

H2afv Cas9-CKO Strategy

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Project Overview

Project Name

H2afv

Project type

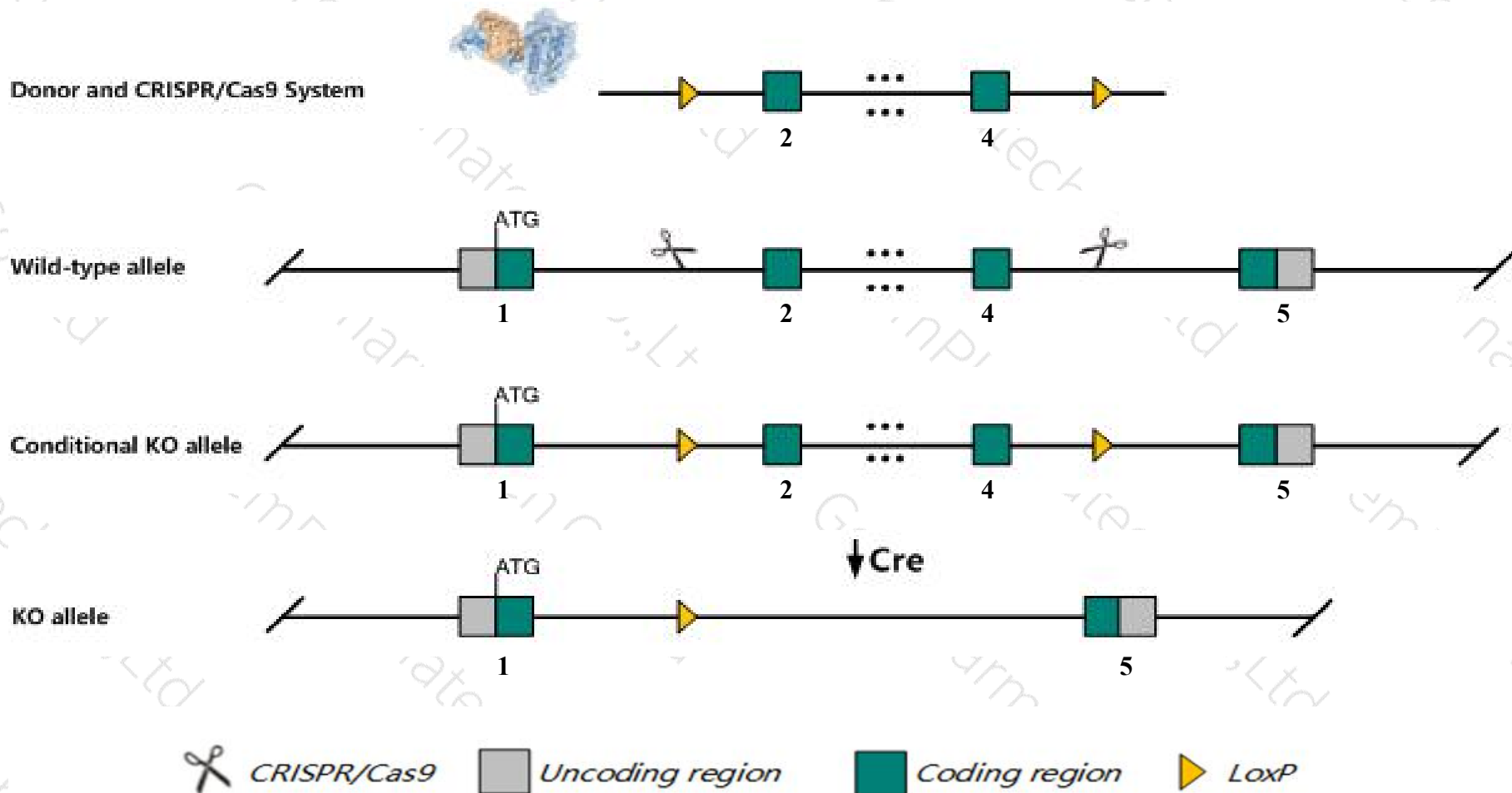
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *H2afv* gene. The schematic diagram is as follows:



Technical routes

- The *H2afv* gene has 2 transcripts. According to the structure of *H2afv* gene, exon2-exon4 of *H2afv*-202 (ENSMUST00000109737.8) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *H2afv* 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.

Notice

- The *H2afv* gene is located on the Chr11. 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.

H2az2 H2A.Z histone variant 2 [*Mus musculus* (house mouse)]

Gene ID: 77605, updated on 1-Oct-2019

Summary

Official Symbol

Official Full Name

Primary source

See related

Gene type

RefSeq status

Organism

Lineage

Also known as

Summary

Expression

Orthologs

H2az2 provided by MGI

H2A.Z histone variant 2 provided by MGI

MGI:MGI:1924855

Ensembl:ENSMUSG00000041126

protein coding

REVIEWED

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

H2av; H2afv; H2A.Z2; H2a.z-2; Wnt1cre; Wnt1-Cre; Wnt1::Cre; C530002L11Rik; Tg(Wnt1-cre)11Rth

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 encodes a replication-independent histone that is a member of the histone H2A family. [provided by RefSeq, Nov 2015]

Ubiquitous expression in CNS E11.5 (RPKM 129.3), CNS E14 (RPKM 78.5) and 27 other tissues See more

human all

Genomic context

Location: 11; 11 A1

Exon count: 6

See H2az2 in Genome Data Viewer

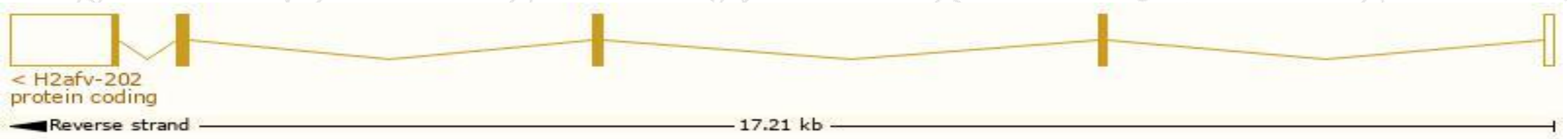
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (6427226..6444511, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (6327229..6344446, complement)

Transcript information (Ensembl)

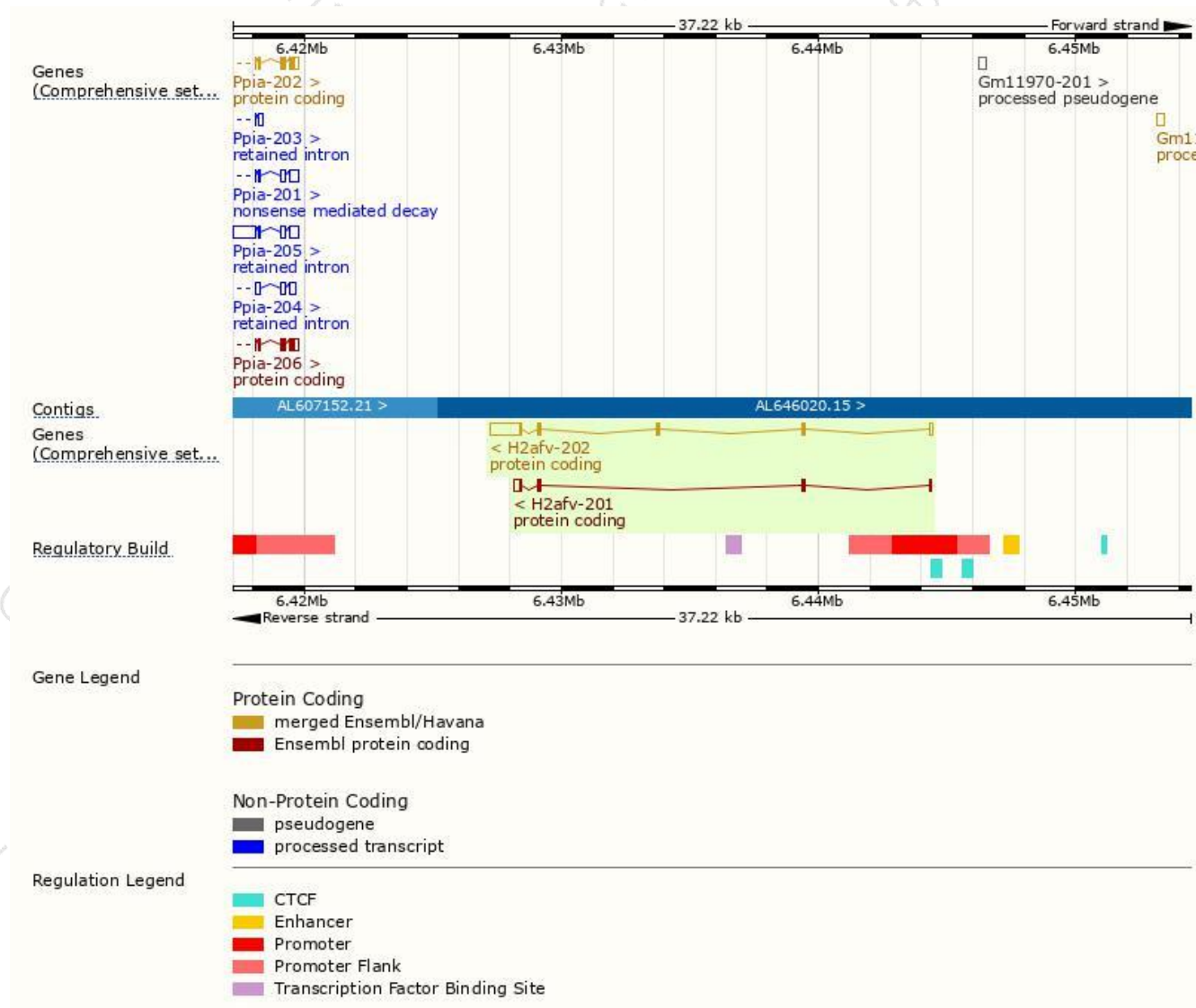
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H2afv-202	ENSMUST00000109737.8	1633	128aa	Protein coding	CCDS48750	B2RVP5 Q3THW5	TSL:1 GENCODE basic APPRIS P1
H2afv-201	ENSMUST00000093346.5	519	90aa	Protein coding	CCDS83779	Q8R029	TSL:1 GENCODE basic

The strategy is based on the design of *H2afv-202* 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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