

Slc12a5 Cas9-CKO Strategy

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Design Date: 2020/01/04

Project Overview



Project Name

Slc12a5

Project type

Cas9-CKO

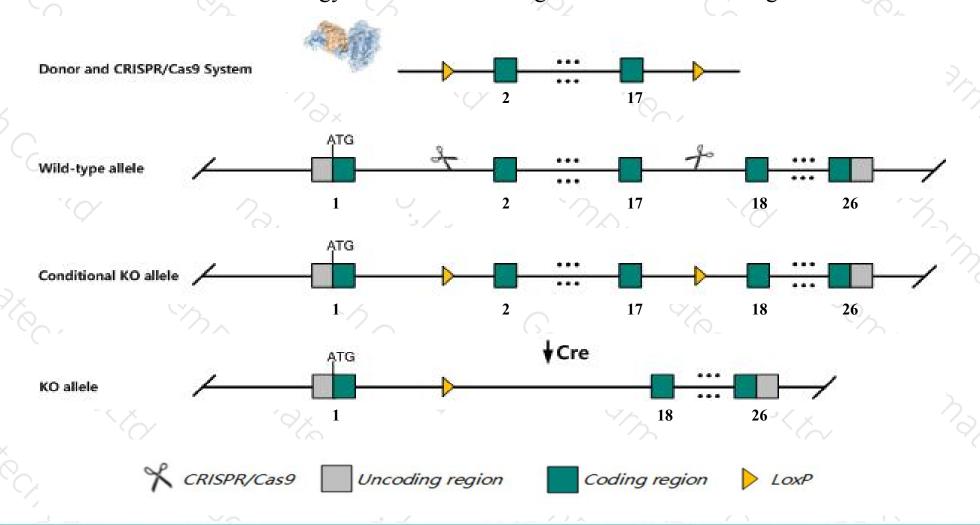
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Slc12a5* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Slc12a5* gene has 10 transcripts. According to the structure of *Slc12a5* gene, exon2-exon17 of *Slc12a5*-201(ENSMUST00000099092.7) transcript is recommended as the knockout region. The region contains 2129bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Slc12a5* 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



- > According to the existing MGI data, mice homozygous for disruptions in this gene die within a few minutes of birth of respiratory failure resulting from a motor nerve defect. Mice homozygous for a hypomorphic allele display postnatal lethality and tonic-clonic seizures.
- The *Slc12a5* 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)



Slc12a5 solute carrier family 12, member 5 [Mus musculus (house mouse)]

Gene ID: 57138, updated on 15-Mar-2020

Summary

☆ ?

Official Symbol Slc12a5 provided by MGI

Official Full Name solute carrier family 12, member 5 provided by MGI

Primary source MGI:MGI:1862037

See related Ensembl: ENSMUSG00000017740

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 KCC2, mKIAA1176

Expression Biased expression in cerebellum adult (RPKM 71.6), cortex adult (RPKM 67.7) and 6 other tissuesSee more

Orthologs <u>human</u> all

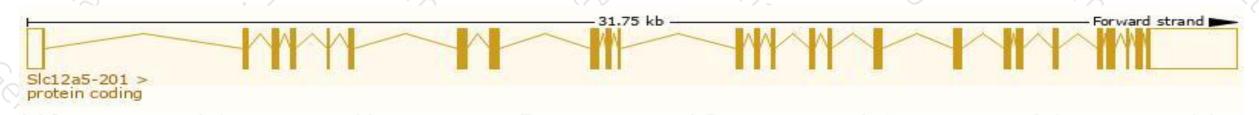
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

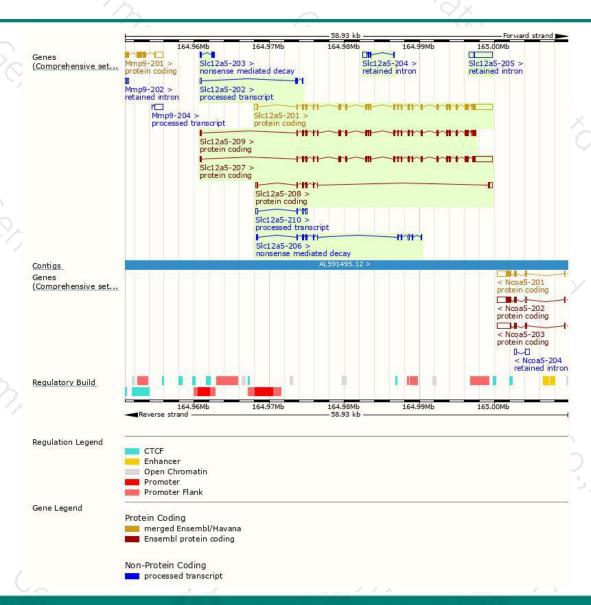
Transcript ID	L.					
	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000099092.7	6028	1115aa	Protein coding	CCDS38332	A0A076FSX1 Q91V14	TSL:1 GENCODE basic APPRIS P2
ENSMUST00000202223.3	5690	<u>1133aa</u>	Protein coding	(4)	A0A076FR46	TSL:1 GENCODE basic
ENSMUST00000202623.3	3574	1138aa	Protein coding	829	A0A076FRG6 Q91V14	TSL:1 GENCODE basic APPRIS ALT2
ENSMUST00000202479.3	1202	<u>231aa</u>	Protein coding		A0A0J9YV84	TSL:5 GENCODE basic
ENSMUST00000202136.1	1106	<u>186aa</u>	Nonsense mediated decay	145	A0A0J9YU26	TSL:5
ENSMUST00000125867.1	422	<u>59aa</u>	Nonsense mediated decay		A0A0J9YUW1	TSL:3
ENSMUST00000208579.1	586	No protein	Processed transcript	-		TSL:5
ENSMUST00000124372.5	465	No protein	Processed transcript	(20	(20)	TSL:2
ENSMUST00000137302.2	2996	No protein	Retained intron		(20	TSL:1
ENSMUST00000135918.1	744	No protein	Retained intron	0-0		TSL:3
	ENSMUST00000202223.3 ENSMUST00000202623.3 ENSMUST00000202479.3 ENSMUST00000202136.1 ENSMUST00000125867.1 ENSMUST00000125867.1 ENSMUST00000124372.5 ENSMUST00000137302.2	ENSMUST00000202223.3 5690 ENSMUST00000202623.3 3574 ENSMUST00000202479.3 1202 ENSMUST00000202136.1 1106 ENSMUST00000125867.1 422 ENSMUST00000208579.1 586 ENSMUST00000124372.5 465 ENSMUST00000137302.2 2996	ENSMUST00000202223.3 5690 1133aa ENSMUST00000202623.3 3574 1138aa ENSMUST00000202479.3 1202 231aa ENSMUST00000202136.1 1106 186aa ENSMUST00000125867.1 422 59aa ENSMUST00000208579.1 586 No protein ENSMUST00000124372.5 465 No protein ENSMUST00000137302.2 2996 No protein	ENSMUST00000202223.3 5690 1133aa Protein coding ENSMUST00000202623.3 3574 1138aa Protein coding ENSMUST00000202479.3 1202 231aa Protein coding ENSMUST00000202136.1 1106 186aa Nonsense mediated decay ENSMUST00000125867.1 422 59aa Nonsense mediated decay ENSMUST000000208579.1 586 No protein Processed transcript ENSMUST00000124372.5 465 No protein Processed transcript ENSMUST00000137302.2 2996 No protein Retained intron	ENSMUST00000202223.3 5690 1133aa Protein coding - ENSMUST00000202623.3 3574 1138aa Protein coding - ENSMUST00000202479.3 1202 231aa Protein coding - ENSMUST00000202136.1 1106 186aa Nonsense mediated decay - ENSMUST00000125867.1 422 59aa Nonsense mediated decay - ENSMUST00000208579.1 586 No protein Processed transcript - ENSMUST00000124372.5 465 No protein Processed transcript - ENSMUST00000137302.2 2996 No protein Retained intron -	ENSMUST00000202223.3 5690 1133aa Protein coding - A0A076FR46 ENSMUST00000202623.3 3574 1138aa Protein coding - A0A076FRG6 Q91V14 ENSMUST00000202479.3 1202 231aa Protein coding - A0A0J9YV84 ENSMUST00000202136.1 1106 186aa Nonsense mediated decay - A0A0J9YU26 ENSMUST00000125867.1 422 59aa Nonsense mediated decay - A0A0J9YUW1 ENSMUST00000124372.5 465 No protein Processed transcript - - ENSMUST00000137302.2 2996 No protein Retained intron - -

The strategy is based on the design of *Slc12a5-201* transcript, the transcription is shown below:



Genomic location distribution





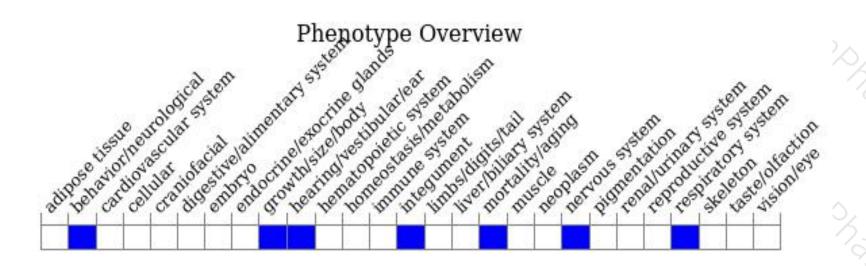
Protein domain





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,mice homozygous for disruptions in this gene die within a few minutes of birth of respiratory failure resulting from a motor nerve defect. Mice homozygous for a hypomorphic allele display postnatal lethality and tonic-clonic seizures.



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





