Spi1 Cas9-CKO Strategy

Designer: Reviewer:

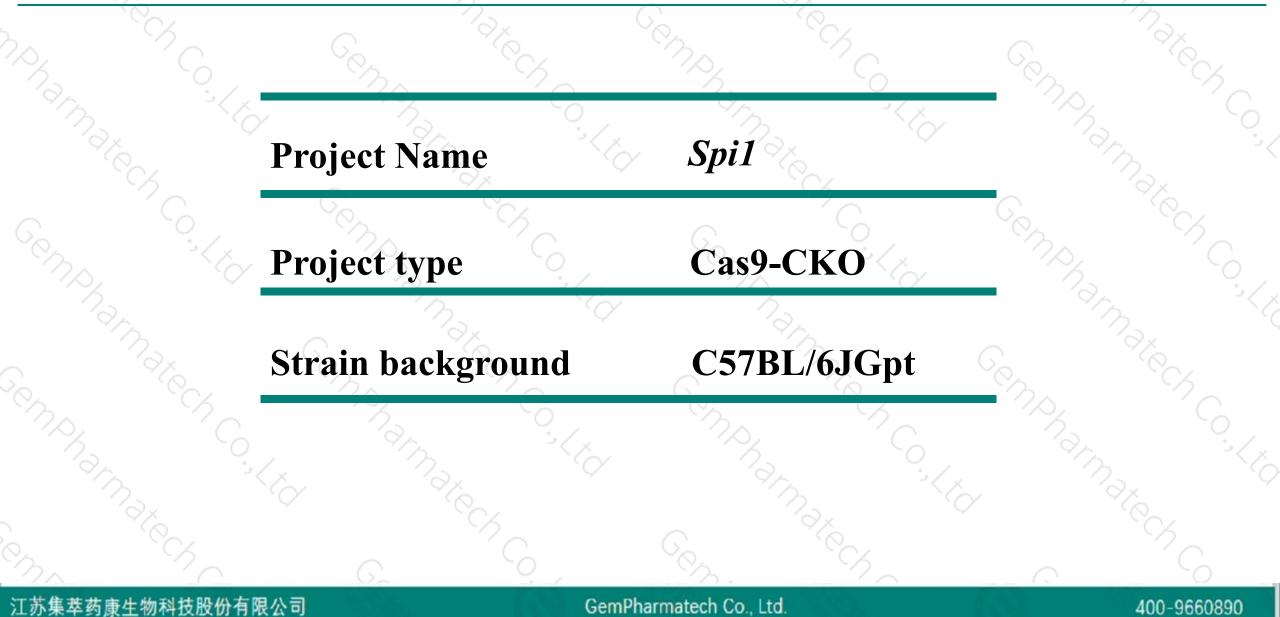
Design Date:

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2020-3-16

Project Overview





Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Spil gene. The schematic diagram is as follows: Donor and CRISPR/Cas9 System **ATG** Wild-type allele ATG **Conditional KO allele** ... Cre **ATG** ... KO allele . . . Cas9/sgRNA Uncoding region Coding region > LoxP

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- The Spil gene has 4 transcripts. According to the structure of Spil gene, exon2 of Spil-201(ENSMUST0000002180.7) transcript is recommended as the knockout region. The region contains 97bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Spi1* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 or cell types.

Notice



- According to the existing MGI data, Nullizygous mice may exhibit fetal or perinatal lethality, absence of myeloid and B cells, and altered T cell and NK cell development. Mice carrying hypomorphic alleles display impaired B-cell and myeloid development, develop T cell derived lymphomas andacute myeloid leukemia, and die prematurely.
- The *Spi1* gene is located on the Chr2. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing

technology level.

Gene information (NCBI)



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Spi1 spleen focus forming virus (SFFV) proviral integration oncogene [Mus musculus (house mouse)]

Gene ID: 20375, updated on 14-Mar-2020

Summary

Official SymbolSpi1 provided by MGIOfficial Full Namespleen focus forming virus (SFFV) proviral integration oncogene provided by MGIPrimary sourceMGI:MGI:98282See relatedEnsembl:ENSMUSG0000002111Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
Murinae; Mus; Mus

Also known as Dis1; PU.1; Dis-1; Sfpi1; Spi-1; Sfpi-1; Tcfpu1; Tfpu.1

Expression Broad expression in spleen adult (RPKM 51.8), lung adult (RPKM 18.0) and 15 other tissues See more

Orthologs human all

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Transcript information (Ensembl)



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

Name 🖕	Transcript ID 👙	bp 🌲	Protein 🖕	Biotype 🍦	CCDS 🖕	UniProt 🖕	Flags	
Spi1-201	ENSMUST0000002180.7	2034	<u>272aa</u>	Protein coding	<u>CCDS16425</u>	<u>P17433</u> & <u>Q3U5L4</u> &	TSL:1 GENCODE basic APPRIS P	
Spi1-204	ENSMUST00000169852.1	544	<u>143aa</u>	Protein coding	2	<u>E9Q6W1</u> &	CDS 3' incomplete TSL:3	
Spi1-203	ENSMUST00000132741.2	402	<u>77aa</u>	Protein coding	28	<u>E9QAI9</u> &	CDS 3' incomplete TSL:3	
Spi1-202	ENSMUST00000131400.1	613	No protein	Processed transcript	58		TSL:2	

The strategy is based on the design of Spi1-201 transcript, The transcription is shown below

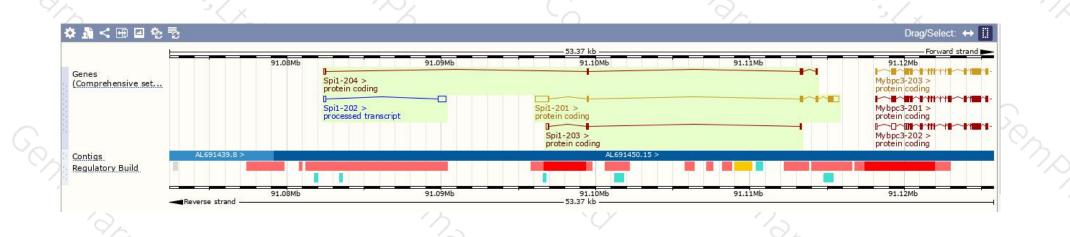
Spi1-201 > protein coding

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Genomic location distribution





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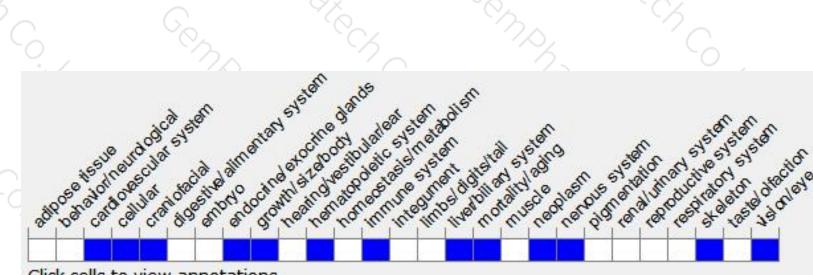
Protein domain



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Mouse phenotype description(MGI)





Click cells to view annotations.

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, Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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



