

Slc44a4 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Slc44a4

Project type

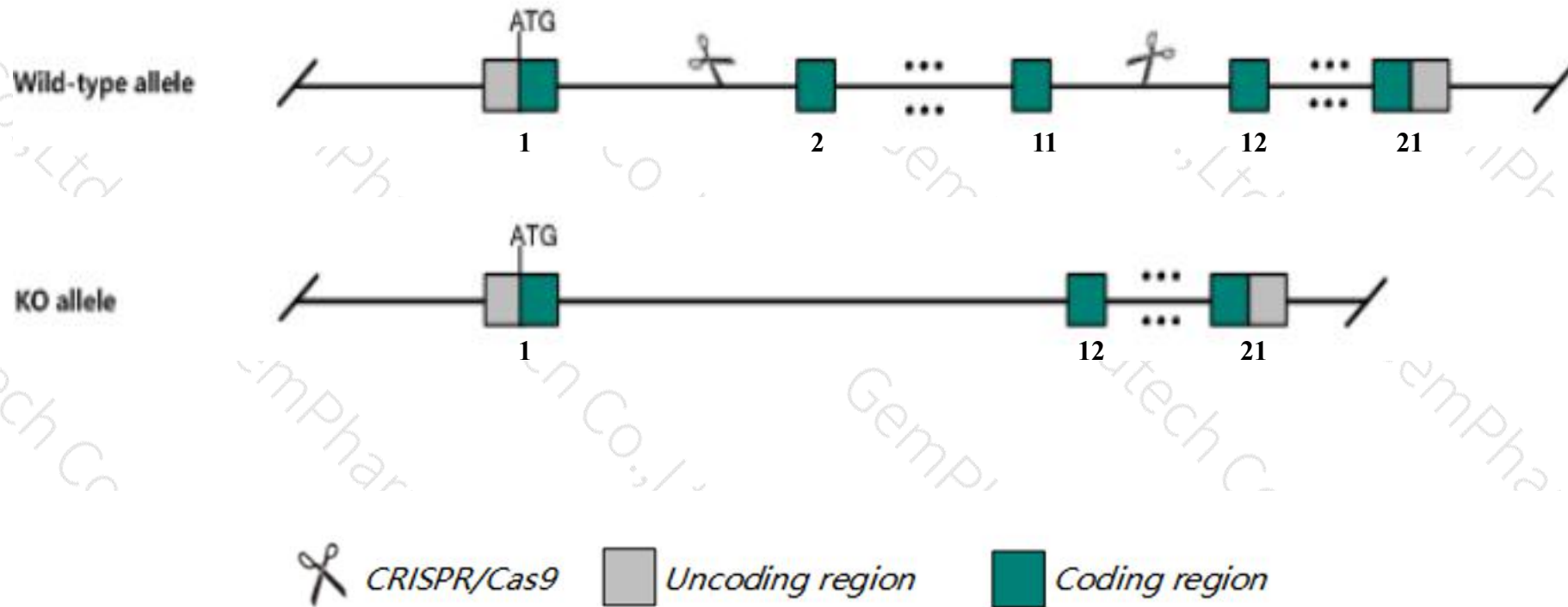
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc44a4* gene. The schematic diagram is as follows:



- The *Slc44a4* gene has 3 transcripts. According to the structure of *Slc44a4* gene, exon2-exon11 of *Slc44a4-201* (ENSMUST00000007249.14) transcript is recommended as the knockout region. The region contains 997bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc44a4* gene. The brief process is as follows: CRISPR/Cas9 system

- The effect on transcript *Slc44a4*-202 is unknown.
- The *Slc44a4* gene is located on the Chr17. 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)

Slc44a4 solute carrier family 44, member 4 [Mus musculus (house mouse)]

Gene ID: 70129, updated on 13-Mar-2020

Summary



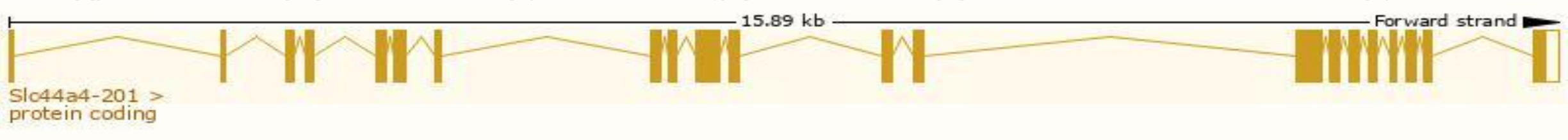
Official Symbol	Slc44a4 provided by MGI
Official Full Name	solute carrier family 44, member 4 provided by MGI
Primary source	MGI:MGI:1917379
See related	Ensembl:ENSMUSG000000007034
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2210409B01Rik, NG22, mTPPT1
Expression	Biased expression in colon adult (RPKM 156.0), large intestine adult (RPKM 85.0) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

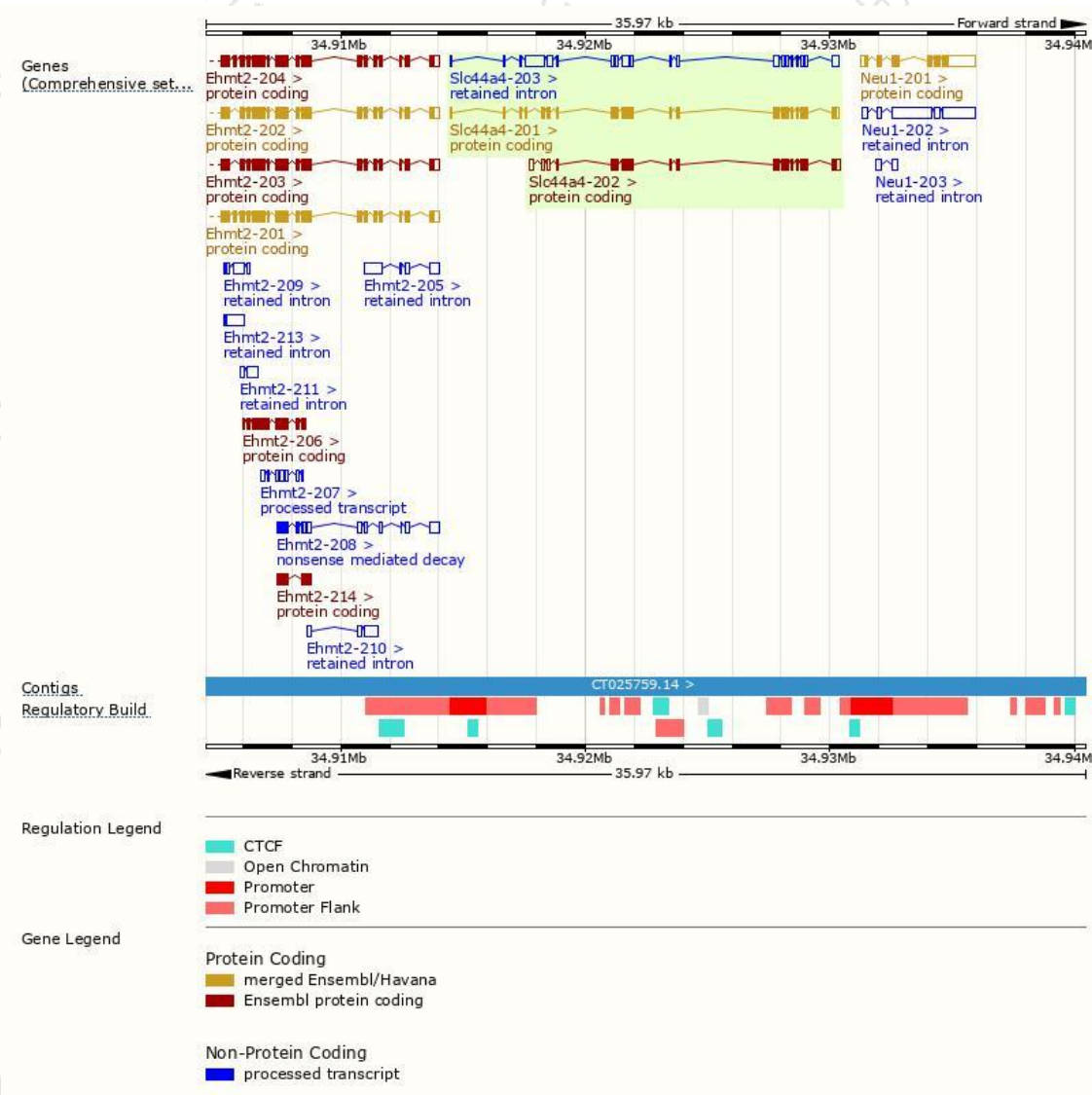
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc44a4-201	ENSMUST00000007249.14	2261	707aa	Protein coding	CCDS37591	Q3ULA4_Q91VA1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Slc44a4-202	ENSMUST00000169230.1	2246	555aa	Protein coding	-	E9PWK0	TSL:1 GENCODE basic
Slc44a4-203	ENSMUST00000173664.1	3055	No protein	Retained intron	-	-	TSL:1

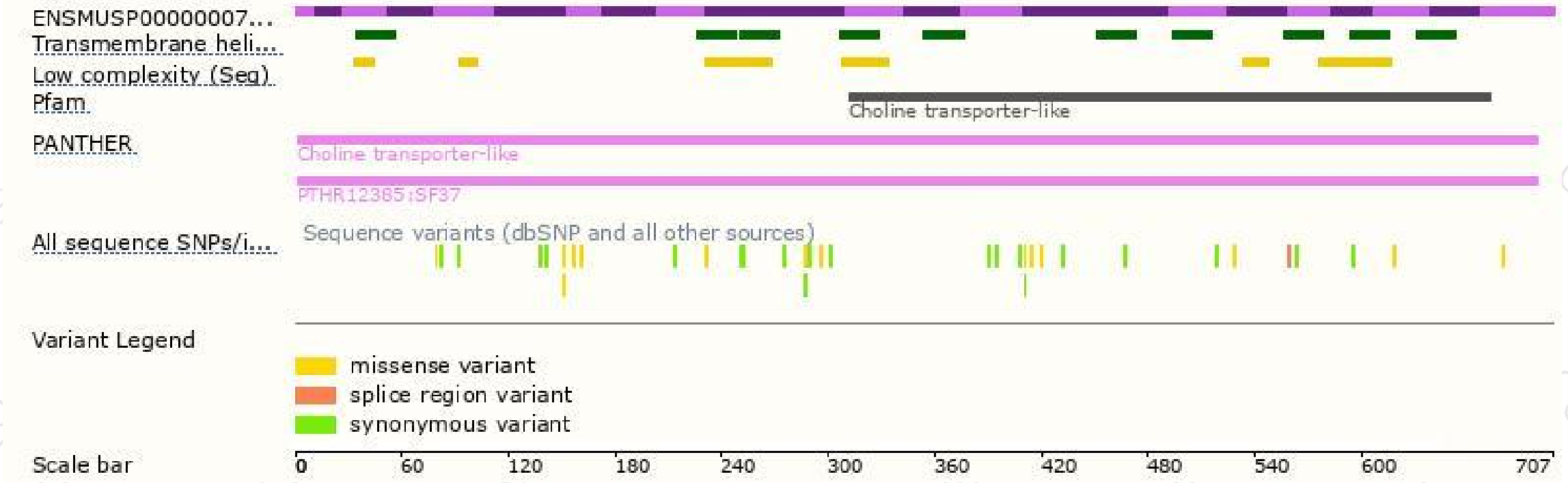
The strategy is based on the design of *Slc44a4-201* transcript,the transcription is shown below



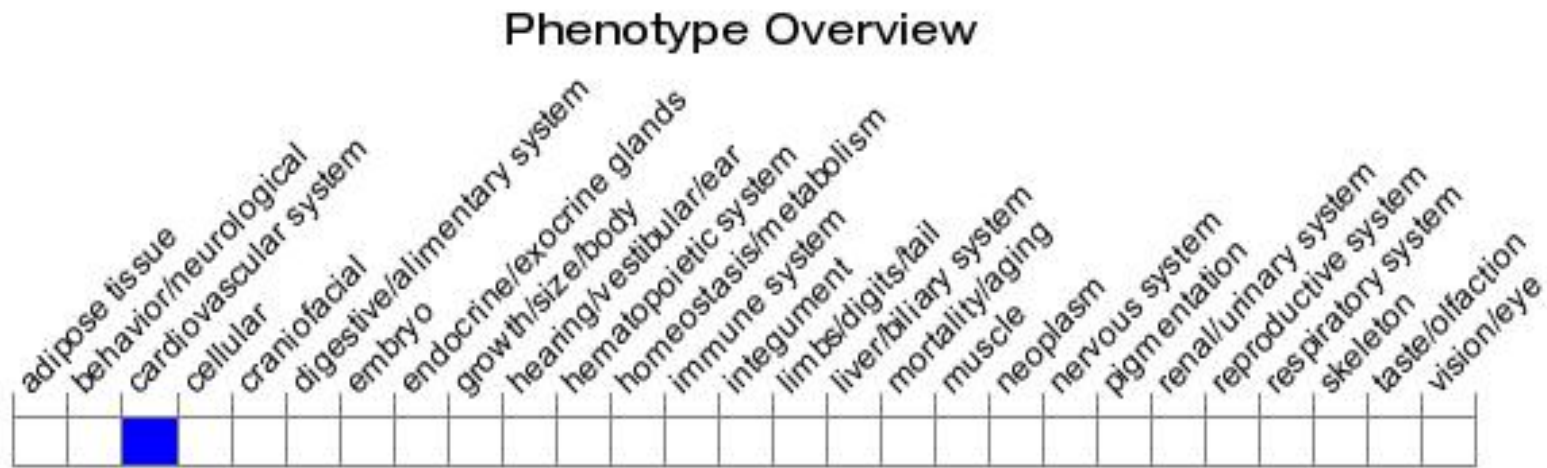
Genomic location distribution



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/>).

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

Tel: 400-9660890

