

***Slc44a5* Cas9-KO Strategy**

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Project Overview

Project Name

Slc44a5

Project type

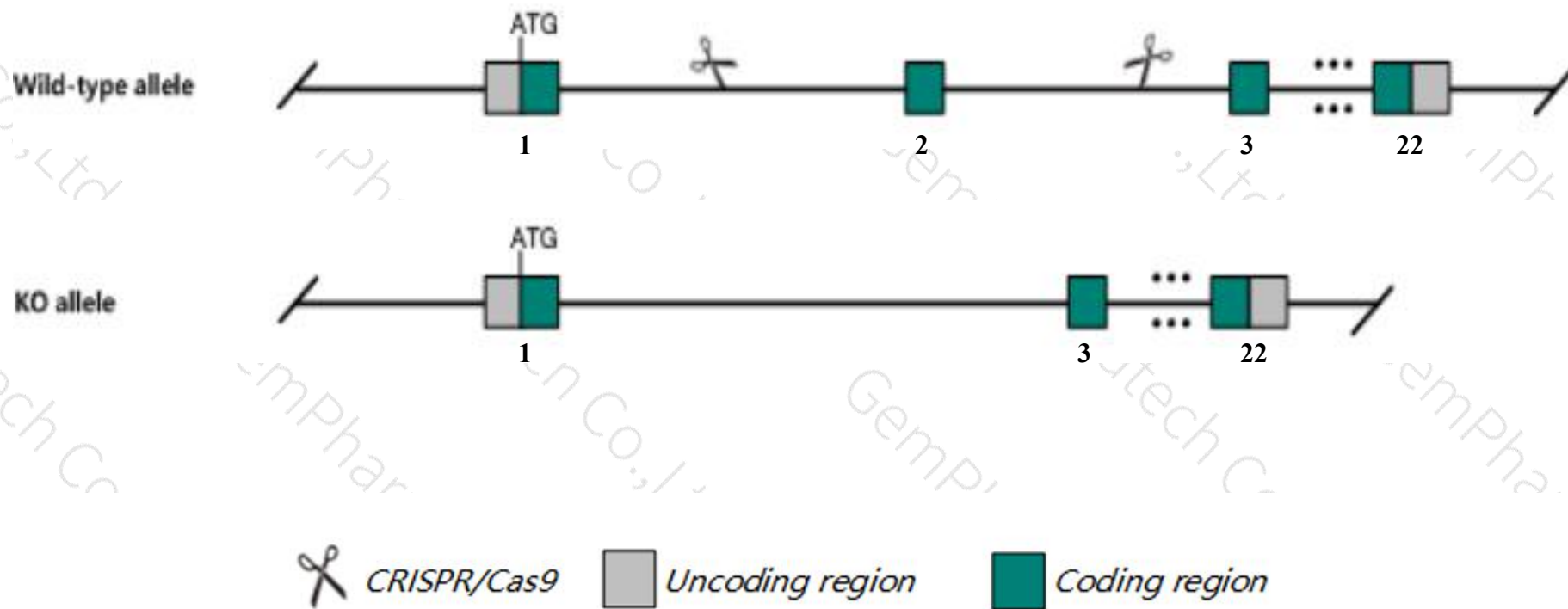
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc44a5* gene. The schematic diagram is as follows:



- The *Slc44a5* gene has 4 transcripts. According to the structure of *Slc44a5* gene, exon2 of *Slc44a5-201* (ENSMUST00000089948.5) transcript is recommended as the knockout region. The region contains 49bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc44a5* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Slc44a5*-202&203 may not be affected.
- The *Slc44a5* 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)

Slc44a5 solute carrier family 44, member 5 [Mus musculus (house mouse)]

Gene ID: 242259, updated on 13-Mar-2020

Summary



Official Symbol	Slc44a5 provided by MGI
Official Full Name	solute carrier family 44, member 5 provided by MGI
Primary source	MGI:MGI:3035141
See related	Ensembl:ENSMUSG00000028360
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA117069, Gm422
Expression	Biased expression in CNS E18 (RPKM 4.0), whole brain E14.5 (RPKM 3.7) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

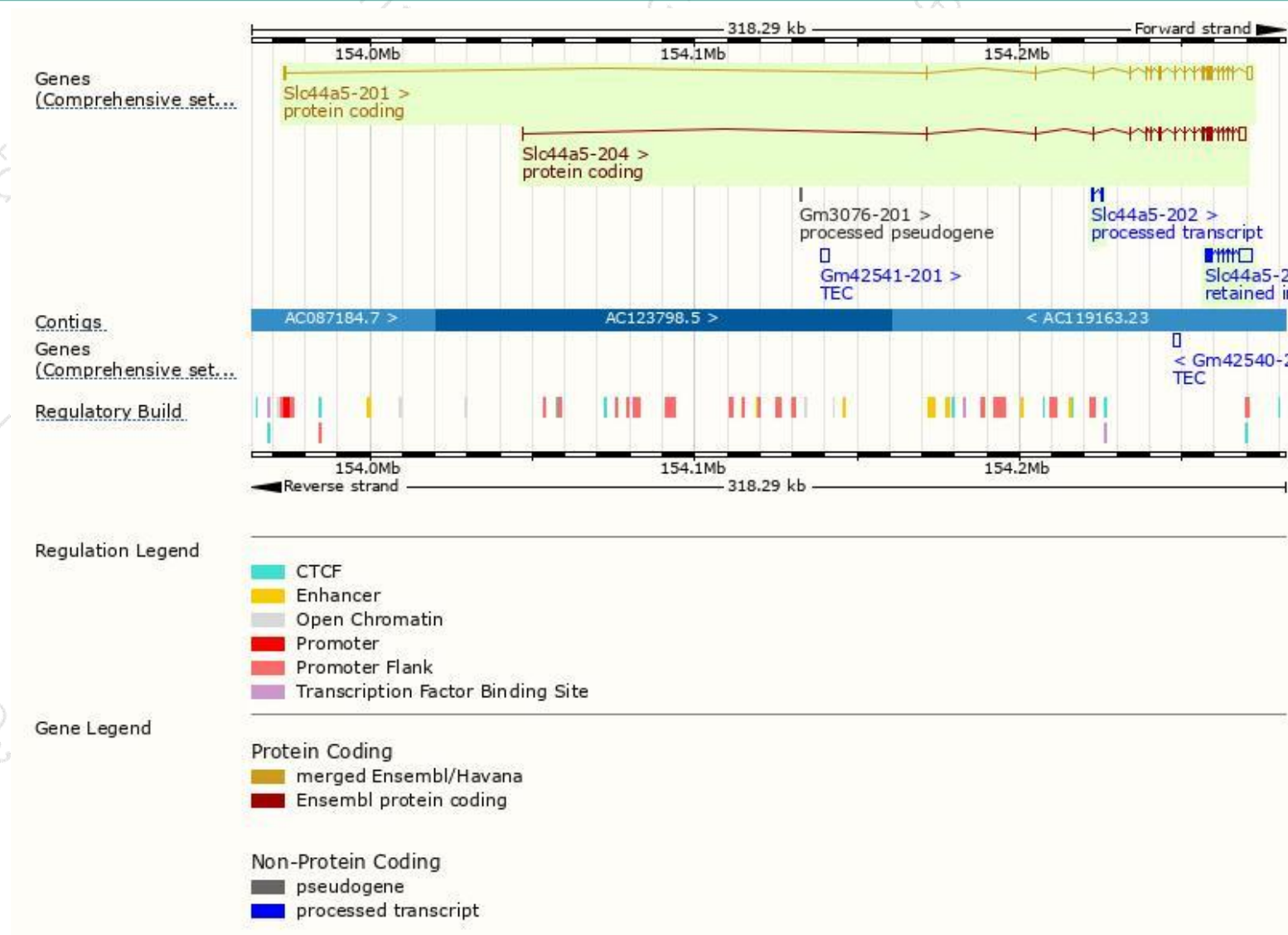
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc44a5-201	ENSMUST00000089948.5	4098	710aa	Protein coding	CCDS38679	Q5RJI2	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 P2
Slc44a5-204	ENSMUST00000239250.1	3853	721aa	Protein coding	-	-	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 ALT2
Slc44a5-202	ENSMUST00000128362.1	550	No protein	Processed transcript	-	-	TSL:2
Slc44a5-203	ENSMUST00000144677.1	5189	No protein	Retained intron	-	-	TSL:1

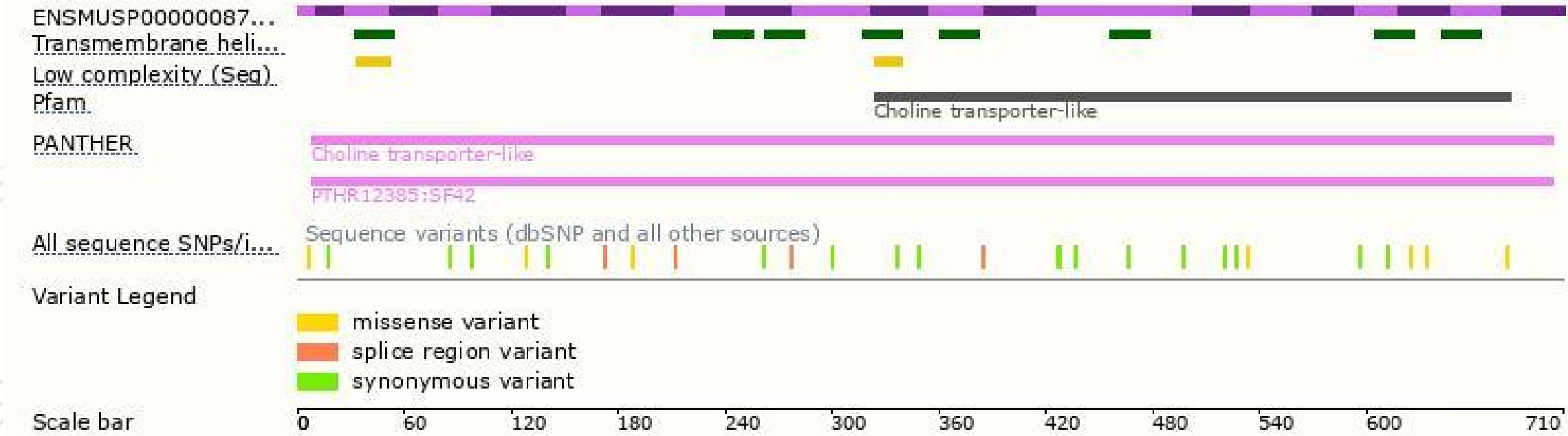
The strategy is based on the design of *Slc44a5-201* transcript,the transcription is shown below



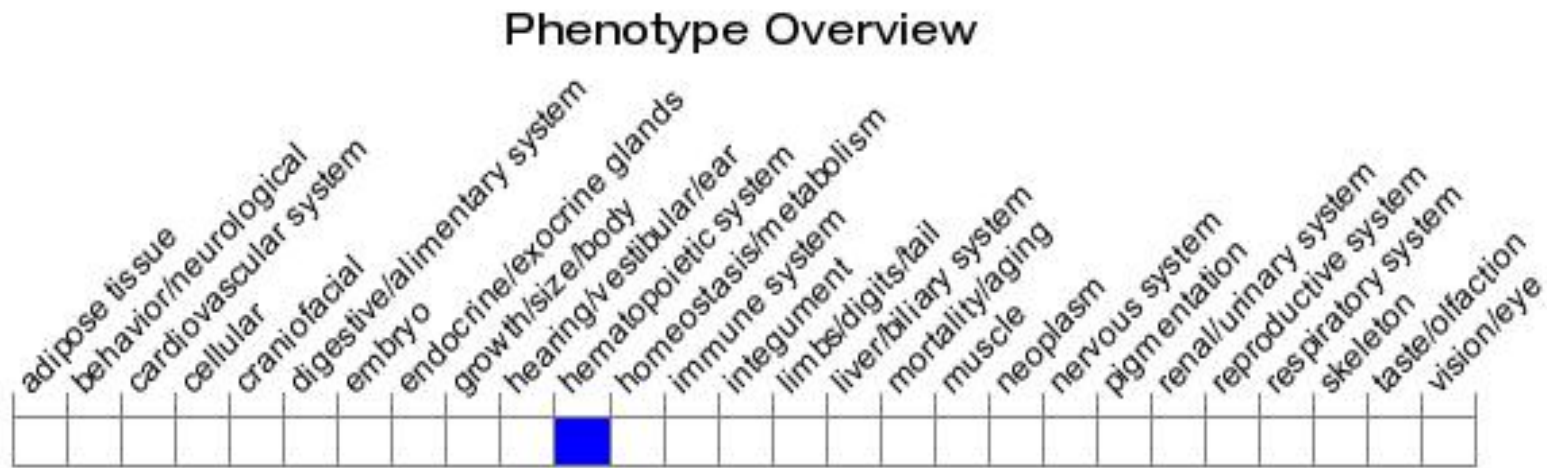
Genomic location distribution



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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