Slc12a7 Cas9-KO Strategy

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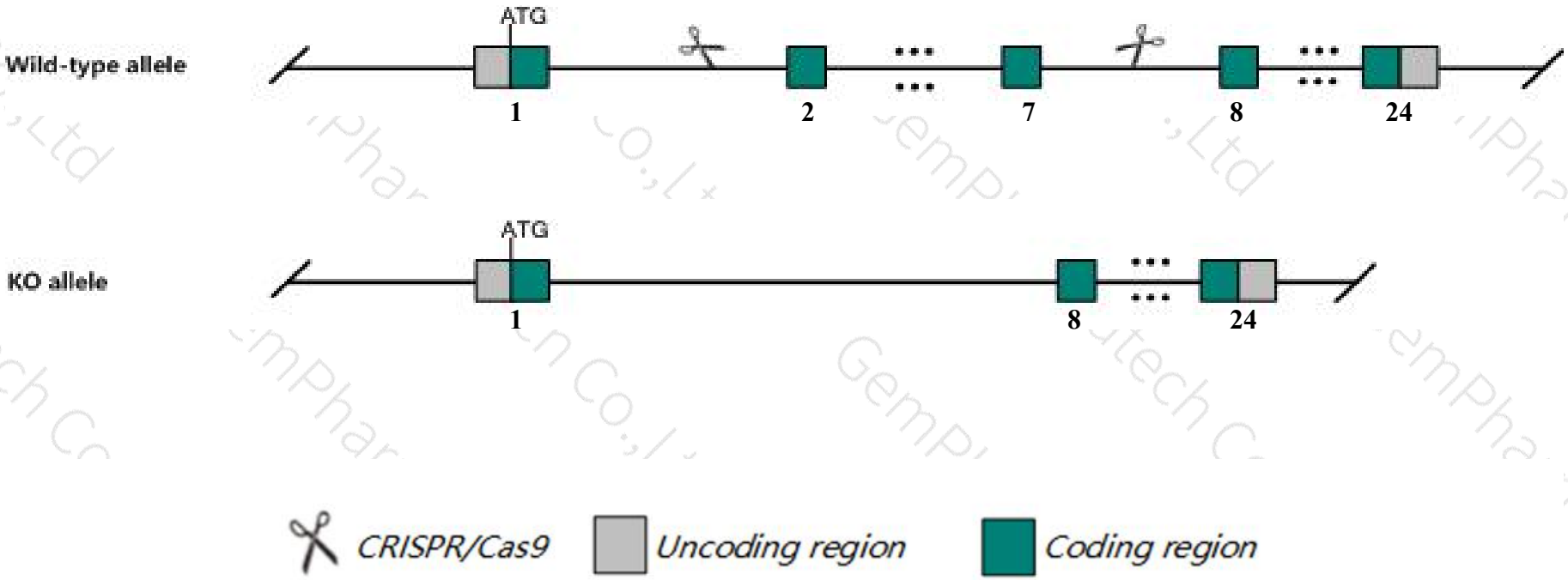
Project Overview

Project Name	***Slc12a7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc12a7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc12a7* gene has 11 transcripts. According to the structure of *Slc12a7* gene, exon2-exon7 of *Slc12a7-201* (ENSMUST00000017900.8) transcript is recommended as the knockout region.The region contains 793bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc12a7* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Hearing is severely impaired in homozygous mutant mice, which also exhibit renal tubular acidosis.
- Transcript *Slc12a7*-204&206&208&211 may not be affected.
- The *Slc12a7* gene is located on the Chr13. 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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Slc12a7 solute carrier family 12, member 7 [*Mus musculus* (house mouse)]

Gene ID: 20499, updated on 12-Aug-2019

Summary

Official Symbol	Slc12a7 provided by MGI
Official Full Name	solute carrier family 12, member 7 provided by MGI
Primary source	MGI:MGI:1342283
See related	Ensembl:ENSMUSG00000017756
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	Kcc4; AA408796; D13Ertd261e
Expression	Ubiquitous expression in ovary adult (RPKM 62.1), heart adult (RPKM 48.1) and 24 other tissues See more
Orthologs	human all

Genomic context

Location: 13 C1; 13 40.15 cM

See Slc12a7 in Genome Data Viewer

Exon count: 30

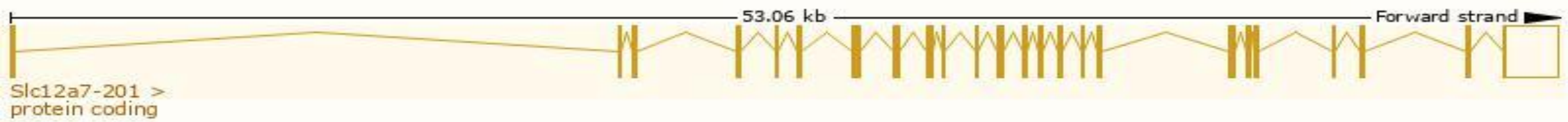
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	13	NC_000079.6 (73733052..73816754)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	13	NC_000079.5 (73901145..73954191)

Transcript information（Ensembl）

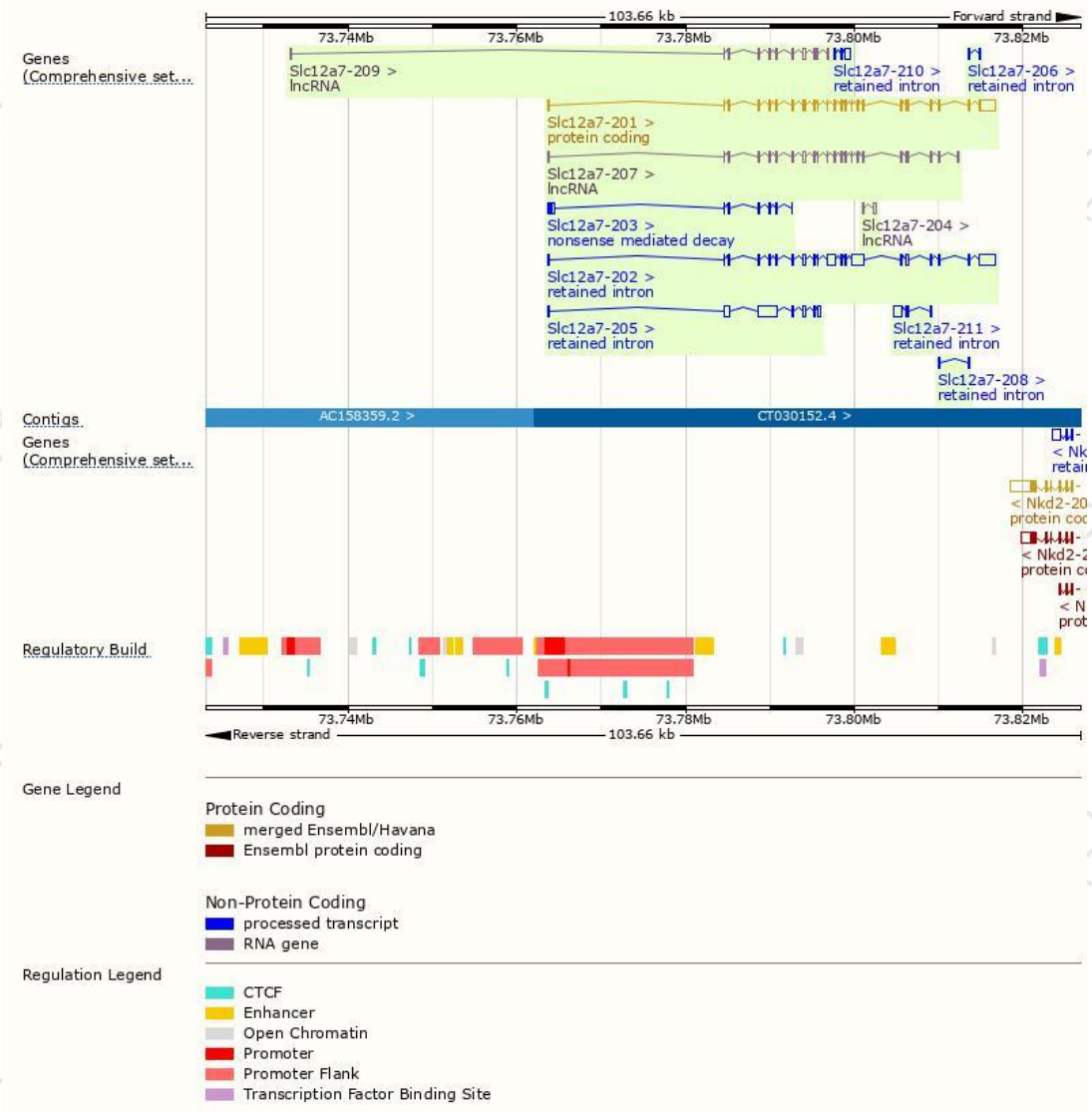
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc12a7-201	ENSMUST00000017900.8	5142	1083aa	Protein coding	CCDS26635	B9EIV8 Q9WVL3	TSL:1 GENCODE basic APPRIS P1
Slc12a7-203	ENSMUST00000220535.1	1433	151aa	Nonsense mediated decay	-	A0A1Y7VMP9	TSL:1
Slc12a7-202	ENSMUST00000220522.1	6987	No protein	Retained intron	-	-	TSL:2
Slc12a7-205	ENSMUST00000221196.1	4059	No protein	Retained intron	-	-	TSL:2
Slc12a7-211	ENSMUST00000223454.1	1504	No protein	Retained intron	-	-	TSL:1
Slc12a7-210	ENSMUST00000223008.1	736	No protein	Retained intron	-	-	TSL:3
Slc12a7-208	ENSMUST00000222309.1	377	No protein	Retained intron	-	-	TSL:3
Slc12a7-206	ENSMUST00000221813.1	356	No protein	Retained intron	-	-	TSL:2
Slc12a7-207	ENSMUST00000222253.1	3242	No protein	lncRNA	-	-	TSL:1
Slc12a7-209	ENSMUST00000222742.1	1813	No protein	lncRNA	-	-	TSL:1
Slc12a7-204	ENSMUST00000220686.1	512	No protein	lncRNA	-	-	TSL:3

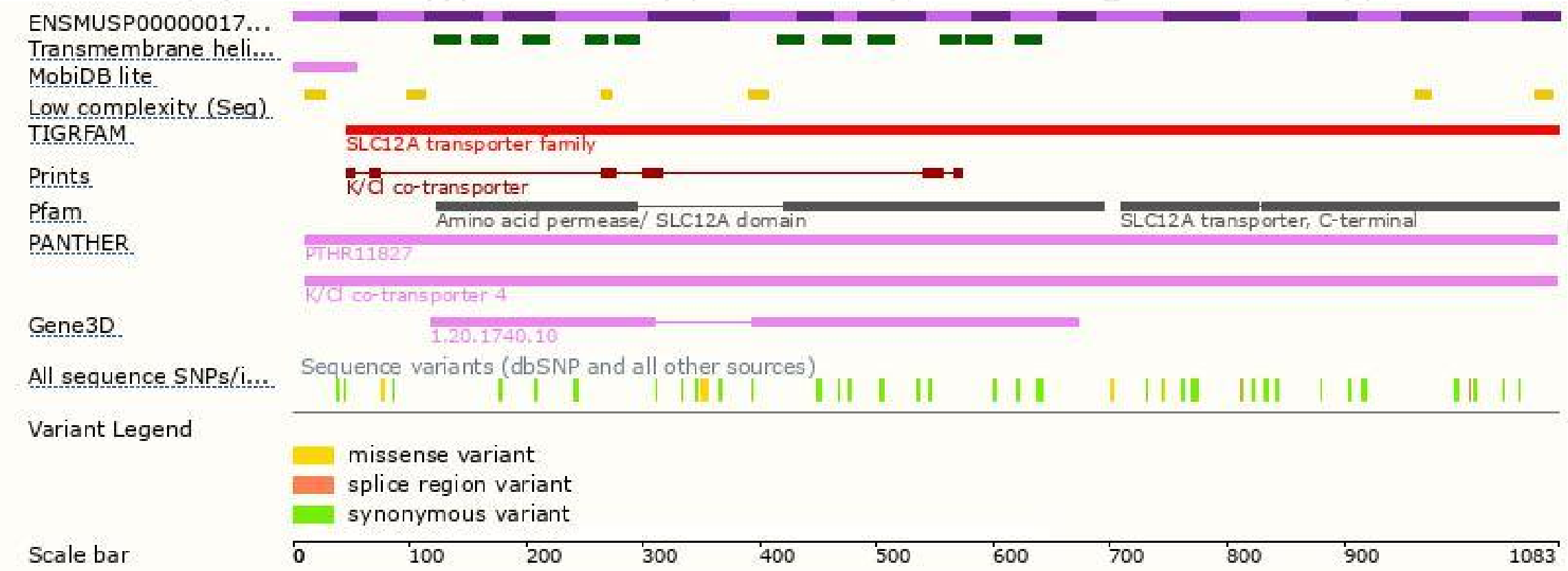
The strategy is based on the design of *Slc12a7-201* transcript,The transcription is shown below



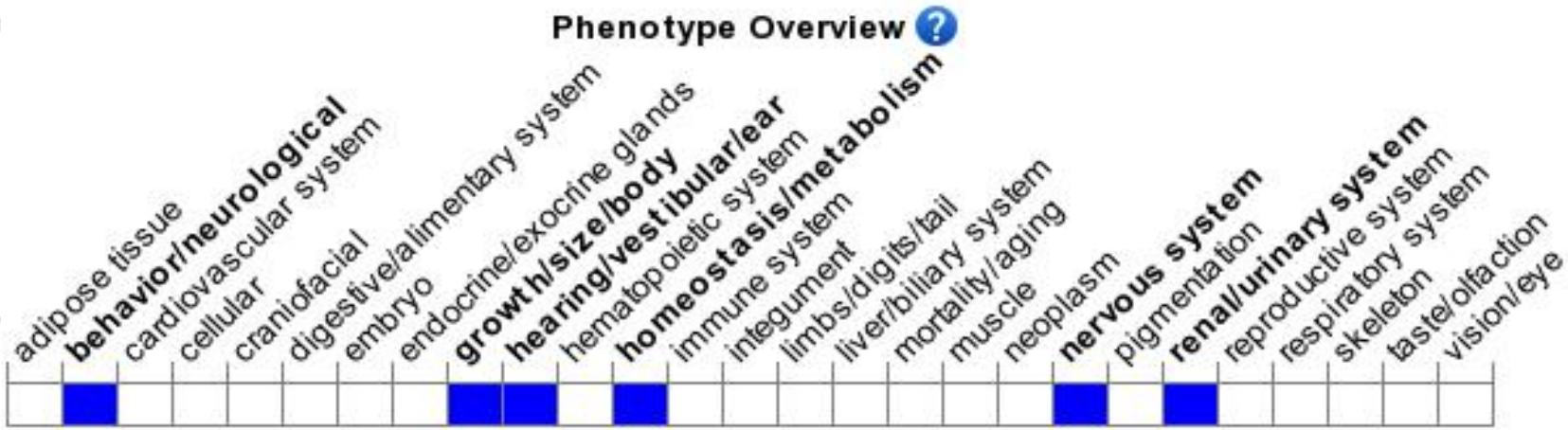
Genomic location distribution



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/).

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

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