

# Hrh1 Cas9-CKO Strategy

Designer: H

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**Design Date:** 

2019-7-22

## **Project Overview**



**Project Name** 

Hrh1

**Project type** 

Cas9-CKO

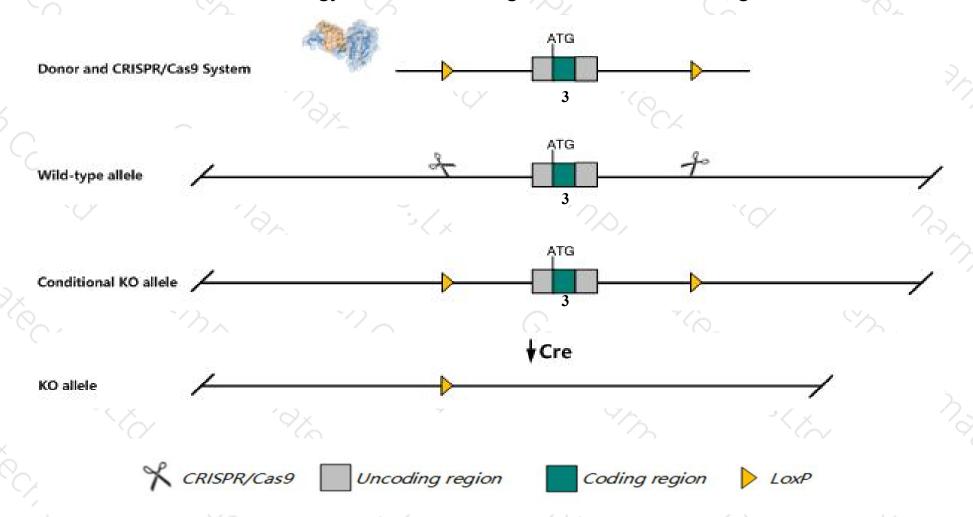
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Hrh1* gene. The schematic diagram is as follows:



### Technical routes



- The *Hrh1* gene has 5 transcripts. According to the structure of *Hrh1* gene, exon3 of *Hrh1-201* (ENSMUST00000088987.2) transcript is recommended as the knockout region. The region contains all 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 *Hrh1* 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, Homozygous null mutants show decrease in exploratory behavior, diurnal activity, aggression, anxiety, serotonin release, respiratory reaction to temperature and leptin response.

  Natural variants affect B. pertussis induced vasoactive amine sensitization.
- > The *Hrh1* gene is located on the Chr6. 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)



#### Hrh1 histamine receptor H1 [Mus musculus (house mouse)]

Gene ID: 15465, updated on 19-Mar-2019

#### Summary

☆ ?

Official Symbol Hrh1 provided by MGI

Official Full Name histamine receptor H1 provided by MGI

Primary source MGI:MGI:107619

See related Ensembl:ENSMUSG00000053004

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 Bphs, H1R, HH1R, Hir

Expression Biased expression in cortex adult (RPKM 2.2), colon adult (RPKM 1.7) and 14 other tissuesSee more

Orthologs human all

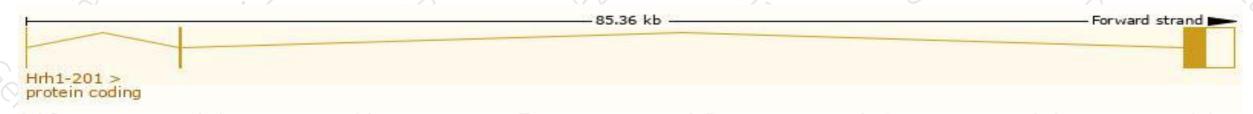
## Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

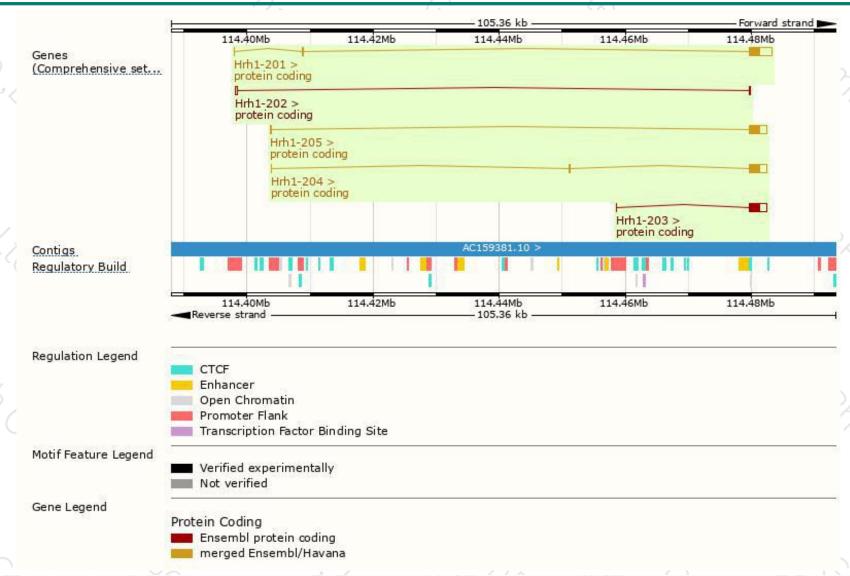
						f km f
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000088987.2	3782	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000161650.2	2978	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000161220.1	2817	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000160780.1	2782	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000160212.1	476	<u>35aa</u>	Protein coding	15 T	E0CXH0	CDS 3' incomplete TSL:2
	ENSMUST00000088987.2 ENSMUST00000161650.2 ENSMUST00000161220.1 ENSMUST00000160780.1	ENSMUST000000161650.2 2978 ENSMUST00000161220.1 2817 ENSMUST00000160780.1 2782	ENSMUST000000161650.2 2978 488aa  ENSMUST00000161220.1 2817 488aa  ENSMUST00000160780.1 2782 488aa	ENSMUST00000088987.2         3782         488aa         Protein coding           ENSMUST00000161650.2         2978         488aa         Protein coding           ENSMUST00000161220.1         2817         488aa         Protein coding           ENSMUST00000160780.1         2782         488aa         Protein coding	ENSMUST00000088987.2         3782         488aa         Protein coding         CCDS20435           ENSMUST00000161650.2         2978         488aa         Protein coding         CCDS20435           ENSMUST00000161220.1         2817         488aa         Protein coding         CCDS20435           ENSMUST00000160780.1         2782         488aa         Protein coding         CCDS20435	ENSMUST00000088987.2         3782         488aa         Protein coding         CCDS20435         B3Y5T0 P70174           ENSMUST00000161650.2         2978         488aa         Protein coding         CCDS20435         B3Y5T0 P70174           ENSMUST00000161220.1         2817         488aa         Protein coding         CCDS20435         B3Y5T0 P70174           ENSMUST00000160780.1         2782         488aa         Protein coding         CCDS20435         B3Y5T0 P70174

The strategy is based on the design of *Hrh1-201* transcript, The transcription is shown below



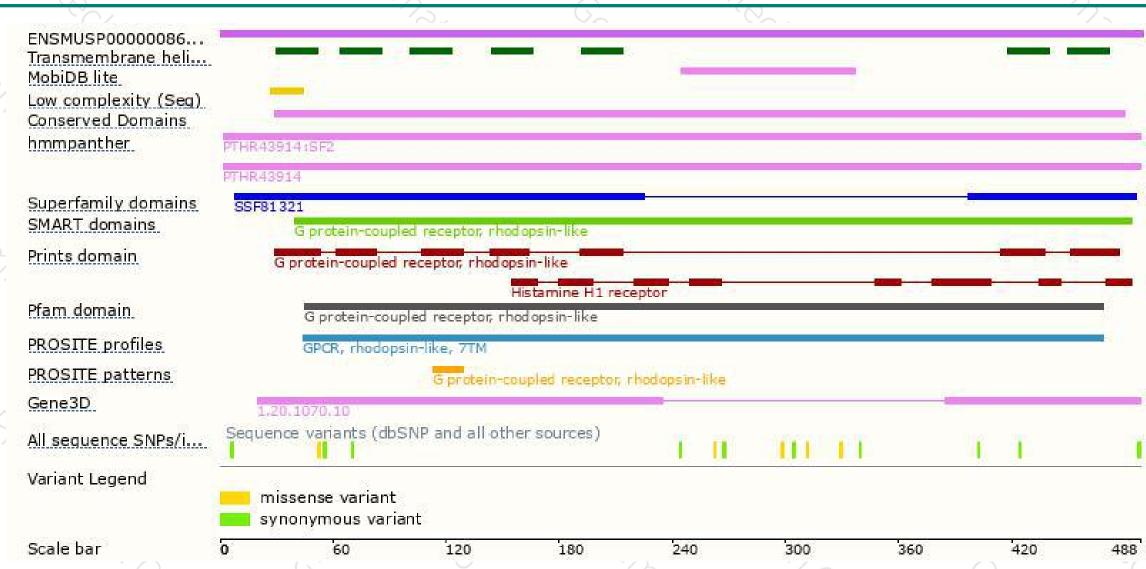
### Genomic location distribution





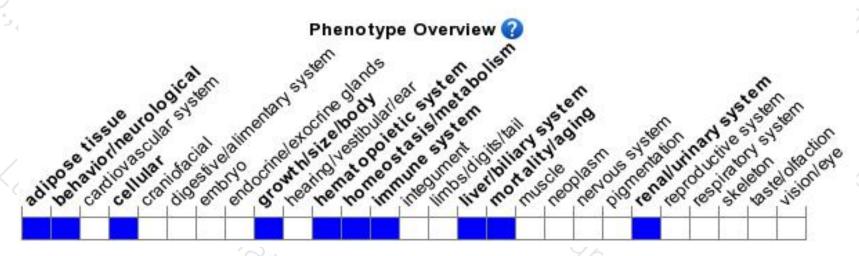
### Protein domain





## 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 null mutants show decrease in exploratory behavior, diurnal activity, aggression, anxiety, serotonin release, respiratory reaction to temperature and leptin response. Natural variants affect B. pertussis induced vasoactive amine sensitization.



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





