Sptan1 Cas9-CKO Strategy Daohua Xu mate ch Co-1 ty Romphamater Control

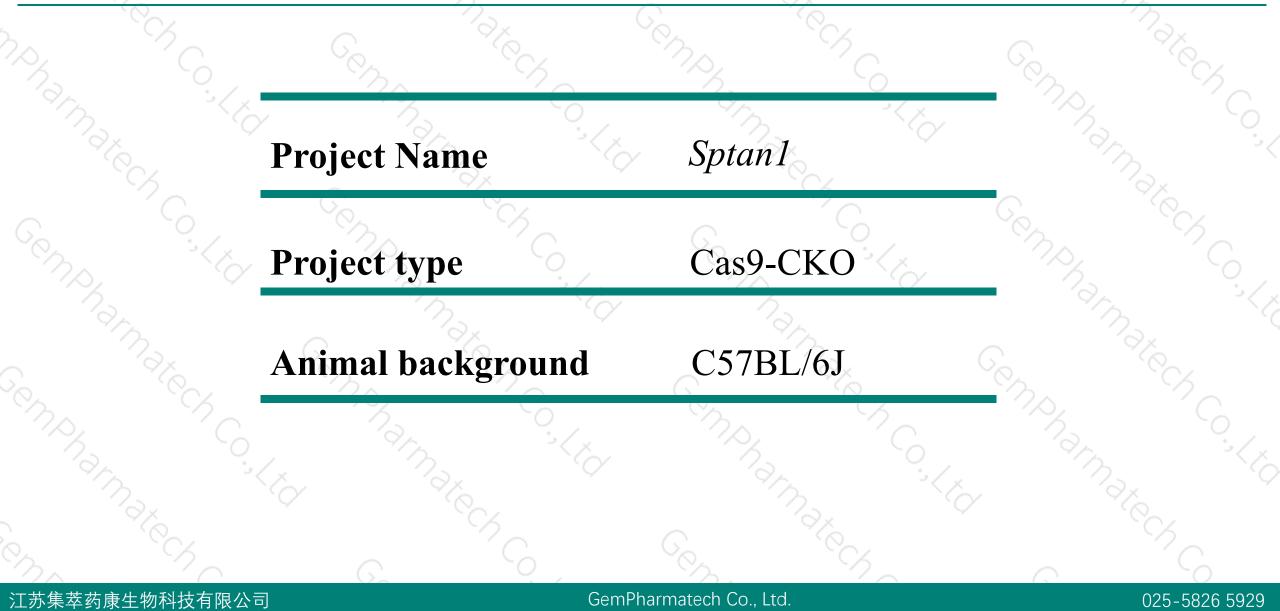
Designer: Enphamatech C. It

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Project Overview

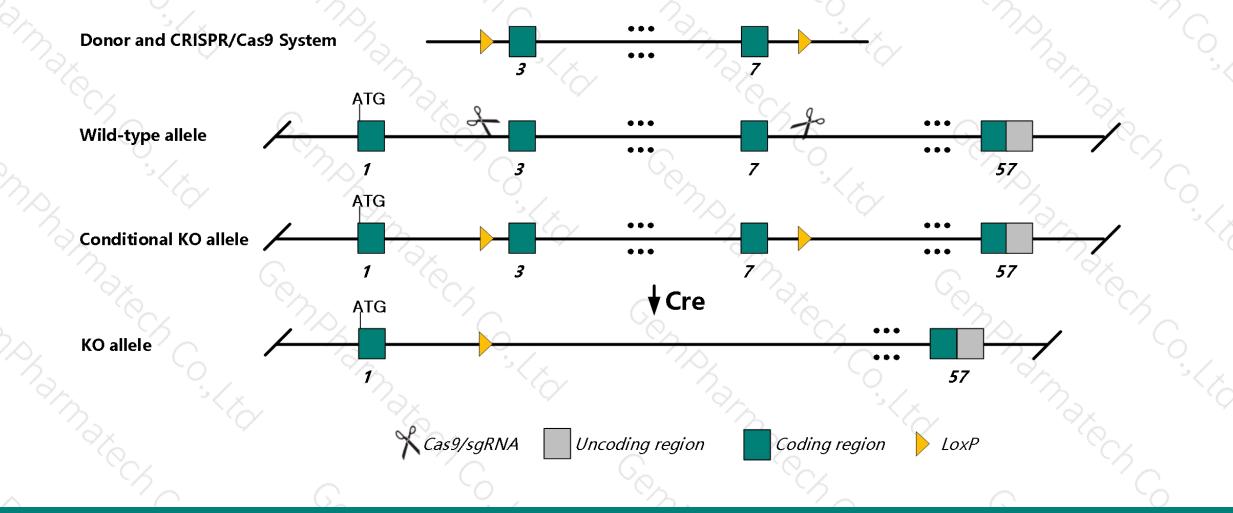




Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Sptan1 gene. The schematic diagram is as follows:



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Technical routes



- The *Sptan1* gene has 16 transcripts, According to the structure of *Sptan1* gene, exon3-exon7 of *Sptan1-208* transcript is recommended as the knockout region. The region contains the 722bp coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Sptan1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed, Cas9, sgRNA and donor were microinjected into fertilized eggs of C57BL/6J mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6J mice which were confirmed positive by PCR-sequencing.
- The flox mice was 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, Homozygous deletion of the exons encoding the CCC region are normal. Mice homozygous for a gene trap allele exhibit embryonic lethality and abnormal nervous system, heart and craniofacial morphology.
- The *Sptan1* gene is located in the Chr2. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information



\$?

Sptan1 spectrin alpha, non-erythrocytic 1 [Mus musculus (house mouse)]

Gene ID: 20740, updated on 3-Jan-2019

Summary

 Official Symbol
 Sptan1 provided by MGI

 Official Full Name
 spectrin alpha, non-erythrocytic 1 provided by MGI

 Primary source
 MGI:MGI:98386

 See related
 Ensembl:ENSMUSG0000057738

 Gene type
 protein coding

 RefSeq status
 VALIDATED

 Organism
 Mus musculus

 Lineage
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Murinae; Mus; Mus

 Also known as
 Spna2; Spna-2; 2610027H02Rik

 Expression
 Broad expression in CNS E18 (RPKM 112.4), cerebellum adult (RPKM 102.7) and 24 other tissues See more

 Ortholos
 human all

(NCBI)

Transcript information (Ensembl)



The gene has 16 transcripts, and all transcripts are shown below :

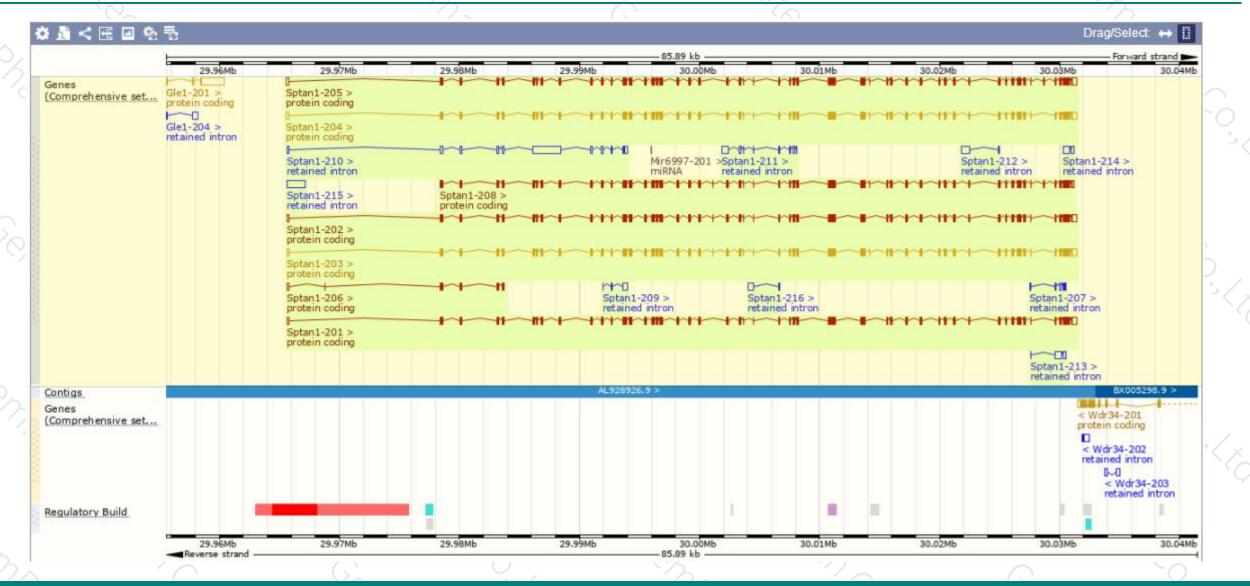
Name 🖕	Transcript ID	bp 🖕	Protein 🖕	Biotype	CCDS 🛊	UniProt	RefSeq	Flags
Sptan1-204	ENSMUST00000113717.7	7958	<u>2457aa</u>	Protein coding	<u>CCDS50559</u> @	A3KGU5@	<u>NM 001177668</u> <u>NP 001171139</u>	TSL:1 GENCODE basic
ptan1-203	ENSMUST00000100225.8	7892	<u>2477aa</u>	Protein coding	<u>CCDS50558</u> @	A3KGU7@	<u>NM 001177667</u> <u>NP 001171138</u> ๗	TSL:1 GENCODE basic APPRIS ALT1
ptan1-208	ENSMUST00000129241.2	7585	<u>2498aa</u>	Protein coding	<u>CCDS38094</u> @	A3KGU9@	<u>NM 001309460</u> @ <u>NP 001296389</u> @	TSL:5 GENCODE basic APPRIS P3
Sptan1-205	ENSMUST00000113719.8	8018	<u>2478aa</u>	Protein coding		<u>E9Q447</u> @	. s=s .	TSL:5 GENCODE basic
Sptan1-202	ENSMUST0000095083.10	7883	<u>2472aa</u>	Protein coding	2	P16546@	15218	TSL:5 GENCODE basic APPRIS ALT1
Sptan1-201	ENSMUST0000046257.13	7820	<u>2452aa</u>	Protein coding	-	P16546@	2 - 3	TSL:5 GENCODE basic APPRIS ALT1
Sptan1-206	ENSMUST00000113741.7	781	<u>219aa</u>	Protein coding	-	A3KGU4@		CDS 3' incomplete TSL:5
Sptan1-210	ENSMUST00000143918.7	3735	No protein	Retained intron		878		TSL:2
ptan1-215	ENSMUST00000202286.1	1471	No protein	Retained intron	-	223 2	10110	TSL:NA
Sptan1-211	ENSMUST00000149038.2	1025	No protein	Retained intron	-	19 1 1	10 - 3	TSL:5
Sptan1-213	ENSMUST00000152453.2	814	No protein	Retained intron	-			TSL:5
Sptan1-212	ENSMUST00000149846.1	800	No protein	Retained intron		852		TSL:3
Sptan1-214	ENSMUST00000201758.1	719	No protein	Retained intron	2	2223 2	12111	TSL:2
ptan1-209	ENSMUST00000131827.2	570	No protein	Retained intron	-		81 - 13	TSL:3
ptan1-216	ENSMUST00000202844.1	477	No protein	Retained intron	-	1.00		TSL:5
ptan1-207	ENSMUST00000124494.4	457	No protein	Retained intron		2972	575	TSL:3

The strategy is based on the design of *Sptan1-208* transcript, The transcription is shown below:

 Image: State of the state of the

Genomic location distribution





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025-5826 5929

Protein domain



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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





