

Hmgn3 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Hmgn3

Project type

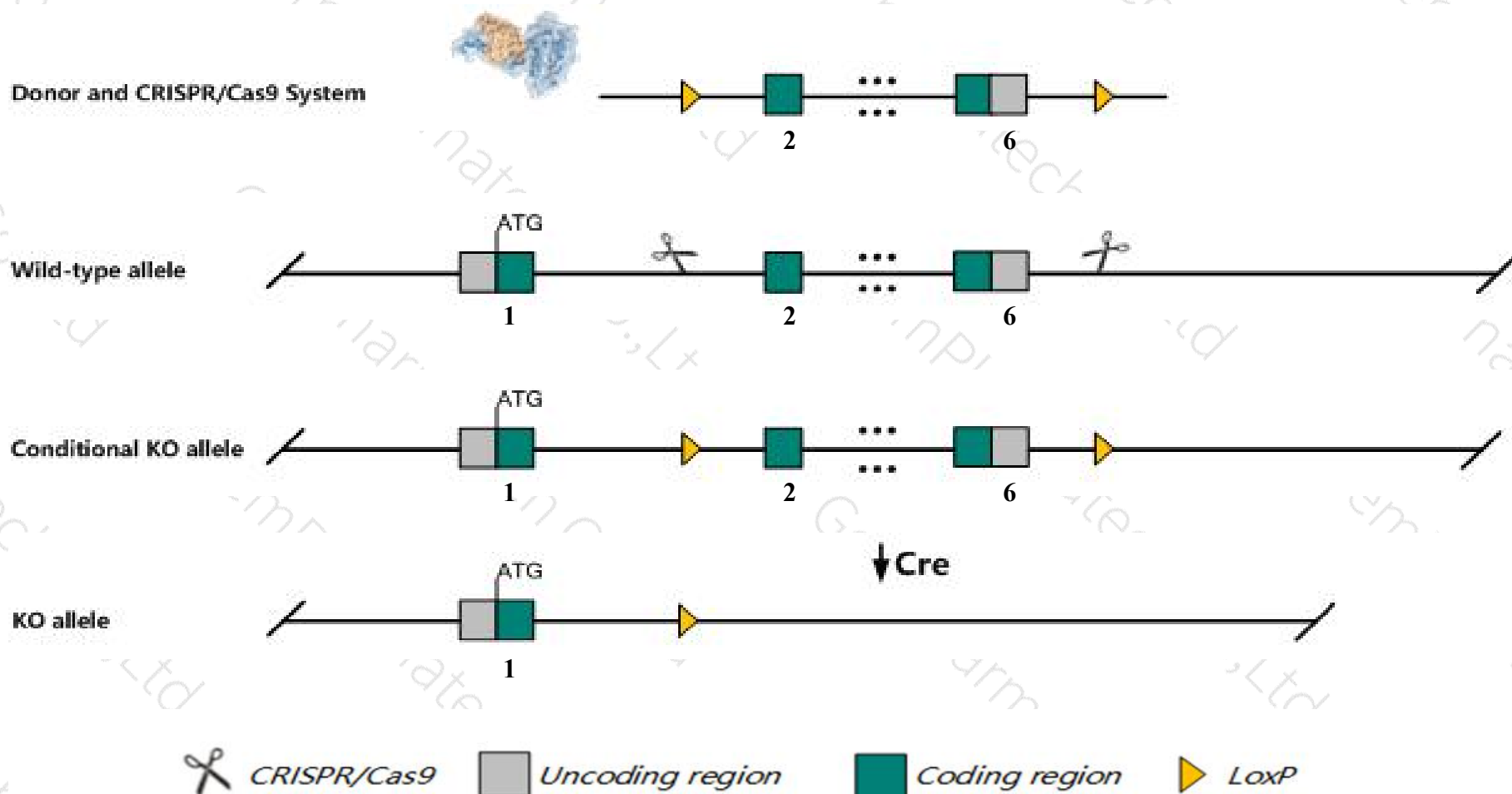
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmgn3* gene. The schematic diagram is as follows:



- The *Hmgn3* gene has 9 transcripts. According to the structure of *Hmgn3* gene, exon2-exon6 of *Hmgn3*-202 (ENSMUST00000162246.8) 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 *Hmgn3* 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 null allele exhibit impaired glucose tolerance with decreased insulin serum levels and increased glucose serum levels during feeding.
- *Gm2065-201* will be knockout.
- The *Hmgn3* gene is located on the Chr9. 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)

Hmgn3 high mobility group nucleosomal binding domain 3 [*Mus musculus* (house mouse)]

Gene ID: 94353, updated on 12-Aug-2019

Summary

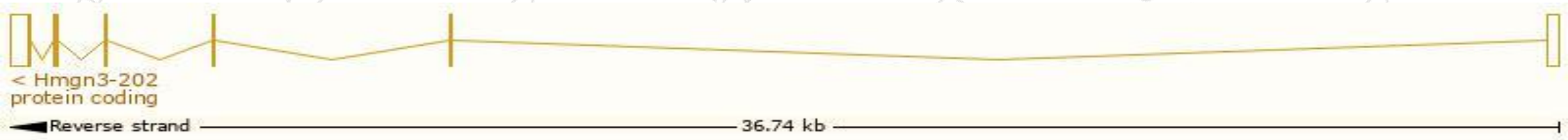
Official Symbol	Hmgn3 provided by MGI
Official Full Name	high mobility group nucleosomal binding domain 3 provided by MGI
Primary source	MGI:MGI:2138069
See related	Ensembl:ENSMUSG00000066456
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TRIP7; BB071015; 1110002A15Rik; 6330514M13Rik
Expression	Biased expression in CNS E18 (RPKM 41.8), CNS E14 (RPKM 31.6) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

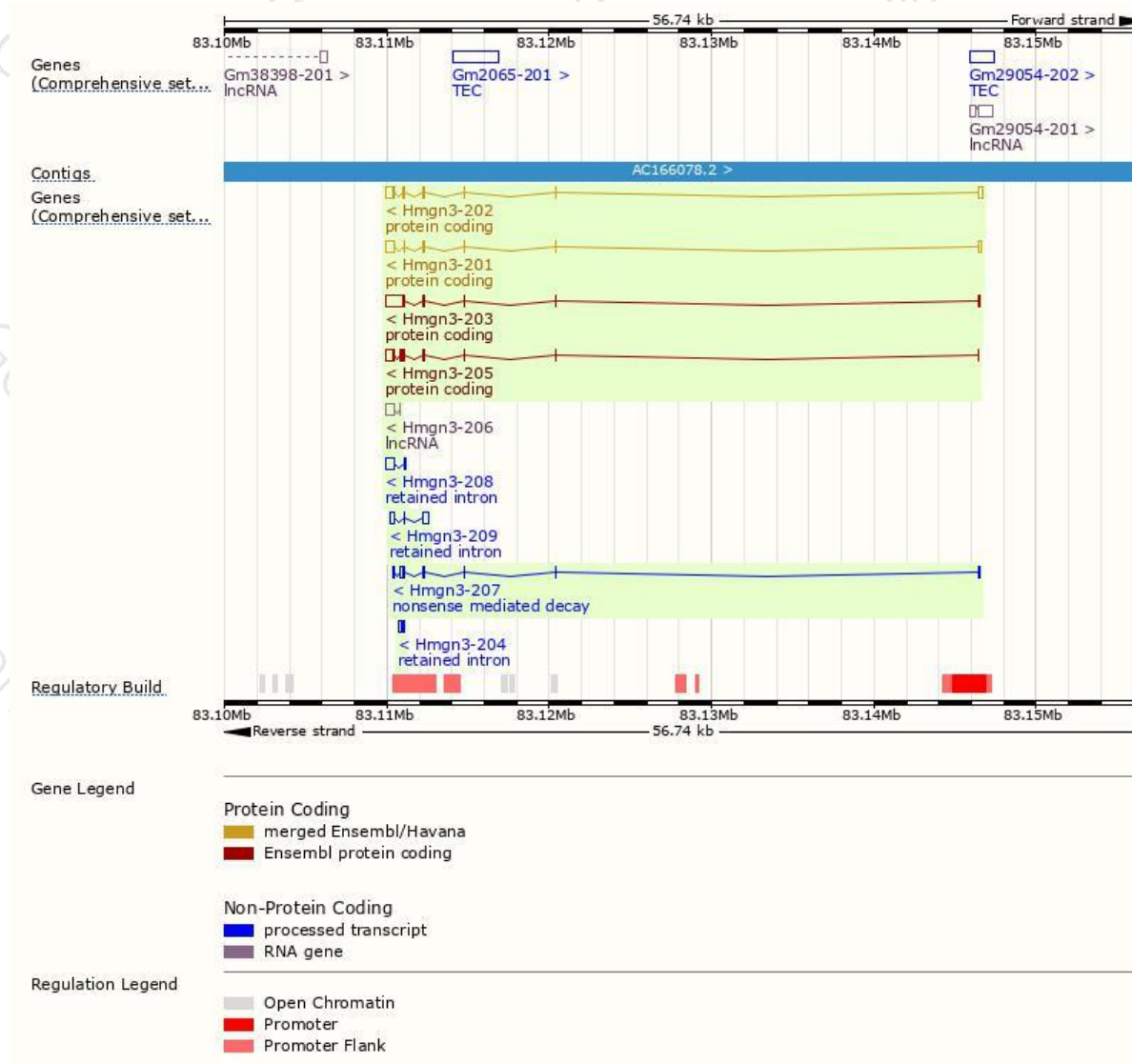
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmgn3-202	ENSMUST00000162246.8	983	99aa	Protein coding	CCDS52872	Q9DCB1	TSL:1 GENCODE basic APPRIS P1
Hmgn3-201	ENSMUST00000161796.8	862	77aa	Protein coding	CCDS52873	Q9DCB1	TSL:1 GENCODE basic
Hmgn3-203	ENSMUST00000185315.6	1391	95aa	Protein coding	-	Q9DCB1	TSL:2 GENCODE basic
Hmgn3-205	ENSMUST00000187193.6	855	128aa	Protein coding	-	A0A087WSB8	TSL:5 GENCODE basic
Hmgn3-207	ENSMUST00000190154.1	546	95aa	Nonsense mediated decay	-	Q9DCB1	TSL:5
Hmgn3-209	ENSMUST00000191105.1	671	No protein	Retained intron	-	-	TSL:2
Hmgn3-208	ENSMUST00000190580.1	560	No protein	Retained intron	-	-	TSL:2
Hmgn3-204	ENSMUST00000185359.1	256	No protein	Retained intron	-	-	TSL:3
Hmgn3-206	ENSMUST00000189777.1	533	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Hmgn3-202* transcript,The transcription is shown below



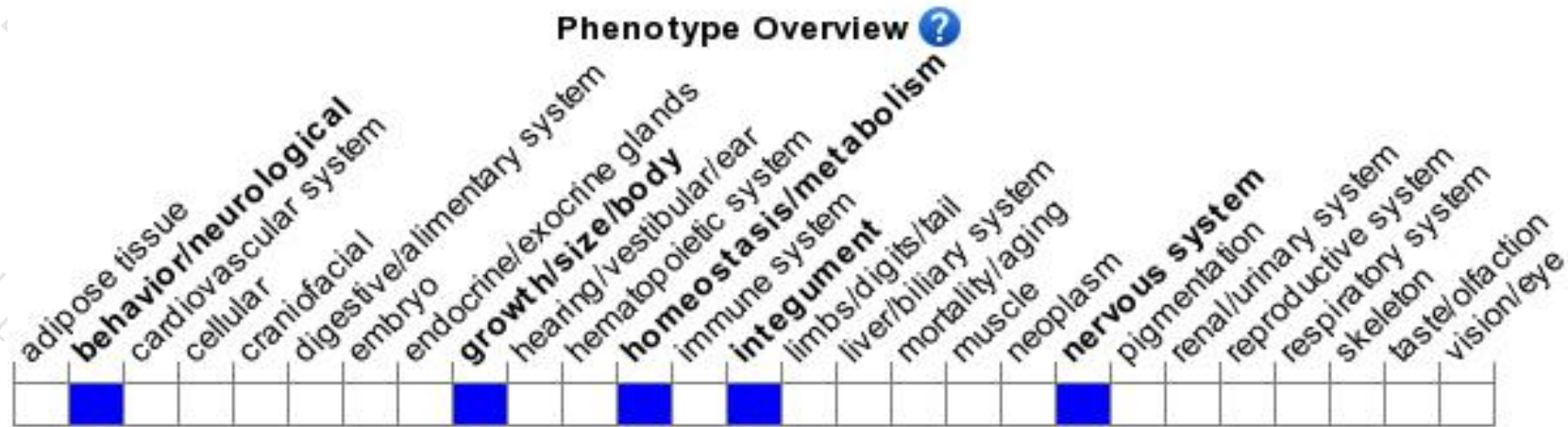
Genomic location distribution



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 homozygous for a null allele exhibit impaired glucose tolerance with decreased insulin serum levels and increased glucose serum levels during feeding.

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

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