

Slc28a3 Cas9-KO Strategy

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Project Overview

Project Name

Slc28a3

Project type

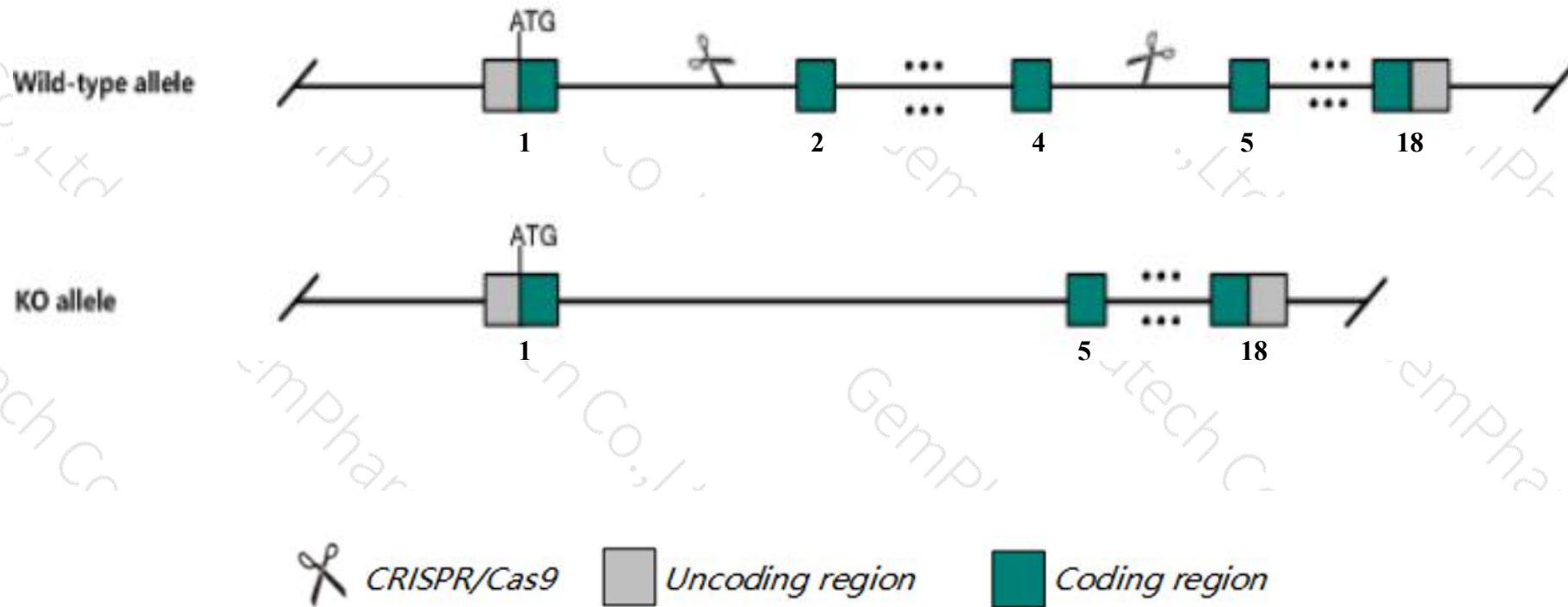
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc28a3* gene. The schematic diagram is as follows:



- The *Slc28a3* gene has 5 transcripts. According to the structure of *Slc28a3* gene, exon2-exon4 of *Slc28a3-201* (ENSMUST00000022036.13) transcript is recommended as the knockout region. The region contains 268bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc28a3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Slc28a3* gene is located on the Chr13. 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.
- Transcript *Slc28a3*-201 may not be affected.
- 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)

Slc28a3 solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 [Mus musculus (house mouse)]

Gene ID: 114304, updated on 13-Mar-2020

Summary



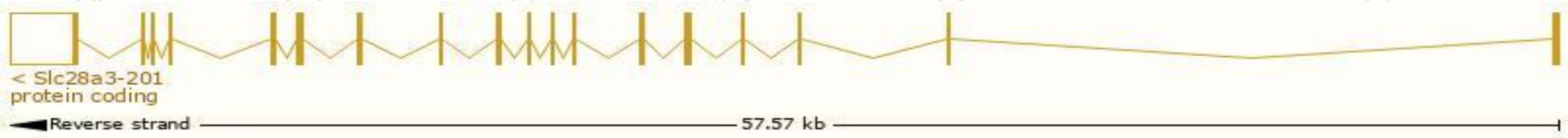
Official Symbol	Slc28a3 provided by MGI
Official Full Name	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 provided by MGI
Primary source	MGI:MGI:2137361
See related	Ensembl:ENSMUSG00000021553
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cnt3
Expression	Biased expression in genital fat pad adult (RPKM 5.2), large intestine adult (RPKM 5.0) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

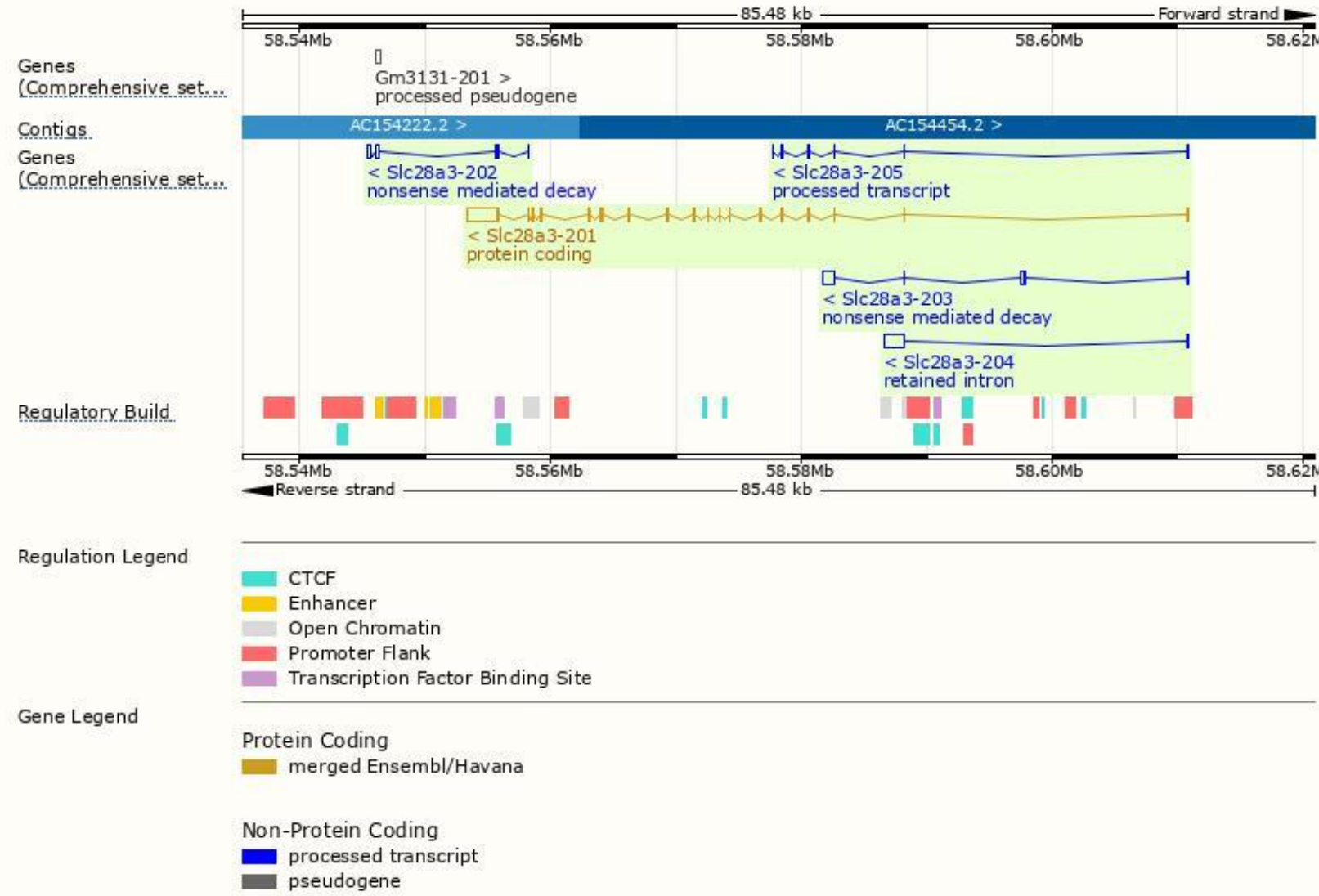
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc28a3-201	ENSMUST00000022036.13	4567	703aa	Protein coding	CCDS26572	Q9ERH8	TSL:1 GENCODE basic APPRIS P1
Slc28a3-203	ENSMUST00000148396.1	1709	68aa	Nonsense mediated decay	-	D6RFS6	TSL:1
Slc28a3-202	ENSMUST00000140760.1	757	61aa	Nonsense mediated decay	-	F6VNY5	CDS 5' incomplete TSL:3
Slc28a3-205	ENSMUST00000224906.1	662	No protein	Processed transcript	-	-	
Slc28a3-204	ENSMUST00000151675.1	1762	No protein	Retained intron	-	-	TSL:1

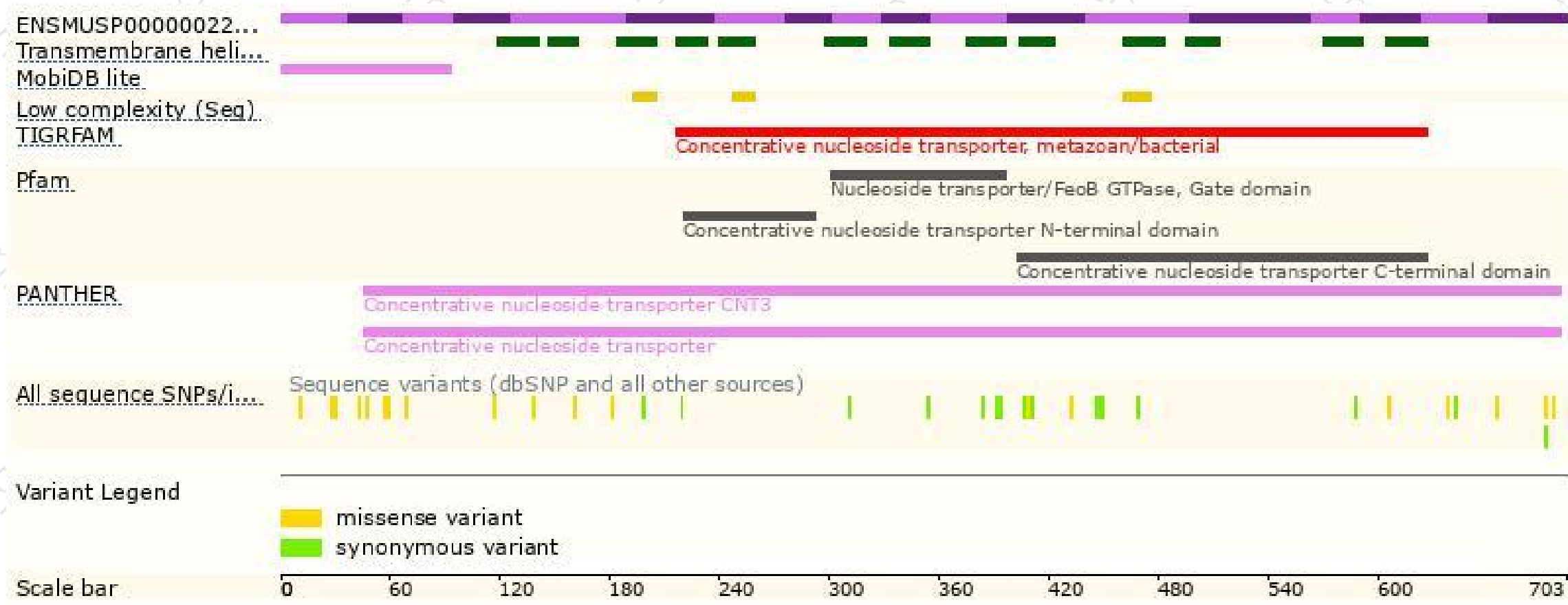
The strategy is based on the design of *Slc28a3-201* transcript,the transcription is shown below:



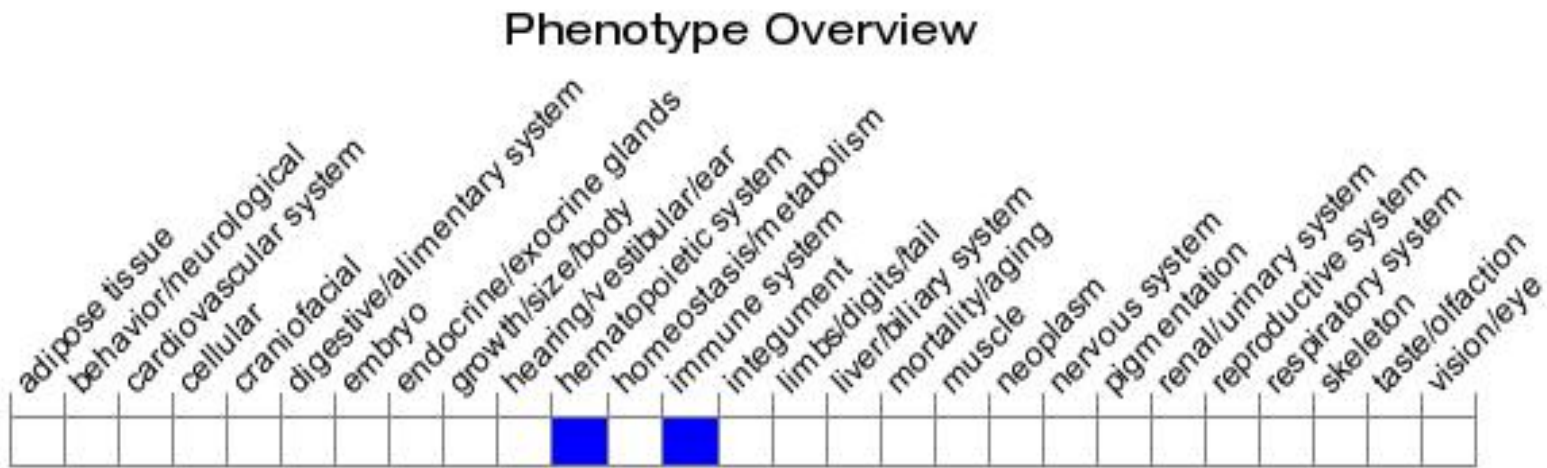
Genomic location distribution



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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