# *Slc9c1* Cas9-KO Strategy

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# Project Overview

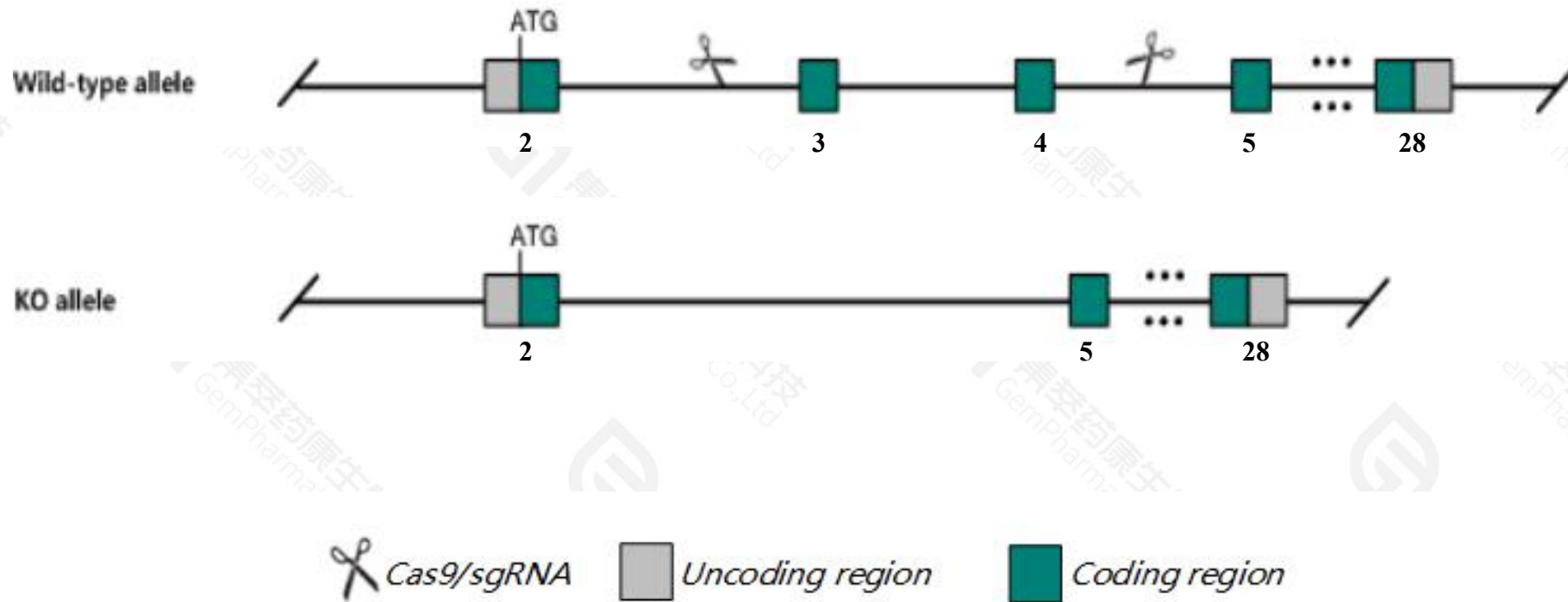| | |
|---|---|
| **Project Name** | *Slc9c1* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc9c1* gene. The schematic diagram is as follows:

# Technical routes

➤ The *Slc9c1* gene has 3 transcripts. According to the structure of *Slc9c1* gene, exon3-exon4 of *Slc9c1-201*(ENSMUST00000159945.8) transcript is recommended as the knockout region.The region contains 230bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Slc9c1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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 null mice display male infertility and asthenozoospermia.

➤ The *Slc9c1* gene is located on the Chr16. 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.

# Gene information （NCBI）

**Slc9c1 solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1 [Mus musculus (house mouse)]**

Gene ID: 208169, updated on 19-Jan-2021

## ▲ Summary

| | |
|---|---|
| **Official Symbol** | Slc9c1 provided by MGI |
| **Official Full Name** | solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1 provided by MGI |
| **Primary source** | MGI:MGI:2685456 |
| **See related** | Ensembl:ENSMUSG00000033210 |
| **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** | Gm610, NHE-10, Slc9, Slc9a10, sNHE, sper, spermNHE |
| **Expression** | Restricted expression toward testis adult (RPKM 10.4)See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------|---------------|-----|---------|---------|------|---------|-------|
| Slc9c1-201 | ENSMUST00000159945.8 | 3836 | 1175aa | Protein coding | CCDS28198 | | TSL:1 , GENCODE basic , APPRIS P1 , |
| Slc9c1-203 | ENSMUST00000162774.7 | 3583 | 163aa | Nonsense mediated decay | - | | CDS 5' incomplete , TSL:1 , |
| Slc9c1-202 | ENSMUST00000162151.3 | 3474 | 520aa | Nonsense mediated decay | - | | CDS 5' incomplete , TSL:1 , |

The strategy is based on the design of *Slc9c1-201* transcript,the transcription is shown below:
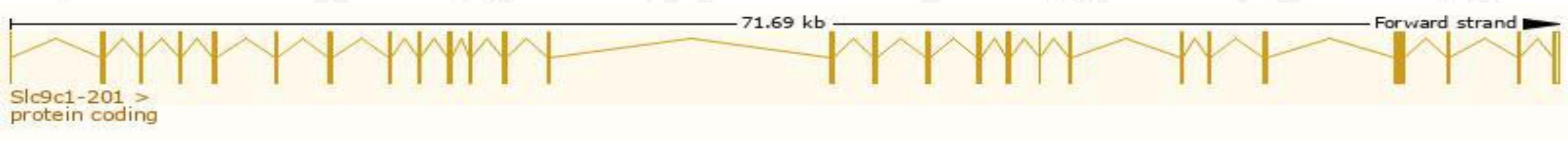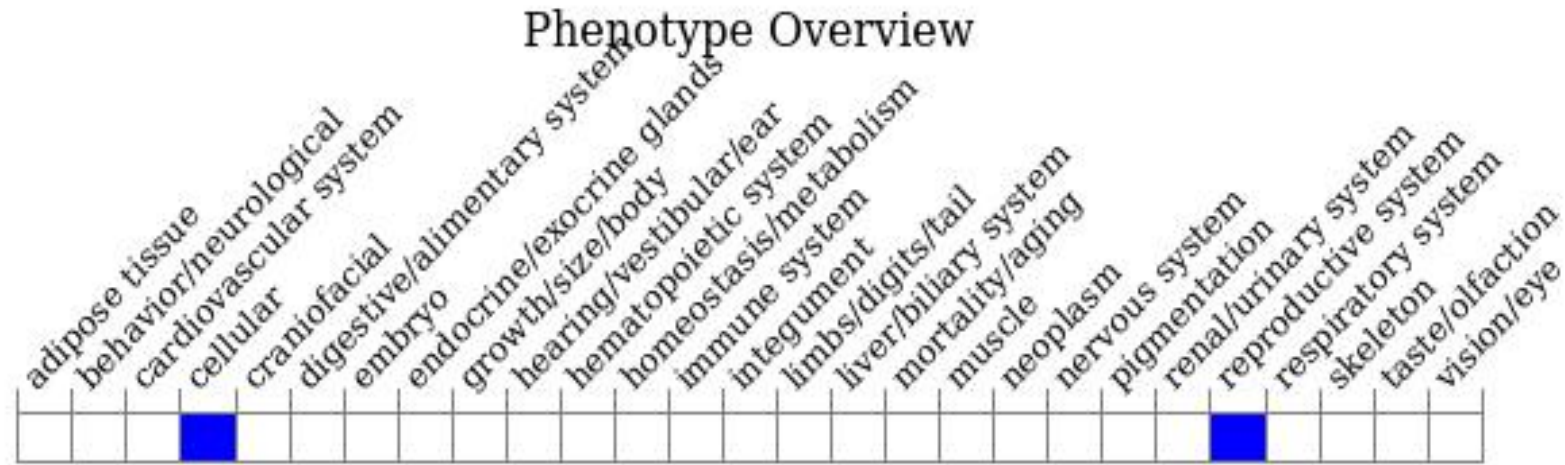
# Genomic location distribution
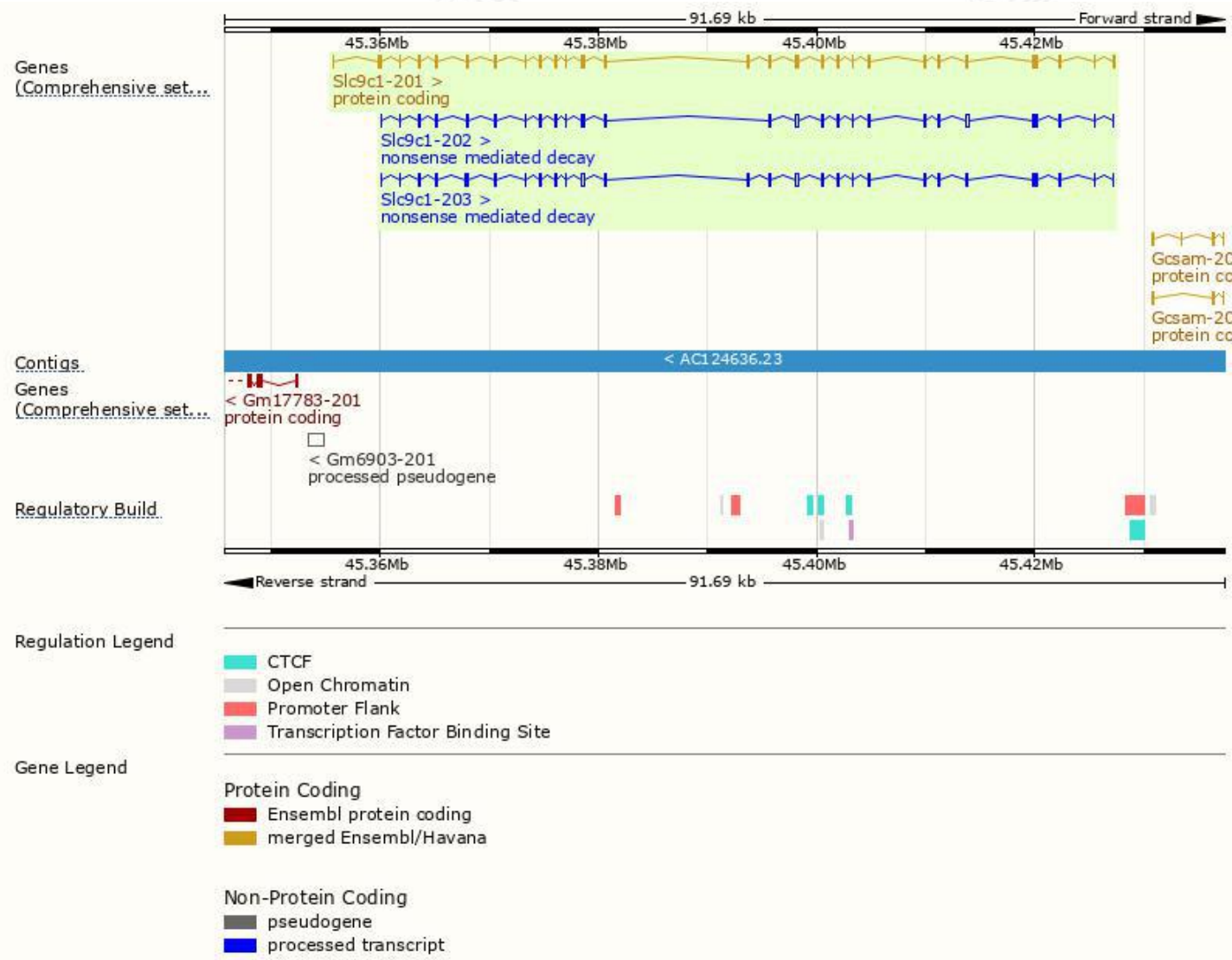
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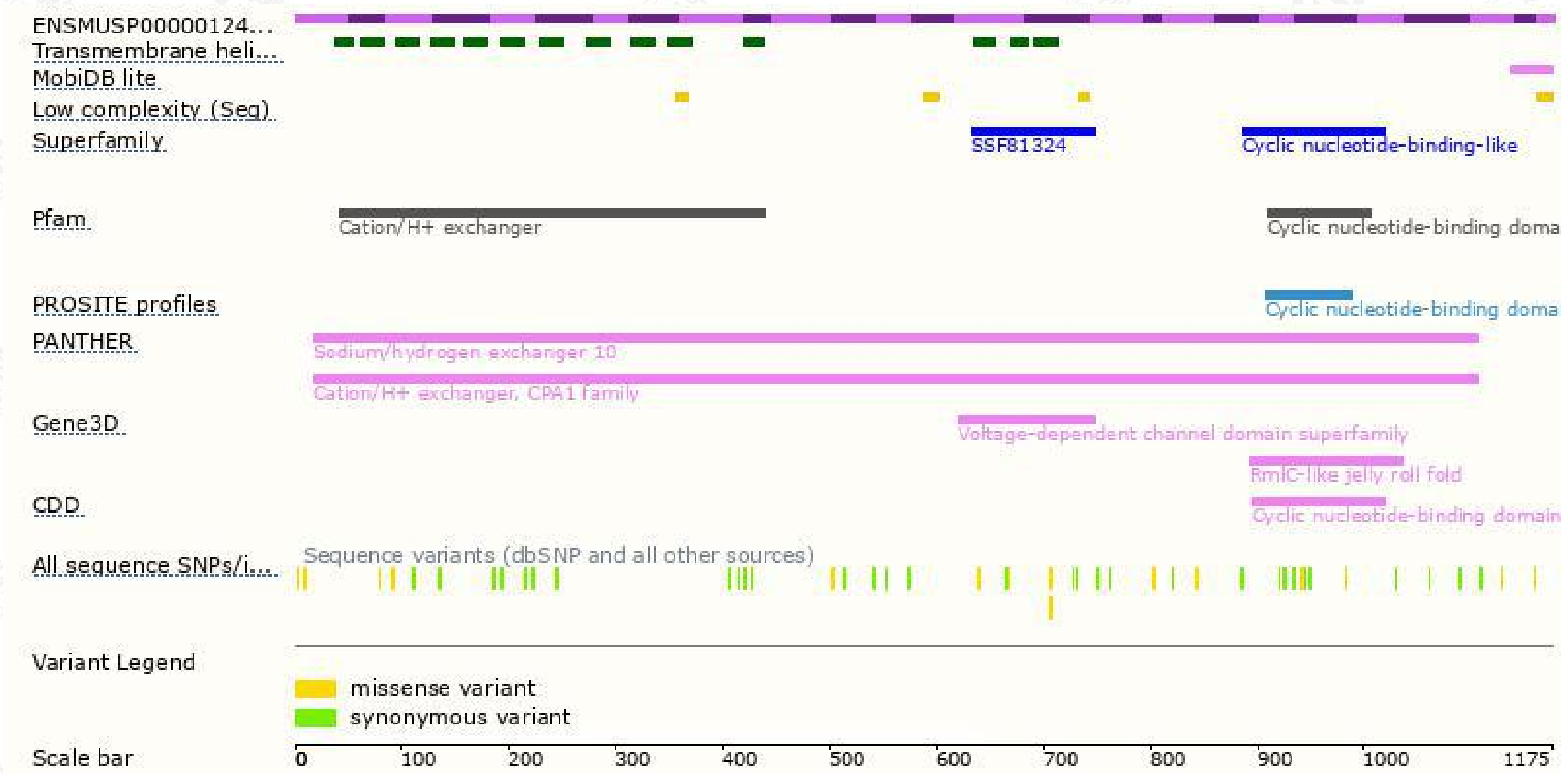
# Mouse phenotype description(MGI )



Phenotype Overview

*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 null mice display male infertility and asthenozoospermia.

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