

Zc3h12d Cas9-KO Strategy

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Project Overview

Project Name

Zc3h12d

Project type

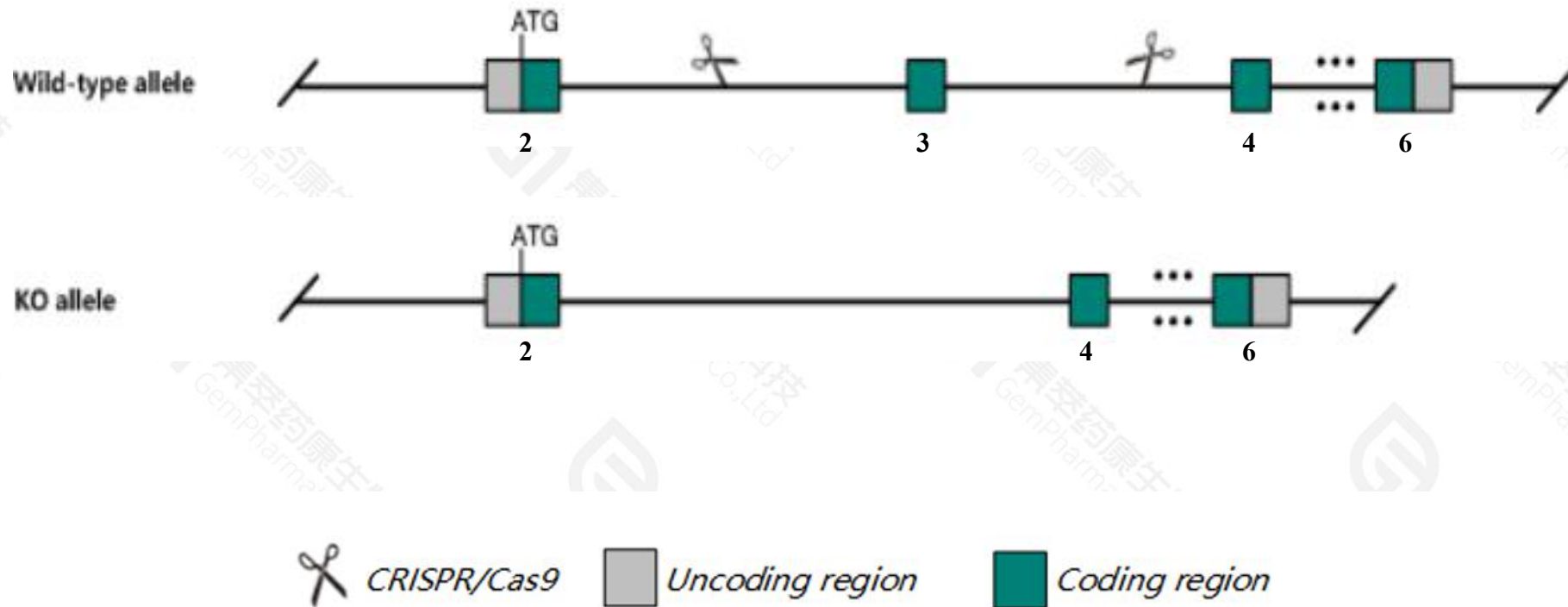
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zc3h12d* gene. The schematic diagram is as follows:



- The *Zc3h12d* gene has 1 transcript. According to the structure of *Zc3h12d* gene, exon3 of *Zc3h12d-201*(ENSMUST00000039484.6) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zc3h12d* 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 disrupted regulation of excessive inflammation.
- The *Zc3h12d* gene is located on the Chr10. 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.

Zc3h12d zinc finger CCCH type containing 12D [Mus musculus (house mouse)]

Gene ID: 237256, updated on 26-Sep-2020

Summary



Official Symbol Zc3h12d provided by [MGI](#)

Official Full Name zinc finger CCCH type containing 12D provided by [MGI](#)

Primary source [MGI:MGI:3045313](#)

See related [Ensembl:ENSMUSG00000039981](#)

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 D730019B10Rik, TF, TFL

Expression Biased expression in spleen adult (RPKM 9.8), duodenum adult (RPKM 3.6) and 9 other tissues [See more](#)

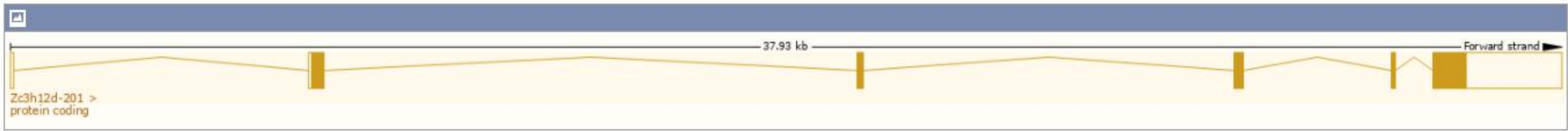
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

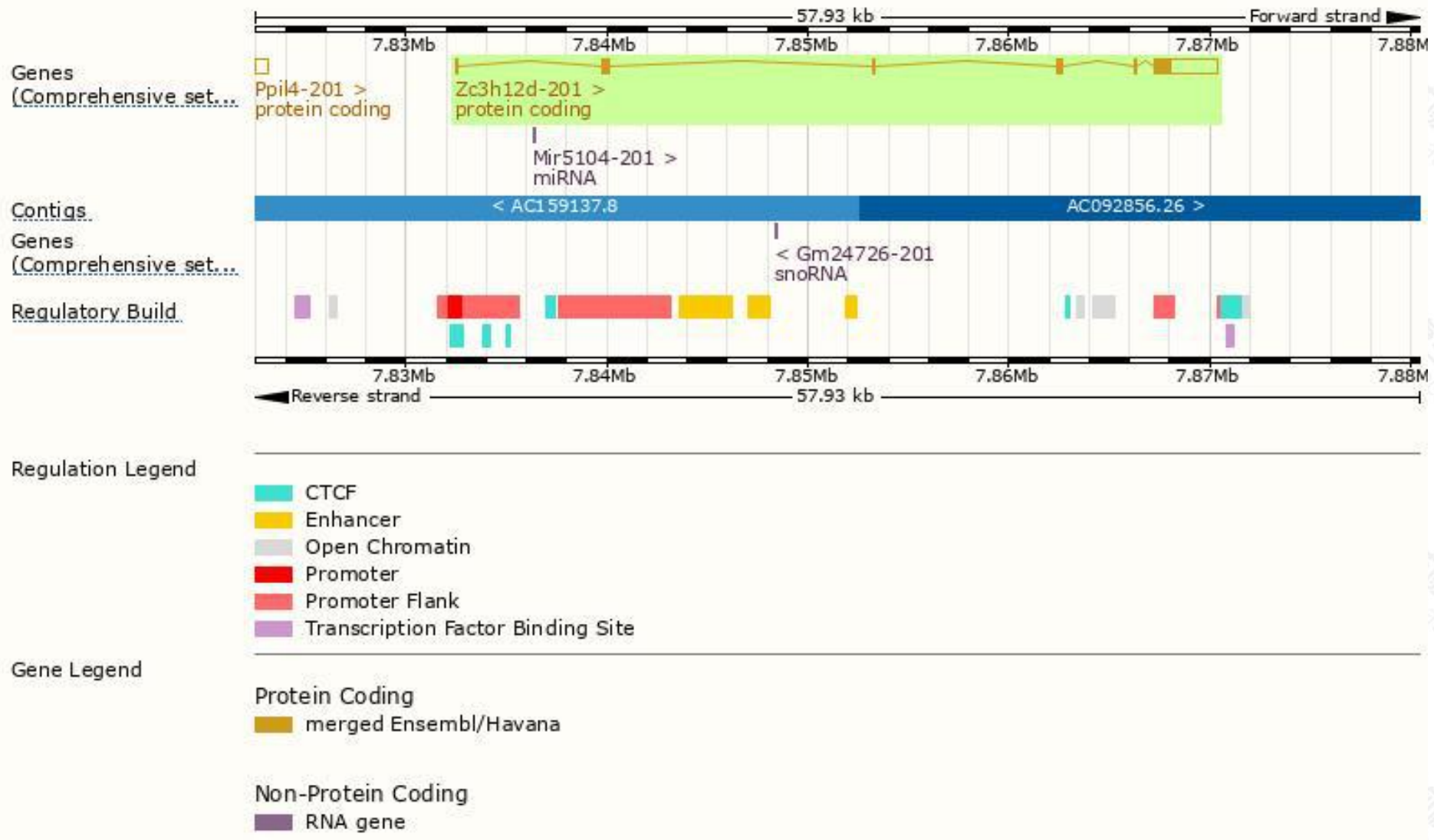
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zc3h12d-201	ENSMUST00000039484.6	4092	533aa	Protein coding	CCDS48496		TSL:1 , GENCODE basic , APPRIS P1 ,

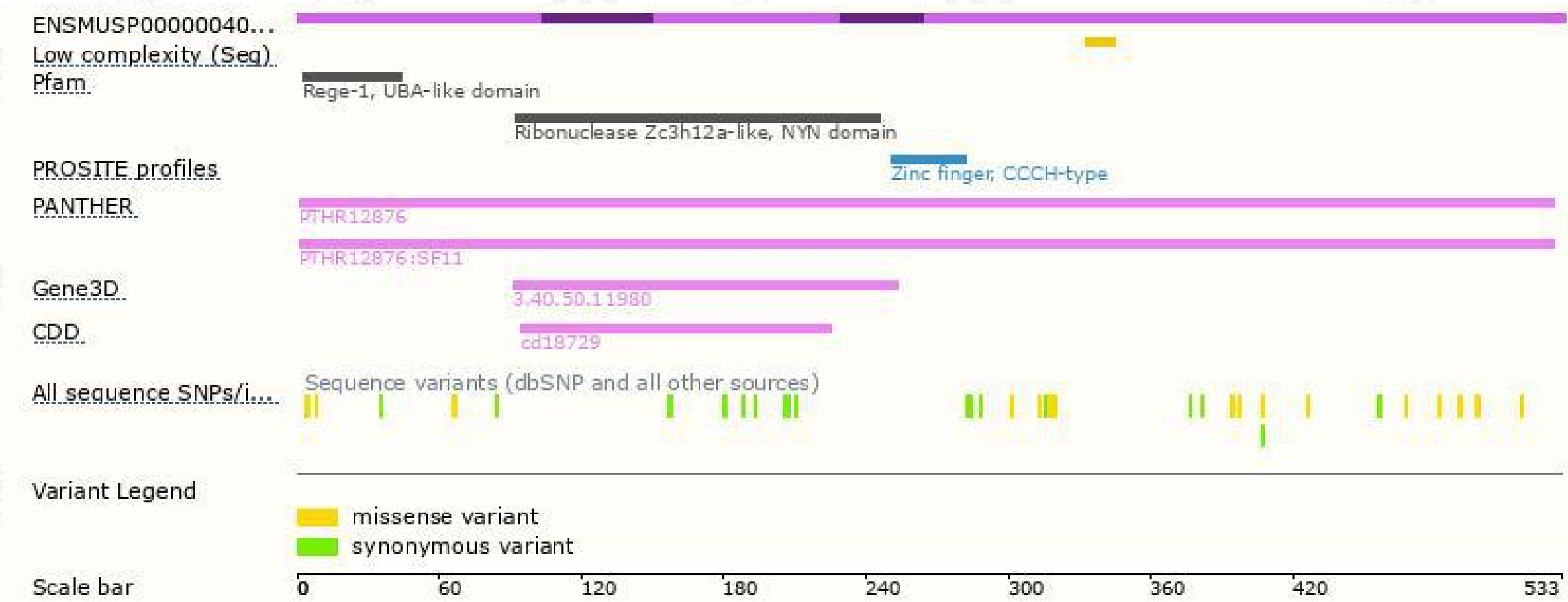
The strategy is based on the design of *Zc3h12d-201* transcript, the transcription is shown below:



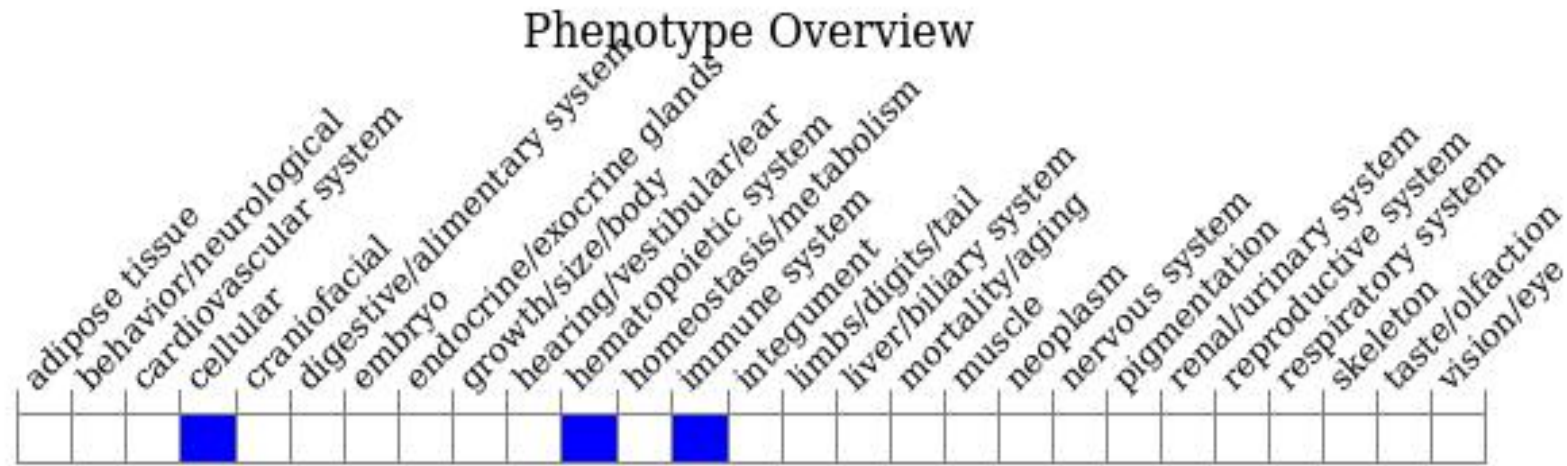
Genomic location distribution



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 disrupted regulation of excessive inflammation.

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