

Slc26a7 Cas9-KO Strategy

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Project Overview

Project Name

Slc26a7

Project type

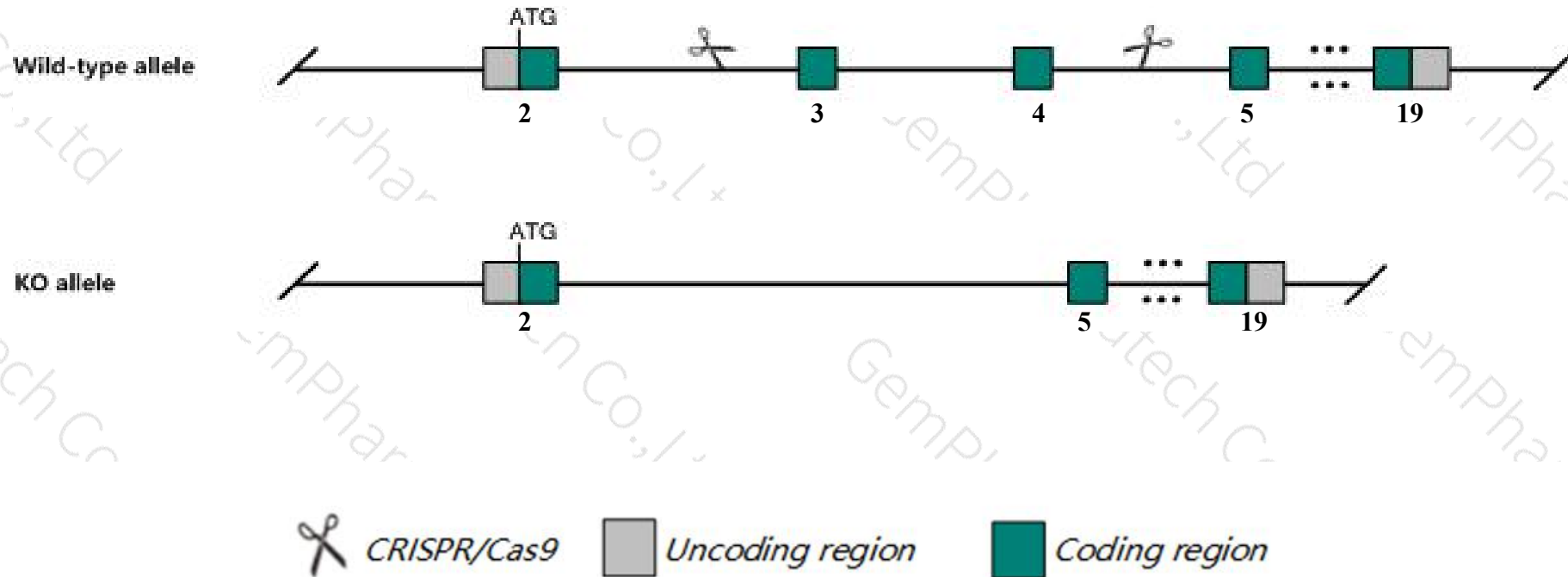
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc26a7* gene. The schematic diagram is as follows:



- The *Slc26a7* gene has 4 transcripts. According to the structure of *Slc26a7* gene, exon3-exon4 of *Slc26a7-201* (ENSMUST00000042221.13) transcript is recommended as the knockout region. The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc26a7* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice deficient for this marker have a reduce arterial pH and reduced serum bicarbonate. Urine is more concentrated and has an elevated pH.
- The *Slc26a7* gene is located on the Chr4. 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)

Slc26a7 solute carrier family 26, member 7 [Mus musculus (house mouse)]

Gene ID: 208890, updated on 31-Jan-2019

Summary



Official Symbol	Slc26a7 provided by MGI
Official Full Name	solute carrier family 26, member 7 provided by MGI
Primary source	MGI:MGI:2384791
See related	Ensembl:ENSMUSG00000040569
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
Expression	Biased expression in limb E14.5 (RPKM 6.8), subcutaneous fat pad adult (RPKM 4.1) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

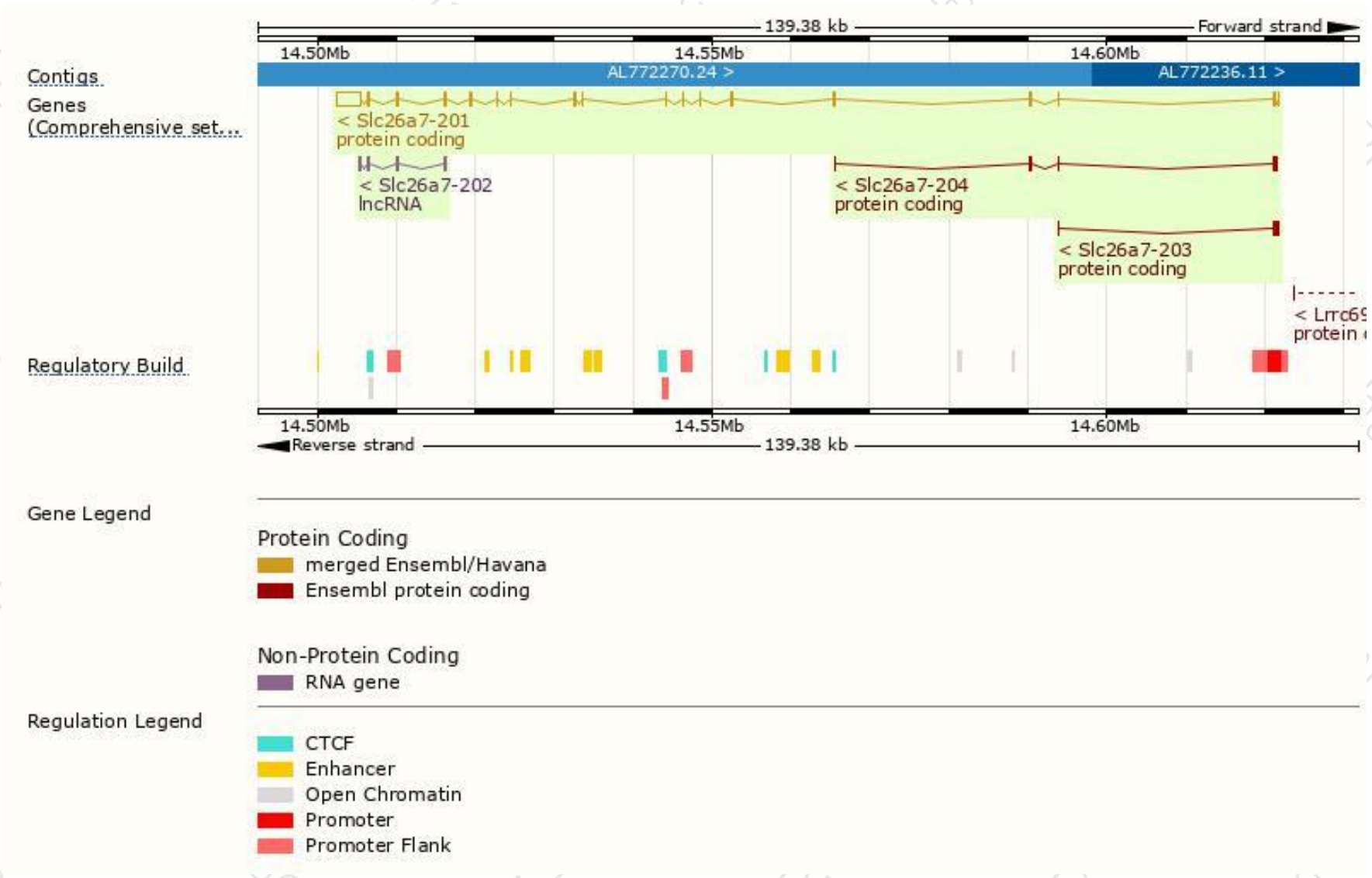
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc26a7-201	ENSMUST00000042221.13	5165	656aa	Protein coding	CCDS17979	Q8R2Z3	TSL:1 GENCODE basic APPRIS P1
Slc26a7-204	ENSMUST00000149633.1	715	200aa	Protein coding	-	A2AJZ5	CDS 3' incomplete TSL:3
Slc26a7-203	ENSMUST00000143105.1	362	99aa	Protein coding	-	A2AJZ6	CDS 3' incomplete TSL:3
Slc26a7-202	ENSMUST00000138042.1	691	No protein	lncRNA	-	-	TSL:2

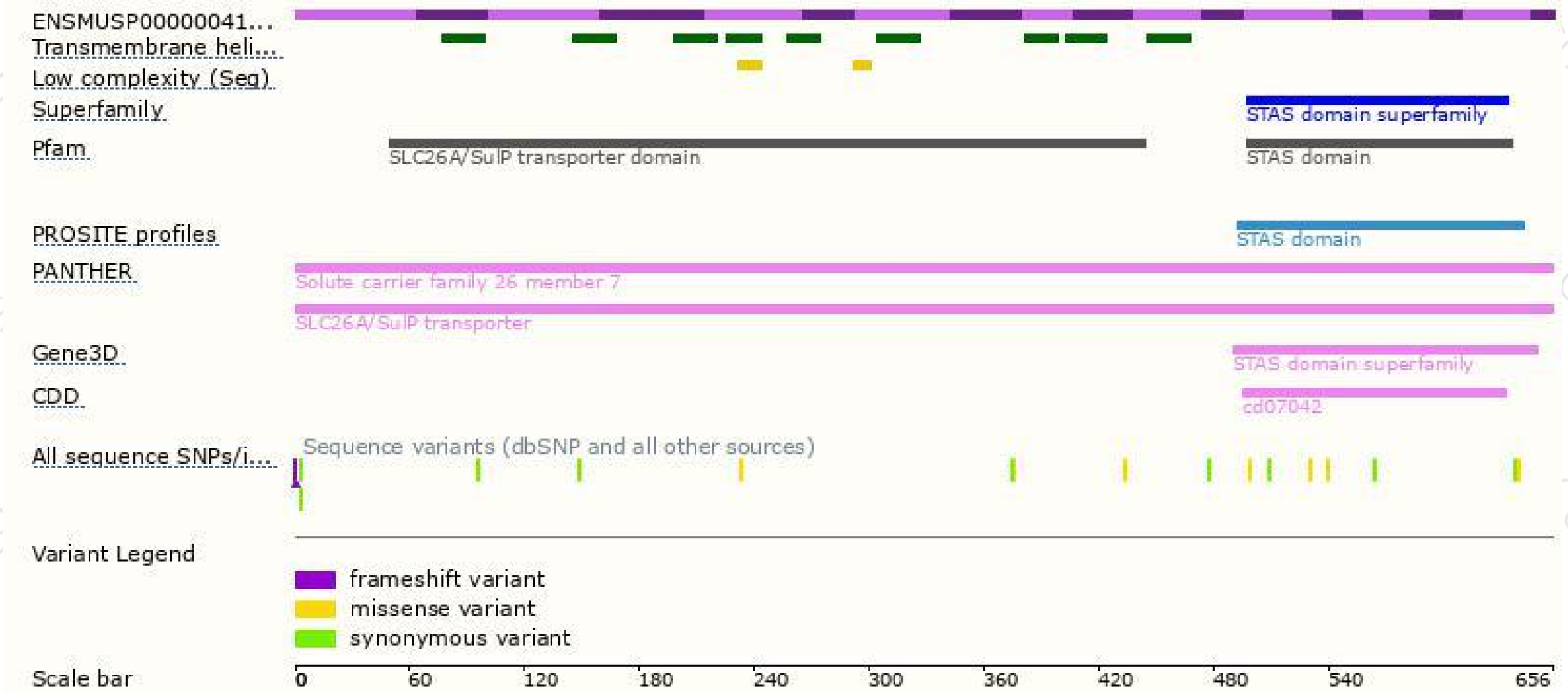
The strategy is based on the design of *Slc26a7-201* transcript,The transcription is shown below



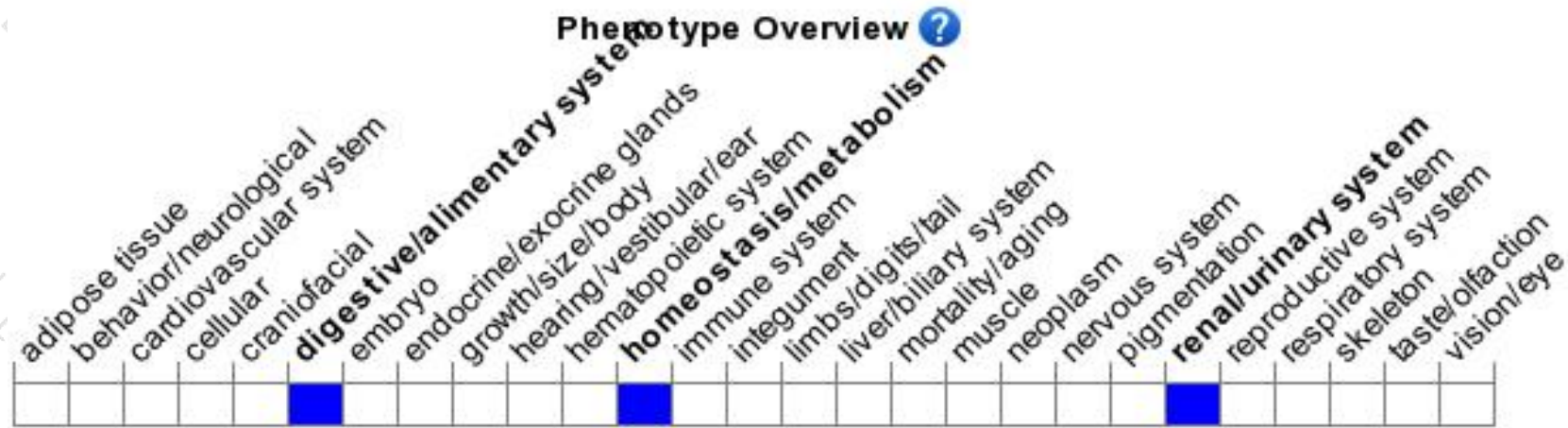
Genomic location distribution



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 deficient for this marker have a reduce arterial pH and reduced serum bicarbonate. Urine is more concentrated and has an elevated pH.

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

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