

Slc9b1 Cas9-CKO Strategy

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Design Date: 2020-3-4

Project Overview



Project Name

Slc9b1

Project type

Cas9-CKO

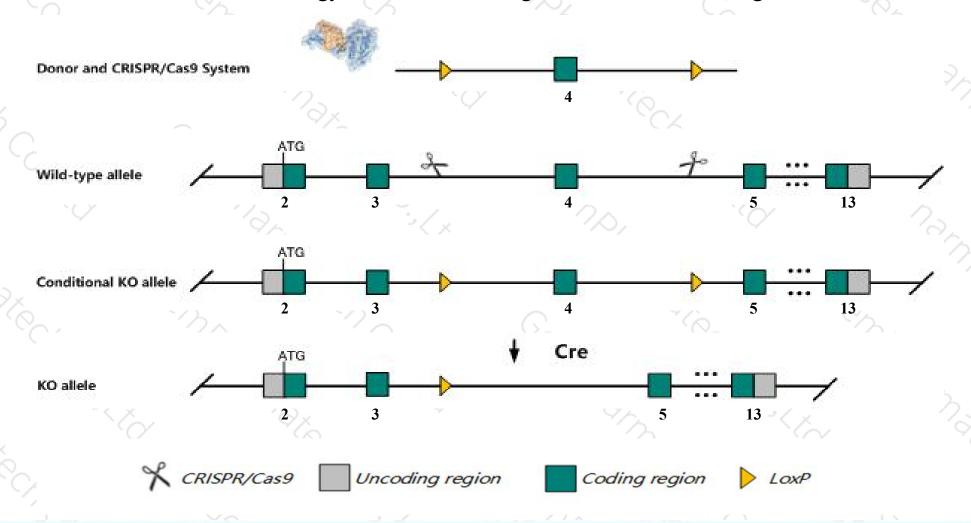
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Slc9b1 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Slc9b1* gene has 9 transcripts. According to the structure of *Slc9b1* gene, exon4 of *Slc9b1-201*(ENSMUST00000078568.11) transcript is recommended as the knockout region. The region contains 298bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Slc9b1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice



- ➤ The *Slc9b1* gene is located on the Chr3. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



SIc9b1 solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1 [Mus musculus (house mouse)]

Gene ID: 74446, updated on 19-Feb-2019

Summary



Official Symbol Slc9b1 provided by MGI

Official Full Name solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1 provided by MGI

Primary source MGI:MGI:1921696

See related Ensembl:ENSMUSG00000050150

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 1700094G20Rik, 4933424B12Rik, 4933425K02Rik, Nhedc1, mtsNHE

Expression Restricted expression toward testis adult (RPKM 25.1)See more

Orthologs human all

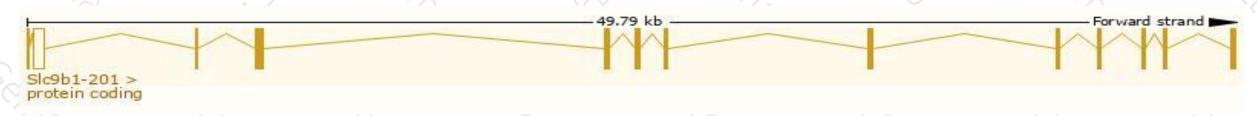
Transcript information (Ensembl)



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

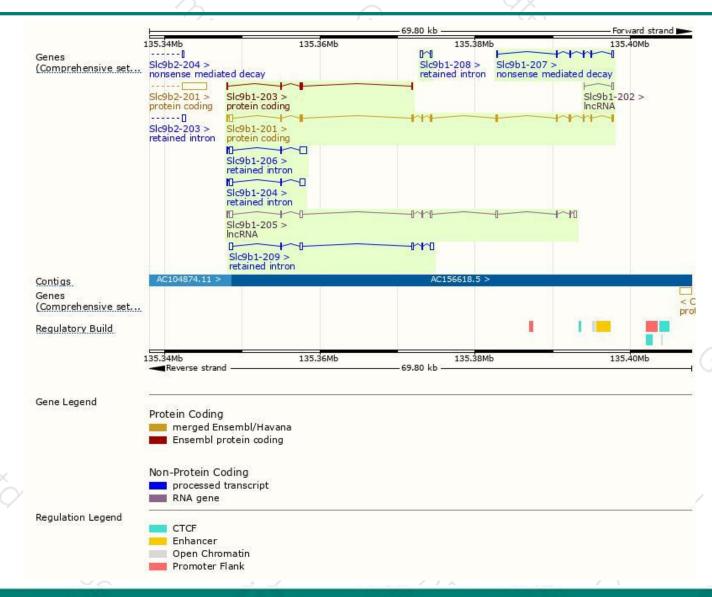
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Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000078568.11	2248	565aa	Protein coding	CCDS17855	G5E8I2	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000159658.7	588	<u>144aa</u>	Protein coding	6.70	E0CY67	CDS 3' incomplete TSL:2
ENSMUST00000161417.5	783	<u>88aa</u>	Nonsense mediated decay	120	F7CTY9	CDS 5' incomplete TSL:5
ENSMUST00000162767.1	1545	No protein	Retained intron	VeV	2	TSL:1
ENSMUST00000160941.7	1407	No protein	Retained intron	153		TSL:1
ENSMUST00000160047.7	1196	No protein	Retained intron	6.00		TSL:1
ENSMUST00000161506.1	492	No protein	Retained intron	120	ů.	TSL:3
ENSMUST00000160460.7	2072	No protein	IncRNA	160	-	TSL:1
ENSMUST00000159276.2	294	No protein	IncRNA	1153	5	TSL:3
	ENSMUST00000159658.7 ENSMUST00000161417.5 ENSMUST00000162767.1 ENSMUST00000160941.7 ENSMUST00000160047.7 ENSMUST00000161506.1 ENSMUST00000160460.7	ENSMUST000001658.11 2248 ENSMUST00000159658.7 588 ENSMUST00000161417.5 783 ENSMUST00000162767.1 1545 ENSMUST00000160941.7 1407 ENSMUST00000160047.7 1196 ENSMUST00000161506.1 492 ENSMUST00000160460.7 2072	ENSMUST00000078568.11 2248 565aa ENSMUST00000159658.7 588 144aa ENSMUST00000161417.5 783 88aa ENSMUST00000162767.1 1545 No protein ENSMUST00000160941.7 1407 No protein ENSMUST00000160047.7 1196 No protein ENSMUST00000161506.1 492 No protein ENSMUST00000160460.7 2072 No protein	ENSMUST00000078568.11 2248 565aa Protein coding ENSMUST00000159658.7 588 144aa Protein coding ENSMUST00000161417.5 783 88aa Nonsense mediated decay ENSMUST00000162767.1 1545 No protein Retained intron ENSMUST00000160941.7 1407 No protein Retained intron ENSMUST00000160047.7 1196 No protein Retained intron ENSMUST00000161506.1 492 No protein Retained intron ENSMUST00000160460.7 2072 No protein IncRNA	ENSMUST00000078568.11 2248 565aa Protein coding CCDS17855 ENSMUST00000159658.7 588 144aa Protein coding - ENSMUST00000161417.5 783 88aa Nonsense mediated decay - ENSMUST00000162767.1 1545 No protein Retained intron - ENSMUST00000160941.7 1407 No protein Retained intron - ENSMUST00000160047.7 1196 No protein Retained intron - ENSMUST00000160460.7 492 No protein Retained intron - ENSMUST00000160460.7 2072 No protein IncRNA -	ENSMUST00000078568.11 2248 565aa Protein coding CCDS17855 G5E8I2 ENSMUST00000159658.7 588 144aa Protein coding - E0CY67 ENSMUST00000161417.5 783 88aa Nonsense mediated decay - F7CTY9 ENSMUST00000162767.1 1545 No protein Retained intron - - ENSMUST00000160941.7 1407 No protein Retained intron - - ENSMUST00000160047.7 1196 No protein Retained intron - - ENSMUST00000160460.1 492 No protein Retained intron - - ENSMUST00000160460.7 2072 No protein IncRNA - -

The strategy is based on the design of Slc9b1-201 transcript, The transcription is shown below



Genomic location distribution





Protein domain







If you have any questions, you are welcome to inquire. Tel: 400-9660890





