# Zfp683 Cas9-KO Strategy

Designer: Ruirui Zhang

Reviewer: Daohua Xu

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## **Project Overview**



**Project Name** 

Zfp683

**Project type** 

Cas9-KO

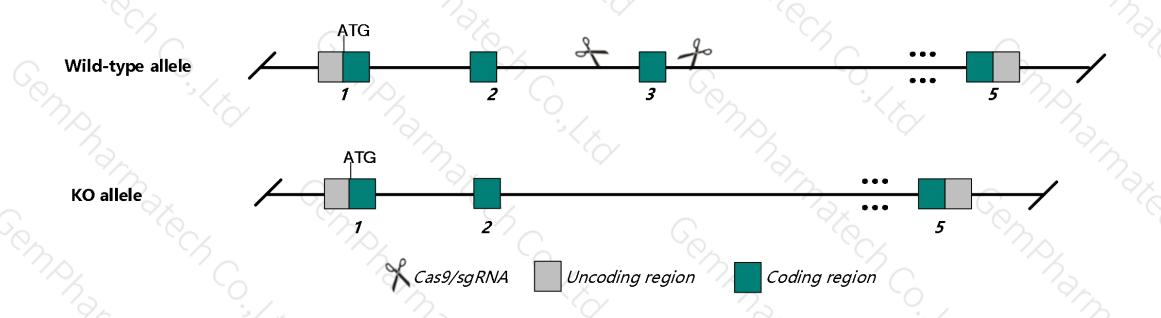
Strain background

C57BL/6JGpt

### **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the Zfp683 gene. The schematic diagram is as follows:



### **Technical routes**



- The *Zfp683* gene has 1 transcript. According to the structure of *Zfp683* gene, exon3 of *Zfp683*-201 (ENSMUST00000105884.2) transcript is recommended as the knockout region. The region contains 668bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Zfp683* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

### **Notice**



- According to the existing MGI data, mice homozygous for a gene trap allele exhibit reduced mature NKT cells and altered susceptibility to MCMV infection.
- The *Zfp683* 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 the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)



Zfp683 zinc finger protein 683 [ Mus musculus (house mouse) ]

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Gene ID: 100503878, updated on 13-Dec-2020

#### Summary

☆ ?

Official Symbol Zfp683 provided by MGI

Official Full Name zinc finger protein 683 provided by MGI

Primary source MGI:MGI:3650254

Gene type pseudo
RefSeq status INFERRED
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Hob; Hobit; Gm13060

Orthologs human all

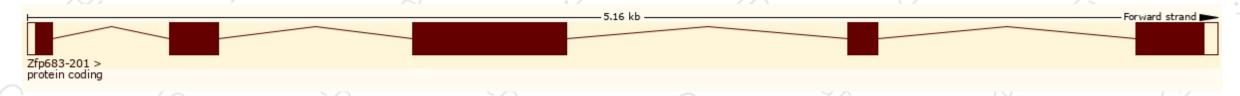
## Transcript information (Ensembl)



The gene has 1 transcripts, and all transcripts are shown below:

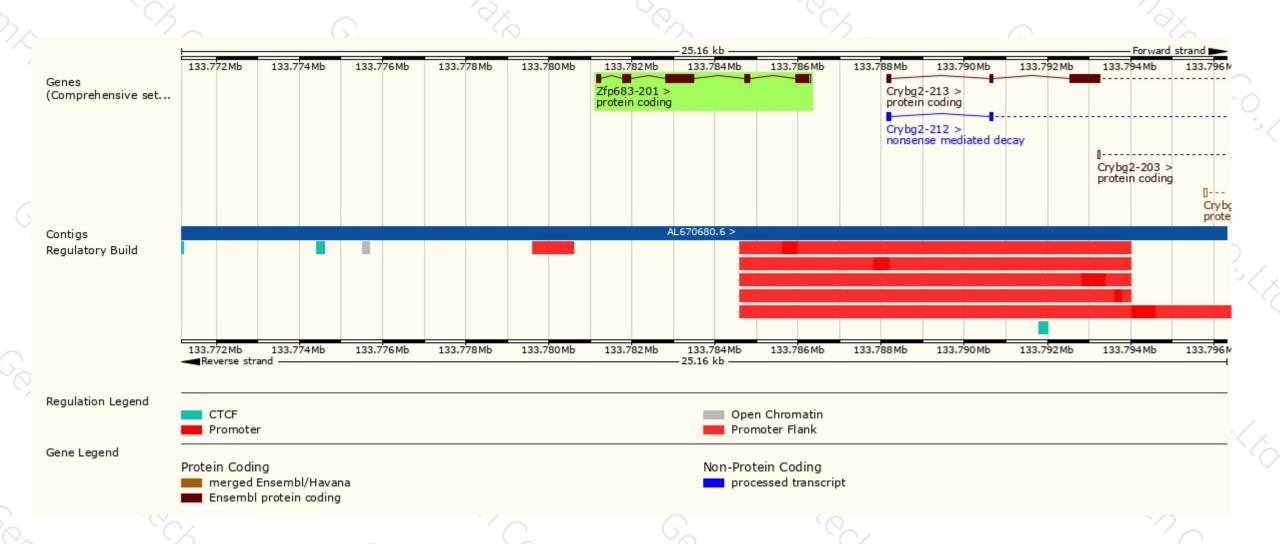
Name 🍦	Transcript ID 🝦	bp 🌲	Protein 🌲	Biotype 🝦	CCDS 🍦	UniProt Match 🍦		Flags	
Zfp683-201	ENSMUST00000105884.2	1471	<u>458aa</u>	Protein coding	-	<u>I7HJS4</u> &	TSL:5	GENCODE basic	APPRIS P1

The strategy is based on the design of *Zfp683*-201 transcript, the transcription is shown below:



### Genomic location (Ensembl)





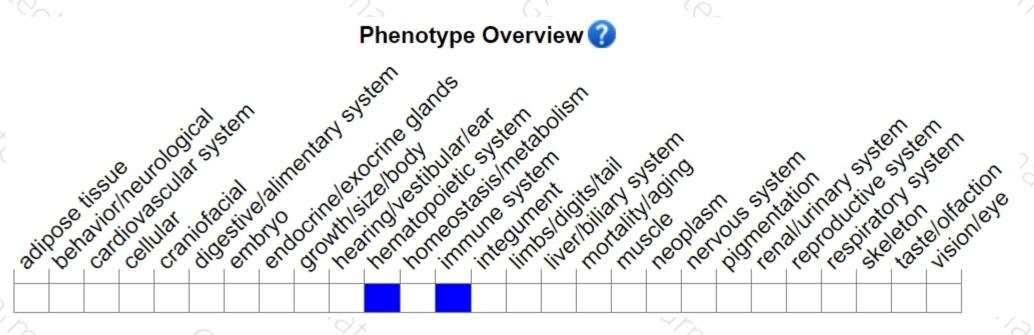
## Protein domain (Ensembl)





### Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

Mice homozygous for a gene trap allele exhibit reduced mature NKT cells and altered susceptibility to MCMV infection.

If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





