

# *Slc2a8* Cas9-KO Strategy

**Designer:**

**Yang Zeng**

**Reviewer:**

**Jia Yu**

**Design Date:**

**2020-2-10**

# Project Overview

**Project Name**

*Slc2a8*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc2a8* gene. The schematic diagram is as follows:



- The *Slc2a8* gene has 8 transcripts. According to the structure of *Slc2a8* gene, exon1-exon10 of *Slc2a8-201* (ENSMUST00000028129.12) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc2a8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for one null allele show reduced spermatozoan ATP levels, mitochondrial membrane potential and sperm motility, and a slight deviation from the expected Mendelian frequency. Homozygotes for another null allele show increased hippocampus cell proliferation and cardiac P-wave duration.
- The *Slc2a8* 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.



# Gene information (NCBI)

## Slc2a8 solute carrier family 2, (facilitated glucose transporter), member 8 [Mus musculus (house mouse)]

Gene ID: 56017, updated on 31-Jan-2019

### Summary



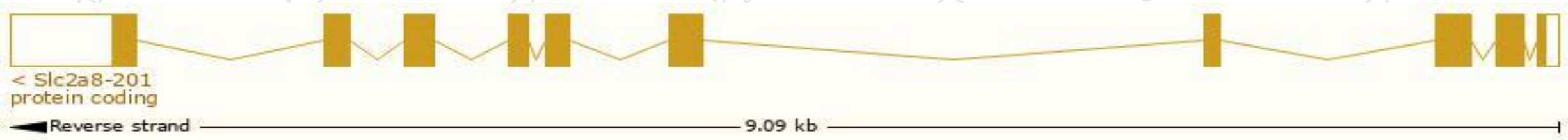
<b>Official Symbol</b>	Slc2a8 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 2, (facilitated glucose transporter), member 8 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1860103</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000026791</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>	D2Erd44e, GLUT8, GlutX1
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 64.4), ovary adult (RPKM 28.5) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

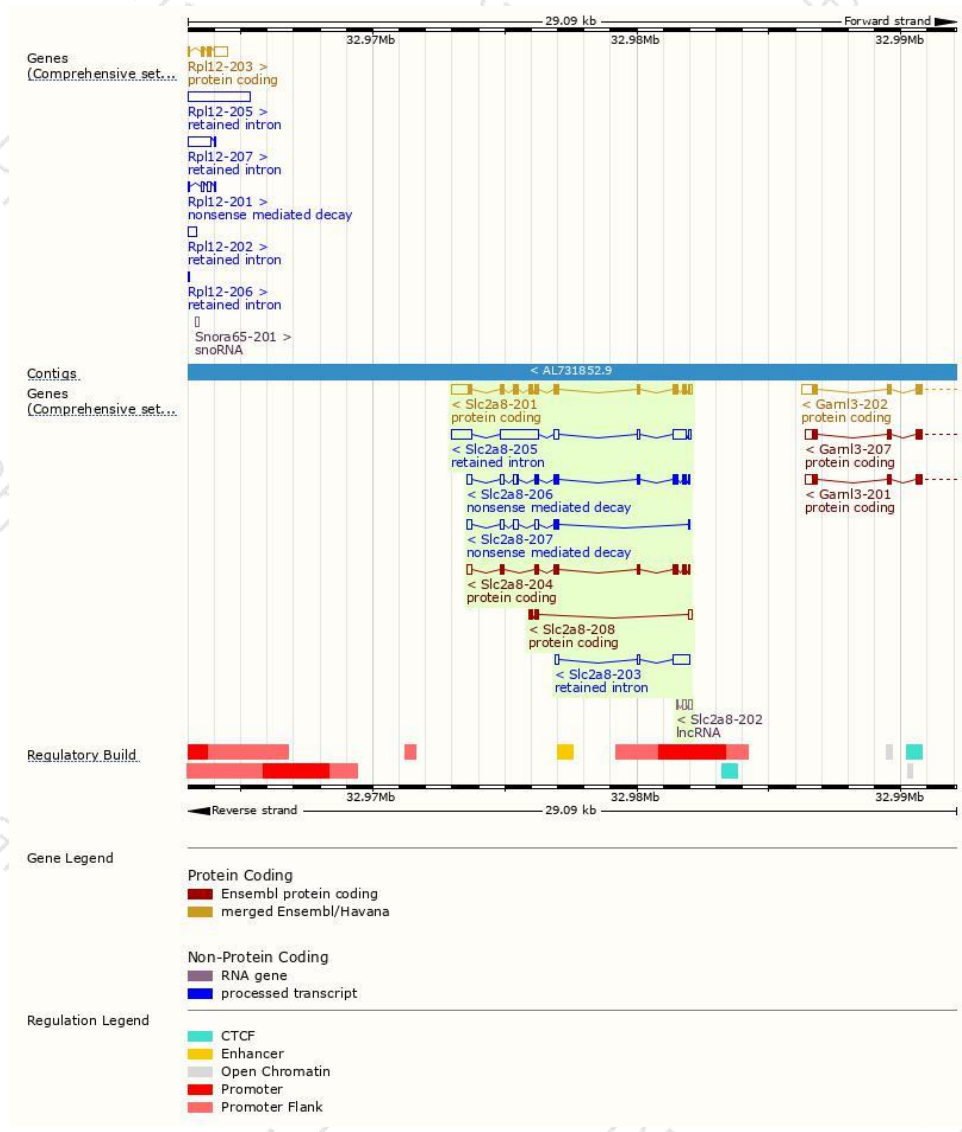
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc2a8-201	<a href="#">ENSMUST00000028129.12</a>	2108	<a href="#">477aa</a>	Protein coding	<a href="#">CCDS15937</a>	<a href="#">Q9JIF3</a>	TSL:1 GENCODE basic APPRIS P1
Slc2a8-204	<a href="#">ENSMUST00000153484.6</a>	1168	<a href="#">329aa</a>	Protein coding	-	<a href="#">Q2TK26</a>	TSL:1 GENCODE basic
Slc2a8-208	<a href="#">ENSMUST00000195863.1</a>	360	<a href="#">60aa</a>	Protein coding	-	<a href="#">A0A0A6YX81</a>	CDS 3' incomplete TSL:2
Slc2a8-206	<a href="#">ENSMUST00000193695.1</a>	1339	<a href="#">291aa</a>	Nonsense mediated decay	-	<a href="#">Q2TK27</a>	TSL:1
Slc2a8-207	<a href="#">ENSMUST00000194066.5</a>	869	<a href="#">71aa</a>	Nonsense mediated decay	-	<a href="#">A0A0A6YXF7</a>	TSL:1
Slc2a8-205	<a href="#">ENSMUST00000191777.5</a>	3120	No protein	Retained intron	-	-	TSL:2
Slc2a8-203	<a href="#">ENSMUST00000130769.1</a>	909	No protein	Retained intron	-	-	TSL:2
Slc2a8-202	<a href="#">ENSMUST00000123643.1</a>	343	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Slc2a8-201* transcript,The transcription is shown below



# Genomic location distribution

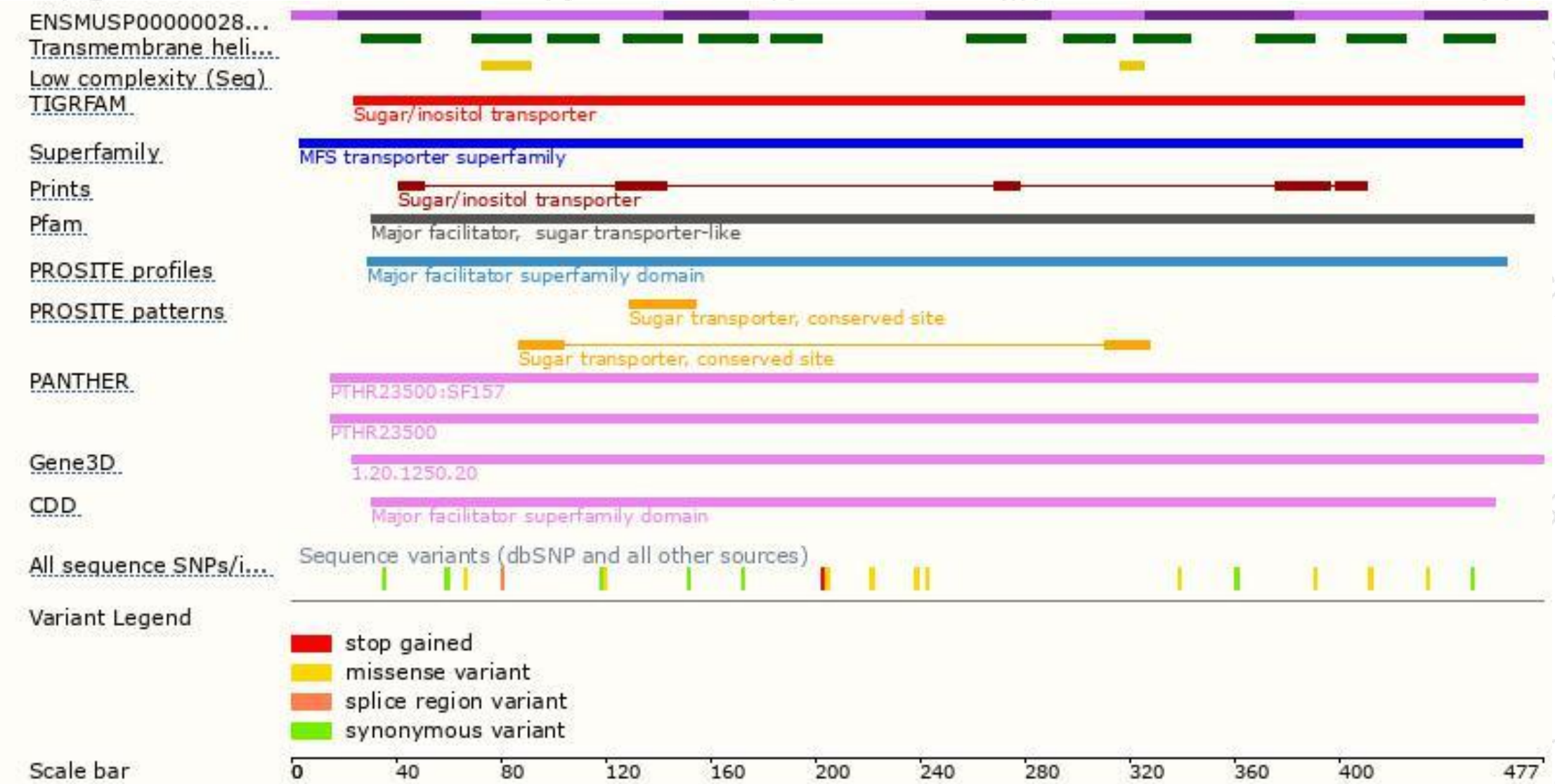




# Protein domain



集萃药康  
GemPharmatech



# 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, Homozygotes for one null allele show reduced spermatozoan ATP levels, mitochondrial membrane potential and sperm motility, and a slight deviation from the expected Mendelian frequency. Homozygotes for another null allele show increased hippocampus cell proliferation and cardiac P-wave duration.

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

Tel: 400-9660890

