Selenom Cas9-CKO Strategy

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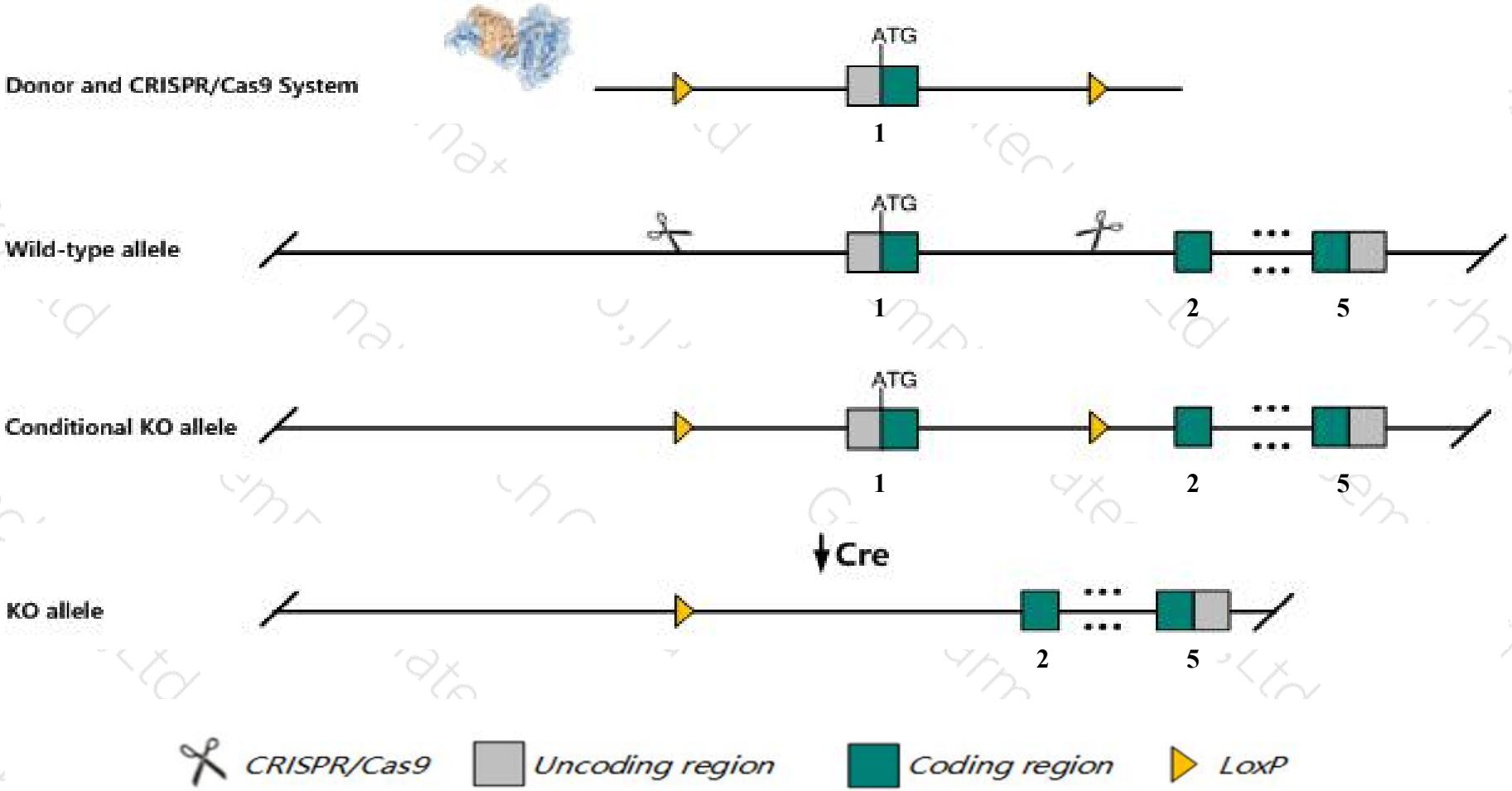
Project Overview

Project Name	***Selenom***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

➢ The *Selenom* gene has 3 transcripts. According to the structure of *Selenom* gene, exon1 of *Selenom-201*(ENSMUST00000094469.4) transcript is recommended as the knockout region.The region contains start codon ATG.Knock out the region will result in disruption of protein function.

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

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit obesity without cognitive deficits.

➢ The *Selenom* gene is located on the Chr11. 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）

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Selenom selenoprotein M [Mus musculus (house mouse)]

Gene ID: 114679, updated on 13-Mar-2020

Summary

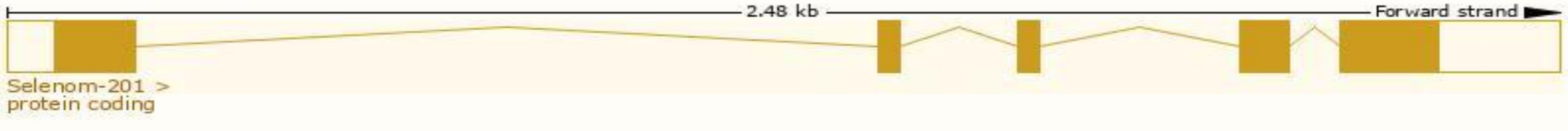
Official Symbol	Selenom provided by MGI
Official Full Name	selenoprotein M provided byMGI
Primary source	MGI:MGI:2149786
See related	Ensembl:ENSMUSG00000075702
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1500040L08Rik, A230103K18, Selm, Sepm
Summary	The protein encoded by this gene belongs to the selenoprotein M/SEP15 family. The exact function of this protein is not known. It is localized in the perinuclear region, is highly expressed in the brain, and may be involved in neurodegenerative disorders. Transgenic mice with targeted deletion of this gene exhibit increased weight gain, suggesting a role for this gene in the regulation of body weight and energy metabolism. This protein is a selenoprotein, containing the rare amino acid selenocysteine (Sec). 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. [provided by RefSeq, Dec 2016]
Expression	Broad expression in colon adult (RPKM 163.0), cerebellum adult (RPKM 154.9) and 22 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

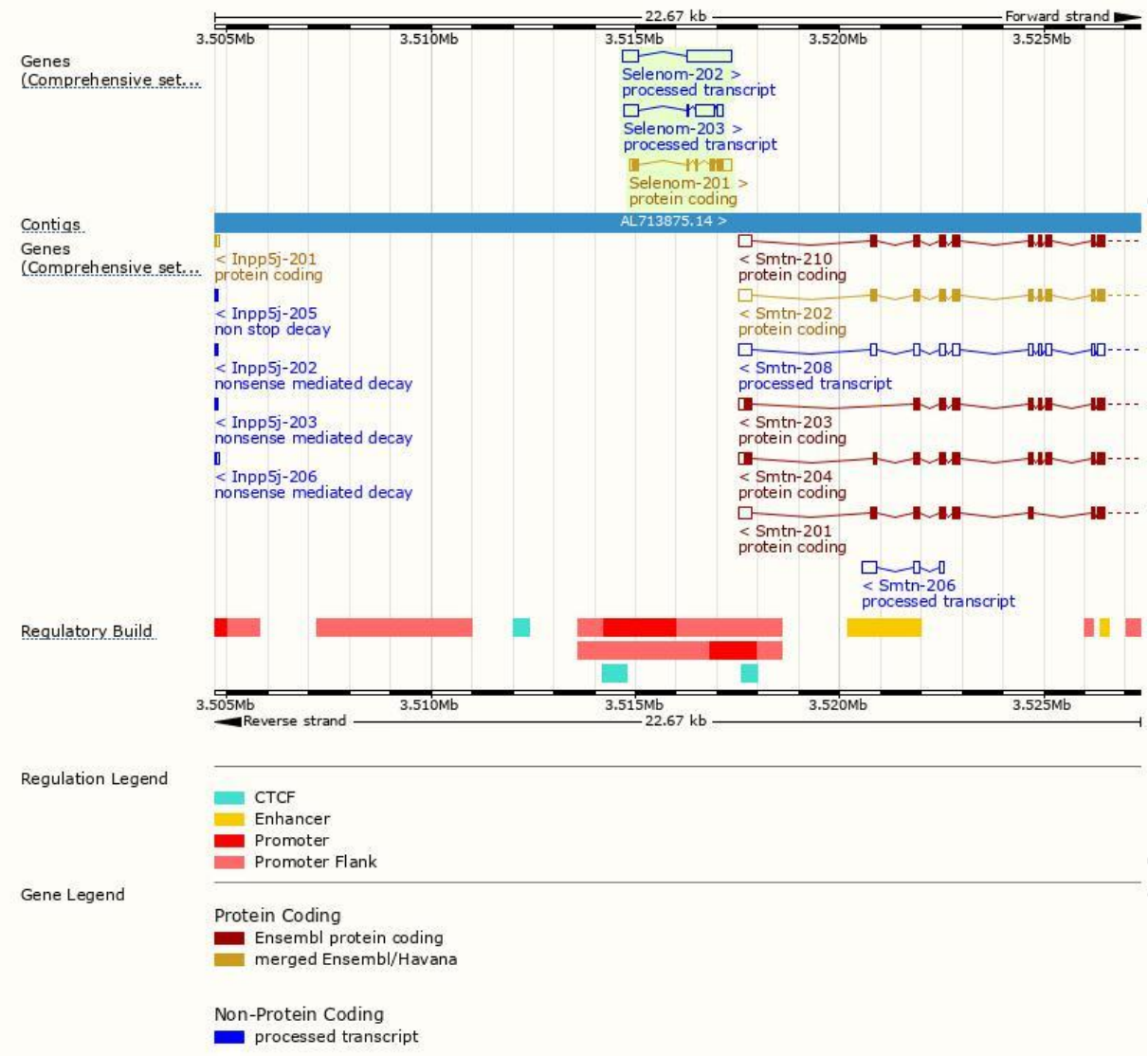
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selenom-201	ENSMUST00000094469.4	707	145aa	Protein coding	CCDS24365	Q8VHC3	TSL:1 GENCODE basic APPRIS P1
Selenom-202	ENSMUST00000123677.1	1478	No protein	Processed transcript	-	-	TSL:2
Selenom-203	ENSMUST00000131865.1	972	No protein	Processed transcript	-	-	TSL:3

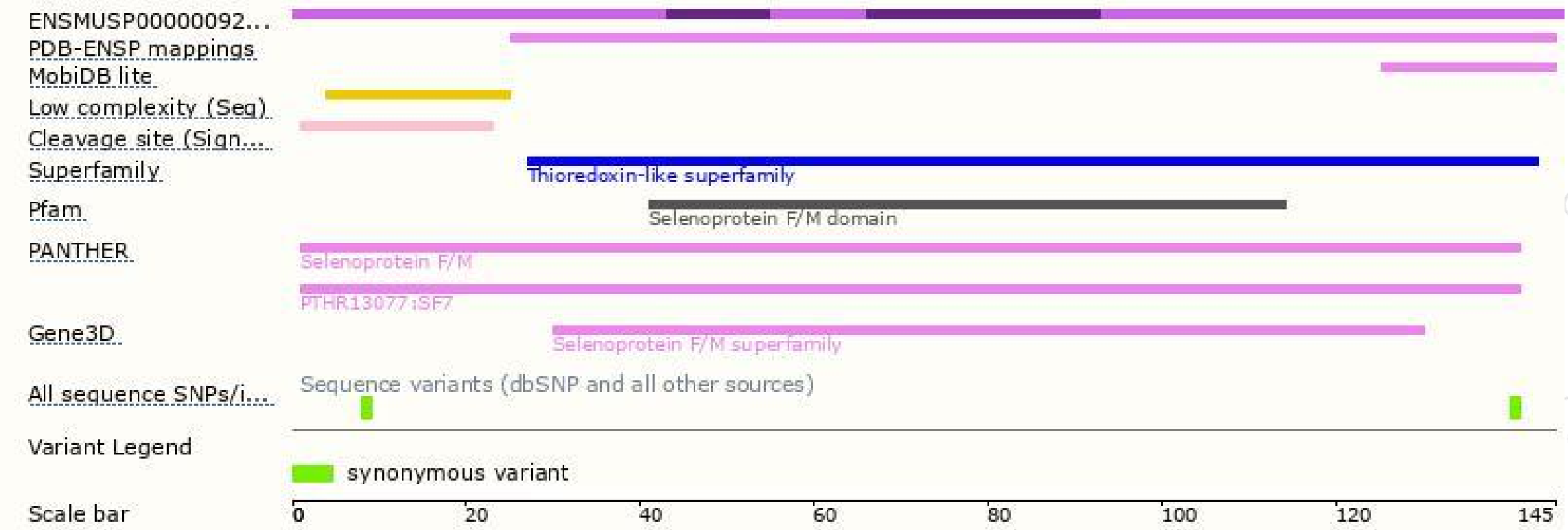
The strategy is based on the design of *Selenom-201* transcript,the transcription is shown below:



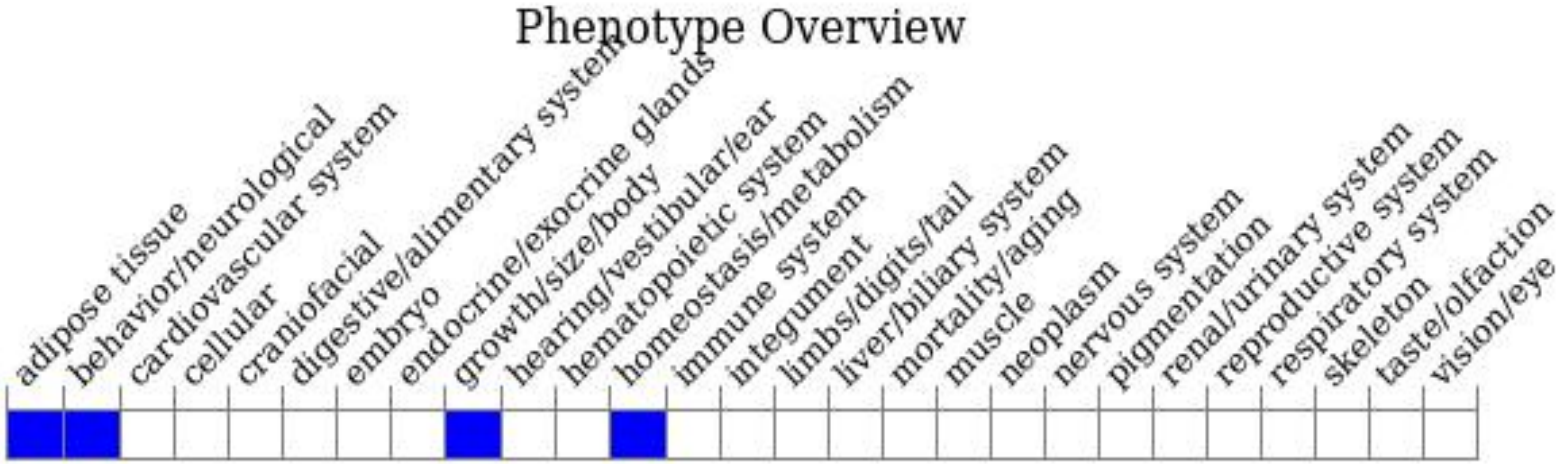
Genomic location distribution



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/).

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

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