

Snx5 Cas9-KO Strategy

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Project Overview

Project Name

$Snx5$

Project type

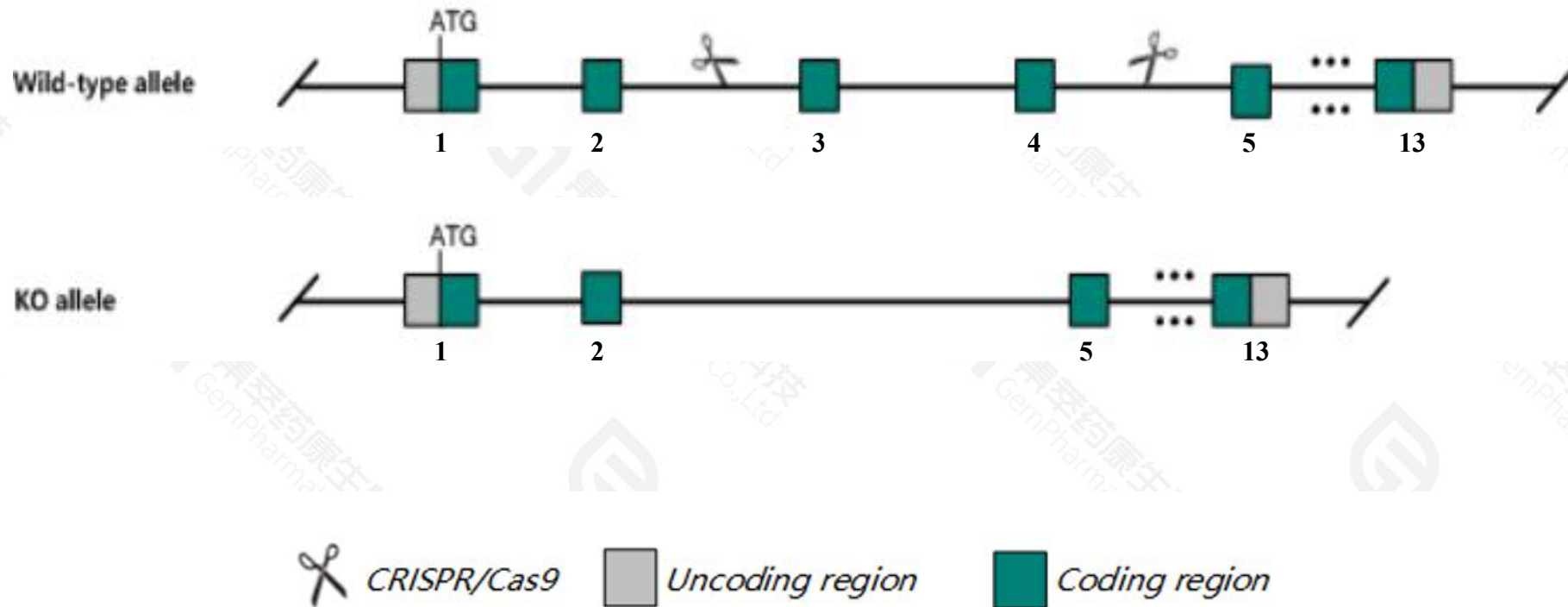
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snx5* gene. The schematic diagram is as follows:



- The *Snx5* gene has 8 transcripts. According to the structure of *Snx5* gene, exon3-exon4 of *Snx5*-201(ENSMUST00000028909.5) transcript is recommended as the knockout region. The region contains 233bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snx5* 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, mice homozygous for a gene trap allele exhibit impaired alveolar epithelial differentiation of type I cells, respiratory failure and lethality during the perinatal and postnatal periods.
- The *Snx5* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Snx5 sorting nexin 5 [Mus musculus (house mouse)]

Gene ID: 69178, updated on 1-Mar-2021

Summary



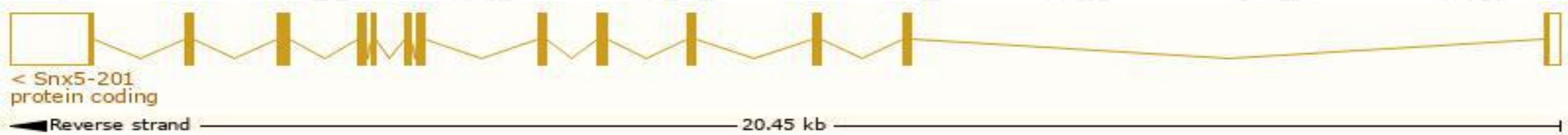
Official Symbol	Snx5 provided by MGI
Official Full Name	sorting nexin 5 provided by MGI
Primary source	MGI:MGI:1916428
See related	Ensembl:ENSMUSG00000027423
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0910001N05Rik, 1810032P22Rik, AU019504, D2Ert52, D2Ert52e
Expression	Ubiquitous expression in placenta adult (RPKM 42.1), liver E14 (RPKM 37.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

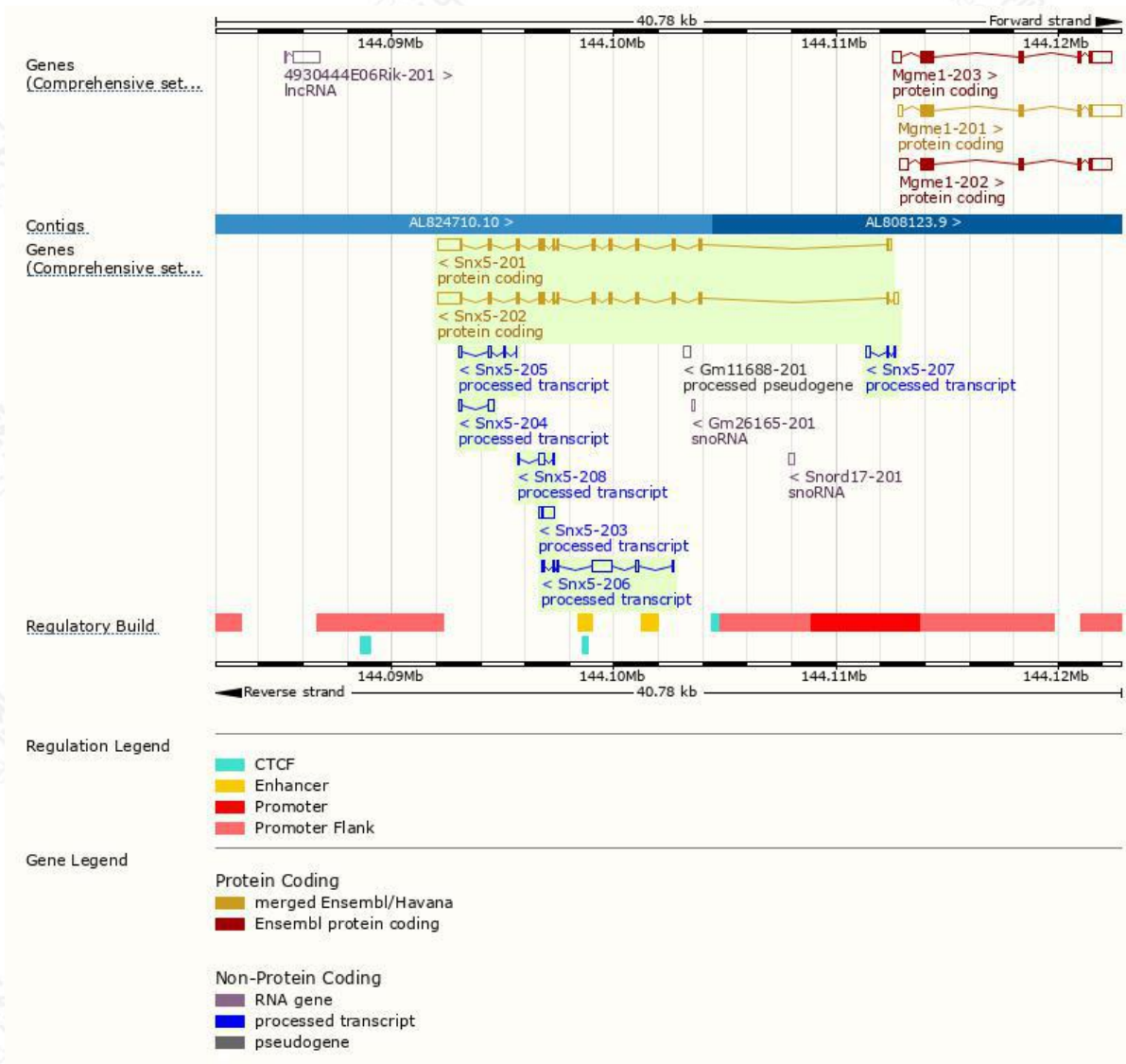
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snx5-202	ENSMUST00000110030.10	2512	404aa	Protein coding	CCDS16815		TSL:1 , GENCODE basic , APPRIS P1 ,
Snx5-201	ENSMUST00000028909.5	2419	404aa	Protein coding	CCDS16815		TSL:1 , GENCODE basic , APPRIS P1 ,
Snx5-206	ENSMUST00000153033.2	1296	No protein	Processed transcript	-		TSL:5 ,
Snx5-203	ENSMUST00000124389.2	602	No protein	Processed transcript	-		TSL:3 ,
Snx5-208	ENSMUST00000156936.2	378	No protein	Processed transcript	-		TSL:3 ,
Snx5-205	ENSMUST00000138745.2	369	No protein	Processed transcript	-		TSL:3 ,
Snx5-204	ENSMUST00000125285.2	350	No protein	Processed transcript	-		TSL:2 ,
Snx5-207	ENSMUST00000155509.2	306	No protein	Processed transcript	-		TSL:5 ,

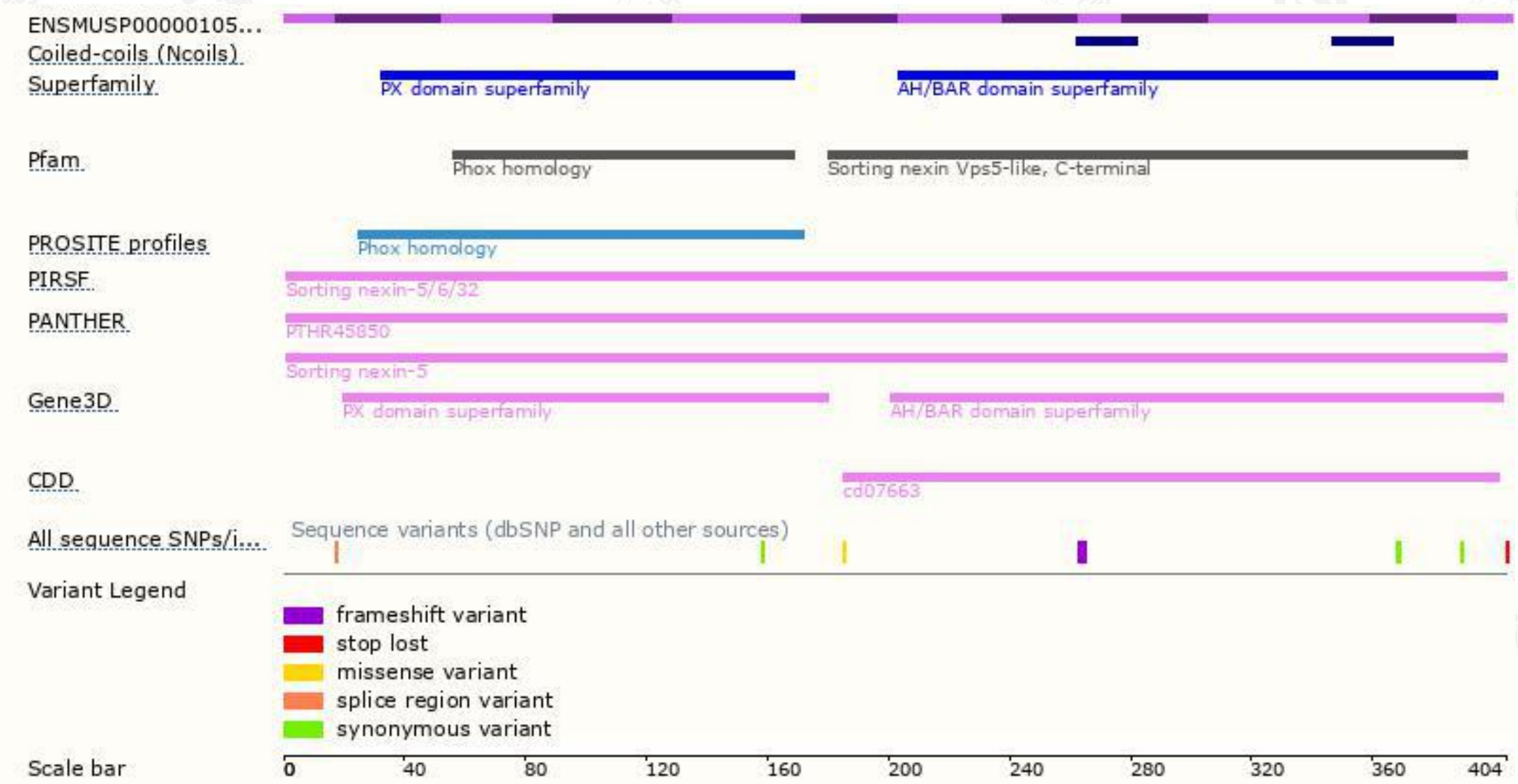
The strategy is based on the design of *Snx5-201* transcript,the transcription is shown below:



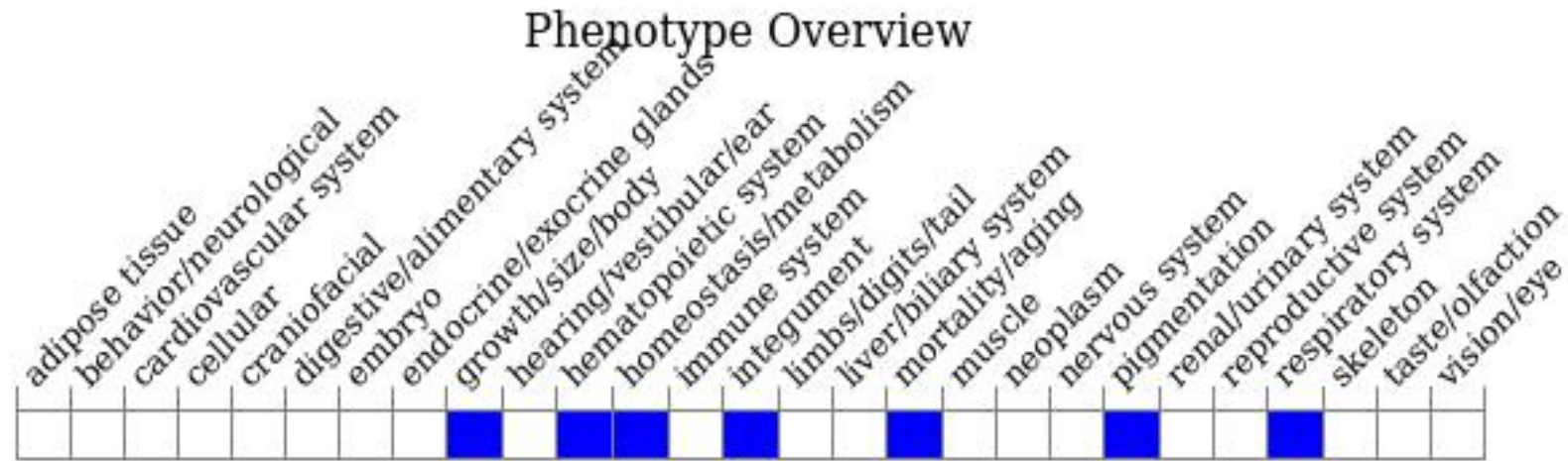
Genomic location distribution



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, mice homozygous for a gene trap allele exhibit impaired alveolar epithelial differentiation of type I cells, respiratory failure and lethality during the perinatal and postnatal periods.

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