

Slc9a3r2 Cas9-KO Strategy

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Project Overview

Project Name

Slc9a3r2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc9a3r2* gene. The schematic diagram is as follows:



- The *Slc9a3r2* gene has 7 transcripts. According to the structure of *Slc9a3r2* gene, exon1-exon5 of *Slc9a3r2-201* (ENSMUST00000002572.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc9a3r2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele are viable, fertile and overtly normal and display normal cAMP- and cGMP-activated CFTR transepithelial chloride transport and bicarbonate secretion in the small intestine.
- The *Slc9a3r2* gene is located on the Chr17. 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)

Slc9a3r2 solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 [Mus musculus (house mouse)]

Gene ID: 65962, updated on 19-Mar-2019

Summary



Official Symbol Slc9a3r2 provided by [MGI](#)

Official Full Name solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 provided by [MGI](#)

Primary source [MGI:MGI:1890662](#)

See related [Ensembl:ENSMUSG000000002504](#)

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 0610011L07Rik, 1200011K07Rik, 2010007A20Rik, E3karp, NHERF-2, Nherf2, Octs2, Sip-1, Sip1, Sryip1, Tka-1

Expression Broad expression in lung adult (RPKM 219.2), ovary adult (RPKM 58.5) and 18 other tissues [See more](#)

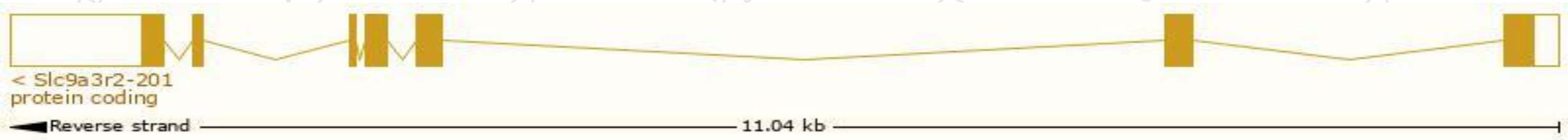
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

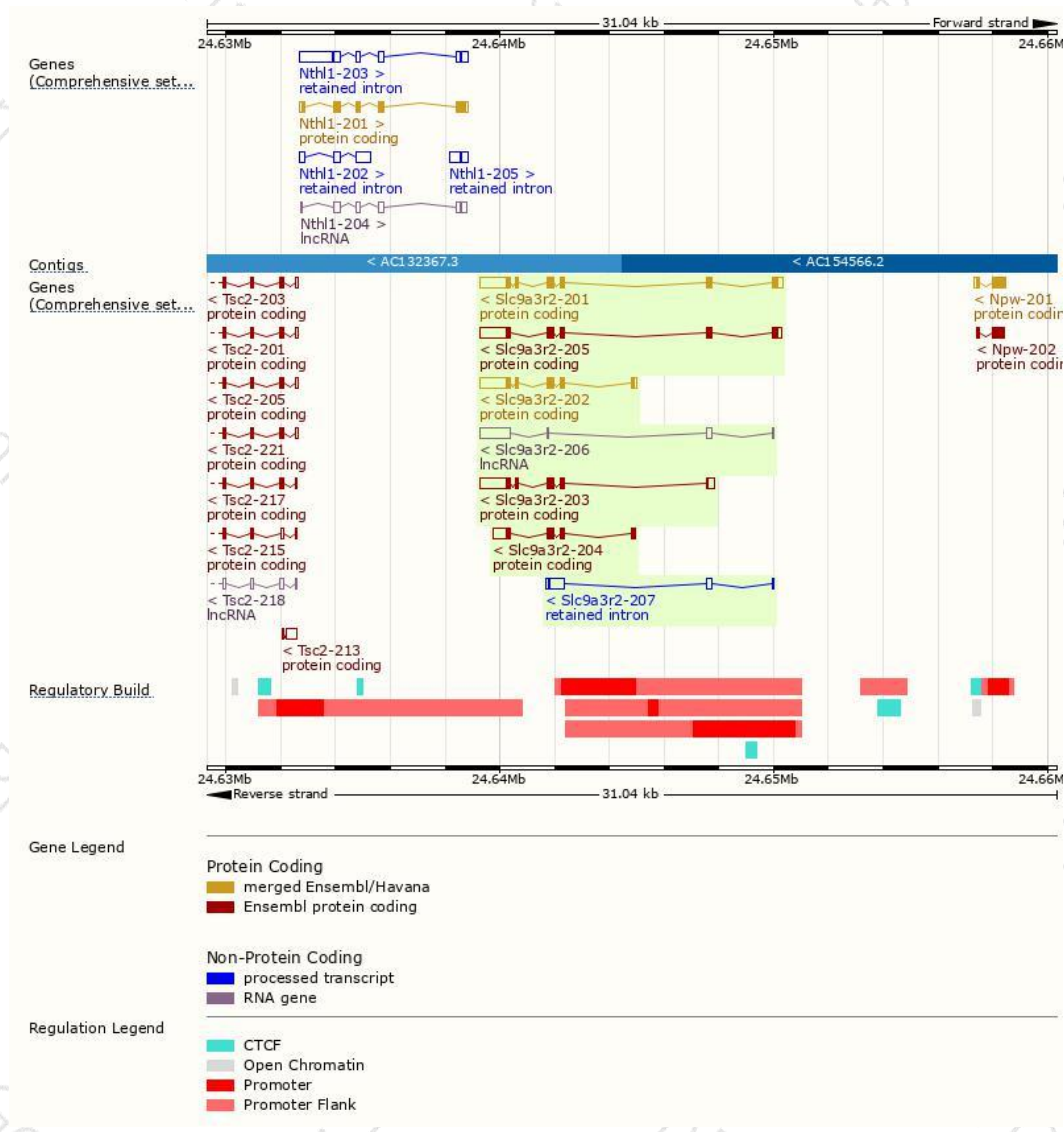
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc9a3r2-201	ENSMUST00000002572.5	2136	337aa	Protein coding	CCDS28488	A0A0R4IZX2	TSL:1 GENCODE basic APPRIS P1
Slc9a3r2-202	ENSMUST00000019684.12	1717	226aa	Protein coding	CCDS28489	A0A0R4J006	TSL:1 GENCODE basic
Slc9a3r2-205	ENSMUST00000234557.1	2035	316aa	Protein coding	-	Q6NS54	GENCODE basic
Slc9a3r2-203	ENSMUST00000234121.1	1840	231aa	Protein coding	-	-	GENCODE basic
Slc9a3r2-204	ENSMUST00000234505.1	1137	205aa	Protein coding	-	-	GENCODE basic
Slc9a3r2-207	ENSMUST00000235042.1	874	No protein	Retained intron	-	-	
Slc9a3r2-206	ENSMUST00000234912.1	1420	No protein	lncRNA	-	-	

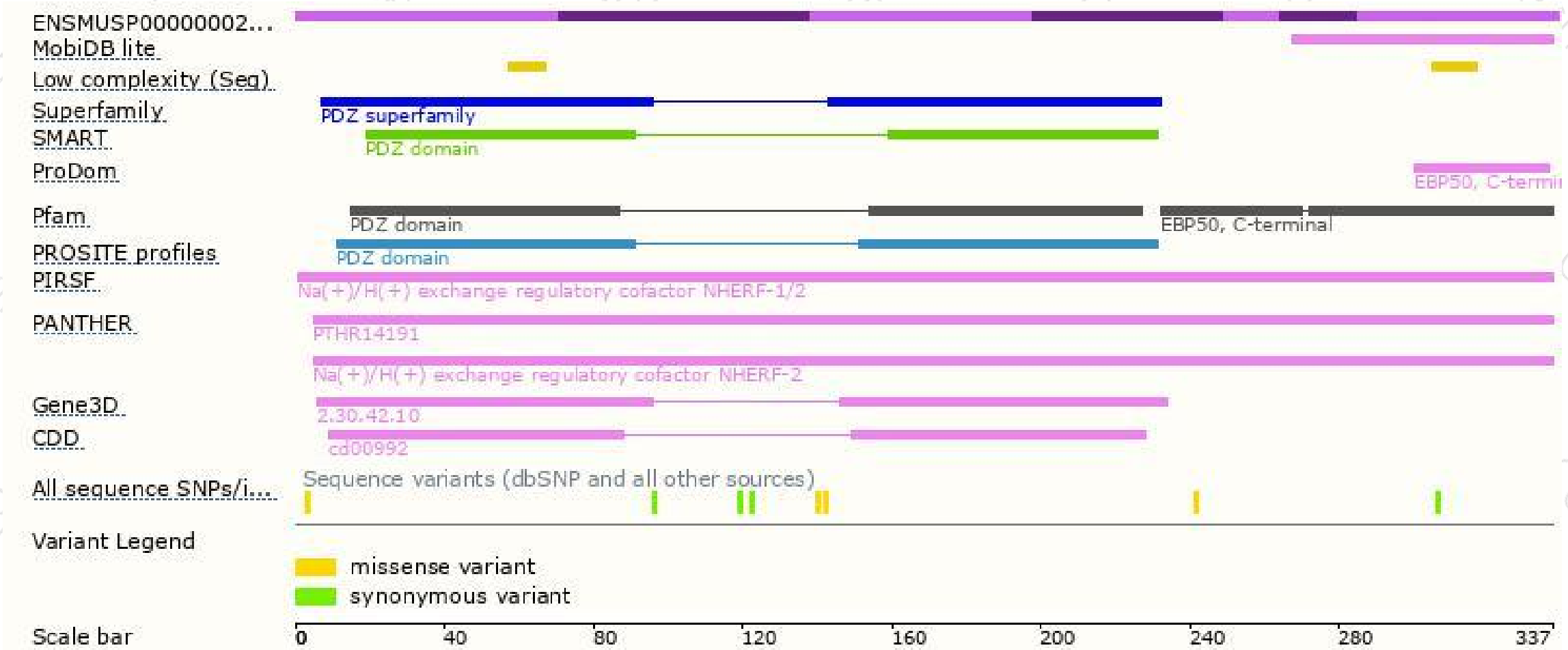
The strategy is based on the design of *Slc9a3r2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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