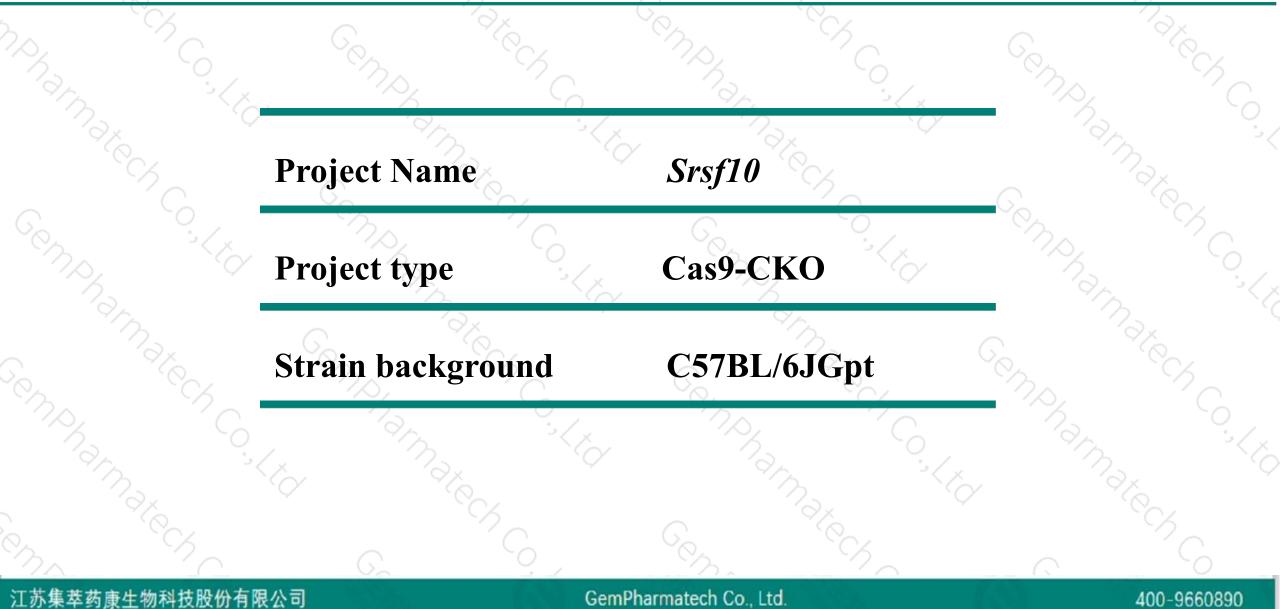


Srsf10 Cas9-CKO Strategy

Designer: Huan Wang Design Date: 2019-8-8

Project Overview



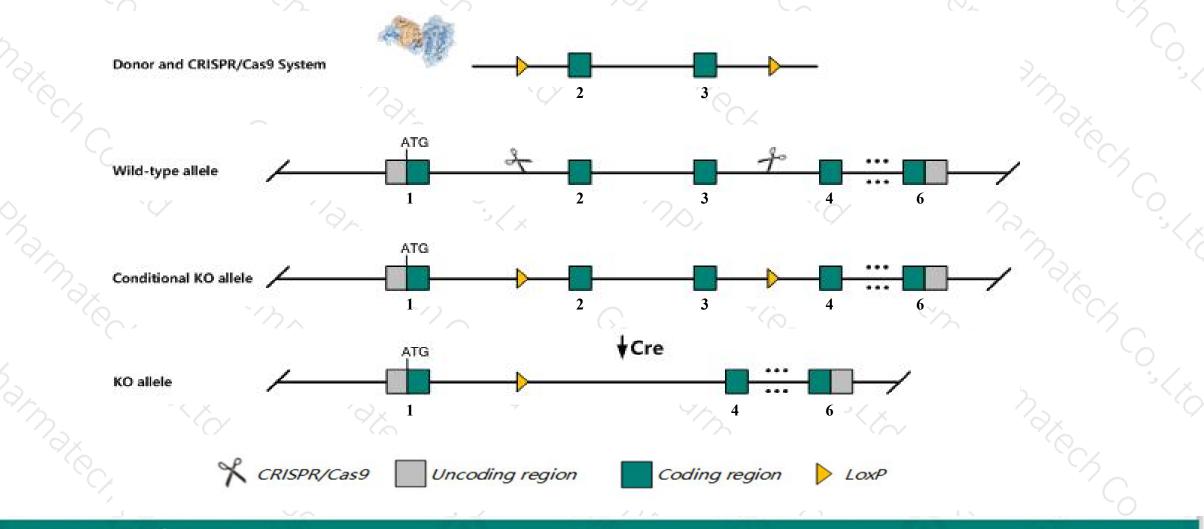


Conditional Knockout strategy



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



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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 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.



- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



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

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

Summary

| Official Symbol | Srsf10 provided by MGI |
|----------------------|--------------------------------------------------------------------------------------------------------------------------------------|
| Official Full Name | serine/arginine-rich splicing factor 10 provided by MGI |
| Primary source | MGI:MGI:1333805 |
| See related | Ensembl:ENSMUSG0000028676 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; |
| | Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | FUSIP2, Fusip1, NSSR1, NSSR2, Nssr, SRrp40, Sfrs13a, Srsf13a, TASR, TASR1, TASR2 |
| Expression | Ubiquitous expression in CNS E11.5 (RPKM 24.5), limb E14.5 (RPKM 19.6) and 28 other tissues See more |
| Orthologs | human all |

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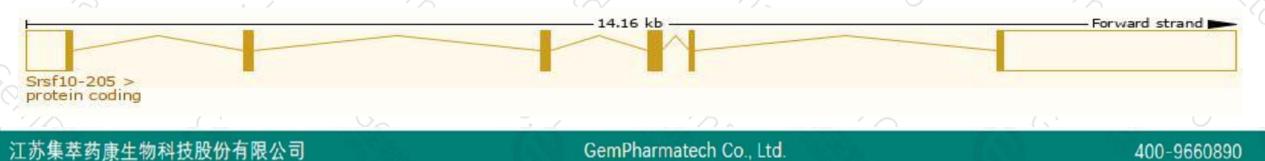
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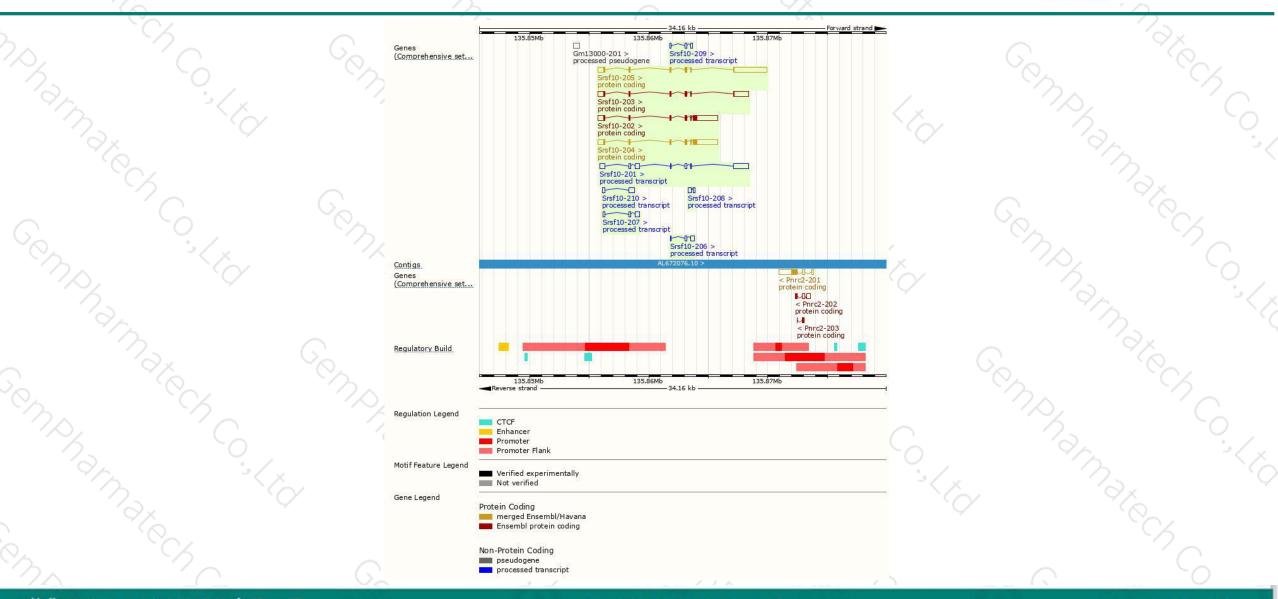
The gene has 10 transcripts, all transcripts are shown below:

| 5 | | | | | | > () | the second s | - 2 [- y | | | |
|---|------------|----------------------|------|--------------|----------------|--------------------|----------------------------------------------------------------------------------------------------------------|---------------------------------|--|--|--|
| 2 | Name 🍦 | Transcript ID 🔹 | bp 🖕 | Protein 🖕 | Biotype 🍦 | CCDS 🖕 | UniProt 🖕 | Flags 🍦 | | | |
| | Srsf10-210 | ENSMUST00000154447.1 | 677 | No protein | IncRNA | - | (, ,) | TSL:1 | | | |
| | Srsf10-209 | ENSMUST00000149878.7 | 394 | No protein | IncRNA | - | (1 - 3) | TSL:3 | | | |
| | Srsf10-208 | ENSMUST00000142002.1 | 423 | No protein | IncRNA | i.e | 0.70 | TSL:2 | | | |
| | Srsf10-207 | ENSMUST00000129718.1 | 717 | No protein | IncRNA | - | 070 | TSL:1 | | | |
| | Srsf10-206 | ENSMUST00000129198.1 | 522 | No protein | IncRNA | - | 0.70 | TSL:3 | | | |
| ~ | Srsf10-205 | ENSMUST00000126641.1 | 3754 | <u>183aa</u> | Protein coding | <u>CCDS18791</u> & | <u>Q3UA07</u> മ <u>Q9R0U0</u> മ | TSL:1 GENCODE basic APPRIS P3 | | | |
| 1 | Srsf10-204 | ENSMUST00000105853.9 | 3058 | <u>262aa</u> | Protein coding | CCDS38922 | Q9R0U0团 | TSL:1 GENCODE basic APPRIS ALT1 | | | |
| | Srsf10-203 | ENSMUST00000102544.8 | 2225 | <u>182aa</u> | Protein coding | CCDS71494@ | Q3TFP0 团 | TSL:1 GENCODE basic APPRIS ALT1 | | | |
| | Srsf10-202 | ENSMUST0000097844.8 | 3055 | <u>261aa</u> | Protein coding | <u>CCDS71493</u> & | Q9R0U0团 | TSL:2 GENCODE basic APPRIS ALT1 | | | |
| | Srsf10-201 | ENSMUST0000030438.14 | 2493 | No protein | IncRNA | - | 0.70 | TSL:5 | | | |

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



Genomic location distribution



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Protein domain



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|-------|--------------------------------------------------------|------------------------------------------------------------------------------------------------------------|---------------|----------------------------------------|---------------------|----------------------------------------|------|-------|--------------|-----|----------|
| * / . | ENSMUSP00000114 MobiDB lite Low complexity (Seg) | | | | | | | | | - | |
| | hmmpanther | and the second second | \$23147 | | ANY ON THE OWNER OF | | | | | | |
| ?>_ | Superfamily domains SMART domains | Serine/arginine-rich splicing factor 10. RNA-binding domain superfamily RNA recognition motif domain | | | | | | | | | |
| | Pfam domain | RNA recognition motif domain | | | | | | | | | |
| | PROSITE profiles | | | motif domain | | | | | | | |
| | Gene3D | Nucleot | ide-binding a | lpha-beta plait | domain supe | rfamily | | | | | |
| 5, | All sequence SNPs/i | /i Sequence variants (dbSNP and all other sources) | | | | | | | | | 2 |
| | Variant Legend | | | | | | | | | | |
| | Scale bar | 0 | 20 | 40 | 60 | 80 | 100 | 120 | 140 | 160 | 183 |
| | AX CA | | | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | | | 1970 | | \checkmark | | 3 |
| 2 | - ⁷ .C. | | G_ | \sim | _ | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | | · ^ _ | | S | 8 |

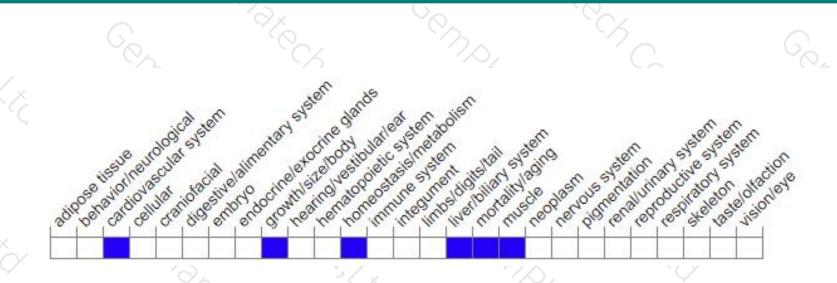
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Mouse phenotype description(MGI)





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.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



