

# H2-Oa Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

**Design Date:** 2020-3-13

## **Project Overview**



**Project Name** 

*H2-Oa* 

**Project type** 

Cas9-KO

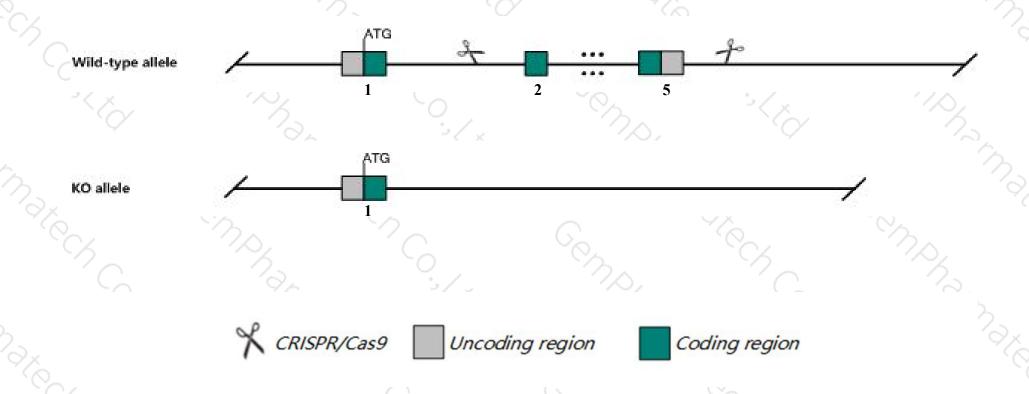
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *H2-Oa* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *H2-Oa* gene has 7 transcripts. According to the structure of *H2-Oa* gene, exon2-exon5 of *H2-Oa-201* (ENSMUST00000025192.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *H2-Oa* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > According to the existing MGI data, Homozygous inactivation of this gene results in abnormal antigen presentation via MHC class II. Mice homozygous for a knock-out allele show enhanced selection of CD4+ single positive thymocytes. Mice homozygous for a different knock-out allele show increased serum IgG1 levels.
- > The flox region overlap with part of the BC051537 gene, which may affect the regulation of this gene.
- The *H2-Oa* gene is located on the Chr17. 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)



#### H2-Oa histocompatibility 2, O region alpha locus [ Mus musculus (house mouse) ]

Gene ID: 15001, updated on 5-Nov-2019

#### Summary

△ ?

Official Symbol H2-Oa provided by MGI

Official Full Name histocompatibility 2, O region alpha locus provided by MGI

Primary source MGI:MGI:95924

See related Ensembl: ENSMUSG00000024334

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 H-20a

Expression Biased expression in spleen adult (RPKM 116.7), thymus adult (RPKM 40.6) and 3 other tissues See more

Orthologs human all

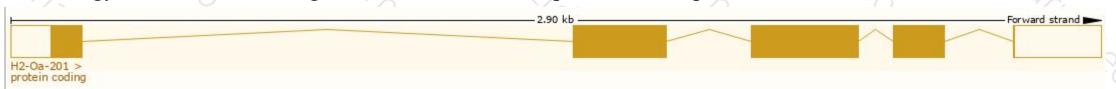
# Transcript information (Ensembl)



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

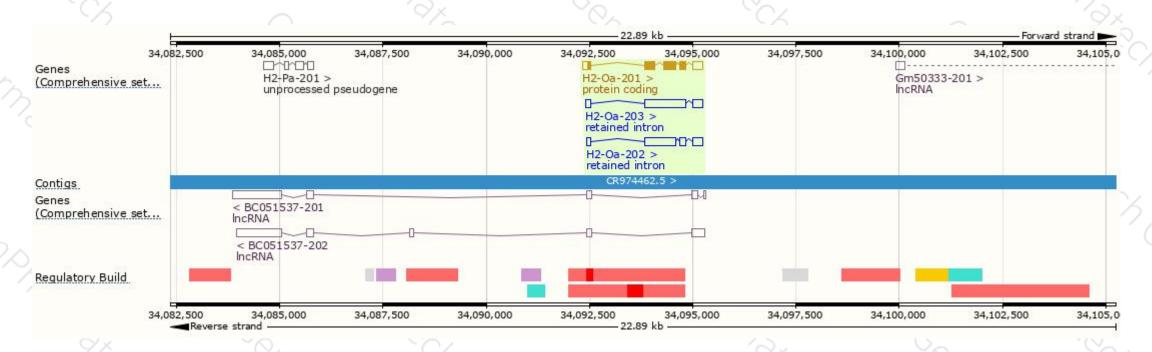
Name 4	Transcript ID #	bp 🌲	Protein 4	Biotype	CCDS 🍦	UniProt #	Flags	
H2-Oa-201	ENSMUST00000025192.7	1088	250aa	Protein coding	CCDS37577 ₽	Q9QWV1₽	TSL:1 GENCODE basic	APPRIS P1
H2-Oa-203	ENSMUST00000236684.1	1340	No protein	Retained intron	70	5)	-	
H2-Oa-202	ENSMUST00000174670.1	1231	No protein	Retained intron	373		TSL:1	

The strategy is based on the design of *H2-Oa-201* transcript, The transcription is shown below



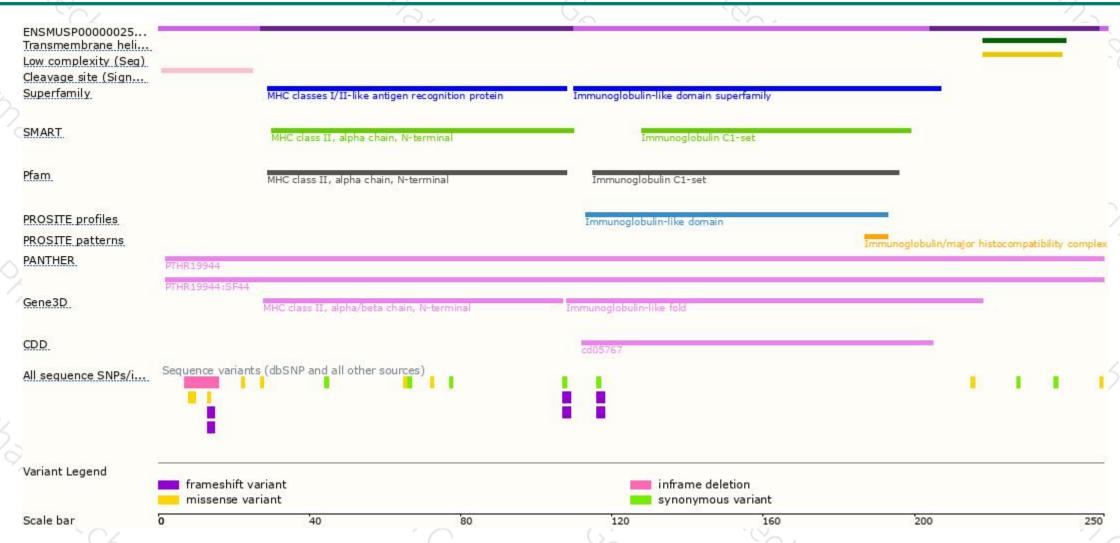
### Genomic location distribution





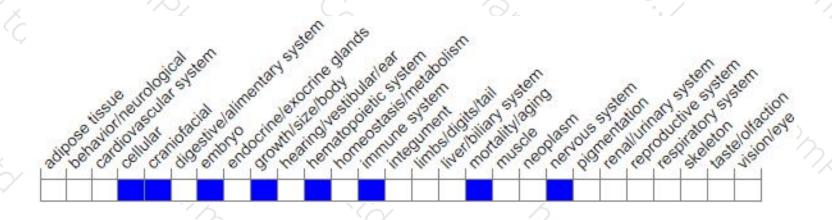
### Protein domain





# 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, Homozygous inactivation of this gene results in abnormal antigen presentation via MHC class II. Mice homozygous for a knock-out allele show enhanced selection of CD4+ single positive thymocytes. Mice homozygous for a different knock-out allele show increased serum IgG1 levels.



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





