GemPharmatech™

Srsf2 Cas9-CKO Strategy

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Overview

Target Gene Name

- Srsf2

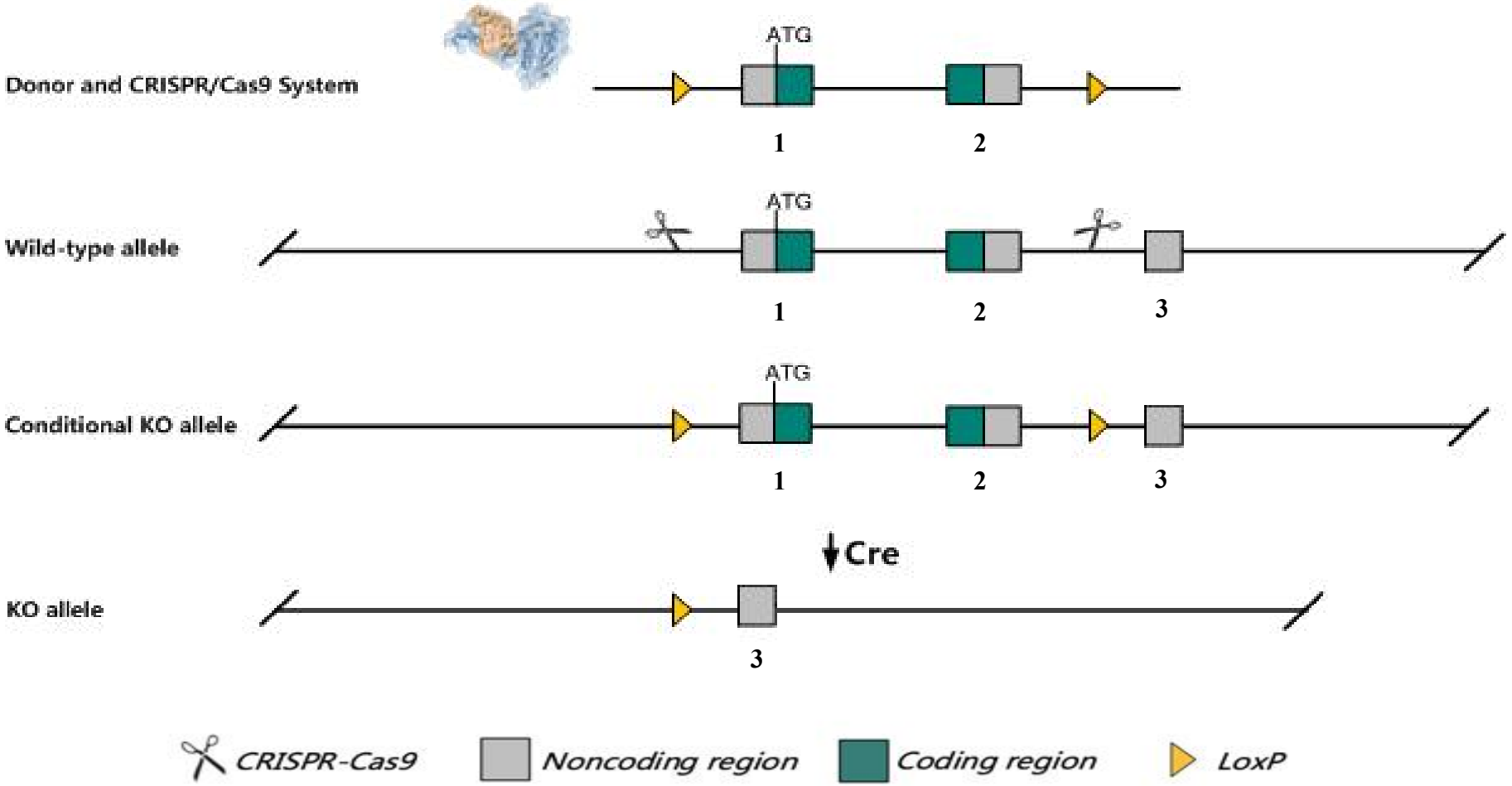
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Srsf2* gene.

Technical Information

- The *Srsf2* gene has 6 transcripts. According to the structure of *Srsf2* gene, exon1-exon2 of *Srsf2*-201 (ENSMUST00000092404.13) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Srsf2* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Srsf2 serine and arginine-rich splicing factor 2 [Mus musculus (house mouse)]

Gene ID: 20382, updated on 14-Apr-2023

Summary

Official Symbol	Srsf2 provided by MGI
Official Full Name	serine and arginine-rich splicing factor 2 provided by MGI
Primary source	MGI:MGI:98284
See related	Ensembl:ENSMUSG00000034120
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	D11Wsu175e, MRF-1, Pr264, SC35, Sfrs10, Sfrs2
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 ovary adult (RPKM 340.2), thymus adult (RPKM 275.9) and 28 other tissuesSee more
Orthologs	human all

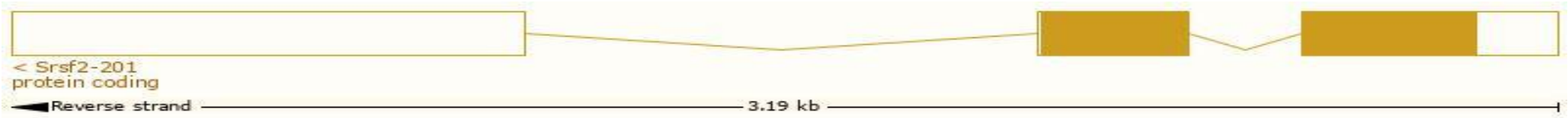
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

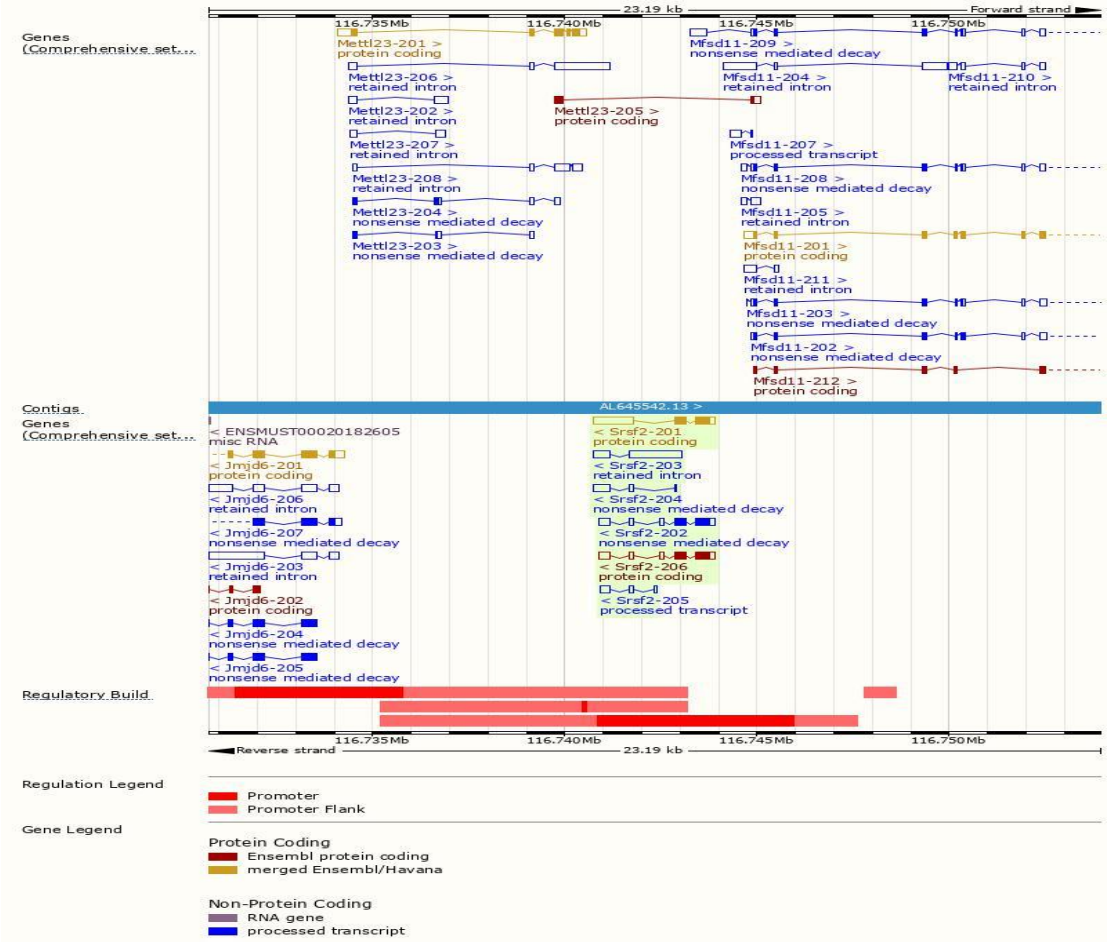
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf2-201	ENSMUST00000092404.12	1899	221aa	Protein coding	CCDS25680		A single transcript chosen for a gene which is the most conserved, most highly expressed, has the longest coding sequence and is represented in other key resources, such as NCBI and UniProt. This is defined in detail on http://www.ensembl.org/info/genome/genebuild/canonical.html Ensembl Canonical , The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS P1 , TSL:1 ,
Srsf2-206	ENSMUST00000190993.7	1326	221aa	Protein coding	CCDS25680		The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS P1 , TSL:2 ,
Srsf2-202	ENSMUST00000136914.8	1336	221aa	Nonsense mediated decay	CCDS25680		TSL:2 ,
Srsf2-204	ENSMUST00000176834.8	620	19aa	Nonsense mediated decay			TSL:3 , CDS 5' incomplete ,
Srsf2-205	ENSMUST00000177429.2	433	No protein	Protein coding CDS not defined			TSL:3 ,
Srsf2-203	ENSMUST00000138484.3	1814	No protein	Retained intron			TSL:1 ,

The strategy is based on the design of *Srsf2*-201 transcript, the transcription is shown below:



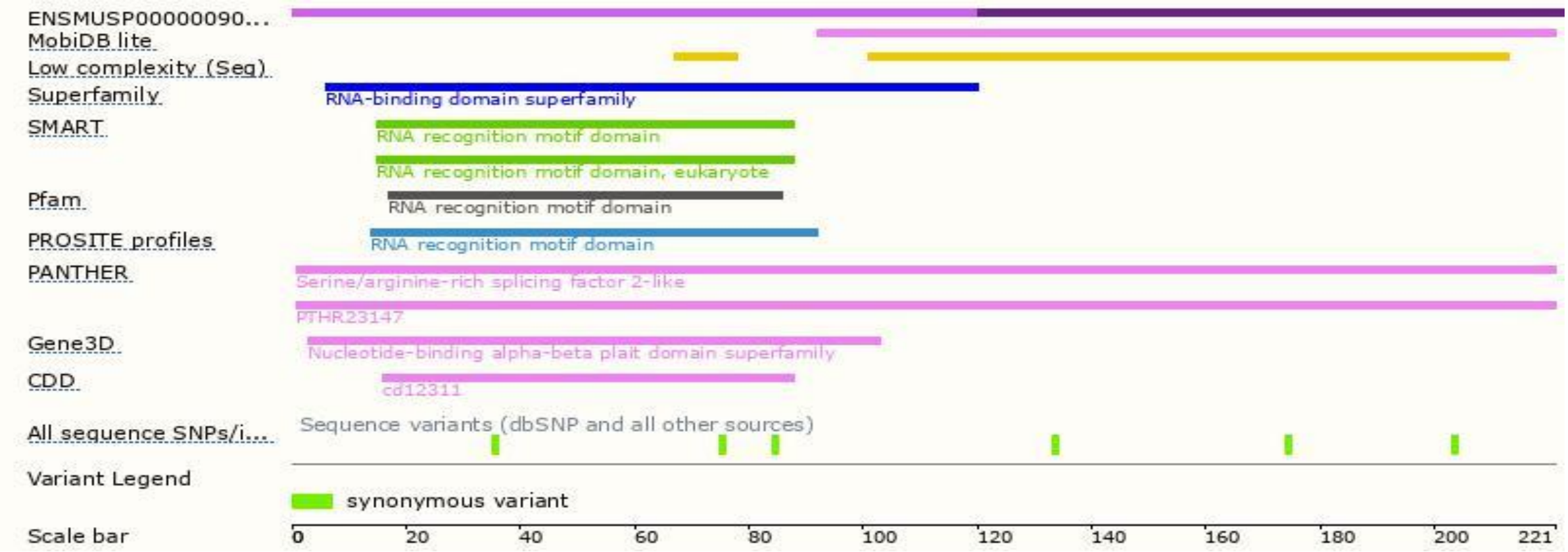
Source: https://www.ensembl.org

Genomic Information



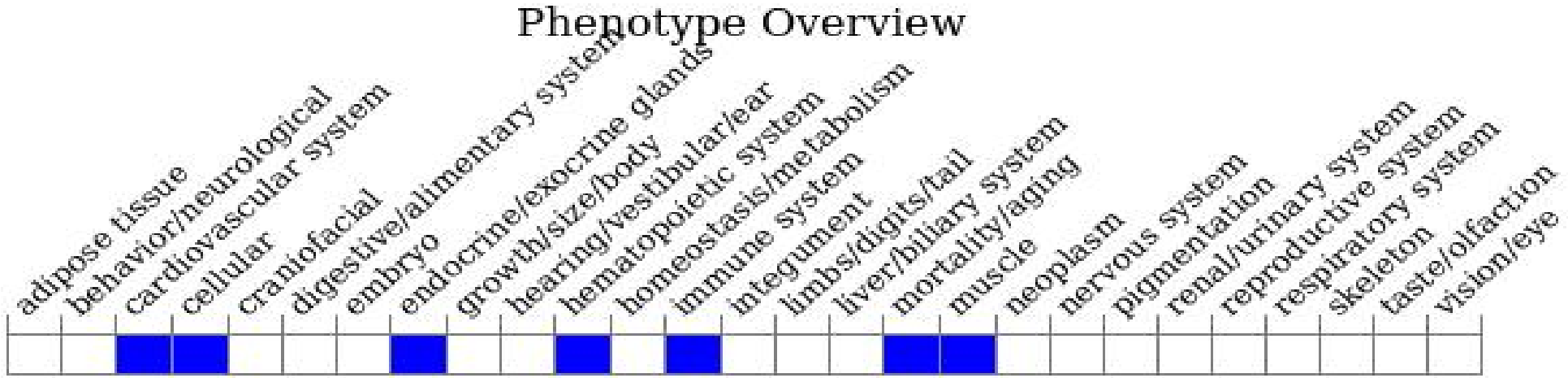
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Homozygous mutants are embryonic lethal. Deaths occur prior to E7.5. Cre induced inactivation of this pre-mRNA splicing factor in the thymus impairs T-cell maturation. Inactivation in ventricular cardiomyocytes results in dilated cardiomyopathy without gross changes in cardiomyocyte development.

Source: https://www.informatics.jax.org

Important Information

- According to MGI information，homozygous mutants are embryonic lethal. Deaths occur prior to E7.5. Cre induced inactivation of this pre-mRNA splicing factor in the thymus impairs T-cell maturation. Inactivation in ventricular cardiomyocytes results in dilated cardiomyopathy without gross changes in cardiomyocyte development.
- The loxp insertion site of this strategy may affect the 5-terminal regulation of the *Mfsd11* gene.
- At the same time as knocking out the target gene, this strategy will knock out the introns of the transcript of *Mettl23*-205, with unknown effects,this strategy may affect the 3-terminal regulation of the *Mettl23* gene.
- This strategy may affect the 5-terminal regulation of the target gene.
- *Srsf2* is located on Chr11. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.