

Srsf4 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-2-19

Project Overview

Project Name

Srsf4

Project type

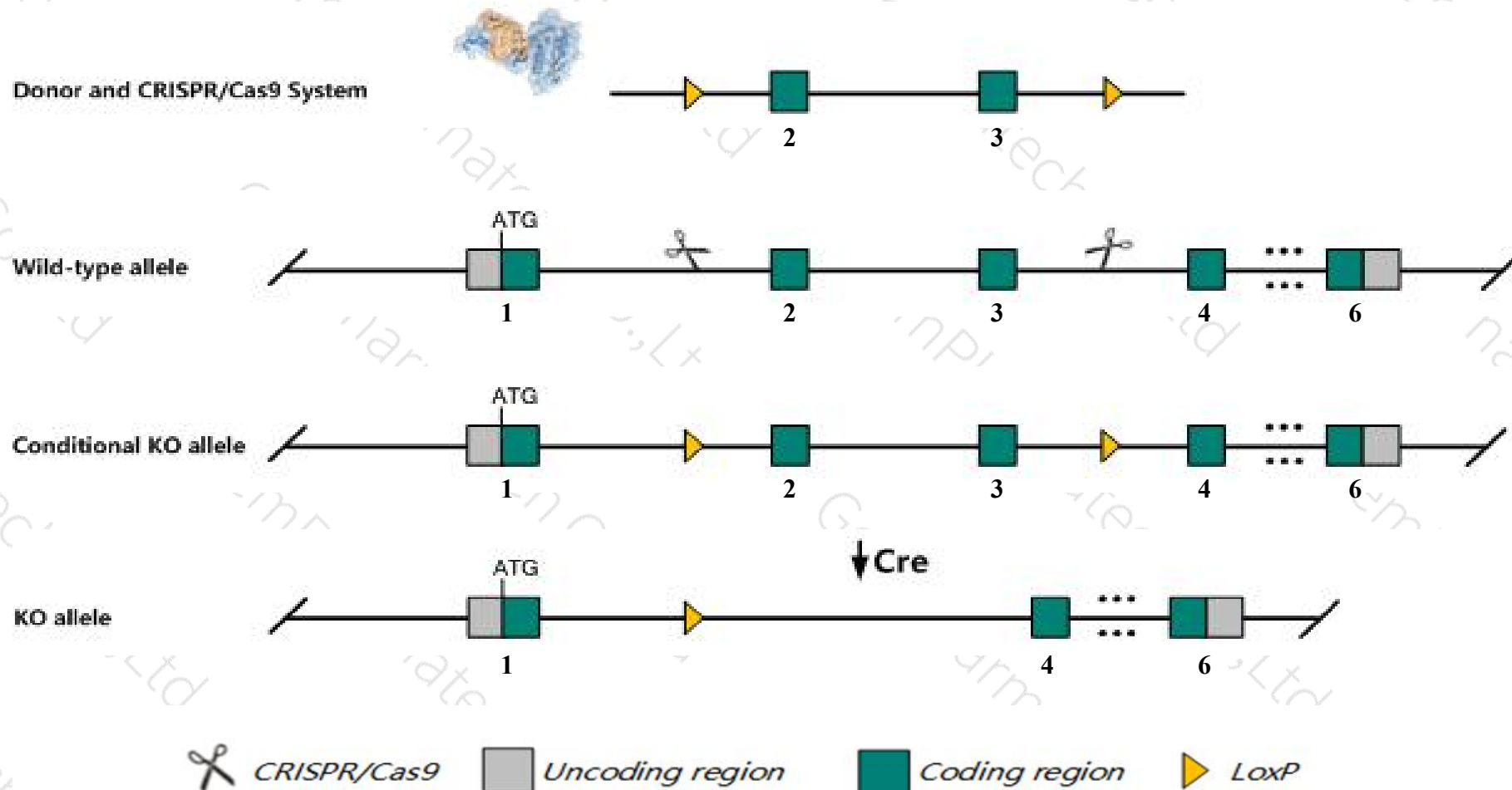
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf4* gene. The schematic diagram is as follows:



- The *Srsf4* gene has 4 transcripts. According to the structure of *Srsf4* gene, exon2-exon3 of *Srsf4-202* (ENSMUST00000053819.5) transcript is recommended as the knockout region. The region contains 256bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srsf4* 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 *Srsf4* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Srsf4 serine/arginine-rich splicing factor 4 [Mus musculus (house mouse)]

Gene ID: 57317, updated on 4-Apr-2019

Summary



Official Symbol	Srsf4 provided by MGI
Official Full Name	serine/arginine-rich splicing factor 4 provided by MGI
Primary source	MGI:MGI:1890577
See related	Ensembl:ENSMUSG000000028911
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	5730499P16Rik, AW550192, MNCb-2616, SRp75, Sfrs4
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. [provided by RefSeq, Sep 2010]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 39.5), CNS E14 (RPKM 24.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

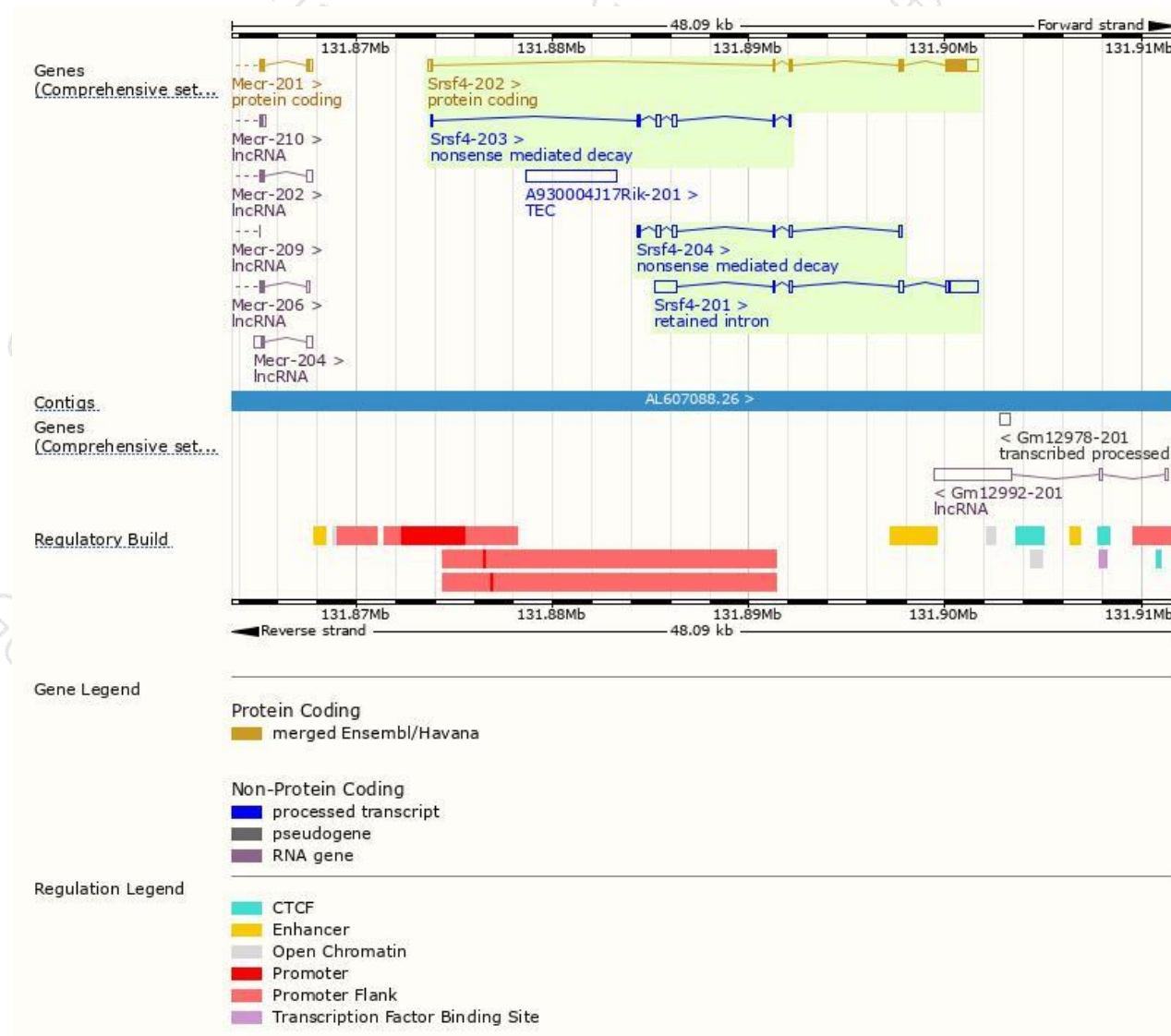
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf4-202	ENSMUST00000053819.5	2257	491aa	Protein coding	CCDS51315	Q542V3	TSL:1 GENCODE basic APPRIS P1
Srsf4-204	ENSMUST00000134943.6	980	31aa	Nonsense mediated decay	-	A0A0A6YXU8	CDS 5' incomplete TSL:5
Srsf4-203	ENSMUST00000129966.7	851	56aa	Nonsense mediated decay	-	A0A0A6YWA5	CDS 5' incomplete TSL:5
Srsf4-201	ENSMUST00000030743.9	3100	No protein	Retained intron	-	-	TSL:1

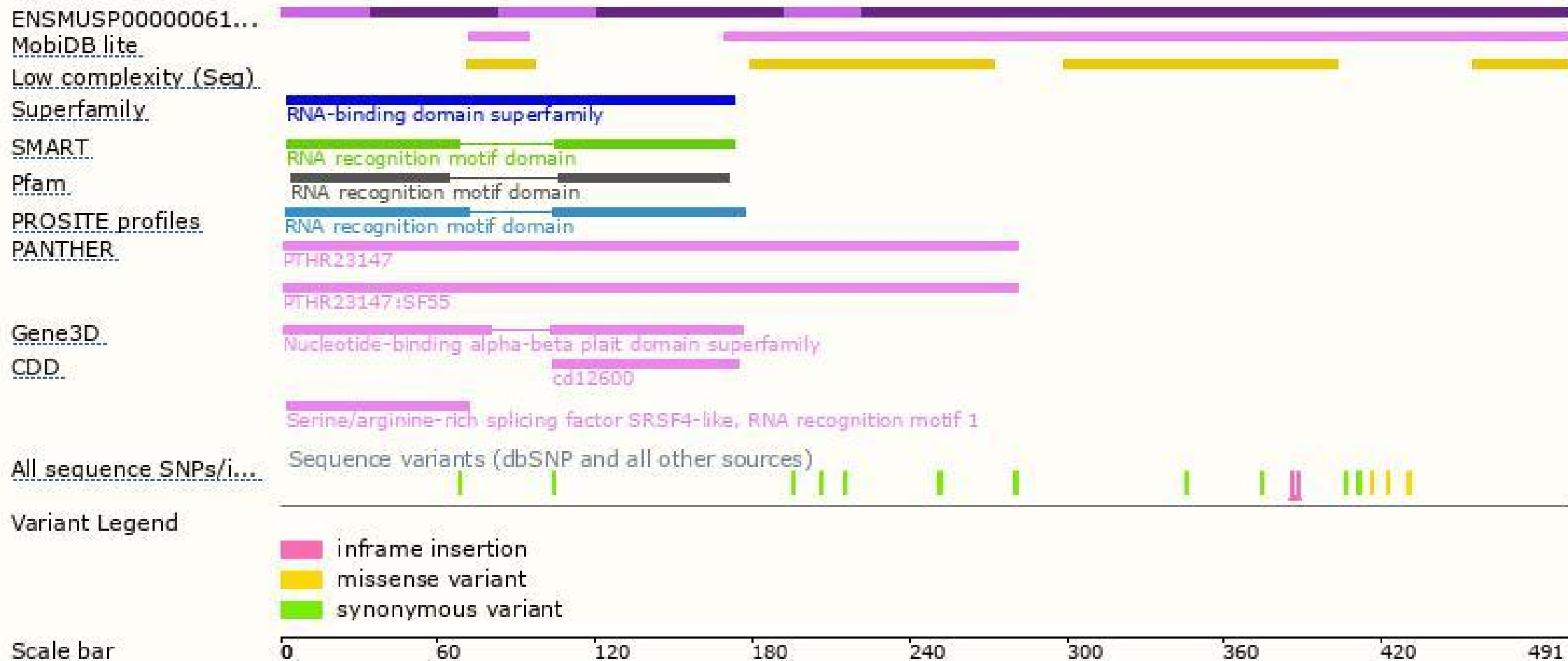
The strategy is based on the design of *Srsf4-202* transcript,The transcription is shown below



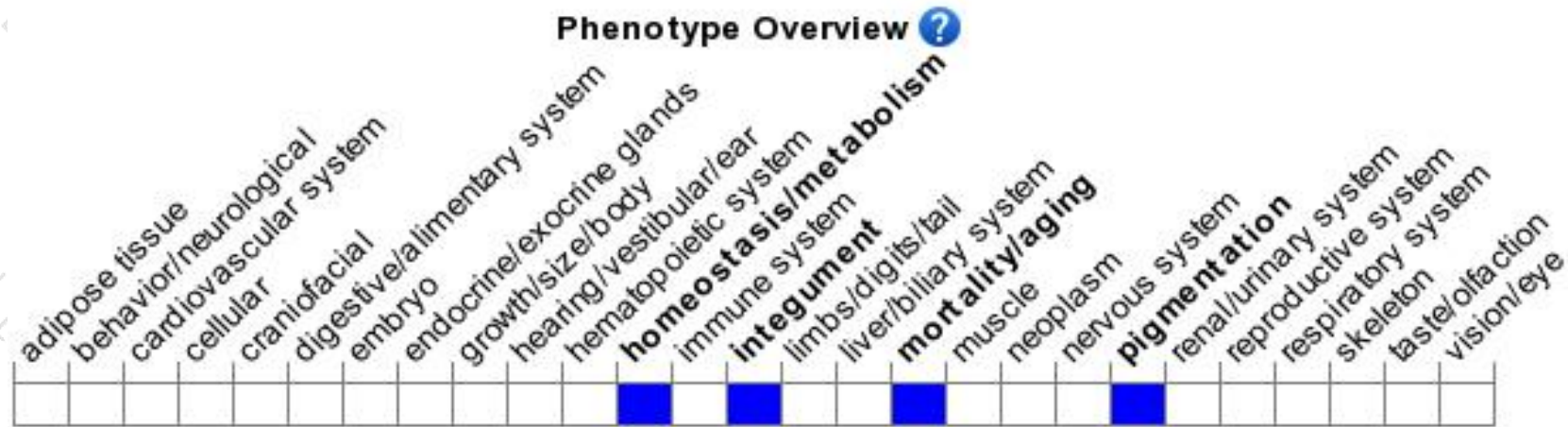
Genomic location distribution



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/>).

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

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