

Setx Cas9-CKO Strategy

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Project Overview

Project Name

Setx

Project type

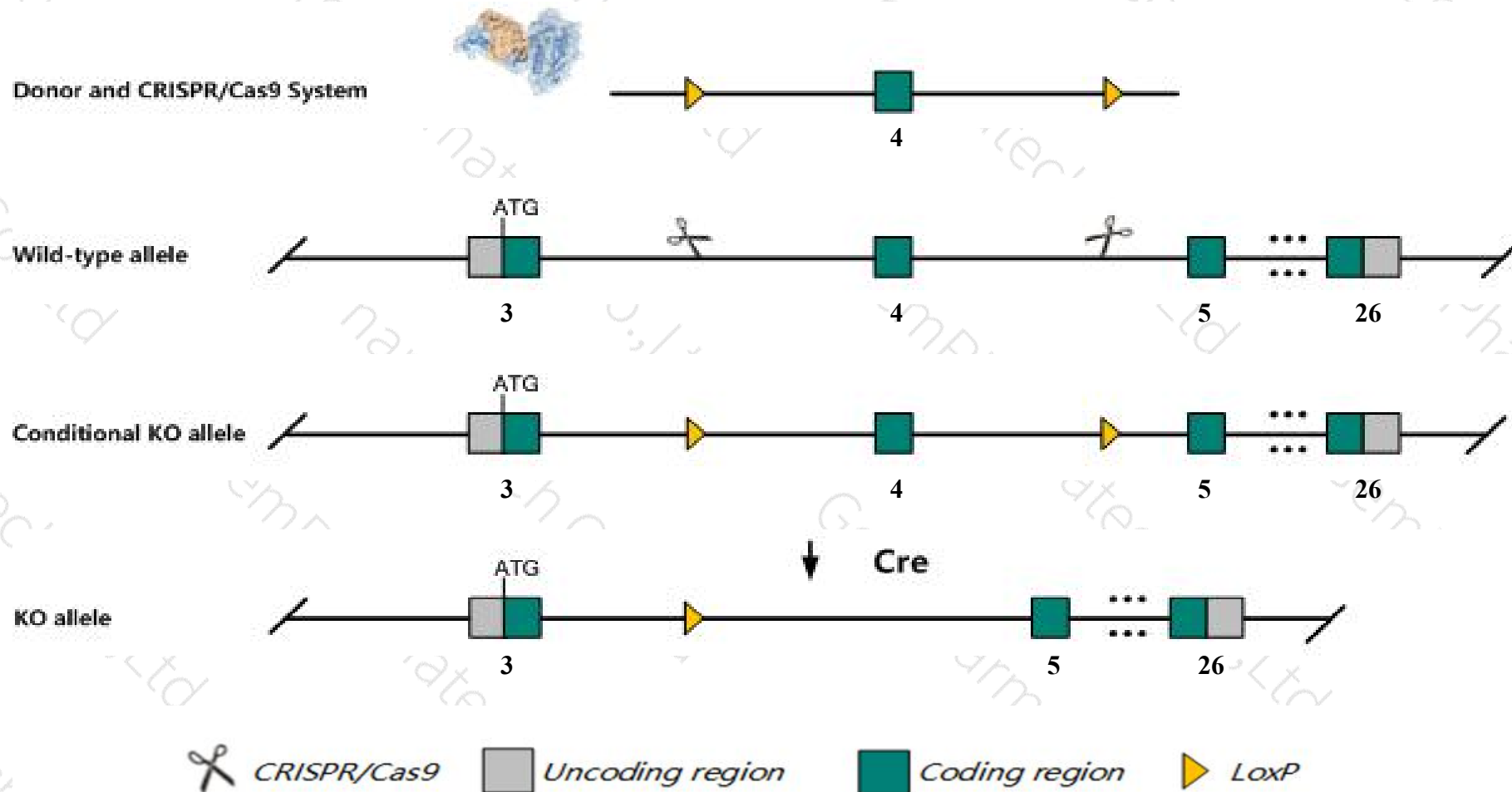
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Setx* gene has 5 transcripts. According to the structure of *Setx* gene, exon4 of *Setx-201* (ENSMUST00000061578.8) transcript is recommended as the knockout region. The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Setx* 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 male infertility due to arrested male meiosis and reduced female fertility.
- The *Setx* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Setx senataxin [Mus musculus (house mouse)]

Gene ID: 269254, updated on 13-Mar-2020

Summary



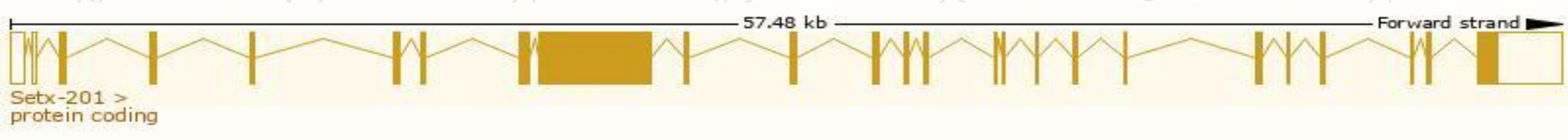
Official Symbol	Setx provided by MGI
Official Full Name	senataxin provided by MGI
Primary source	MGI:MGI:2443480
See related	Ensembl:ENSMUSG00000043535
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A130090N03, A930037J23Rik, AOA2, AW060766, Als4, SCAR1, Sen1, mKIAA0625
Expression	Broad expression in testis adult (RPKM 26.8), CNS E11.5 (RPKM 4.6) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

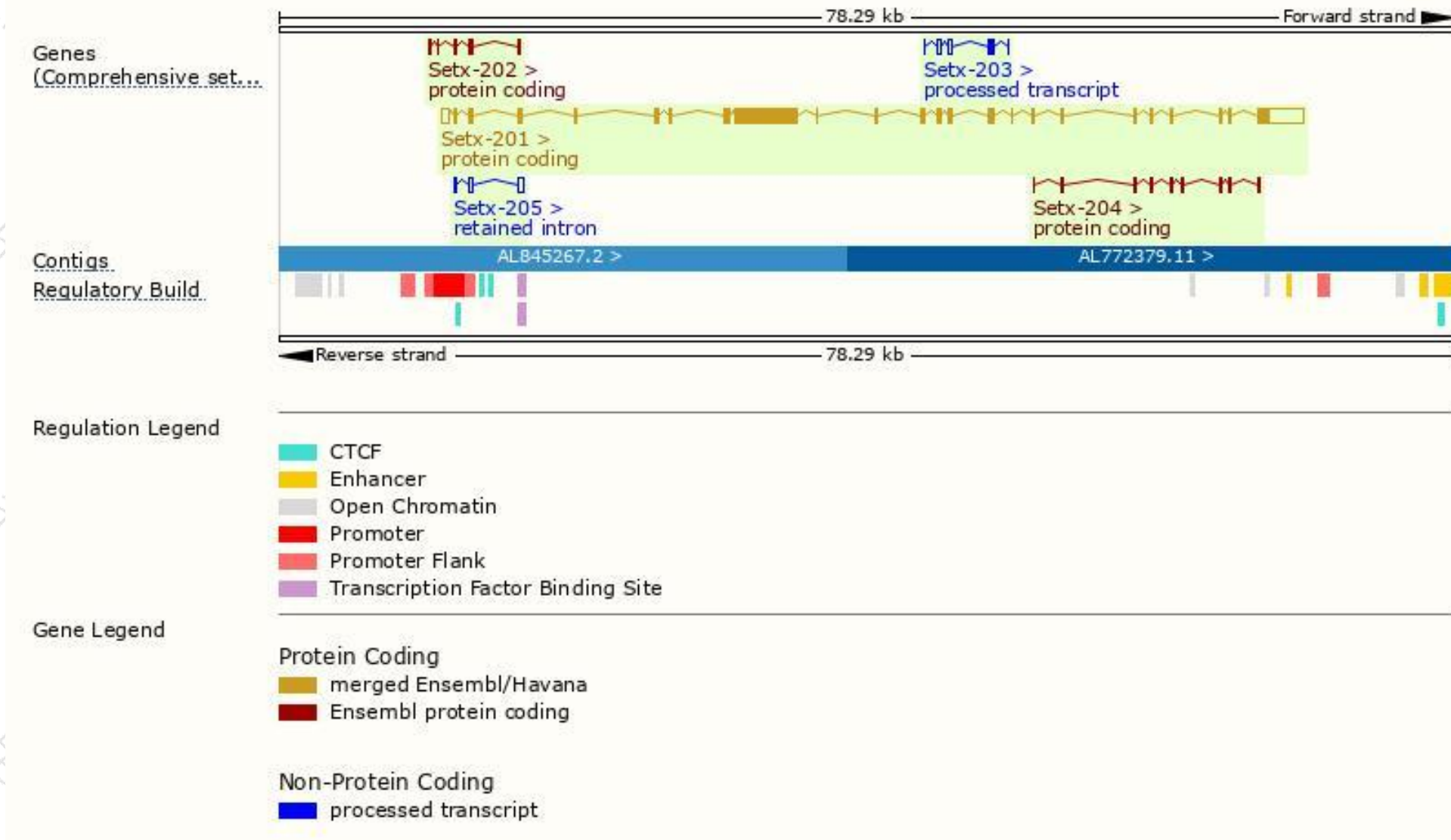
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setx-201	ENSMUST00000061578.8	10970	2646aa	Protein coding	CCDS38090	A2AKX3	TSL:5 GENCODE basic APPRIS P1
Setx-202	ENSMUST00000129544.7	525	81aa	Protein coding	-	A0A0A0MQJ0	CDS 3' incomplete TSL:3
Setx-203	ENSMUST00000135992.1	577	No protein	Processed transcript	-	-	TSL:5
Setx-204	ENSMUST00000145422.1	1141	381aa	Protein coding	-	F6R186	CDS 5' and 3' incomplete TSL:5
Setx-205	ENSMUST00000154910.1	538	No protein	Retained intron	-	-	TSL:3

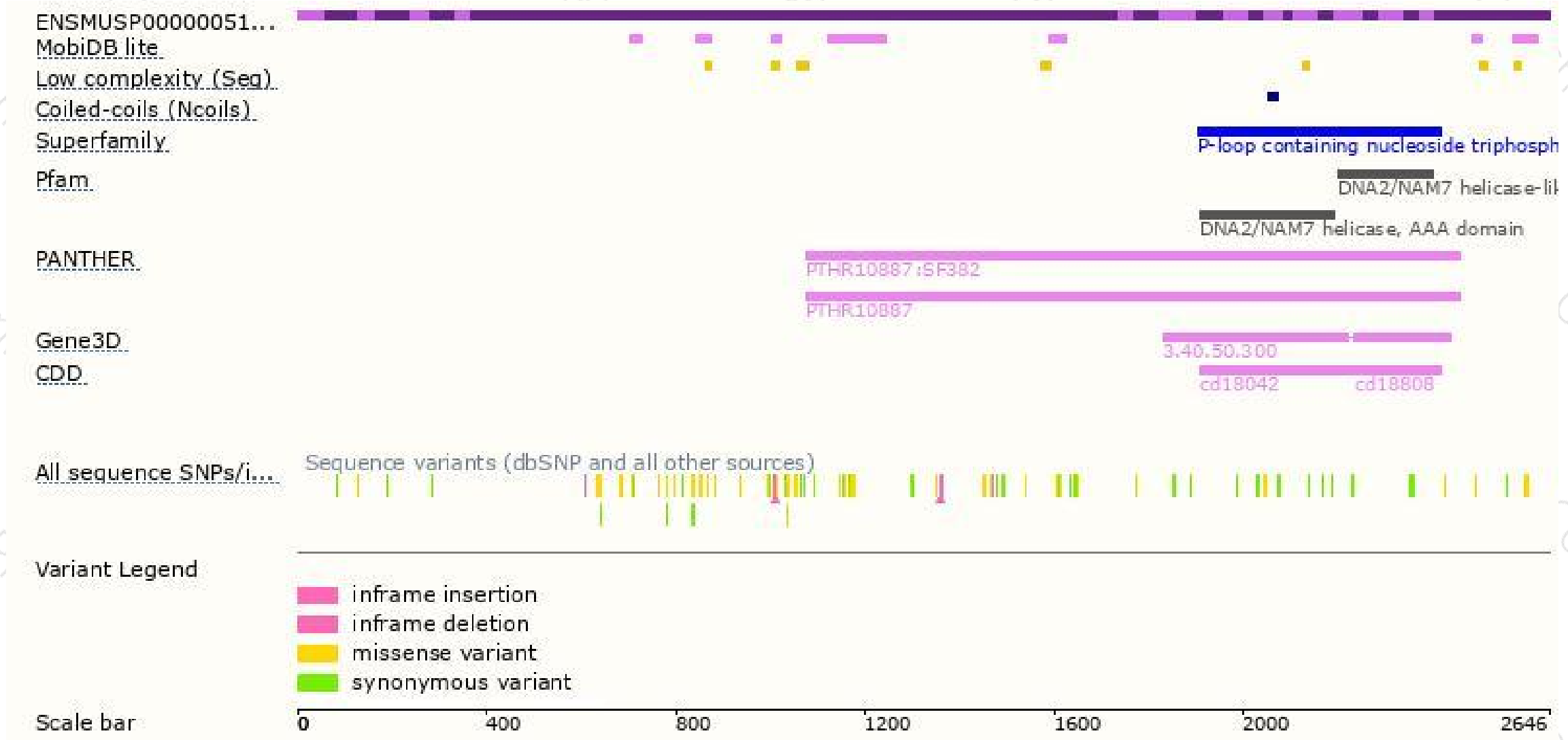
The strategy is based on the design of *Setx-201* transcript,The transcription is shown below



Genomic location distribution

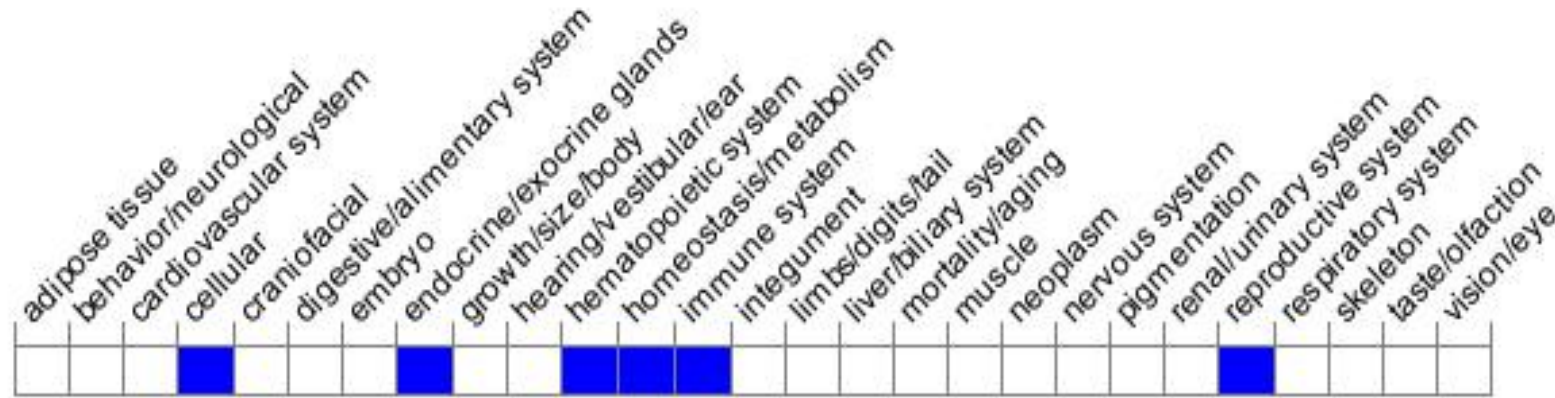


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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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