Srsf4 Cas9-KO Strategy

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Project Overview

Project Name	*Srsf4*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ 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

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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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

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

▲Summary

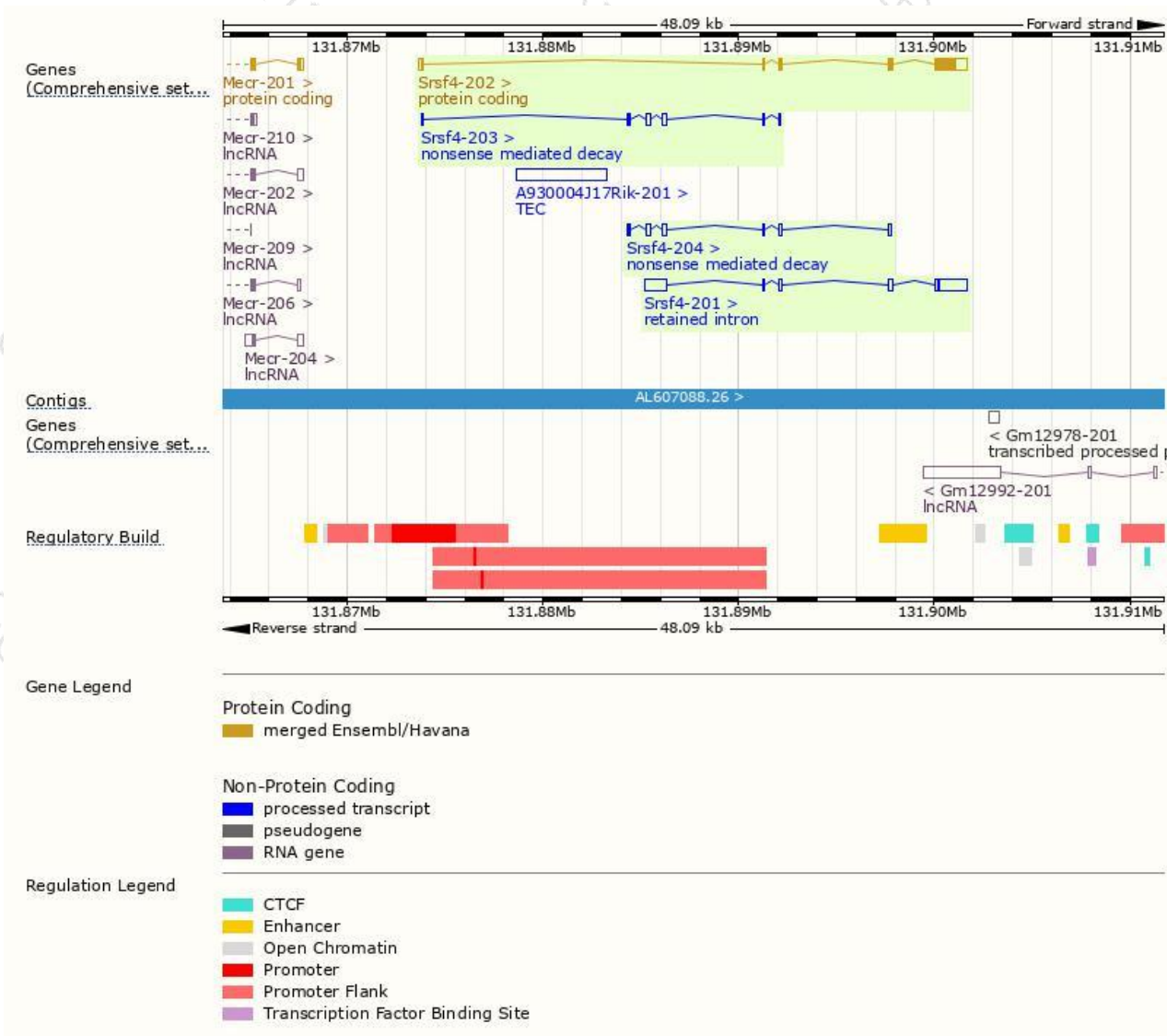|	
Official Symbol	Srsf4 provided by MGI
Official Full Name	serine/arginine-rich splicing factor 4 provided byMGI
Primary source	MGI:MGI:1890577
See related	Ensembl:ENSMUSG00000028911
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; 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 tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

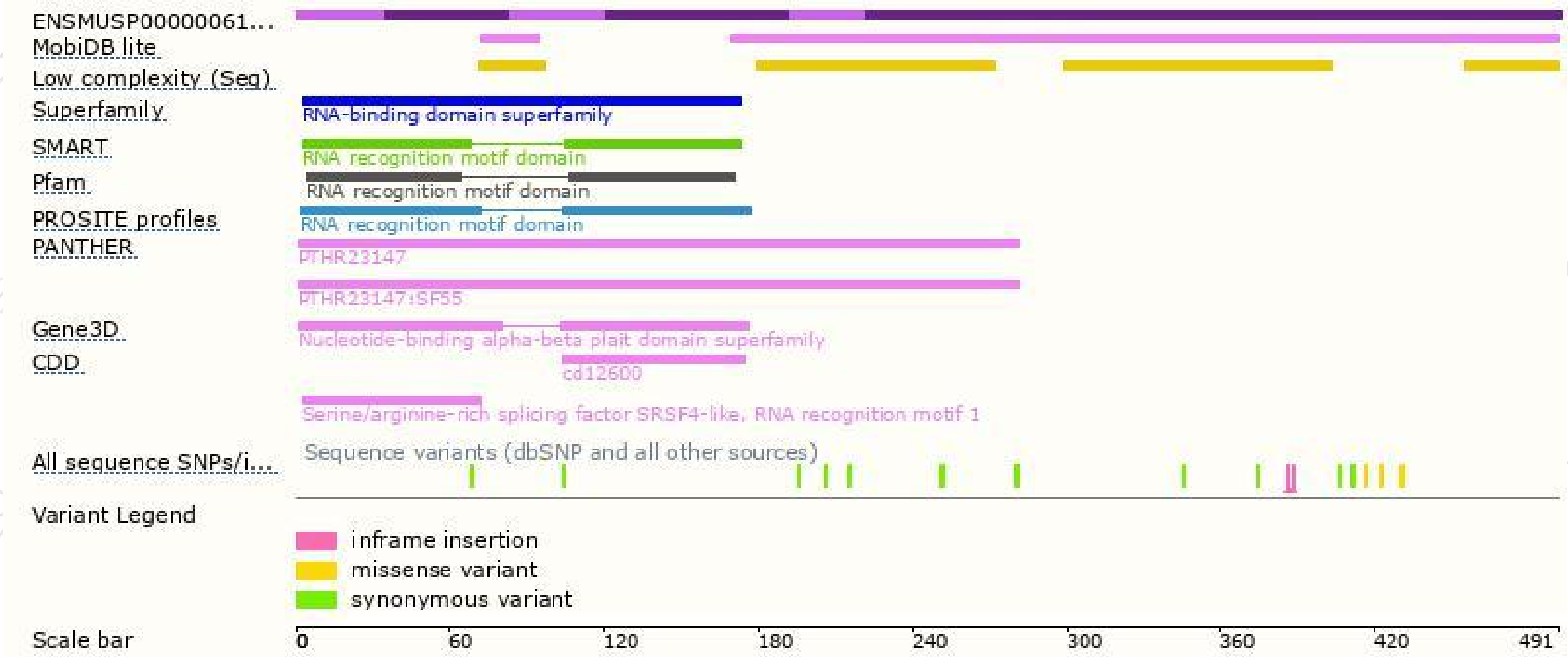| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf4-202	ENSMUST00000053819.5	2257	491aa	Protein coding	CCDS51315	Q542V3	TSL:1 GENCODE basic APPRIS P1
Srsf4-204	ENSMUST00000134943.6	980	31aa	Nonsense mediated decay	-	A0A0A6YXU8	CDS 5' incomplete TSL:5
Srsf4-203	ENSMUST00000129966.7	851	56aa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

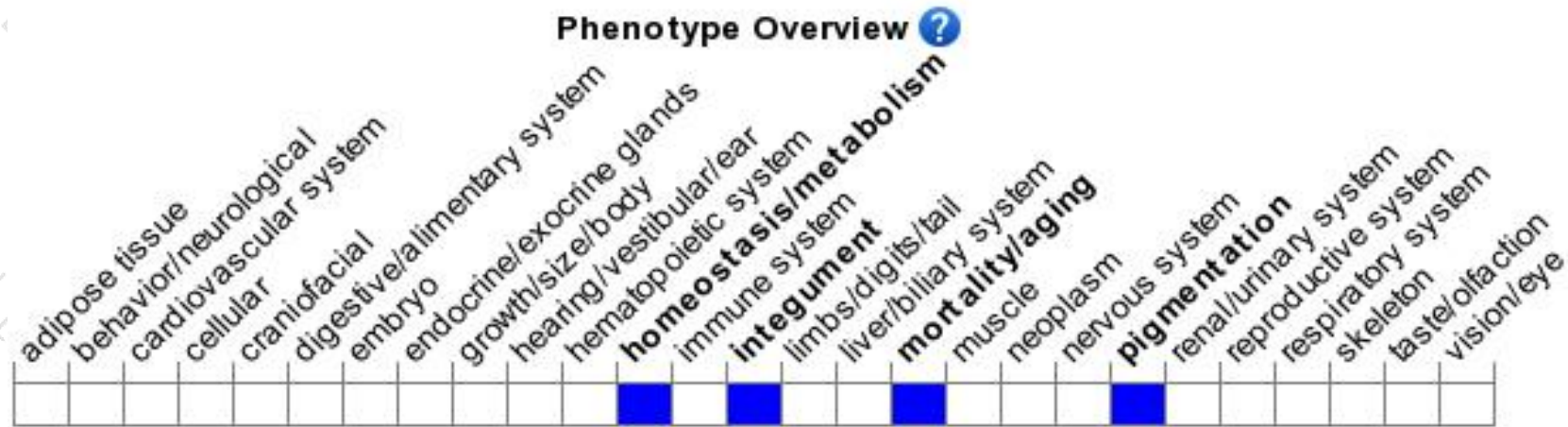The strategy is based on the design of *Srsf4-202* transcript,The transcription is shown below

28.09 kb — Forward strand

Srsf4-202 >
protein coding

Genomic location distribution

Protein domain

ENSMUSP00000061...	
MobiDB lite	
Low complexity (Seg)	
Superfamily	RNA-binding domain superfamily
SMART	RNA recognition motif domain
Pfam	RNA recognition motif domain
PROSITE profiles	RNA recognition motif domain
PANTHER	PTHR23147
	PTHR23147:SF55
Gene3D	Nucleotide-binding alpha-beta plait domain superfamily
CDD	cd12600
	Serine/arginine-rich splicing factor SRSF4-like, RNA recognition motif 1
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend
- inframe insertion
- missense variant
- synonymous variant

Scale bar: 0   60   120   180   240   300   360   420   491

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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