

Spns1 Cas9-KO Strategy

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Design Date: 2021-4-13

Project Overview

Project Name

Spns1

Project type

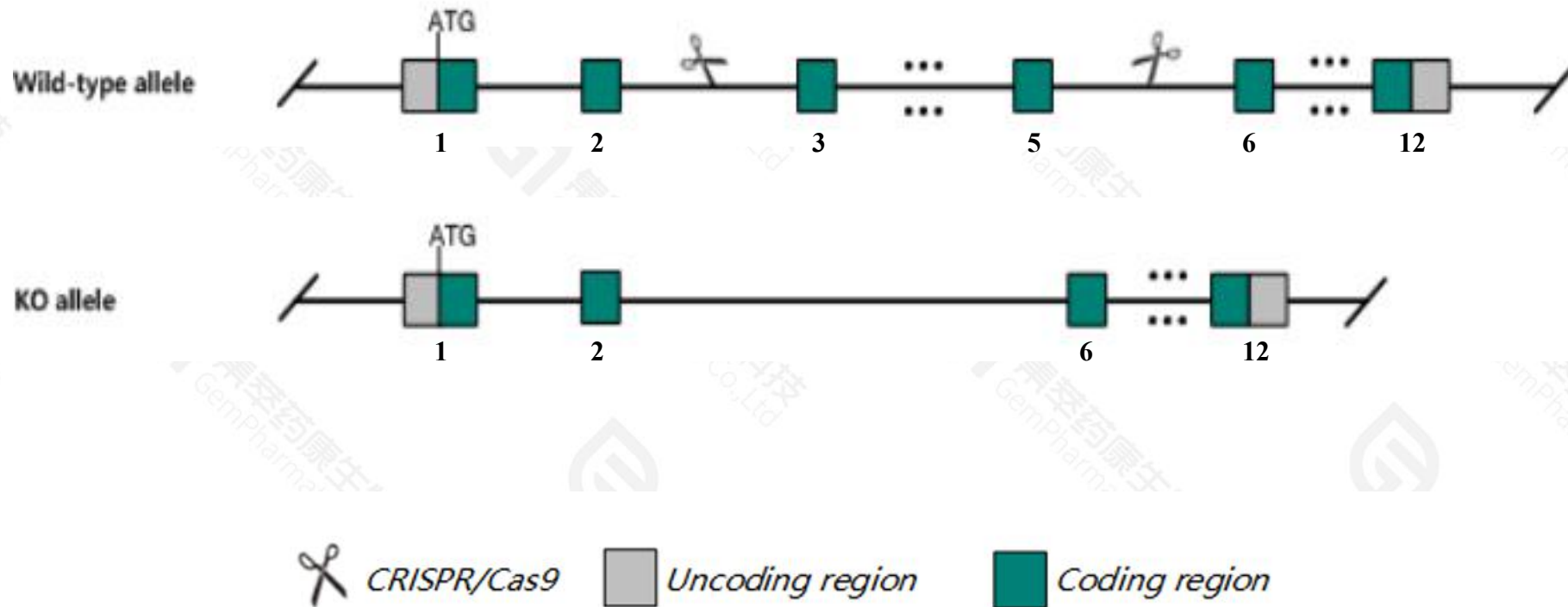
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Spns1* gene. The schematic diagram is as follows:



- The *Spns1* gene has 13 transcripts. According to the structure of *Spns1* gene, exon3-exon5 of *Spns1*-201(ENSMUST00000032994.15) transcript is recommended as the knockout region. The region contains 356bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Spns1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous mutation results in lethality before weaning.
- The *Spns1* 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.

Spns1 spinster homolog 1 [Mus musculus (house mouse)]

Gene ID: 73658, updated on 25-Sep-2020

Summary



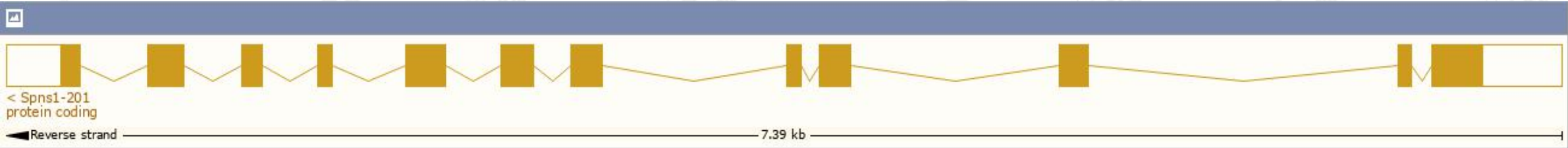
Official Symbol	Spns1 provided by MGI
Official Full Name	spinster homolog 1 provided by MGI
Primary source	MGI:MGI:1920908
See related	Ensembl:ENSMUSG00000030741
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2210013K02Rik, Spin1, Spinl
Expression	Ubiquitous expression in thymus adult (RPKM 51.4), lung adult (RPKM 38.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

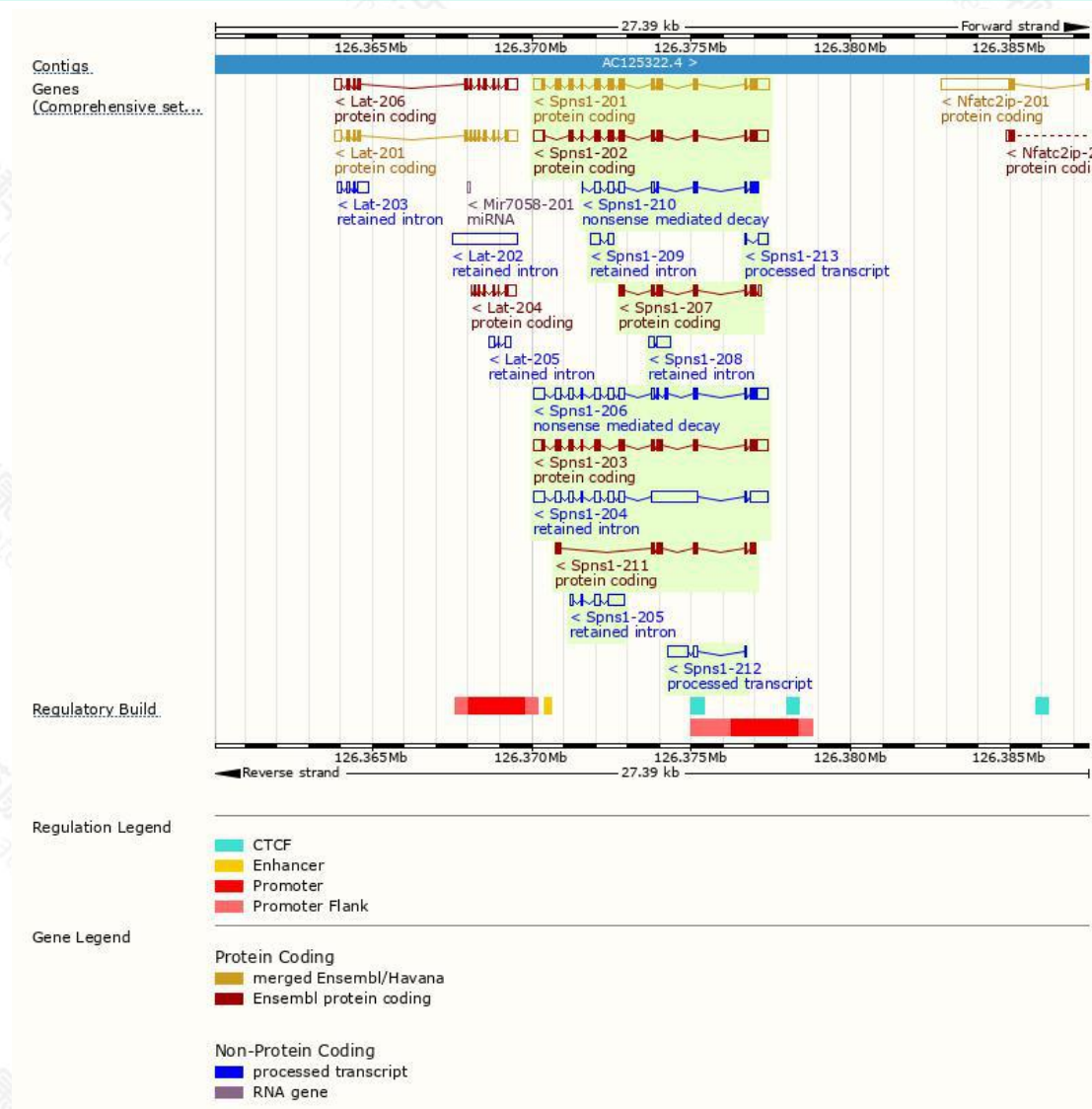
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spns1-201	ENSMUST00000032994.15	2219	528aa	Protein coding	CCDS21826		TSL:1 , GENCODE basic , APPRIS P1 ,
Spns1-203	ENSMUST00000119846.8	2017	476aa	Protein coding	-		TSL:5 , GENCODE basic ,
Spns1-202	ENSMUST00000119754.8	2001	453aa	Protein coding	-		TSL:5 , GENCODE basic ,
Spns1-207	ENSMUST00000150476.3	867	239aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Spns1-211	ENSMUST00000205930.2	787	262aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Spns1-206	ENSMUST00000138141.8	2152	165aa	Nonsense mediated decay	-		TSL:1 ,
Spns1-210	ENSMUST00000205366.2	1100	167aa	Nonsense mediated decay	-		TSL:5 ,
Spns1-212	ENSMUST00000206094.2	829	No protein	Processed transcript	-		TSL:3 ,
Spns1-213	ENSMUST00000206377.2	346	No protein	Processed transcript	-		TSL:3 ,
Spns1-204	ENSMUST00000126810.8	3251	No protein	Retained intron	-		TSL:2 ,
Spns1-205	ENSMUST00000137263.3	821	No protein	Retained intron	-		TSL:2 ,
Spns1-208	ENSMUST00000150748.2	619	No protein	Retained intron	-		TSL:3 ,
Spns1-209	ENSMUST00000152000.2	435	No protein	Retained intron	-		TSL:1 ,

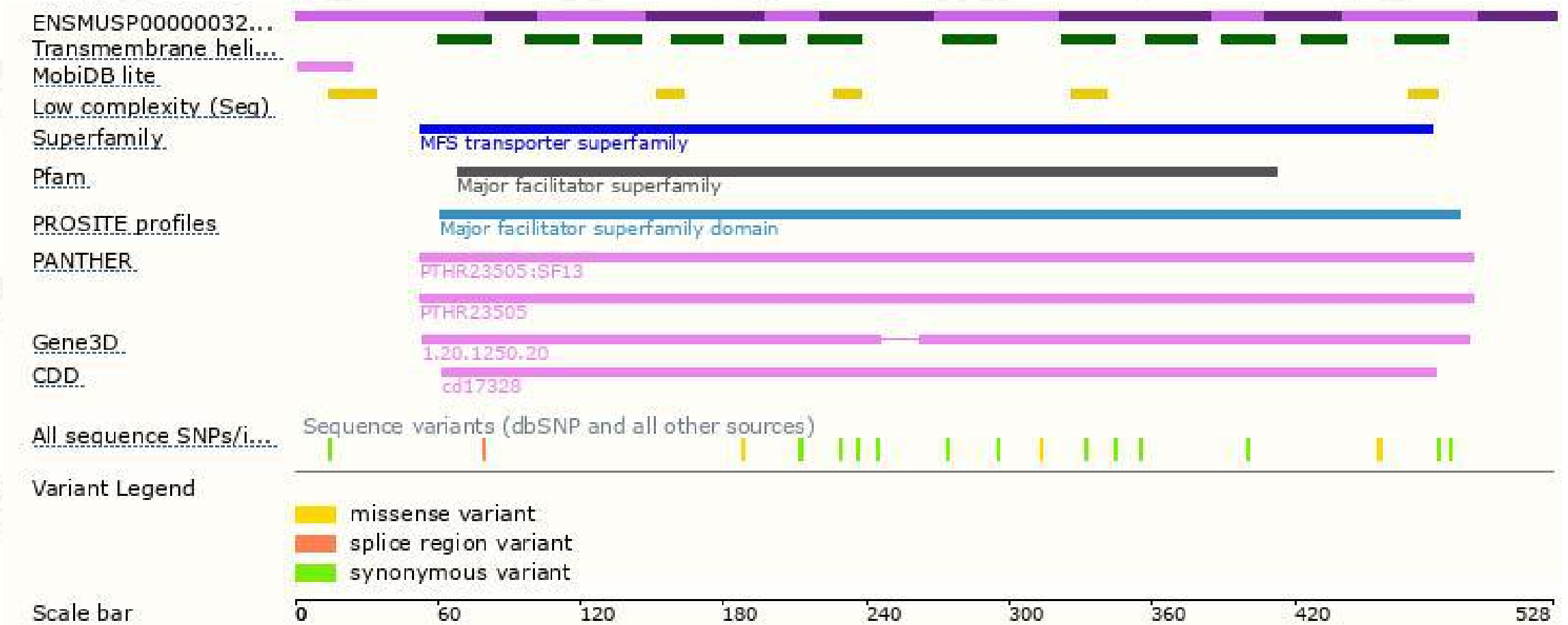
The strategy is based on the design of *Spns1-201* transcript,the transcription is shown below:



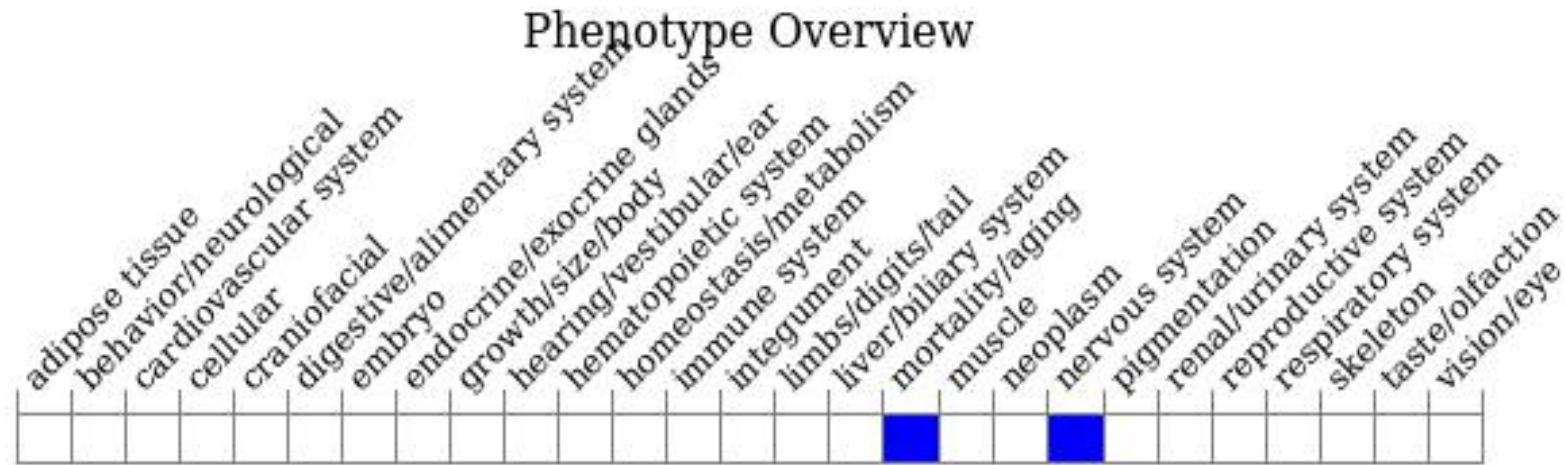
Genomic location distribution



Protein domain



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, homozygous mutation results in lethality before weaning.

If you have any questions, you are welcome to inquire.
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