

Sec24d Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

Design Date: 2020-7-24

Project Overview

Project Name

Sec24d

Project type

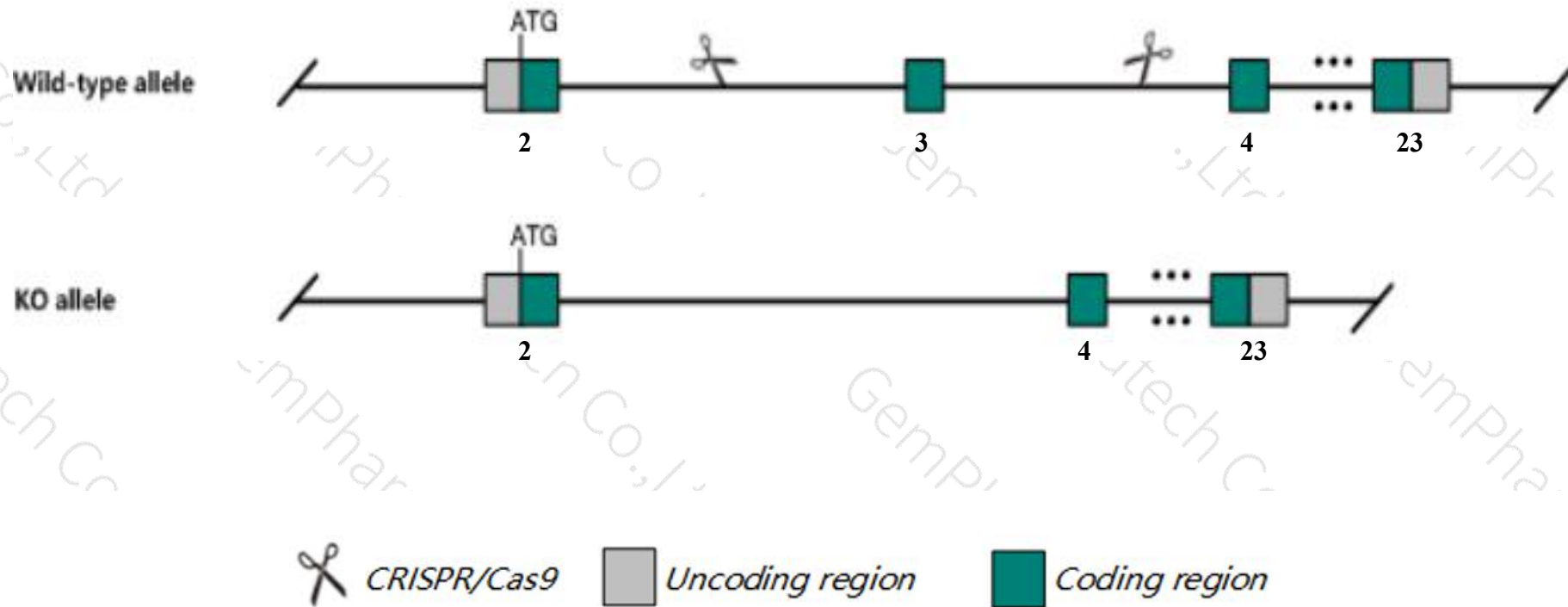
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec24d* gene. The schematic diagram is as follows:



- The *Sec24d* gene has 8 transcripts. According to the structure of *Sec24d* gene, exon3 of *Sec24d-201*(ENSMUST00000047923.11) transcript is recommended as the knockout region. The region contains 124bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sec24d* 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 knock-out allele exhibit early embryonic lethality. A hypomorphic gene trap allele results in lethality during organogenesis.
- The transcript of *Sec24d*-202&203&204&205&207&208 may not be affected.
- The *Sec24d* gene is located on the Chr3. 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)

Sec24d Sec24 related gene family, member D (*S. cerevisiae*) [*Mus musculus* (house mouse)]

Gene ID: 69608, updated on 13-Mar-2020

Summary



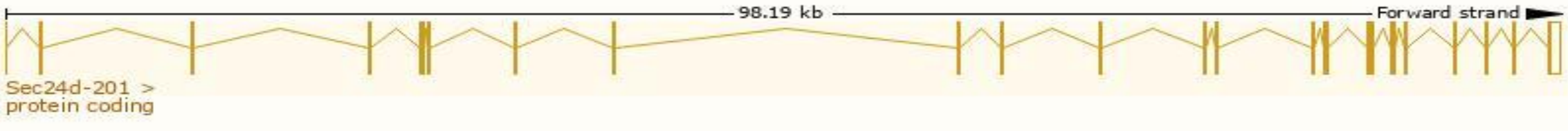
Official Symbol	Sec24d provided by MGI
Official Full Name	Sec24 related gene family, member D (<i>S. cerevisiae</i>) provided by MGI
Primary source	MGI:MGI:1916858
See related	Ensembl:ENSMUSG00000039234
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310020L09Rik, Gm1349
Expression	Broad expression in adrenal adult (RPKM 64.8), duodenum adult (RPKM 50.4) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

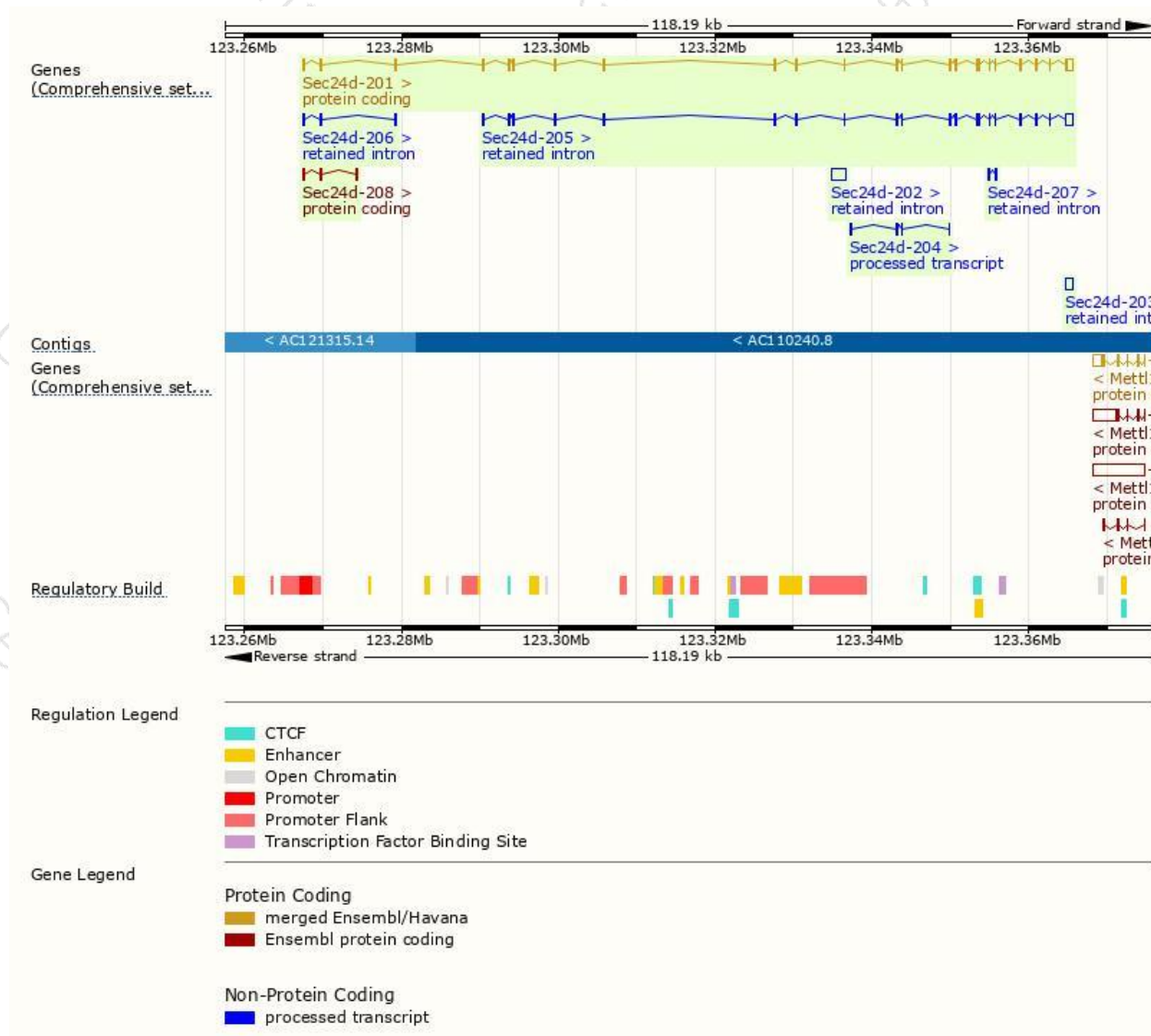
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec24d-201	ENSMUST00000047923.11	3903	1032aa	Protein coding	CCDS38621	Q6NXL1	TSL:1 GENCODE basic APPRIS P1
Sec24d-208	ENSMUST00000200333.1	307	47aa	Protein coding	-	A0A0G2JGJ5	TSL:1 GENCODE basic
Sec24d-204	ENSMUST00000196631.1	376	No protein	Processed transcript	-	-	TSL:3
Sec24d-205	ENSMUST00000197291.4	3649	No protein	Retained intron	-	-	TSL:5
Sec24d-202	ENSMUST00000196167.1	1947	No protein	Retained intron	-	-	TSL:NA
Sec24d-203	ENSMUST00000196482.1	923	No protein	Retained intron	-	-	TSL:NA
Sec24d-207	ENSMUST00000200309.1	421	No protein	Retained intron	-	-	TSL:2
Sec24d-206	ENSMUST00000198210.1	409	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Sec24d-201* transcript,the transcription is shown below:



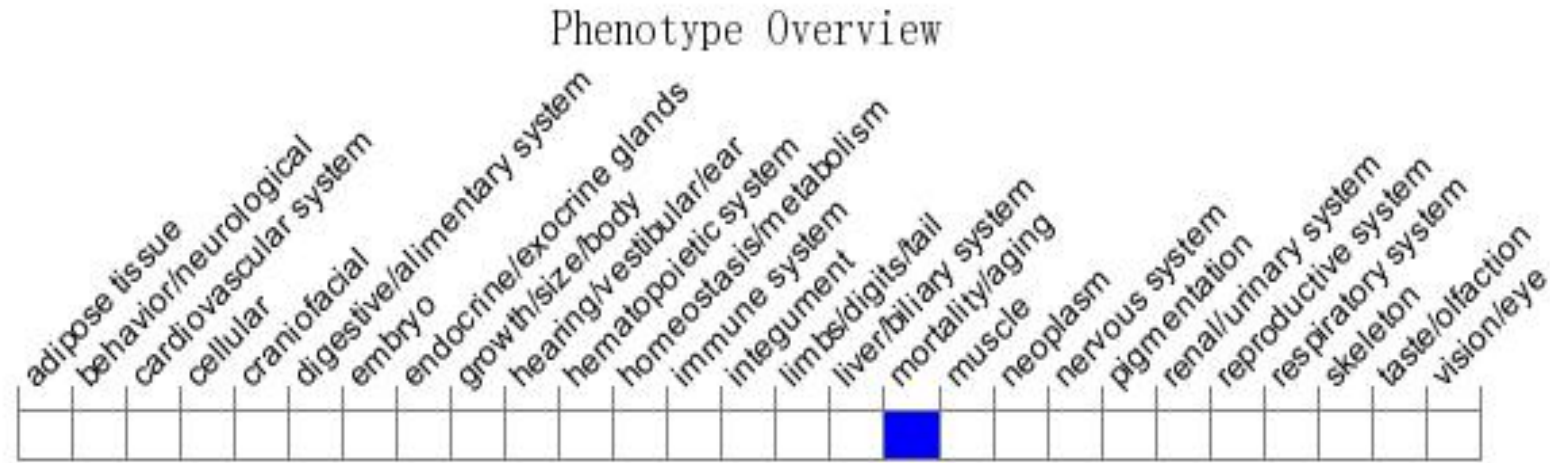
Genomic location distribution



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 early embryonic lethality. A hypomorphic gene trap allele results in lethality during organogenesis.

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

Tel: 400-9660890

