

Dzip3 Cas9-KO Strategy

Designer: Huimin Su

Reviewer: Ruiuri Zhang

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Project Overview

Project Name

Dzip3

Project type

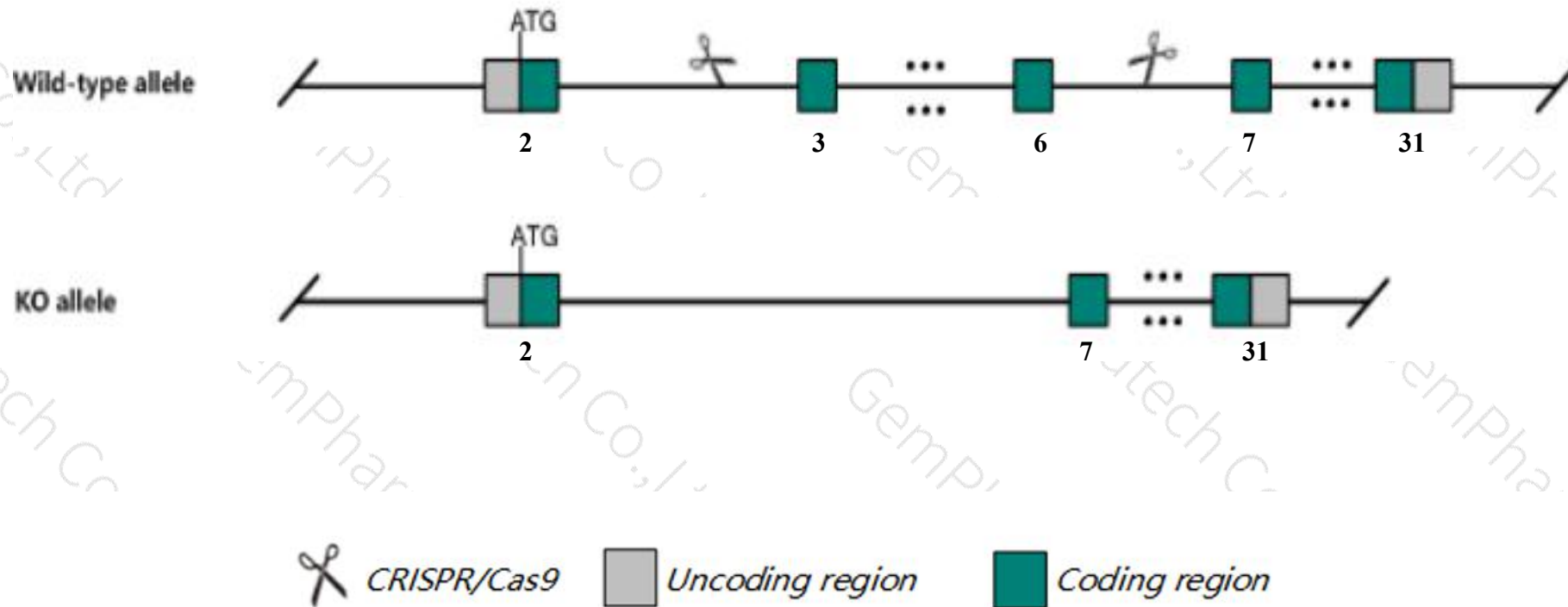
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dzip3* gene. The schematic diagram is as follows:



- The *Dzip3* gene has 7 transcripts. According to the structure of *Dzip3* gene, exon3-exon6 of *Dzip3-201*(ENSMUST00000114516.7) transcript is recommended as the knockout region. The region contains 427bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dzip3* 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 an ENU-induced allele exhibit embryonic lethality.
- Transcript *Dzip3-207* is incomplete, so the effect on it is unknown.
- The *Dzip3* gene is located on the Chr16. 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)

Dzip3 DAZ interacting protein 3, zinc finger [Mus musculus (house mouse)]

Gene ID: 224170, updated on 13-Mar-2020

Summary



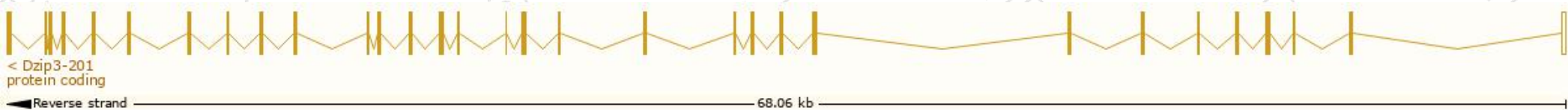
Official Symbol	Dzip3 provided by MGI
Official Full Name	DAZ interacting protein 3, zinc finger provided by MGI
Primary source	MGI:MGI:1917433
See related	Ensembl:ENSMUSG00000064061
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310047C04Rik, 2A-HUB, 6430549P11Rik, A230104G20
Expression	Broad expression in CNS E18 (RPKM 15.0), CNS E14 (RPKM 12.5) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

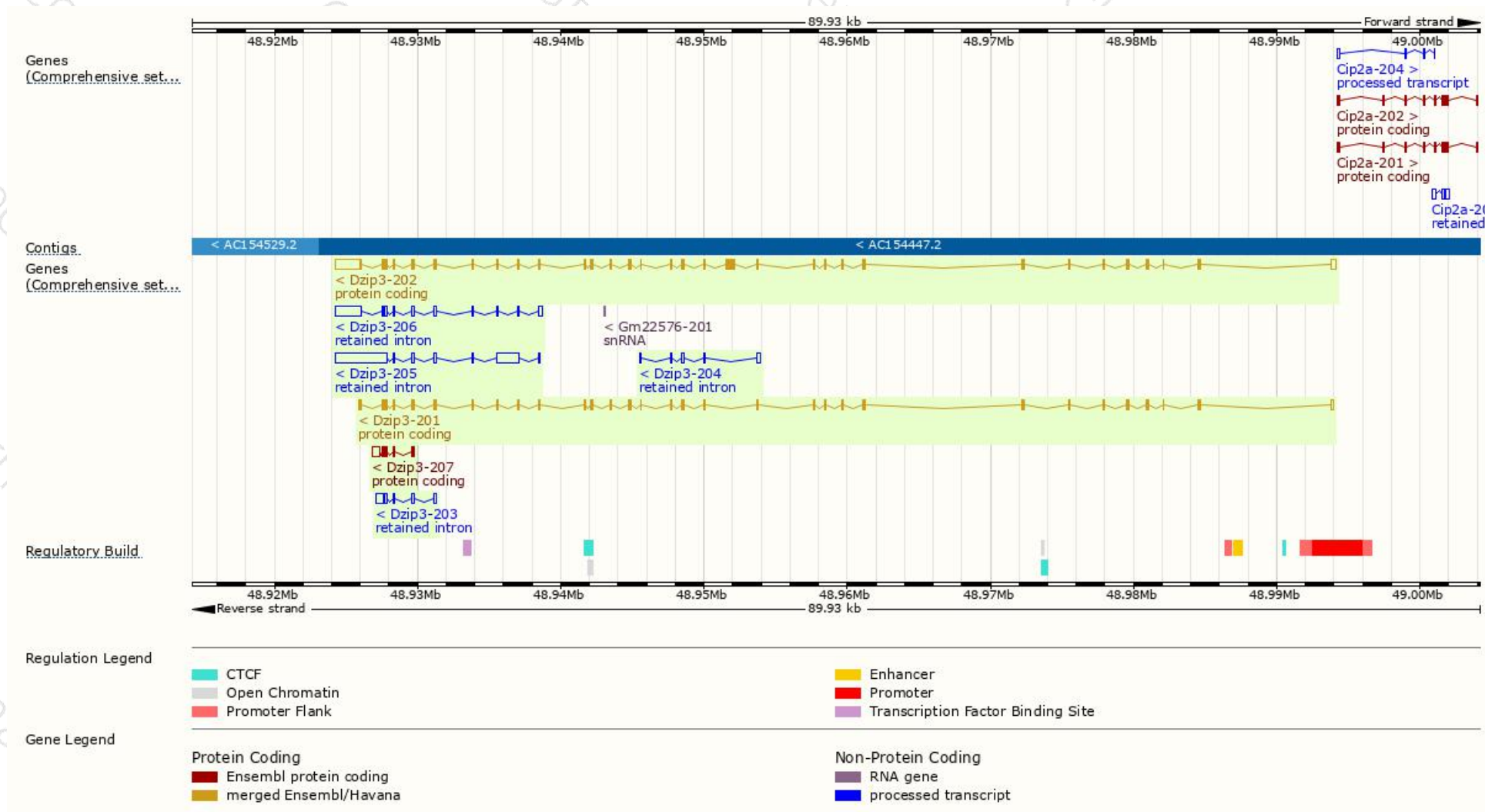
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dzip3-207	ENSMUST00000151950.1	961	167aa	Protein coding	-	F6Z1P8	CDS 5' incomplete TSL:2
Dzip3-201	ENSMUST00000114516.7	3331	998aa	Protein coding	CCDS37353	Q7TPV2	TSL:1 GENCODE basic APPRIS P3
Dzip3-202	ENSMUST00000121869.7	5820	1204aa	Protein coding	CCDS49866	E9QNZ2	TSL:5 GENCODE basic APPRIS ALT2
Dzip3-205	ENSMUST00000139350.7	5835	No protein	Retained intron	-	-	TSL:1
Dzip3-206	ENSMUST00000147358.7	3021	No protein	Retained intron	-	-	TSL:5
Dzip3-203	ENSMUST00000123961.1	1071	No protein	Retained intron	-	-	TSL:2
Dzip3-204	ENSMUST00000133377.1	563	No protein	Retained intron	-	-	TSL:3

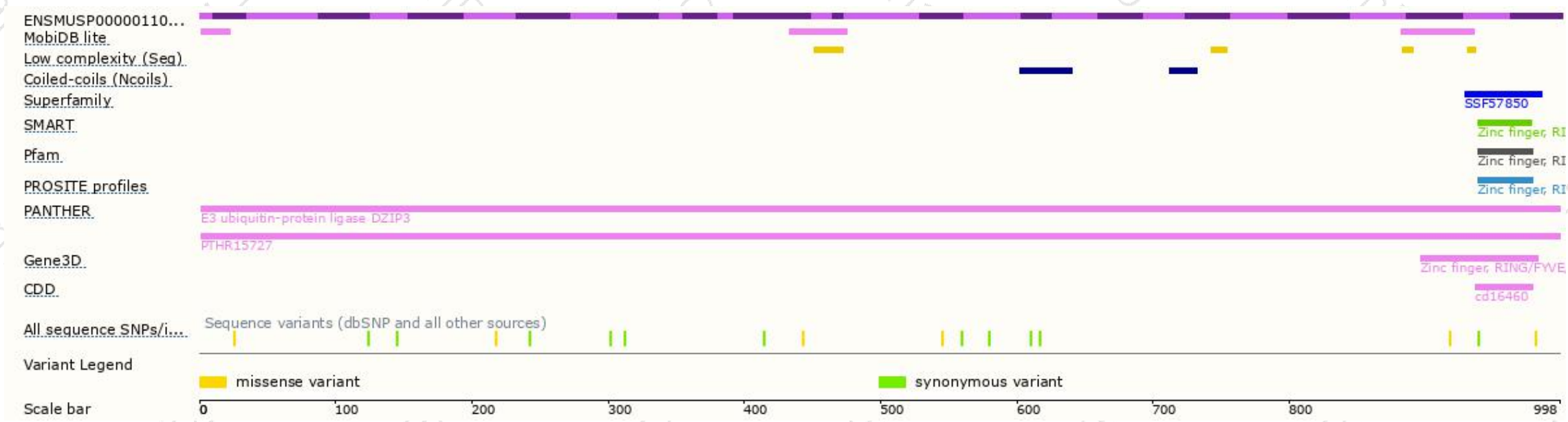
The strategy is based on the design of *Dzip3-201* transcript,the transcription is shown below:



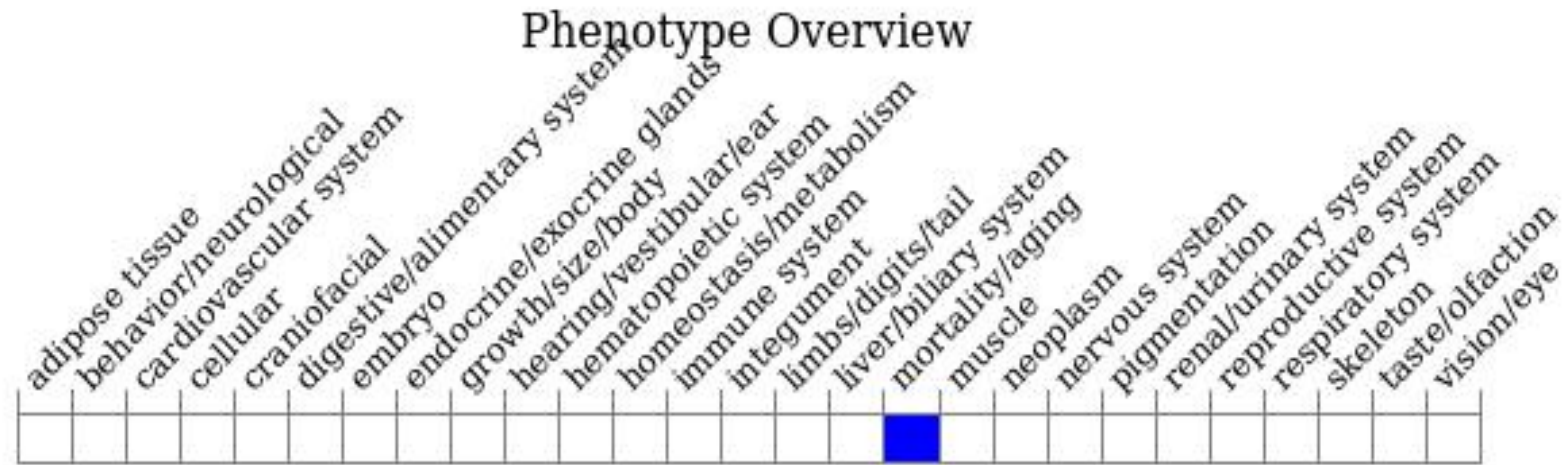
Genomic location distribution



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 an ENU-induced allele exhibit embryonic lethality.

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

Tel: 400-9660890

