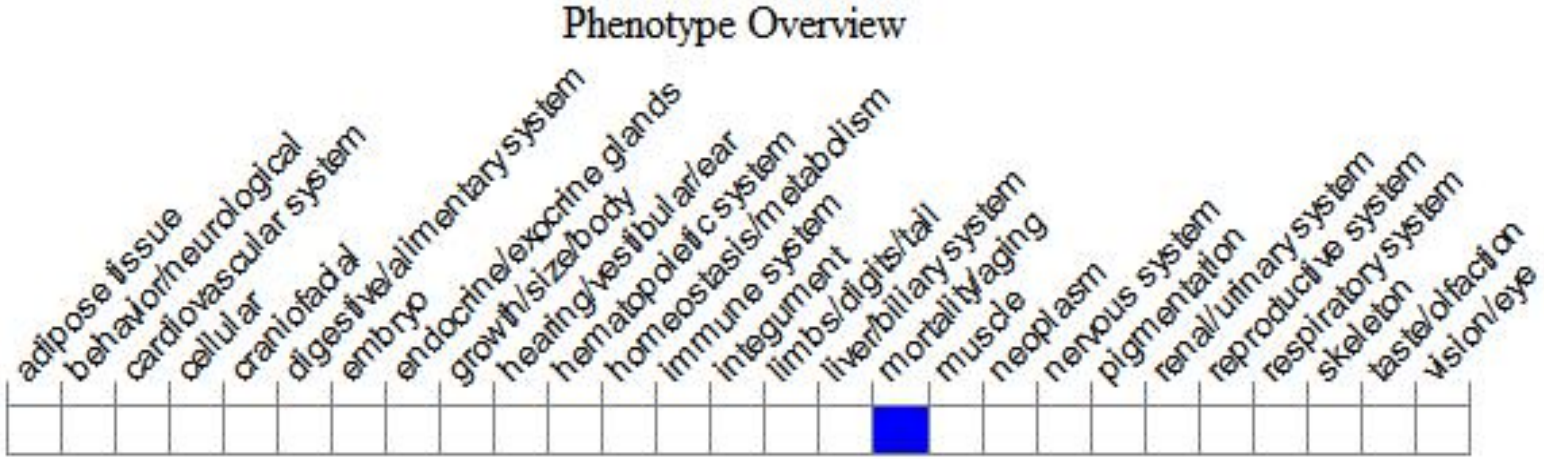
Genomic location distribution



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/).

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd