

Slc14a1 Cas9-KO Strategy

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Date: 2019-12-13

Project Overview

Project Name

Slc14a1

Project type

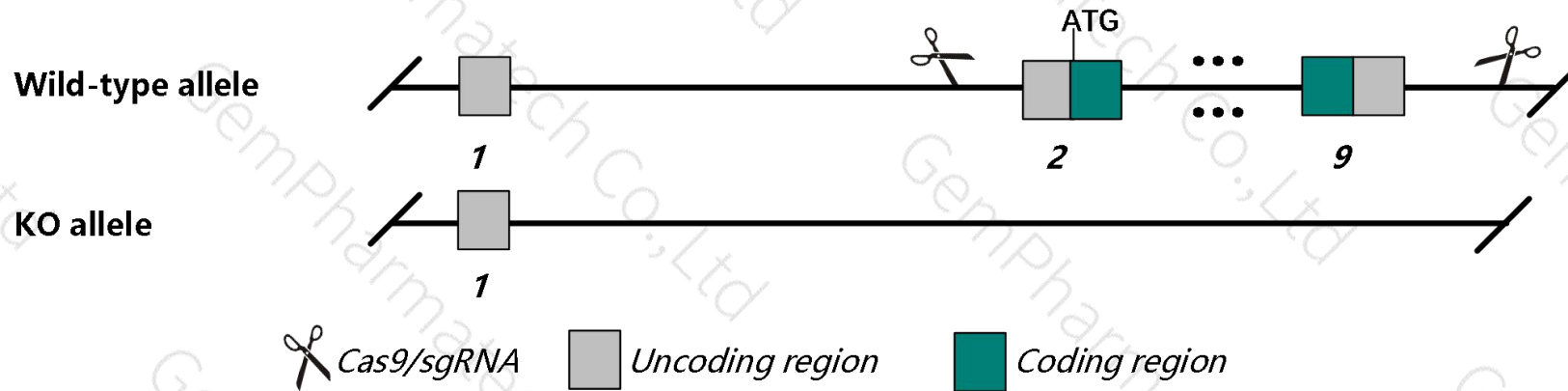
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc14a1* gene. The schematic diagram is as follows:



- The *Slc14a1* gene has 3 transcripts. According to the structure of *Slc14a1* gene, exon2-exon9 of *Slc14a1-201* (ENSMUST00000091813.11) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc14a1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene display a grossly normal phenotype although they have an inability to concentrate urea in urine.
- The *Slc14a1* gene is located on the Chr18. 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)

Slc14a1 solute carrier family 14 (urea transporter), member 1 [*Mus musculus* (house mouse)]

Gene ID: 108052, updated on 10-Oct-2019

Summary

Official Symbol Slc14a1 provided by [MGI](#)
Official Full Name solute carrier family 14 (urea transporter), member 1 provided by [MGI](#)
Primary source [MGI:MGI:1351654](#)
See related [Ensembl:ENSMUSG00000059336](#)
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 UT-B; Utb1; 2610507K20Rik; 3021401A05Rik
Expression Biased expression in ovary adult (RPKM 19.4), bladder adult (RPKM 19.2) and 13 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 18; 18 E3

See Slc14a1 in [Genome Data Viewer](#)

Exon count: 11

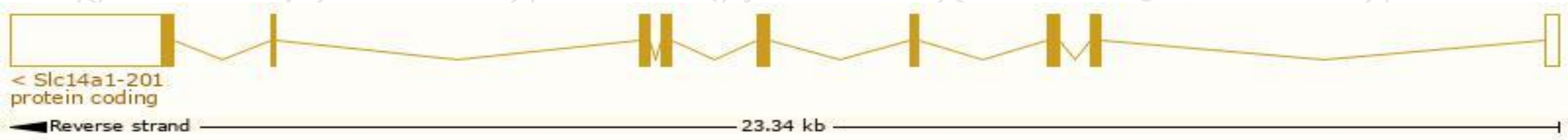
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (78100091..78142119, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (78296830..78338858, complement)

Transcript information (Ensembl)

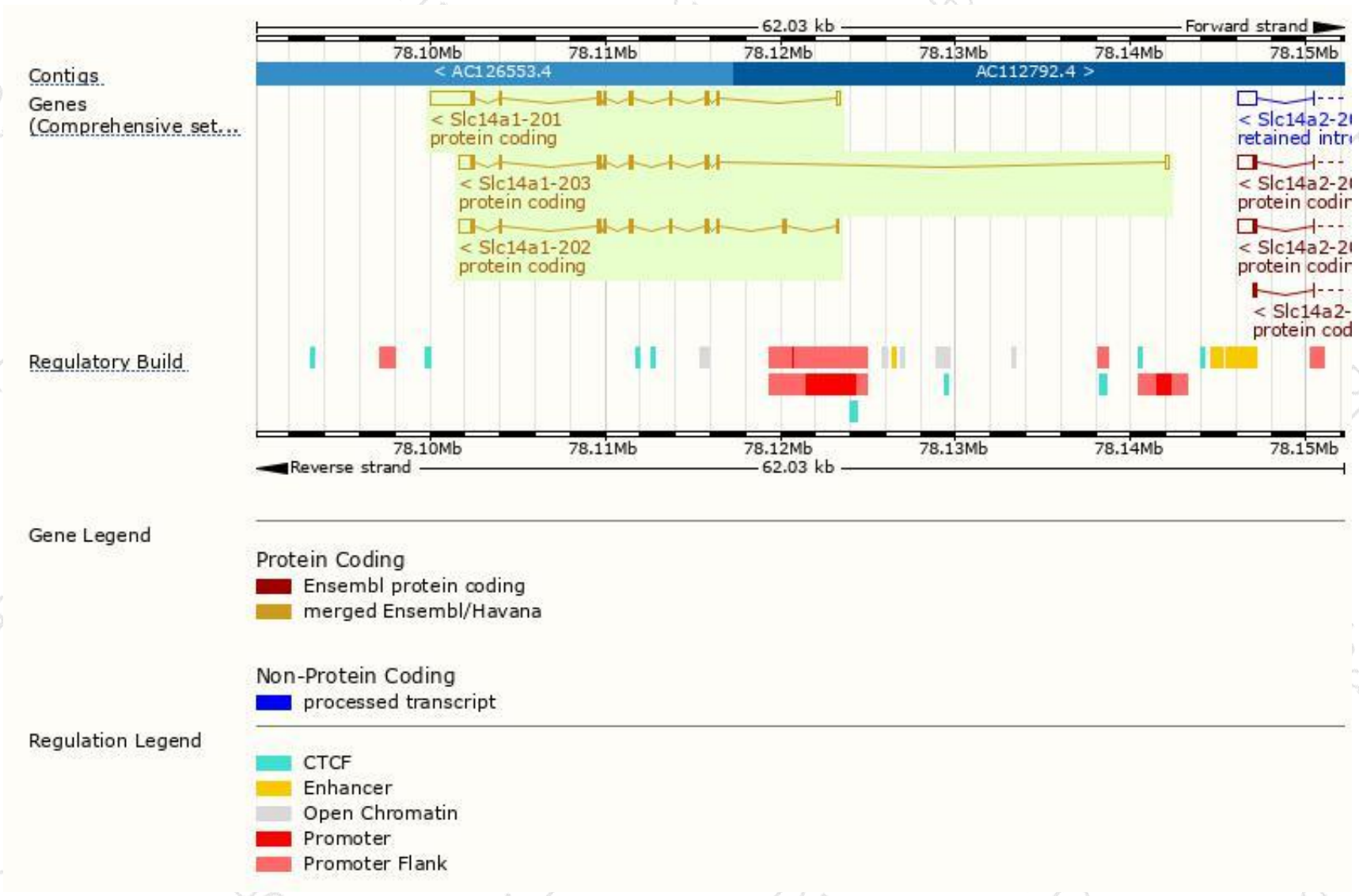
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc14a1-201	ENSMUST00000091813.11	3665	384aa	Protein coding	CCDS29360	Q8VHL0	TSL:1 GENCODE basic APPRIS P3
Slc14a1-202	ENSMUST00000160292.7	2217	440aa	Protein coding	CCDS50330	Q8VHL0	TSL:1 GENCODE basic APPRIS ALT 2
Slc14a1-203	ENSMUST00000160639.1	2047	384aa	Protein coding	CCDS29360	Q8VHL0	TSL:1 GENCODE basic APPRIS P3

The strategy is based on the design of *Slc14a1-201* transcript,The transcription is shown below



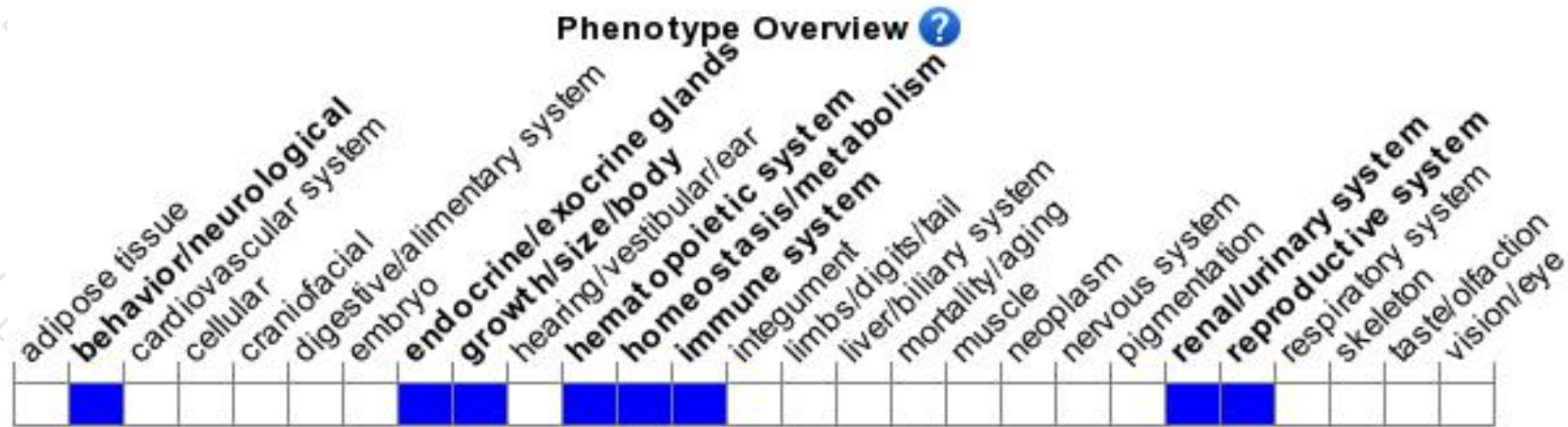
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for disruptions in this gene display a grossly normal phenotype although they have an inability to concentrate urea in urine.

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

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