

# *H2aj* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*H2aj*

**Project type**

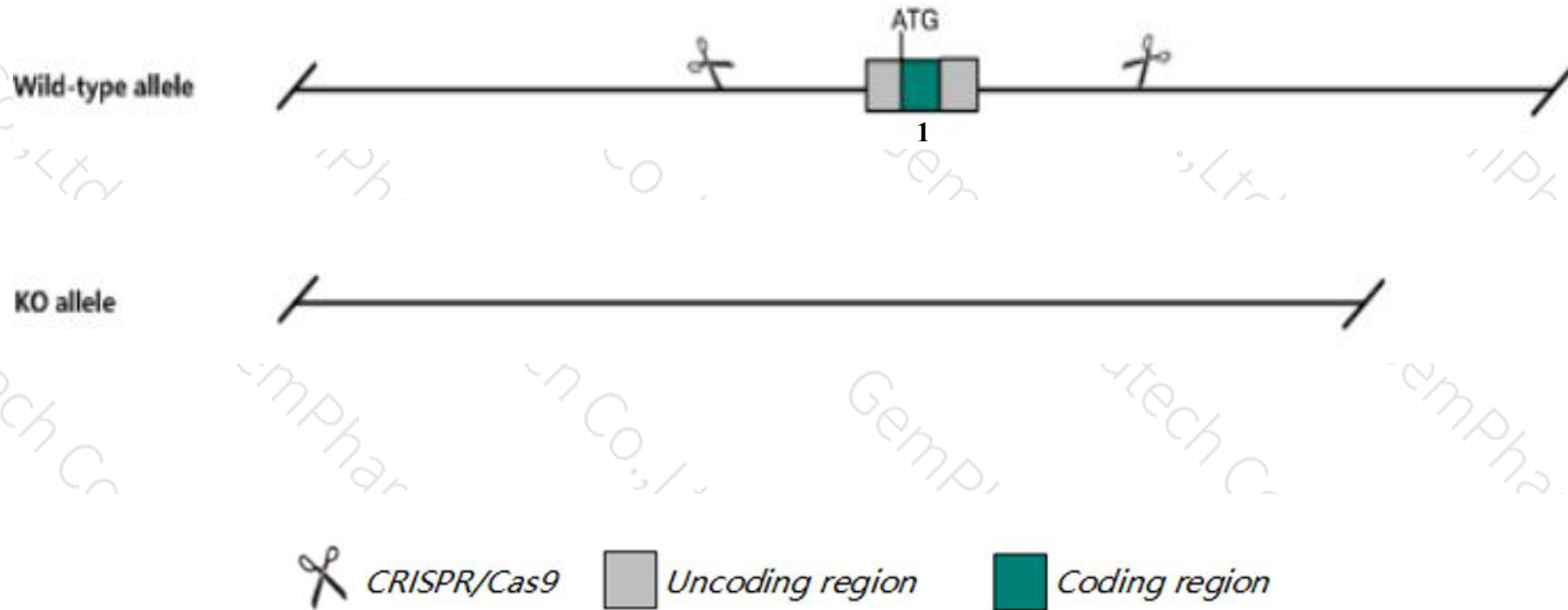
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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 v

- *Gm44364*-201 gene may be destroyed.
- The knockout 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

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

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

### Summary



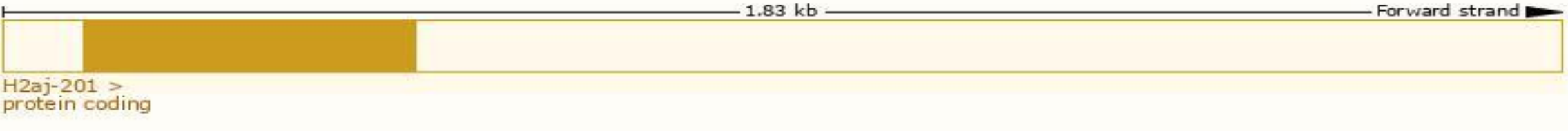
<b>Official Symbol</b>	H2aj provided by <a href="#">MGI</a>
<b>Official Full Name</b>	H2J.A histone provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:3606192</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000060032</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	E130307C13, H2afj
<b>Summary</b>	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]
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

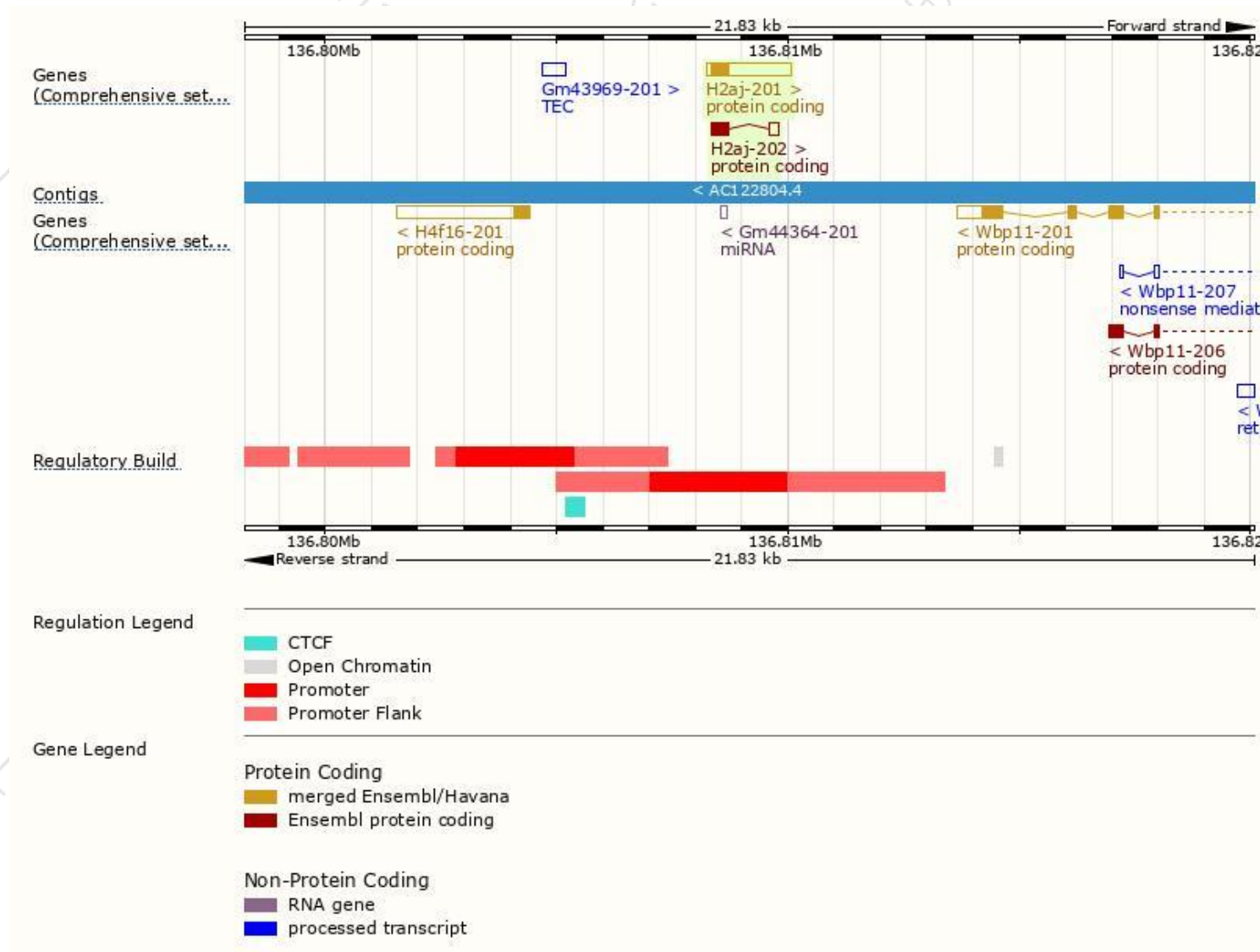
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H2aj-201	<a href="#">ENSMUST00000074556.6</a>	1831	<a href="#">129aa</a>	Protein coding	<a href="#">CCDS20654</a>	<a href="#">Q8R1M2</a>	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	<a href="#">ENSMUST00000203982.1</a>	577	<a href="#">126aa</a>	Protein coding	-	<a href="#">A0A0N4SV66</a>	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

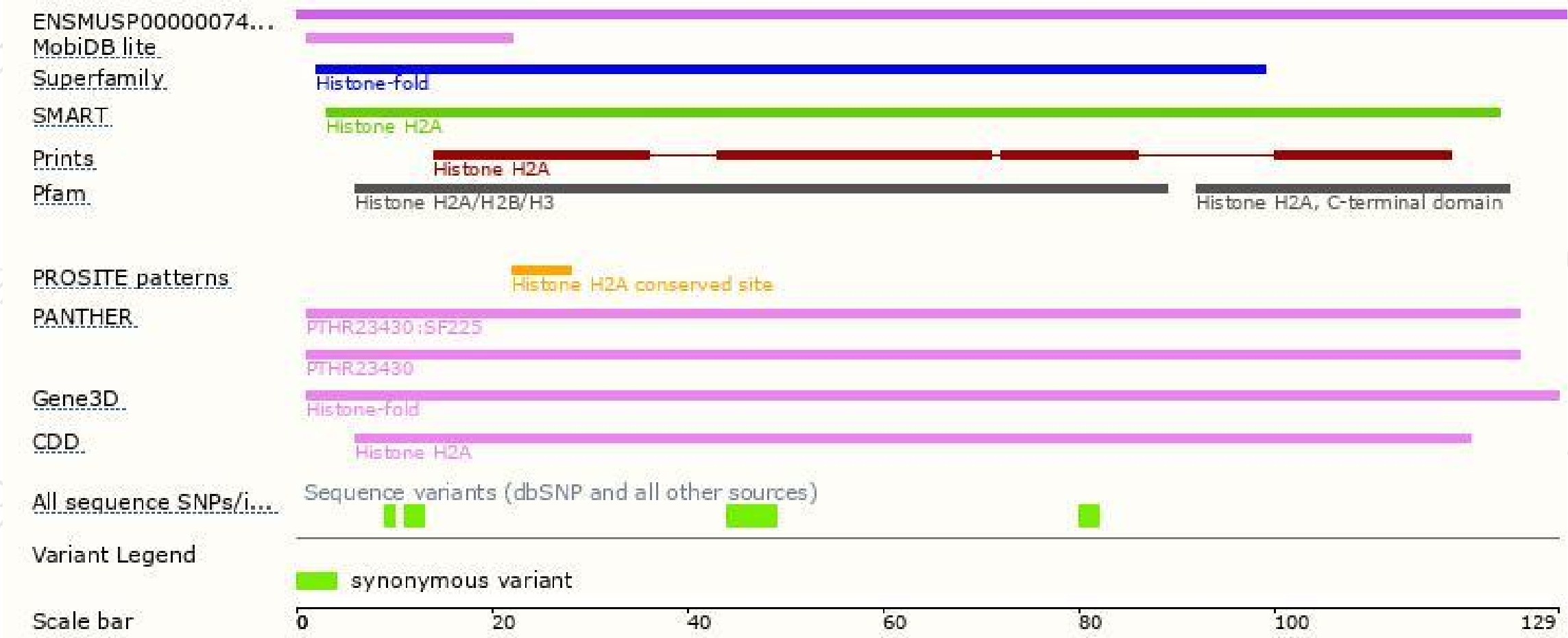


# Genomic location distribution





# Protein domain



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

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