

Hnrnp1 Cas9-CKO Strategy

Designer: Xiangli Bian

Reviewer: Yao Yu

Design Date: 2023-10-30

Overview

Target Gene Name

- *Hnrnph1*

Project Type

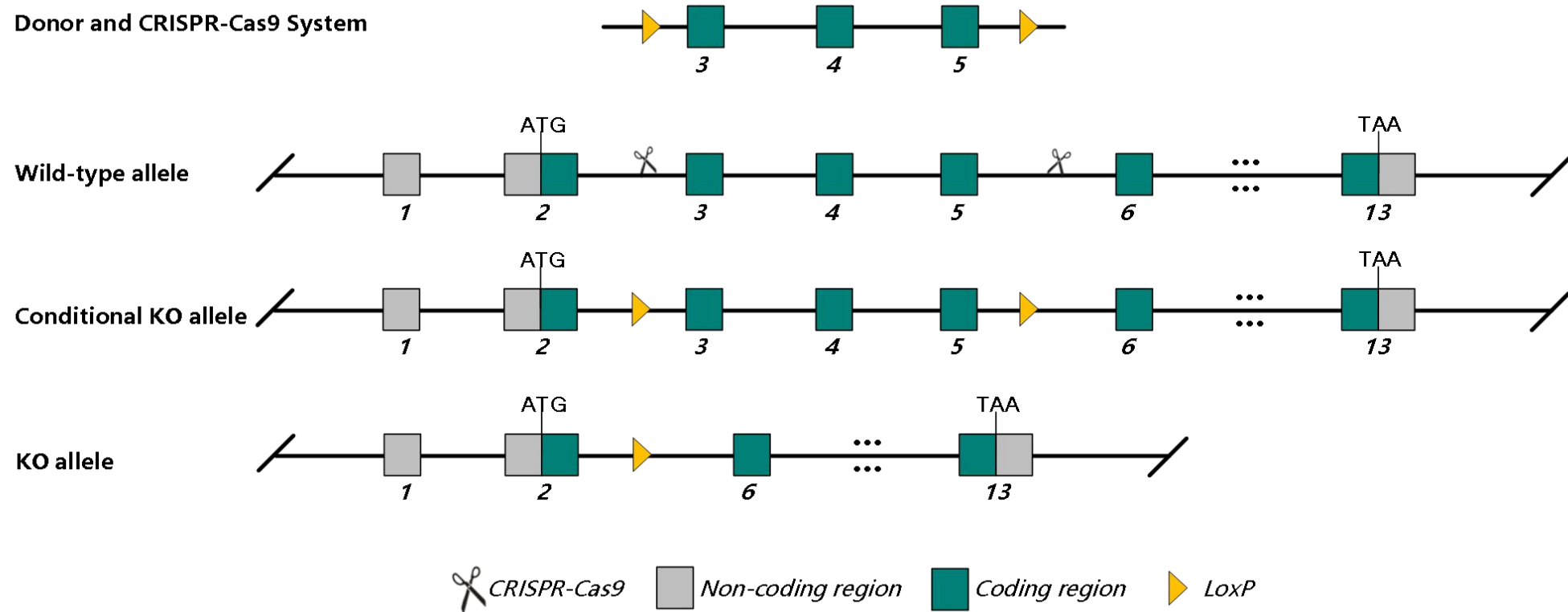
- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Hnrnp1* gene.

Technical Information

- The *Hnrnp1* gene has 18 transcripts. According to the structure of *Hnrnp1* gene, exon 3-5 of *Hnrnp1*-202 (ENSMUST00000077817.8) is recommended as the knockout region. The region contains 439 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Hnrnp1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Hnrnp1 heterogeneous nuclear ribonucleoprotein H1 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 59013, updated on 11-Oct-2023

Summary

Official Symbol Hnrnp1 provided by [MGI](#)
Official Full Name heterogeneous nuclear ribonucleoprotein H1 provided by [MGI](#)
Primary source [MGI:MGI:1891925](#)
See related [Ensembl:ENSMUSG00000007850](#) [AllianceGenome:MGI:1891925](#)
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 Hnrnp1; Hnrph1; E430005G16Rik
Summary Predicted to enable RNA binding activity; enzyme binding activity; and identical protein binding activity. Acts upstream of or within cellular response to interleukin-7. Predicted to be located in cytosol and nucleus. Predicted to be part of catalytic step 2 spliceosome. Predicted to be active in nucleoplasm. Is expressed in brain; gut; liver; metanephros; and respiratory system. Human ortholog(s) of this gene implicated in Sjogren's syndrome. Orthologous to human HNRNPH1 (heterogeneous nuclear ribonucleoprotein H1). [provided by Alliance of Genome Resources, Apr 2022]
Expression Broad expression in CNS E11.5 (RPKM 294.5), CNS E14 (RPKM 202.8) and 17 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: 11 B1.3; 11 30.56 cM

See Hnrnp1 in [Genome Data Viewer](#)

Exon count: 16

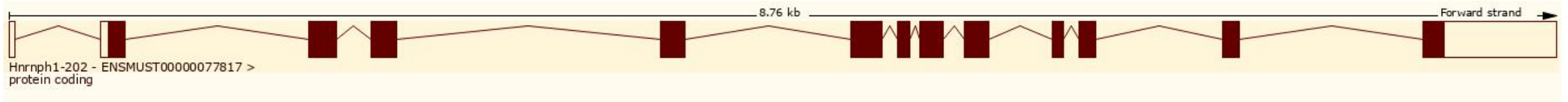
<https://www.ncbi.nlm.nih.gov/gene/59013>

Transcript Information

The gene has 18 transcripts, all transcripts are shown below:

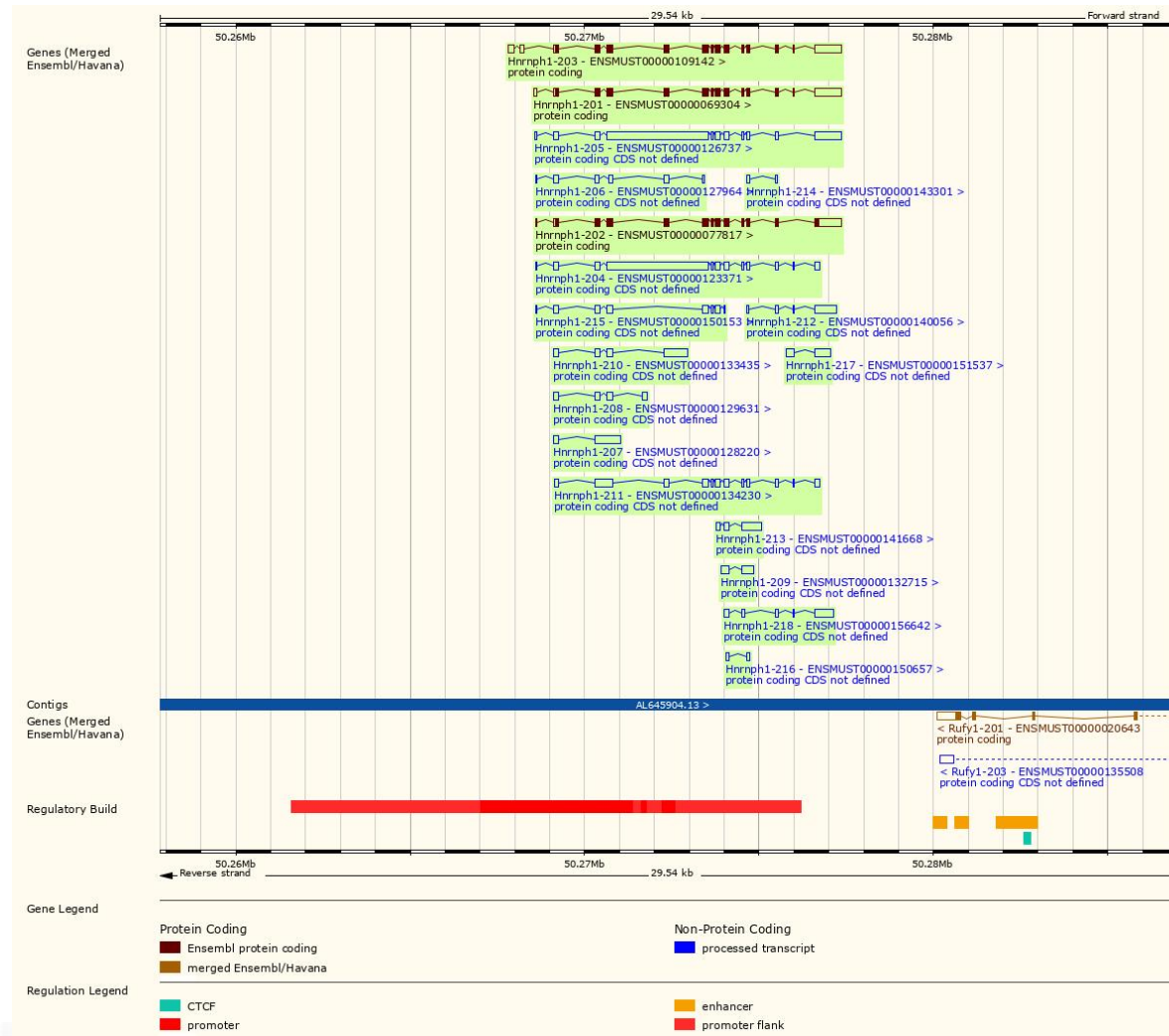
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000077817.8	Hnrnp1-202	2126	472aa	Protein coding	CCDS83800	Q8C2Q7	Ensembl Canonical	GENCODE basic APPRIS ALT1 TSL:1
ENSMUST00000109142.8	Hnrnp1-203	2427	449aa	Protein coding	CCDS24634	Q35737 Q811L7	GENCODE basic	APPRIS P4 TSL:1
ENSMUST00000069304.14	Hnrnp1-201	2225	449aa	Protein coding	CCDS24634	Q35737 Q811L7	GENCODE basic	APPRIS P4 TSL:1
ENSMUST00000126737.8	Hnrnp1-205	4577	No protein	Protein coding CDS not defined		-	TSL:1	
ENSMUST00000123371.8	Hnrnp1-204	4002	No protein	Protein coding CDS not defined		-	TSL:1	
ENSMUST00000134230.8	Hnrnp1-211	1724	No protein	Protein coding CDS not defined		-	TSL:5	
ENSMUST00000133435.2	Hnrnp1-210	1116	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000156642.8	Hnrnp1-218	914	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000150153.8	Hnrnp1-215	870	No protein	Protein coding CDS not defined		-	TSL:5	
ENSMUST00000128220.8	Hnrnp1-207	860	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000141668.8	Hnrnp1-213	832	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000140056.2	Hnrnp1-212	816	No protein	Protein coding CDS not defined		-	TSL:3	
ENSMUST00000151537.2	Hnrnp1-217	677	No protein	Protein coding CDS not defined		-	TSL:1	
ENSMUST00000129631.8	Hnrnp1-208	582	No protein	Protein coding CDS not defined		-	TSL:3	
ENSMUST00000132715.2	Hnrnp1-209	582	No protein	Protein coding CDS not defined		-	TSL:3	
ENSMUST00000127964.8	Hnrnp1-206	581	No protein	Protein coding CDS not defined		-	TSL:5	
ENSMUST00000150657.2	Hnrnp1-216	163	No protein	Protein coding CDS not defined		-	TSL:5	
ENSMUST00000143301.2	Hnrnp1-214	159	No protein	Protein coding CDS not defined		-	TSL:3	

The strategy is based on the design of *Hnrnp1-202* transcript, the transcription is shown below:

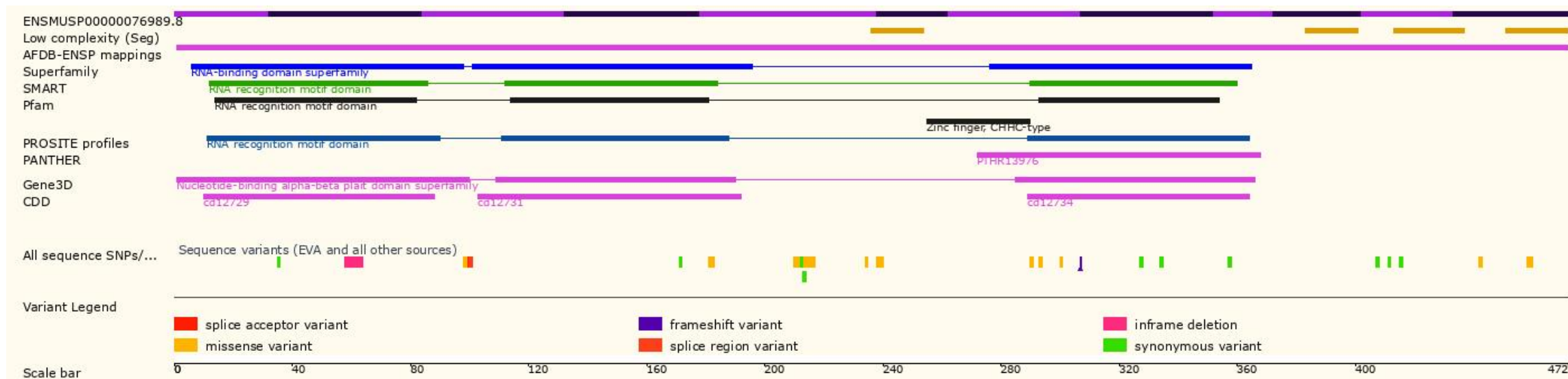


Source: <http://asia.ensembl.org/>

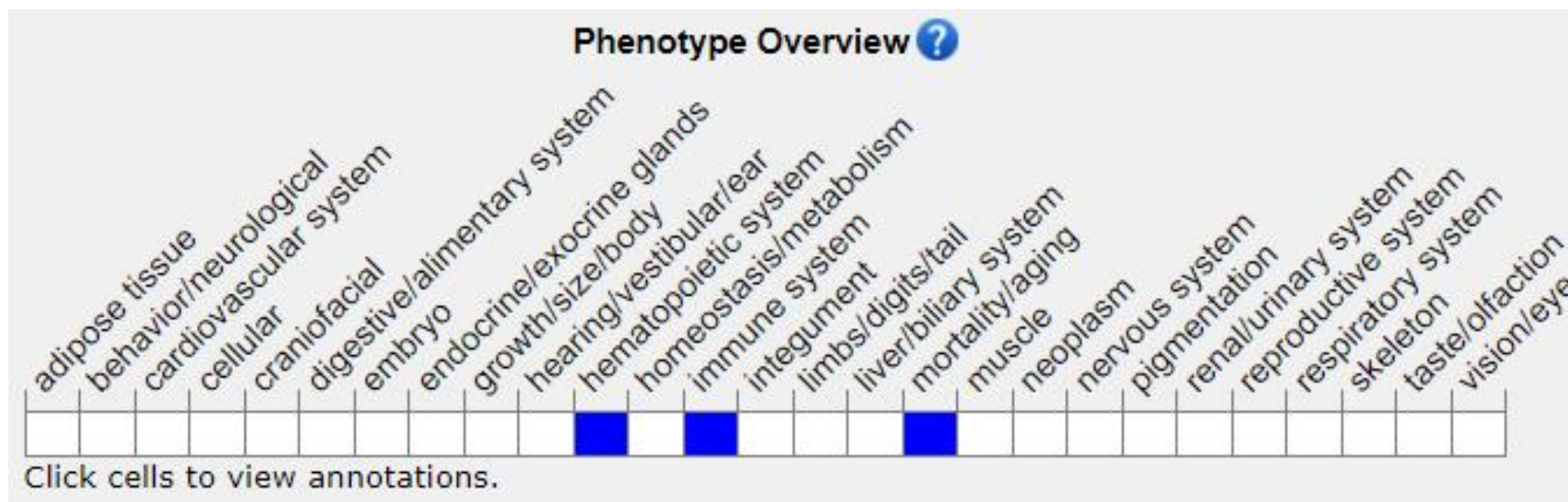
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



Important Information

- This strategy may not affect *Hnrnph1*-209, *Hnrnph1*-212, *Hnrnph1*-213, *Hnrnph1*-214, *Hnrnph1*-216, *Hnrnph1*-217 and *Hnrnph1*-218 transcript.
- A loxp will be inserted exon 4 of *Hnrnph1*-204 transcript, which may affect the regulation of the transcript.
- A loxp will be inserted exon 4 of *Hnrnph1*-205 transcript, which may affect the regulation of the transcript.
- *Hnrnph1* is located on Chr 11. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.