

Slc11a1 Cas9-CKO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

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Project Overview

Project Name

Slc11a1

Project type

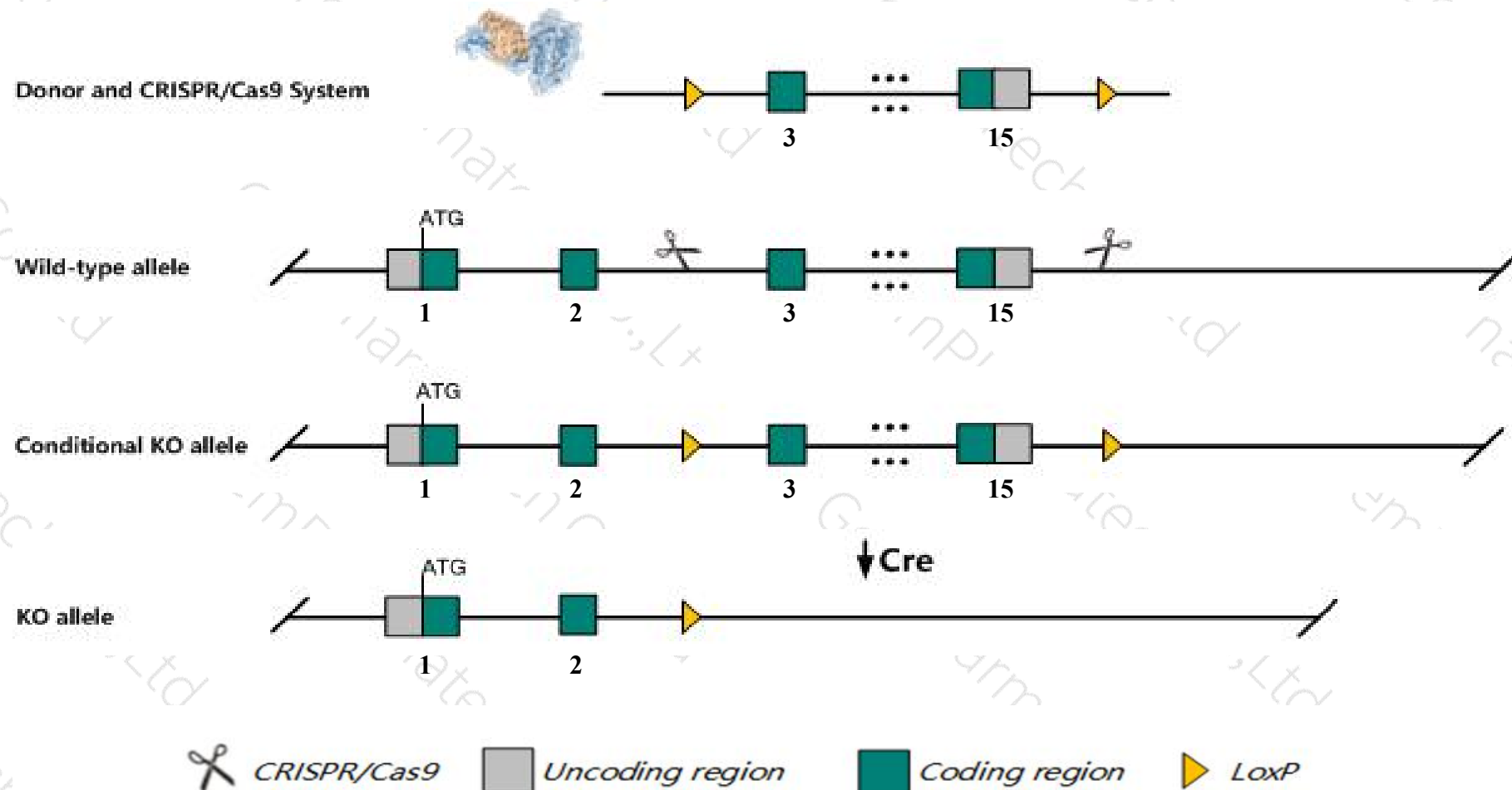
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc11a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slc11a1* gene has 11 transcripts. According to the structure of *Slc11a1* gene, exon3-exon15 of *Slc11a1-201* (ENSMUST00000027368.5) transcript is recommended as the knockout region. The region contains most 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 *Slc11a1* 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.

- According to the existing MGI data, Mutations in this gene are associated with susceptibility to infection with pathogens, including Myobacterium, Salmonella and Leishmania. Depending on the mutation, mutants may exhibit either increased or decreased susceptibility to infection.
- The *Slc11a1* gene is located on the Chr1. 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)

Slc11a1 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 [*Mus musculus* (house mouse)]

Gene ID: 18173, updated on 12-Aug-2019

Summary

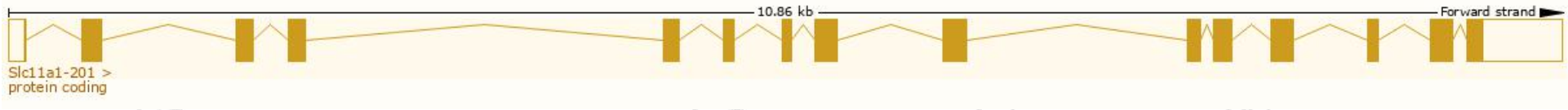
Official Symbol	Slc11a1 provided by MGI
Official Full Name	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 provided by MGI
Primary source	MGI:MGI:1345275
See related	Ensembl:ENSMUSG00000026177
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bcg; Ity; Lsh; ity; Ity1; Nramp; Nramp1
Expression	Broad expression in spleen adult (RPKM 37.5), mammary gland adult (RPKM 13.7) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

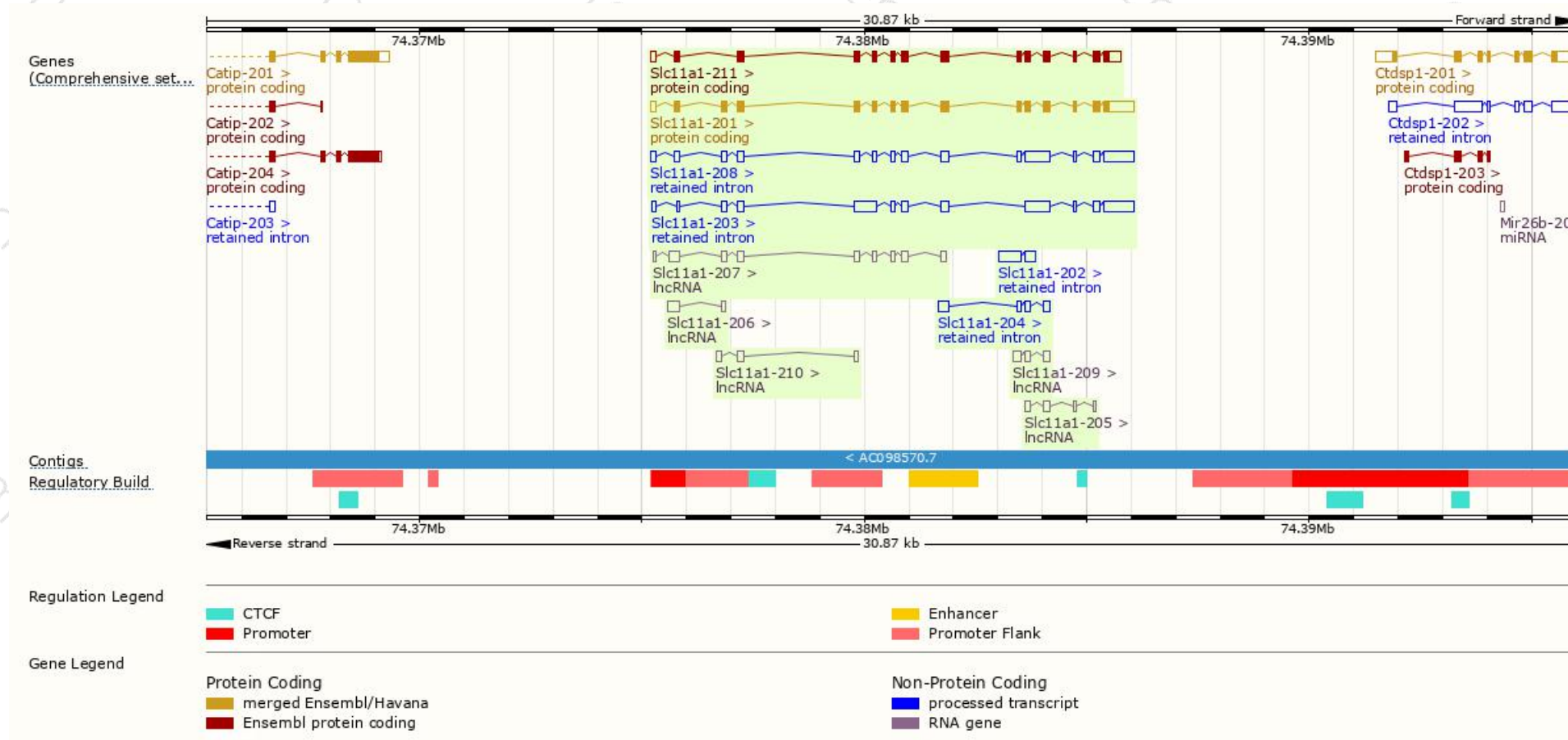
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc11a1-201	ENSMUST00000027368.5	2315	548aa	Protein coding	CCDS15047	P41251	TSL:1 GENCODE basic APPRIS P2
Slc11a1-211	ENSMUST00000187516.6	1893	507aa	Protein coding	-	A0A087WNR0	TSL:5 GENCODE basic APPRIS ALT2
Slc11a1-203	ENSMUST00000131511.7	2726	No protein	Retained intron	-	-	TSL:2
Slc11a1-208	ENSMUST00000147233.7	2584	No protein	Retained intron	-	-	TSL:2
Slc11a1-202	ENSMUST00000127487.1	704	No protein	Retained intron	-	-	TSL:3
Slc11a1-204	ENSMUST00000133896.7	604	No protein	Retained intron	-	-	TSL:5
Slc11a1-207	ENSMUST00000136786.7	1055	No protein	lncRNA	-	-	TSL:5
Slc11a1-209	ENSMUST00000149166.7	457	No protein	lncRNA	-	-	TSL:2
Slc11a1-205	ENSMUST00000134189.1	426	No protein	lncRNA	-	-	TSL:5
Slc11a1-206	ENSMUST00000135137.1	378	No protein	lncRNA	-	-	TSL:2
Slc11a1-210	ENSMUST00000155865.1	331	No protein	lncRNA	-	-	TSL:3

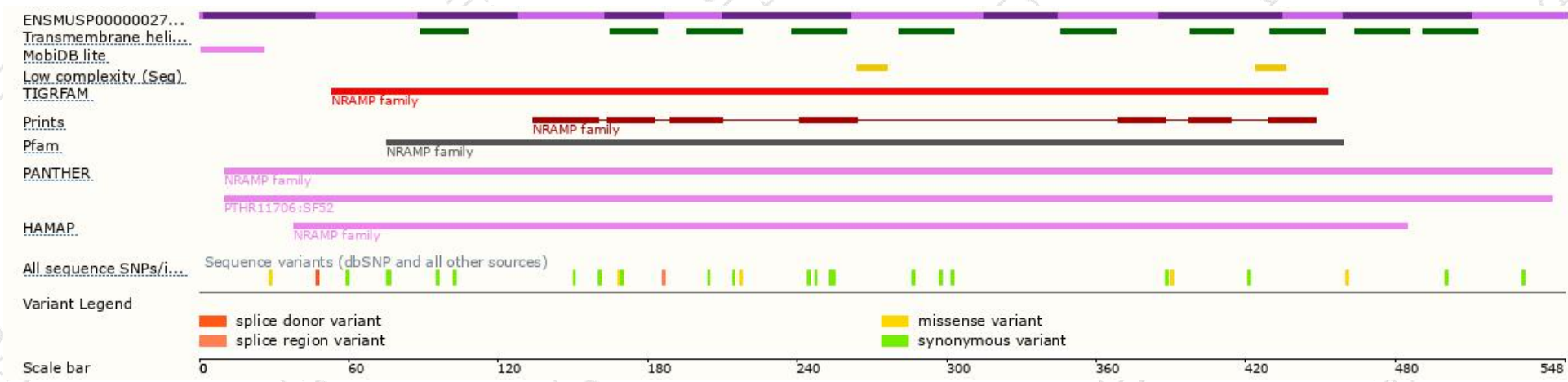
The strategy is based on the design of *Slc11a1-201* transcript,The transcription is shown below



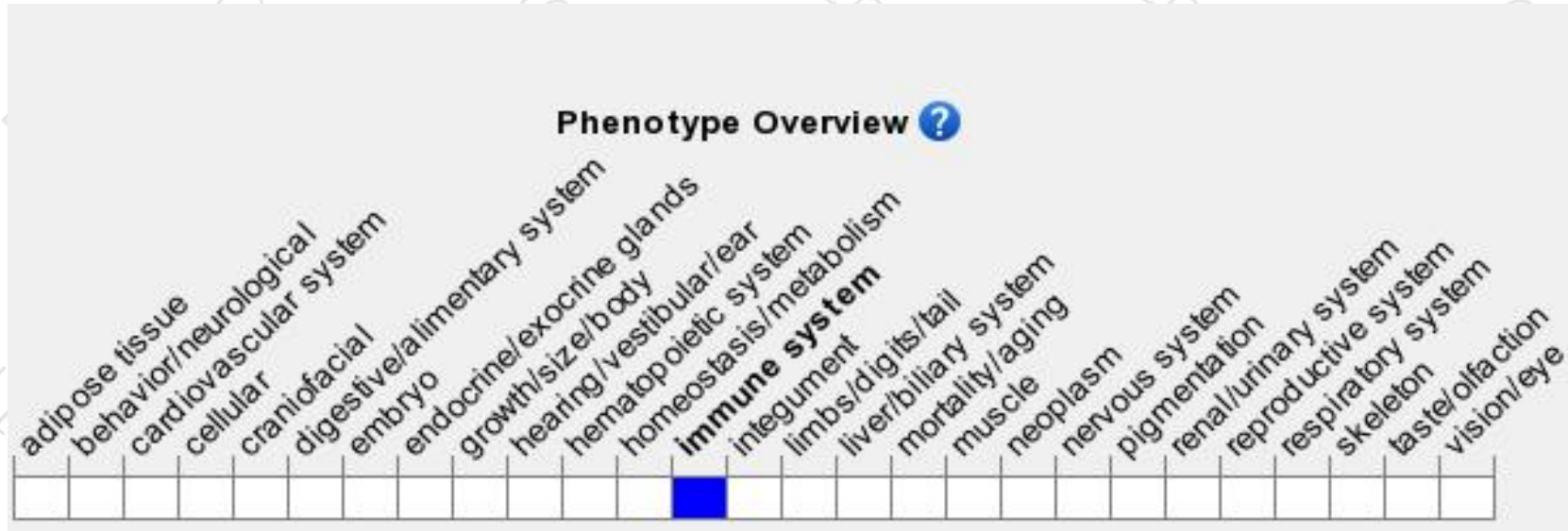
Genomic location distribution



Protein domain



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, Mutations in this gene are associated with susceptibility to infection with pathogens, including Myobacterium, Salmonella and Leishmania. Depending on the mutation, mutants may exhibit either increased or decreased susceptibility to infection.

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

Tel: 400-9660890

