Slc4a7 Cas9-KO Strategy

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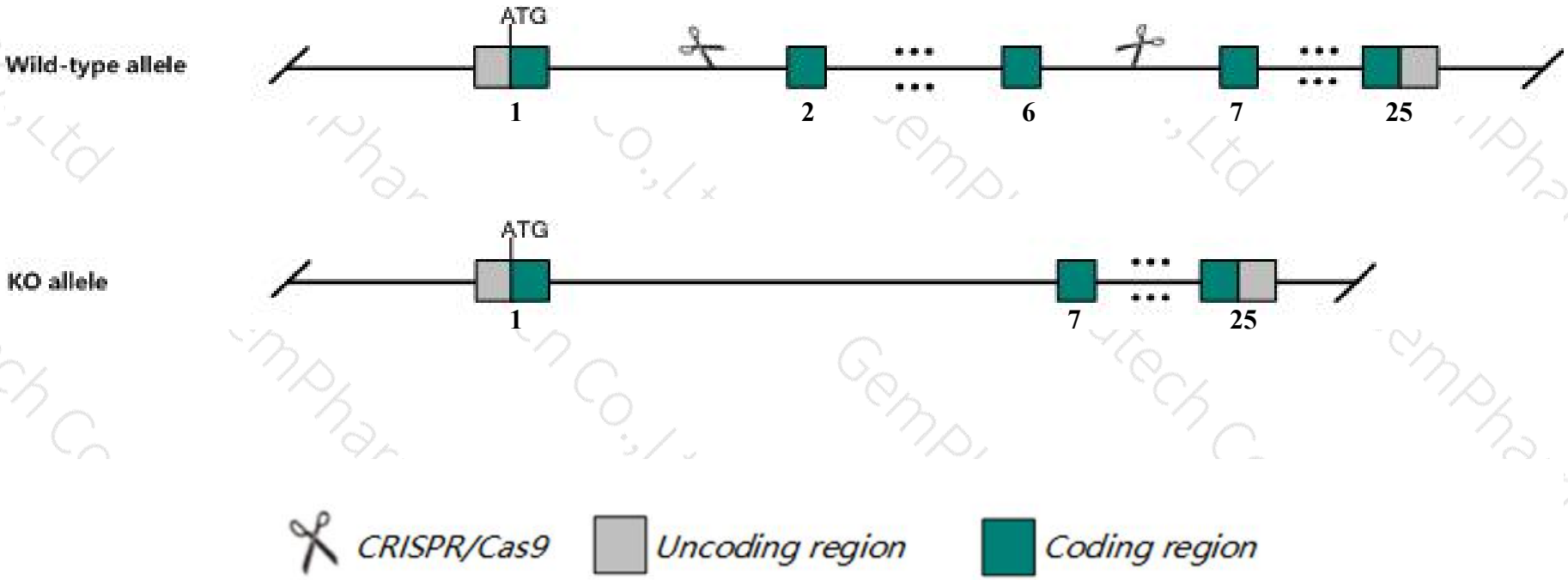
Project Overview

Project Name	***Slc4a7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc4a7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc4a7* gene has 25 transcripts. According to the structure of *Slc4a7* gene, exon2-exon6 of *Slc4a7-201* (ENSMUST00000057015.7) transcript is recommended as the knockout region.The region contains 718bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc4a7* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a disruption at this locus display defects of the auditory and visual systems similar to those observed in patients with Ushers syndrome. Mice homozygous for a gene trap allele exhibit disruption in sodium/bicarbonate function that impacts vasodilation and hypertension.

- The *Slc4a7* gene is located on the Chr14. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Slc4a7 solute carrier family 4, sodium bicarbonate cotransporter, member 7 [Mus musculus (house mouse)]

Gene ID: 218756, updated on 5-Mar-2019

Summary

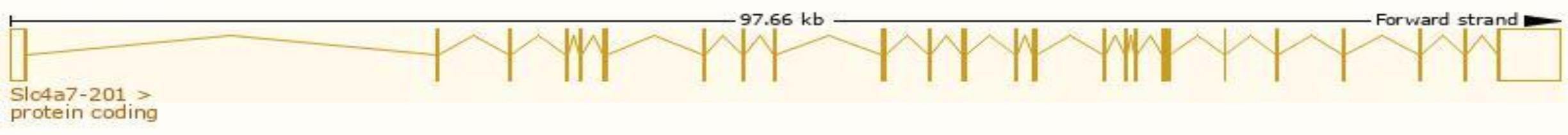
Official Symbol	Slc4a7 provided by MGI
Official Full Name	solute carrier family 4, sodium bicarbonate cotransporter, member 7 provided byMGI
Primary source	MGI:MGI:2443878
See related	Ensembl:ENSMUSG00000021733
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E430014N10Rik, NBC3, NBCn1, NBCn1-G, Tg(Thy1-SNCA)12Mjff
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 6.9), CNS E14 (RPKM 6.6) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

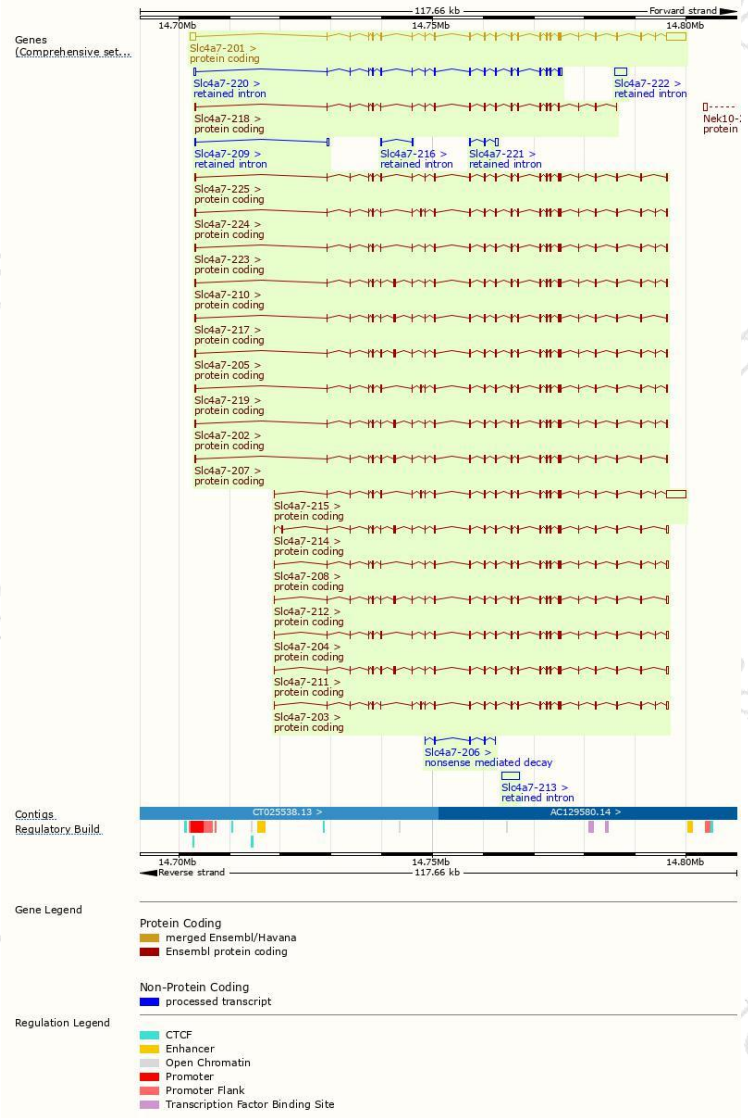
The gene has 25 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc4a7-201	ENSMUST00000057015.7	8132	1131aa	Protein coding	CCDS36810	F8VQC9	TSL:1 GENCODE basic APPRIS P2
Slc4a7-215	ENSMUST00000224952.2	7297	1146aa	Protein coding	-	A0A286YDB4 H6WZF5	GENCODE basic
Slc4a7-214	ENSMUST00000224752.2	4265	1212aa	Protein coding	-	A0A286YCX8	GENCODE basic
Slc4a7-211	ENSMUST00000224333.2	4097	1215aa	Protein coding	-	A0A286YDK8	GENCODE basic
Slc4a7-205	ENSMUST00000223761.2	4070	1254aa	Protein coding	-	A0A286YD14 J9RV59	GENCODE basic
Slc4a7-212	ENSMUST00000224672.2	4053	1200aa	Protein coding	-	A0A286YCU2 E3UVT9	GENCODE basic
Slc4a7-210	ENSMUST00000224222.2	4052	1248aa	Protein coding	-	A0A286YCS4	GENCODE basic
Slc4a7-202	ENSMUST00000223607.2	4037	1243aa	Protein coding	-	A0A286YCS4	GENCODE basic
Slc4a7-207	ENSMUST00000223981.2	3968	1220aa	Protein coding	-	A0A286YD46	GENCODE basic
Slc4a7-217	ENSMUST00000225175.2	3923	1205aa	Protein coding	-	A0A286YDA9 J9RDH0	GENCODE basic
Slc4a7-203	ENSMUST00000223695.2	3851	1133aa	Protein coding	-	A0A286YDZ8 I1VGT6	GENCODE basic
Slc4a7-204	ENSMUST00000223740.2	3831	1126aa	Protein coding	-	A0A286YCE1 E3UVT8	GENCODE basic
Slc4a7-208	ENSMUST00000224049.2	3792	1113aa	Protein coding	-	A0A286YCQ1 H6WZ45	GENCODE basic
Slc4a7-219	ENSMUST00000225238.2	3761	1151aa	Protein coding	-	A0A286YCH3 I1VGT4	GENCODE basic
Slc4a7-224	ENSMUST00000225979.2	3723	1138aa	Protein coding	-	A0A286YED8 I1VGT5	GENCODE basic
Slc4a7-223	ENSMUST00000225630.2	3663	1118aa	Protein coding	-	A0A286YDX4 D3Y272	GENCODE basic APPRIS ALT2
Slc4a7-225	ENSMUST00000226079.2	3594	1095aa	Protein coding	-	A0A286YD88 D3Y273	GENCODE basic APPRIS ALT2
Slc4a7-218	ENSMUST00000225232.2	2964	932aa	Protein coding	-	A0A286YDJ7	CDS 3' incomplete
Slc4a7-206	ENSMUST00000223771.1	426	88aa	Nonsense mediated decay	-	A0A286YDR1	CDS 5' incomplete
Slc4a7-213	ENSMUST00000224750.1	3401	No protein	Retained intron	-	-	
Slc4a7-220	ENSMUST00000225496.1	3025	No protein	Retained intron	-	-	
Slc4a7-222	ENSMUST00000225613.1	2378	No protein	Retained intron	-	-	
Slc4a7-221	ENSMUST00000225508.1	761	No protein	Retained intron	-	-	
Slc4a7-209	ENSMUST00000224197.1	679	No protein	Retained intron	-	-	
Slc4a7-216	ENSMUST00000225078.1	484	No protein	Retained intron	-	-	

The strategy is based on the design of *Slc4a7-201* transcript,The transcription is shown below

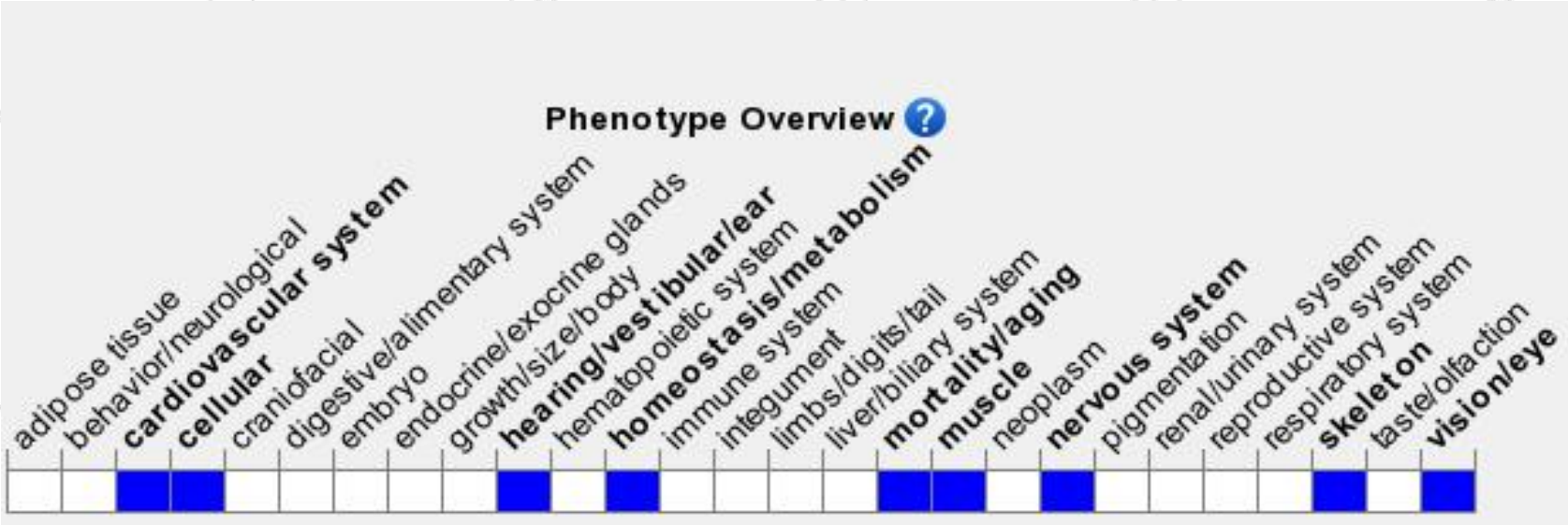


Genomic location distribution



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 a disruption at this locus display defects of the auditory and visual systems similar to those observed in patients with Ushers syndrome. Mice homozygous for a gene trap allele exhibit disruption in sodium/bicarbonate function that impacts vasodilation and hypertension.

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

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