

Slc38a3 Cas9-KO Strategy

Designer: Huimin Su

Reviewer: Ruiuri Zhang

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Project Overview

Project Name

Slc38a3

Project type

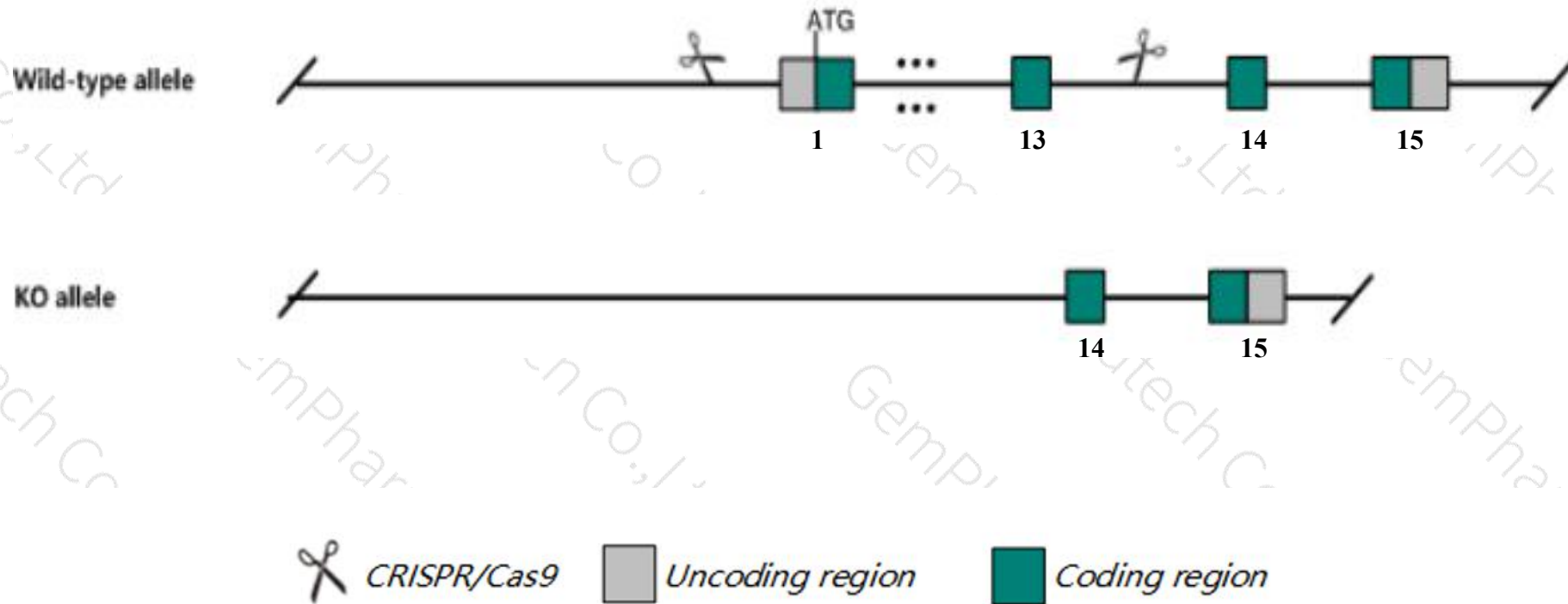
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc38a3* gene. The schematic diagram is as follows:



- The *Slc38a3* gene has 14 transcripts. According to the structure of *Slc38a3* gene, exon1-exon13 of *Slc38a3-202* (ENSMUST00000167868.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc38a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for an enu allele exhibit complete postnatal lethality between p18 and p20, altered amino acid levels in the serum, liver and brain, and decreased ammonia excretion.
- The *Slc38a3* gene is located on the Chr9. 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)

Slc38a3 solute carrier family 38, member 3 [*Mus musculus* (house mouse)]

Gene ID: 76257, updated on 13-Mar-2020

Summary

Official Symbol Slc38a3 provided by [MGI](#)

Official Full Name solute carrier family 38, member 3 provided by [MGI](#)

Primary source [MGI:MGI:1923507](#)

See related [Ensembl:ENSMUSG00000010064](#)

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 Sn1; Nat1; mNAT; Snat3; D9Ucla2; Slc38-3; 0610012J02Rik

Expression Biased expression in liver adult (RPKM 1073.0), liver E18 (RPKM 123.2) and 1 other tissue [See more](#)

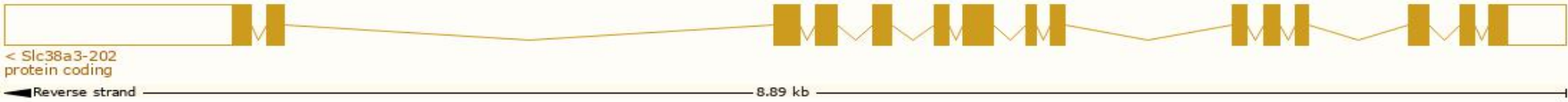
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

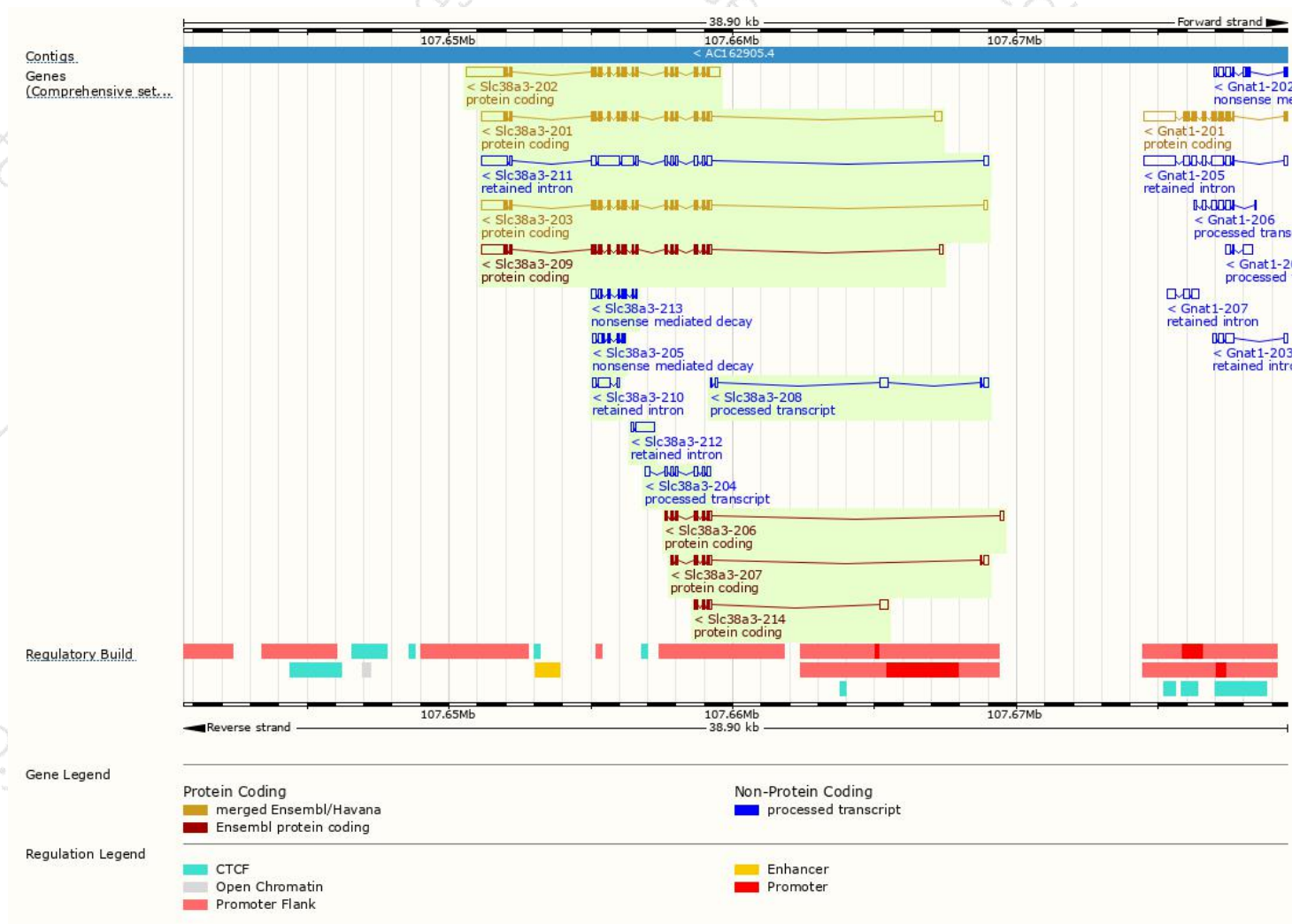
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc38a3-202	ENSMUST00000167868.7	3151	505aa	Protein coding	CCDS23503	Q9DCP2	TSL:1 GENCODE basic APPRIS P1
Slc38a3-201	ENSMUST0000010208.13	2585	505aa	Protein coding	CCDS23503	Q9DCP2	TSL:1 GENCODE basic APPRIS P1
Slc38a3-209	ENSMUST00000193932.5	2463	505aa	Protein coding	CCDS23503	Q9DCP2	TSL:1 GENCODE basic APPRIS P1
Slc38a3-203	ENSMUST00000177567.7	2456	505aa	Protein coding	CCDS23503	Q9DCP2	TSL:1 GENCODE basic APPRIS P1
Slc38a3-206	ENSMUST00000192323.5	696	181aa	Protein coding	-	A0A0A6YX60	CDS 3' incomplete TSL:3
Slc38a3-207	ENSMUST00000192990.5	691	154aa	Protein coding	-	A0A0A6YWF5	CDS 3' incomplete TSL:3
Slc38a3-214	ENSMUST00000195843.1	638	99aa	Protein coding	-	A0A0A6YWH4	CDS 3' incomplete TSL:3
Slc38a3-213	ENSMUST00000195739.1	703	160aa	Nonsense mediated decay	-	A0A0A6YWC0	CDS 5' incomplete TSL:3
Slc38a3-205	ENSMUST00000192211.1	641	125aa	Nonsense mediated decay	-	A0A0A6YW18	CDS 5' incomplete TSL:3
Slc38a3-204	ENSMUST00000191923.1	731	No protein	Processed transcript	-	-	TSL:3
Slc38a3-208	ENSMUST00000193495.1	624	No protein	Processed transcript	-	-	TSL:3
Slc38a3-211	ENSMUST00000194895.5	3133	No protein	Retained intron	-	-	TSL:2
Slc38a3-212	ENSMUST00000195033.1	780	No protein	Retained intron	-	-	TSL:2
Slc38a3-210	ENSMUST00000194230.1	614	No protein	Retained intron	-	-	TSL:5

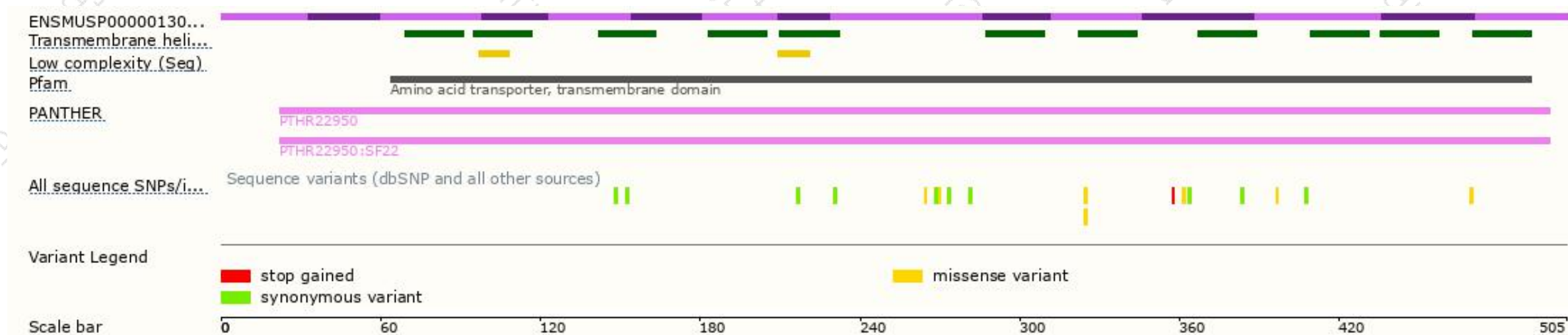
The strategy is based on the design of *Slc38a3-202* transcript, the transcription is shown below



Genomic location distribution

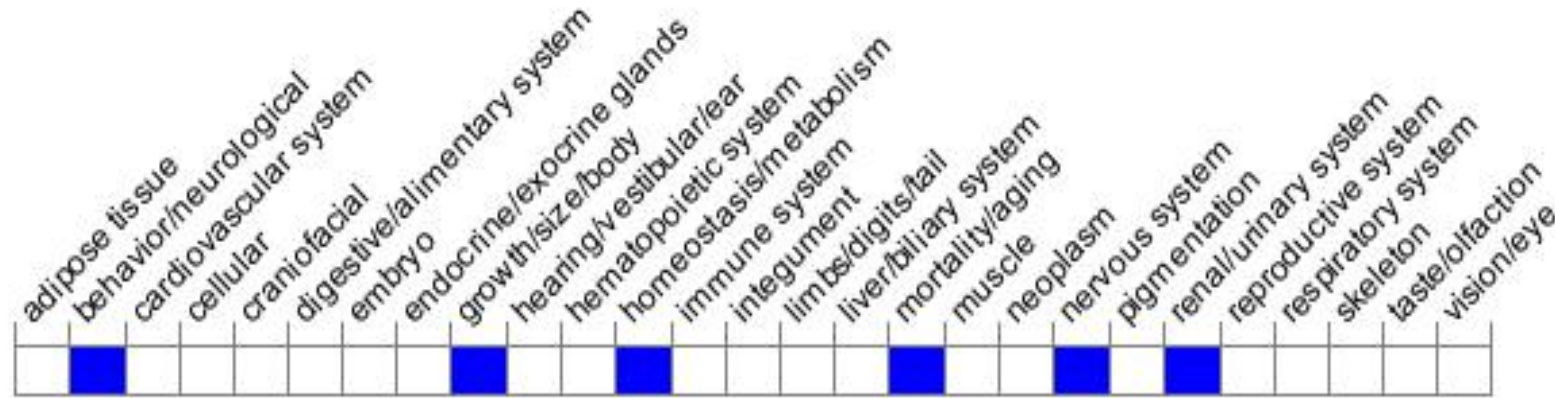


Protein domain



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/>).

According to the existing MGI data, Mice homozygous for an ENU allele exhibit complete postnatal lethality between P18 and P20, altered amino acid levels in the serum, liver and brain, and decreased ammonia excretion.

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

Tel: 400-9660890

