

# *Srsf10* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-8-8**

# Project Overview

**Project Name**

***Srsf10***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf10* gene. The schematic diagram is as follows:



- The *Srsf10* gene has 10 transcripts. According to the structure of *Srsf10* gene, exon2-exon3 of *Srsf10-205* (ENSMUST00000126641.1) transcript is recommended as the knockout region. The region contains 209bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srsf10* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit fetal and neonatal lethality associated with edema and cardiac defects.
- The *Srsf10* 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)

## Srsf10 serine/arginine-rich splicing factor 10 [Mus musculus (house mouse)]

Gene ID: 14105, updated on 3-Feb-2019

### Summary



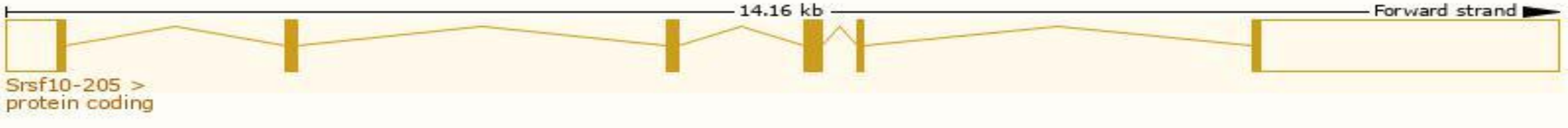
<b>Official Symbol</b>	Srsf10 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	serine/arginine-rich splicing factor 10 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1333805</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000028676</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	FUSIP2, Fusip1, NSSR1, NSSR2, Nssr, SRp40, Sfrs13a, Srsf13a, TASR, TASR1, TASR2
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 24.5), limb E14.5 (RPKM 19.6) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

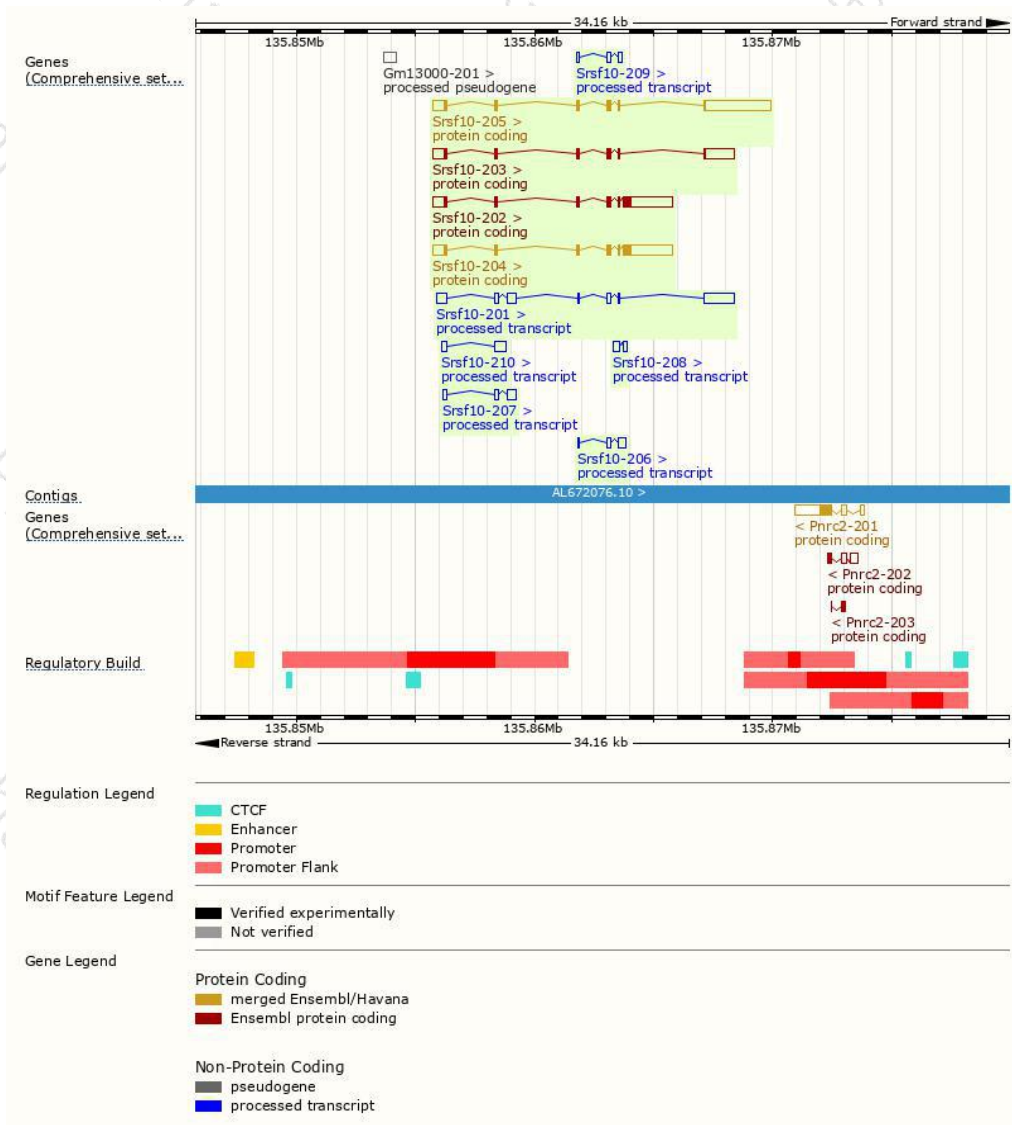
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf10-210	<a href="#">ENSMUST00000154447.1</a>	677	No protein	lncRNA	-	-	TSL:1
Srsf10-209	<a href="#">ENSMUST00000149878.7</a>	394	No protein	lncRNA	-	-	TSL:3
Srsf10-208	<a href="#">ENSMUST00000142002.1</a>	423	No protein	lncRNA	-	-	TSL:2
Srsf10-207	<a href="#">ENSMUST00000129718.1</a>	717	No protein	lncRNA	-	-	TSL:1
Srsf10-206	<a href="#">ENSMUST00000129198.1</a>	522	No protein	lncRNA	-	-	TSL:3
Srsf10-205	<a href="#">ENSMUST00000126641.1</a>	3754	<a href="#">183aa</a>	Protein coding	<a href="#">CCDS18791</a>	<a href="#">Q3UA07</a> <a href="#">Q9R0U0</a>	TSL:1 GENCODE basic APPRIS P3
Srsf10-204	<a href="#">ENSMUST00000105853.9</a>	3058	<a href="#">262aa</a>	Protein coding	<a href="#">CCDS38922</a>	<a href="#">Q9R0U0</a>	TSL:1 GENCODE basic APPRIS ALT1
Srsf10-203	<a href="#">ENSMUST00000102544.8</a>	2225	<a href="#">182aa</a>	Protein coding	<a href="#">CCDS71494</a>	<a href="#">Q3TFP0</a>	TSL:1 GENCODE basic APPRIS ALT1
Srsf10-202	<a href="#">ENSMUST00000097844.8</a>	3055	<a href="#">261aa</a>	Protein coding	<a href="#">CCDS71493</a>	<a href="#">Q9R0U0</a>	TSL:2 GENCODE basic APPRIS ALT1
Srsf10-201	<a href="#">ENSMUST00000030438.14</a>	2493	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Srsf10-205* transcript,The transcription is shown below

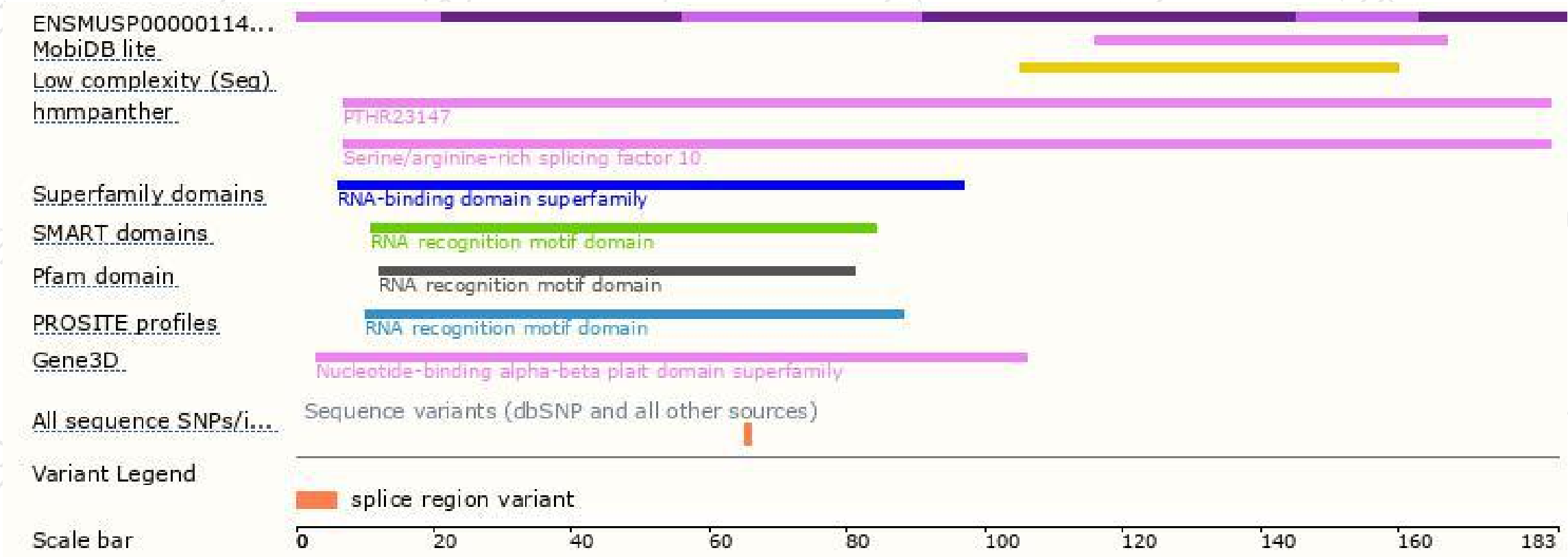


# Genomic location distribution

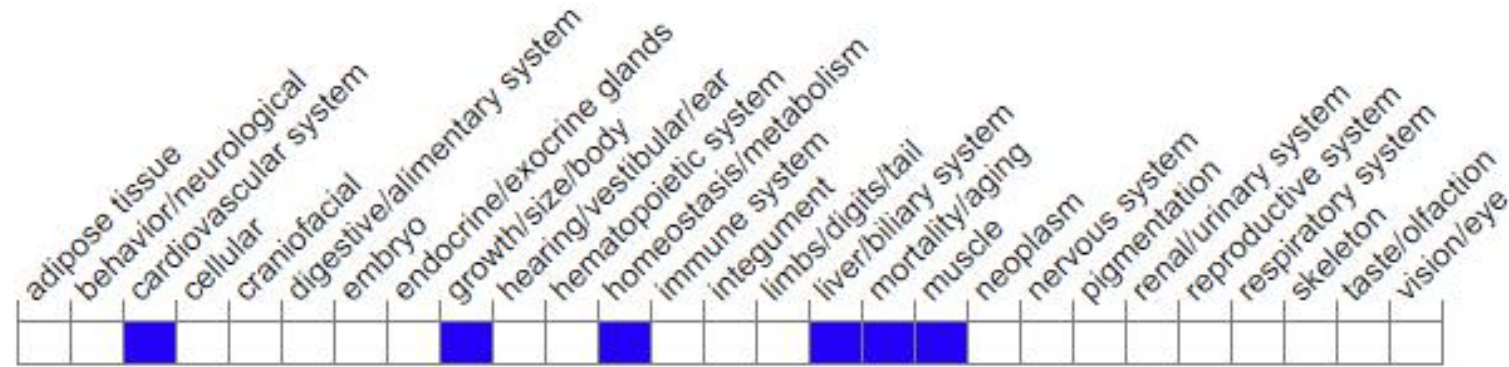




# Protein domain



# 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 null allele exhibit fetal and neonatal lethality associated with edema and cardiac defects.

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

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