

Slc12a6 Cas9-CKO Strategy

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Project Overview

Project Name

Slc12a6

Project type

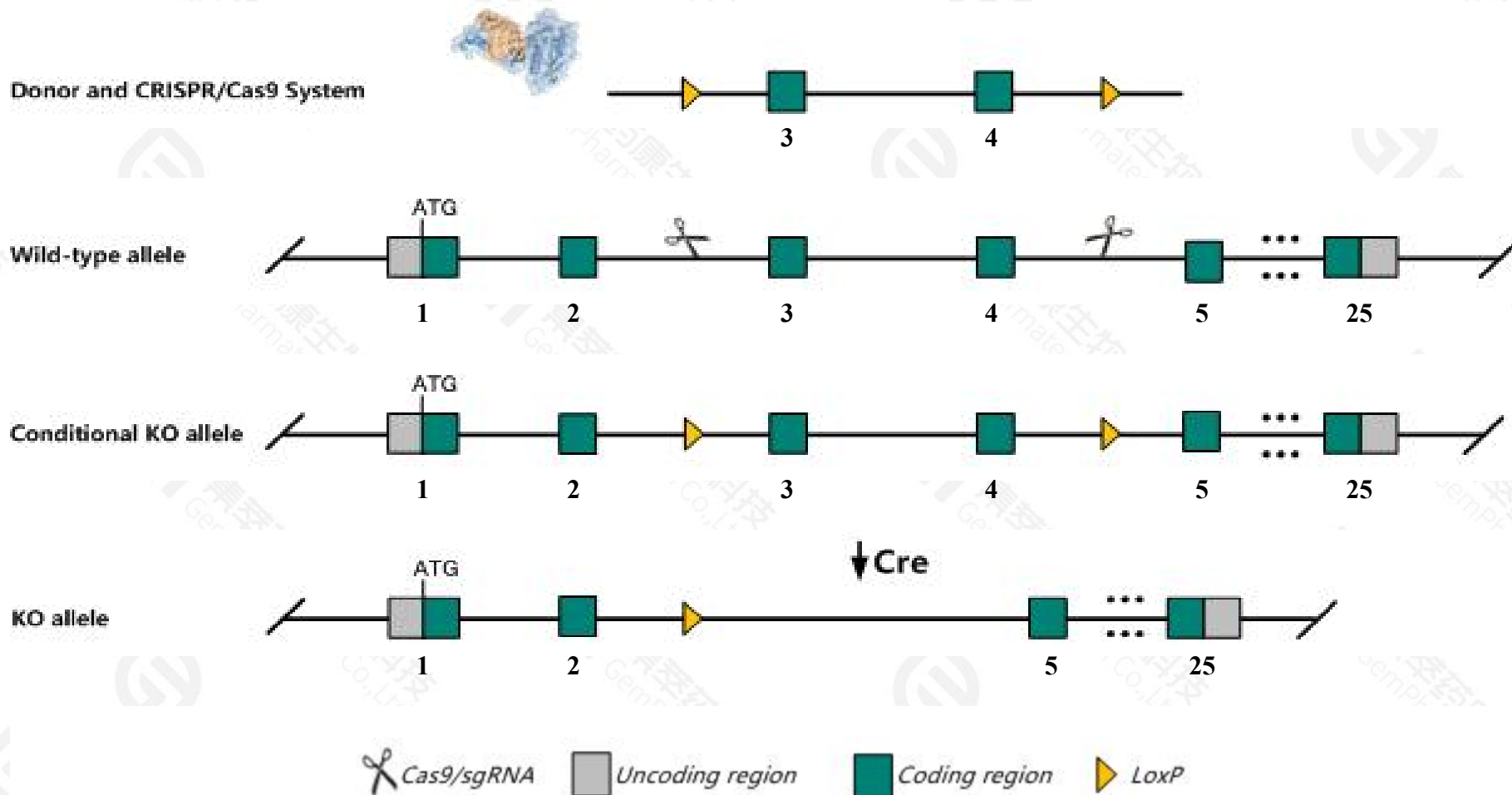
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc12a6* gene. The schematic diagram is as follows:



- The *Slc12a6* gene has 8 transcripts. According to the structure of *Slc12a6* gene, exon3-exon4 of *Slc12a6-201*(ENSMUST00000028549.14) transcript is recommended as the knockout region. The region contains 227bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc12a6* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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.

- The flox region contains functional region of the *Gm21985-201* gene. Knockout the region may affect the function of *Gm21985-201* gene
- According to the existing MGI data, homozygotes for targeted null mutations exhibit locomotor deficits, progressive neurodegeneration, slow progressive deafness and failure to breed.
- The *Slc12a6* gene is located on the Chr2. 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)

Slc12a6 solute carrier family 12, member 6 [Mus musculus (house mouse)]

Gene ID: 107723, updated on 18-Jan-2021

Summary



Official Symbol Slc12a6 provided by [MGI](#)

Official Full Name solute carrier family 12, member 6 provided by [MGI](#)

Primary source [MGI:MGI:2135960](#)

See related [Ensembl:ENSMUSG00000027130](#)

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 9530023I19Rik, KCC3, ga, gaxp

Expression Ubiquitous expression in bladder adult (RPKM 21.4), thymus adult (RPKM 18.0) and 28 other tissues [See more](#)

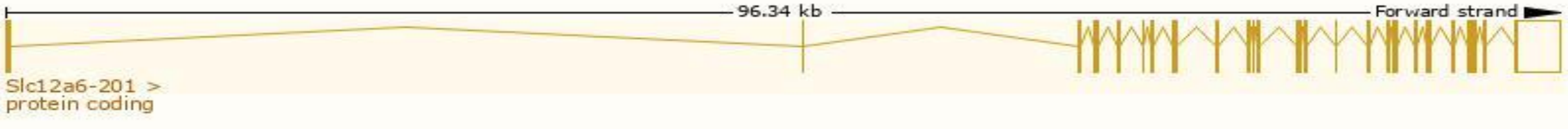
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

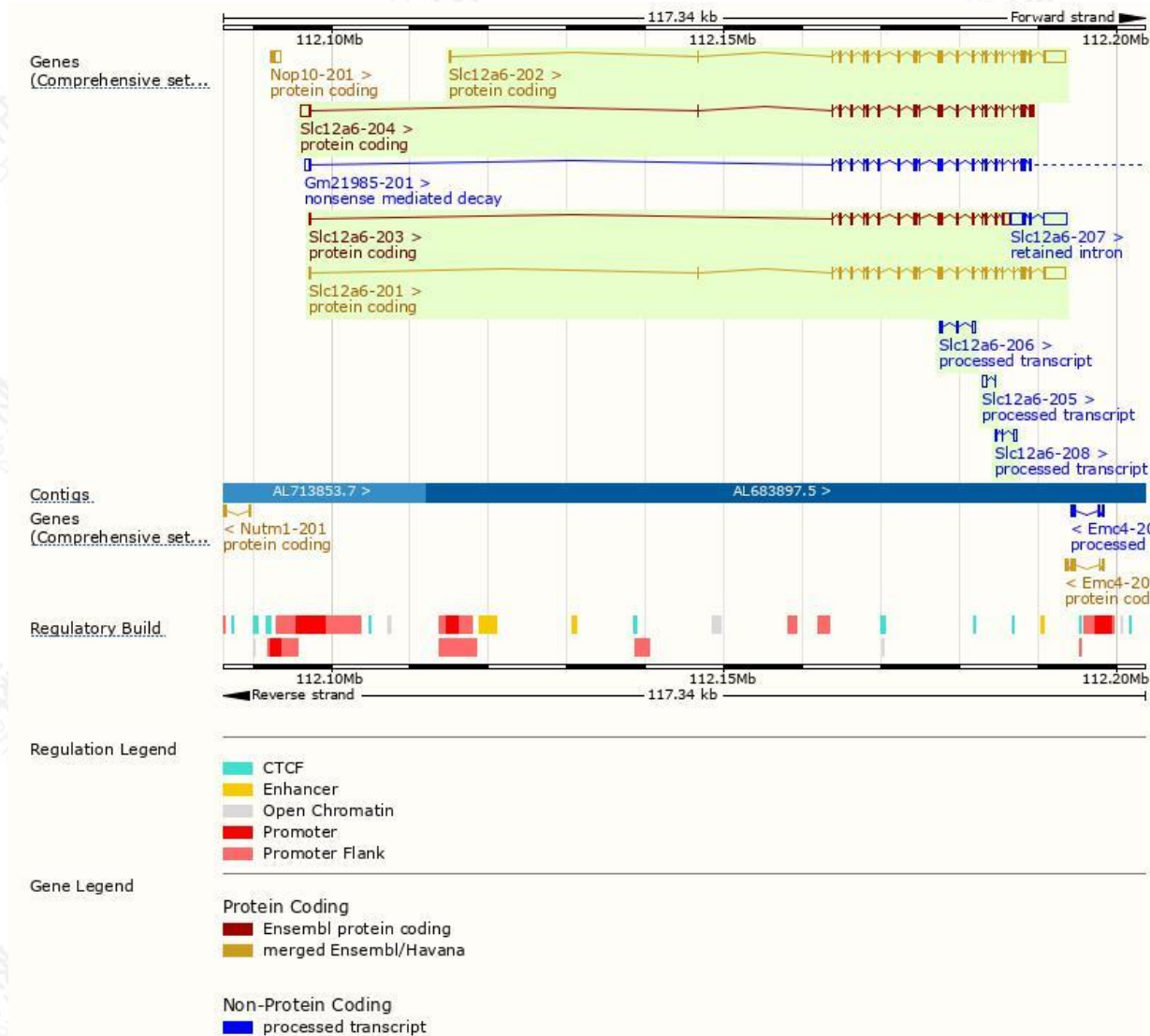
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc12a6-201	ENSMUST00000028549.14	6105	1150aa	Protein coding	CCDS16551		TSL:1 , GENCODE basic , APPRIS P4 ,
Slc12a6-202	ENSMUST00000053666.8	6060	1099aa	Protein coding	CCDS16552		TSL:1 , GENCODE basic , APPRIS ALT1 ,
Slc12a6-204	ENSMUST00000110991.9	4556	1128aa	Protein coding	-		TSL:1 , GENCODE basic ,
Slc12a6-203	ENSMUST00000110987.9	3722	946aa	Protein coding	-		TSL:1 , GENCODE basic ,
Slc12a6-208	ENSMUST00000156470.2	766	No protein	Processed transcript	-		TSL:3 ,
Slc12a6-206	ENSMUST00000133840.2	652	No protein	Processed transcript	-		TSL:3 ,
Slc12a6-205	ENSMUST00000132752.2	600	No protein	Processed transcript	-		TSL:3 ,
Slc12a6-207	ENSMUST00000137896.2	4464	No protein	Retained intron	-		TSL:2 ,

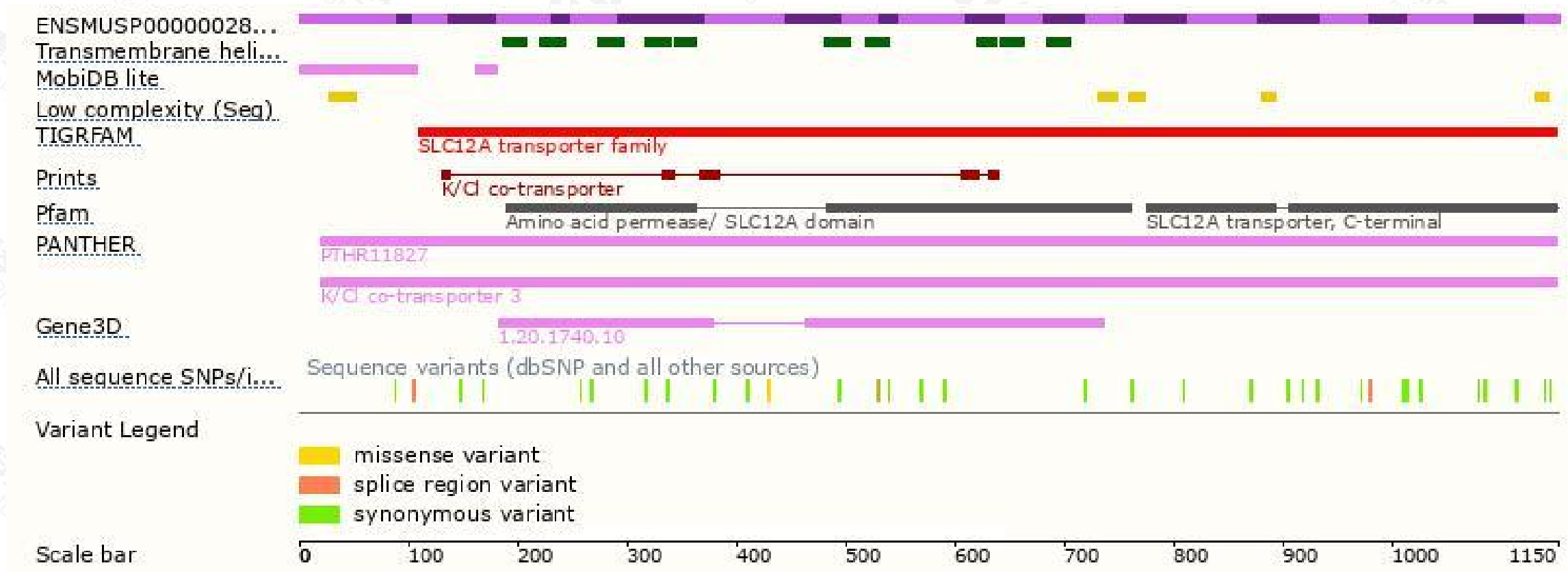
The strategy is based on the design of *Slc12a6-201* transcript,the transcription is shown below:



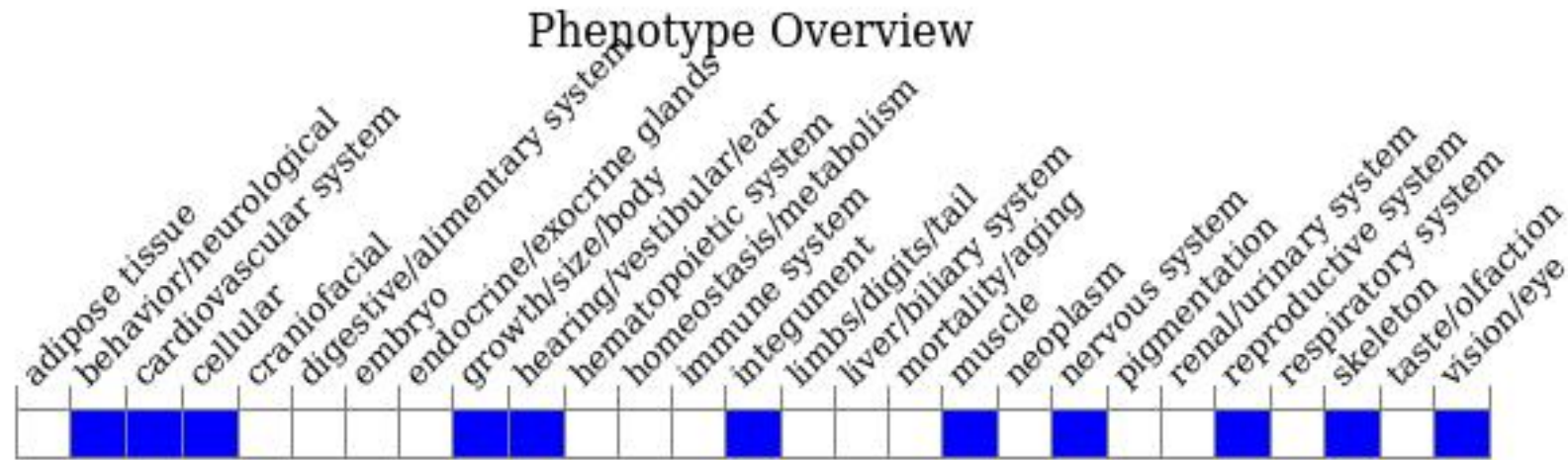
Genomic location distribution



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, homozygotes for targeted null mutations exhibit locomotor deficits, progressive neurodegeneration, slow progressive deafness and failure to breed.

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

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