GemPharmatech™

H1f2 Cas9-KO Strategy

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Overview

Target Gene Name

- *H1f2*

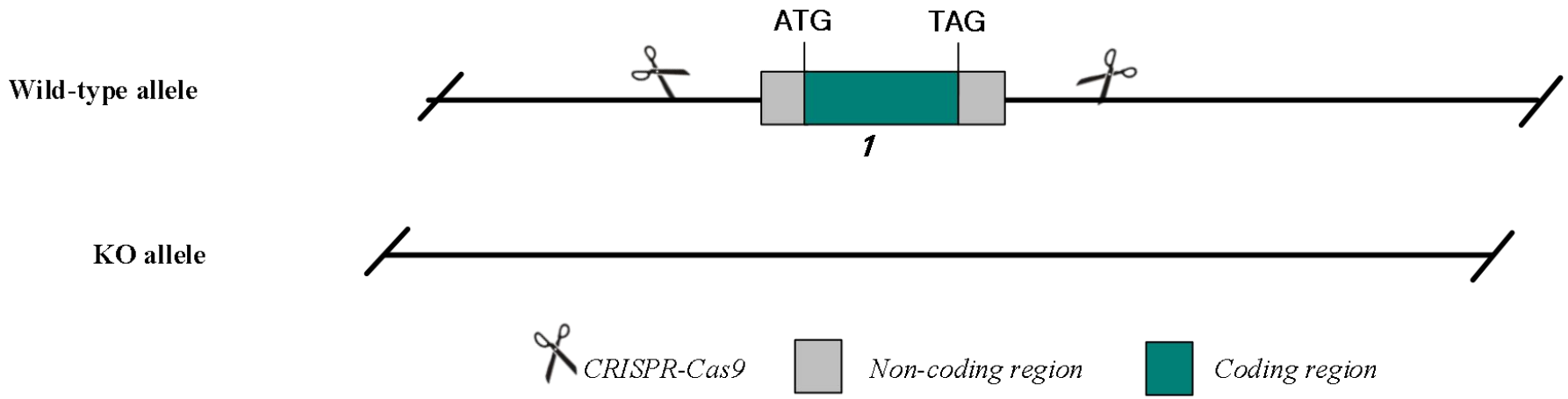
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *H1f2* gene.

Technical Information

- The *H1f2* gene has 1 transcript. According to the structure of *H1f2* gene, exon1 of *H1f2*-201 (ENSMUST00000040914.3) transcript is recommended as the knockout region. The region contains all coding sequences, which may disrupt the function of *H1f2*.
- In this project we use CRISPR-Cas9 technology to modify *H1f2* gene. The brief process is as follows: Cas9 and gRNAs 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.

Gene Information

H1f2 H1.2 linker histone, cluster member [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 50708, updated on 31-Oct-2023

Summary

Official Symbol	H1f2 provided by MGI
Official Full Name	H1.2 linker histone, cluster member provided by MGI
Primary source	MGI:MGI:1931526
See related	Ensembl:ENSMUSG00000036181 AllianceGenome:MGI:1931526
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	H1c; H1-2; H1.2; His1a; H1var1; Hist1h1c; 0610008C09Rik
Summary	Histones are basic nuclear proteins responsible for nucleosome structure of the chromosomal fiber in eukaryotes. Two molecules of each of the four core histones (H2A, H2B, H3, and H4) form an octamer, around which approximately 146 bp of DNA is wrapped in repeating units, called nucleosomes. The linker histone, H1, interacts with linker DNA between nucleosomes and functions in the compaction of chromatin into higher order structures. This gene is intronless and encodes a member of the histone H1 family. Transcripts from this gene lack polyA tails but instead contain a palindromic termination element. [provided by RefSeq, Feb 2014]
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

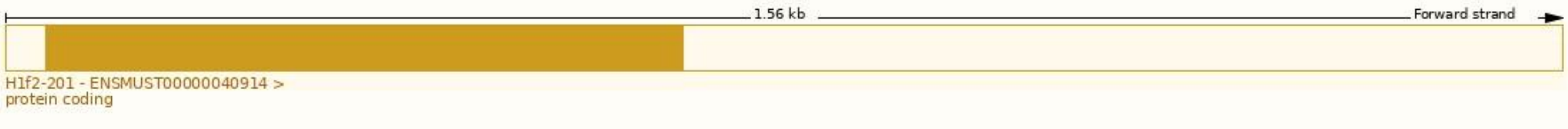
Transcript Information

The gene has 1 transcript, the transcript is shown below:

Show/hide columns (1 hidden) Filter

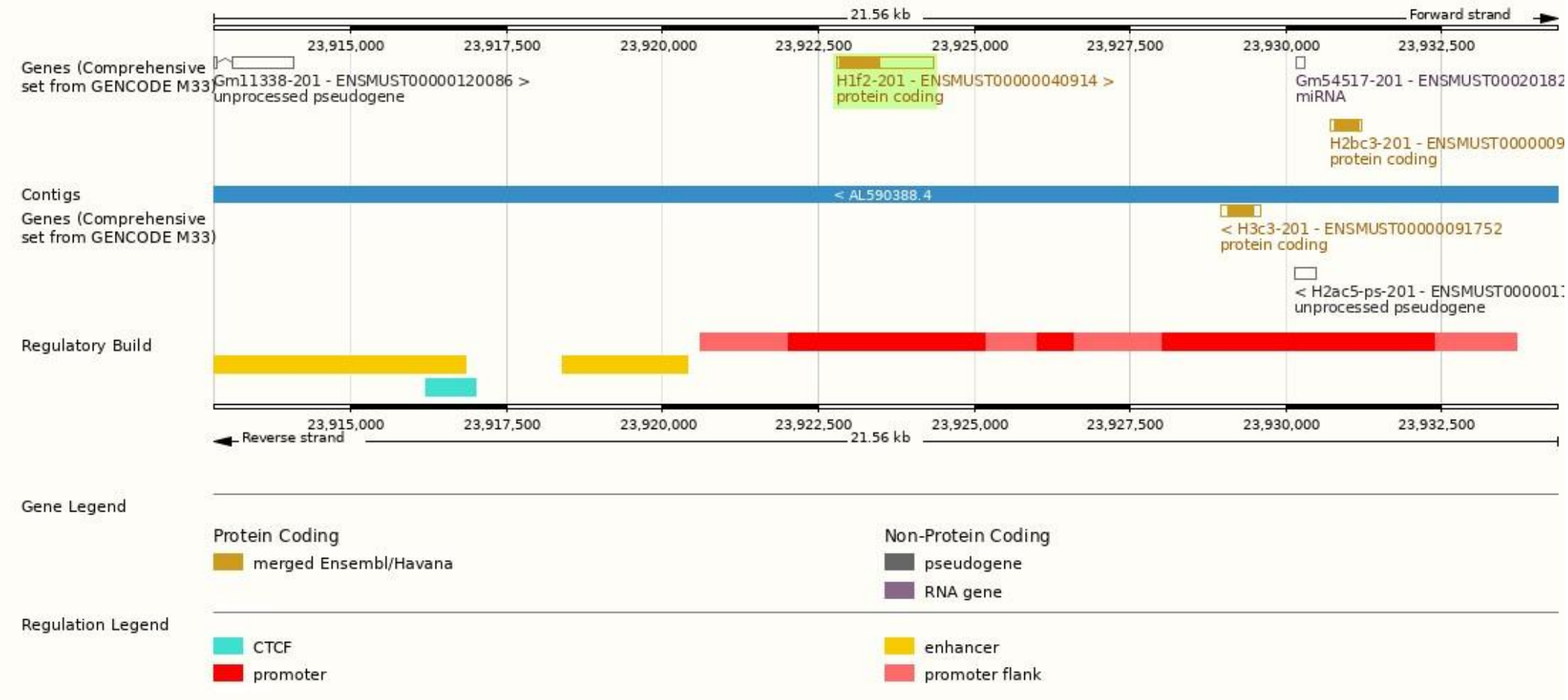
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000040914.3	H1f2-201	1560	212aa	Protein coding	CCDS26361	P15864 Q5SZA3	Ensembl Canonical GENCODE basic APPRIS P1 TSL:NA

The strategy is based on the design of *H1f2*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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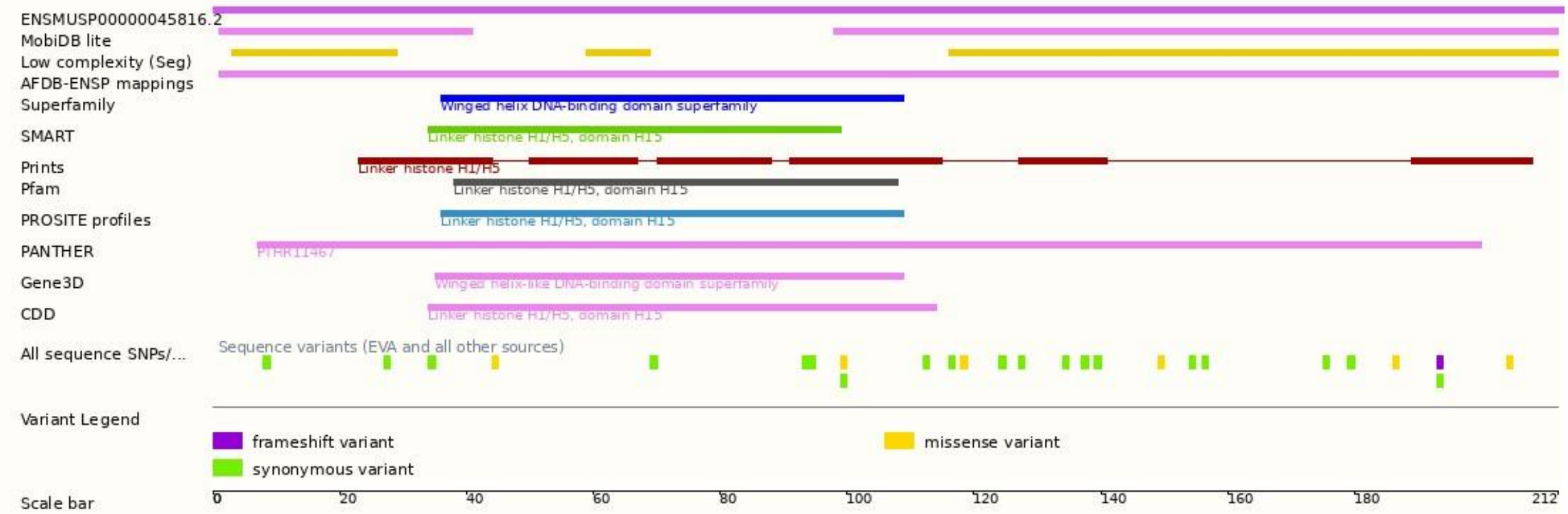
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Important Information

- The loxp insertion is on the predicted promoter region, which may affect the expression of *H1f2*.
- *H1f2* is located on Chr13. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.