

Srsf3 Cas9-KO Strategy

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Reviewer:

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Design Date:

2020-1-13

Project Overview

Project Name

Srsf3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf3* gene. The schematic diagram is as follows:



- The *Srsf3* gene has 10 transcripts. According to the structure of *Srsf3* gene, exon2 of *Srsf3-202* (ENSMUST00000130216.2) 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 *Srsf3* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutant mice die at early embryonic stages.
- The *Srsf3* gene is located on the Chr17. 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)

Srsf3 serine/arginine-rich splicing factor 3 [Mus musculus (house mouse)]

Gene ID: 20383, updated on 31-Jan-2019

Summary



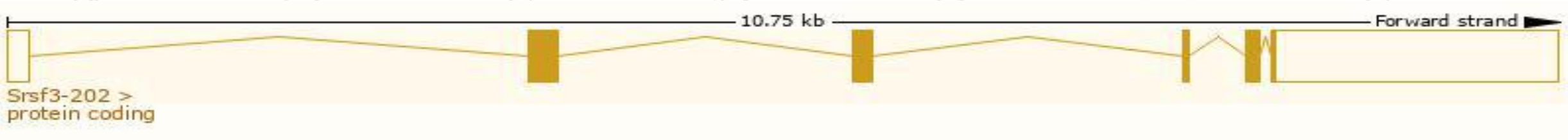
Official Symbol	Srsf3 provided by MGI
Official Full Name	serine/arginine-rich splicing factor 3 provided by MGI
Primary source	MGI:MGI:98285
See related	Ensembl:ENSMUSG000000071172
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AL024116, Sfrs3, X16
Summary	The protein encoded by this gene is a member of the serine/arginine (SR)-rich family of pre-mRNA splicing factors, which constitute part of the spliceosome. Each of these factors contains an RNA recognition motif (RRM) for binding RNA and an RS domain for binding other proteins. The RS domain is rich in serine and arginine residues and facilitates interaction between different SR splicing factors. In addition to being critical for mRNA splicing, the SR proteins have also been shown to be involved in mRNA export from the nucleus and in translation. Two transcript variants, one protein-coding and the other not protein-coding, have been found for this gene. [provided by RefSeq, Sep 2010]
Expression	Broad expression in CNS E11.5 (RPKM 128.5), CNS E14 (RPKM 91.1) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

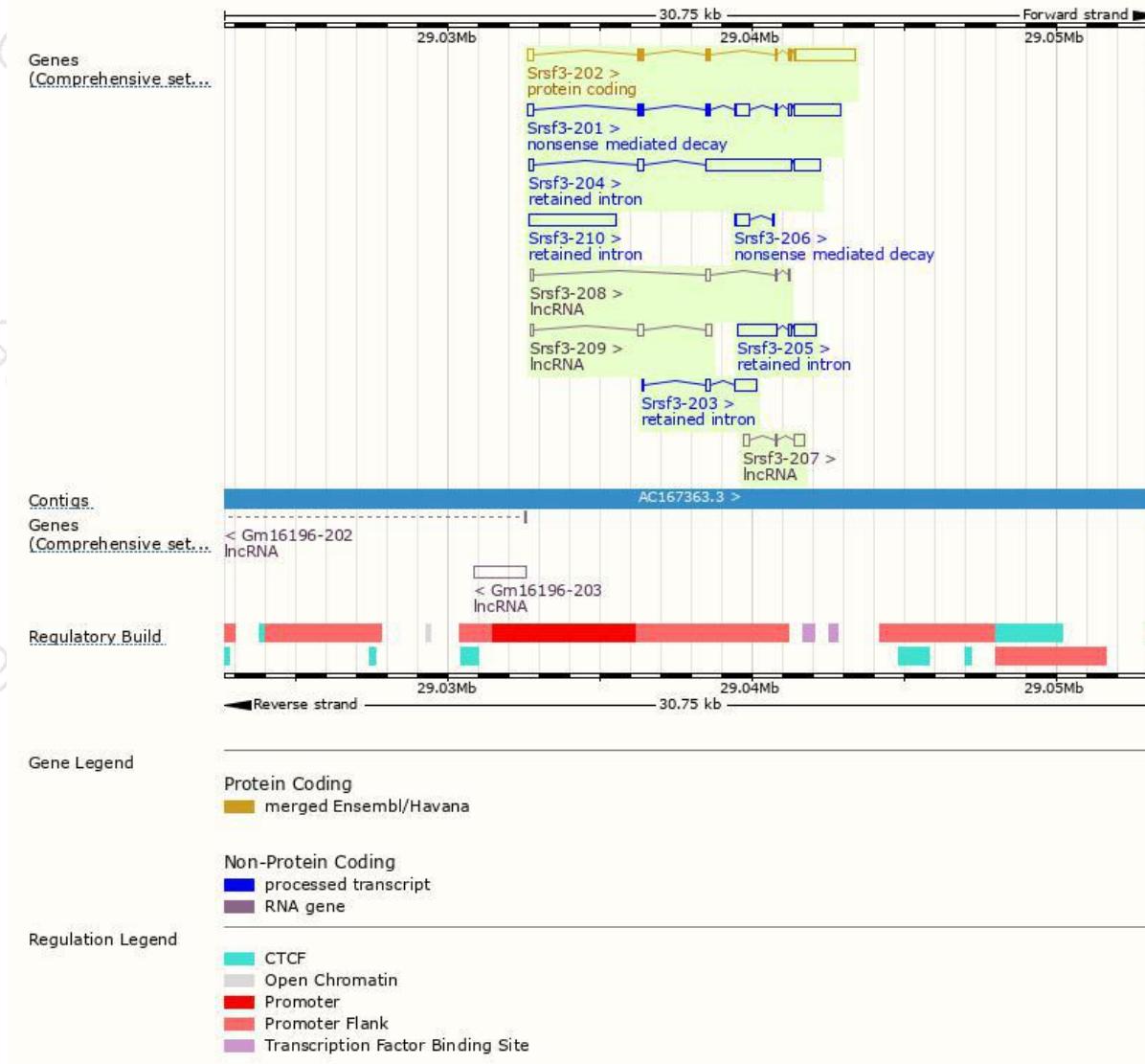
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf3-202	ENSMUST00000130216.2	2618	164aa	Protein coding	CCDS28590	P84104	TSL:1 GENCODE basic APPRIS P1
Srsf3-201	ENSMUST00000037776.15	2594	124aa	Nonsense mediated decay	-	P84104 Q3U781	TSL:1
Srsf3-206	ENSMUST00000233010.1	526	11aa	Nonsense mediated decay	-	A0A3B2W3M9	CDS 5' incomplete
Srsf3-204	ENSMUST00000147265.8	4010	No protein	Retained intron	-	-	TSL:1
Srsf3-210	ENSMUST00000233885.1	2836	No protein	Retained intron	-	-	
Srsf3-205	ENSMUST00000150157.2	2110	No protein	Retained intron	-	-	TSL:2
Srsf3-203	ENSMUST00000144551.1	893	No protein	Retained intron	-	-	TSL:2
Srsf3-207	ENSMUST00000233105.1	594	No protein	lncRNA	-	-	
Srsf3-209	ENSMUST00000233209.1	518	No protein	lncRNA	-	-	
Srsf3-208	ENSMUST00000233127.1	319	No protein	lncRNA	-	-	

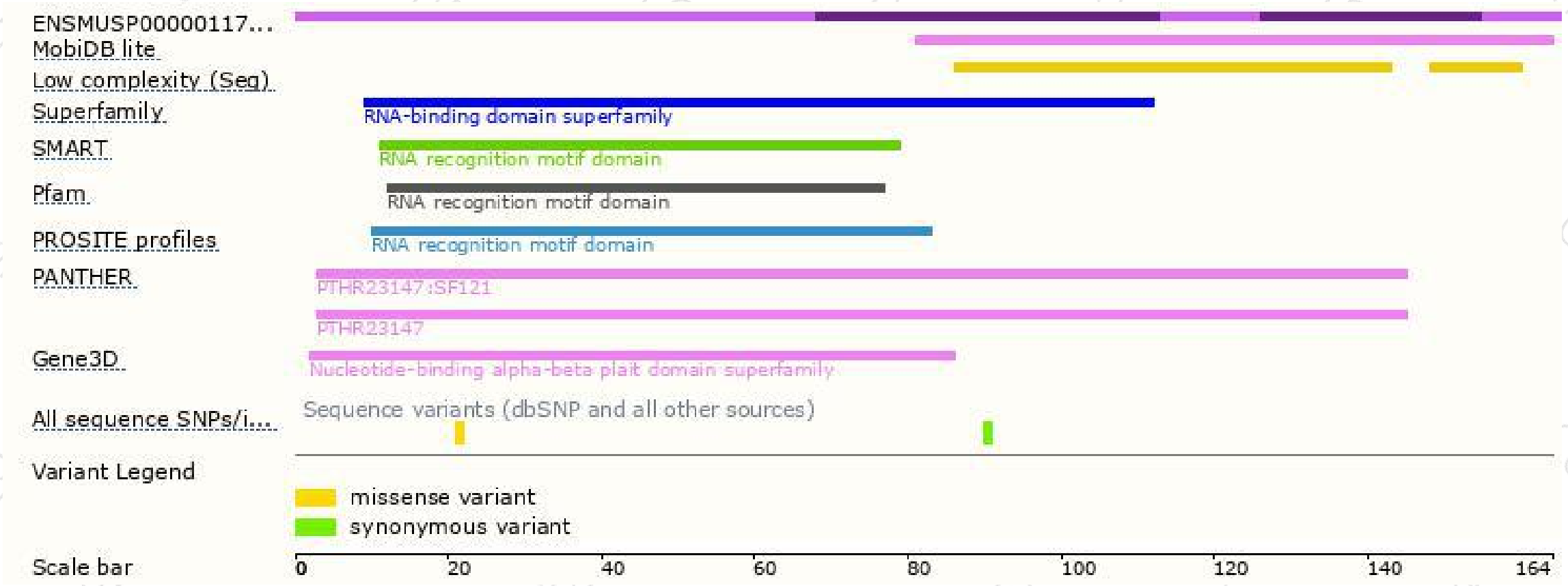
The strategy is based on the design of *Srsf3-202* transcript,The transcription is shown below



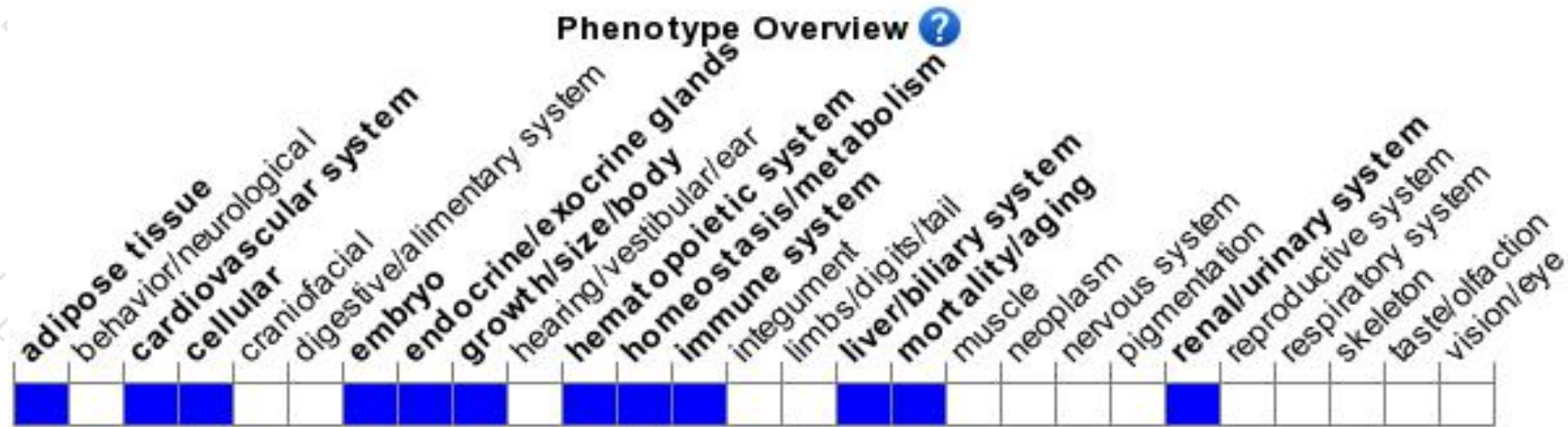
Genomic location distribution



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, Homozygous mutant mice die at early embryonic stages.

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

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