

***Kctd1* Cas9-CKO Strategy**

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Project Overview

Project Name

Kctd1

Project type

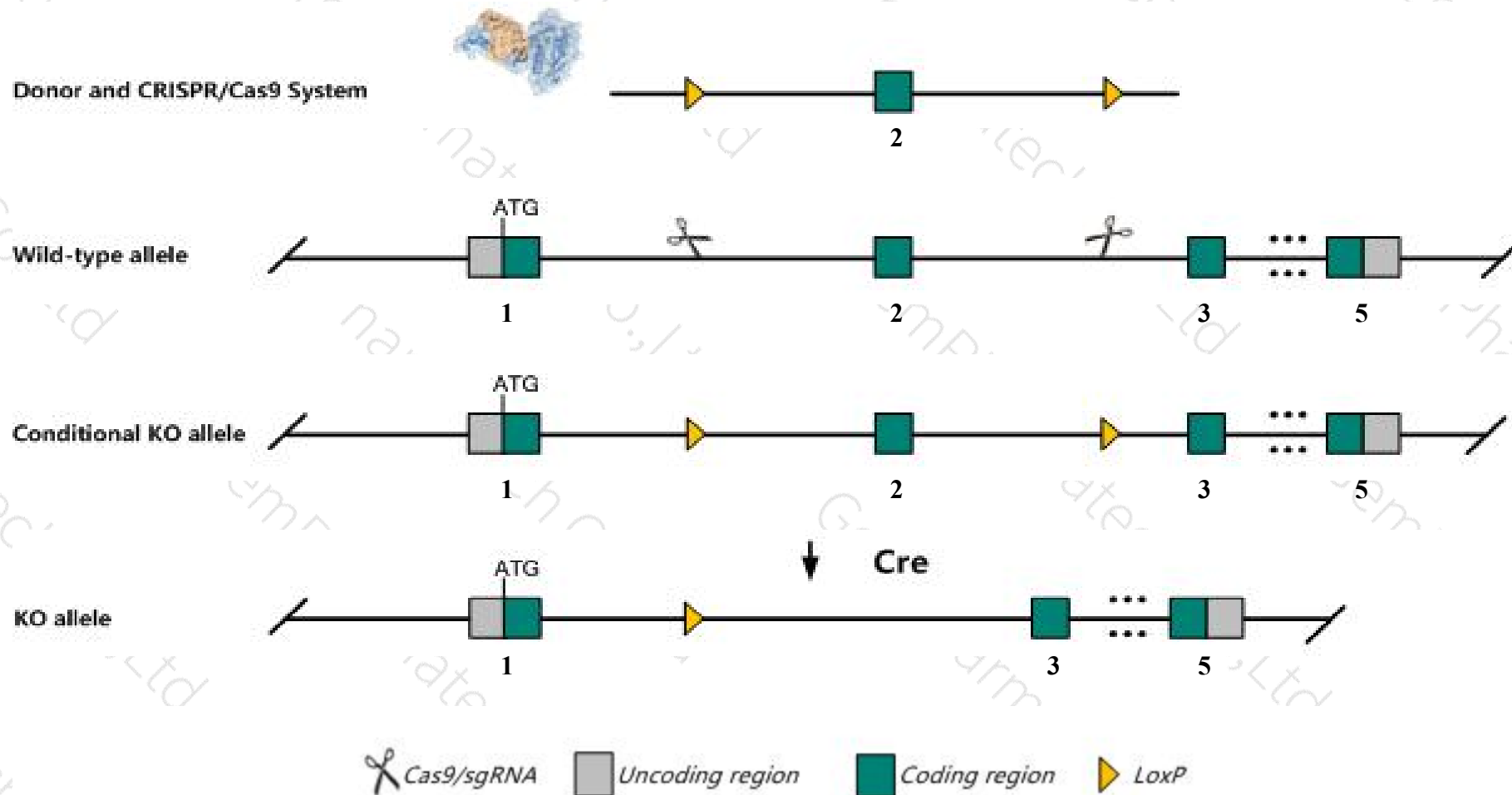
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- 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: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

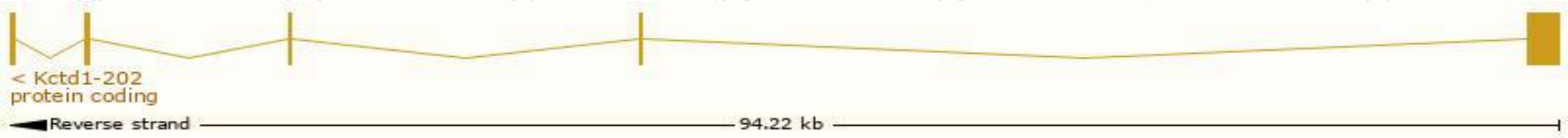
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

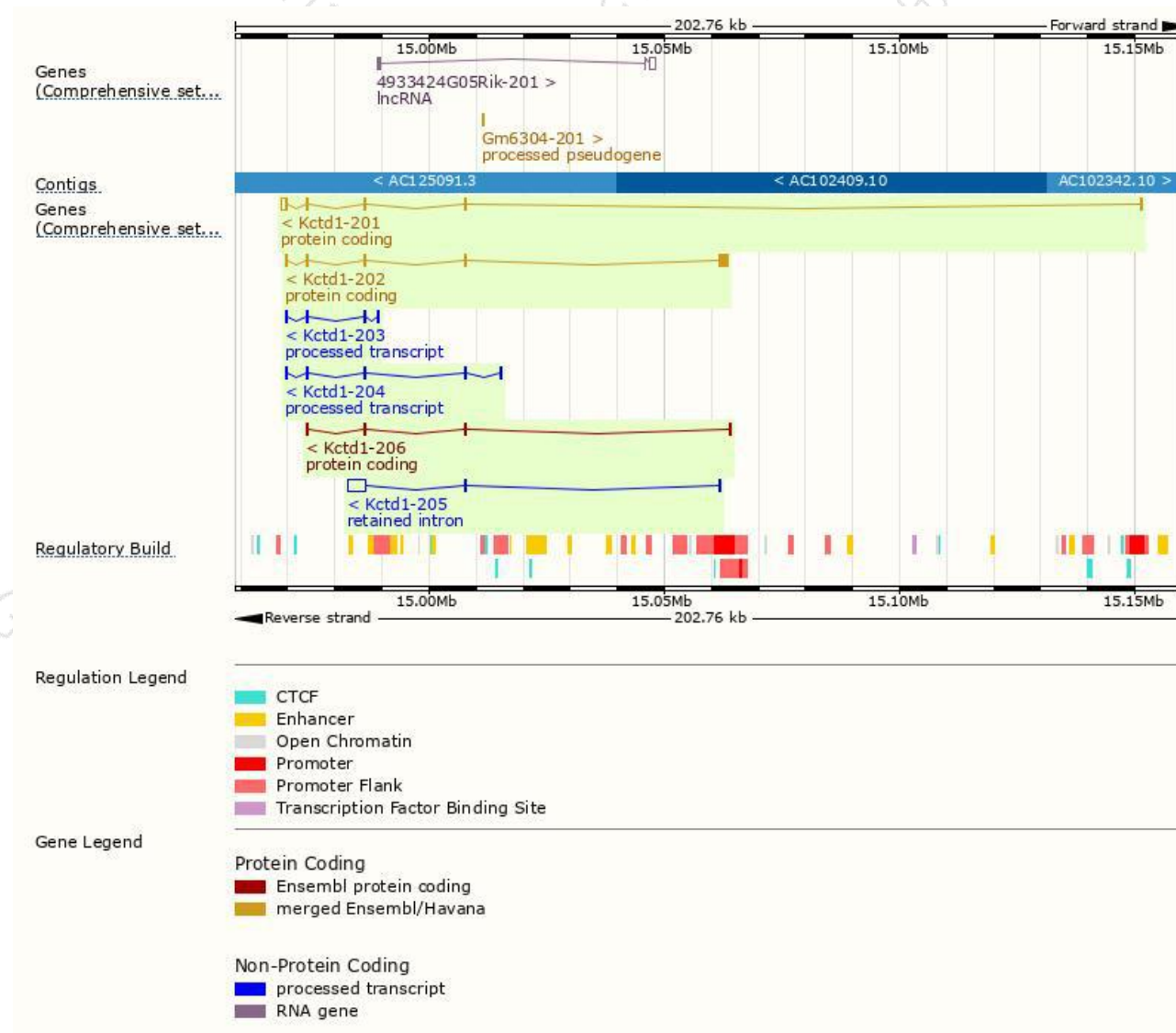
The gene has 6 transcripts,all transcripts are shown below:

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:



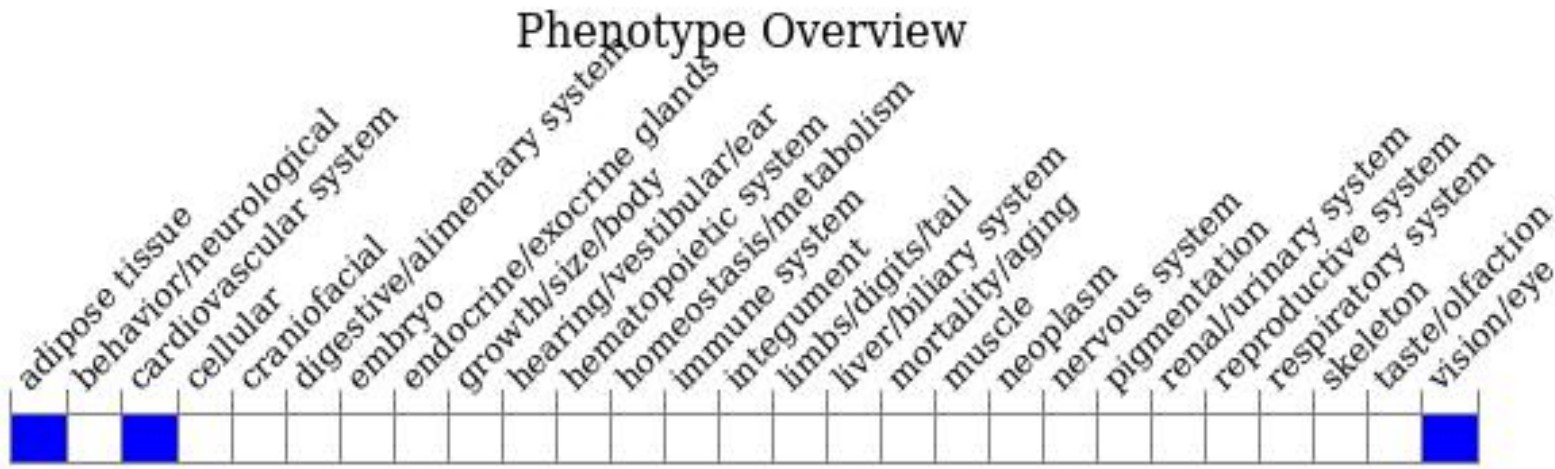
Genomic location distribution



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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