

# *Slc44a3* Cas9-CKO Strategy

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**Reviewer:** Yanhua Shen

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# Project Overview

**Project Name**

*Slc44a3*

**Project type**

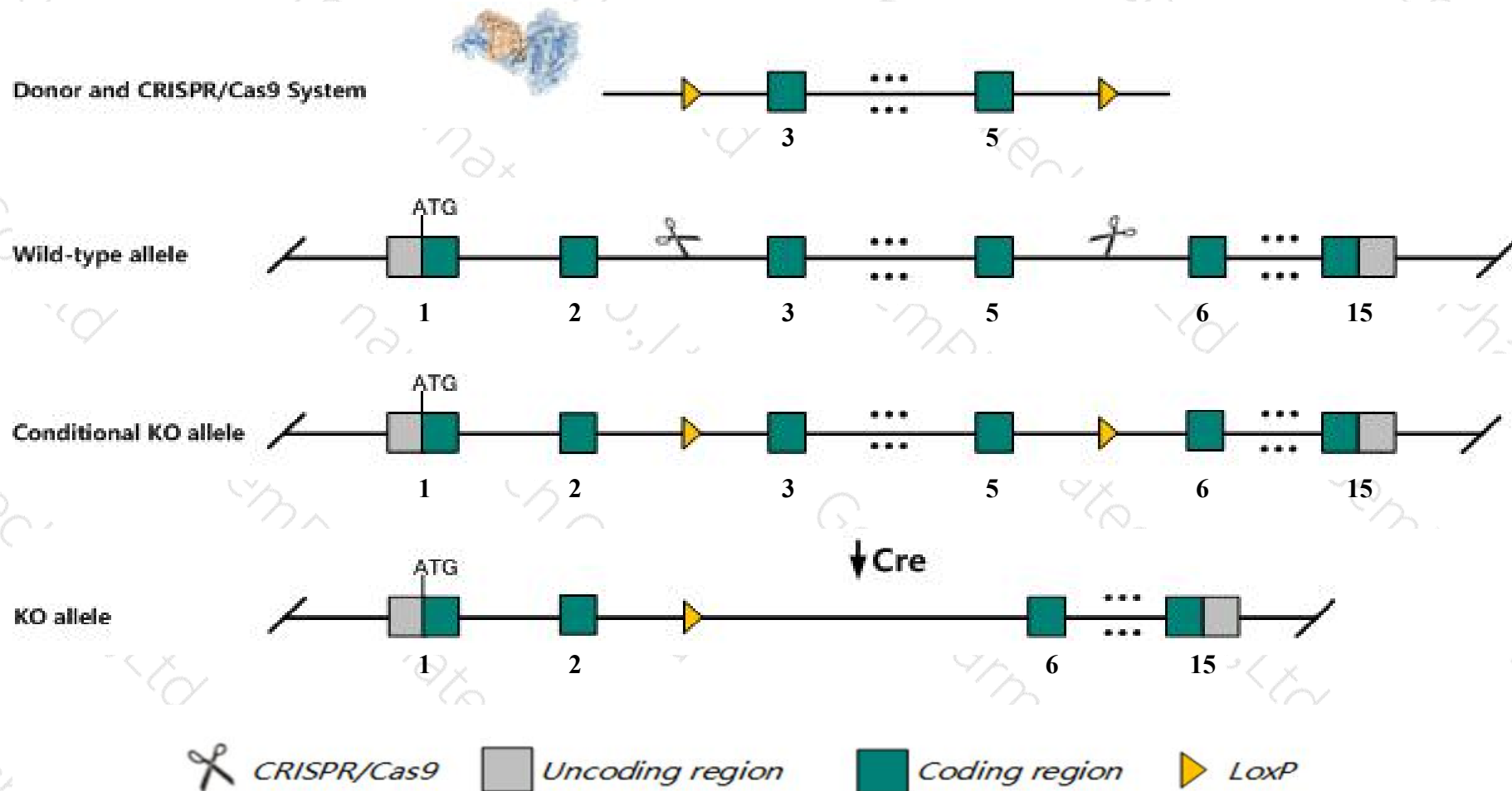
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional 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 and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- Transcript *Slc44a3*-202 may not be affected.
- The floxed 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

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

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

### Summary



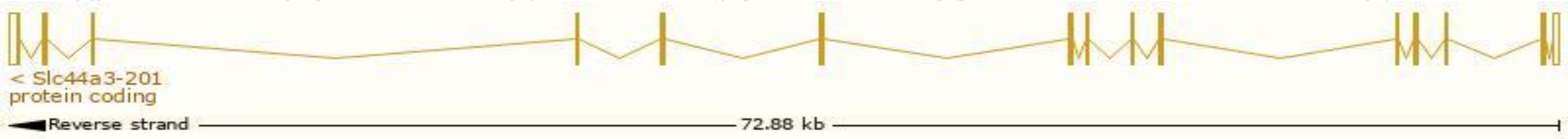
<b>Official Symbol</b>	Slc44a3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 44, member 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2384860</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000039865</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	BC010552
<b>Expression</b>	Broad expression in colon adult (RPKM 11.7), adrenal adult (RPKM 10.2) and 17 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

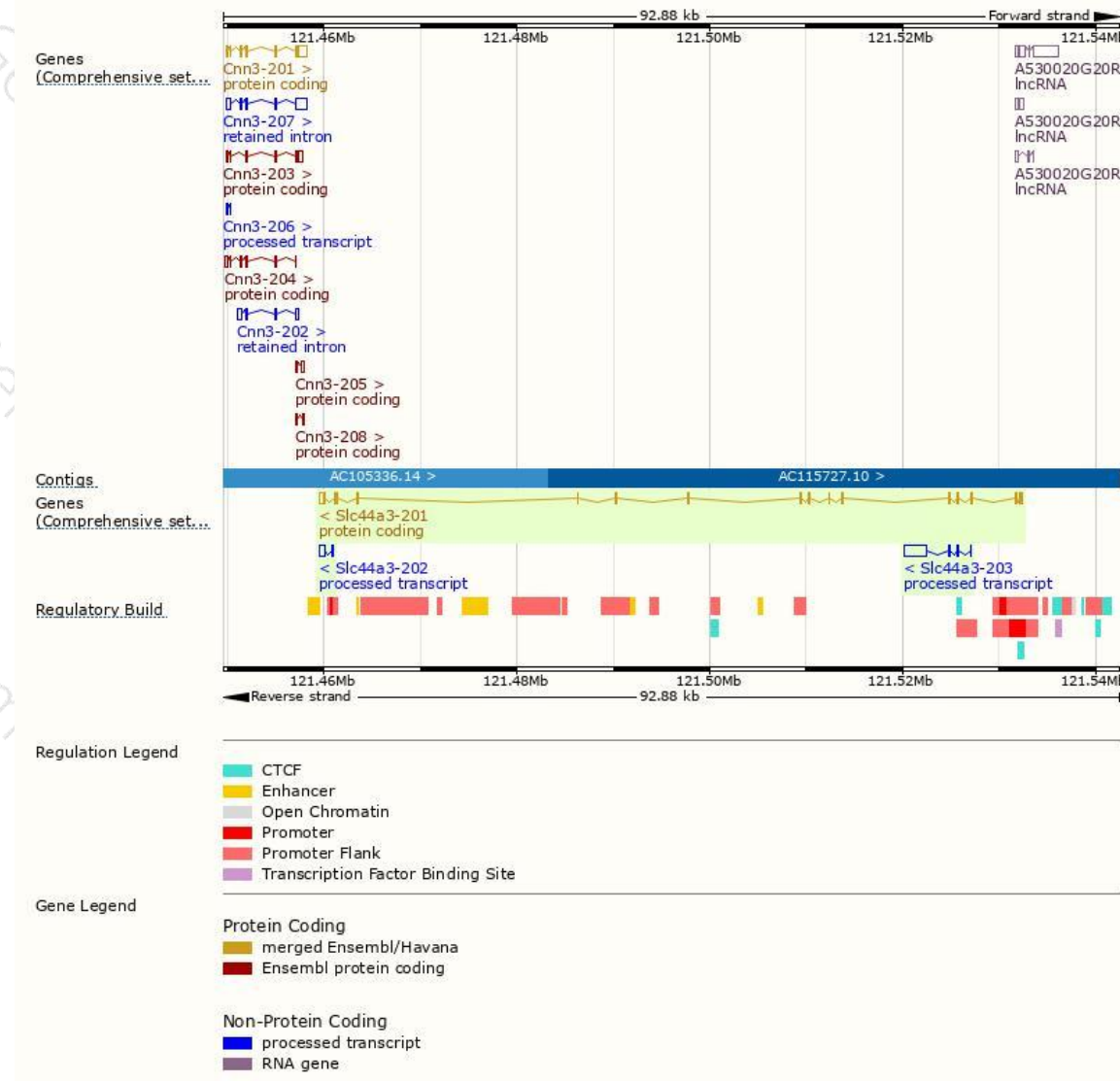
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc44a3-201	<a href="#">ENSMUST00000039197.8</a>	2620	<a href="#">656aa</a>	Protein coding	<a href="#">CCDS51060</a>	<a href="#">Q921V7</a>	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	<a href="#">ENSMUST00000199422.1</a>	2646	No protein	Processed transcript	-	-	TSL:1
Slc44a3-202	<a href="#">ENSMUST00000198335.1</a>	615	No protein	Processed transcript	-	-	TSL:3

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

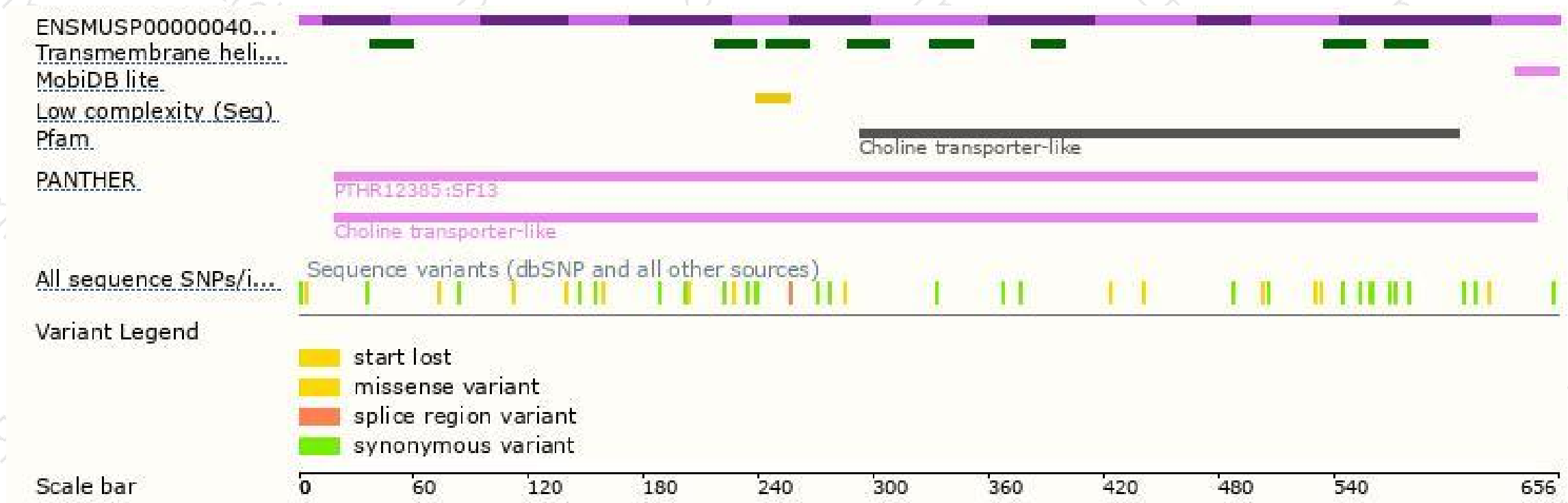


# Genomic location distribution



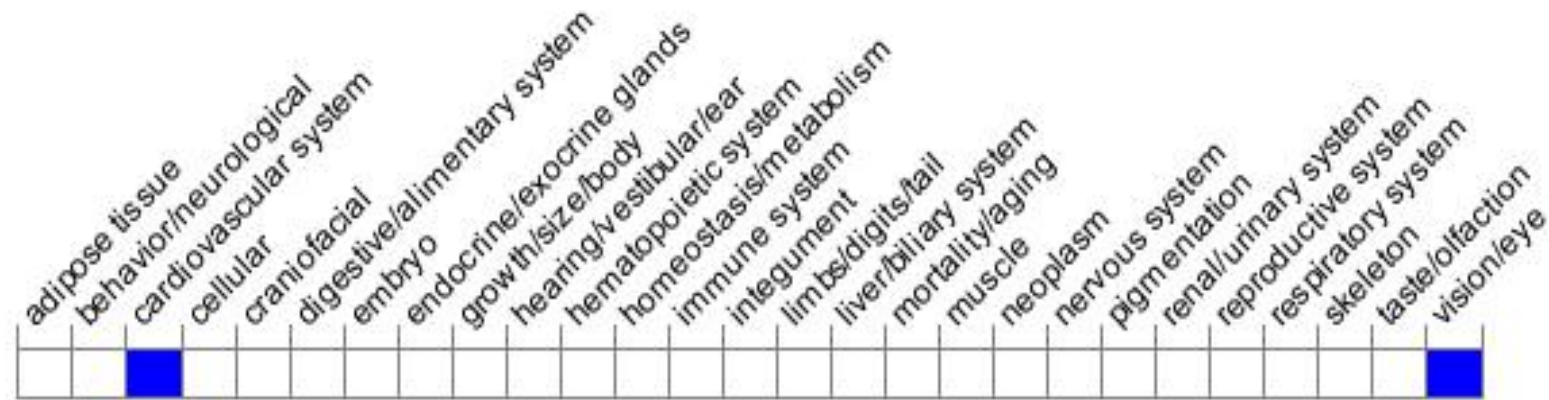


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview



*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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