

Hrh1 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Hrh1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 v

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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 tissues See more
Orthologs	human all

Transcript information (Ensembl)

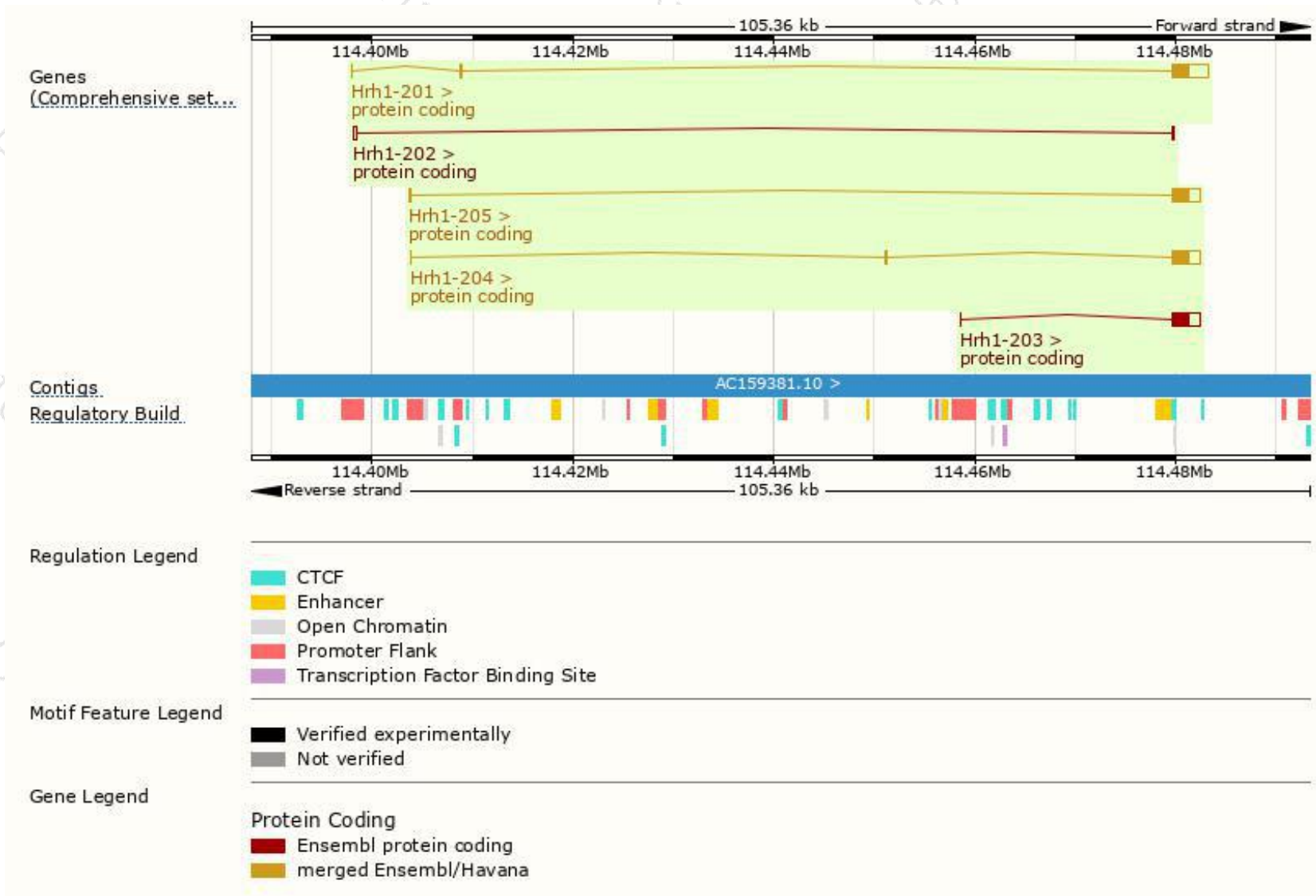
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hrh1-201	ENSMUST00000088987.2	3782	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
Hrh1-205	ENSMUST00000161650.2	2978	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
Hrh1-204	ENSMUST00000161220.1	2817	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:1 GENCODE basic APPRIS P1
Hrh1-203	ENSMUST00000160780.1	2782	488aa	Protein coding	CCDS20435	B3Y5T0 P70174	TSL:5 GENCODE basic APPRIS P1
Hrh1-202	ENSMUST00000160212.1	476	35aa	Protein coding	-	E0CXH0	CDS 3' incomplete TSL:2

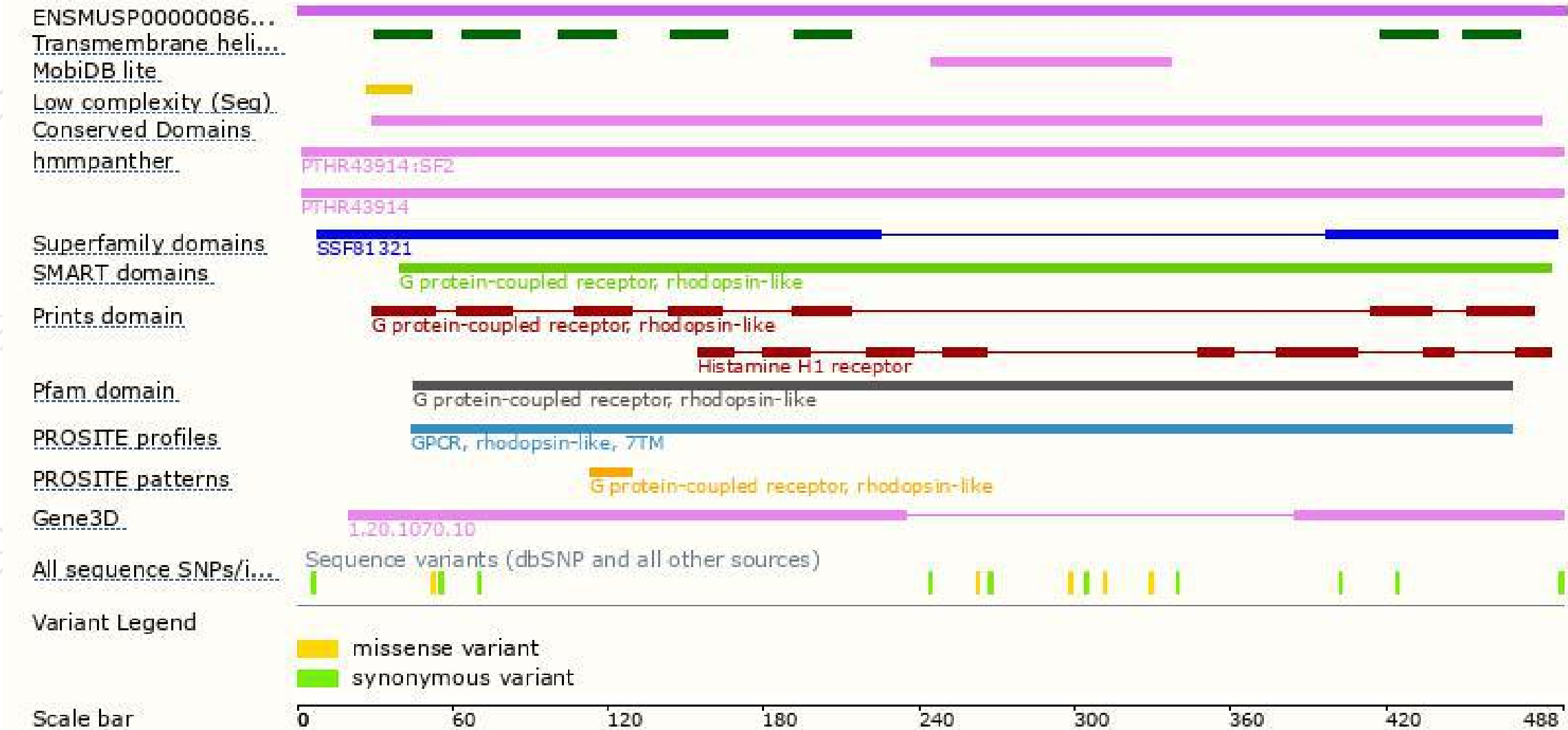
The strategy is based on the design of *Hrh1-201* transcript,The transcription is shown below



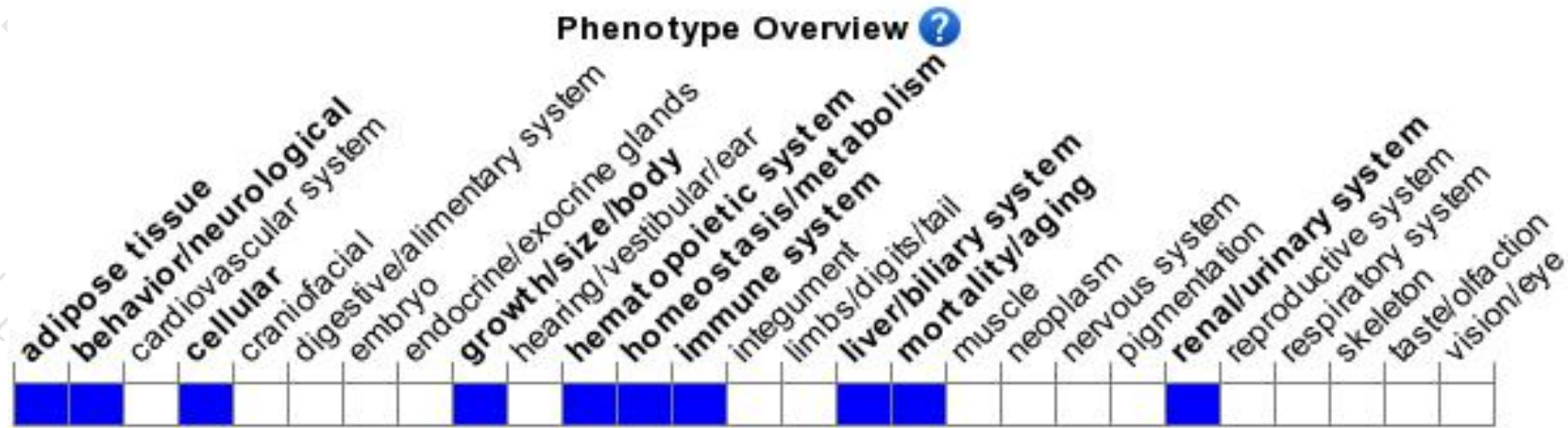
Genomic location distribution



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.

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