# *Slc2a9* Cas9-KO Strategy

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# Project Overview

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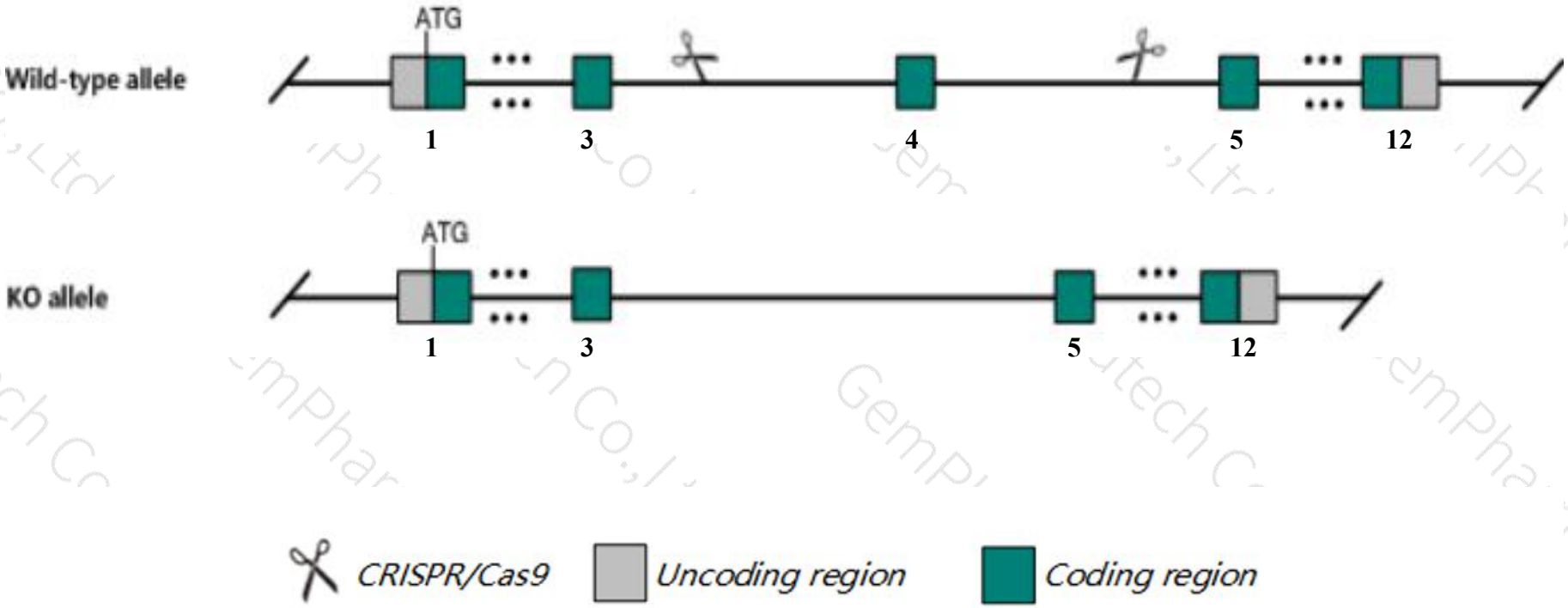
|---|---|
| **Project Name** | ***Slc2a9*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc2a9* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Slc2a9* gene has 12 transcripts. According to the structure of *Slc2a9* gene, exon4 of *Slc2a9-203*(ENSMUST00000067886.11) transcript is recommended as the knockout region.The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc2a9* 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.

# Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele show partial prenatal lethality, polydipsia, hyperuricemia, hyperuricosuria and polyuria, and develop urate nephropathy, characterized by obstructive lithiasis, tubulointerstitial inflammation, cortical fibrosis, renal insufficiency and reduced male weight.

➢ Transcript *Slc2a9-212* may not be affected.

➢ The *Slc2a9* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

## Slc2a9 solute carrier family 2 (facilitated glucose transporter), member 9 [ *Mus musculus* (house mouse) ]

Gene ID: 117591, updated on 26-Jun-2020

### Summary

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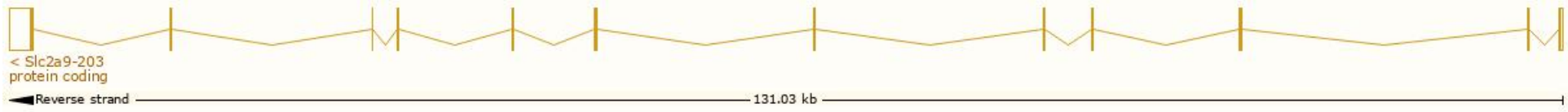
|---|---|
| **Official Symbol** | Slc2a9 provided by MGI |
| **Official Full Name** | solute carrier family 2 (facilitated glucose transporter), member 9 provided by MGI |
| **Primary source** | MGI:MGI:2152844 |
| **See related** | Ensembl:ENSMUSG00000005107 |
| **Gene type** | protein coding |
| **RefSeq 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** | Glut9; GLUT-9; SLC2A9B; SLC2a9A |
| **Expression** | Broad expression in liver adult (RPKM 6.8), large intestine adult (RPKM 5.0) and 16 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

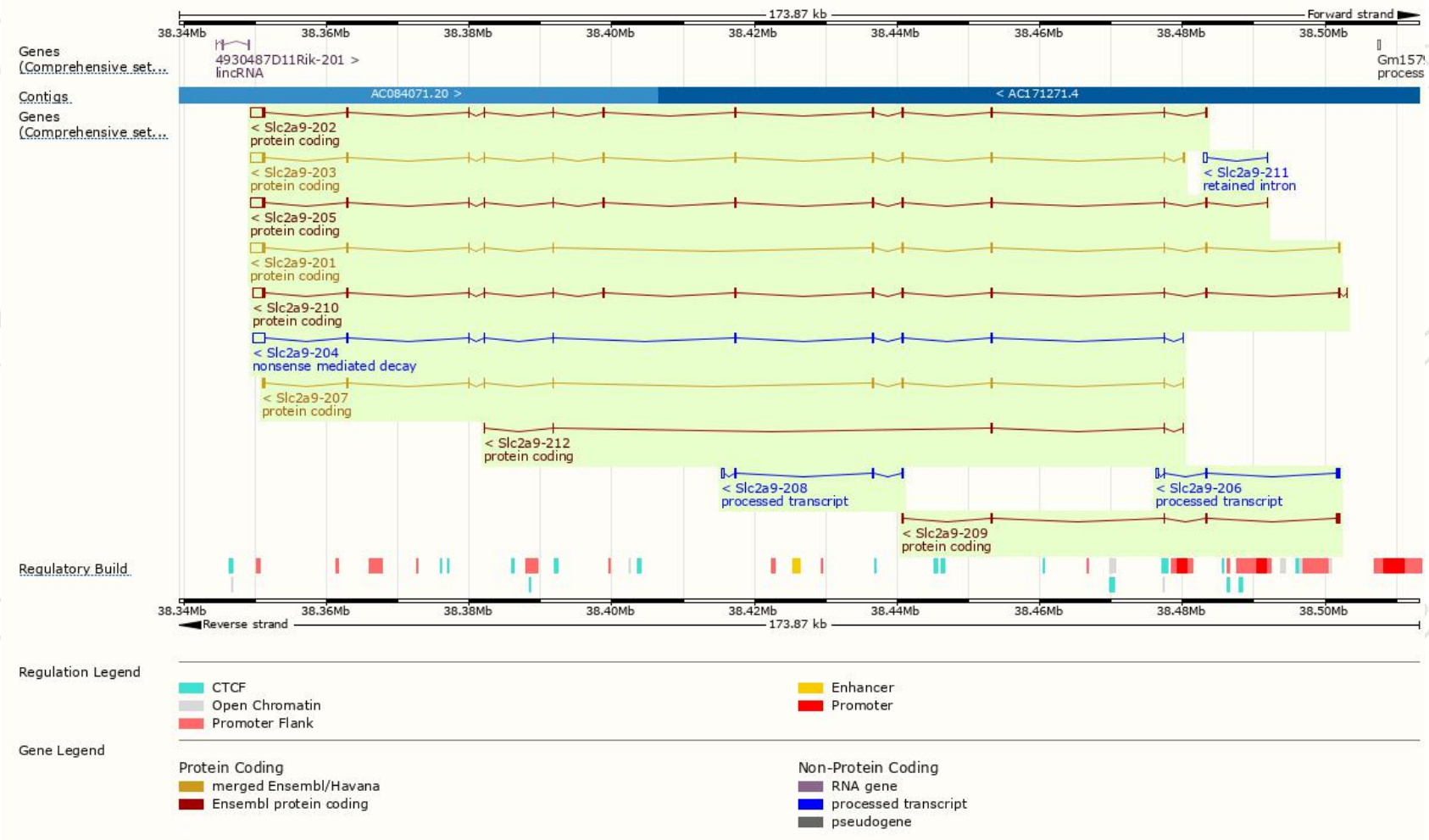
The gene has 12 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein ▲ | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Slc2a9-209 | ENSMUST00000147664.7 | 652 | 144aa | Protein coding | - | A0A5H1ZRL9 | CDS 3' incomplete TSL:2 |
| Slc2a9-212 | ENSMUST00000156272.7 | 526 | 158aa | Protein coding | - | A0A5H1ZRN5 | CDS 3' incomplete TSL:5 |
| Slc2a9-204 | ENSMUST00000122970.7 | 2900 | 281aa | Nonsense mediated decay | - | A0A5H1ZRL6 | TSL:1 |
| Slc2a9-201 | ENSMUST00000005238.12 | 3243 | 416aa | Protein coding | CCDS19256 | Q3T9X0 | TSL:1 GENCODE basic |
| Slc2a9-207 | ENSMUST00000143758.7 | 1296 | 431aa | Protein coding | CCDS51482 | Q3T9X0 | TSL:1 GENCODE basic |
| Slc2a9-205 | ENSMUST00000129099.7 | 3462 | 523aa | Protein coding | CCDS51484 | Q3T9X0 | TSL:5 GENCODE basic APPRIS ALT2 |
| Slc2a9-202 | ENSMUST00000067872.11 | 3403 | 523aa | Protein coding | CCDS51484 | Q3T9X0 | TSL:1 GENCODE basic APPRIS ALT2 |
| Slc2a9-210 | ENSMUST00000155634.7 | 3164 | 523aa | Protein coding | CCDS51484 | Q3T9X0 | TSL:5 GENCODE basic APPRIS ALT2 |
| Slc2a9-203 | ENSMUST00000067886.11 | 3602 | 538aa | Protein coding | CCDS51483 | Q3T9X0 | TSL:1 GENCODE basic APPRIS P4 |
| Slc2a9-206 | ENSMUST00000140462.1 | 776 | No protein | Processed transcript | - | - | TSL:3 |
| Slc2a9-208 | ENSMUST00000144290.1 | 770 | No protein | Processed transcript | - | - | TSL:3 |
| Slc2a9-211 | ENSMUST00000156076.1 | 427 | No protein | Retained intron | - | - | TSL:3 |

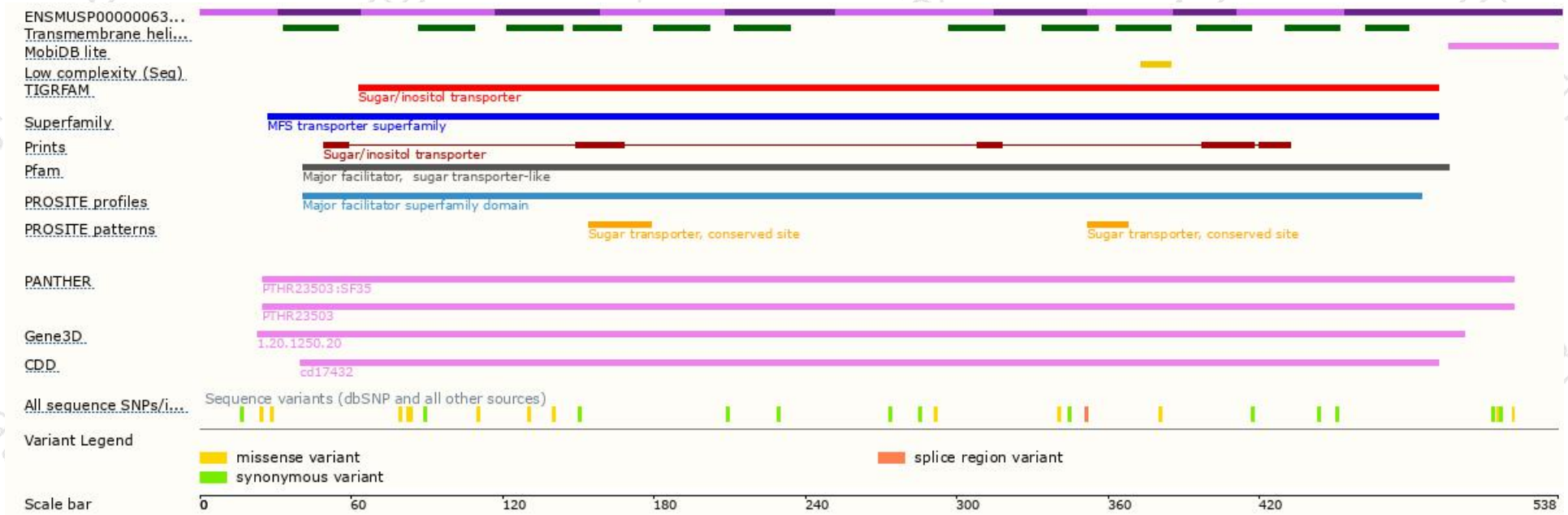
The strategy is based on the design of *Slc2a9-203* transcript,the transcription is shown below:



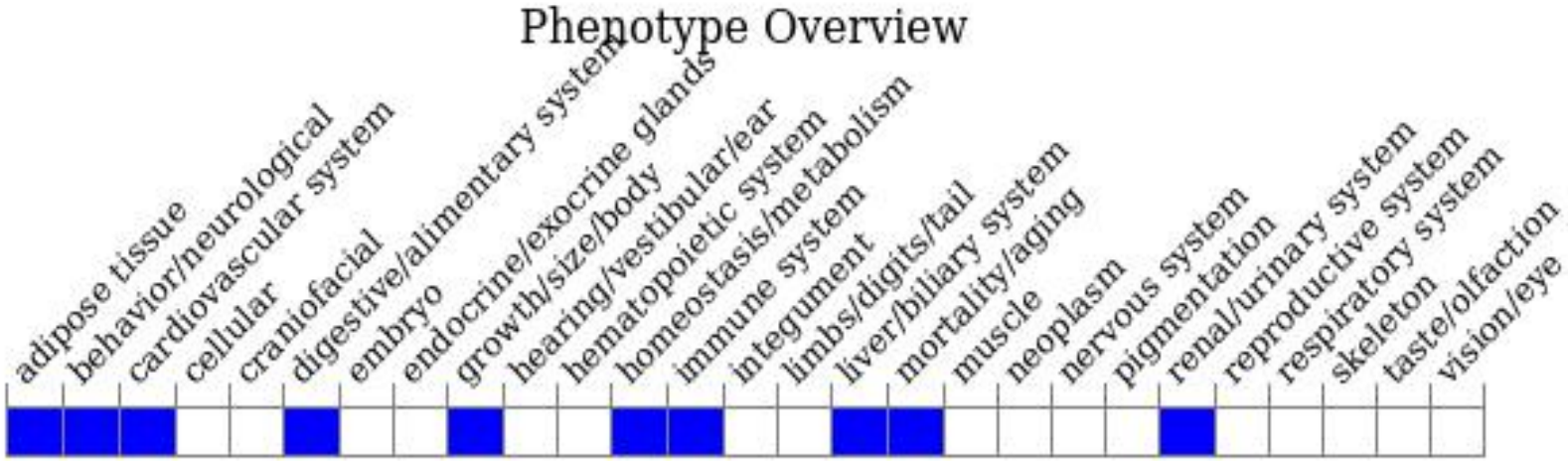
# Genomic location distribution



# 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 knock-out allele show partial prenatal lethality, polydipsia, hyperuricemia, hyperuricosuria and polyuria, and develop urate nephropathy, characterized by obstructive lithiasis, tubulointerstitial inflammation, cortical fibrosis, renal insufficiency and reduced male weight.

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

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