

# Snx14 Cas9-KO Strategy

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# Overview

## Target Gene Name

- Snx14

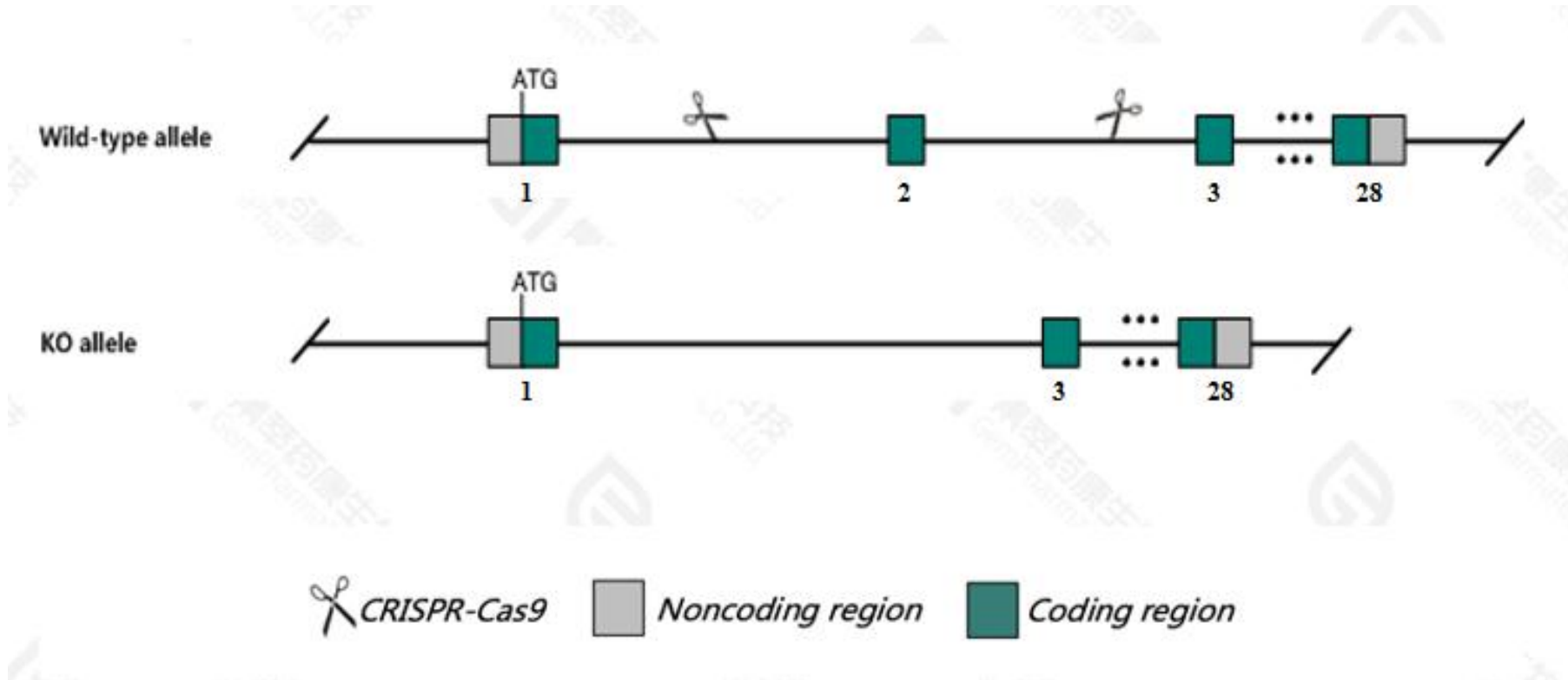
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Snx14* gene.

# Technical Information

- The *Snx14* gene has 9 transcripts. According to the structure of *Snx14* gene, exon2 of *Snx14-209*(ENSMUST00000239462.2) transcript is recommended as the knockout region. The region contains 121bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Snx14* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

# Gene Information

## **Snx14** sorting nexin 14 [ *Mus musculus* (house mouse) ]

Gene ID: 244962, updated on 5-Jan-2023

[Download Datasets](#)

### Summary

|                    |   |
|--------------------|---|
| Official Symbol    | Snx14 provided by <a href="#">MGI</a>   |
| Official Full Name | sorting nexin 14 provided by <a href="#">MGI</a>  |
| Primary source     | <a href="#">MGI:MGI:2155664</a>   |
| See related        | <a href="#">Ensembl:ENSMUSG00000032422</a> <a href="#">AllianceGenome:MGI:2155664</a>   |
| Gene type          | protein coding  |
| RefSeq status      | VALIDATED   |
| Organism           | <a href="#">Mus musculus</a>  |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus   |
| Also known as      | YR-14; B830022K16; C330035N22Rik  |
| Summary            | Predicted to enable phosphatidylinositol-3,5-bisphosphate binding activity. Predicted to be involved in autophagosome maturation. Predicted to act upstream of or within protein transport. Predicted to be located in cytosol and lysosome. Predicted to be active in late endosome. Human ortholog(s) of this gene implicated in autosomal recessive spinocerebellar ataxia 20. Orthologous to human SNX14 (sorting nexin 14). [provided by Alliance of Genome Resources, Apr 2022] |
| Expression         | Ubiquitous expression in bladder adult (RPKM 4.9), CNS E18 (RPKM 4.5) and 28 other tissues <a href="#">See more</a>   |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>   |
| <b>NEW</b>         | Try the new <a href="#">Gene table</a><br>Try the new <a href="#">Transcript table</a>  |

### Genomic context

Location: 9; 9 E3.1

Exon count: 30

See Snx14 in [Genome Data Viewer](#)

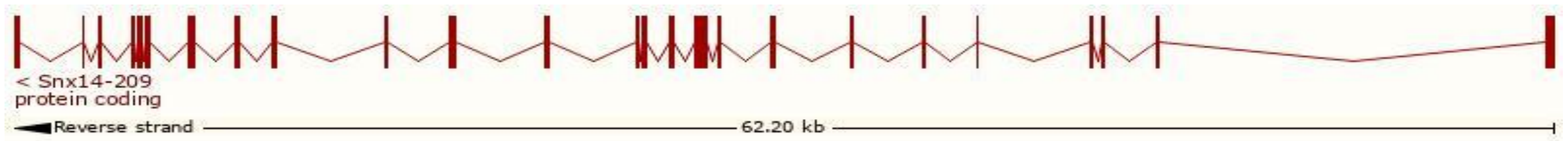
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

| Transcript ID                        | Name                      | bp   | Protein               | Biotype                 | CCDS                      | UniProt Match              | Flags                           |
|--------------------------------------|---------------------------|------|-----------------------|-------------------------|---------------------------|----------------------------|---------------------------------|
| <a href="#">ENSMUST00000239462.2</a> | <a href="#">Snx14-209</a> | 3112 | <a href="#">964aa</a> | Protein coding          | <a href="#">CCDS23387</a> | <a href="#">Q8BHY8</a>     | Ensembl Canonical Gencode basic |
| <a href="#">ENSMUST00000165315.9</a> | <a href="#">Snx14-204</a> | 3109 | <a href="#">937aa</a> | Protein coding          |                           | <a href="#">A0A6Q6RCM4</a> | Gencode basic APPRIS P4 TSL:1   |
| <a href="#">ENSMUST00000174806.9</a> | <a href="#">Snx14-207</a> | 3082 | <a href="#">946aa</a> | Protein coding          |                           | <a href="#">G3UX33</a>     | Gencode basic APPRIS ALT1 TSL:5 |
| <a href="#">ENSMUST00000173039.9</a> | <a href="#">Snx14-206</a> | 2970 | <a href="#">893aa</a> | Protein coding          |                           | <a href="#">G3UXB6</a>     | Gencode basic TSL:5             |
| <a href="#">ENSMUST00000173011.9</a> | <a href="#">Snx14-205</a> | 2238 | <a href="#">665aa</a> | Protein coding          |                           | <a href="#">G3UX13</a>     | Gencode basic TSL:5             |
| <a href="#">ENSMUST00000126405.3</a> | <a href="#">Snx14-201</a> | 2633 | <a href="#">183aa</a> | Nonsense mediated decay |                           | <a href="#">D6RH84</a>     | TSL:1                           |
| <a href="#">ENSMUST00000187610.2</a> | <a href="#">Snx14-208</a> | 2269 | No protein            | Retained intron         |                           | -                          | TSL:NA                          |
| <a href="#">ENSMUST00000140439.8</a> | <a href="#">Snx14-203</a> | 1765 | No protein            | Retained intron         |                           | -                          | TSL:1                           |
| <a href="#">ENSMUST00000126563.3</a> | <a href="#">Snx14-202</a> | 1075 | No protein            | Retained intron         |                           | -                          | TSL:2                           |

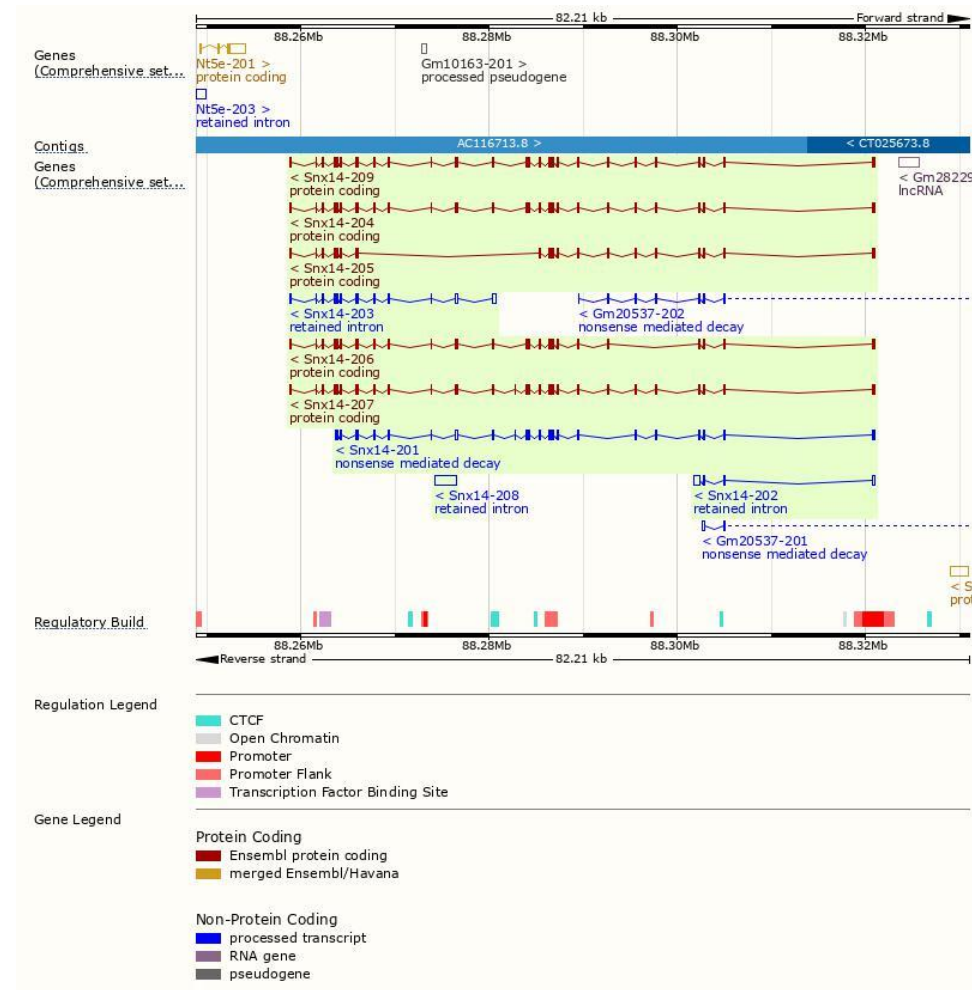
The strategy is based on the design of *Snx14-209* transcript, the transcription is shown below:



Source: <https://www.ensembl.org>



# Genomic Information

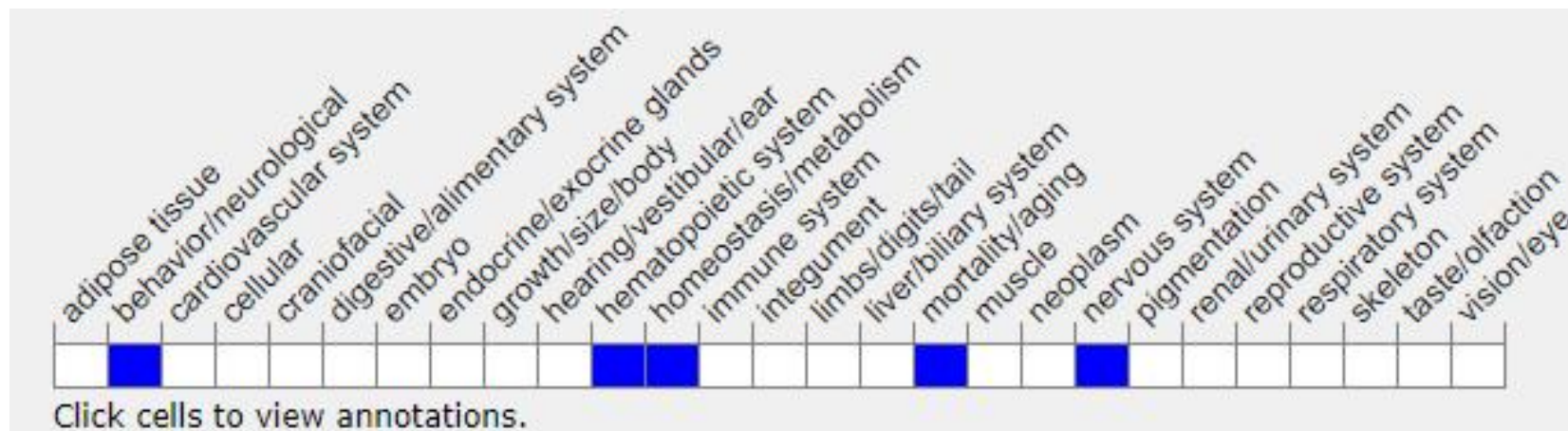


# Protein Information





# Mouse Phenotype Information (MGI)



- Phenotypes affected by the gene are marked in blue. Data quoted from MGI database (<http://www.informatics.jax.org/>).

# Important Information

- *Gm20537* gene will be destroyed.
- The *Snx14* gene is located on the Chr9. 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.