

Zc2hc1a Cas9-CKO Strategy

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Design Date: 2020-3-22

Project Overview

Project Name

Zc2hc1a

Project type

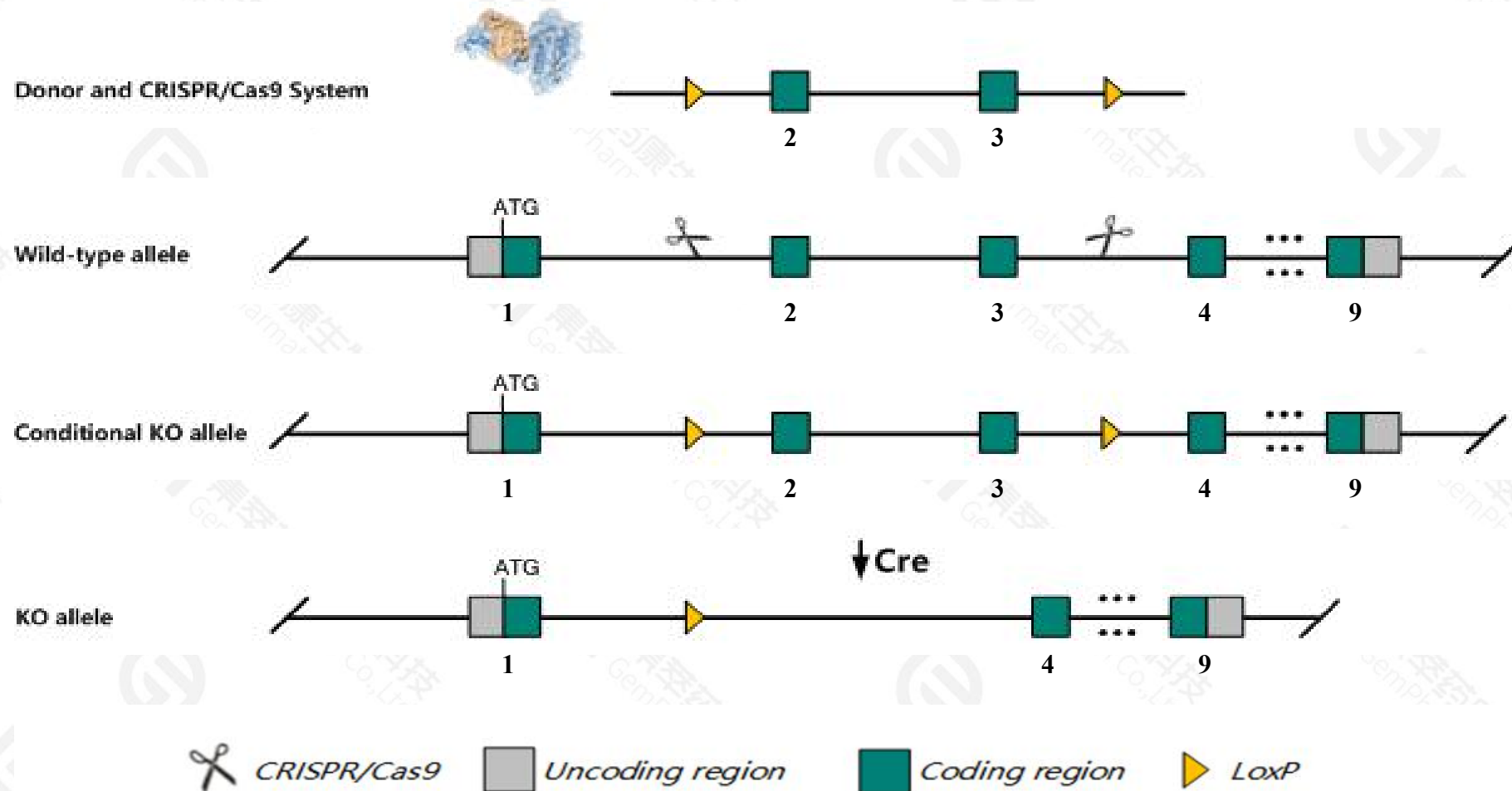
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zc2hc1a* gene. The schematic diagram is as follows:



Technical routes

- The *Zc2hc1a* gene has 3 transcripts. According to the structure of *Zc2hc1a* gene, exon2-exon3 of *Zc2hc1a-201*(ENSMUST00000051064.9) transcript is recommended as the knockout region. The region contains 194bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zc2hc1a* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Zc2hc1a* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Zc2hc1a zinc finger, C2HC-type containing 1A [Mus musculus (house mouse)]

Gene ID: 67306, updated on 17-Dec-2020

Summary



Official Symbol Zc2hc1a provided by [MGI](#)

Official Full Name zinc finger, C2HC-type containing 1A provided by [MGI](#)

Primary source [MGI:MGI:1914556](#)

See related [Ensembl:ENSMUSG00000043542](#)

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 3110050N22Rik, AI790358, AU023959, Fam16, Fam164a

Expression Broad expression in CNS E18 (RPKM 22.4), whole brain E14.5 (RPKM 18.1) and 16 other tissues [See more](#)

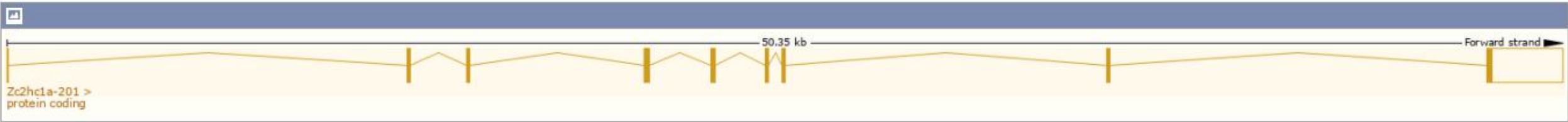
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

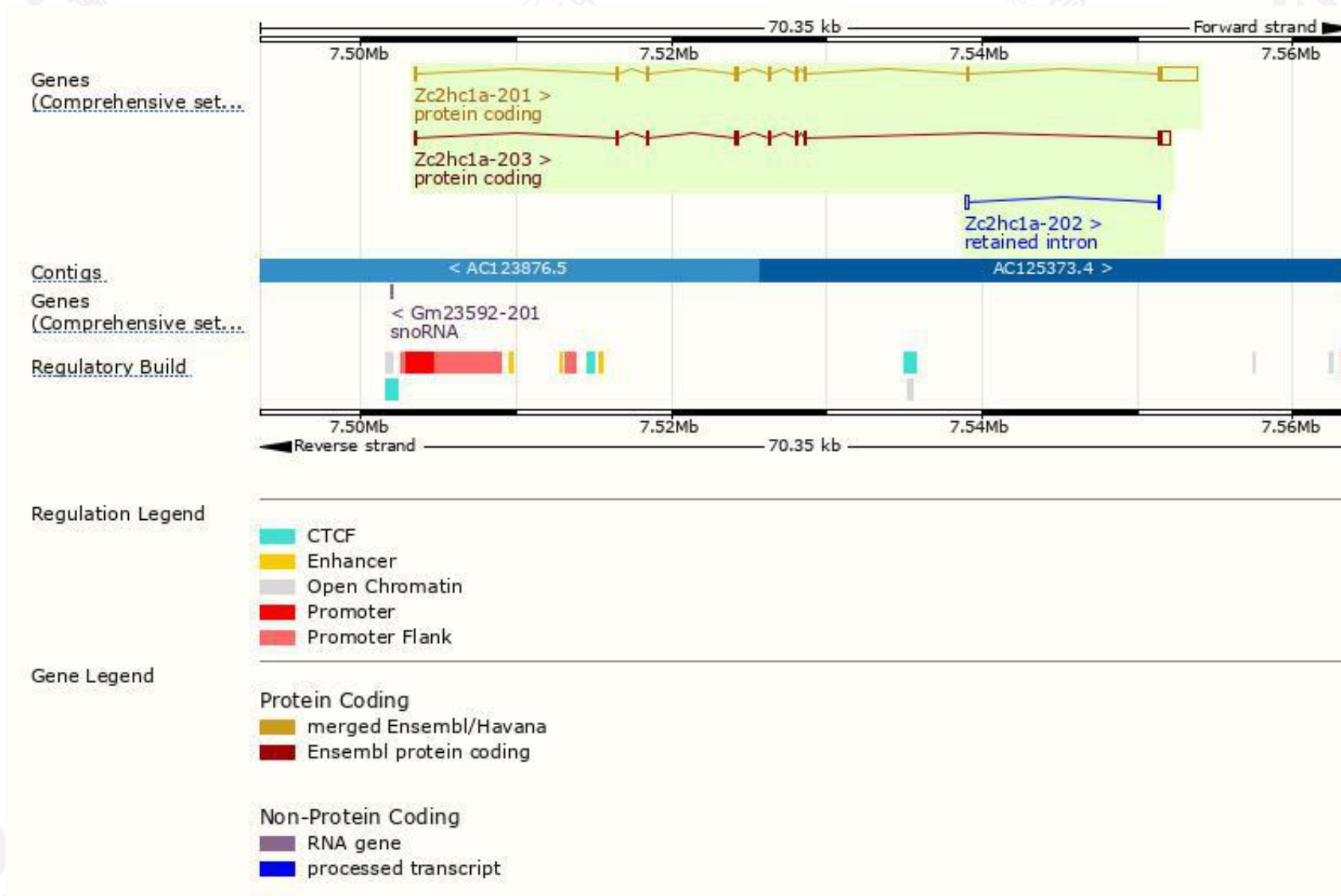
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zc2hc1a-201	ENSMUST00000051064.9	3292	324aa	Protein coding	CCDS17230		TSL:1 , GENCODE basic , APPRIS P1 ,
Zc2hc1a-203	ENSMUST00000193010.2	1420	288aa	Protein coding	-		TSL:1 , GENCODE basic ,
Zc2hc1a-202	ENSMUST00000192835.2	443	No protein	Retained intron	-		TSL:1 ,

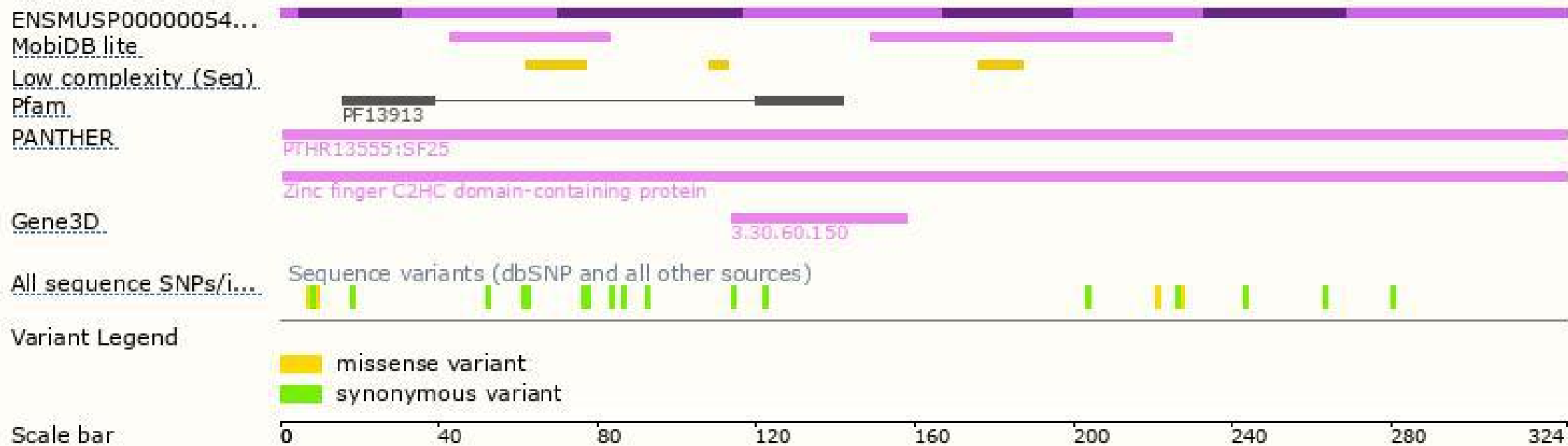
The strategy is based on the design of *Zc2hc1a-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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