

# *Slc7a3* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Slc7a3*

**Project type**

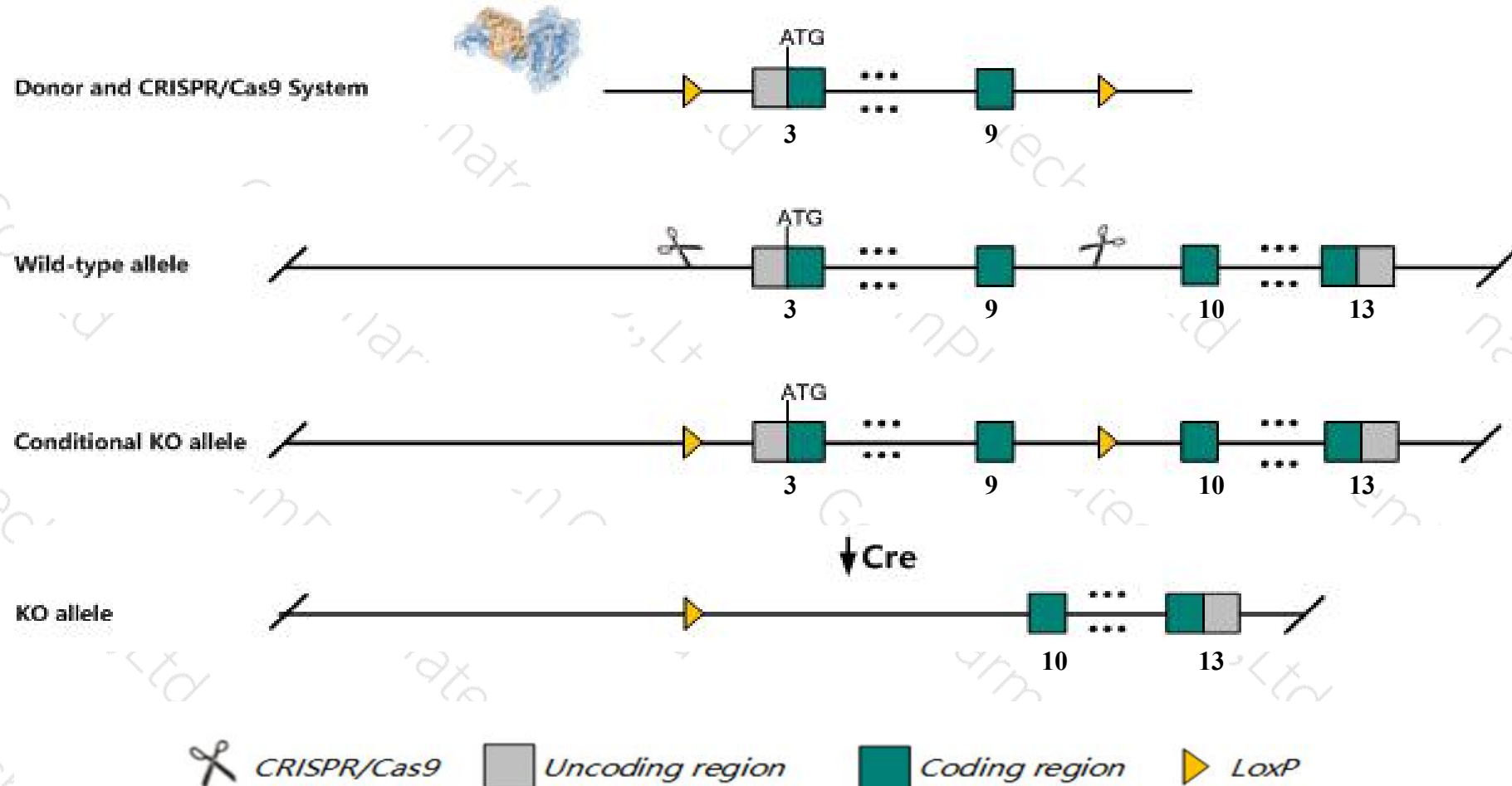
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a3* gene. The schematic diagram is as follows:



- The *Slc7a3* gene has 7 transcripts. According to the structure of *Slc7a3* gene, exon3-exon9 of *Slc7a3*-203 (ENSMUST00000113710.7) 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 *Slc7a3* 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 *Slc7a3* gene is located on the ChrX. 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)

**Slc7a3** solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 [ *Mus musculus* (house mouse) ]

Gene ID: 11989, updated on 14-Aug-2019

## Summary

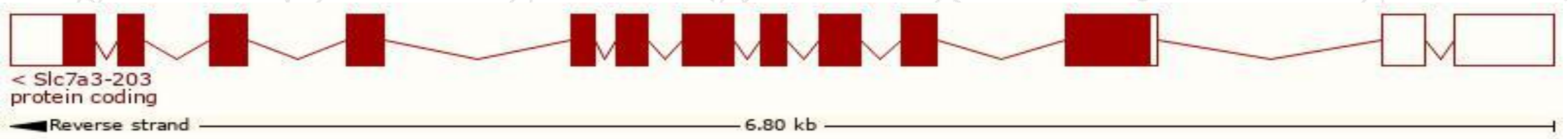
Official Symbol	Slc7a3 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 provided by MGI
Primary source	MGI:MGI:1100521
See related	Ensembl:ENSMUSG00000031297
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CAT3; Atrc3; CAT-3; SLC7A1; SLC7A2
Summary	The protein encoded by this gene is a member of the system y+ cationic amino acid transporter family. Proteins of this family allow uptake of arginine from extracellular media. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2014]
Expression	Broad expression in CNS E18 (RPKM 4.8), limb E14.5 (RPKM 1.7) and 17 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

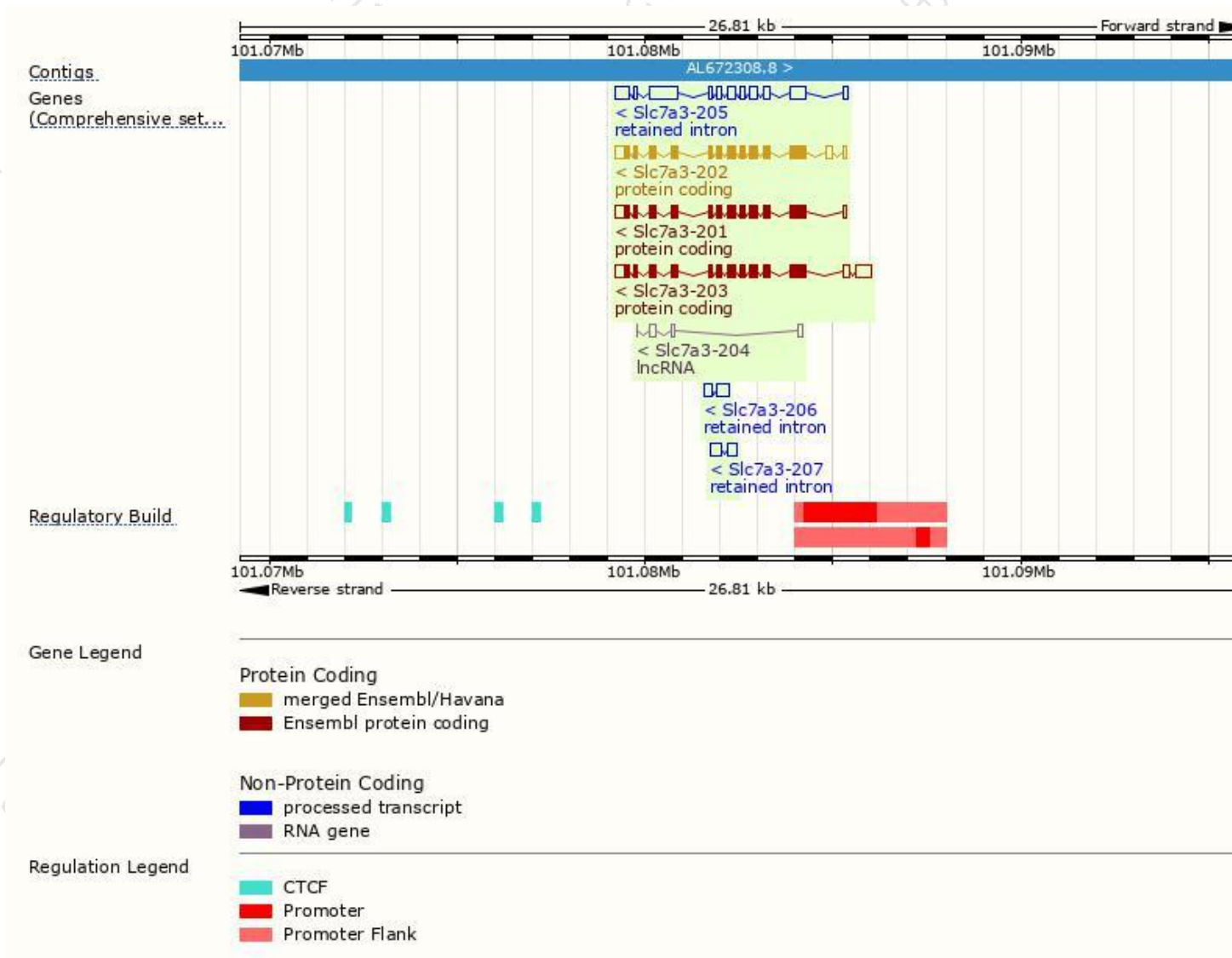
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a3-203	<a href="#">ENSMUST00000113710.7</a>	2750	<a href="#">618aa</a>	Protein coding	<a href="#">CCDS30309</a>	<a href="#">P70423</a>	TSL:5 GENCODE basic APPRIS P1
Slc7a3-202	<a href="#">ENSMUST00000101362.7</a>	2371	<a href="#">618aa</a>	Protein coding	<a href="#">CCDS30309</a>	<a href="#">P70423</a>	TSL:1 GENCODE basic APPRIS P1
Slc7a3-201	<a href="#">ENSMUST00000073927.4</a>	2232	<a href="#">618aa</a>	Protein coding	<a href="#">CCDS30309</a>	<a href="#">P70423</a>	TSL:1 GENCODE basic APPRIS P1
Slc7a3-205	<a href="#">ENSMUST00000138162.1</a>	2717	No protein	Retained intron	-	-	TSL:2
Slc7a3-206	<a href="#">ENSMUST00000144410.1</a>	570	No protein	Retained intron	-	-	TSL:2
Slc7a3-207	<a href="#">ENSMUST00000151922.1</a>	544	No protein	Retained intron	-	-	TSL:3
Slc7a3-204	<a href="#">ENSMUST00000126282.1</a>	367	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Slc7a3-203* transcript,The transcription is shown below

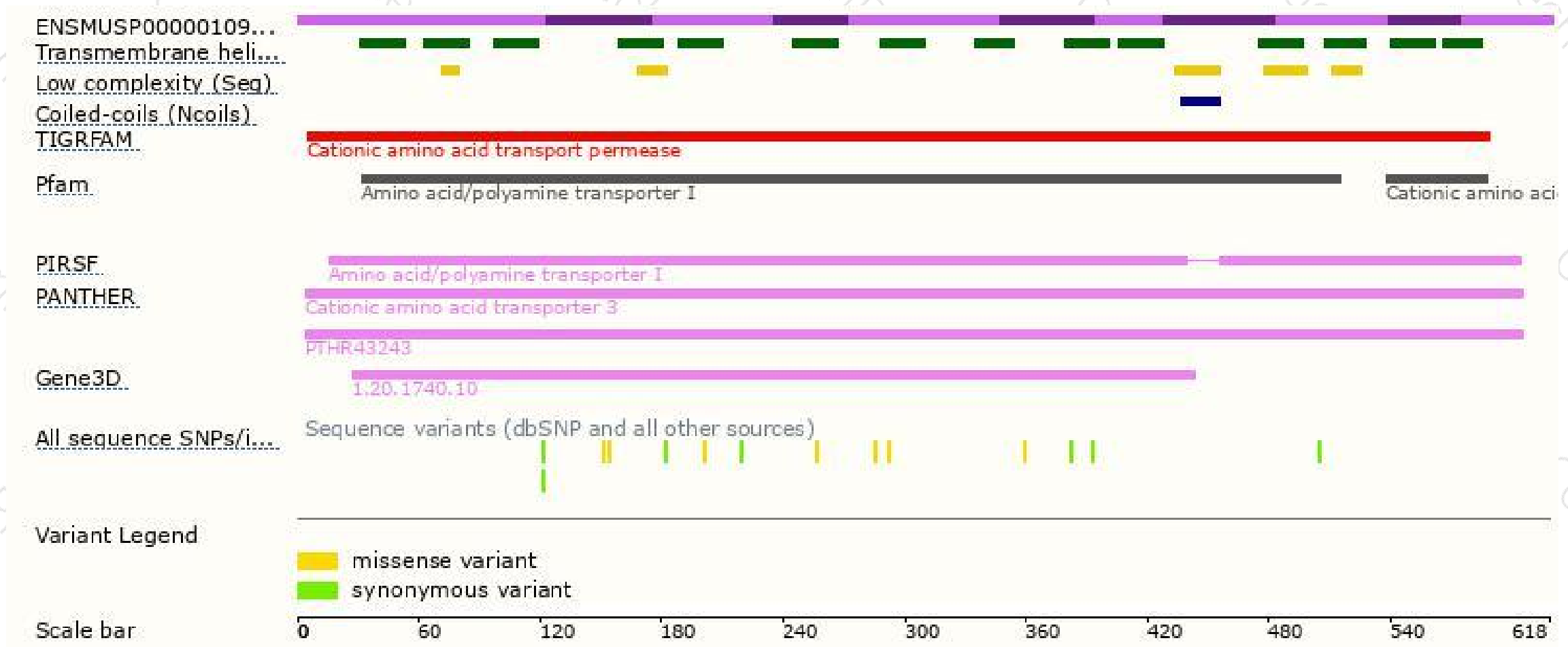


# Genomic location distribution





# Protein domain



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

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