Selenoh Cas9-KO Strategy

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Project Overview

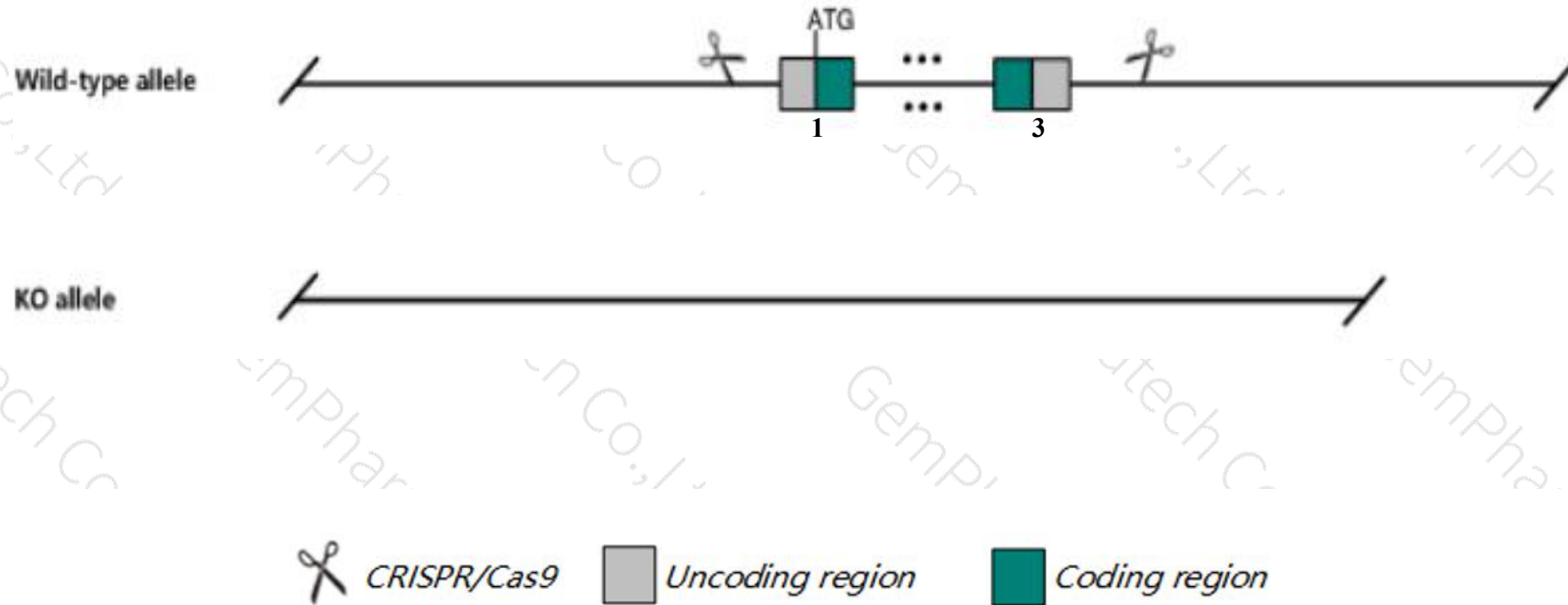|	
Project Name	*Selenoh*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Selenoh* gene has 6 transcripts. According to the structure of *Selenoh* gene, exon1-exon3 of *Selenoh-201*(ENSMUST00000102646.2) 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 *Selenoh* 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

➢ The partial sequence of the intron of *Gm28635* gene will be deleted.

➢ The *Selenoh* gene is located on the Chr2. 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）

Selenoh selenoprotein H [Mus musculus (house mouse)]

Gene ID: 72657, updated on 13-Mar-2020

▲ Summary

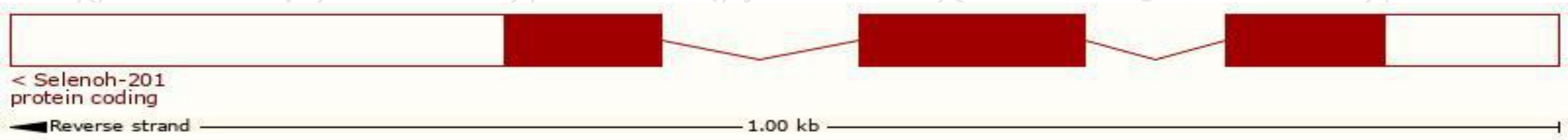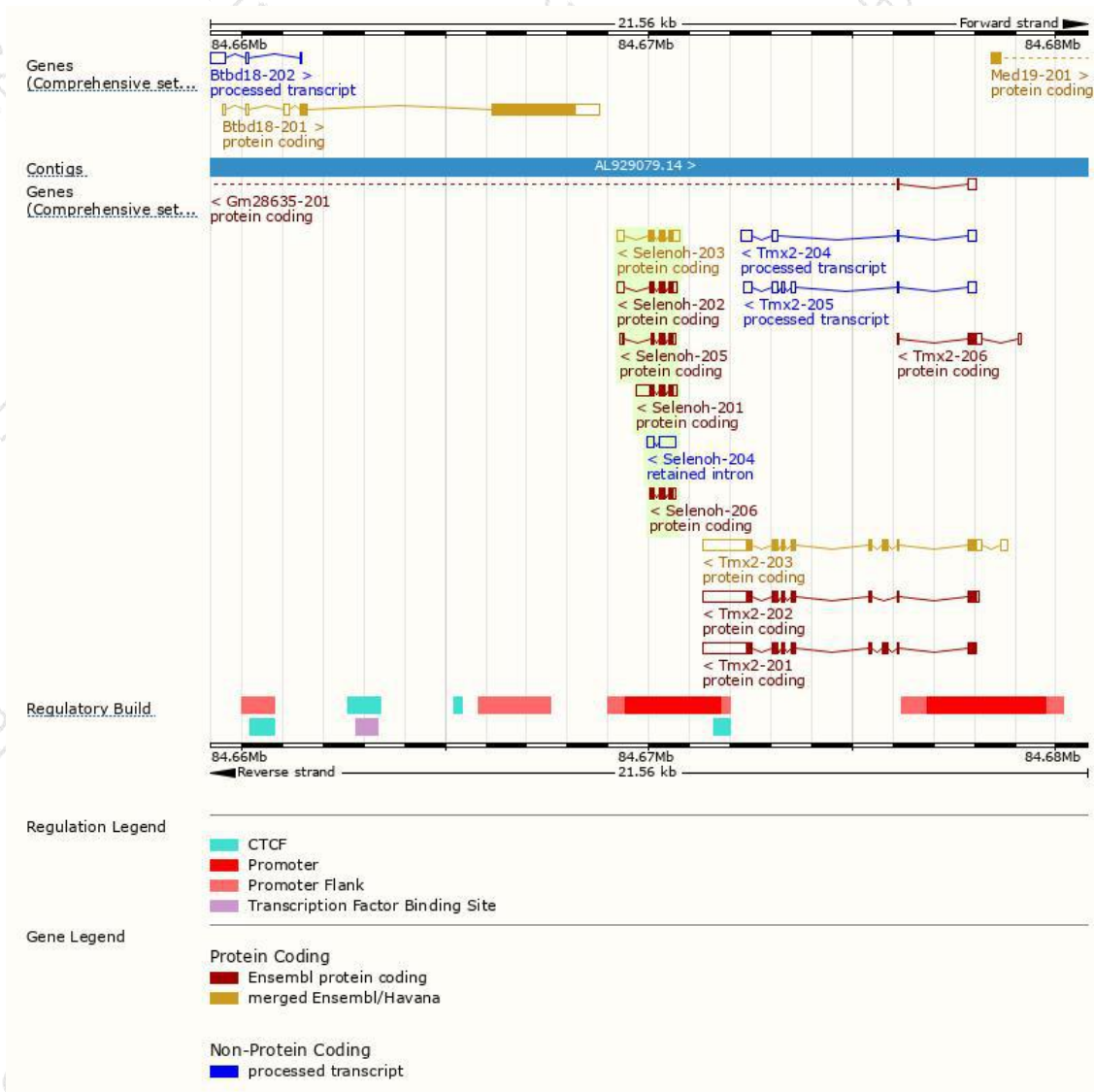|	
Official Symbol	Selenoh provided by MGI
Official Full Name	selenoprotein H provided by MGI
Primary source	MGI:MGI:1919907
See related	Ensembl:ENSMUSG00000076437
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2700094K13Rik, Selh
Summary	This gene encodes a nucleolar protein, which belongs to the SelWTH family. It functions as an oxidoreductase, and has been shown to protect neurons against UVB-induced damage by inhibiting apoptotic cell death pathways, promote mitochondrial biogenesis and mitochondrial function, and suppress cellular senescence through genome maintenance and redox regulation. This protein is a selenoprotein, containing the rare amino acid selenocysteine (Sec) at its active site. 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. Alternatively spliced transcript variants have been found for this gene. [provided by RefSeq, May 2016]
Expression	Broad expression in CNS E11.5 (RPKM 111.9), limb E14.5 (RPKM 56.8) and 25 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selenoh-201	ENSMUST00000102646.2	783	116aa	Protein coding	CCDS16187	Q3UQA7	TSL:1 GENCODE basic APPRIS P2
Selenoh-203	ENSMUST00000117299.8	747	116aa	Protein coding	CCDS16187	Q3UQA7	TSL:1 GENCODE basic APPRIS P2
Selenoh-202	ENSMUST00000102647.9	654	116aa	Protein coding	CCDS16187	Q3UQA7	TSL:1 GENCODE basic APPRIS P2
Selenoh-205	ENSMUST0000189636.6	499	123aa	Protein coding	-	A0A087WPM0	TSL:3 GENCODE basic APPRIS ALT2
Selenoh-206	ENSMUST0000189988.1	390	101aa	Protein coding	-	A0A087WNU1	TSL:3 GENCODE basic
Selenoh-204	ENSMUST00000154179.1	599	No protein	Retained intron	-	-	TSL:2

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

< Selenoh-201
protein coding

◀ Reverse strand ————————— 1.00 kb —————————

Genomic location distribution

Protein domain

ENSMUSP00000112...	
Low complexity (Seg)	
TIGRFAM	Selenoprotein, Rdx-type
Superfamily	Thioredoxin-like superfamily
Pfam	Selenoprotein, Rdx-type
PANTHER	PTHR33638
	PTHR33638:SF1
Gene3D	3.40.30.10
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	
	▬ missense variant
Scale bar	0 10 20 30 40 50 60 70 80 90 100 116
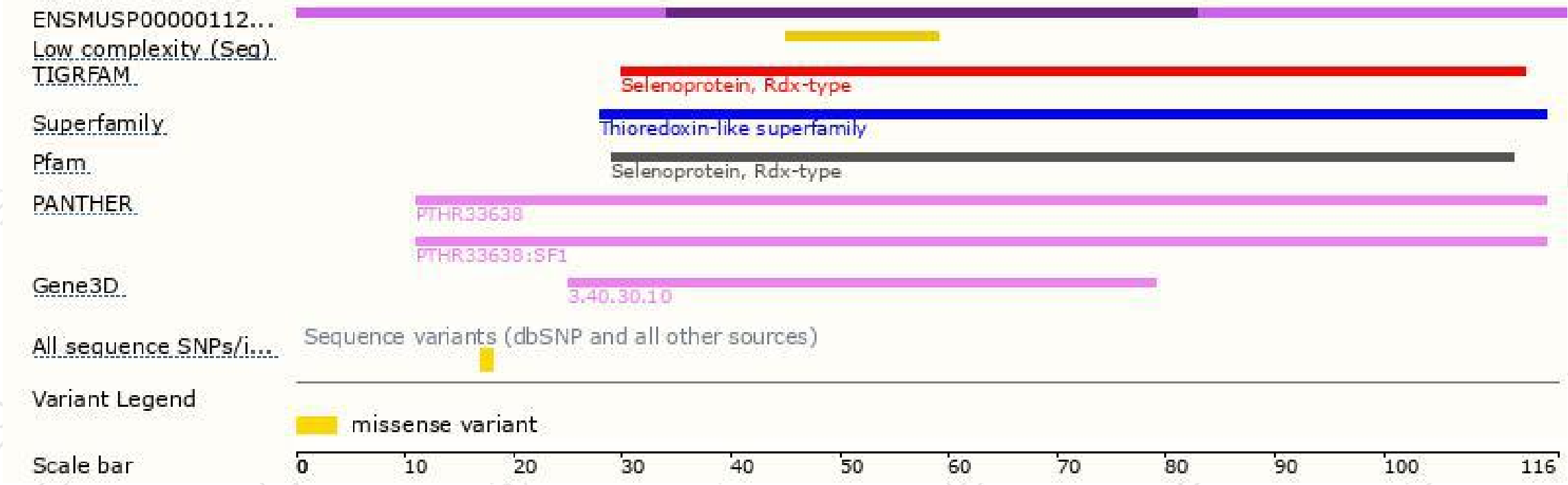
If you have any questions, you are welcome to inquire.
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