

Hmgn2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Hmgn2

Project type

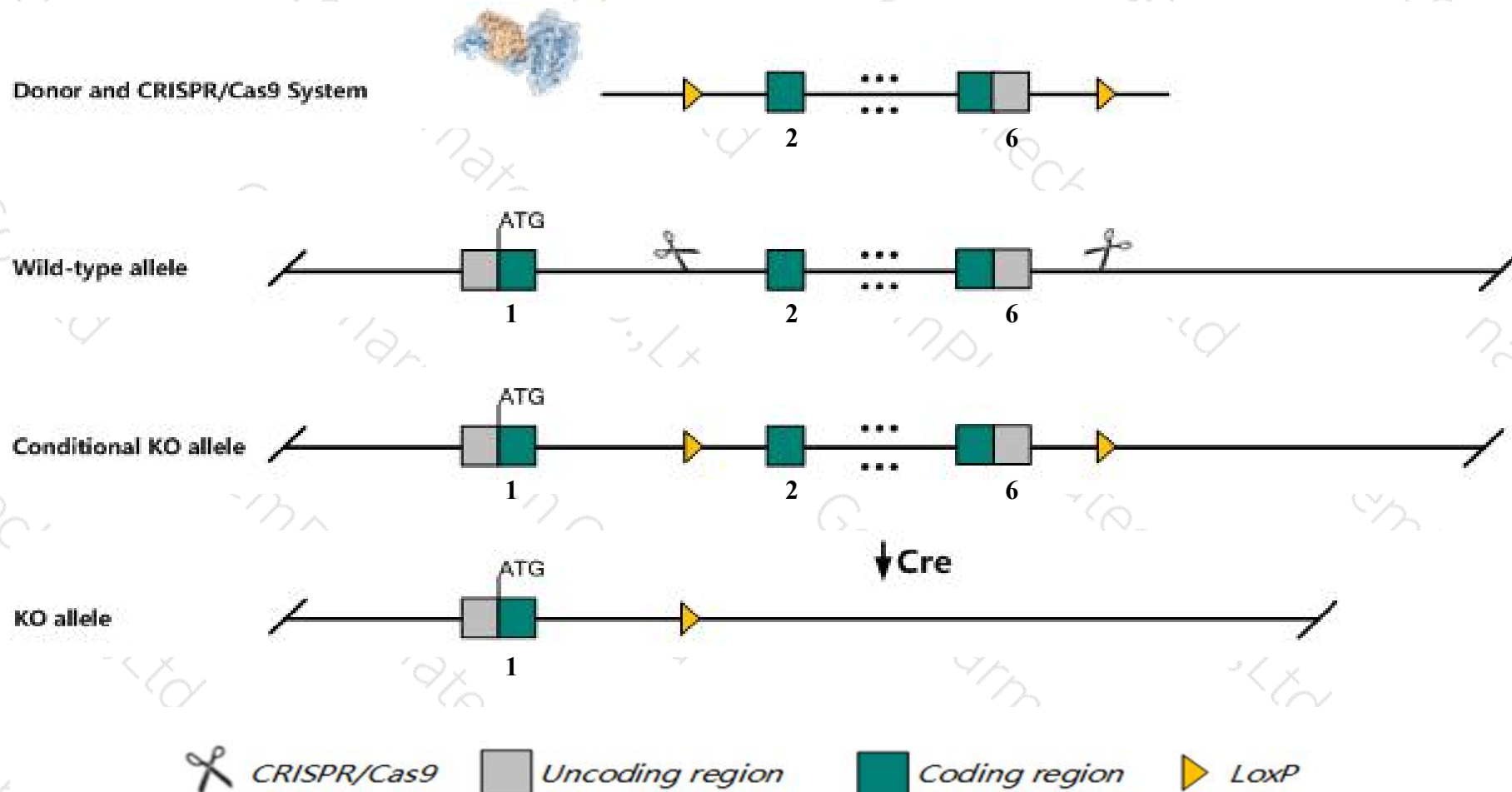
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmgn2* gene. The schematic diagram is as follows:



Technical routes

- The *Hmgn2* gene has 13 transcripts. According to the structure of *Hmgn2* gene, exon2-exon6 of *Hmgn2*-203 (ENSMUST00000102553.10) 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 *Hmgn2* 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

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable.
- Transcripts 206, 210, 212 will be destroyed.
- The effect on transcripts 204, 205 is unknown.
- The *Hmgn2* gene is located on the Chr4. 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)

Hmgn2 high mobility group nucleosomal binding domain 2 [*Mus musculus* (house mouse)]

Gene ID: 15331, updated on 3-Nov-2019

Summary

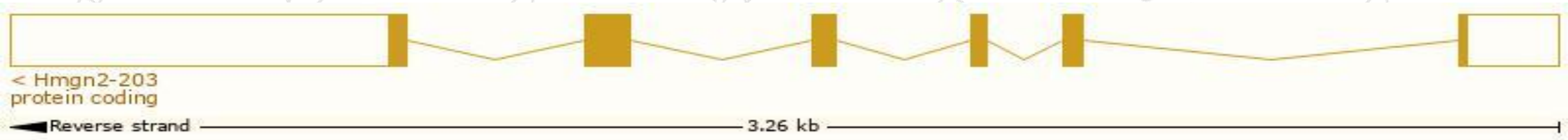
Official Symbol	Hmgn2 provided by MGI
Official Full Name	high mobility group nucleosomal binding domain 2 provided by MGI
Primary source	MGI:MGI:96136
See related	Ensembl:ENSMUSG000000003038
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Hmg17; HMG-17
Expression	Biased expression in CNS E11.5 (RPKM 375.6), limb E14.5 (RPKM 204.2) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

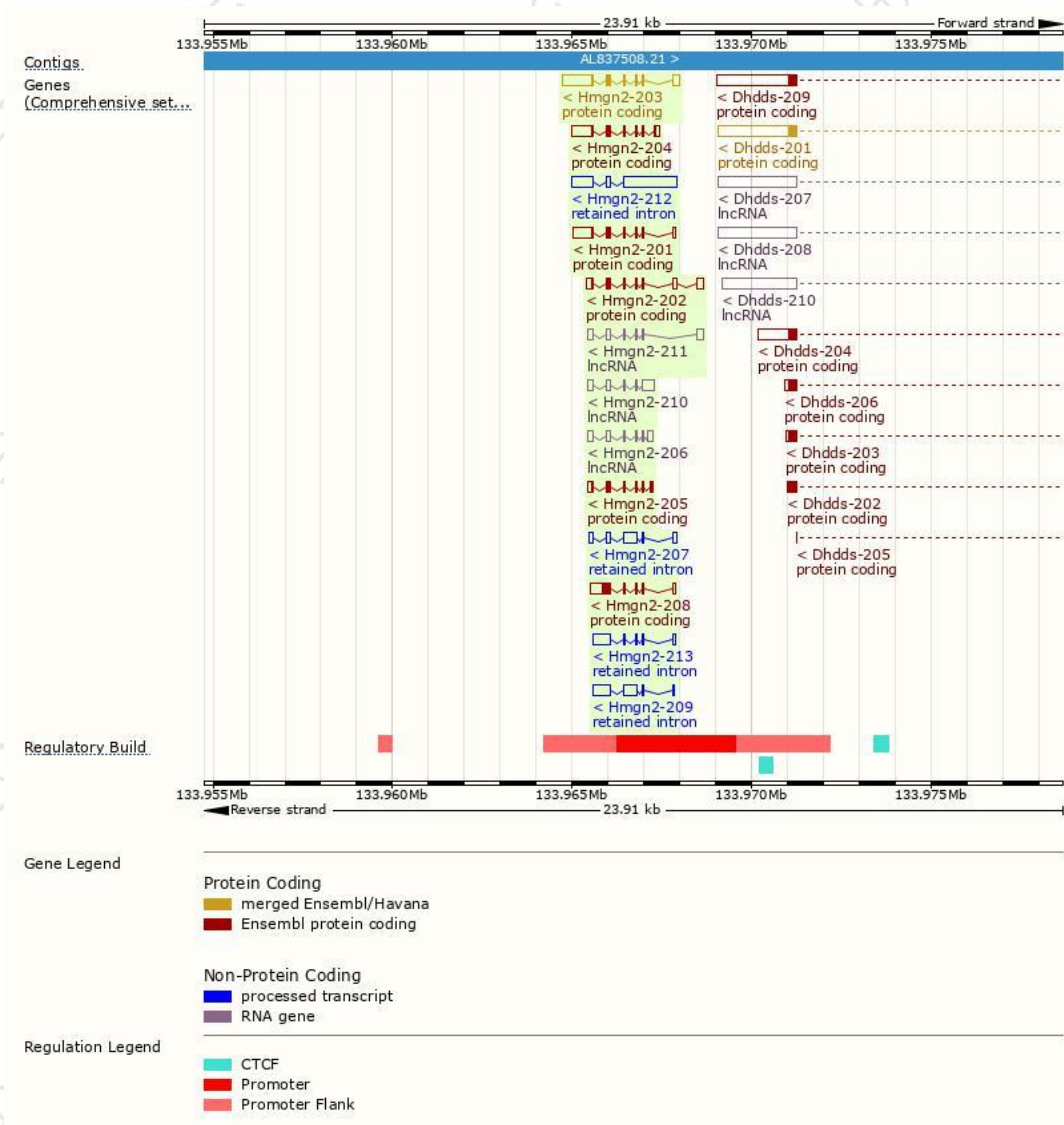
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmgn2-203	ENSMUST00000102553.10	1265	90aa	Protein coding	CCDS18759	P09602 Q5BL14	TSL:1 GENCODE basic APPRIS P2
Hmgn2-202	ENSMUST00000102552.7	676	90aa	Protein coding	CCDS18759	P09602 Q5BL14	TSL:2 GENCODE basic APPRIS P2
Hmgn2-204	ENSMUST00000105893.7	973	96aa	Protein coding	-	A3KGL9	TSL:3 GENCODE basic
Hmgn2-201	ENSMUST00000100472.9	881	92aa	Protein coding	-	Q5XK38	TSL:2 GENCODE basic APPRIS ALT 1
Hmgn2-208	ENSMUST00000136327.1	772	109aa	Protein coding	-	B7ZCQ3	TSL:2 GENCODE basic
Hmgn2-205	ENSMUST00000123234.7	432	112aa	Protein coding	-	F6W687	CDS 5' incomplete TSL:3
Hmgn2-212	ENSMUST00000145025.7	2159	No protein	Retained intron	-	-	TSL:1
Hmgn2-209	ENSMUST00000136859.1	927	No protein	Retained intron	-	-	TSL:2
Hmgn2-207	ENSMUST00000130809.7	711	No protein	Retained intron	-	-	TSL:5
Hmgn2-213	ENSMUST00000153622.7	681	No protein	Retained intron	-	-	TSL:2
Hmgn2-210	ENSMUST00000137456.7	630	No protein	lncRNA	-	-	TSL:2
Hmgn2-211	ENSMUST00000138458.7	544	No protein	lncRNA	-	-	TSL:5
Hmgn2-206	ENSMUST00000125266.7	503	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Hmgn2-203* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000099...

MobiDB lite

Low complexity (Seg)

SMART

High mobility group protein HMGN

Prints

High mobility group protein HMGN

Pfam

High mobility group protein HMGN

PROSITE patterns

High mobility group protein HMGN

PANTHER

PTHR23087

PTHR23087:SF13

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

Y

R

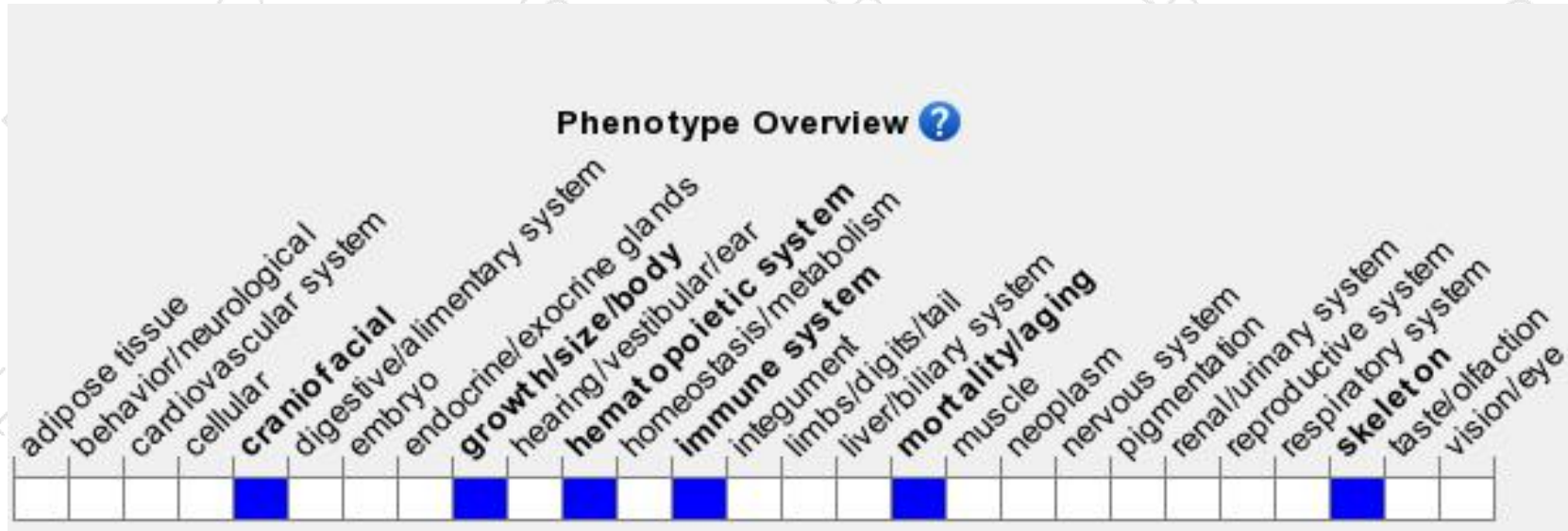
Variant Legend

synonymous variant

Scale bar

0 8 16 24 32 40 48 56 64 72 80 90

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 knock-out allele are viable.

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

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