

Kcnk1 Cas9-KO Strategy

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Design Date:

2020-2-10

Project Overview

Project Name

Kcnk1

Project type

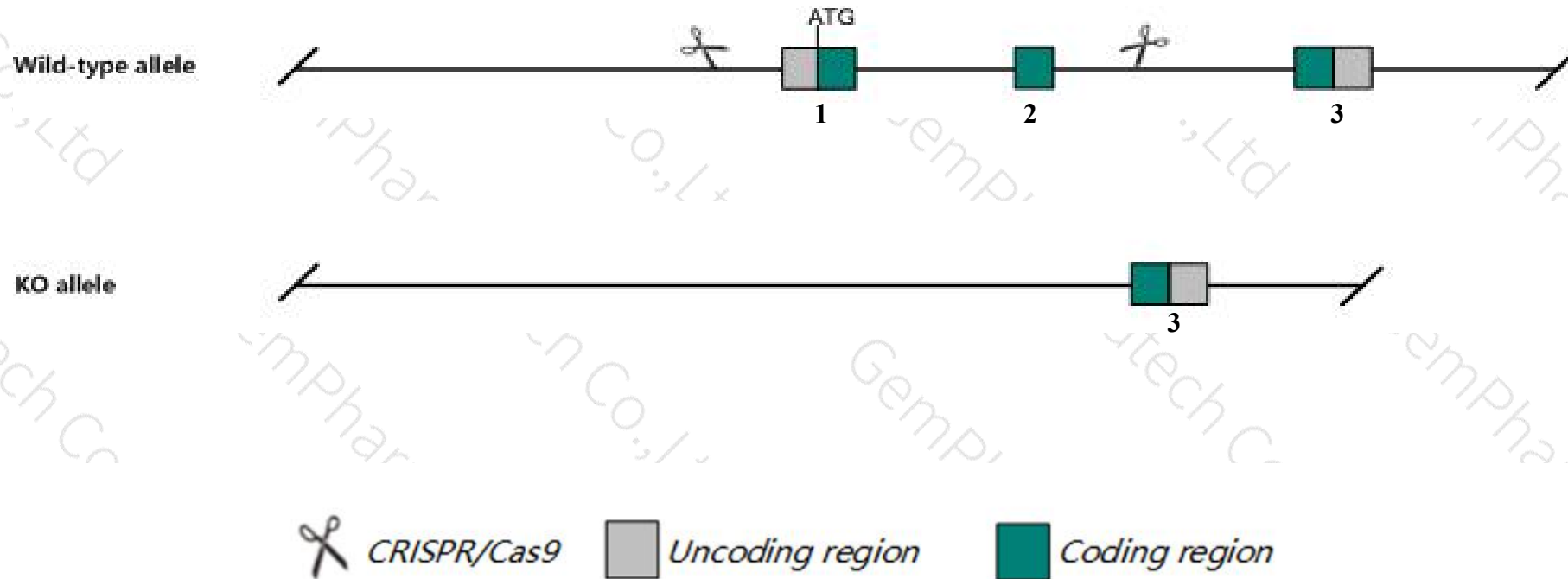
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnk1* gene. The schematic diagram is as follows:



- The *Kcnk1* gene has 2 transcripts. According to the structure of *Kcnk1* gene, exon1-exon2 of *Kcnk1-201* (ENSMUST00000046765.9) 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 *Kcnk1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null mutation reduced urinary flow rates and on a low phosphate diet display an attenuated ability to increase renal phosphate reabsorption.
- The *Kcnk1* gene is located on the Chr8. 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)

Kcnk1 potassium channel, subfamily K, member 1 [Mus musculus (house mouse)]

Gene ID: 16525, updated on 3-Feb-2019

Summary



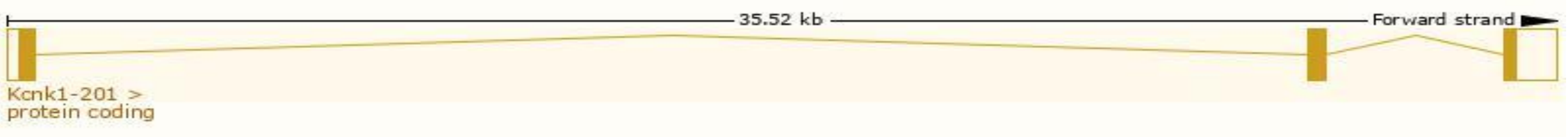
Official Symbol	Kcnk1 provided by MGI
Official Full Name	potassium channel, subfamily K, member 1 provided by MGI
Primary source	MGI:MGI:109322
See related	Ensembl:ENSMUSG00000033998
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI788889, TWIK-1
Expression	Broad expression in genital fat pad adult (RPKM 45.9), cerebellum adult (RPKM 26.7) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

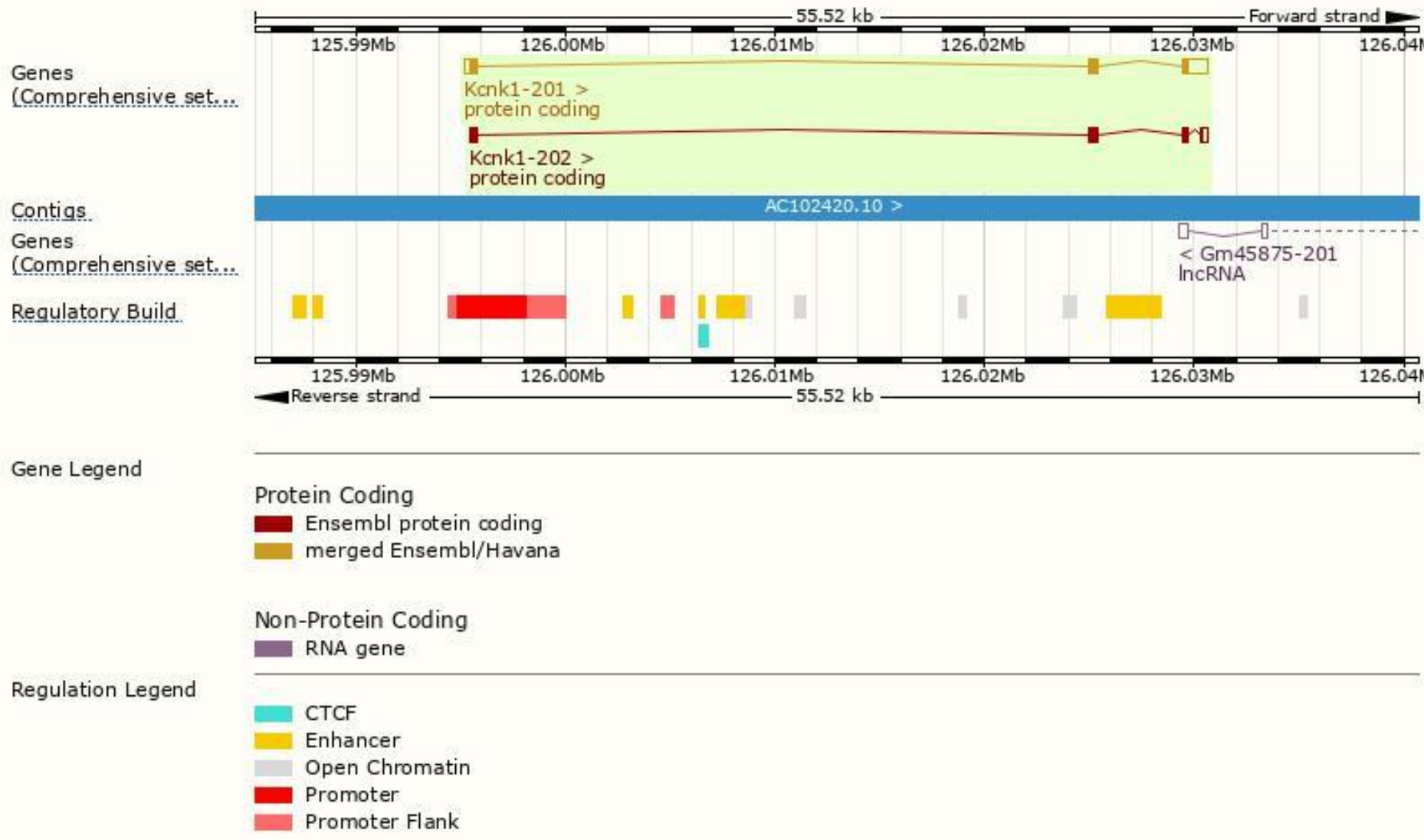
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnk1-201	ENSMUST00000046765.9	2235	336aa	Protein coding	CCDS22783	Q08581	TSL:1 GENCODE basic APPRIS P1
Kcnk1-202	ENSMUST00000212831.1	1309	328aa	Protein coding	-	A0A1D5RMH2	TSL:5 GENCODE basic

The strategy is based on the design of *Kcnk1-201* transcript,The transcription is shown below



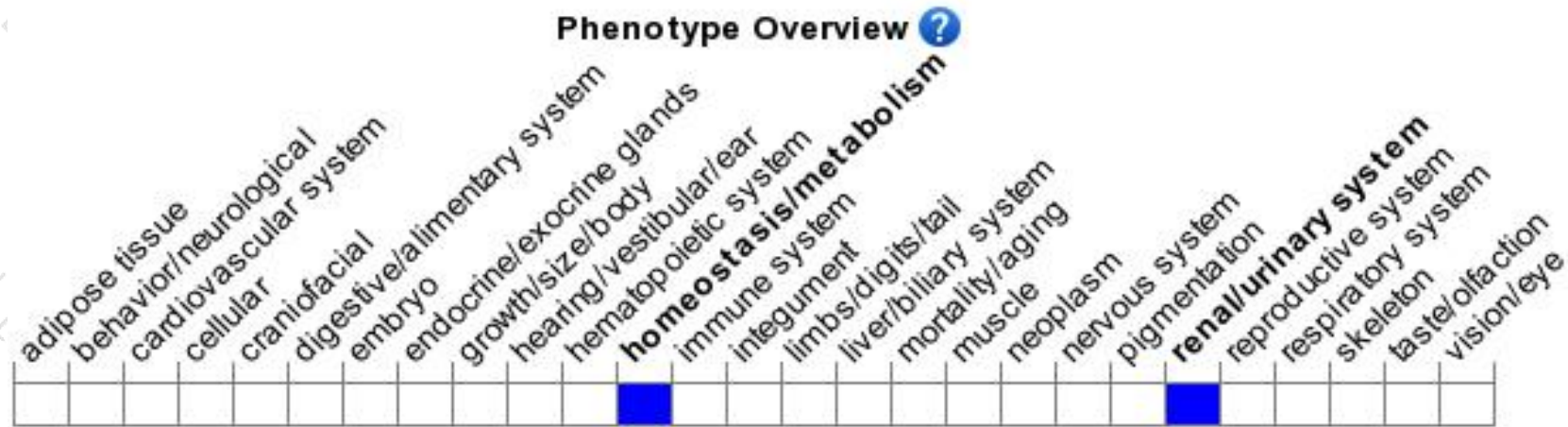
Genomic location distribution



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 a null mutation reduced urinary flow rates and on a low phosphate diet display an attenuated ability to increase renal phosphate reabsorption.

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

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