

Slc12a9 Cas9-KO Strategy

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Project Overview

Project Name

Slc12a9

Project type

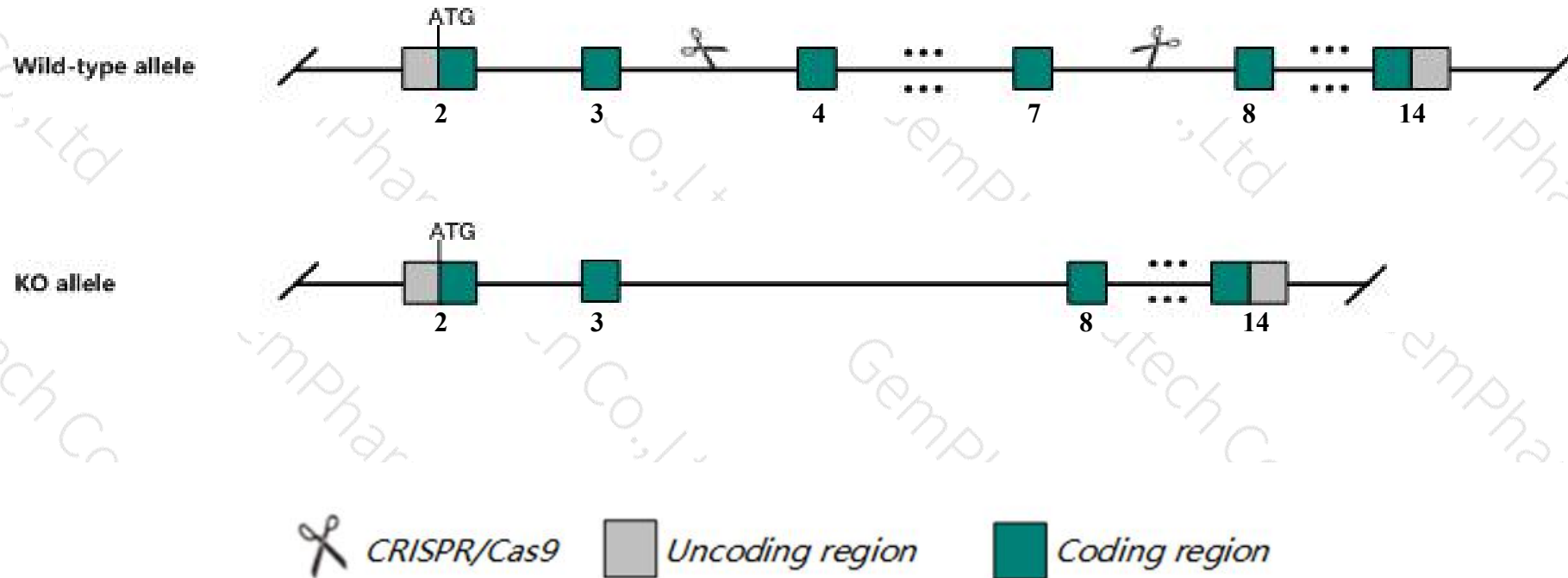
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc12a9* gene. The schematic diagram is as follows:



- The *Slc12a9* gene has 4 transcripts. According to the structure of *Slc12a9* gene, exon4-exon7 of *Slc12a9-201* (ENSMUST00000039991.13) transcript is recommended as the knockout region. The region contains 661bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc12a9* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Slc12a9* gene is located on the Chr5. 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)

Slc12a9 solute carrier family 12 (potassium/chloride transporters), member 9 [Mus musculus (house mouse)]

Gene ID: 83704, updated on 31-Jan-2019

Summary



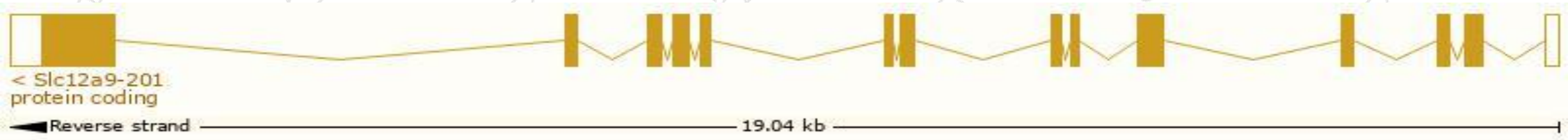
Official Symbol	Slc12a9 provided by MGI
Official Full Name	solute carrier family 12 (potassium/chloride transporters), member 9 provided by MGI
Primary source	MGI:MGI:1933532
See related	Ensembl:ENSMUSG000000037344
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CIP1
Expression	Ubiquitous expression in ovary adult (RPKM 11.1), adrenal adult (RPKM 11.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

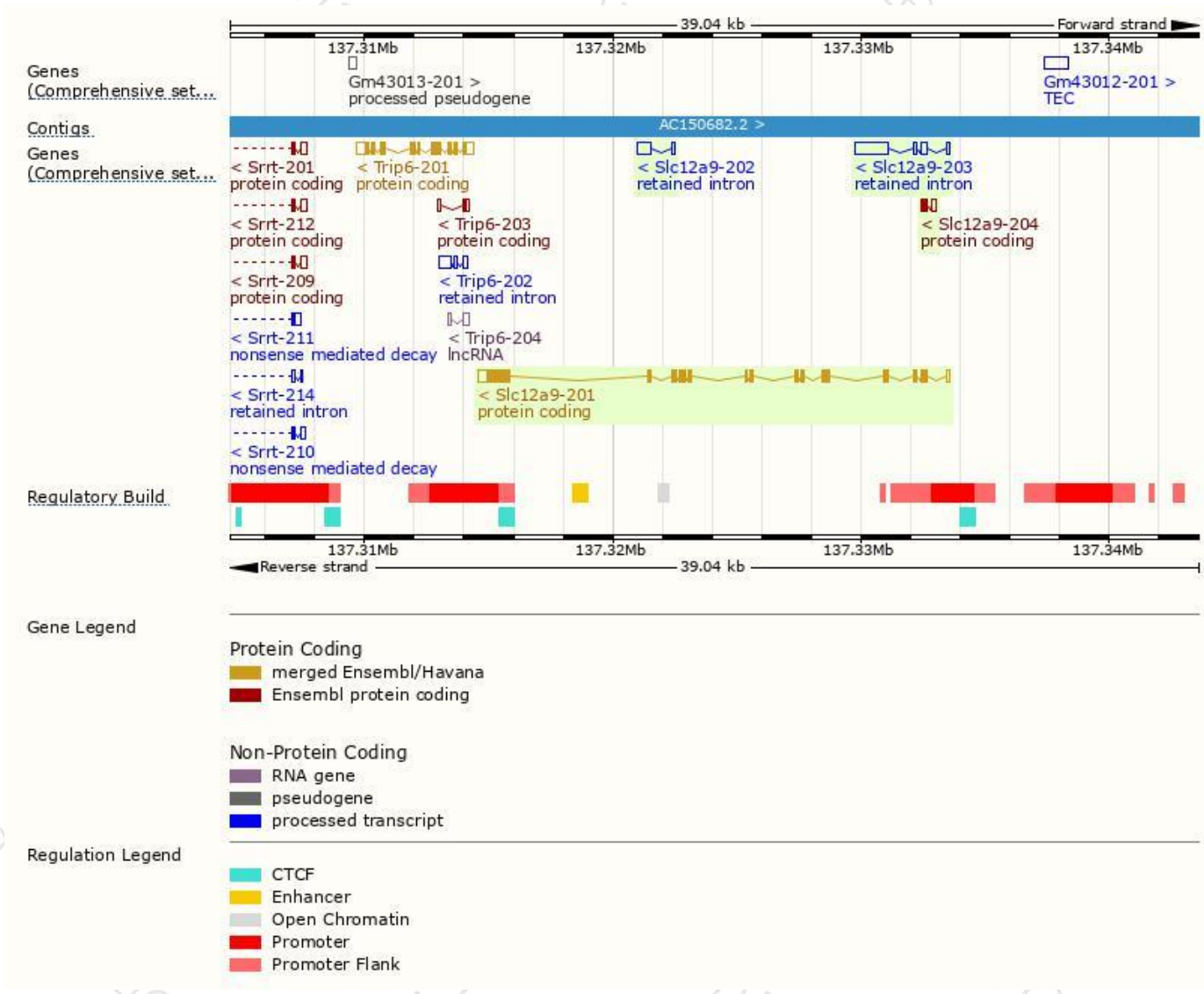
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc12a9-201	ENSMUST00000039991.13	3330	914aa	Protein coding	CCDS19766	Q99MR3	TSL:1 GENCODE basic APPRIS P1
Slc12a9-204	ENSMUST00000156646.2	365	60aa	Protein coding	-	D3Z362	CDS 3' incomplete TSL:5
Slc12a9-203	ENSMUST00000149847.1	1815	No protein	Retained intron	-	-	TSL:1
Slc12a9-202	ENSMUST00000141517.1	637	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Slc12a9-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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