

Set Cas9-KO Strategy

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Project Overview

Project Name

Set

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Set* gene has 7 transcripts. According to the structure of *Set* gene, exon2 of *Set-201* (ENSMUST00000067996.6) transcript is recommended as the knockout region. The region contains 58bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Set* gene. The brief process is as follows: CRISPR/Cas9 system we

- The *Set* 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)

Set SET nuclear oncogene [Mus musculus (house mouse)]

Gene ID: 56086, updated on 31-Jan-2019

Summary



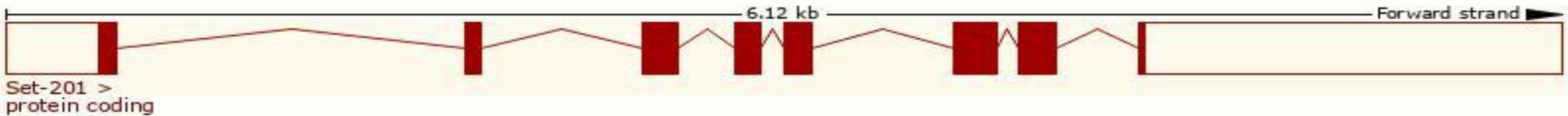
Official Symbol	Set provided by MGI
Official Full Name	SET nuclear oncogene provided by MGI
Primary source	MGI:MGI:1860267
See related	Ensembl:ENSMUSG00000054766
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610030F17Rik, 5730420M11Rik, AA407739, I-2PP2A, StF-IT-1, TAF-I
Expression	Ubiquitous expression in CNS E11.5 (RPKM 163.2), CNS E14 (RPKM 62.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

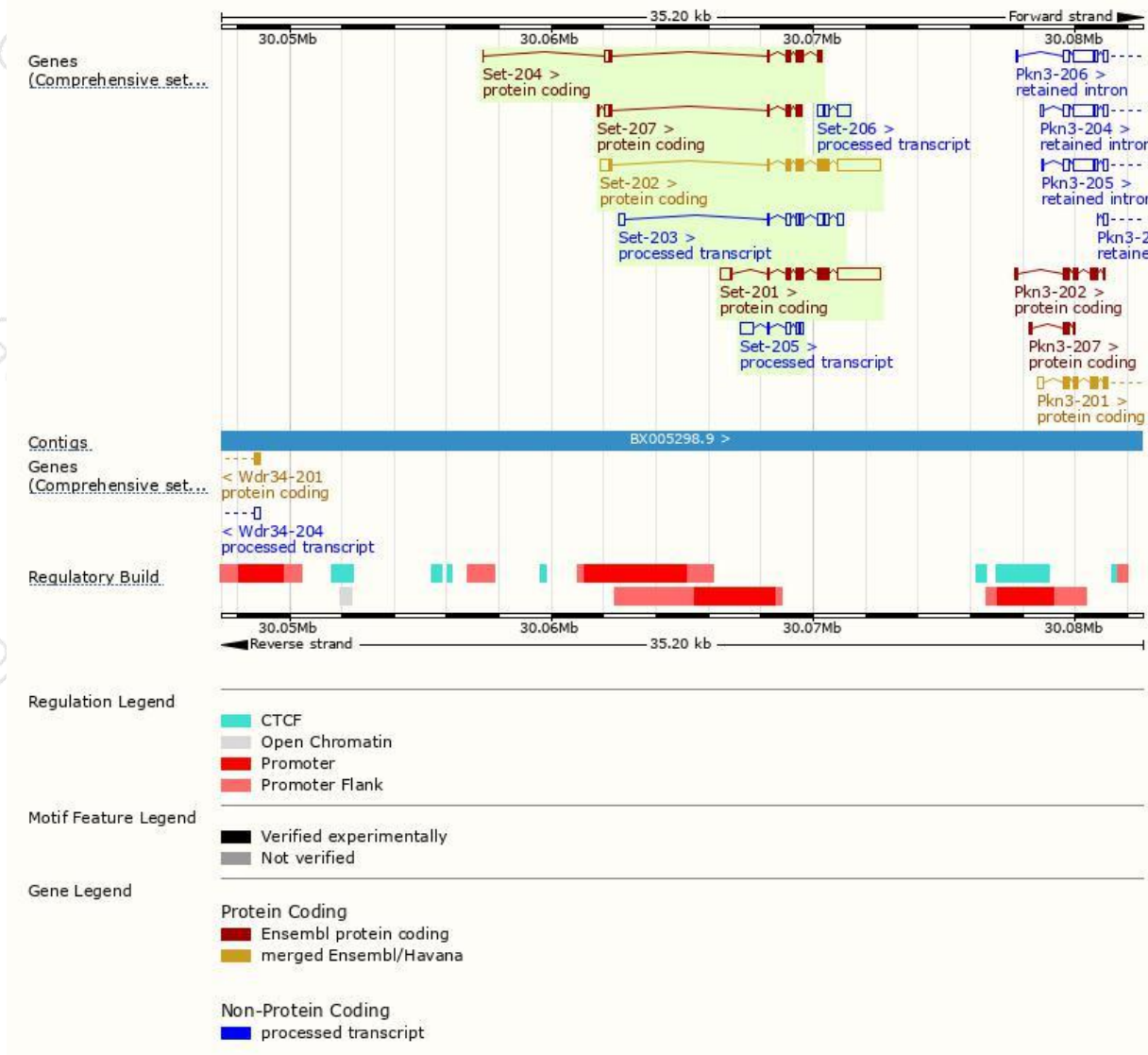
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Set-201	ENSMUST00000067996.6	2834	277aa	Protein coding	CCDS57162	Q9EQU5	TSL:1 GENCODE basic APPRIS ALT2
Set-202	ENSMUST00000102866.9	2824	289aa	Protein coding	CCDS15866	Q3T9S3 Q9EQU5	TSL:1 GENCODE basic APPRIS P3
Set-204	ENSMUST00000134364.7	790	215aa	Protein coding	-	A2BE93	CDS 3' incomplete TSL:5
Set-207	ENSMUST00000149578.7	633	151aa	Protein coding	-	A2BE92	CDS 3' incomplete TSL:3
Set-203	ENSMUST00000125824.7	1112	No protein	Processed transcript	-	-	TSL:5
Set-205	ENSMUST00000137291.1	952	No protein	Processed transcript	-	-	TSL:5
Set-206	ENSMUST00000147590.1	844	No protein	Processed transcript	-	-	TSL:2

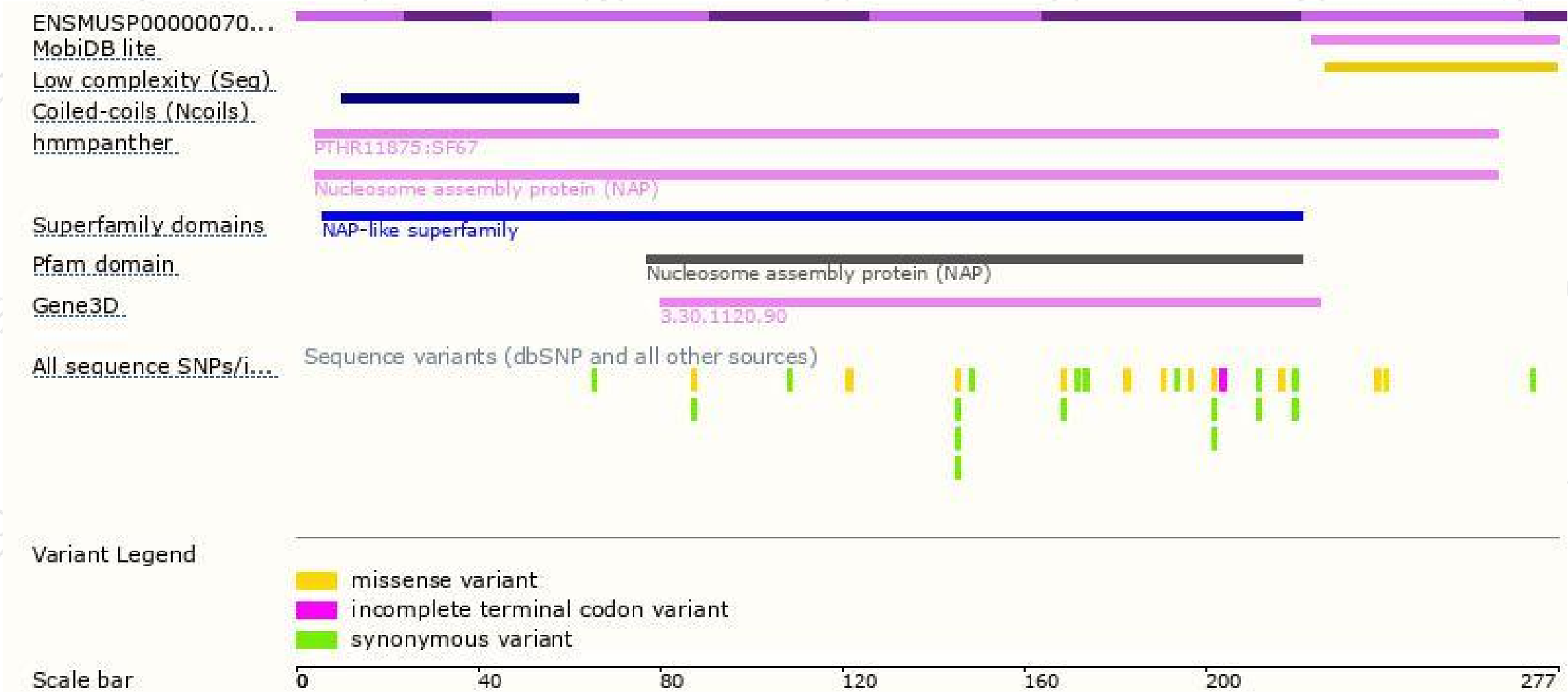
The strategy is based on the design of *Set-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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