

H1f1 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

H1f1

Project type

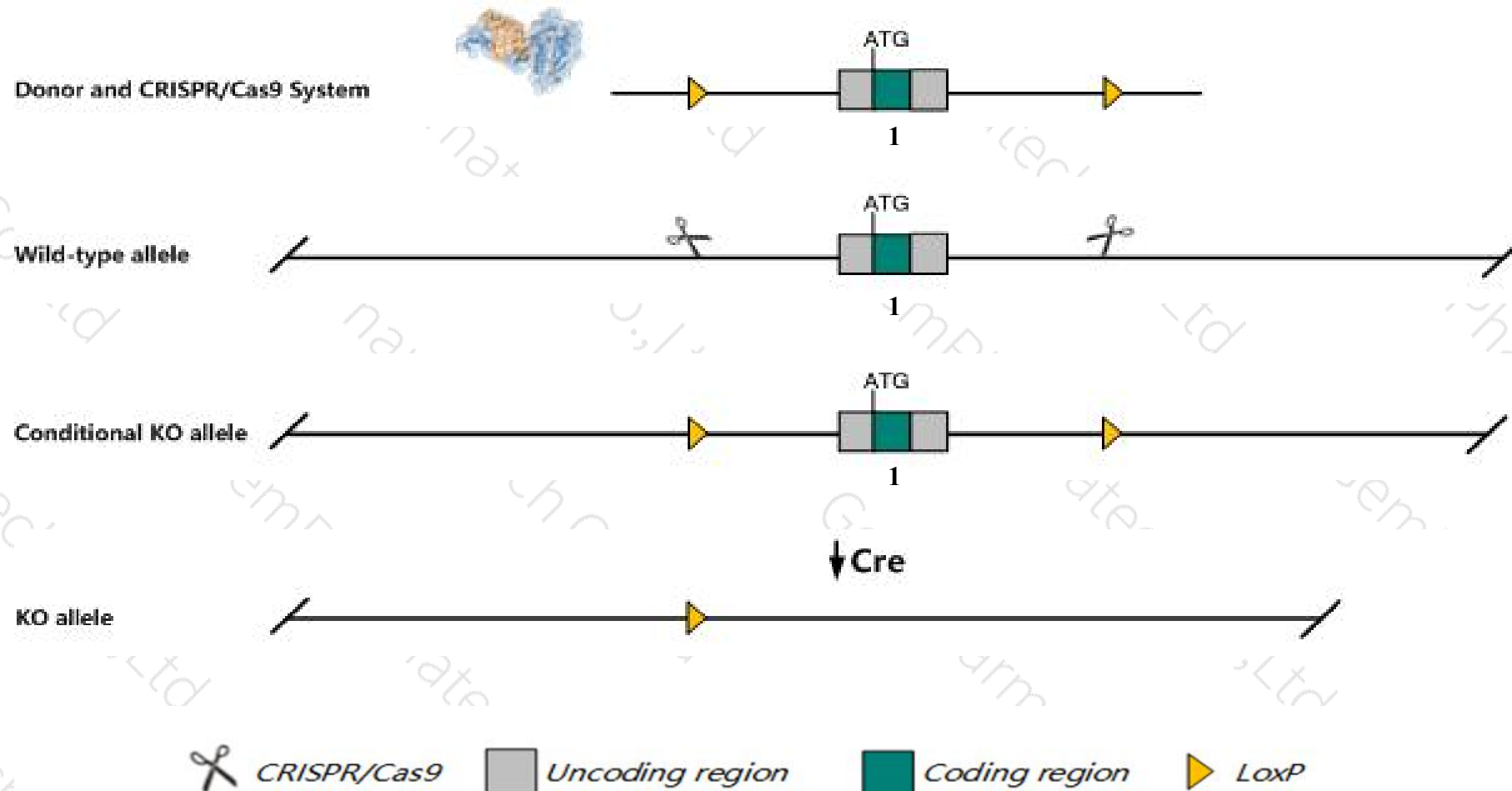
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hlf1* gene. The schematic diagram is as follows:



Technical routes

- The *H1f1* gene has 1 transcript. According to the structure of *H1f1* gene, exon1 of *H1f1*-201 (ENSMUST00000055770.3) 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 *H1f1* 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.

- According to the existing MGI data, mice homozygous for a targeted null mutation are viable, fertile and do not exhibit any defects in the reproductive system or in spermatogenesis.
- The KO region may affect the function of *H3c1*, *H4c1*, *H4c* and *4930558J22Rik* gene.
- The *H1f1* gene is located on the Chr13. 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)

H1f1 H1.1 linker histone, cluster member [Mus musculus (house mouse)]

Gene ID: 80838, updated on 13-Mar-2020

Summary



Official Symbol H1f1 provided by [MGI](#)

Official Full Name H1.1 linker histone, cluster member provided by [MGI](#)

Primary source [MGI:MGI:1931523](#)

See related [Ensembl:ENSMUSG00000049539](#)

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 H1-1, H1.1, H1a, H1var3, Hist1h1a

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 replication-dependent histone that is a member of the histone H1 family. Transcripts from this gene lack polyA tails but instead contain a palindromic termination element. [provided by RefSeq, Aug 2015]

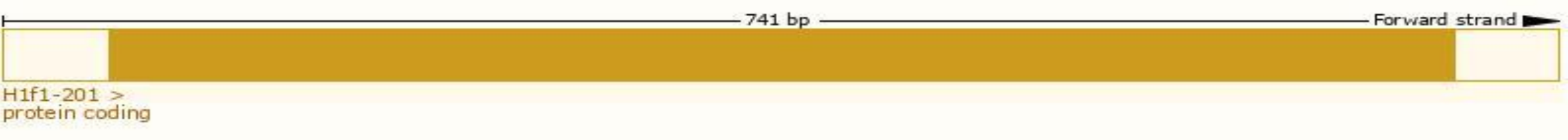
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

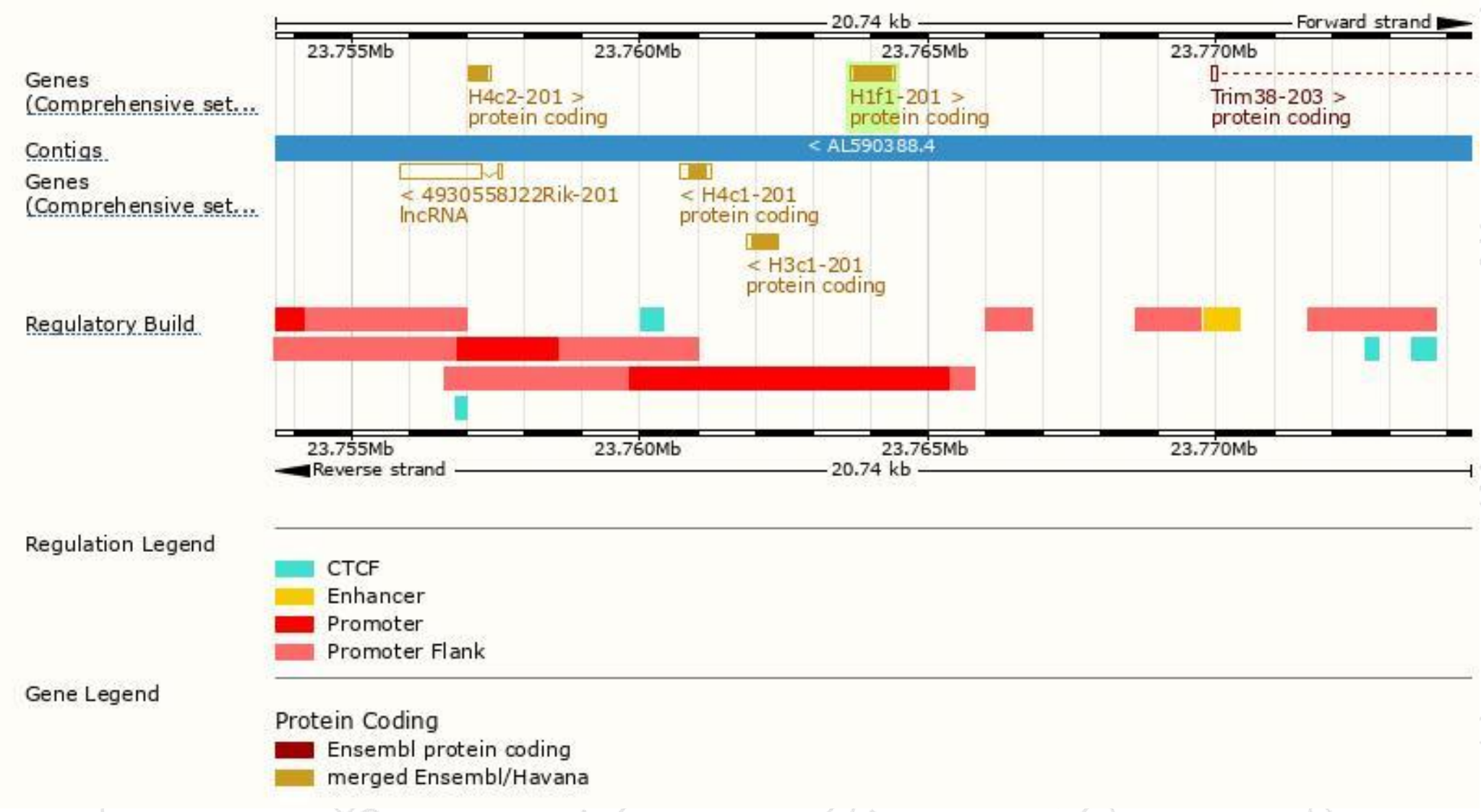
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H1f1-201	ENSMUST00000055770.3	741	213aa	Protein coding	CCDS26369	P43275	TSL:NA GENCODE basic APPRIS P1

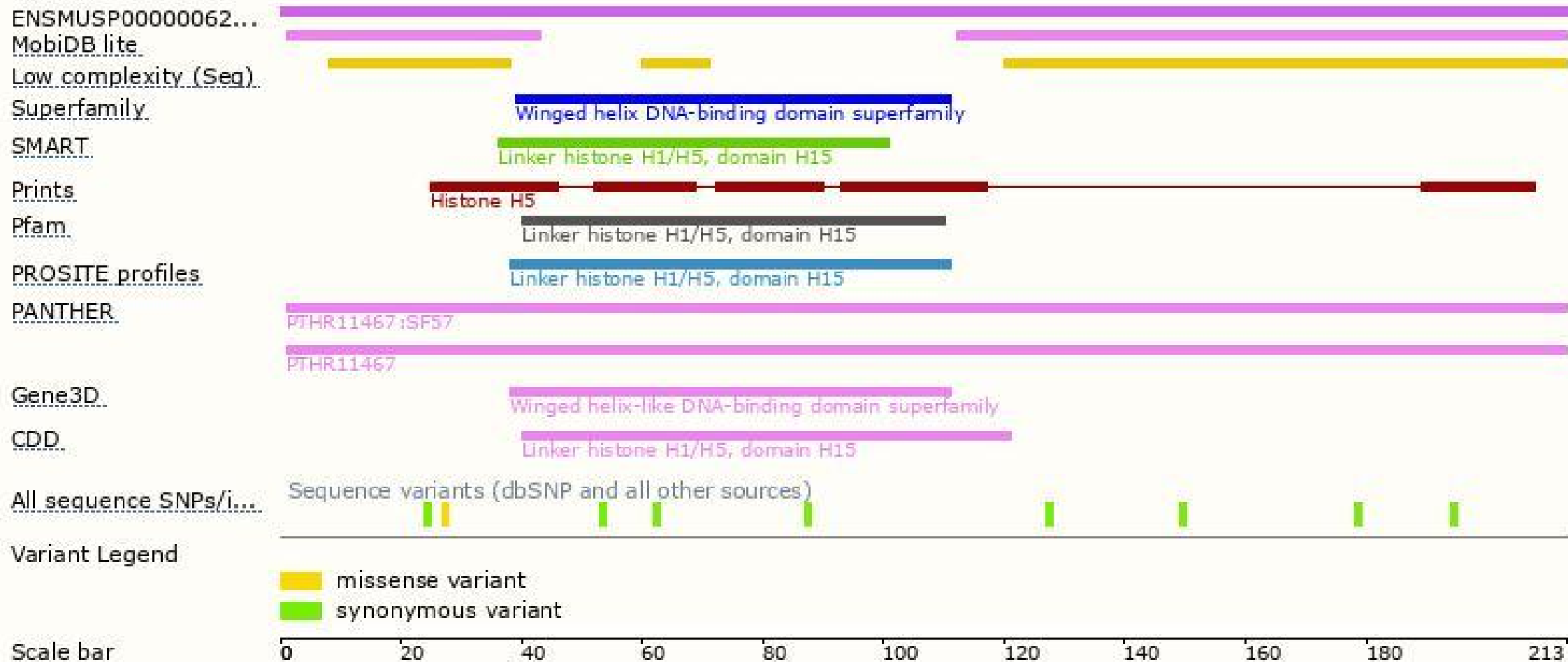
The strategy is based on the design of *H1f1-201* transcript, The transcription is shown below



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.

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