

***Kctd10* Cas9-KO Strategy**

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Project Overview

Project Name

Kctd10

Project type

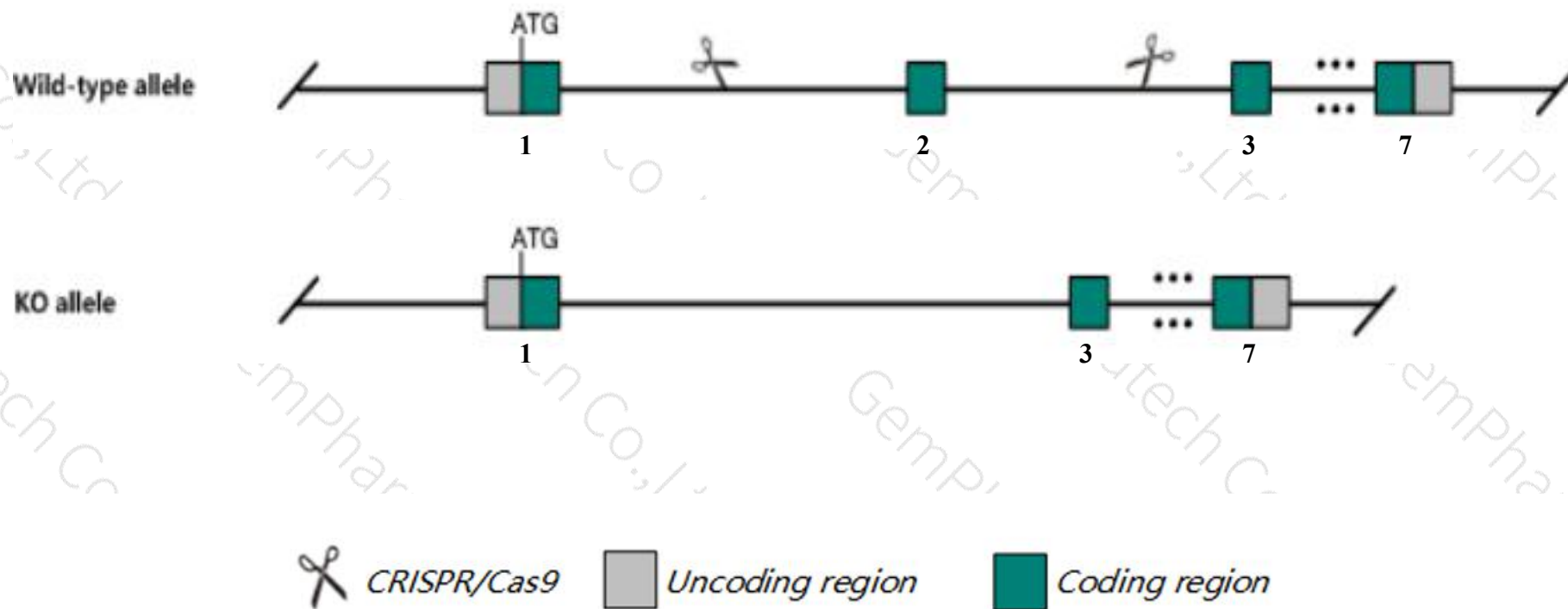
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kctd10* gene. The schematic diagram is as follows:



- The *Kctd10* gene has 7 transcripts. According to the structure of *Kctd10* gene, exon2 of *Kctd10-201* (ENSMUST00000001125.5) transcript is recommended as the knockout region. The region contains 214bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kctd10* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit embryonic lethality between e10.5 and e11.5, abnormal vasculature, absent vitelline circulation, enlarged pericardium, thin myocardium and defective heart valve defect formation.
- The *Kctd10* 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)

Kctd10 potassium channel tetramerisation domain containing 10 [Mus musculus (house mouse)]

Gene ID: 330171, updated on 13-Mar-2020

Summary



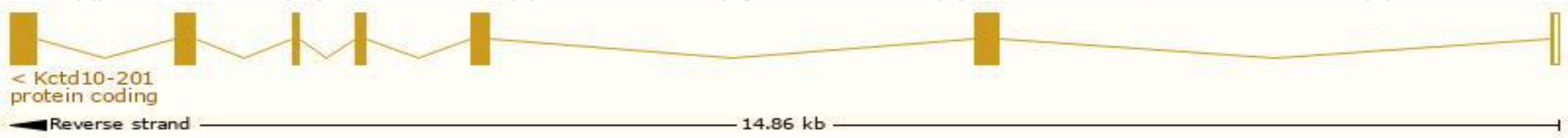
Official Symbol	Kctd10 provided by MGI
Official Full Name	potassium channel tetramerisation domain containing 10 provided by MGI
Primary source	MGI:MGI:2141207
See related	Ensembl:ENSMUSG000000001098
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW536343, C87062, mBACURD3
Expression	Ubiquitous expression in lung adult (RPKM 118.3), colon adult (RPKM 56.8) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

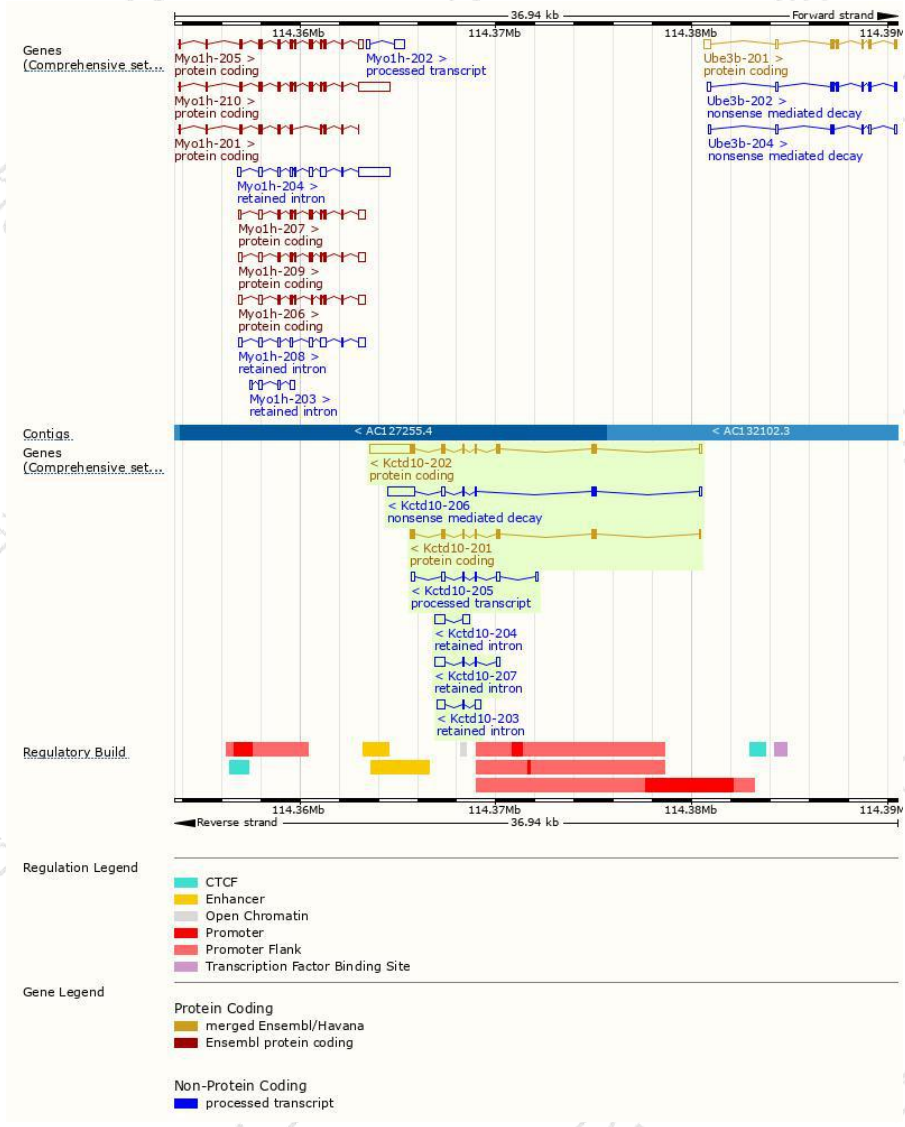
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kctd10-202	ENSMUST00000102581.10	3103	315aa	Protein coding	CCDS19563	Q922M3	TSL:1 GENCODE basic APPRIS P3
Kctd10-201	ENSMUST00000001125.5	1026	316aa	Protein coding	CCDS51623	F8WGGQ9	TSL:5 GENCODE basic APPRIS ALT1
Kctd10-206	ENSMUST00000134532.8	2019	100aa	Nonsense mediated decay	-	S4R2A3	TSL:5
Kctd10-205	ENSMUST00000134173.7	777	No protein	Processed transcript	-	-	TSL:5
Kctd10-204	ENSMUST00000132646.1	850	No protein	Retained intron	-	-	TSL:5
Kctd10-207	ENSMUST00000135170.7	791	No protein	Retained intron	-	-	TSL:3
Kctd10-203	ENSMUST00000123538.1	786	No protein	Retained intron	-	-	TSL:1

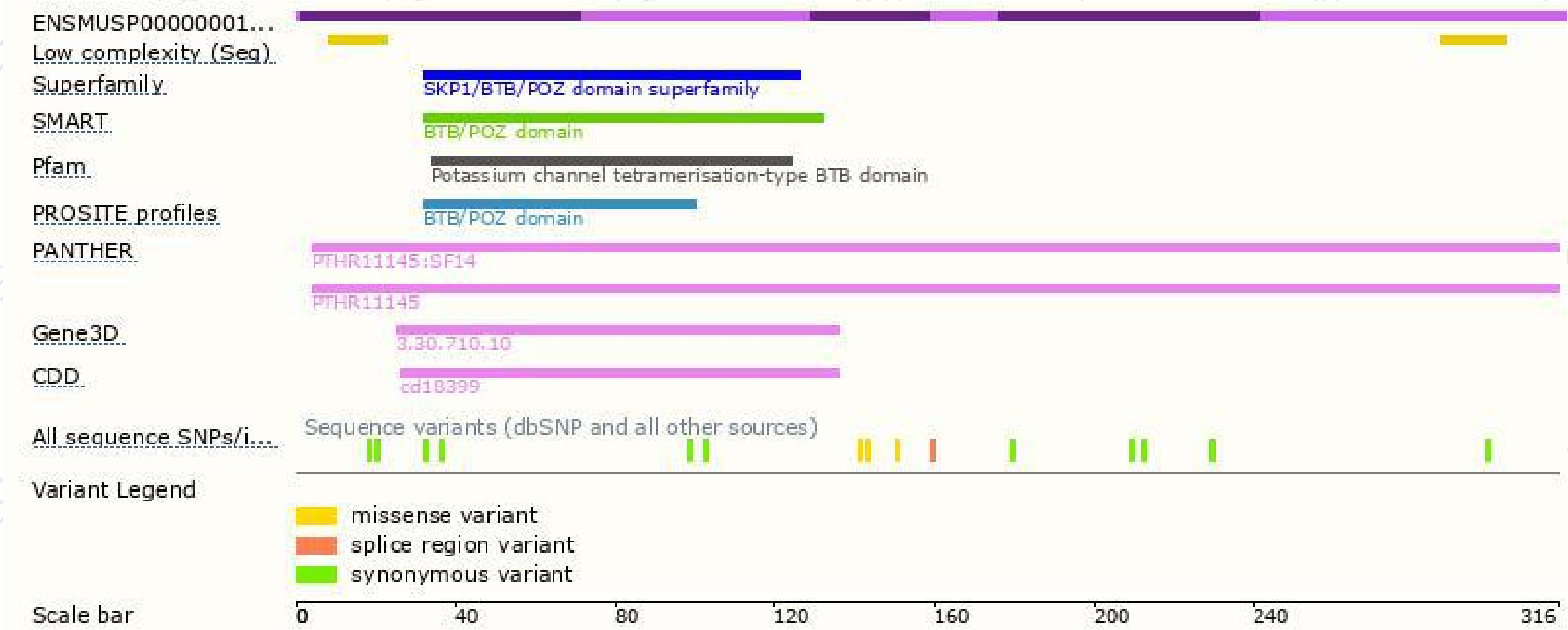
The strategy is based on the design of *Kctd10-201* transcript,the transcription is shown below:



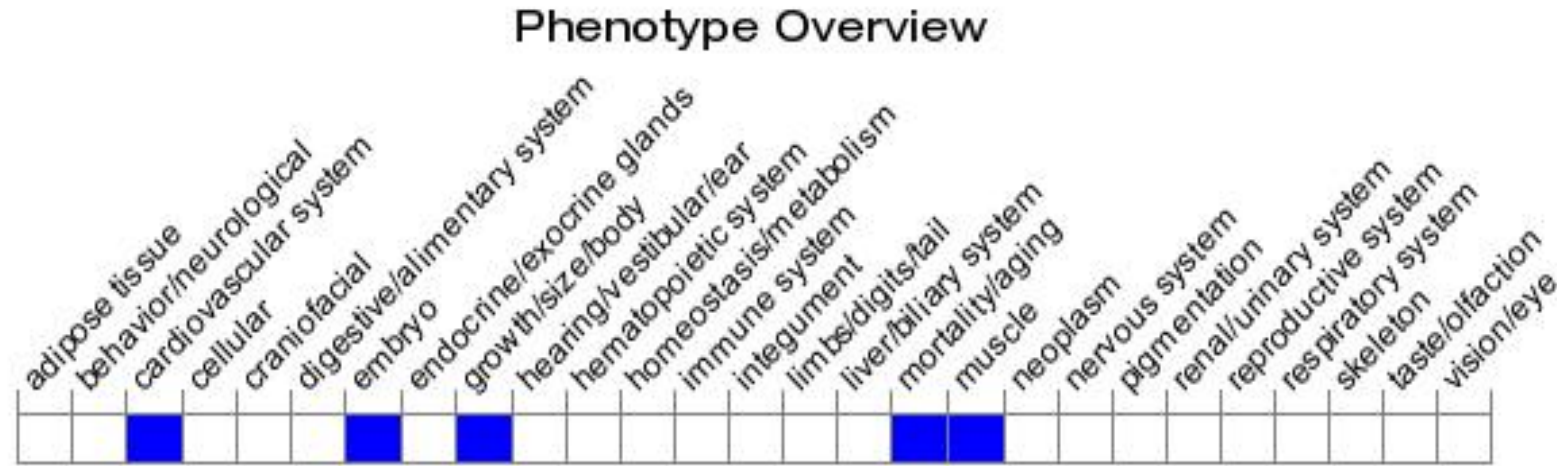
Genomic location distribution



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 knock-out allele exhibit embryonic lethality between E10.5 and E11.5, abnormal vasculature, absent vitelline circulation, enlarged pericardium, thin myocardium and defective heart valve defect formation.

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

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