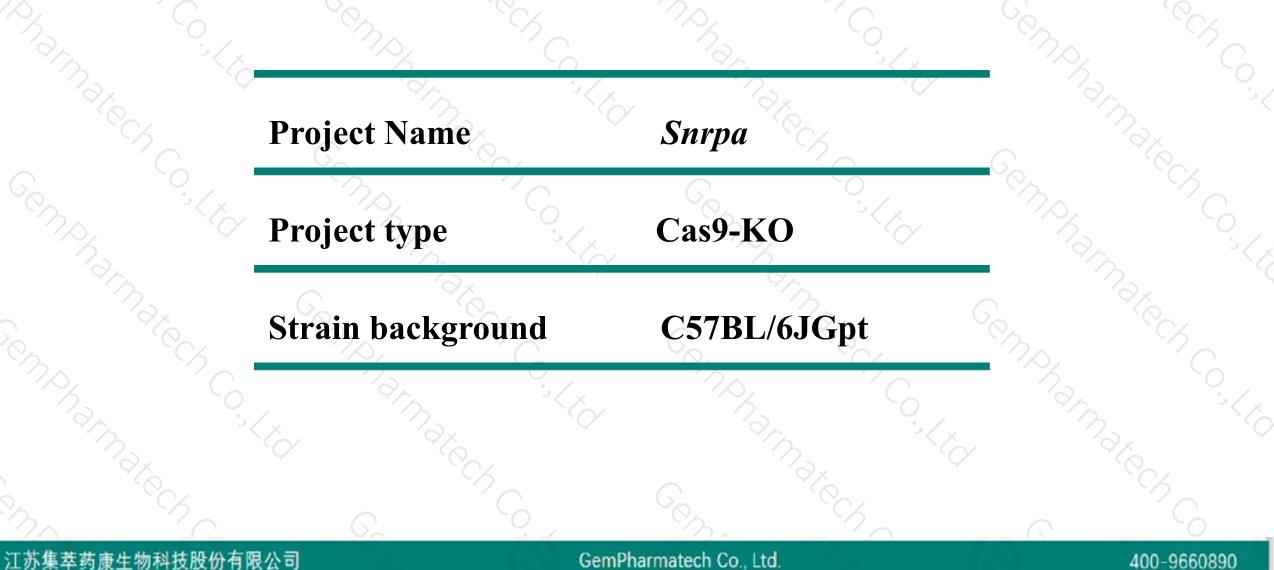


Snrpa Cas9-KO Strategy

Designer:Xueting Zhang Reviewer:Yanhua Shen Date:2019-10-17

Project Overview



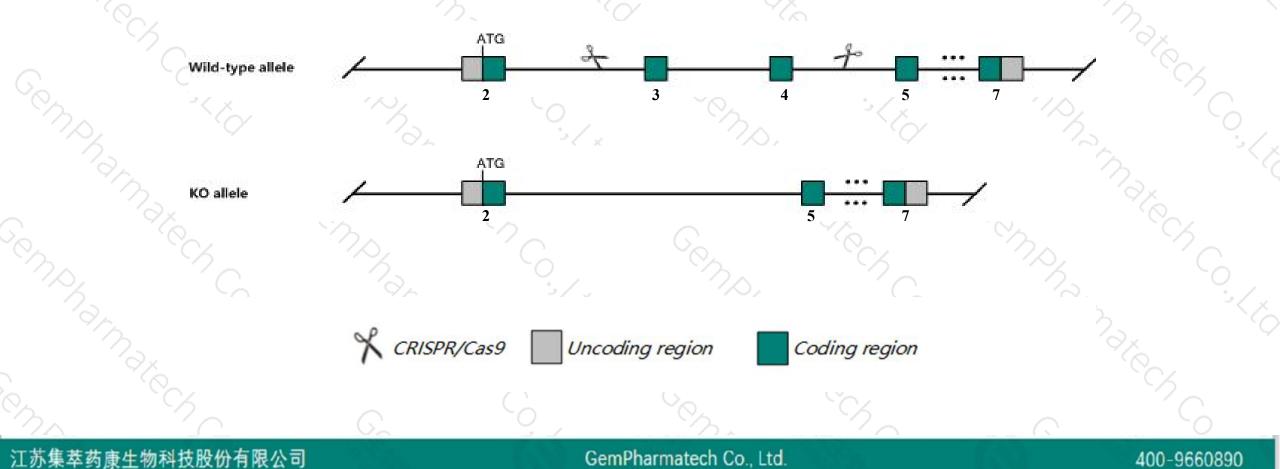


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Knockout strategy



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





- The Snrpa gene has 7 transcripts. According to the structure of Snrpa gene, exon3-exon4 of Snrpa-201 (ENSMUST0000080356.9) transcript is recommended as the knockout region. The region contains 350bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Snrpa gene. The brief process is as follows: CRISPR/Cas9 system



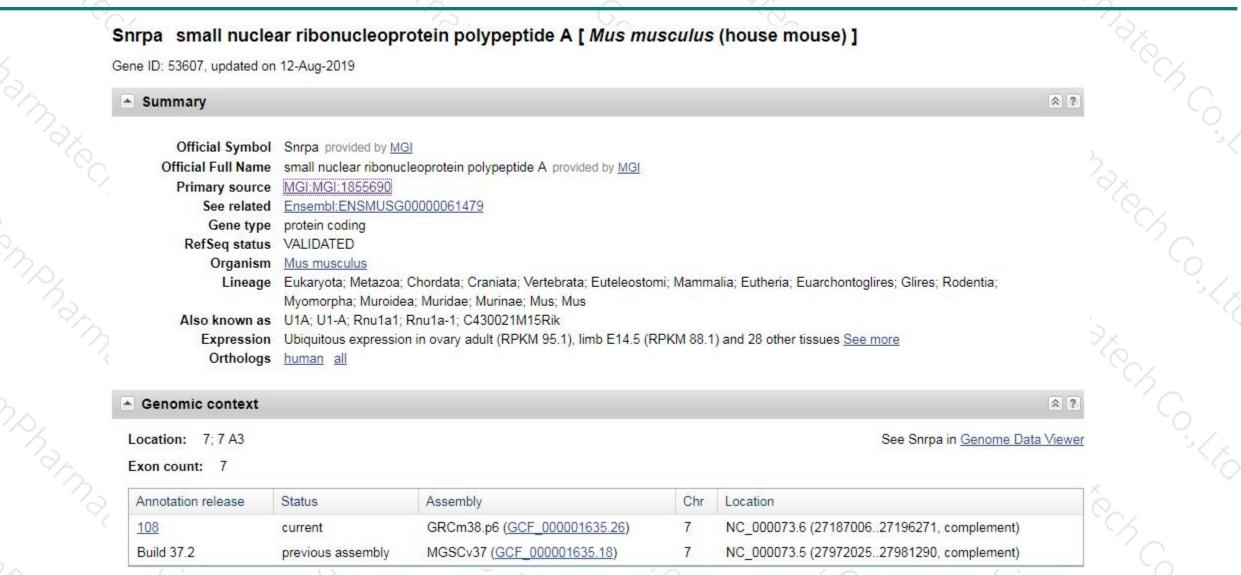
- The knockout region is near to the N-terminal of BC024978 gene, this strategy may influence the regulatory function of the N-terminal of BC024978 gene.
- ➤ Transcript Snrpa-205&207 may not be affected.
- The Snrpa gene is located on the Chr7. If the knockout mice are crossed with other mice strains 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)

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Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

	<i>I</i>		2 21		la l	
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST0000080356.9	1365	<u>287aa</u>	Protein coding	CCDS21014	<u>Q62189</u>	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000122202.7	1336	<u>287aa</u>	Protein coding	CCDS21014	<u>Q62189</u>	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000163311.8	1288	<u>287aa</u>	Protein coding <u>CCDS21014</u> <u>Q62189</u> TS		TSL:2 GENCODE basic APPRIS P1	
ENSMUST00000126211.1	968	<u>247aa</u>	Protein coding - D3Z0S6		CDS 3' incomplete TSL:2	
ENSMUST00000141378.1	510	<u>44aa</u>	Nonsense mediated decay	5	D6RI83	TSL:3
ENSMUST00000206439.1	1690	No protein	Retained intron	-		TSL:NA
ENSMUST00000148491.1	509	No protein	Retained intron	2	28	TSL:1
	ENSMUST0000080356.9 ENSMUST00000122202.7 ENSMUST00000163311.8 ENSMUST00000126211.1 ENSMUST00000141378.1 ENSMUST00000206439.1	ENSMUST0000080356.9 1365 ENSMUST00000122202.7 1336 ENSMUST00000163311.8 1288 ENSMUST00000126211.1 968 ENSMUST00000141378.1 510 ENSMUST00000206439.1 1690	ENSMUST0000080356.9 1365 287aa ENSMUST0000122202.7 1336 287aa ENSMUST0000163311.8 1288 287aa ENSMUST0000126211.1 968 247aa ENSMUST0000141378.1 510 44aa ENSMUST000026439.1 1690 No protein	ENSMUST0000080356.91365287aaProtein codingENSMUST00000122202.71336287aaProtein codingENSMUST00000163311.81288287aaProtein codingENSMUST00000126211.1968247aaProtein codingENSMUST00000141378.151044aaNonsense mediated decayENSMUST00000206439.11690No proteinRetained intron	ENSMUST0000080356.91365287aaProtein codingCCDS21014ENSMUST0000122202.71336287aaProtein codingCCDS21014ENSMUST0000163311.81288287aaProtein codingCCDS21014ENSMUST0000126211.1968247aaProtein coding-ENSMUST0000141378.151044aaNonsense mediated decay-ENSMUST0000206439.11690No proteinRetained intron-	ENSMUST0000080356.91365287aaProtein codingCCDS21014Q62189ENSMUST0000122202.71336287aaProtein codingCCDS21014Q62189ENSMUST0000163311.81288287aaProtein codingCCDS21014Q62189ENSMUST0000126211.1968247aaProtein codingCDS21014D32086ENSMUST0000141378.151044aaNonsense mediated decay-D6RI83ENSMUST0000206439.11690No proteinRetained intron

The strategy is based on the design of Snrpa-201 transcript, The transcription is shown below

< Snrpa-201 protein coding

Reverse strand

- 9.27 kb

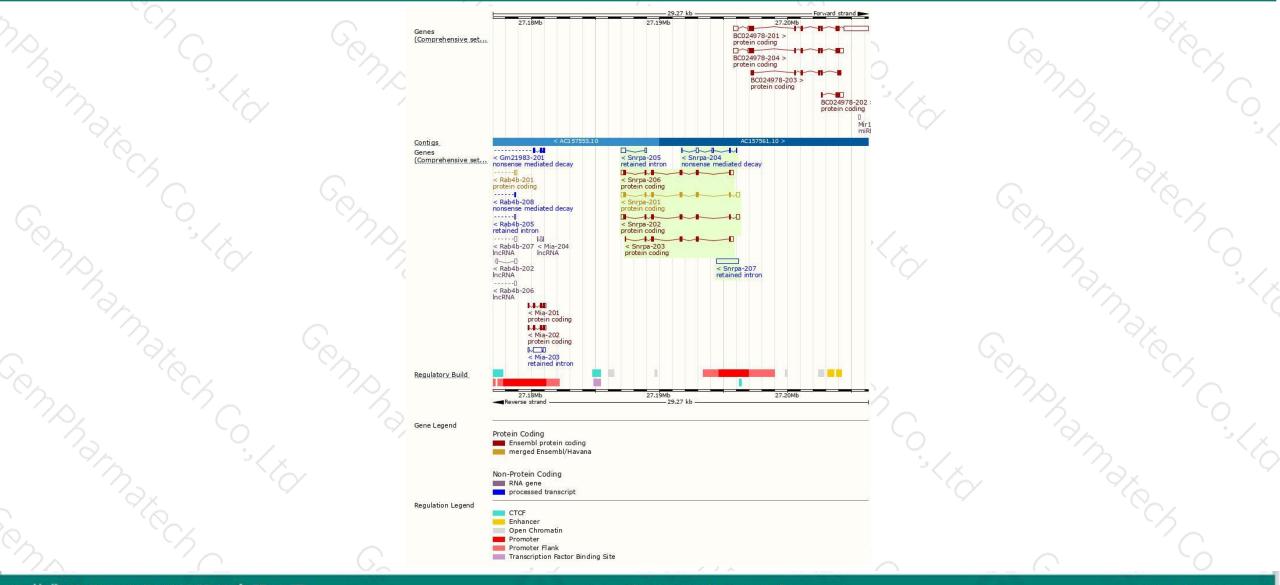
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Genomic location distribution





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Protein domain



25.	20			95 ·		0		
- A.	ENSMUSP00000079 MobiDB lite Low complexity (Seg)					-	50	
	Superfamily	RNA-binding	domain superfamily					~
	SMART	RNA recogn	Itlon motif domain					
	Pfam.	RNA recogn	nition motif domain			10		
Gon	PROSITE profiles PANTHER	RNA recogni PTHR10501	tion motif domain					
	Gene3D	PTHR10501 (S Nucleotide-bin	F21 ding alpha-beta plait doma	in superfamily		0		
	CDD	U1 small nud	ear ribonucleoprotein A, RI	NA recognition motif 1		U1 small nucle	ar ribonucleoprotein A.	
Senz	All sequence SNPs/i	Sequence varian	ts (dbSNP and all other :	sources)	[1,1](1)		6	
	Variant Legend	missense va						
2	Scale bar	0 4	0 80	120	160	200	240 287	
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江苏集萃	药康生物科技股份有限公	公司	G	emPharmatech Co., I	_td.	1433	400-9660890)



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



