

***Kctd1* Cas9-KO Strategy**

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Project Overview

Project Name

Kctd1

Project type

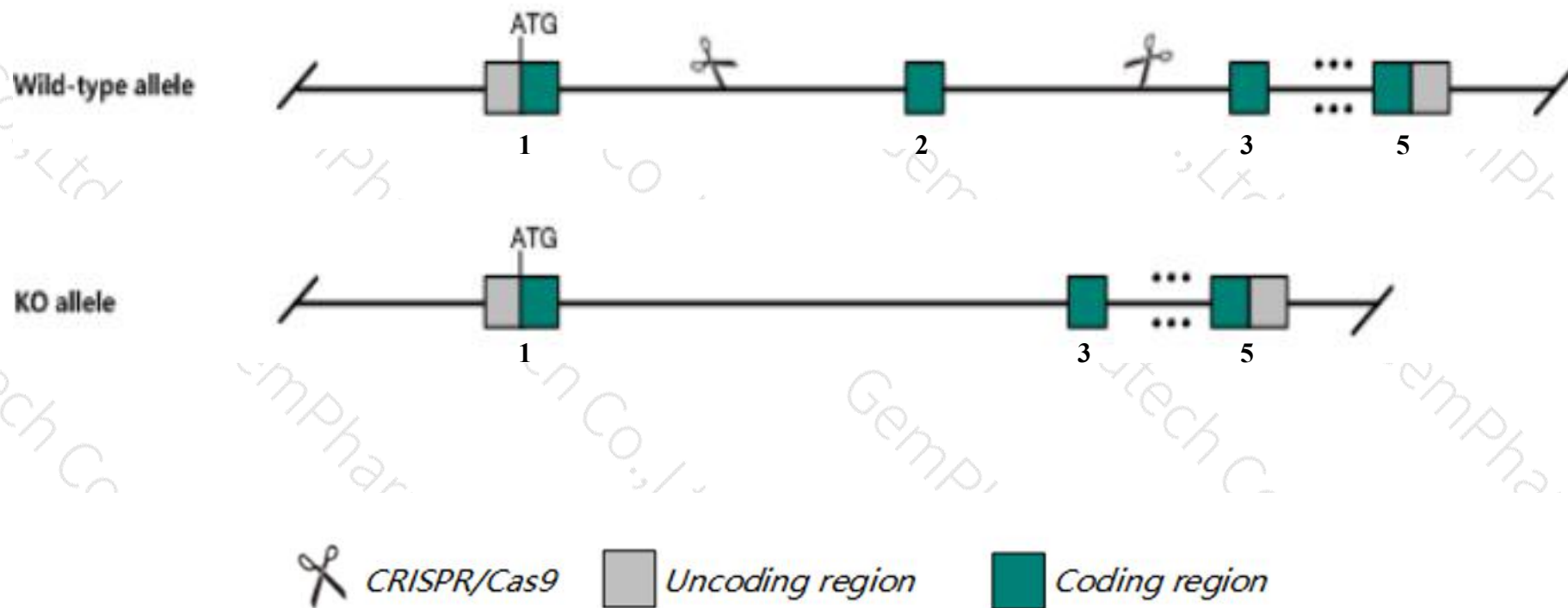
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kctd1* gene. The schematic diagram is as follows:



- The *Kctd1* gene has 6 transcripts. According to the structure of *Kctd1* gene, exon2 of *Kctd1*-202(ENSMUST00000168989.8) transcript is recommended as the knockout region. The region contains 179bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kctd1* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- This strategy may affect the function of *Mrpl27*-ps-201 and *4933424G05Rik*-201 gene.
- The *Kctd1* 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)

Kctd1 potassium channel tetramerisation domain containing 1 [Mus musculus (house mouse)]

Gene ID: 106931, updated on 13-Mar-2020

Summary



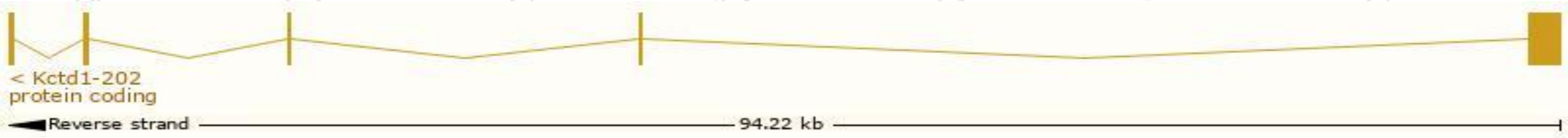
Official Symbol	Kctd1 provided by MGI
Official Full Name	potassium channel tetramerisation domain containing 1 provided by MGI
Primary source	MGI:MGI:1918269
See related	Ensembl:ENSMUSG00000036225
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4933402K10Rik, AI661543, AW553000
Expression	Broad expression in adrenal adult (RPKM 5.1), frontal lobe adult (RPKM 4.7) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

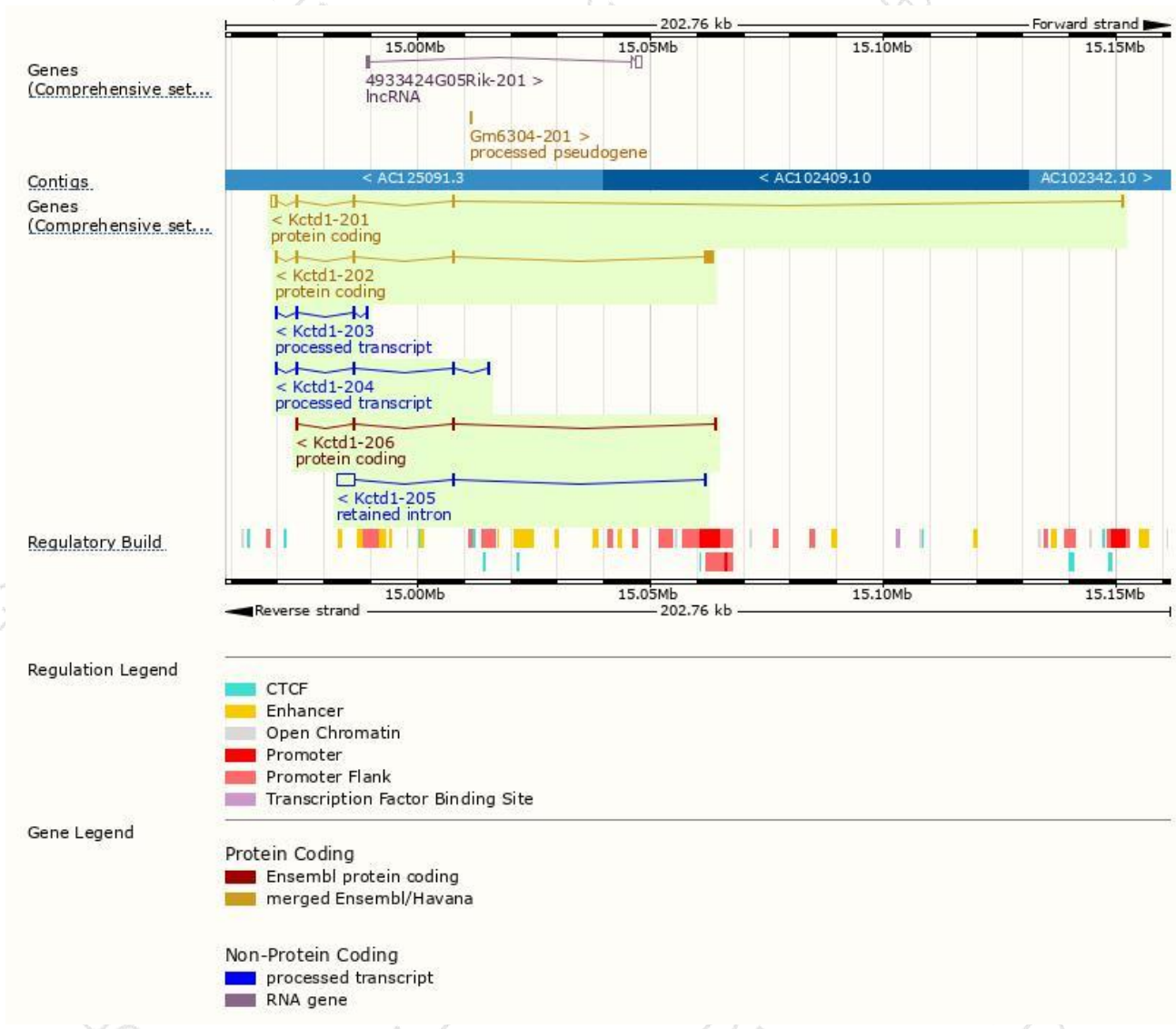
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kctd1-202	ENSMUST00000168989.8	2777	861aa	Protein coding	CCDS50228	E9Q6T9	TSL:1 GENCODE basic APPRIS P1
Kctd1-201	ENSMUST00000025992.6	1772	265aa	Protein coding	CCDS50229	Q5M956	TSL:1 GENCODE basic
Kctd1-206	ENSMUST00000234864.1	749	180aa	Protein coding	-	A0A3Q4EG48	CDS 3' incomplete
Kctd1-203	ENSMUST00000233993.1	1092	No protein	Processed transcript	-	-	
Kctd1-204	ENSMUST00000234221.1	920	No protein	Processed transcript	-	-	
Kctd1-205	ENSMUST00000234685.1	4061	No protein	Retained intron	-	-	

The strategy is based on the design of *Kctd1-202* transcript,the transcription is shown below:



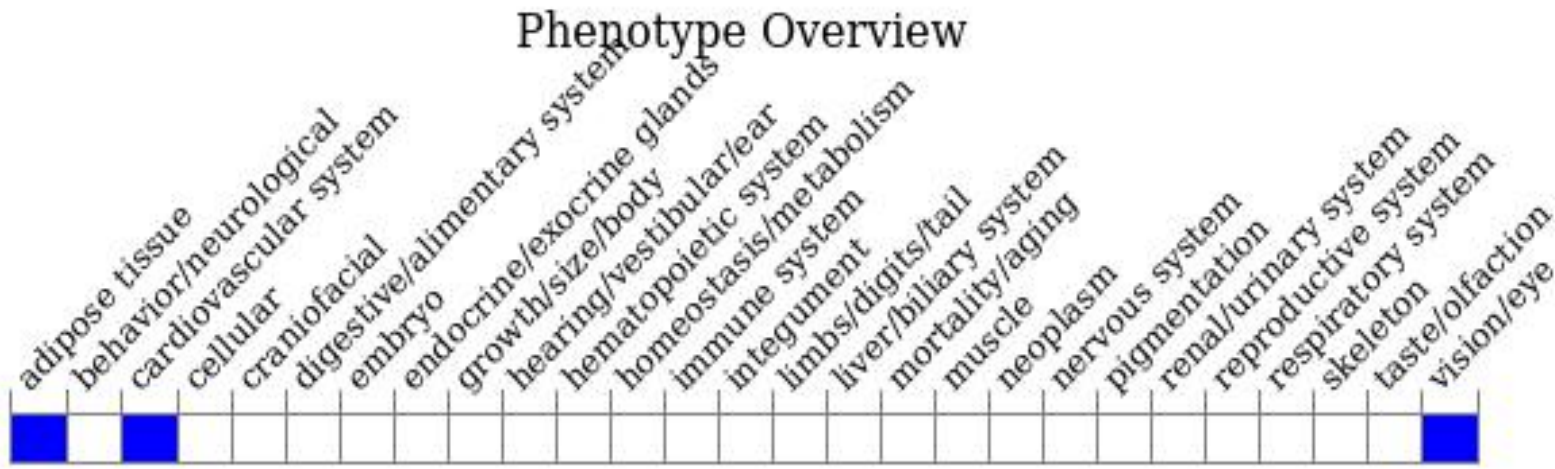
Genomic location distribution



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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