

# Zc3h12a Cas9-CKO Strategy

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Reviewer: Huimin Su

**Design Date:** 2019-11-26

# **Project Overview**



**Project Name** 

Zc3h12a

**Project type** 

Cas9-CKO

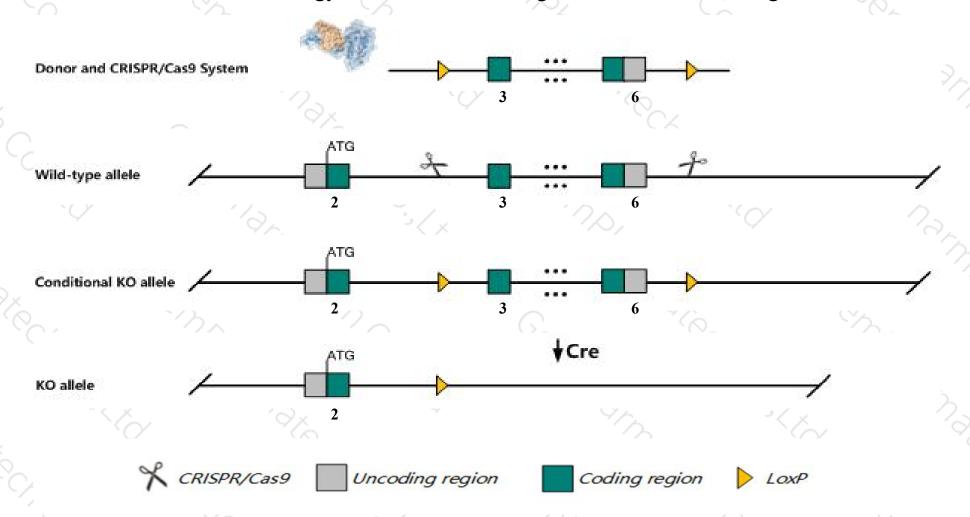
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Zc3h12a gene. The schematic diagram is as follows:



### Technical routes



- The Zc3h12a gene has 2 transcripts. According to the structure of Zc3h12a gene, exon3-exon6 of Zc3h12a-201 (ENSMUST00000036188.7) transcript is recommended as the knockout region. The region contains 1348bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Zc3h12a 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.

### **Notice**



- > According to the existing MGI data, Mice homozygous for a null allele exhibit splenomegaly, lymphadenopathy, hyperimmunoglobulinemia, increased auto-antibodies, and defective IL6 post-transcriptional regulation.
- The Zc3h12a gene is located on the Chr4. 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)



#### Zc3h12a zinc finger CCCH type containing 12A [Mus musculus (house mouse)]

Gene ID: 230738, updated on 25-Mar-2019

#### Summary

☆ ?

Official Symbol Zc3h12a provided by MGI

Official Full Name zinc finger CCCH type containing 12A provided by MGI

Primary source MGI:MGI:2385891

See related Ensembl:ENSMUSG00000042677

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 BC036563, MCPIP, MCPIP-1, Mcpip1, Reg1

Expression Broad expression in large intestine adult (RPKM 23.3), spleen adult (RPKM 14.6) and 15 other tissuesSee more

Orthologs <u>human</u> all

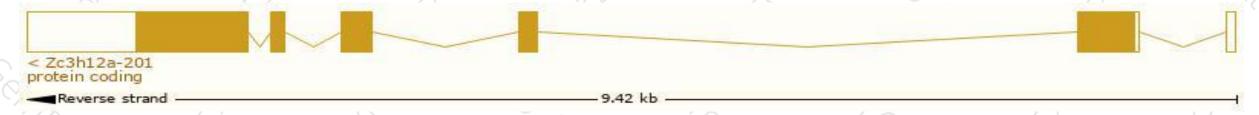
# Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

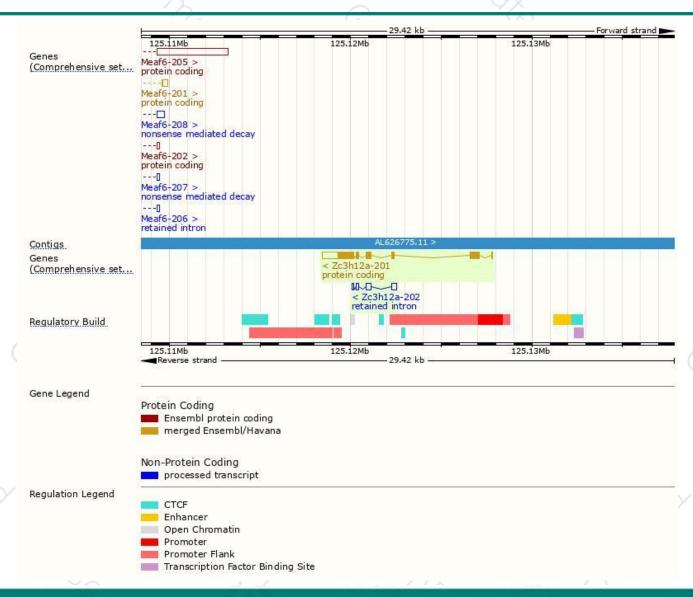
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zc3h12a-201	ENSMUST00000036188.7	2755	<u>596aa</u>	Protein coding	CCDS18638	Q5D1E7	TSL:1 GENCODE basic APPRIS P1
Zc3h12a-202	ENSMUST00000131685.1	660	No protein	Retained intron	<del>-</del> 88	-	TSL:1

The strategy is based on the design of Zc3h12a-201 transcript, The transcription is shown below



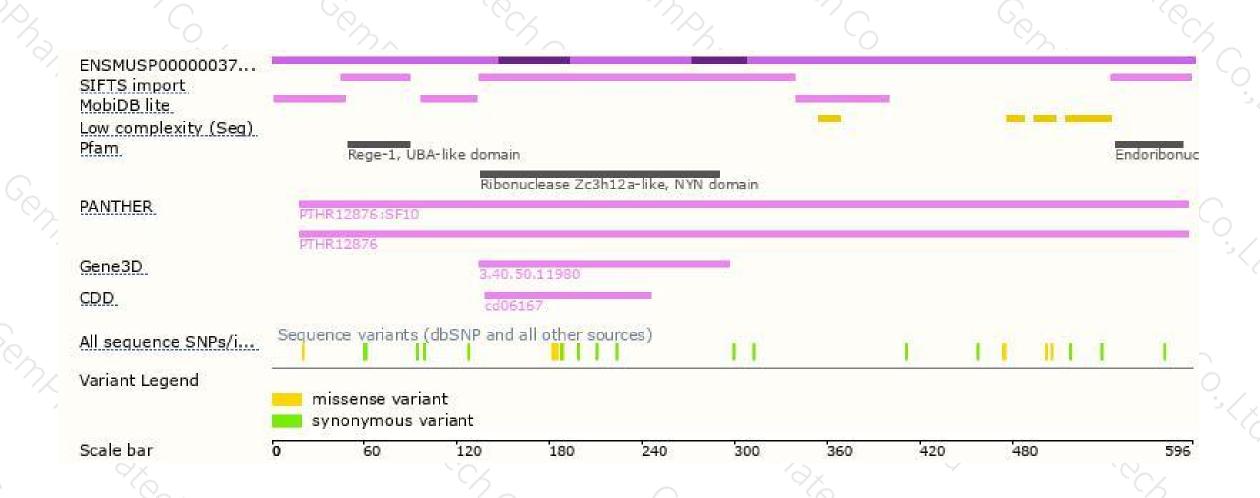
### Genomic location distribution





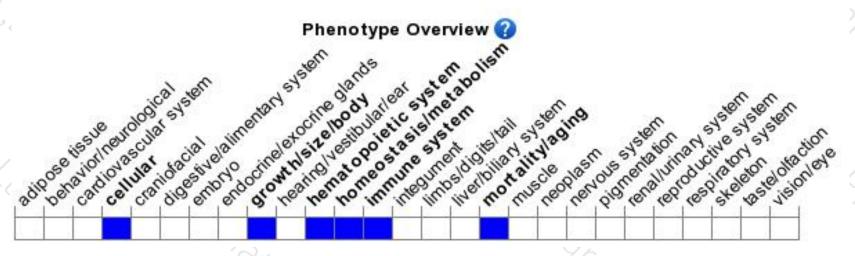
### Protein domain





# 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 null allele exhibit splenomegaly, lymphadenopathy, hyperimmunoglobulinemia, increased auto-antibodies, and defective IL6 post-transcriptional regulation.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





