

Sfpq Cas9-KO Strategy

Designer: Yanhua Shen
Reviewer: Xueting Zhang
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Project Overview

Project Name

Sfpq

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Sfpq* gene has 6 transcripts. According to the structure of *Sfpq* gene, exon1-exon9 of *Sfpq-201* (ENSMUST00000030623.7) 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 *Sfpq* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a gene trap allele die. Heterozygous mice show abnormality in entrainment of circadian rhythm.
- The *Sfpq* gene is located on the Chr4. 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)

Sfpq splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [*Mus musculus* (house mouse)]

Gene ID: 71514, updated on 12-Aug-2019

Summary

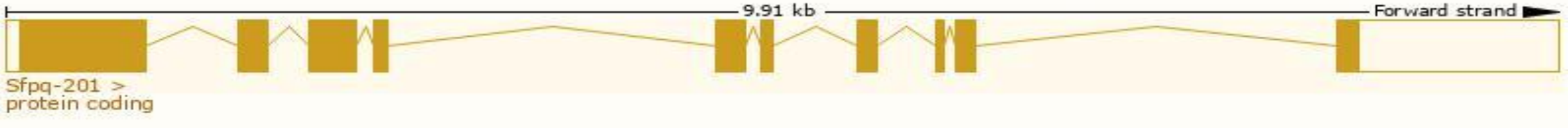
Official Symbol	Sfpq provided by MGI
Official Full Name	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) provided by MGI
Primary source	MGI:MGI:1918764
See related	Ensembl:ENSMUSG00000028820
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PSF; REP1; Gm12940; AU021830; D4Ertd314e; 1110004P21Rik; 2810416M14Rik; 5730453G22Rik; 9030402K04Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 54.6), CNS E14 (RPKM 39.2) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

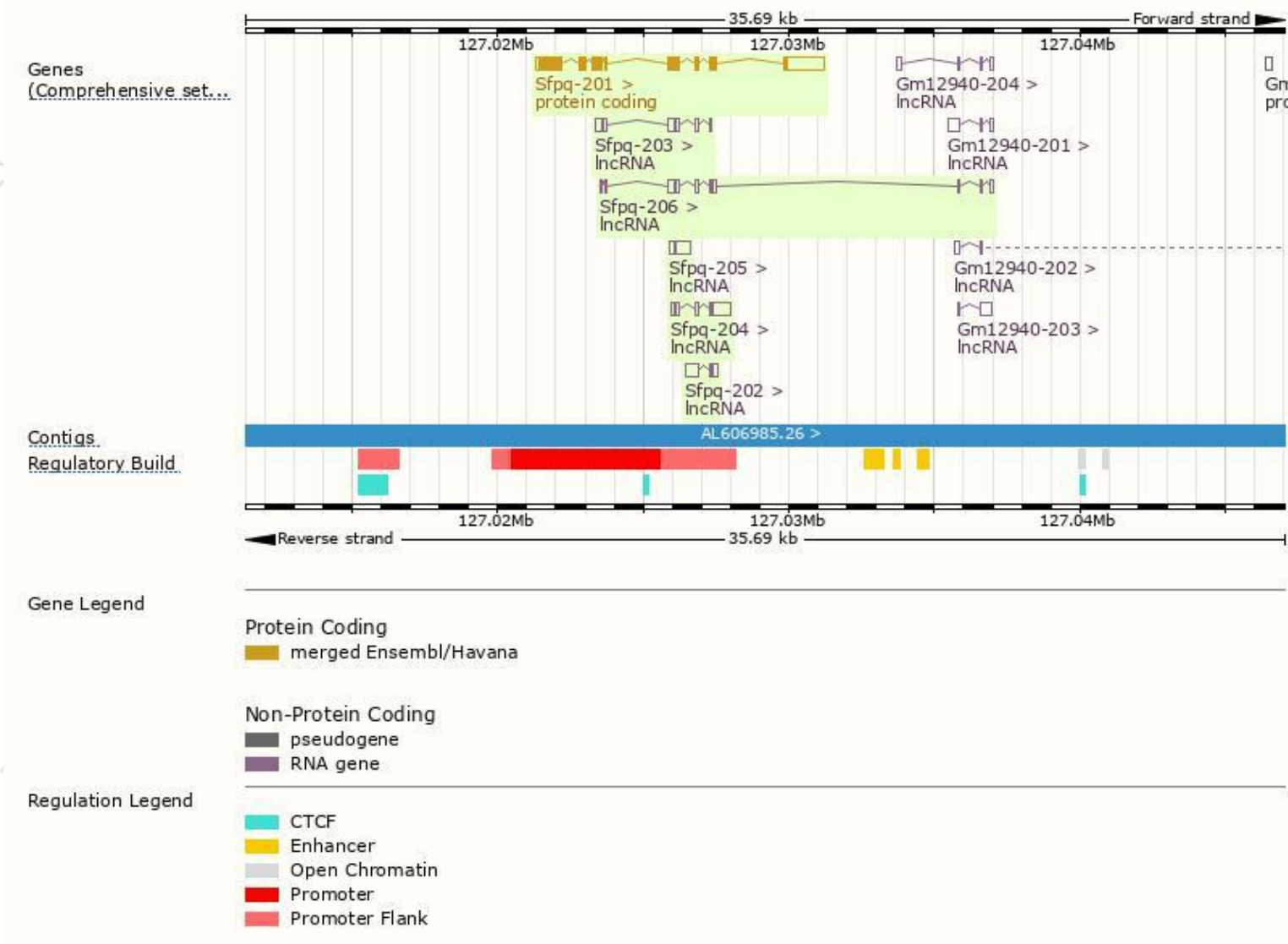
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sfpq-201	ENSMUST00000030623.7	3465	699aa	Protein coding	CCDS18662	Q8VIJ6	TSL:1 GENCODE basic APPRIS P1
Sfpq-204	ENSMUST00000143168.7	967	No protein	lncRNA	-	-	TSL:2
Sfpq-206	ENSMUST00000146285.7	925	No protein	lncRNA	-	-	TSL:5
Sfpq-203	ENSMUST00000140682.7	755	No protein	lncRNA	-	-	TSL:3
Sfpq-202	ENSMUST00000125453.1	644	No protein	lncRNA	-	-	TSL:2
Sfpq-205	ENSMUST00000144630.1	600	No protein	lncRNA	-	-	TSL:3

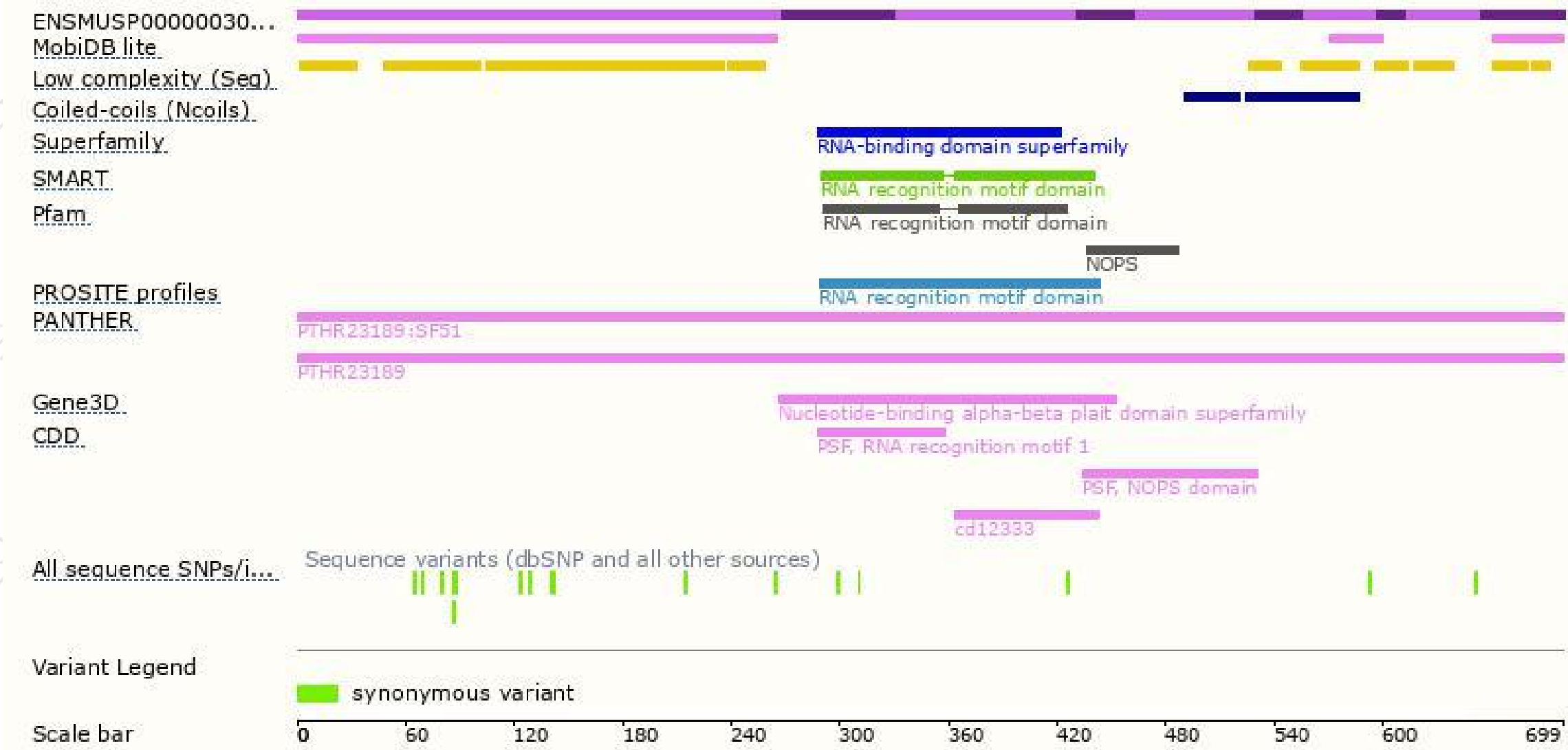
The strategy is based on the design of *Sfpq-201* transcript,The transcription is shown below



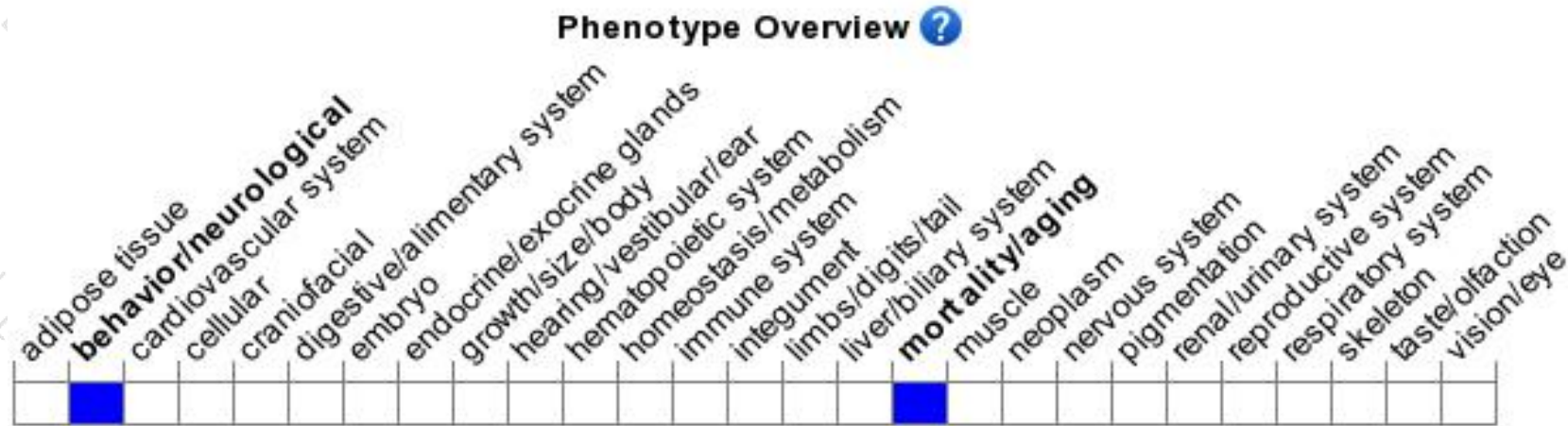
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a gene trap allele die. Heterozygous mice show abnormality in entrainment of circadian rhythm.

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

Tel: 400-9660890

