Selenop Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

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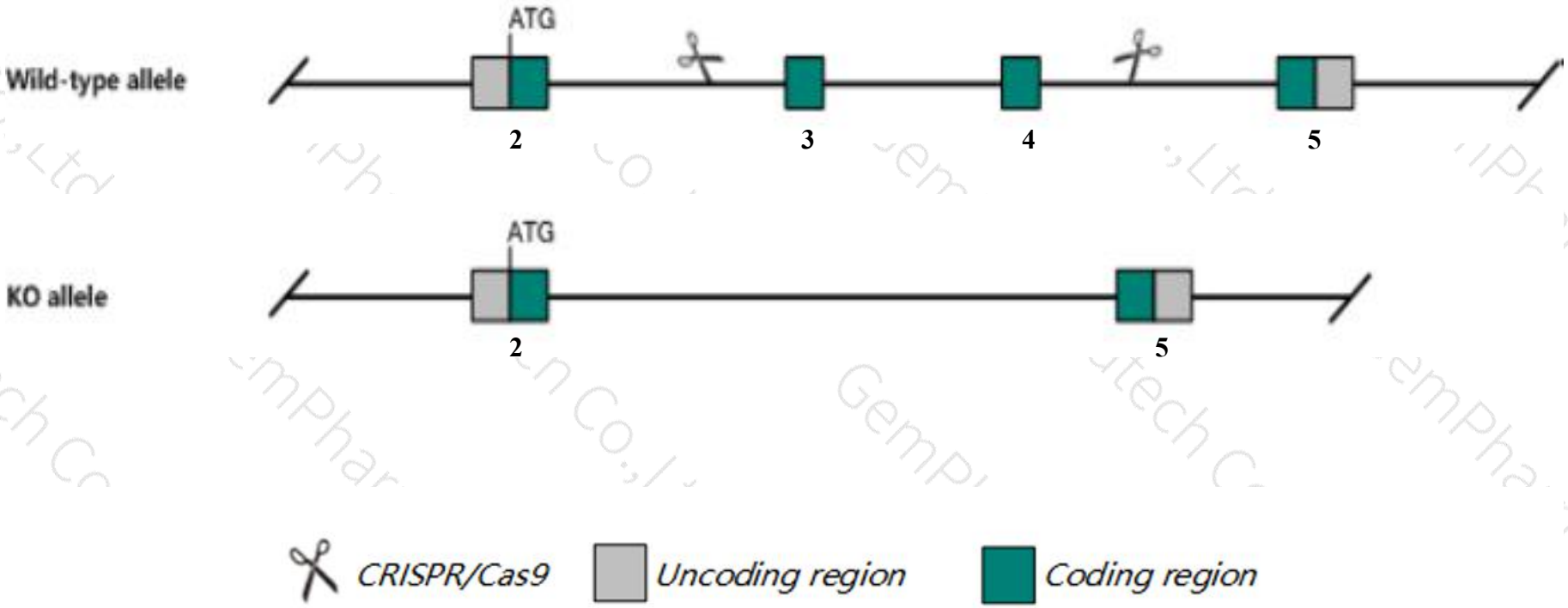
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Selenop* gene has 7 transcripts. According to the structure of *Selenop* gene, exon3-exon4 of *Selenop-203* (ENSMUST00000159216.8) transcript is recommended as the knockout region.The region contains 331bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,homozygotes for targeted null mutations exhibit ataxia, spasticity, impaired growth, reduced male fertility, and excess mortality.

- The *Selenop* gene is located on the Chr15. 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）

集萃药康 GemPharmatech

Selenop selenoprotein P [Mus musculus (house mouse)]

Gene ID: 20363, updated on 13-Mar-2020

Summary

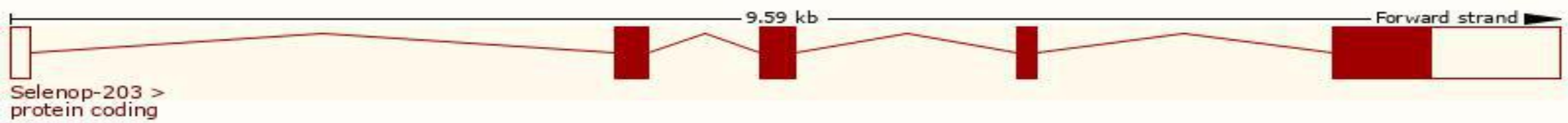
Official Symbol	Selenop provided by MGI
Official Full Name	selenoprotein P provided byMGI
Primary source	MGI:MGI:894288
See related	Ensembl:ENSMUSG00000064373
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU018766, D15Ucla1, Se-P, Sepp1, selp
Summary	This gene encodes a selenoprotein that is predominantly expressed in the liver and secreted into the plasma. This selenoprotein is unique in that it contains multiple selenocysteine (Sec) residues per polypeptide (10 in mouse), and accounts for most of the selenium in plasma. It has been implicated as an extracellular antioxidant, and in the transport of selenium to extra-hepatic tissues via apolipoprotein E receptor-2 (apoER2). Mice lacking this gene exhibit neurological dysfunction, suggesting its importance in normal brain function. Sec is encoded by the UGA codon, which normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, designated the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon, rather than as a stop signal. The mRNA for this selenoprotein contains two SECIS elements. Alternatively spliced transcript variants differing in 5' non-coding region have been described for this gene. Expression of these variants varies in different tissues and developmental stages (PMID:23064117). [provided by RefSeq, Feb 2017]
Expression	Broad expression in liver E18 (RPKM 1163.6), liver adult (RPKM 814.0) and 18 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

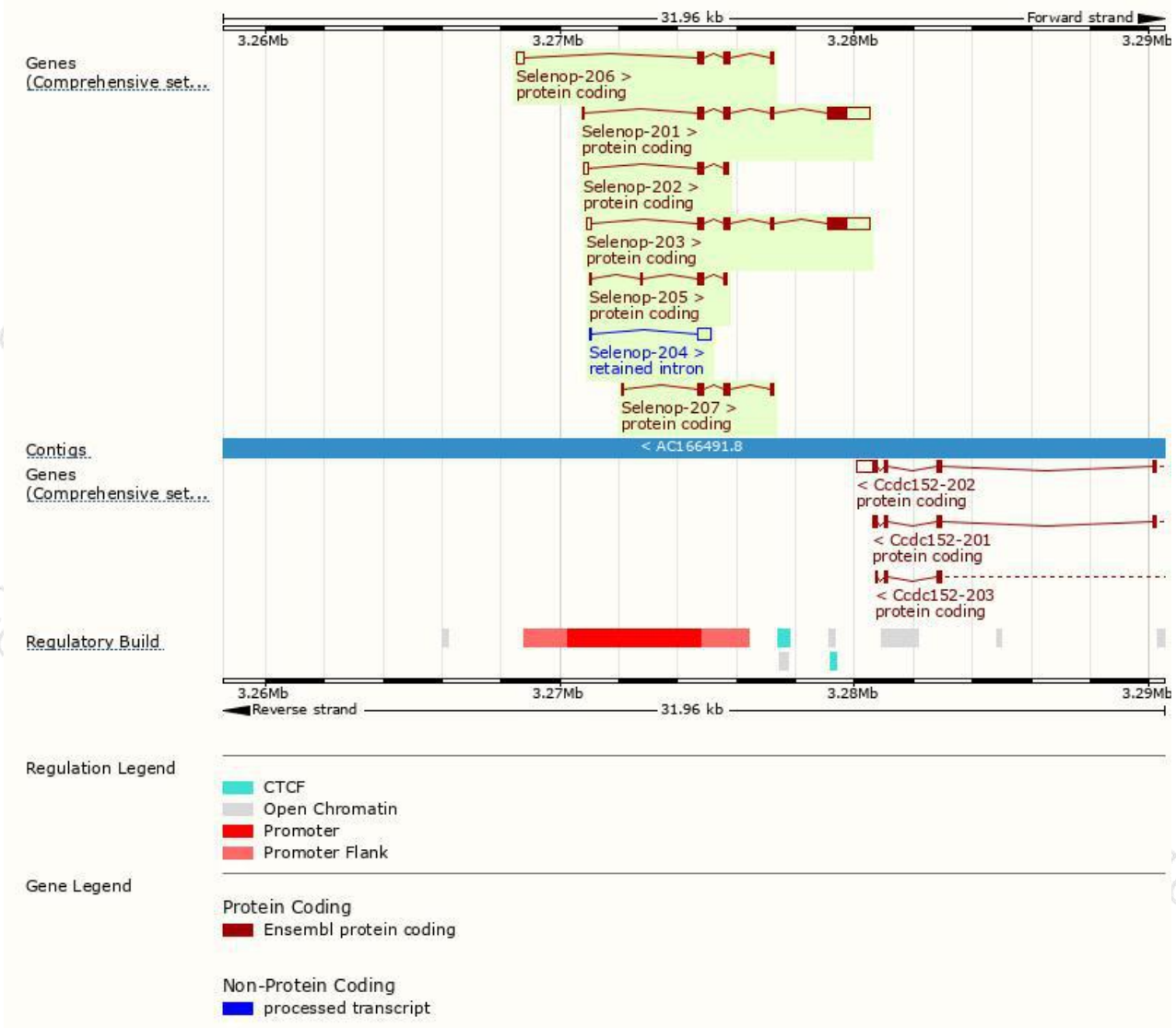
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selenop-203	ENSMUST00000159216.8	2085	380aa	Protein coding	CCDS27357	P70274	TSL:5 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
Selenop-201	ENSMUST00000082424.10	2013	380aa	Protein coding	CCDS27357	P70274	TSL:5 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
Selenop-206	ENSMUST00000160787.8	768	177aa	Protein coding	-	E0CX80	CDS 3' incomplete TSL:5
Selenop-207	ENSMUST00000160930.1	627	177aa	Protein coding	-	E0CX80	CDS 3' incomplete TSL:3
Selenop-202	ENSMUST00000159158.7	527	124aa	Protein coding	-	E0CZ76	CDS 3' incomplete TSL:2
Selenop-205	ENSMUST00000160311.1	420	110aa	Protein coding	-	E0CY03	CDS 3' incomplete TSL:2
Selenop-204	ENSMUST00000159247.1	516	No protein	Retained intron	-	-	TSL:2

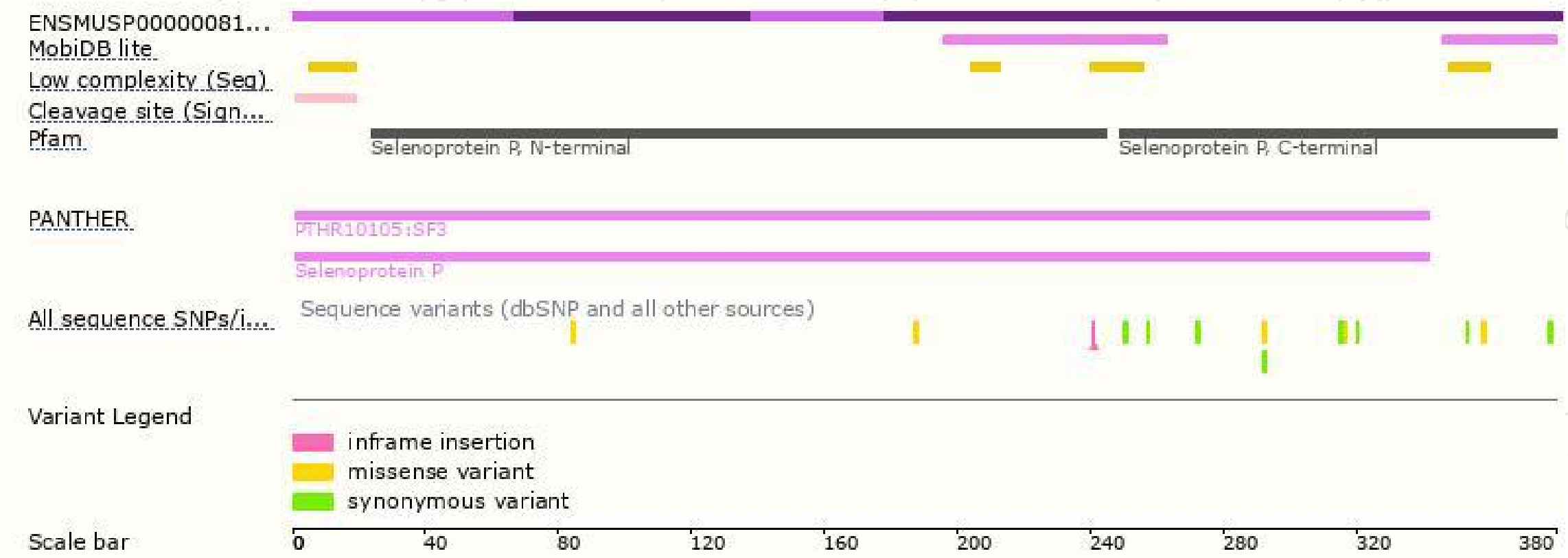
The strategy is based on the design of *Selenop-203* transcript,the transcription is shown below:



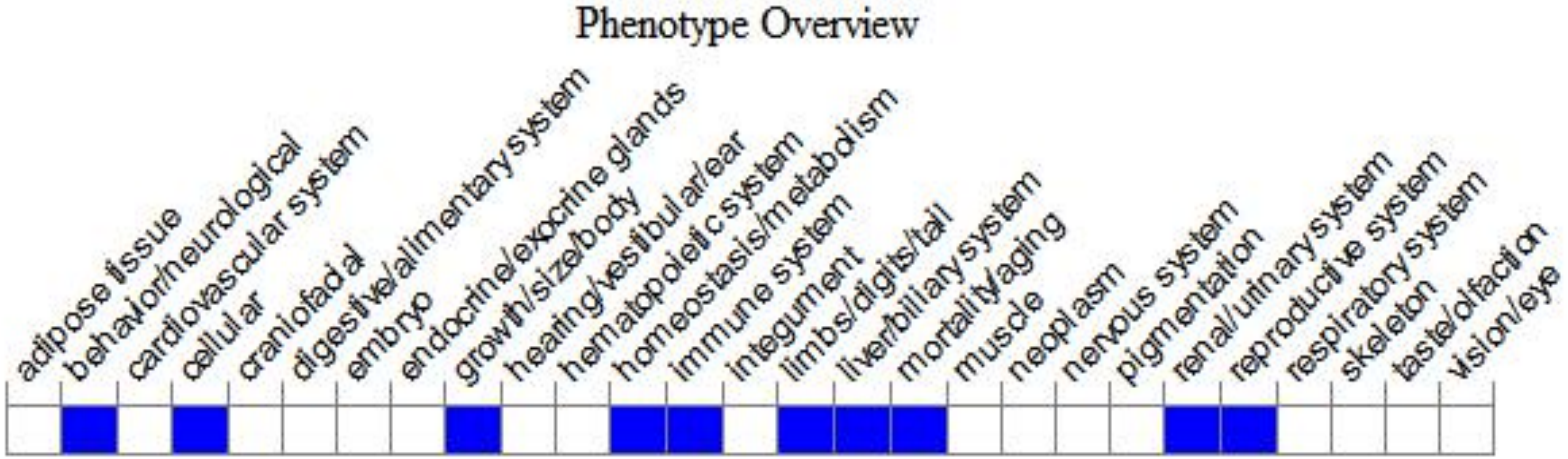
Genomic location distribution



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,homozygotes for targeted null mutations exhibit ataxia, spasticity, impaired growth, reduced male fertility, and excess mortality.

集萃药康
GemPharmatech

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd