

Slc44a3 Cas9-KO Strategy

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Design Date: 2020-4-17

Project Overview

Project Name

Slc44a3

Project type

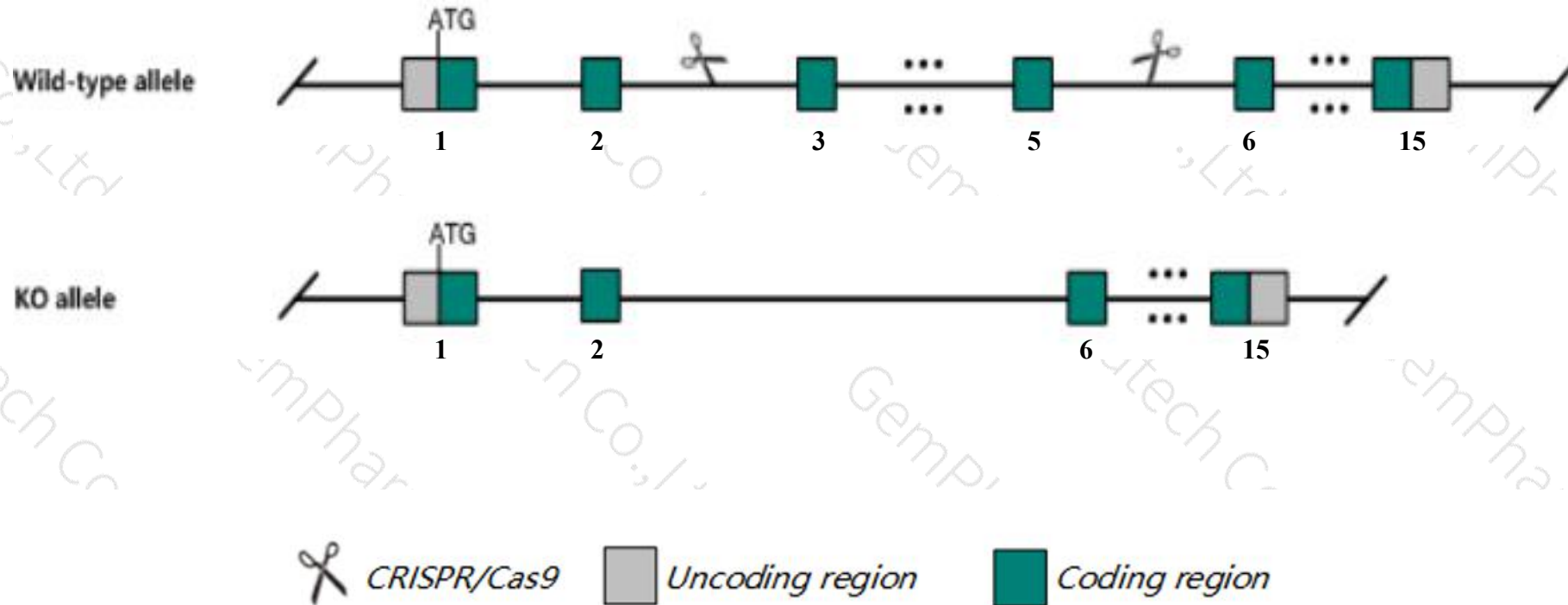
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc44a3* gene. The schematic diagram is as follows:



- The *Slc44a3* gene has 3 transcripts. According to the structure of *Slc44a3* gene, exon3-exon5 of *Slc44a3-201* (ENSMUST00000039197.8) transcript is recommended as the knockout region. The region contains 374bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc44a3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- Transcript *Slc44a3*-202 may not be affected.
- The knockout region is near to the N-terminal of *A530020G20Rik* gene, this strategy may influence the regulatory function of the N-terminal of *A530020G20Rik* gene.
- The *Slc44a3* gene is located on the Chr3. 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)

Slc44a3 solute carrier family 44, member 3 [Mus musculus (house mouse)]

Gene ID: 213603, updated on 13-Mar-2020

Summary



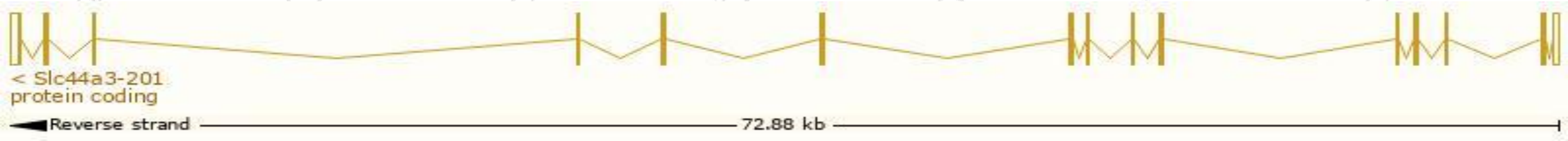
Official Symbol	Slc44a3 provided by MGI
Official Full Name	solute carrier family 44, member 3 provided by MGI
Primary source	MGI:MGI:2384860
See related	Ensembl:ENSMUSG00000039865
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC010552
Expression	Broad expression in colon adult (RPKM 11.7), adrenal adult (RPKM 10.2) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

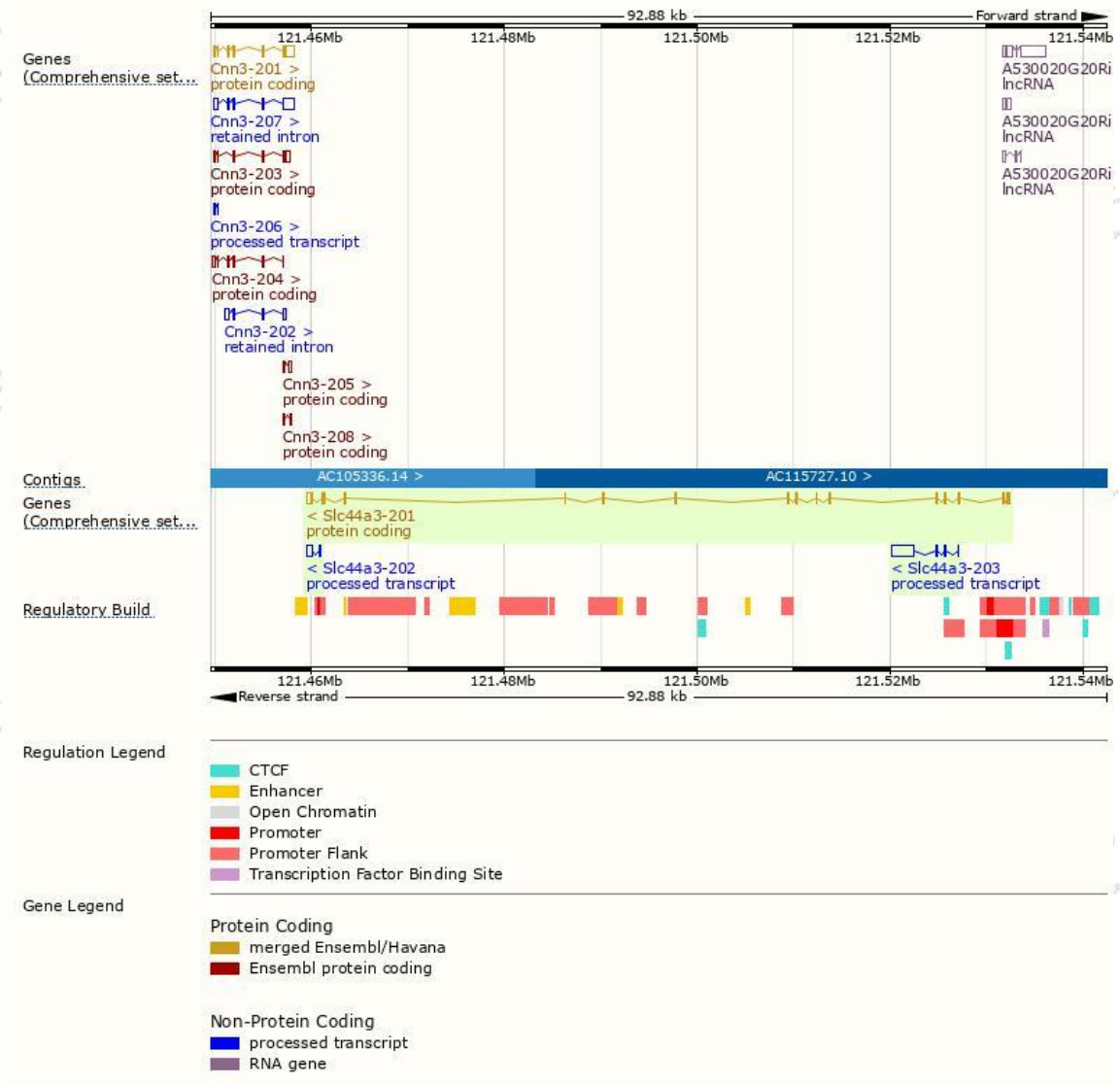
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc44a3-201	ENSMUST00000039197.8	2620	656aa	Protein coding	CCDS51060	Q921V7	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
Slc44a3-203	ENSMUST00000199422.1	2646	No protein	Processed transcript	-	-	TSL:1
Slc44a3-202	ENSMUST00000198335.1	615	No protein	Processed transcript	-	-	TSL:3

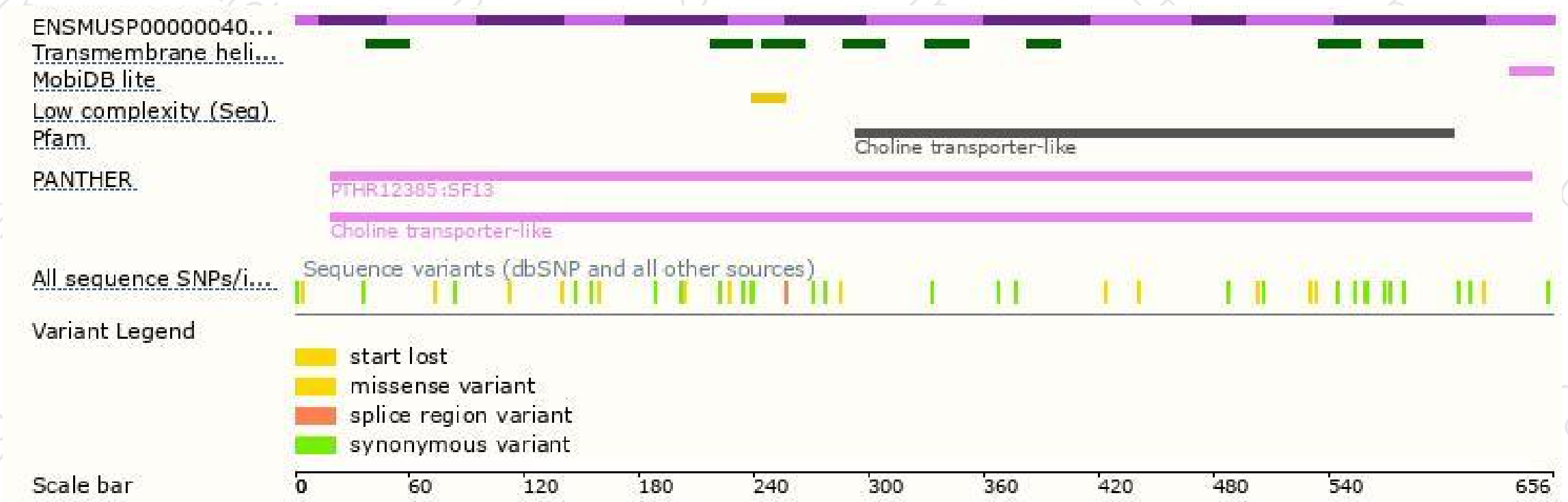
The strategy is based on the design of *Slc44a3-201* transcript,the transcription is shown below



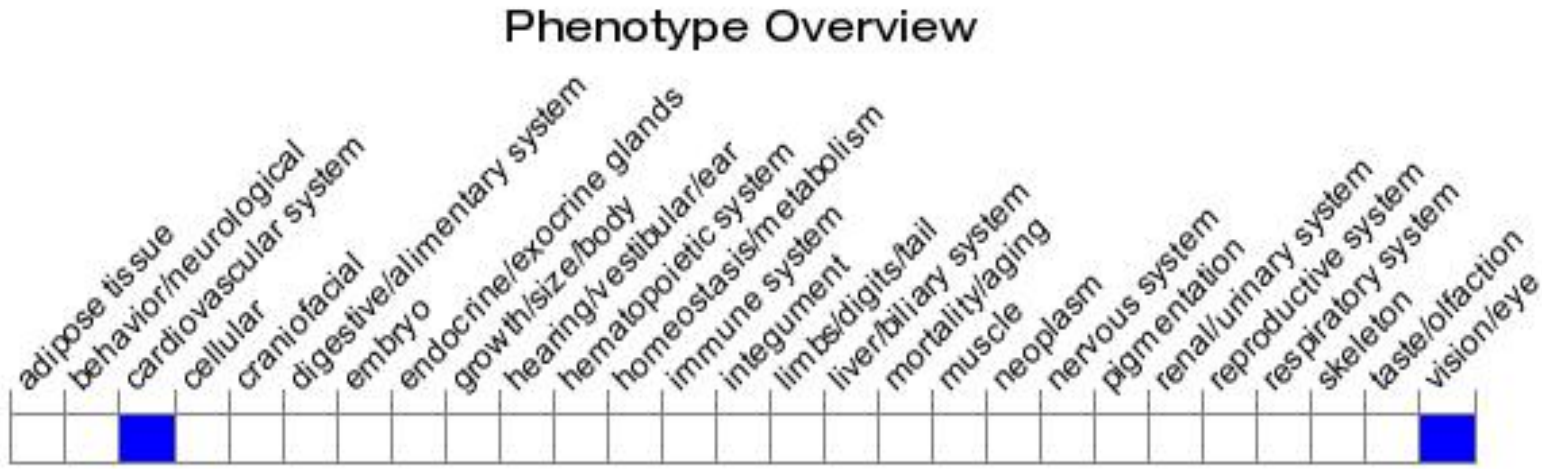
Genomic location distribution



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.

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