

Selenov Cas9-CKO Strategy

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Project Overview

Project Name

Selenov

Project type

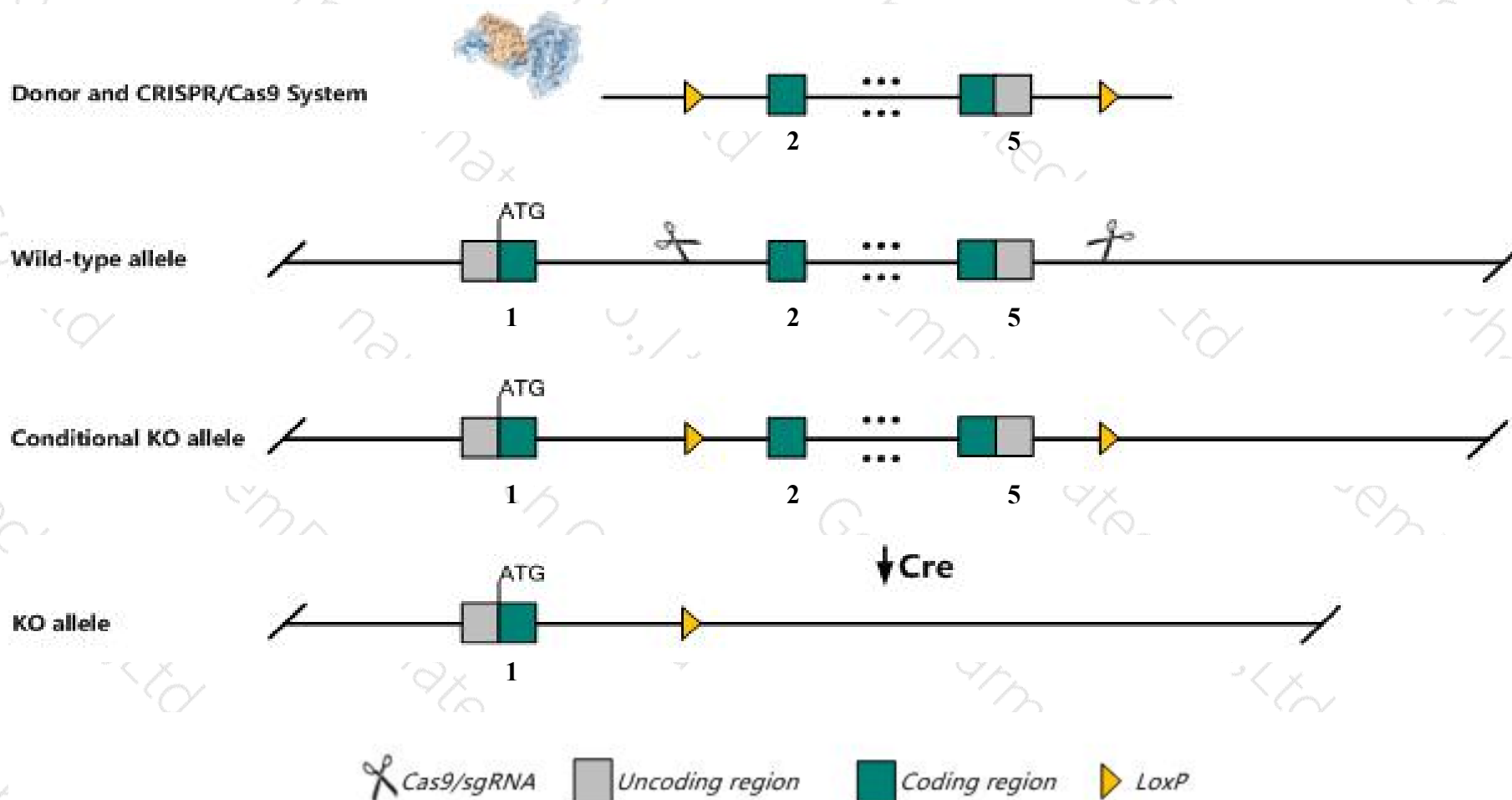
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Selenov* gene has 2 transcripts. According to the structure of *Selenov* gene, exon2-exon5 of *Selenov-201*(ENSMUST00000056589.13) transcript is recommended as the knockout region. The region contains 232bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Selenov* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, male mice homozygous for a mutation are viable and show normal fertility.
- The *Selenov* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Selenov selenoprotein V [Mus musculus (house mouse)]

Gene ID: 280621, updated on 13-Mar-2020

Summary



Official Symbol Selenov provided by [MGI](#)

Official Full Name selenoprotein V provided by [MGI](#)

Primary source [MGI:MGI:3608324](#)

See related [Ensembl:ENSMUSG00000046750](#)

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 Selv

Summary This gene encodes a selenoprotein containing a selenocysteine (Sec) residue, which is encoded by the UGA codon that normally signals 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 specifically expressed in the testis. It belongs to the SelWTH family, which possesses a thioredoxin-like fold and a conserved CxxU (C is cysteine, U is Sec) motif, suggesting a redox function for this gene. [provided by RefSeq, Apr 2017]

Expression Restricted expression toward testis adult (RPKM 175.4)[See more](#)

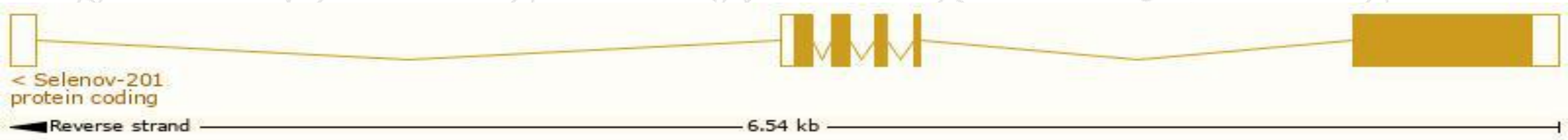
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

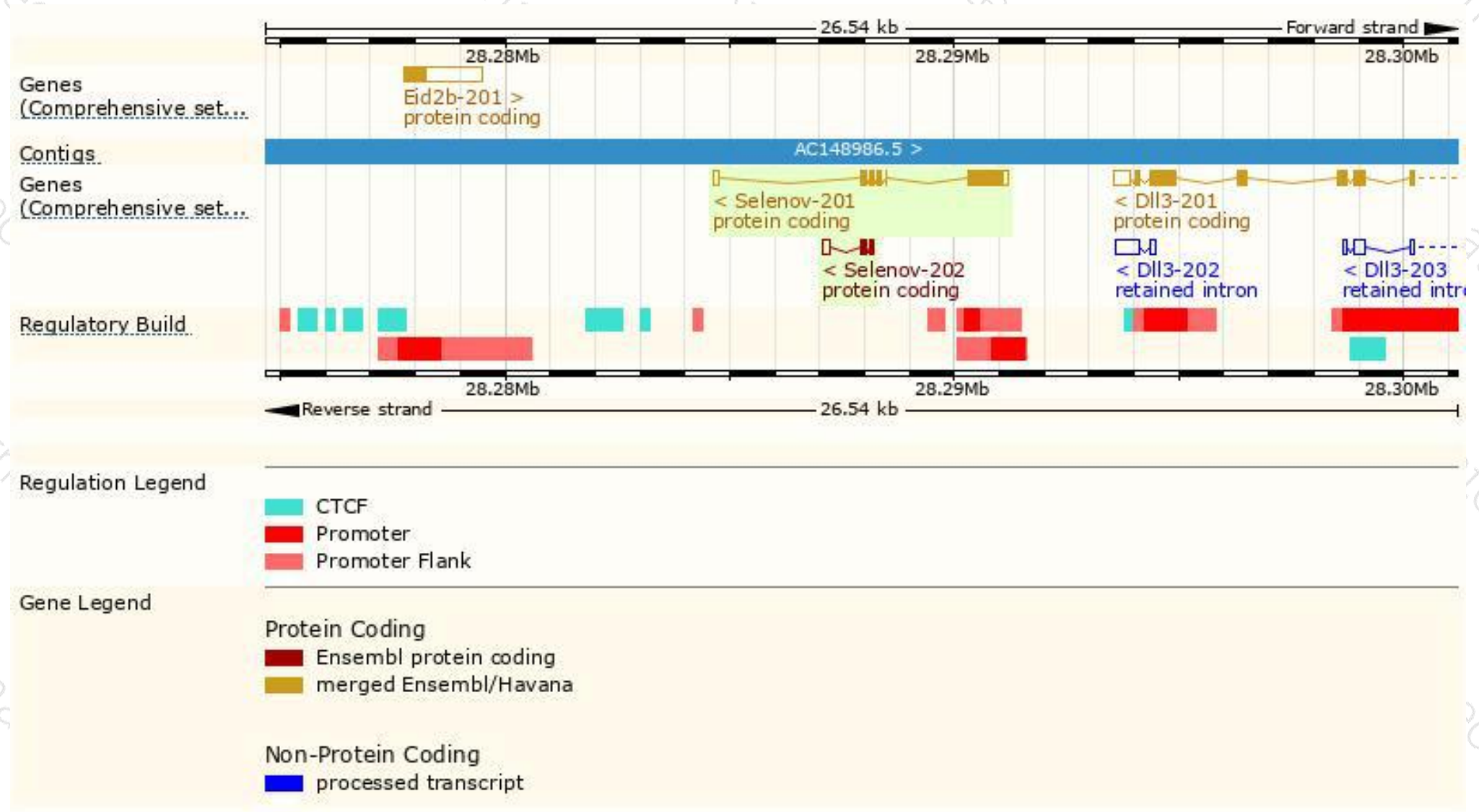
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selenov-201	ENSMUST00000056589.13	1267	328aa	Protein coding	CCDS39855	D3YXG1 Q5FWB9	TSL:1 GENCODE basic APPRIS P1
Selenov-202	ENSMUST00000156408.1	383	46aa	Protein coding	-	F6TYD6	CDS 5' incomplete TSL:3

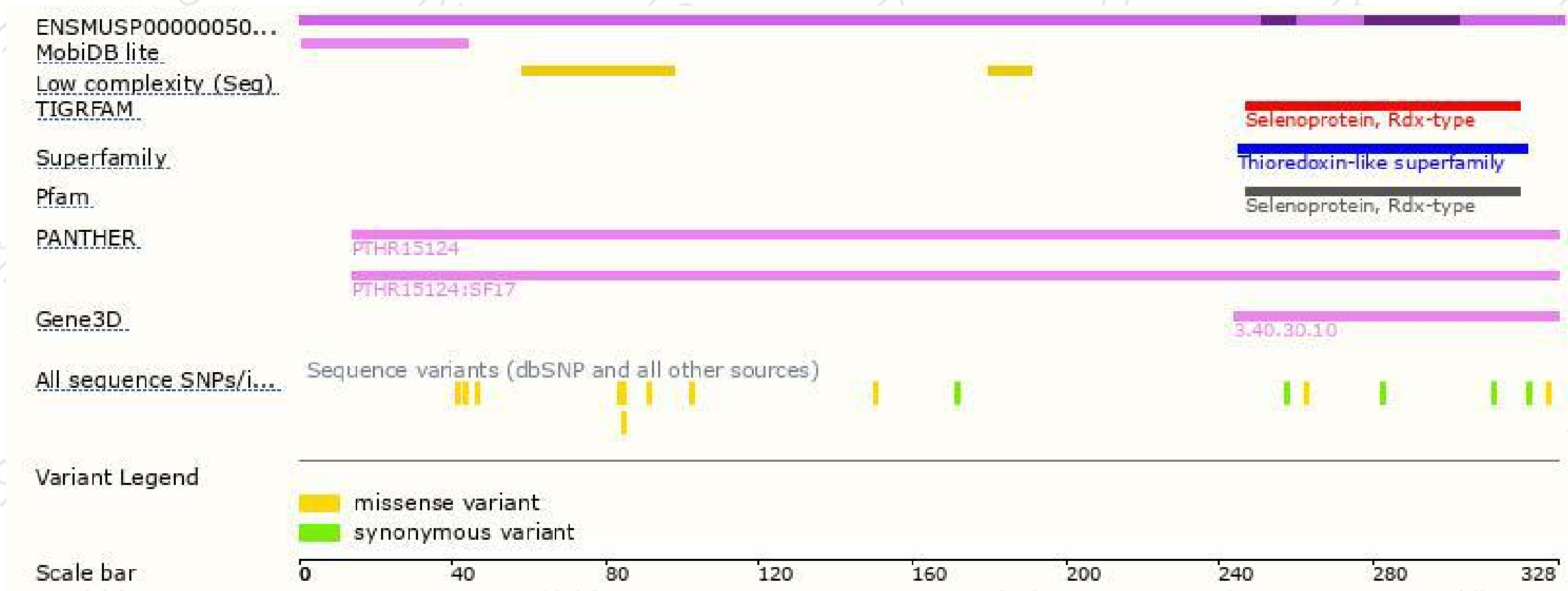
The strategy is based on the design of *Selenov-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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