

Kctd9 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

Design Date: 2020-8-12

Project Overview

Project Name

Kctd9

Project type

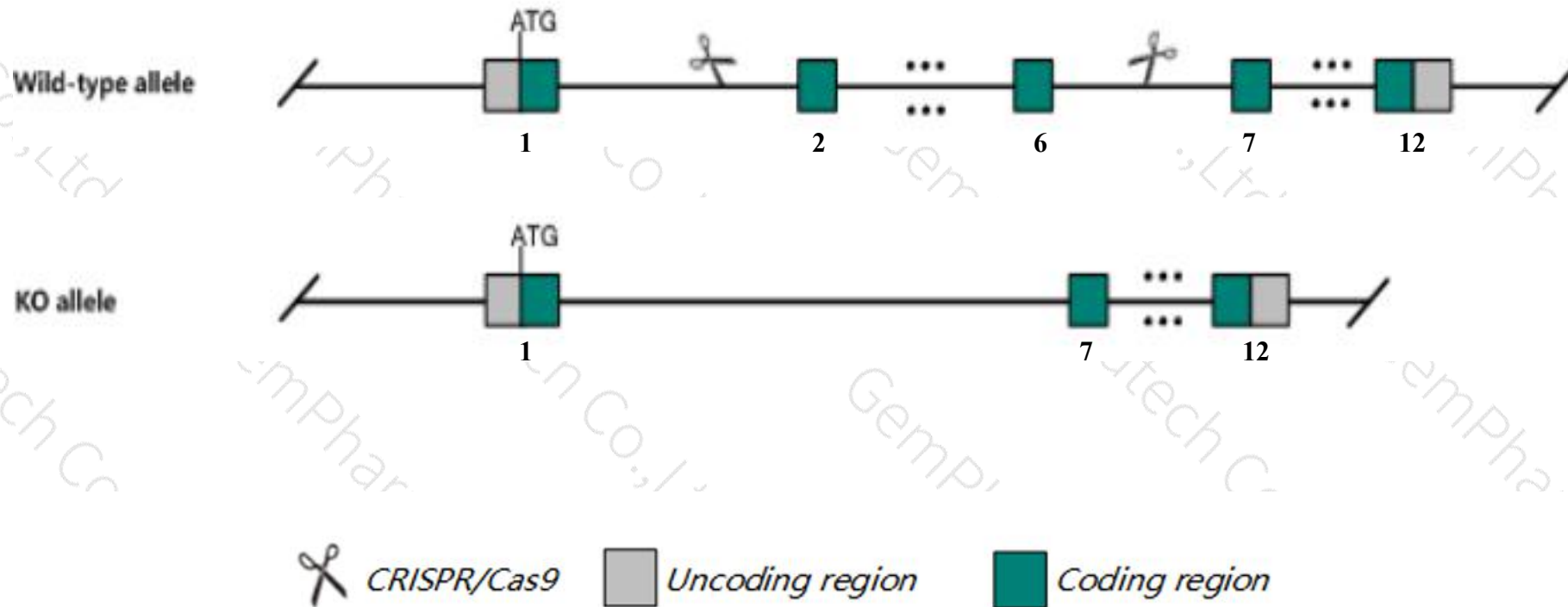
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kctd9* gene. The schematic diagram is as follows:



- The *Kctd9* gene has 6 transcripts. According to the structure of *Kctd9* gene, exon2-exon6 of *Kctd9*-204(ENSMUST00000150768.7) transcript is recommended as the knockout region. The region contains 451bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kctd9* 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.

- According to the existing MGI data, mice homozygous for a null allele exhibit impaired NK cell development and effector function.
- The effect on transcript *Kctd9*-202&203&205 is unknown.
- The *Kctd9* gene is located on the Chr14. 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)

Kctd9 potassium channel tetramerisation domain containing 9 [Mus musculus (house mouse)]

Gene ID: 105440, updated on 13-Mar-2020

Summary



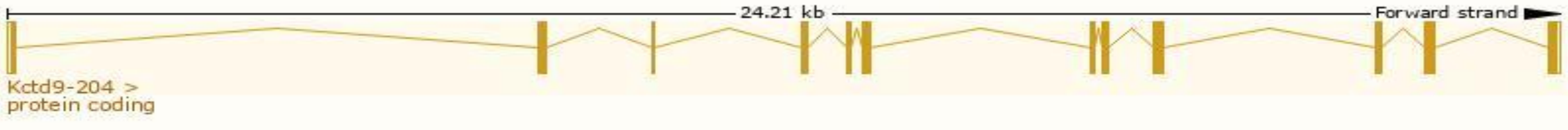
Official Symbol	Kctd9 provided by MGI
Official Full Name	potassium channel tetramerisation domain containing 9 provided by MGI
Primary source	MGI:MGI:2145579
See related	Ensembl:ENSMUSG00000034327
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in placenta adult (RPKM 5.9), bladder adult (RPKM 5.3) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

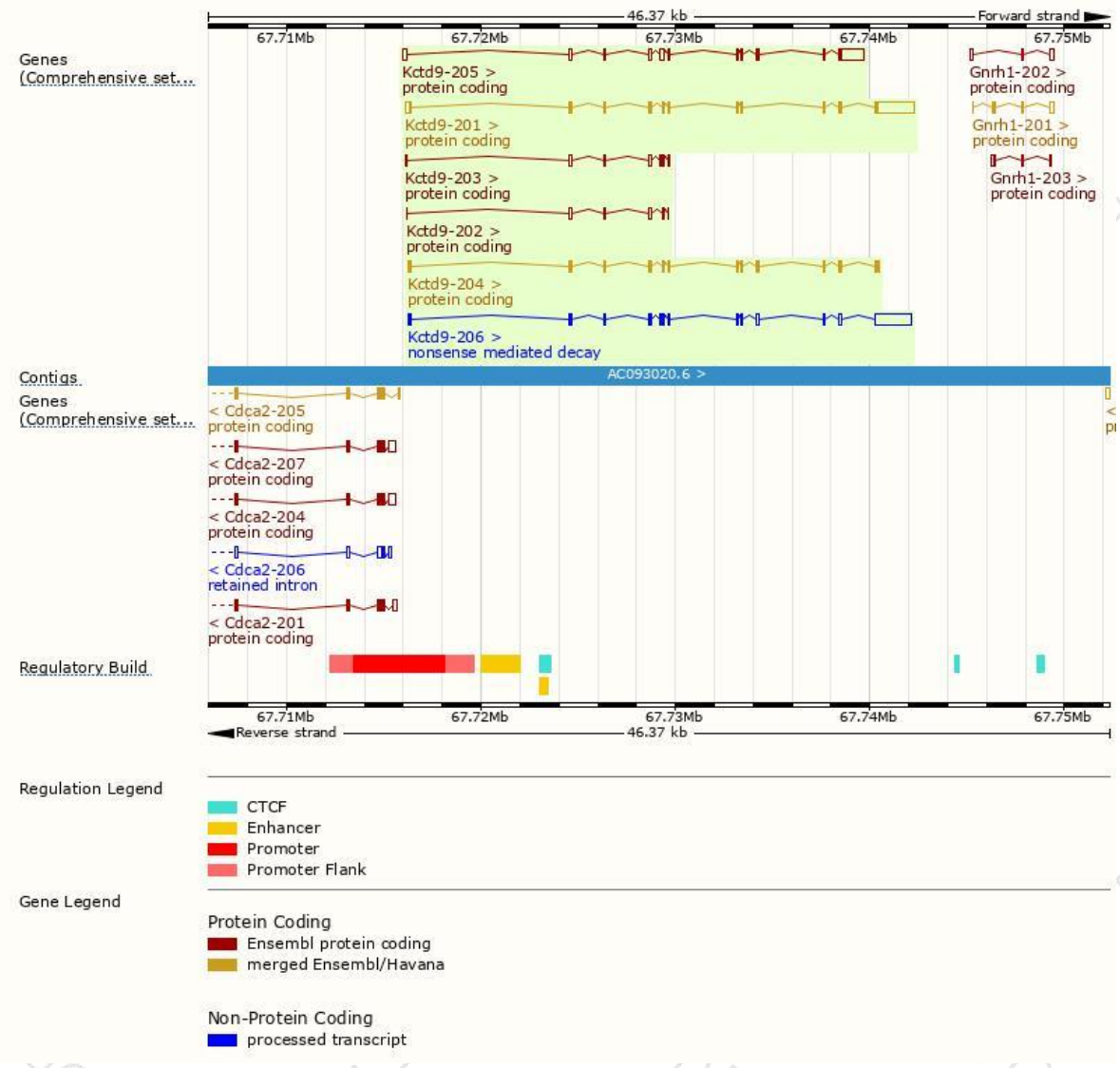
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kctd9-201	ENSMUST00000078053.12	3157	339aa	Protein coding	CCDS27230	Q80UN1	TSL:1 GENCODE basic
Kctd9-204	ENSMUST00000150768.7	1302	389aa	Protein coding	CCDS49531	E9PUA6	TSL:5 GENCODE basic APPRIS P1
Kctd9-205	ENSMUST00000152243.7	2528	245aa	Protein coding	-	D3YZ64	TSL:2 GENCODE basic
Kctd9-203	ENSMUST00000145542.7	470	40aa	Protein coding	-	D3Z7J5	CDS 3' incomplete TSL:5
Kctd9-202	ENSMUST00000125212.1	356	10aa	Protein coding	-	A0A1C7ZMZ1	CDS 3' incomplete TSL:5
Kctd9-206	ENSMUST00000156700.1	3098	135aa	Nonsense mediated decay	-	D6RH42	TSL:2

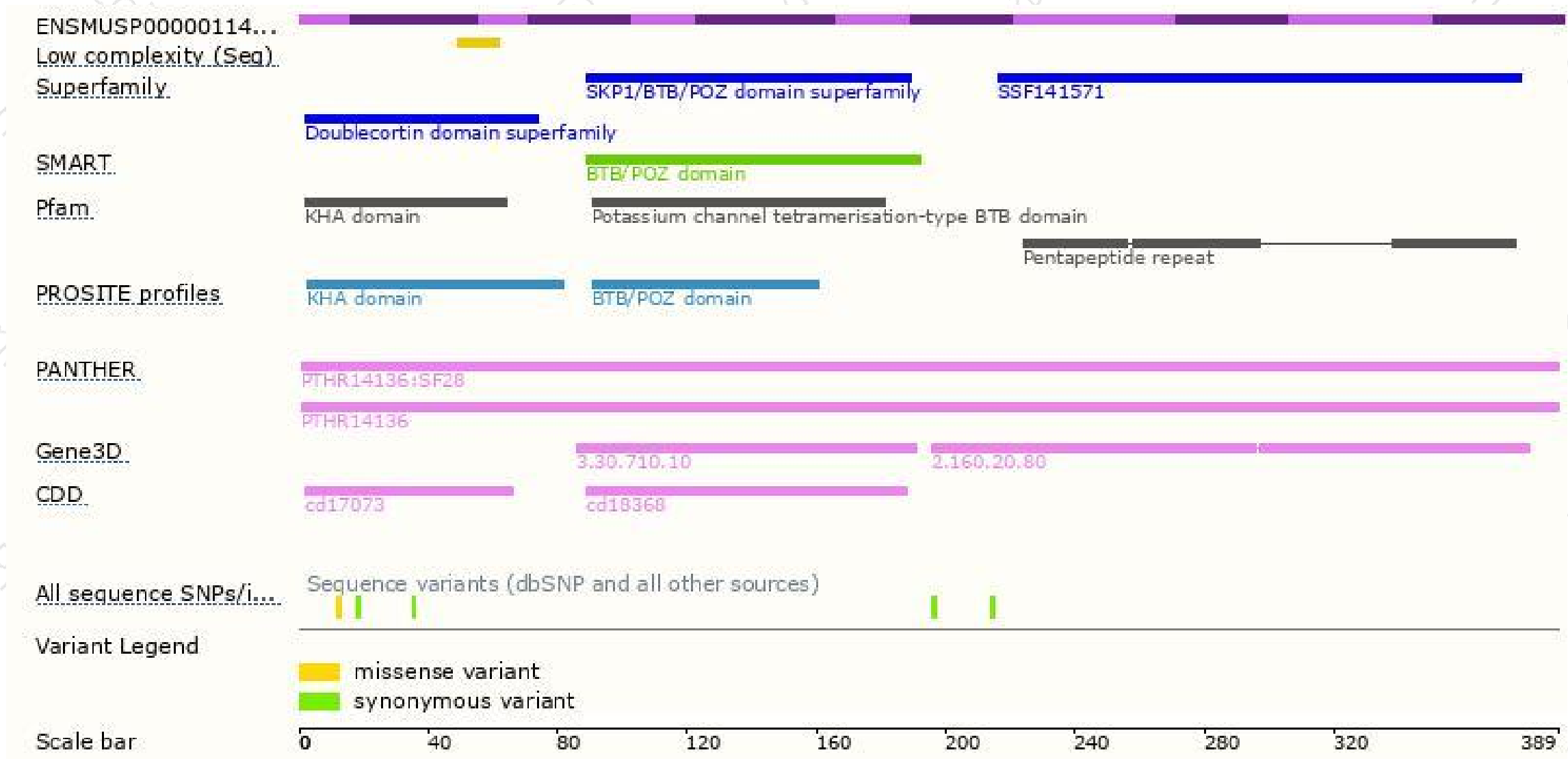
The strategy is based on the design of *Kctd9-204* transcript,the transcription is shown below:



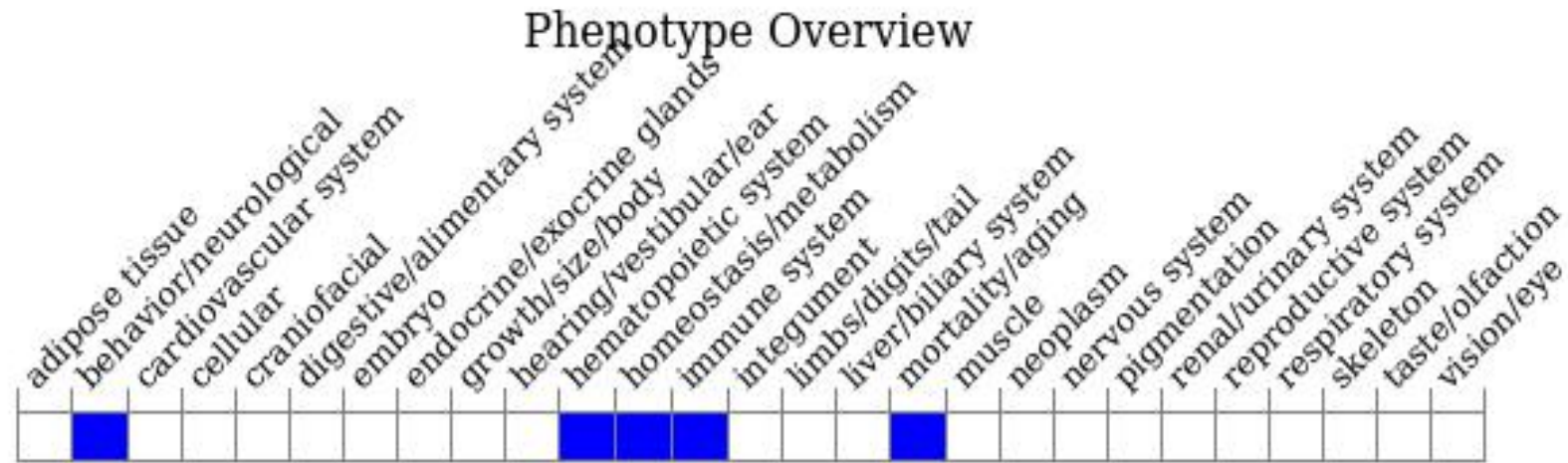
Genomic location distribution



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 allele exhibit impaired NK cell development and effector function.

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

Tel: 400-9660890

