

Slc7a4 Cas9-KO Strategy

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Design Date: 2024-4-24

Overview

Target Gene Name

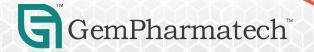
• Slc7a4

Project Type

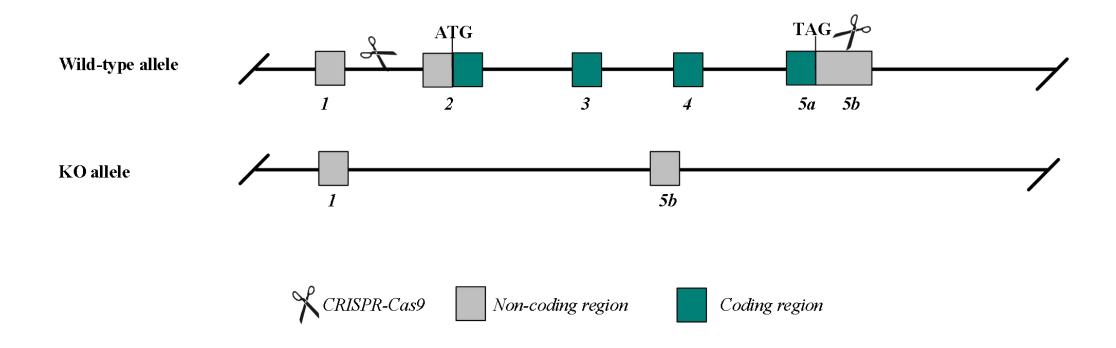
• Cas9-KO

Genetic Background

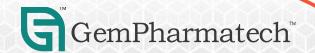
• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Slc7a4 gene.



Technical Information

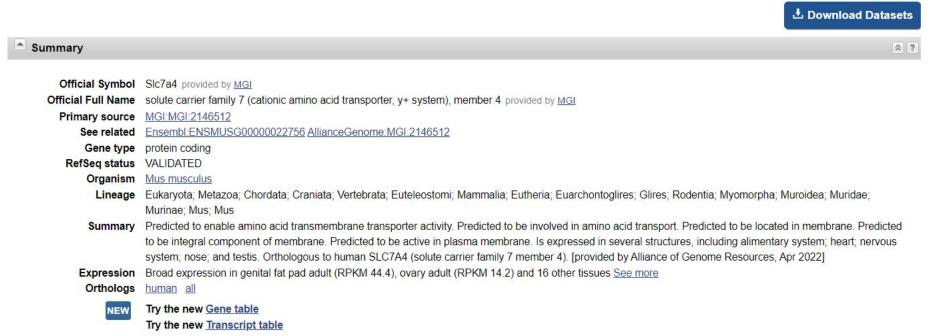
- The *Slc7a4* gene has 11 transcripts. According to the structure of *Slc7a4* gene, exon 2-exon 5 of *Slc7a4*-202 (ENSMUST00000172164.10) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Slc7a4* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 ontarget amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



Gene Information

Slc7a4 solute carrier family 7 (cationic amino acid transporter, y+ system), member 4 [Mus musculus (house mouse)]

Gene ID: 224022, updated on 11-Apr-2024



Source: https://www.ncbi.nlm.nih.gov/

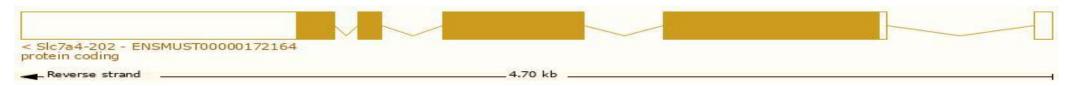


Transcript Information

The gene has 11 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden)								Filter
Transcript ID		Name	bp 🍦	Protein	Biotype	CCDS 🍦	UniProt Match	Flags
NSMUST0000006354	4.11	Slc7a4-201	2758	<u>635aa</u>	Protein coding	CCDS28008 ₽	Q8BLQ7₽	GENCODE basic APPRIS P1 TSL:1
NSMUST0000017216	4.10	Slc7a4-202	3281	<u>635aa</u>	Protein coding	CCDS28008 ₽	Q8BLQ7@	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST0000023128	33.2	Slc7a4-203	455	<u>117aa</u>	Protein coding		A0A338P685₺	CDS 3' incomplete
ENSMUST0000023155	52.2	Slc7a4-204	596	140aa	Protein coding		<u>A0A338P740</u> @	CDS 3' incomplete
ENSMUST000002316	15.2	Slc7a4-205	1711	<u>430aa</u>	Protein coding		A0A338P754@	GENCODE basic
ENSMUST0000023164	15.2	Slc7a4-206	763	242aa	Protein coding		A0A338P6C5₽	CDS 3' incomplete
ENSMUST0000023218	36.2	Slc7a4-207	440	<u>76aa</u>	Protein coding		A0A338P6V0 ₽	CDS 3' incomplete
ENSMUST0000023222	26.2	Slc7a4-208	1920	<u>452aa</u>	Protein coding		Q91WD3@	GENCODE basic
ENSMUST0000023233	36.2	Slc7a4-209	435	81aa	Protein coding		A0A338P7B4₽	CDS 3' incomplete
ENSMUST0000023238	35.2	Slc7a4-210	1714	<u>430aa</u>	Protein coding		A0A338P754₽	GENCODE basic
ENSMUST0000023242	29.2	Slc7a4-211	2577	No protein	Retained intron		-	-

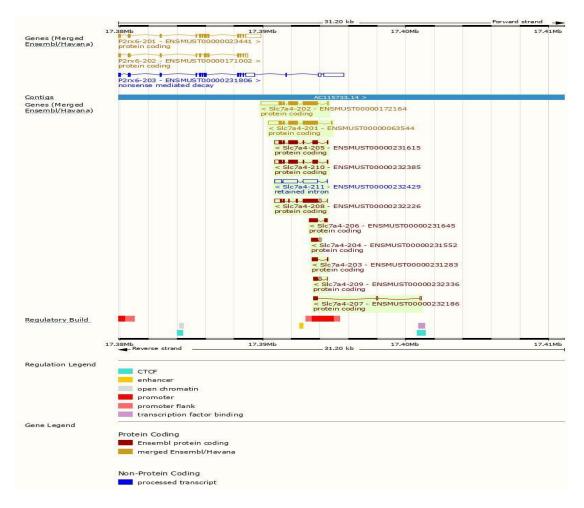
The strategy is based on the design of *Slc7a4*-202 transcript, the transcription is shown below:



Source: https://www.ensembl.org



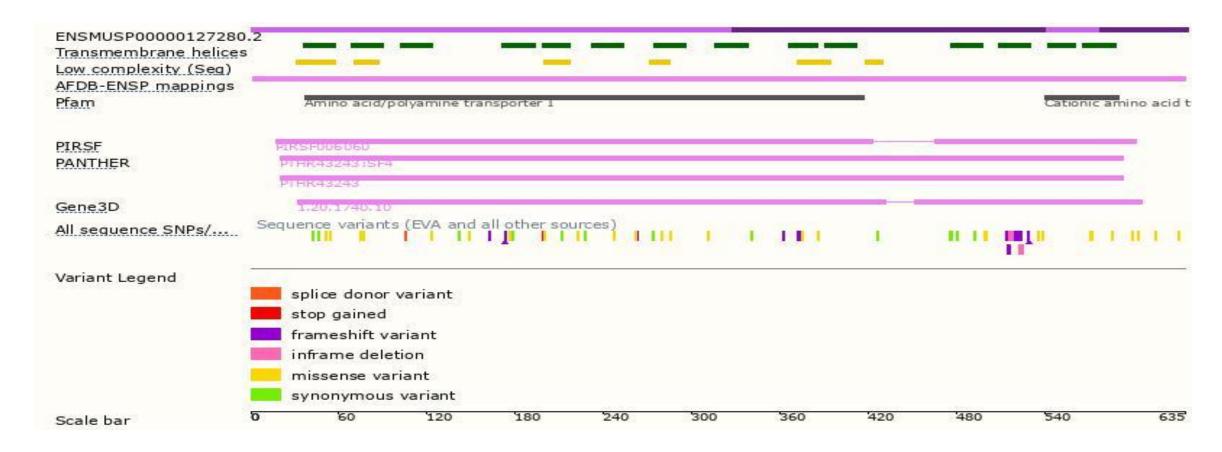
Genomic Information





Source: : https://www.ensembl.org

Protein Information





Source: : https://www.ensembl.org

Important Information

- Transcript *Slc7a4*-203&*Slc7a4*-204&*Slc7a4*-206&*Slc7a4*-207&*Slc7a4*-209 may not be affected.
- The KO region contains the functional region of the P2rx6 gene. Knockout the region may affect its function of P2rx6 gene.
- *Slc7a4* is located on Chr16. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

