

Setmar Cas9-CKO Strategy

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Project Overview

Project Name

Setmar

Project type

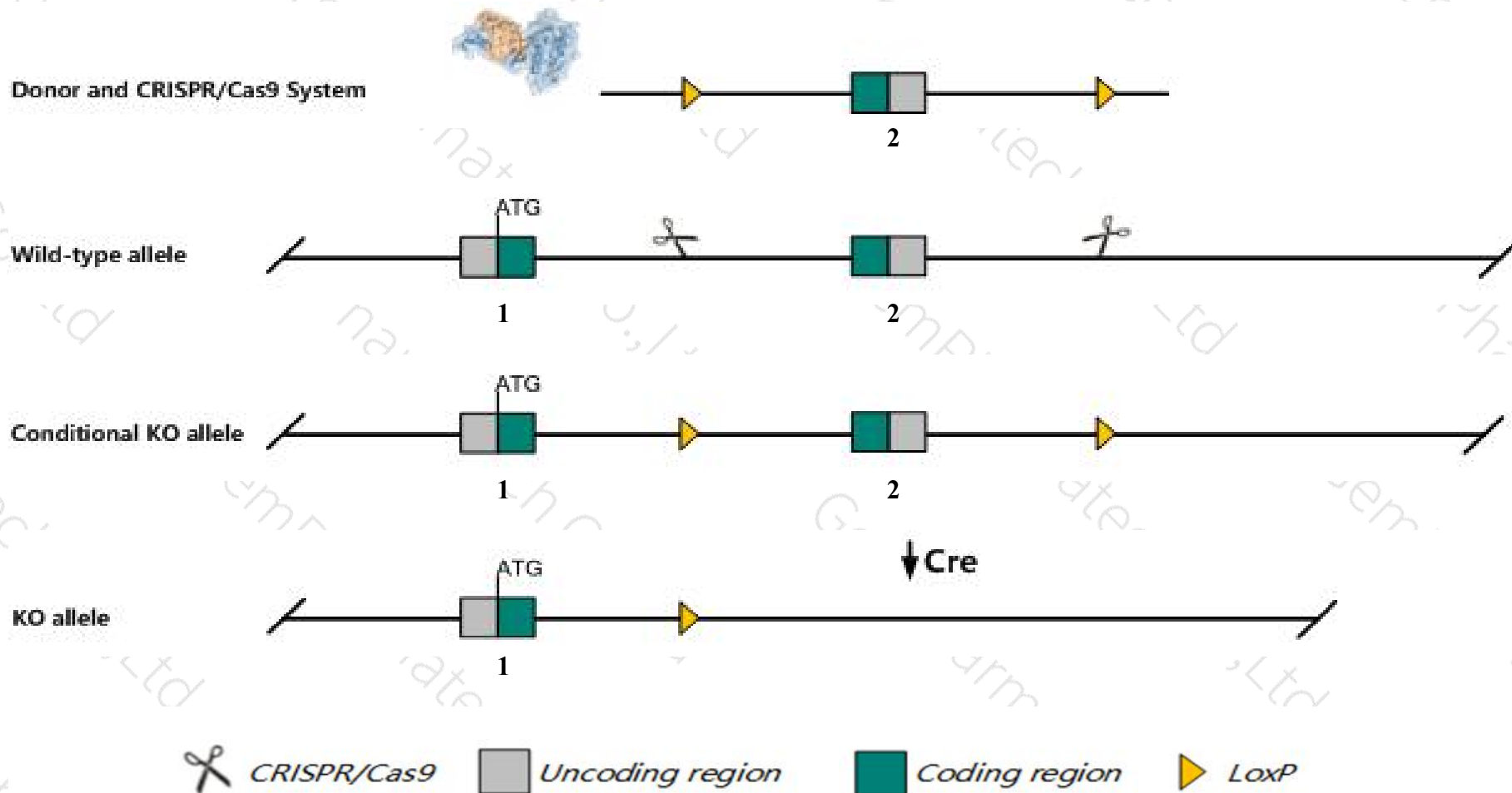
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Setmar* gene has 2 transcripts. According to the structure of *Setmar* gene, exon2 of *Setmar-201* (ENSMUST00000049246.6) transcript is recommended as the knockout region. The region contains most 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 *Setmar* 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

- The *Setmar* gene is located on the Chr6. 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)

Setmar SET domain without mariner transposase fusion [Mus musculus (house mouse)]

Gene ID: 74729, updated on 13-Mar-2020

Summary



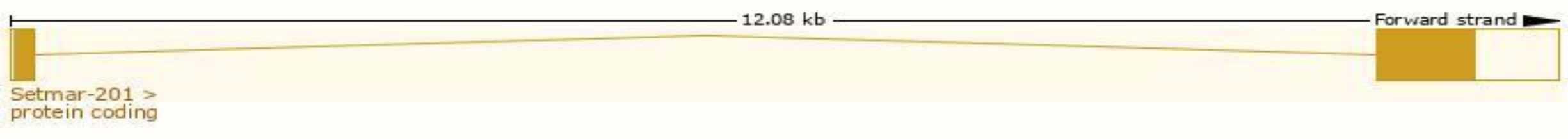
Official Symbol	Setmar provided by MGI
Official Full Name	SET domain without mariner transposase fusion provided by MGI
Primary source	MGI:MGI:1921979
See related	Ensembl:ENSMUSG000000034639
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830404F24Rik, Etet2
Summary	This gene encodes a histone-lysine N-methyltransferase that may be involved in the methylation of histone H3. In anthropoid primates this gene is a fusion gene of a SET histone-lysine N-methyltransferase and a mariner (MAR) family transposase. In all other species this gene contains only the SET domain. [provided by RefSeq, Jan 2013]
Expression	Ubiquitous expression in bladder adult (RPKM 2.7), frontal lobe adult (RPKM 1.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

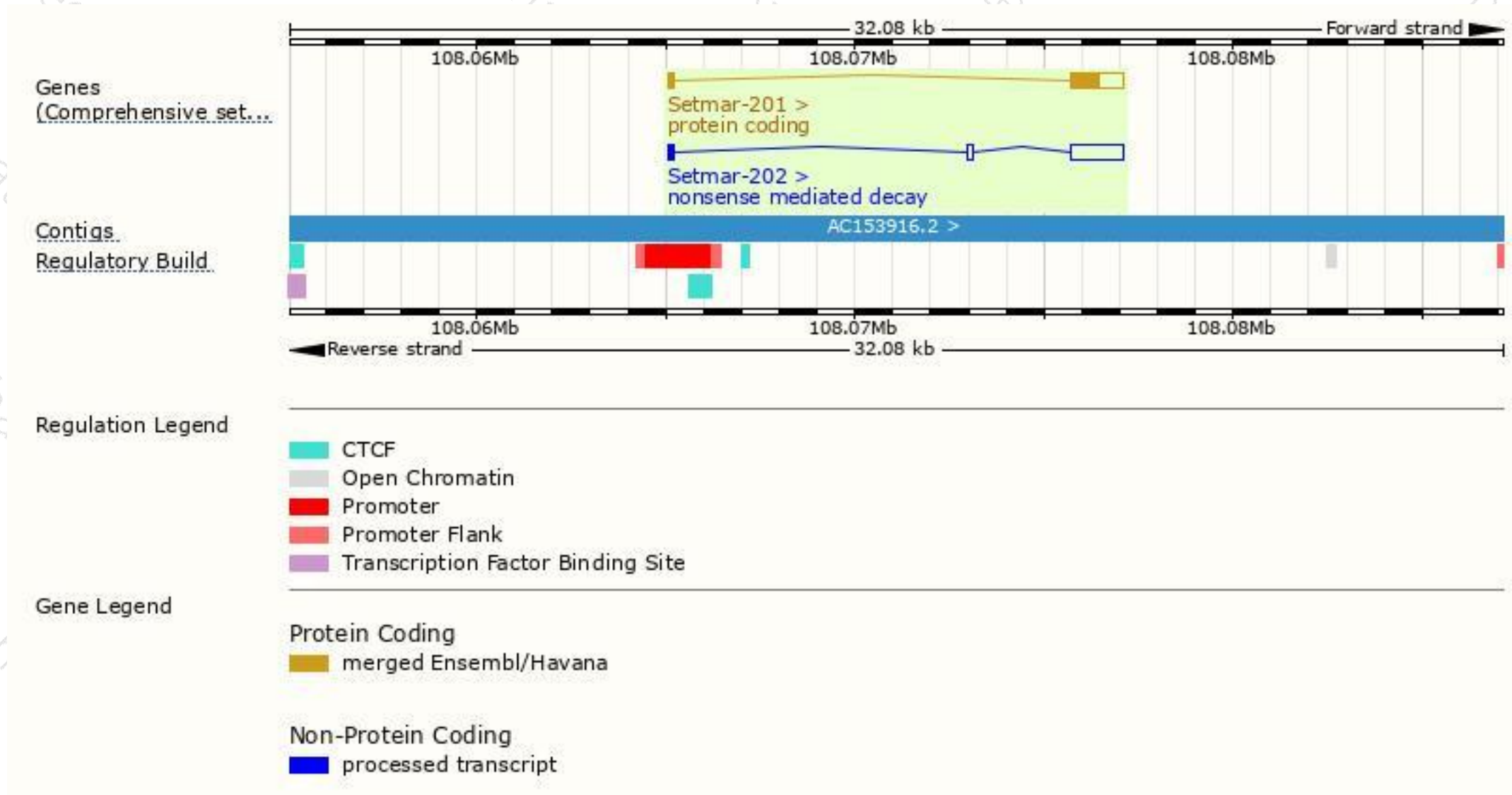
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setmar-201	ENSMUST00000049246.6	1612	309aa	Protein coding	CCDS51867	Q80UJ9	TSL:1 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
Setmar-202	ENSMUST00000138140.2	1748	60aa	Nonsense mediated decay	-	A0A0N4SVW0	TSL:3

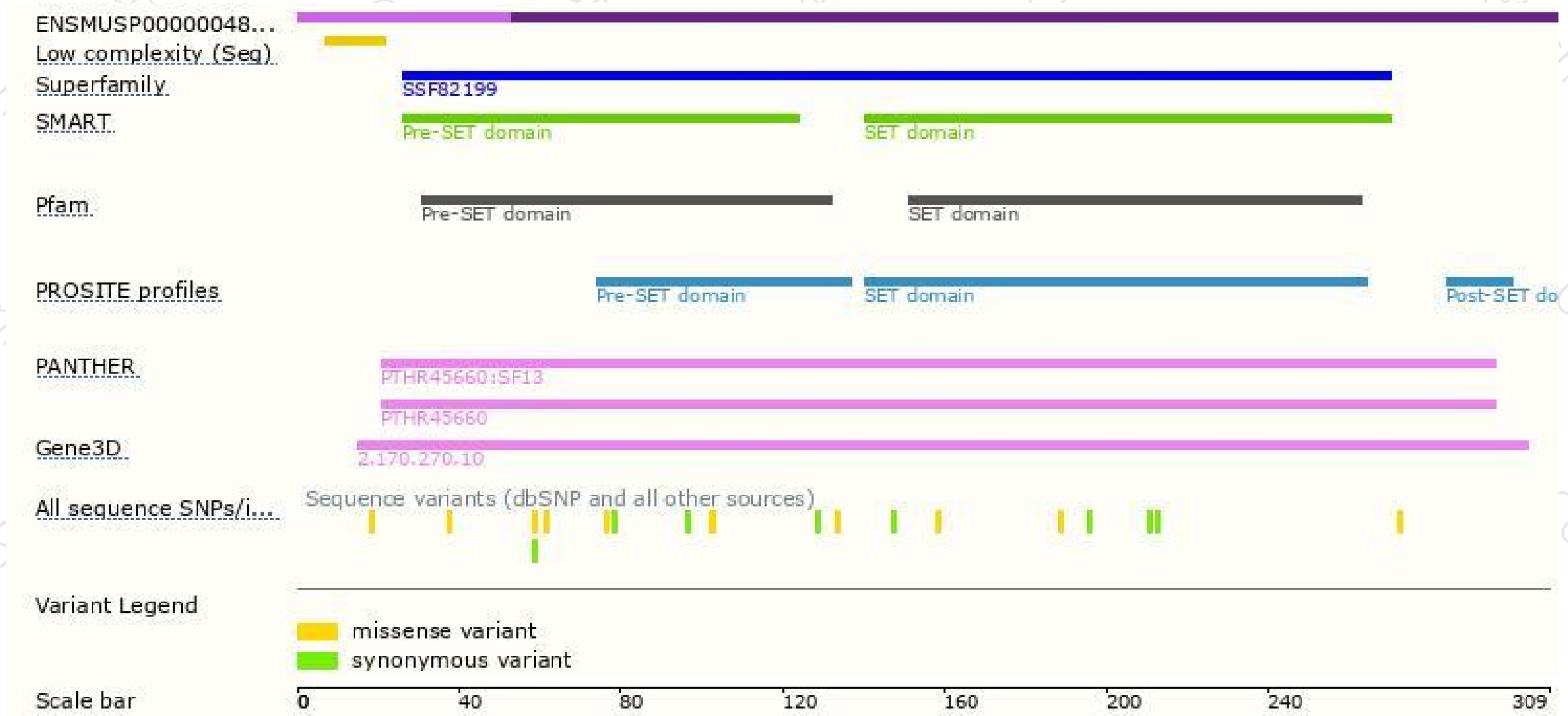
The strategy is based on the design of *Setmar-201* transcript,the transcription is shown below:



Genomic location distribution

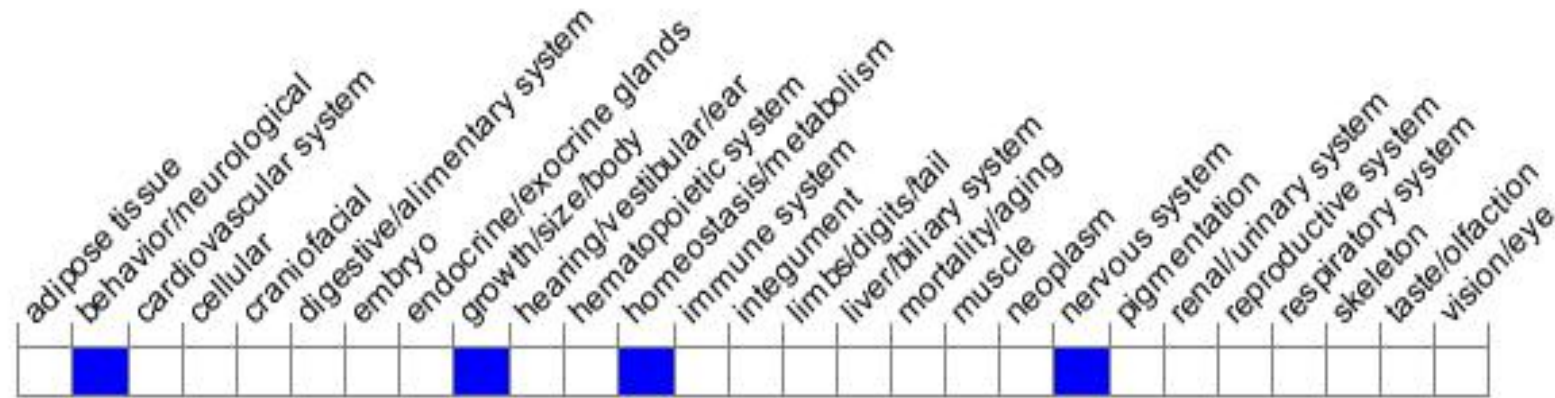


Protein domain



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/>).

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

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