

# *Snd1* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- *Snd1*

## Project Type

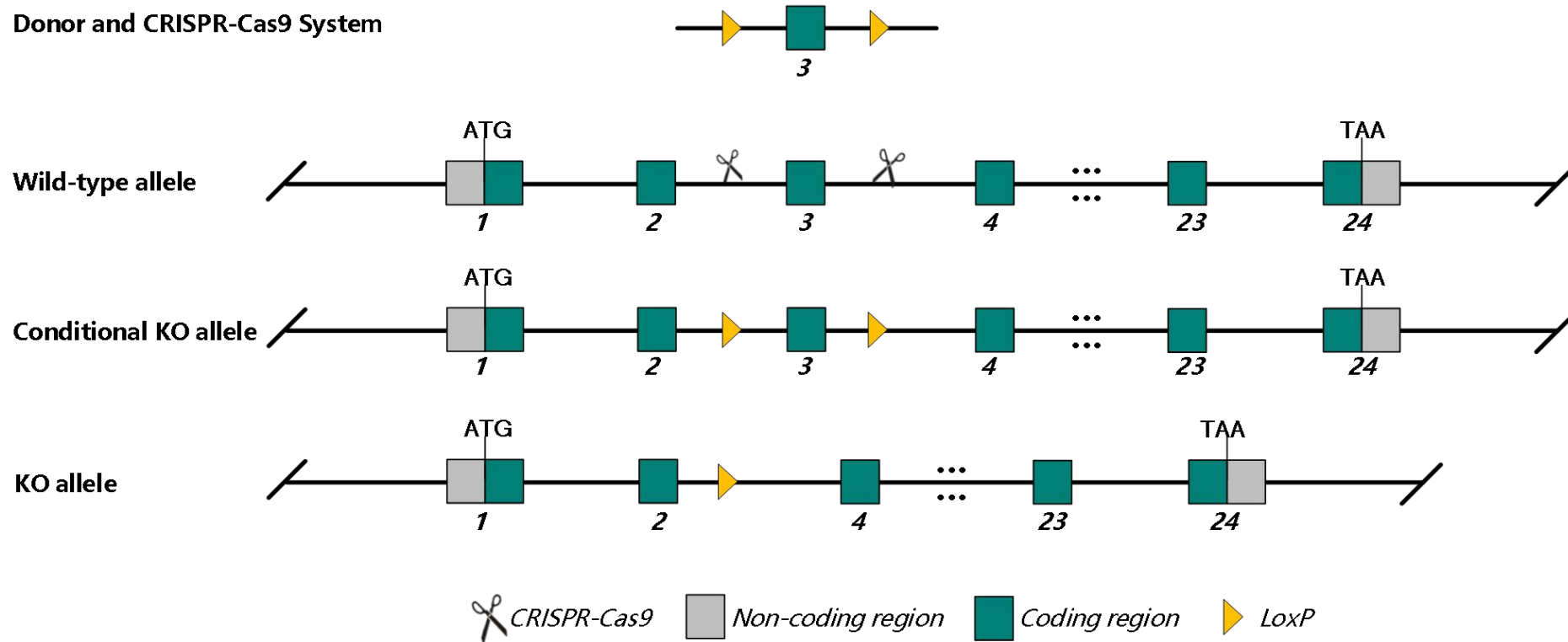
- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Snd1* gene.

# Technical Information

- The *Snd1* gene has 12 transcripts. According to the structure of *Snd1* gene, exon3 of *Snd1*-201 (ENSMUST00000001460.14) is recommended as the knockout region. The region contains 121 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Snd1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

# Gene Information

**Snd1** staphylococcal nuclease and tudor domain containing 1 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 56463, updated on 21-Nov-2023

## Summary

<b>Official Symbol</b>	Snd1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	staphylococcal nuclease and tudor domain containing 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1929266</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000001424</a> <a href="#">AllianceGenome:MGI:1929266</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Tudor-SN
<b>Summary</b>	Predicted to enable RISC complex binding activity; RNA binding activity; and endoribonuclease activity. Predicted to be involved in mRNA catabolic process; miRNA catabolic process; and regulation of cell cycle process. Located in dense body and nucleus. Is expressed in several structures, including central nervous system; early conceptus; limb mesenchyme; reproductive system; and sensory organ. Orthologous to human SND1 (staphylococcal nuclease and tudor domain containing 1). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 40.7), ovary adult (RPKM 37.4) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

## Genomic context

**Location:** 6 A3.3; 6 11.99 cM

See Snd1 in [Genome Data Viewer](#)

**Exon count:** 27

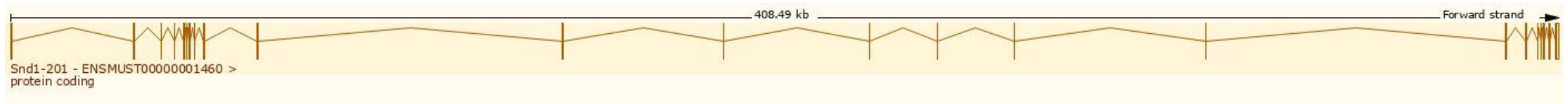
<https://www.ncbi.nlm.nih.gov/gene/56463>

# Transcript Information

The gene has 12 transcripts, all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000164915.8</a>	Snd1-203	3688	<a href="#">262aa</a>	Nonsense mediated decay		<a href="#">E9Q3E9</a>	TSL:1
<a href="#">ENSMUST00000001460.14</a>	Snd1-201	3482	<a href="#">910aa</a>	Protein coding	<a href="#">CCDS19953</a>	<a href="#">Q78PY7</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000167201.2</a>	Snd1-206	3781	<a href="#">608aa</a>	Protein coding		<a href="#">Q3TJ56</a>	Gencode basic TSL:1
<a href="#">ENSMUST00000168362.2</a>	Snd1-207	351	<a href="#">10aa</a>	Protein coding		<a href="#">A0A1C7ZN09</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000183161.2</a>	Snd1-212	2420	No protein	Retained intron		-	TSL:NA
<a href="#">ENSMUST00000165151.2</a>	Snd1-204	718	No protein	Retained intron		-	TSL:2
<a href="#">ENSMUST00000171532.8</a>	Snd1-211	420	No protein	Protein coding CDS not defined		-	TSL:3
<a href="#">ENSMUST00000169579.8</a>	Snd1-209	392	No protein	Protein coding CDS not defined		-	TSL:3
<a href="#">ENSMUST00000166136.2</a>	Snd1-205	366	No protein	Protein coding CDS not defined		-	TSL:3
<a href="#">ENSMUST00000171195.8</a>	Snd1-210	337	No protein	Protein coding CDS not defined		-	TSL:3
<a href="#">ENSMUST00000169321.2</a>	Snd1-208	320	No protein	Protein coding CDS not defined		-	TSL:2
<a href="#">ENSMUST00000163772.2</a>	Snd1-202	110	No protein	Protein coding CDS not defined		-	TSL:1

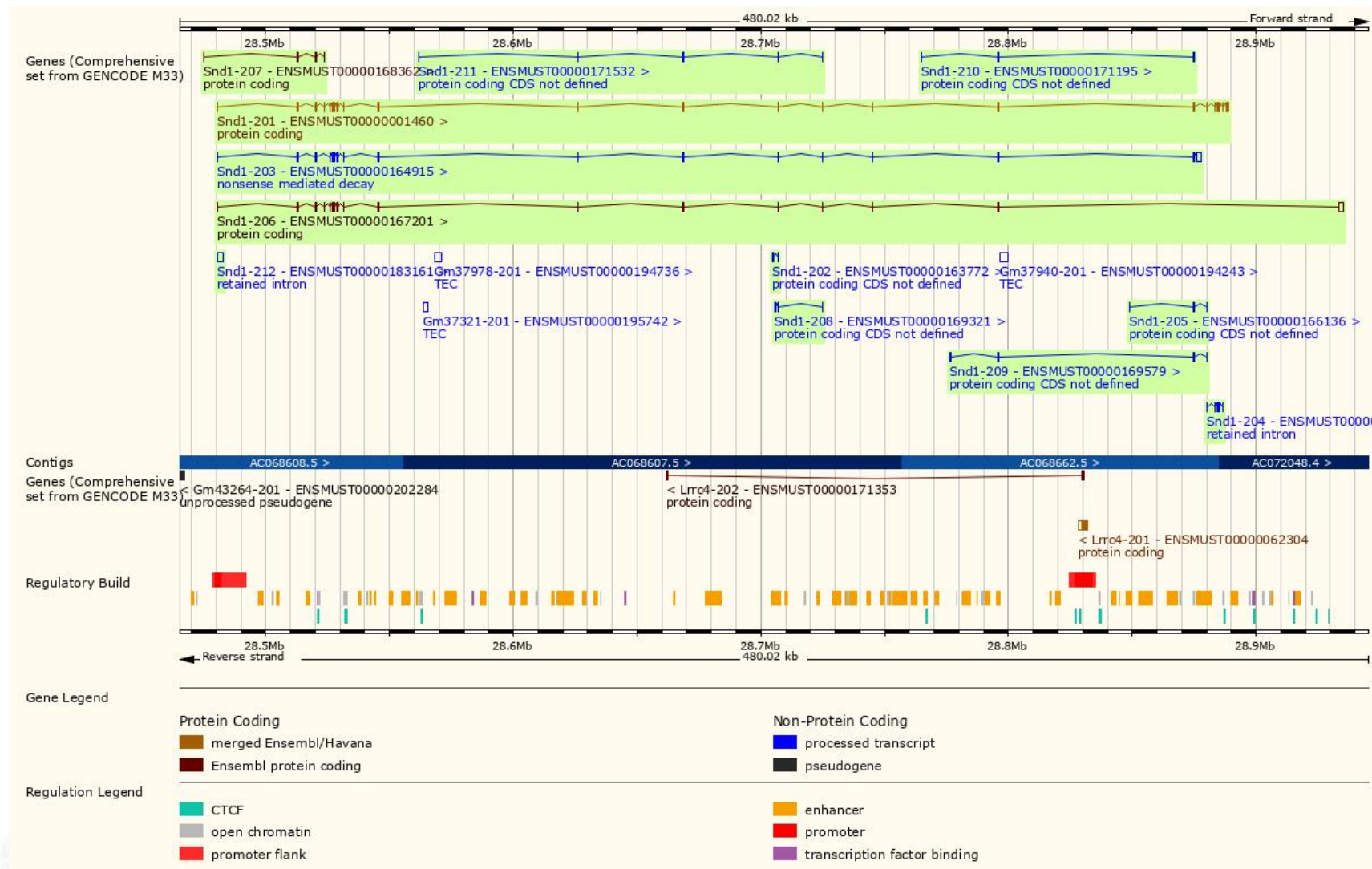
The strategy is based on the design of *Snd1*-201 transcript, the transcription is shown below:



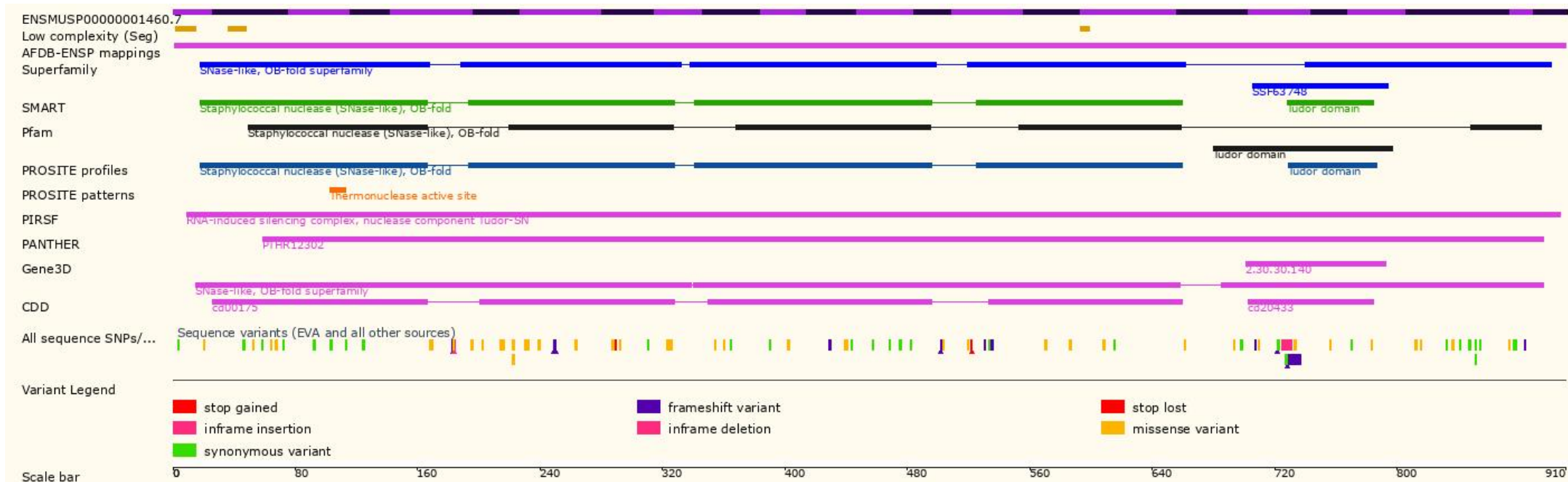
Source: <http://asia.ensembl.org/>



# Genomic Information

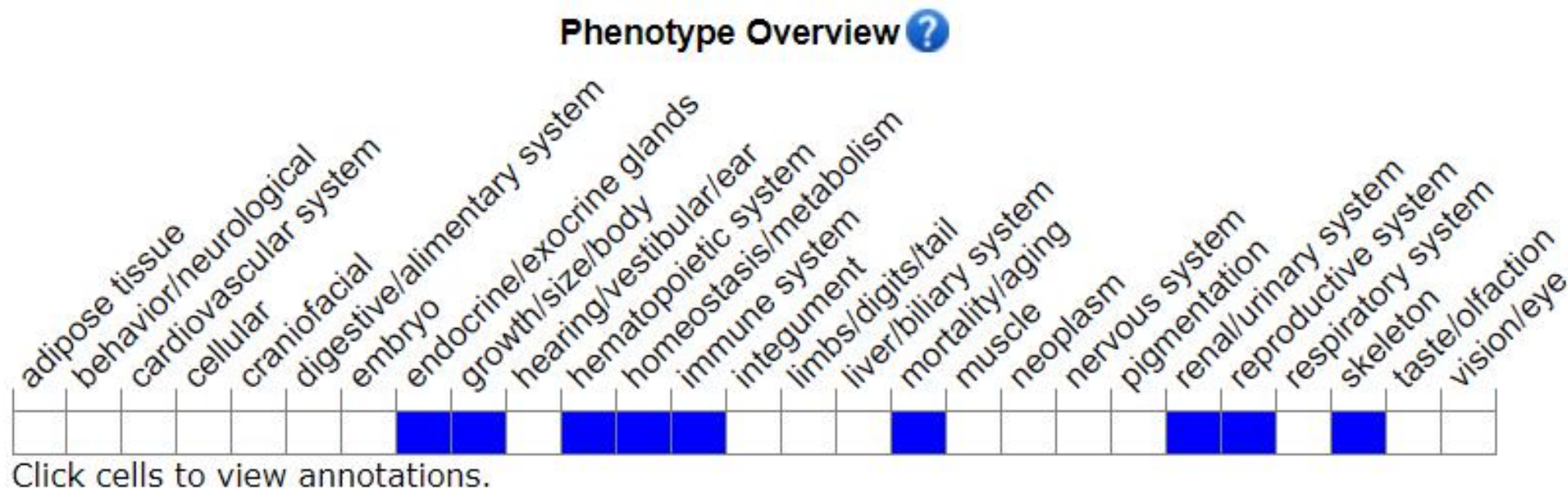


# Protein Information





# Mouse Phenotype Information (MGI)

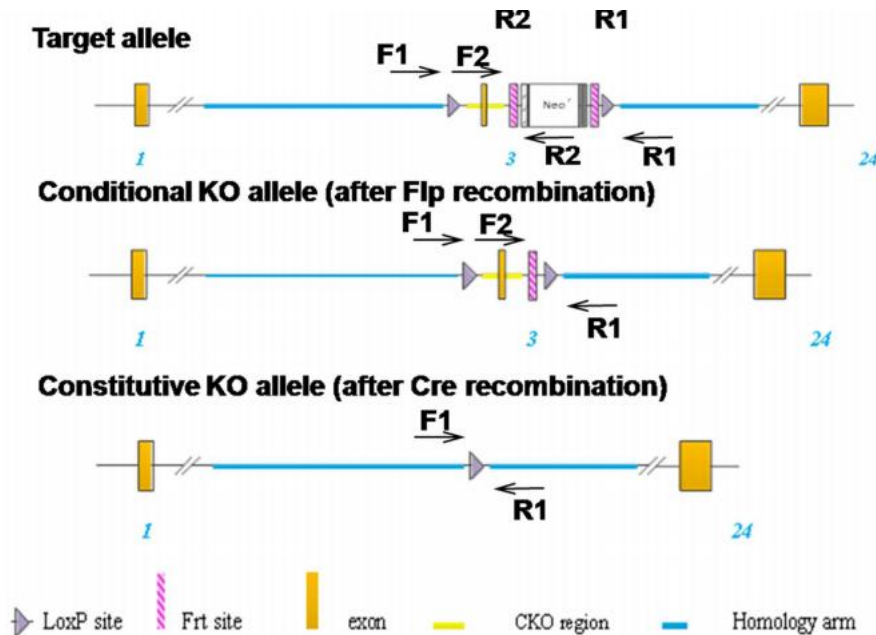


Mice homozygous for a null allele exhibit normal splenic T and B cell ratios and TH1 activity.

# Important Information

- This strategy may not affect *Snd1*-202, *Snd1*-204, *Snd1*-205, *Snd1*-208~*Snd1*-212 transcript.
- *Snd1* is located on Chr 6. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

# Reference



## **S1 Fig. Construction of constitutive SND1 KO mice.**

The mSnd1 gene (GenBank accession number: NM\_019776.2, Ensembl: ENSMUSG00000001424) is located on mouse chromosome 6. Twenty-four exons have been identified, with the ATG start codon in exon 1 and TAA stop codon in exon 24 (Transcript: Snd1-001 ENSMUST00000001460). Exon 3 was selected as conditional knockout region. Deletion of exon 3 should result in the loss of function of the mSnd1 gene. To engineer the targeting vector, homology arms and CKO (conditional KO) region were generated by PCR using BAC clone RP24-333L16 from the C57BL/6J library as template. In the targeting vector, the Neo cassette was flanked by Frt sites, and CKO region was flanked by LoxP sites. DTA will be used for negative selection. The conditional KO allele was obtained after Flp-mediated recombination and the constitutive KO allele was then obtained after Cre-mediated recombination.

<https://doi.org/10.1371/journal.ppat.1009295.s001>

(PDF)

[1] Wang X, Zhang C, Wang S, Rashu R, Thomas R, Yang J, Yang X. SND1 promotes Th1/17 immunity against chlamydial lung infection through enhancing dendritic cell function. PLoS Pathog. 2021 Feb 26;17(2):e1009295. doi: 10.1371/journal.ppat.1009295. PMID: 33635920; PMCID: PMC7946287.