

H3f3b Cas9-CKO Strategy

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Project Overview

Project Name

H3f3b

Project type

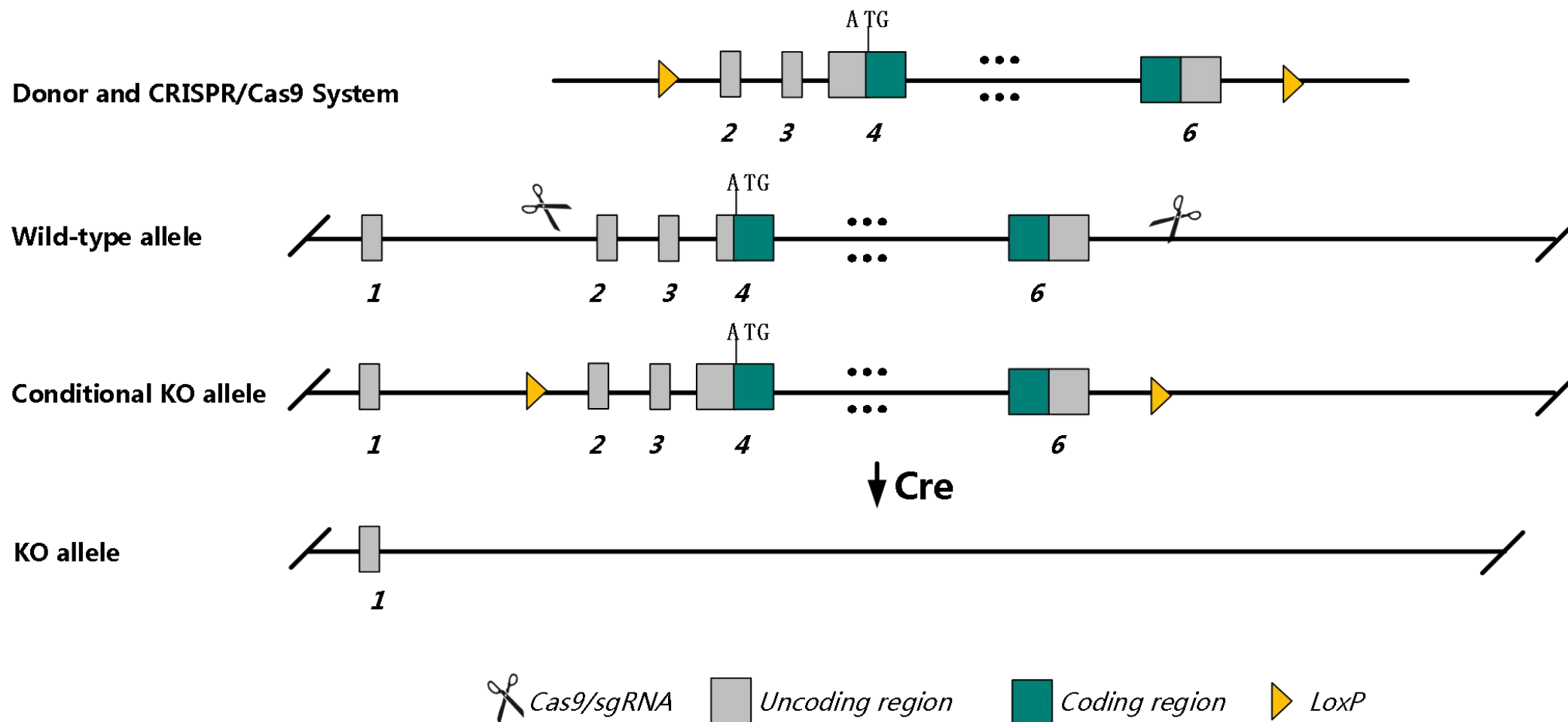
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *H3f3b* gene. The schematic diagram is as follows:



- The *H3f3b* gene has 4 transcripts. According to the structure of *H3f3b* gene, exon2-exon6 of *H3f3b*-202 (ENSMUST00000106454.7) transcript is recommended as the knockout region. The region contains most 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 *H3f3b* 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 heterozygous for a reporter allele exhibit reduced body size and male infertility due to failure of spermiogenesis.
- The *H3f3b* 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.

Gene information (NCBI)

H3f3b H3 histone, family 3B [Mus musculus (house mouse)]

Gene ID: 15081, updated on 31-Jan-2019

Summary



Official Symbol H3f3b provided by [MGI](#)

Official Full Name H3 histone, family 3B provided by [MGI](#)

Primary source [MGI:MGI:1101768](#)

See related [Ensembl:ENSMUSG00000016559](#)

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 9430068D06Rik, H3.3B

Summary Histones are basic nuclear proteins that are responsible for the 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 contains introns and its mRNA is polyadenylated, unlike most histone genes. The protein encoded by this gene is a replication-independent histone that is a member of the histone H3 family. [provided by RefSeq, Nov 2015]

Expression Broad expression in CNS E14 (RPKM 263.1), whole brain E14.5 (RPKM 256.7) and 26 other tissues [See more](#)

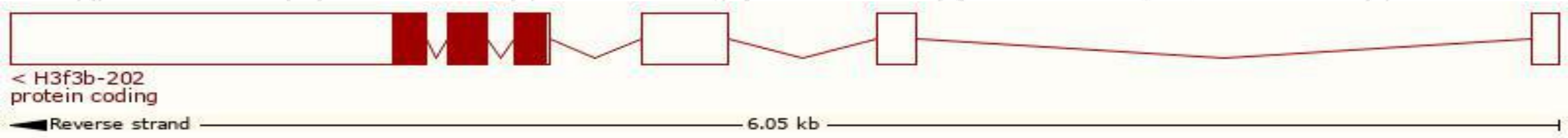
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

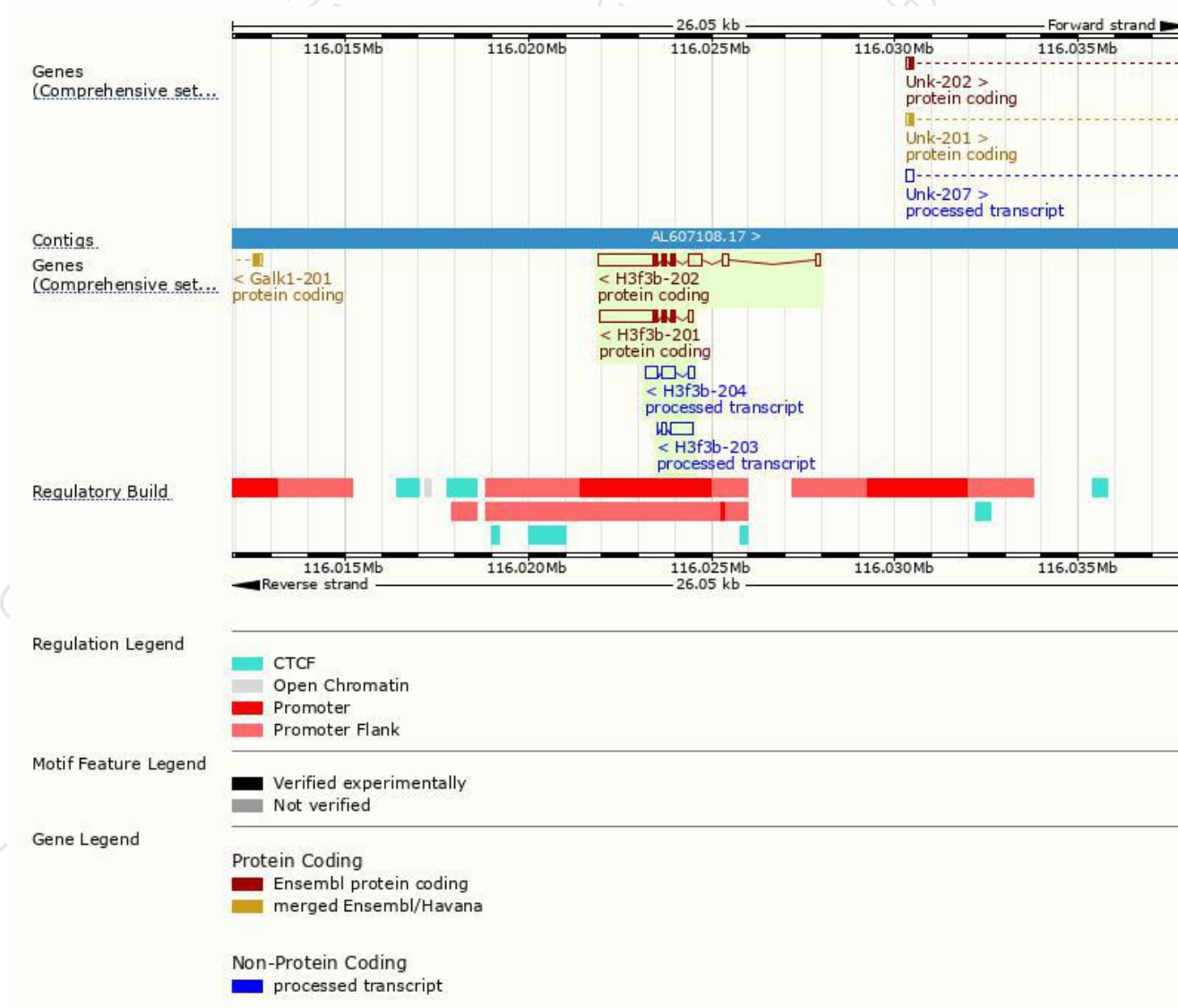
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H3f3b-202	ENSMUST00000106454.7	2514	136aa	Protein coding	CCDS36377	P84244	TSL:5 GENCODE basic APPRIS P1
H3f3b-201	ENSMUST00000016703.7	1993	136aa	Protein coding	CCDS36377	P84244	TSL:1 GENCODE basic APPRIS P1
H3f3b-204	ENSMUST00000139623.1	874	No protein	Processed transcript	-	-	TSL:3
H3f3b-203	ENSMUST00000139378.1	773	No protein	Processed transcript	-	-	TSL:1

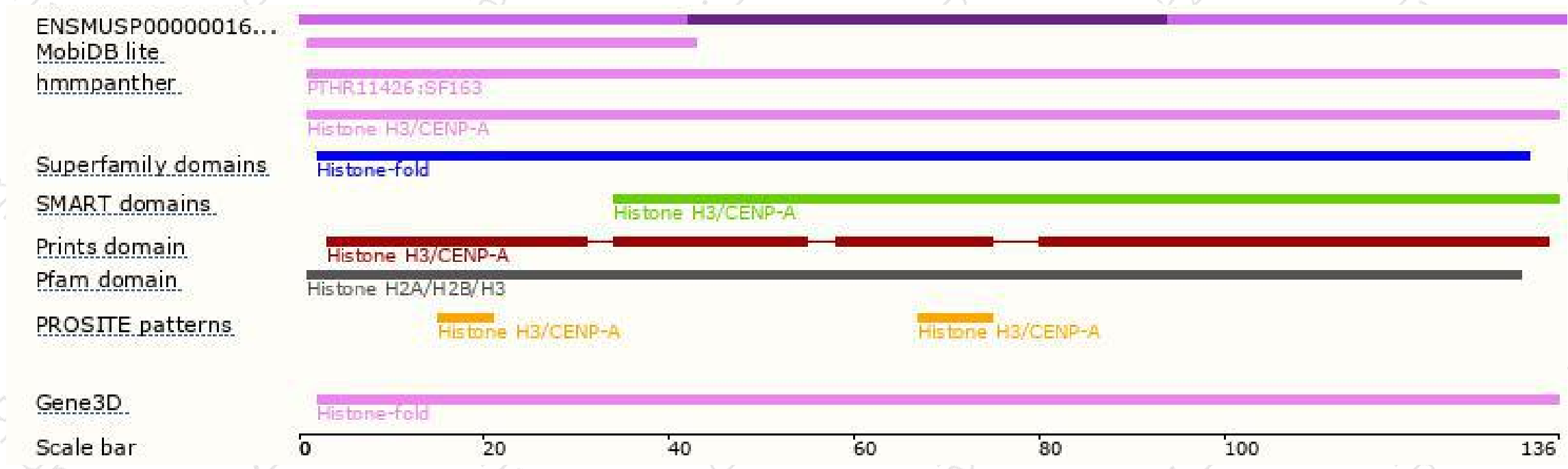
The strategy is based on the design of *H3f3b-202* transcript,The transcription is shown below



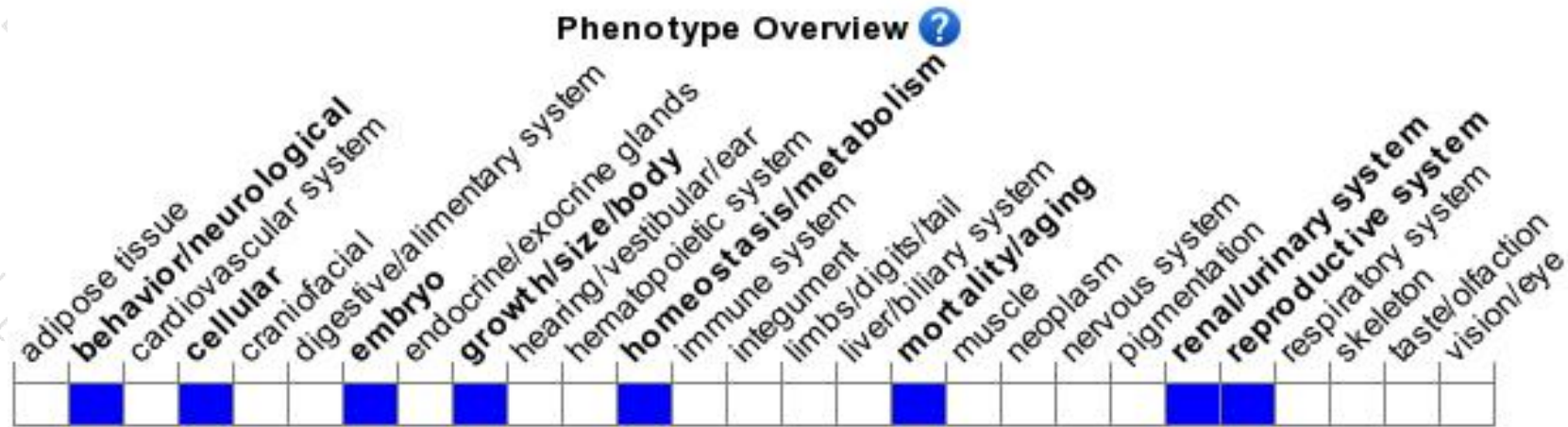
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice heterozygous for a reporter allele exhibit reduced body size and male infertility due to failure of spermiogenesis.

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

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