

H2aj Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

H2aj

Project type

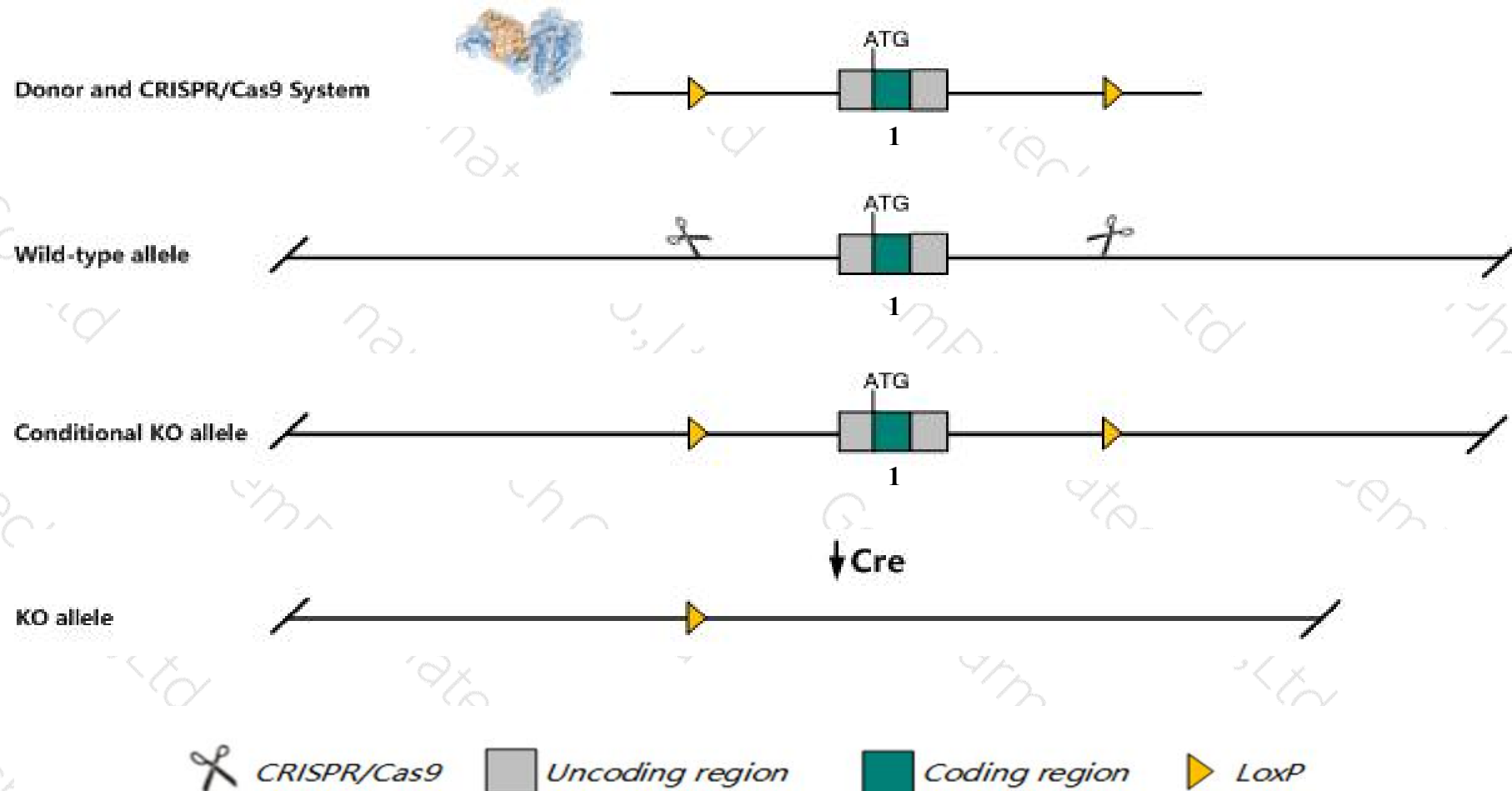
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *H2aj* gene. The schematic diagram is as follows:



- The *H2aj* gene has 2 transcripts. According to the structure of *H2aj* gene, exon1 of *H2aj-201* (ENSMUST00000074556.6) 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 *H2aj* 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.

- *Gm44364*-201 gene may be destroyed.
- The flox region is about 3.7 kb away from the 5th end of the *H4f16*-201 gene, and its effect is unknown.
- The *H2aj* 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)

H2aj H2J.A histone [Mus musculus (house mouse)]

Gene ID: 232440, updated on 13-Mar-2020

Summary



Official Symbol H2aj provided by [MGI](#)

Official Full Name H2J.A histone provided by [MGI](#)

Primary source [MGI:MGI:3606192](#)

See related [Ensembl:ENSMUSG00000060032](#)

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 E130307C13, H2afj

Summary Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Nucleosomes consist of approximately 146 bp of DNA wrapped around a histone octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is located on chromosome 6 and encodes a replication-independent histone that is member of the histone H2A family. [provided by RefSeq, Nov 2015]

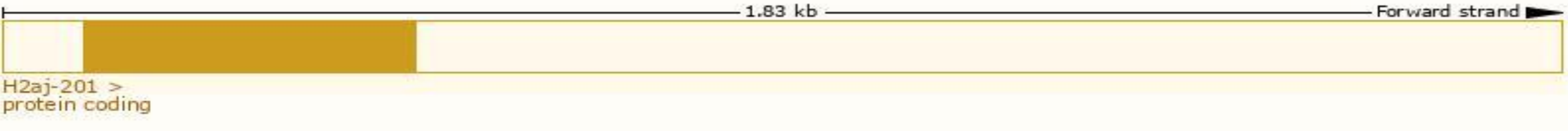
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

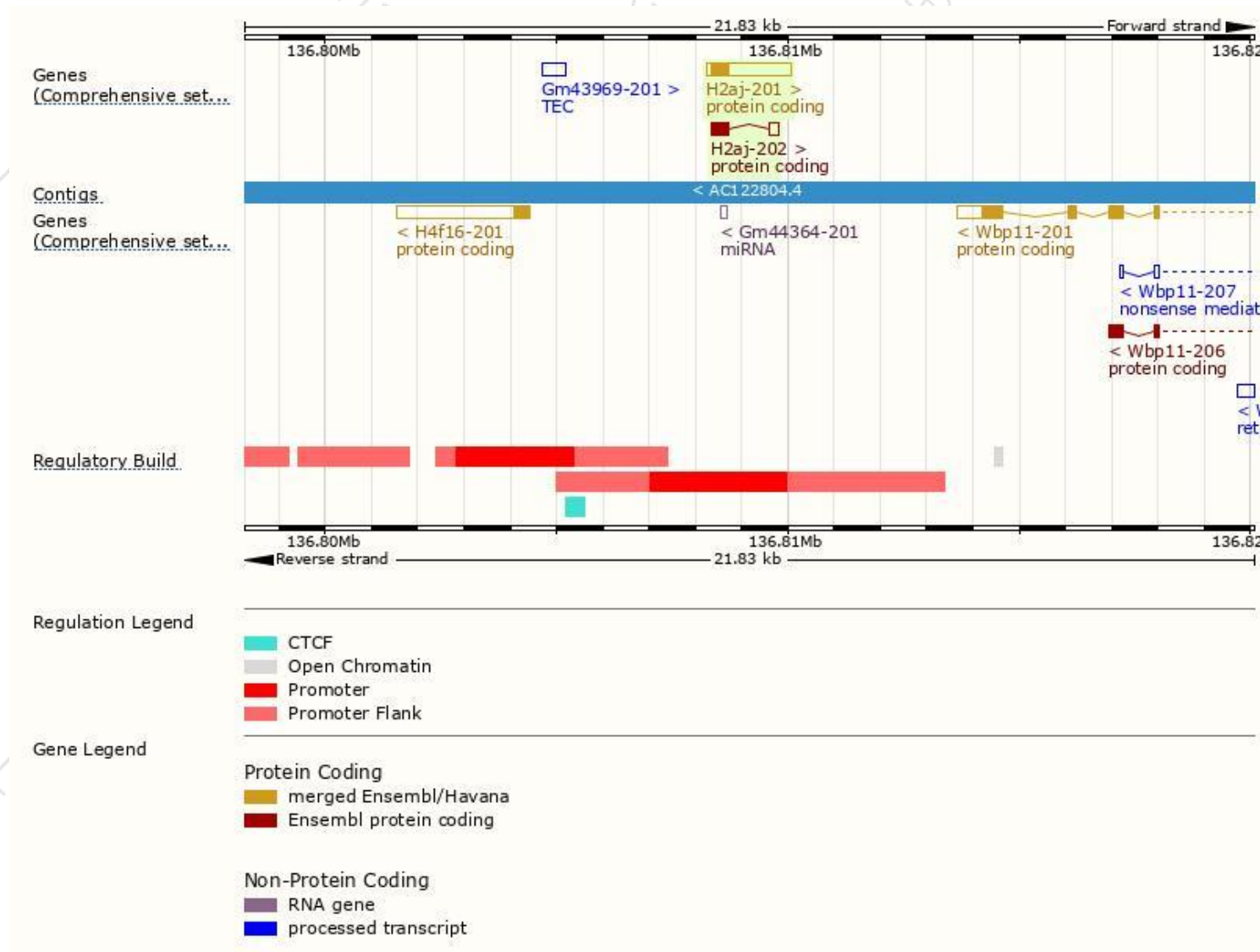
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H2aj-201	ENSMUST00000074556.6	1831	129aa	Protein coding	CCDS20654	Q8R1M2	TSL:NA GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
H2aj-202	ENSMUST00000203982.1	577	126aa	Protein coding	-	A0A0N4SV66	TSL:3 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1

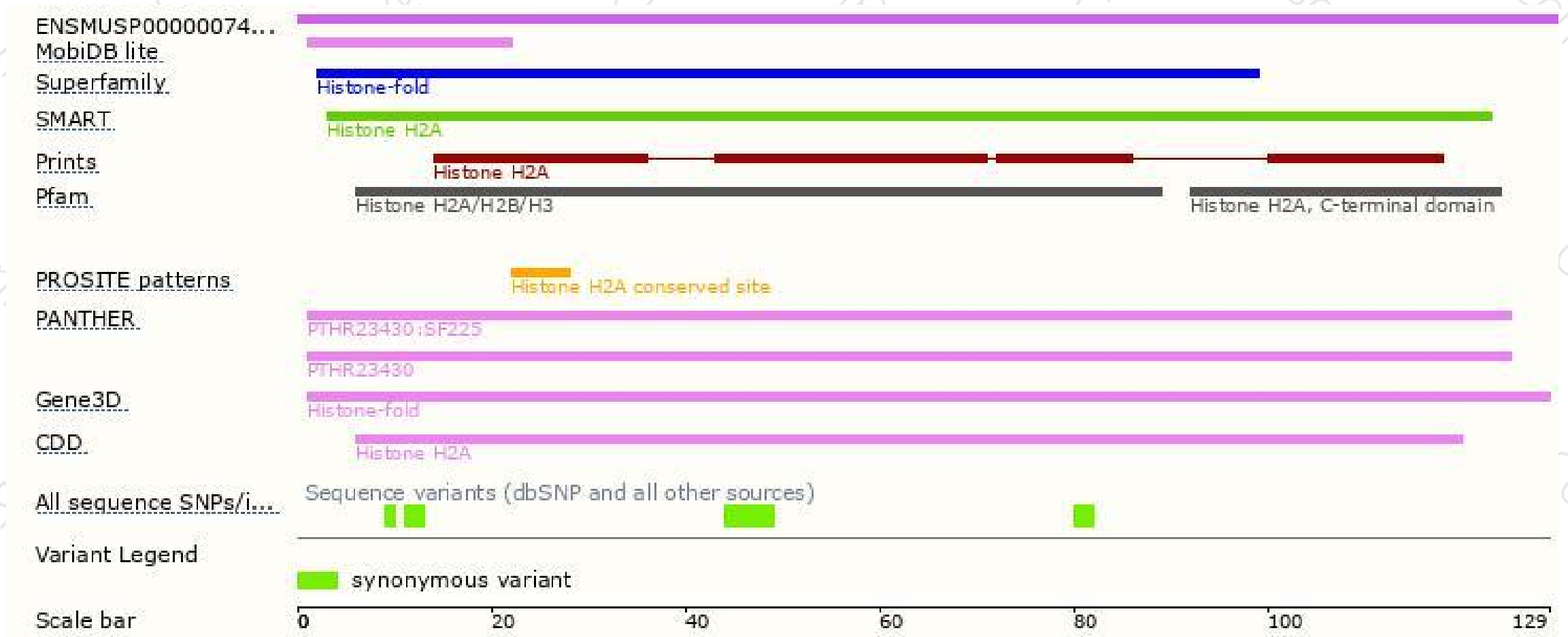
The strategy is based on the design of *H2aj-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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