

Slc26a9 Cas9-KO Strategy

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Design Date:

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Project Overview

Project Name

Slc26a9

Project type

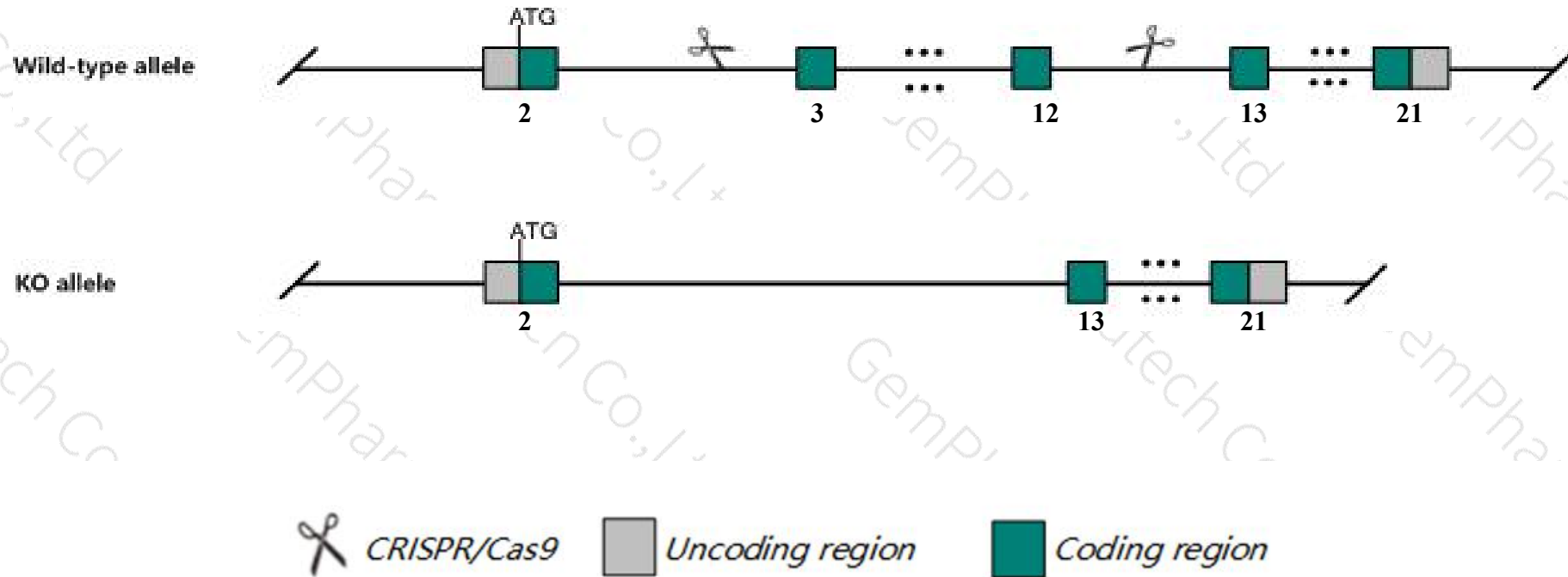
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc26a9* gene. The schematic diagram is as follows:



Technical routes

- The *Slc26a9* gene has 4 transcripts. According to the structure of *Slc26a9* gene, exon3-exon12 of *Slc26a9-201* (ENSMUST00000049027.9) transcript is recommended as the knockout region. The region contains 1264bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc26a9* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a null allele exhibit reduced gastric secretory membranes and loss of gastric acid secretion.
- The *Slc26a9* gene is located on the Chr1. 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.

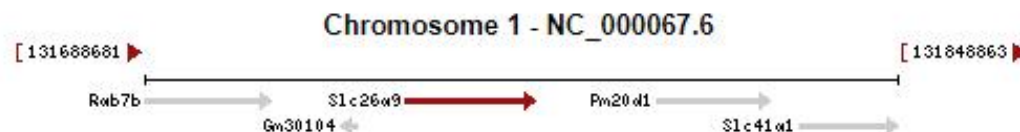
Gene information (NCBI)

Slc26a9 solute carrier family 26, member 9 [*Mus musculus* (house mouse)]

Gene ID: 320718, updated on 12-Aug-2019

Summary

Official Symbol	Slc26a9 provided by MGI
Official Full Name	solute carrier family 26, member 9 provided by MGI
Primary source	MGI:MGI:2444594
See related	Ensembl:ENSMUSG00000042268
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	E030002L01Rik
Expression	Biased expression in stomach adult (RPKM 21.9) and lung adult (RPKM 13.8) See more
Orthologs	human all

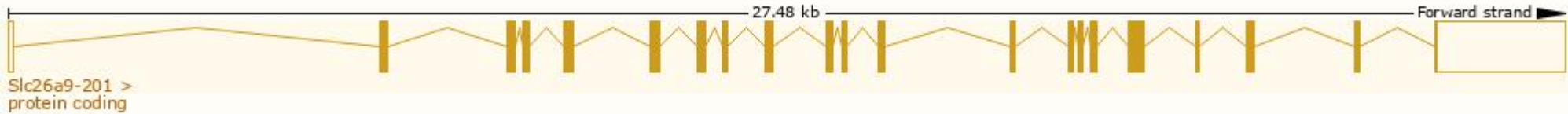


Transcript information (Ensembl)

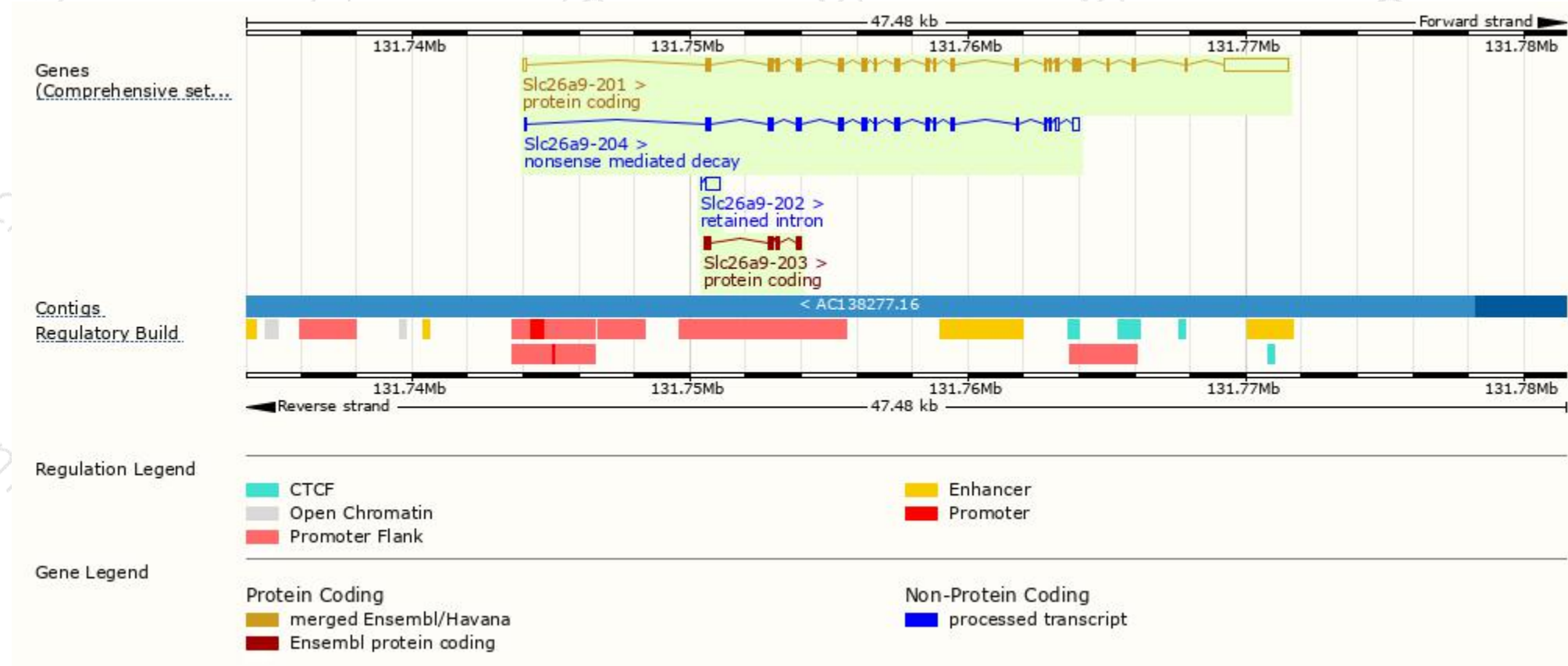
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc26a9-201	ENSMUST00000049027.9	4739	790aa	Protein coding	CCDS15273	A0A0R4J0F7	TSL:1 GENCODE basic APPRIS P1
Slc26a9-203	ENSMUST00000147800.1	644	179aa	Protein coding	-	D3Z1A3	CDS 3' incomplete TSL:3
Slc26a9-204	ENSMUST00000186122.6	1929	478aa	Nonsense mediated decay	-	A0A087WSS7	TSL:5
Slc26a9-202	ENSMUST00000130544.1	541	No protein	Retained intron	-	-	TSL:2

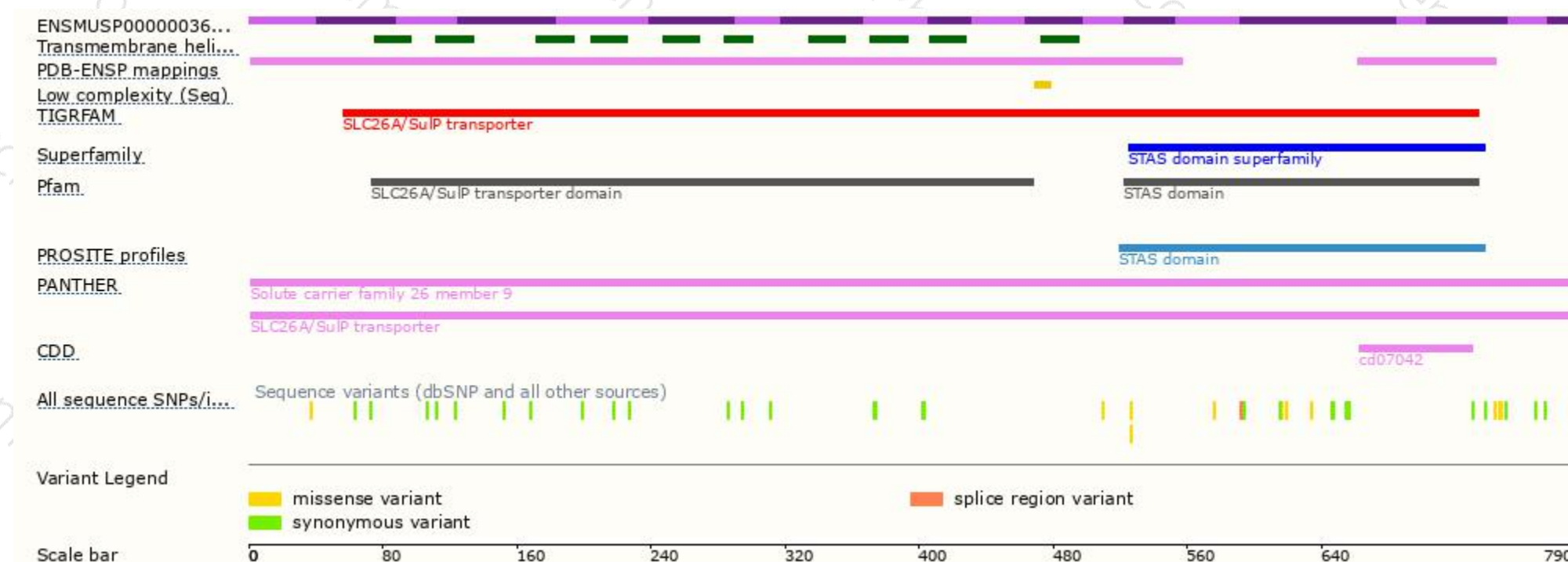
The strategy is based on the design of *Slc26a9-201* transcript,The transcription is shown below



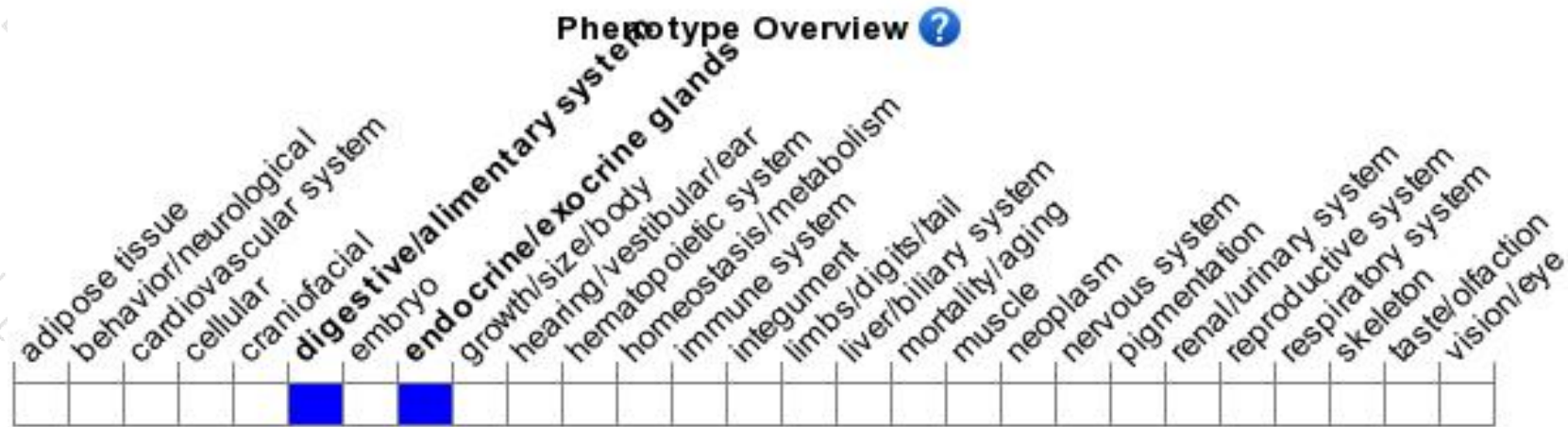
Genomic location distribution



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 null allele exhibit reduced gastric secretory membranes and loss of gastric acid secretion.

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

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