

Srsf11 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Srsf11

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf11* gene. The schematic diagram is as follows:



- The *Srsf11* gene has 19 transcripts. According to the structure of *Srsf11* gene, exon3-exon7 of *Srsf11-204* (ENSMUST00000121326.7) transcript is recommended as the knockout region. The region contains 515bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srsf11* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Srsf11* gene is located on the Chr3. 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)

Srsf11 serine/arginine-rich splicing factor 11 [Mus musculus (house mouse)]

Gene ID: 69207, updated on 31-Jan-2019

Summary



Official Symbol Srsf11 provided by [MGI](#)

Official Full Name serine/arginine-rich splicing factor 11 provided by [MGI](#)

Primary source [MGI:MGI:1916457](#)

See related [Ensembl:ENSMUSG00000055436](#)

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 0610009J05Rik, 2610019N13Rik, BF642805, Sfrs11

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. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov 2014]

Expression Ubiquitous expression in limb E14.5 (RPKM 60.3), CNS E14 (RPKM 43.9) and 28 other tissues [See more](#)

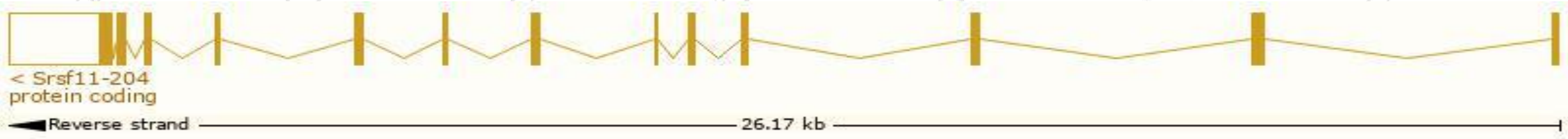
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

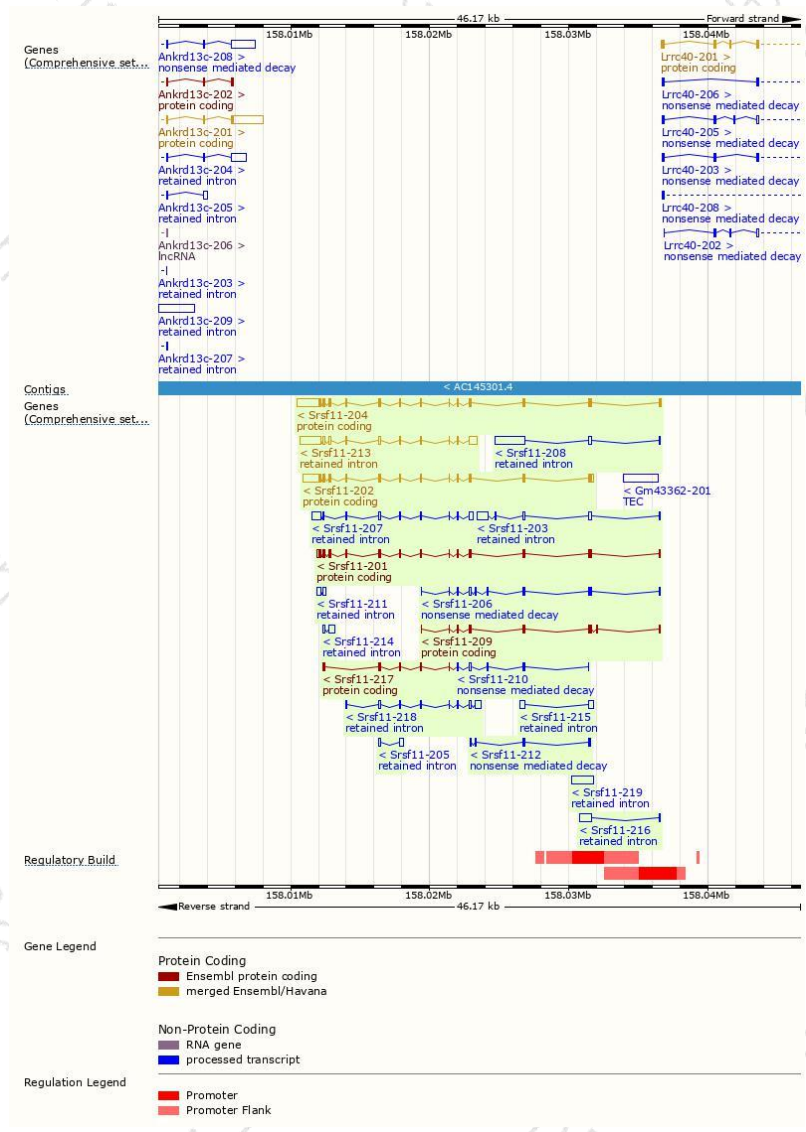
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf11-204	ENSMUST00000121326.7	3106	511aa	Protein coding	CCDS51103	E9Q6E5	TSL:5 GENCODE basic APPRIS P4
Srsf11-202	ENSMUST00000072875.14	2654	476aa	Protein coding	CCDS51102	Q3UIX4	TSL:1 GENCODE basic APPRIS ALT2
Srsf11-201	ENSMUST00000069025.13	1643	500aa	Protein coding	-	F6RDI8	CDS 5' incomplete TSL:5
Srsf11-209	ENSMUST00000137444.7	769	192aa	Protein coding	-	D3Z4B0	CDS 3' incomplete TSL:5
Srsf11-217	ENSMUST00000198705.4	526	175aa	Protein coding	-	A0A0G2JEG1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Srsf11-206	ENSMUST00000126716.8	940	112aa	Nonsense mediated decay	-	D6RE22	TSL:5
Srsf11-210	ENSMUST00000140491.7	397	53aa	Nonsense mediated decay	-	F6X2U6	CDS 5' incomplete TSL:5
Srsf11-212	ENSMUST00000147304.2	392	101aa	Nonsense mediated decay	-	F6TN80	CDS 5' incomplete TSL:3
Srsf11-213	ENSMUST00000152274.8	2952	No protein	Retained intron	-	-	TSL:1
Srsf11-208	ENSMUST00000133090.1	2415	No protein	Retained intron	-	-	TSL:1
Srsf11-207	ENSMUST00000127778.5	1670	No protein	Retained intron	-	-	TSL:1
Srsf11-219	ENSMUST00000199742.1	1570	No protein	Retained intron	-	-	TSL:NA
Srsf11-203	ENSMUST00000089922.11	1309	No protein	Retained intron	-	-	TSL:1
Srsf11-218	ENSMUST00000199520.4	1074	No protein	Retained intron	-	-	TSL:5
Srsf11-216	ENSMUST00000197292.1	930	No protein	Retained intron	-	-	TSL:2
Srsf11-215	ENSMUST00000196034.1	642	No protein	Retained intron	-	-	TSL:2
Srsf11-211	ENSMUST00000145267.1	521	No protein	Retained intron	-	-	TSL:2
Srsf11-214	ENSMUST00000156303.1	474	No protein	Retained intron	-	-	TSL:3
Srsf11-205	ENSMUST00000126377.1	437	No protein	Retained intron	-	-	TSL:2

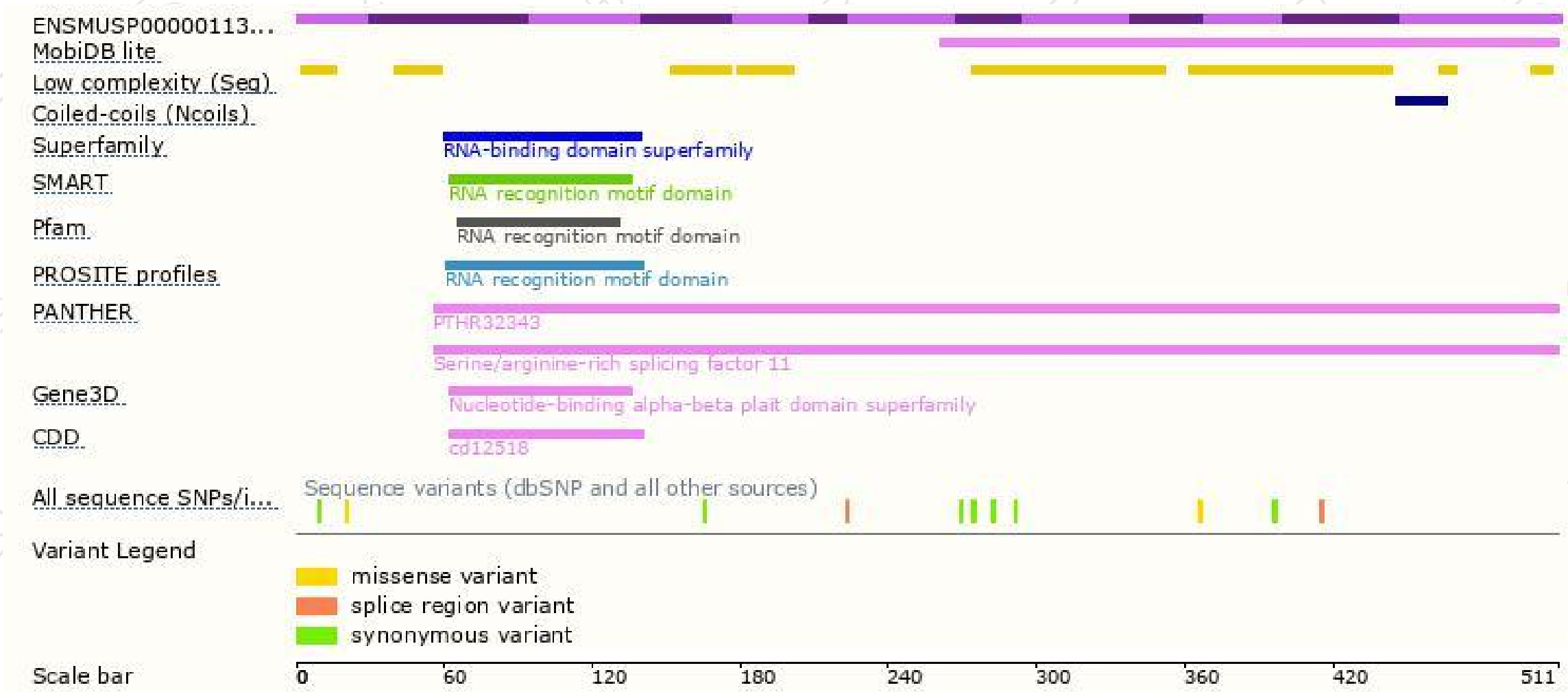
The strategy is based on the design of *Srsf11-204* transcript,The transcription is shown below



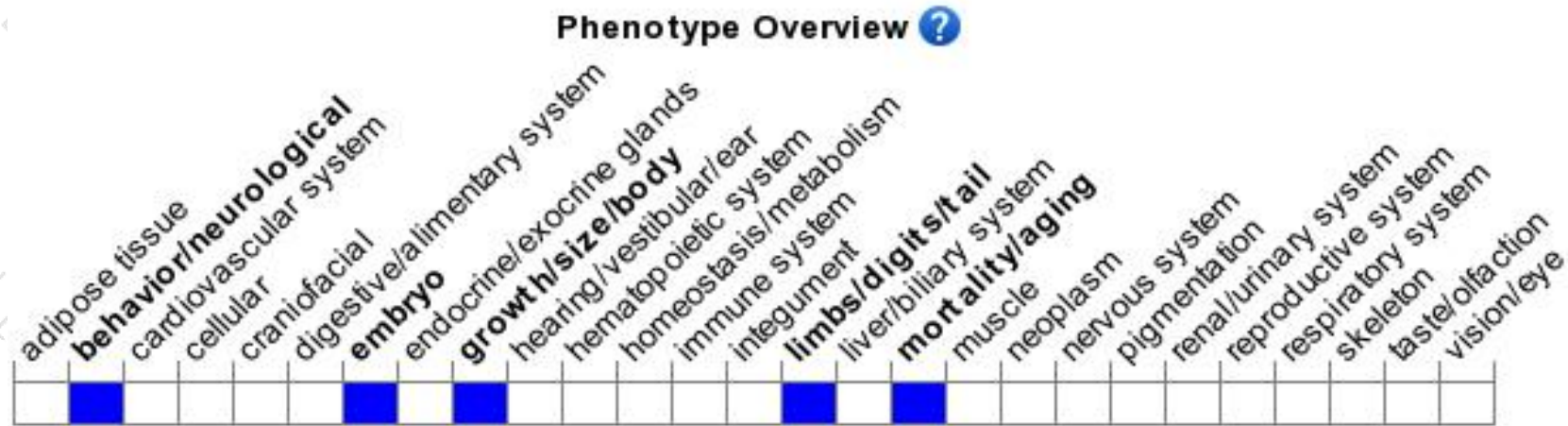
Genomic location distribution



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/>).

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

Tel: 400-9660890

