Snrpn Cas9-CKO Strategy

Designer: Rui Xiong

Reviewer: Miaomiao Cui

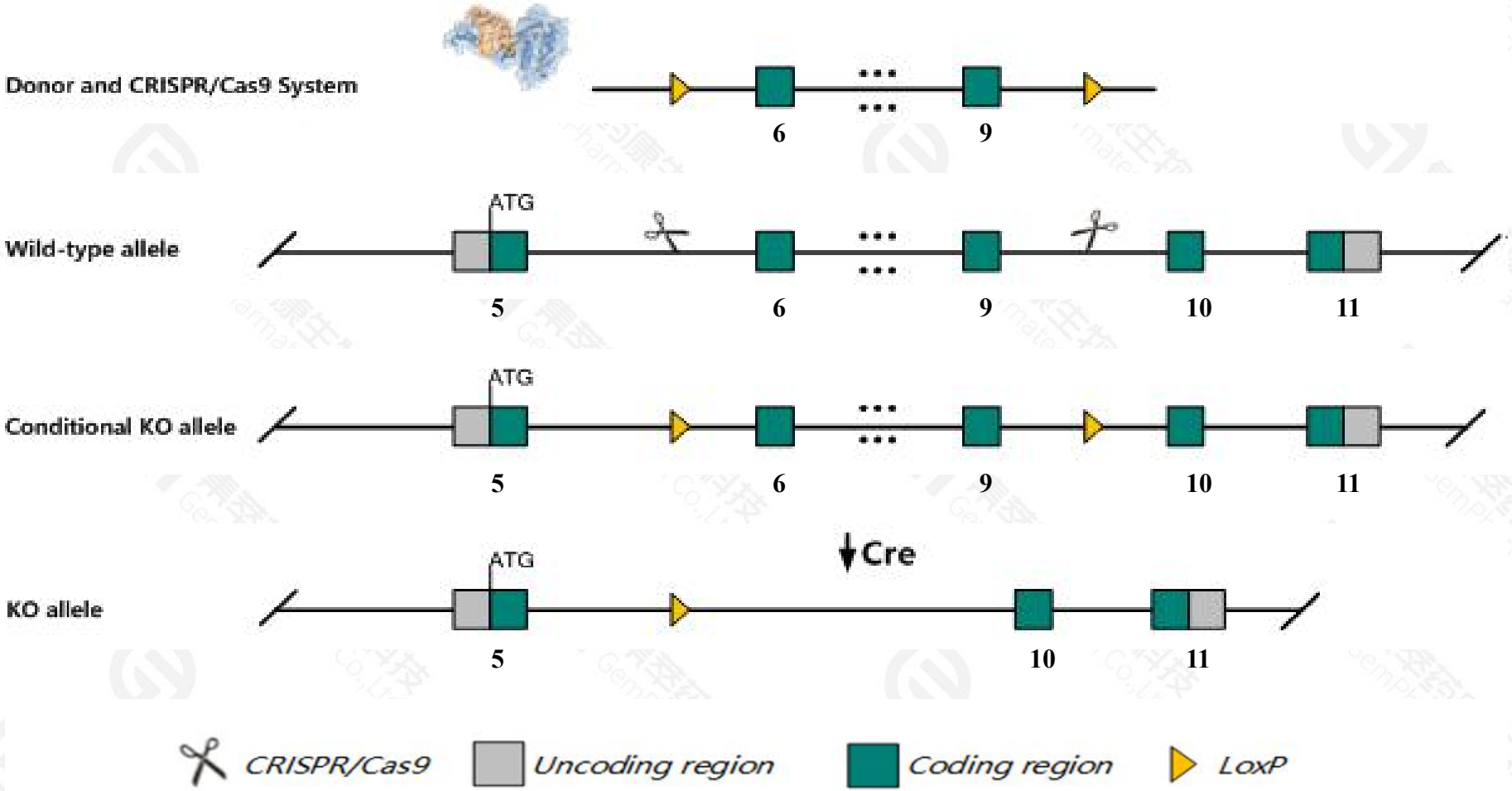
Design Date: 2021-5-27

Project Overview

Project Name	***Snrpn***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

➢ The *Snrpn* gene has 2 transcripts. According to the structure of *Snrpn* gene, exon6-exon9 of *Snrpn-202*(ENSMUST00000098402.5) transcript is recommended as the knockout region.The region contains 556bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Snrpn* 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.

Notice

➢ *Gm38393* gene will be destroyed.

➢ According to the existing MGI data,homozygotes for targeted intragenic deletions are phenotypically normal. Deletions that also encompass neighboring genes on the paternal chromosome exhibit growth retardation, hypotonia, and high mortality.

➢ The *Snrpn* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

集萃药康 GemPharmatech

Snrpn small nuclear ribonucleoprotein N [Mus musculus (house mouse)]

Gene ID: 20646, updated on 25-Sep-2020

Summary

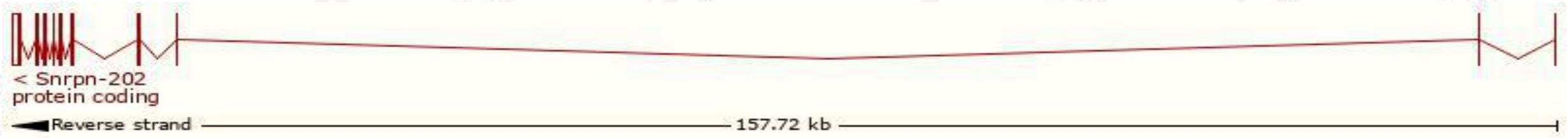
Official Symbol	Snrpn provided by MGI
Official Full Name	small nuclear ribonucleoprotein N provided byMGI
Primary source	MGI:MGI:98347
See related	Ensembl:ENSMUSG00000102252
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410045I01Rik, HCERN3, Peg, Peg4, Pwc, SMN, sm-D, snRNP-N
Summary	This locus represents a paternally-expressed imprinted gene that encodes a component of the small nuclear ribonucleoprotein complex, which functions in pre-mRNA processing. Genomic and genetic changes in this region result in growth defects and lethality; the corresponding region in human is the critical region for Prader-Willi Syndrome. Alternative promoter use and alternative splicing result in a multitude of transcript variants encoding the same protein. Transcript variants may be bicistronic and also encode the SNRPN upstream reading frame protein (Snurf) from an upstream open reading frame. In addition, long spliced transcripts for small nucleolar RNA host gene 14 (Snhg14) may originate from the promoters at this locus and incorporate exons shared with this gene. [provided by RefSeq, Mar 2017]
Expression	Biased expression in cerebellum adult (RPKM 199.4), cortex adult (RPKM 198.6) and 8 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

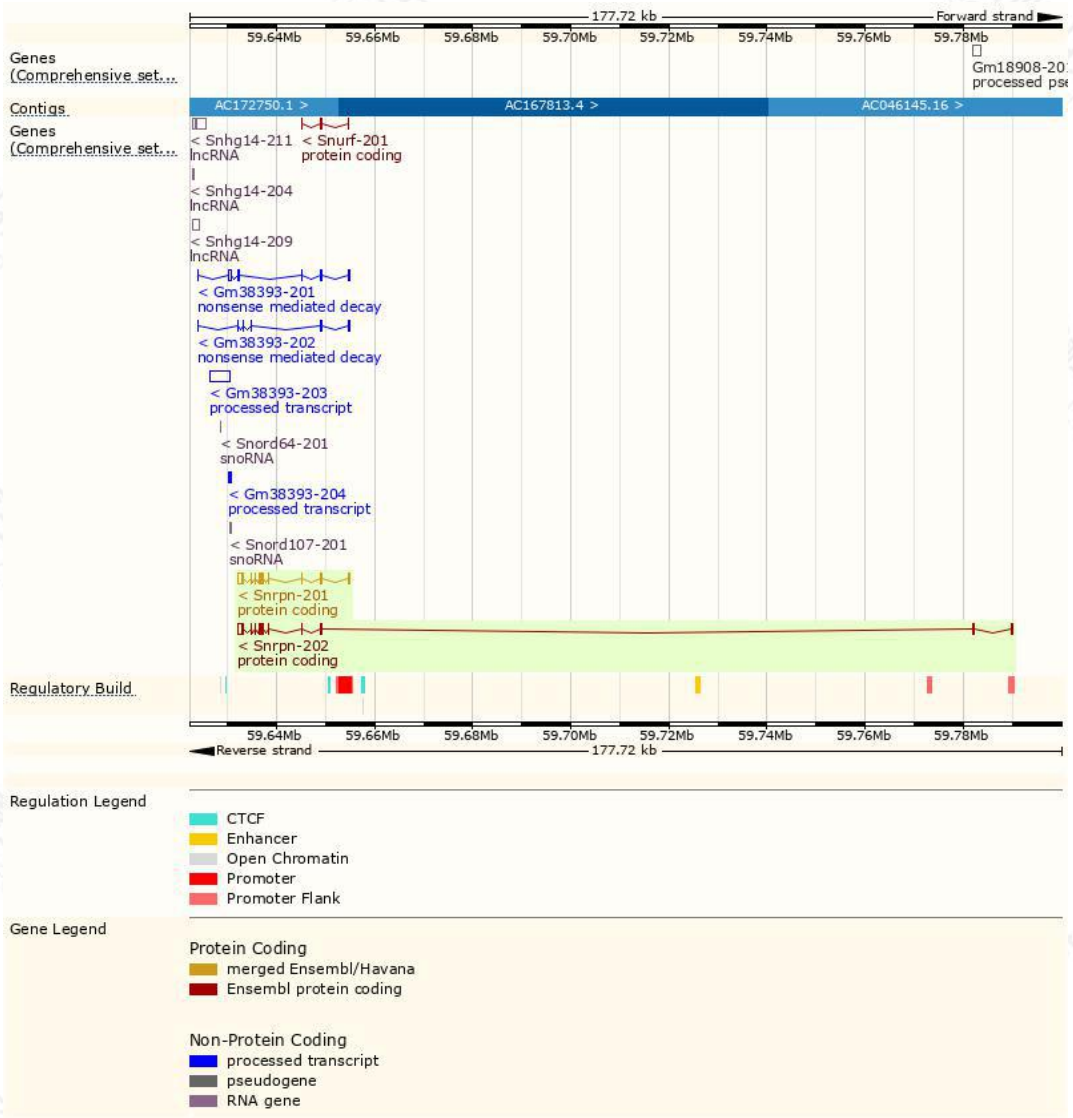
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snrpn-202	ENSMUST00000098402.5	2076	240aa	Protein coding	CCDS39974		TSL:5 , GENCODE basic , APPRIS P1 ,
Snrpn-201	ENSMUST00000059305.17	1932	240aa	Protein coding	CCDS39974		TSL:1 , GENCODE basic , APPRIS P1 ,

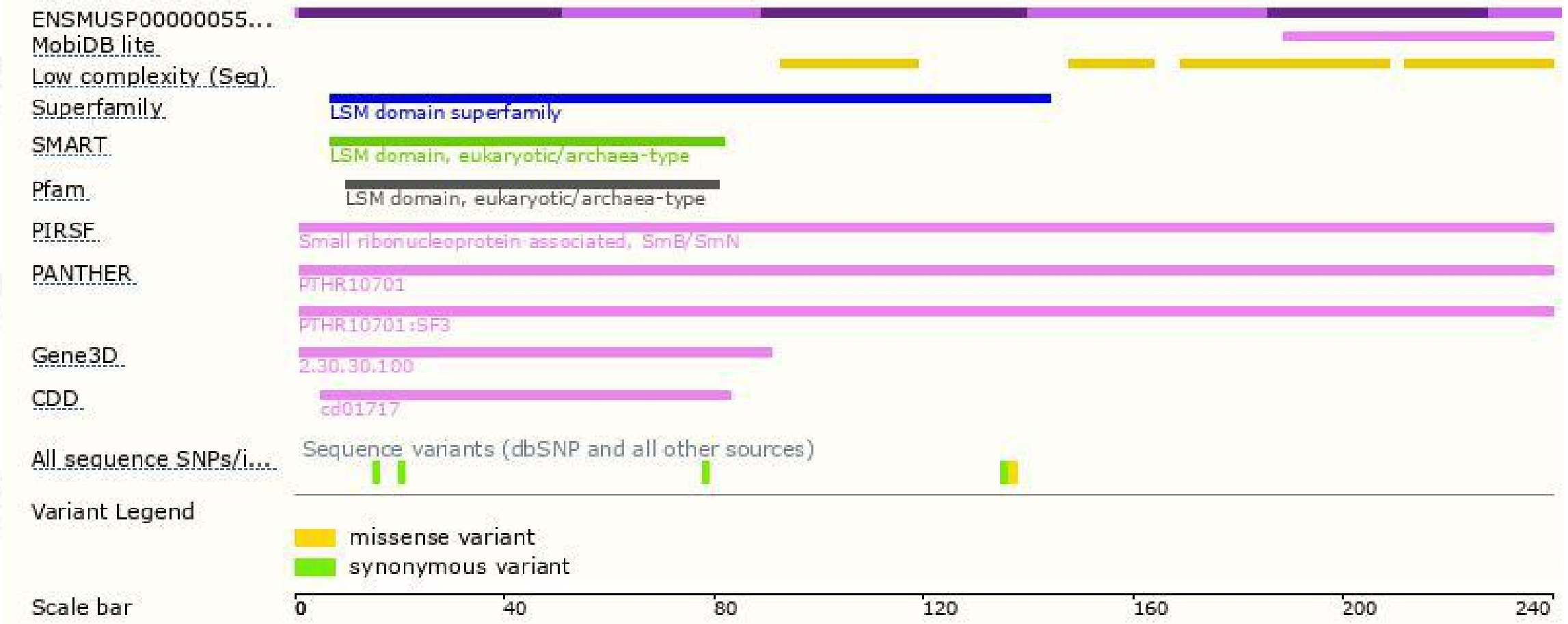
The strategy is based on the design of *Snrpn-202* transcript,the transcription is shown below:



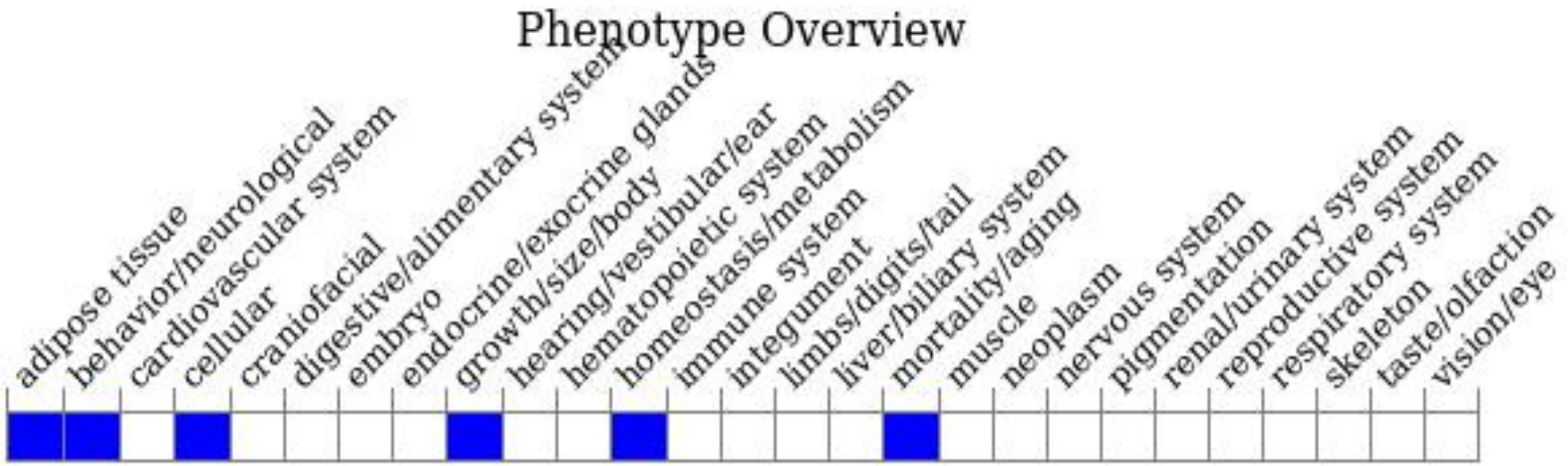
Genomic location distribution



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,homozygotes for targeted intragenic deletions are phenotypically normal. Deletions that also encompass neighboring genes on the paternal chromosome exhibit growth retardation, hypotonia, and high mortality.

集萃药康
GemPharmatech

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

集萃药康生物科技
GemPharmatech Co.,Ltd