

Hmgn1 Cas9-KO Strategy

Designer:

Ruirui Zhang

Reviewer:

Huimin Su

Design Date:

2020-2-21

Project Overview

Project Name

Hmgn1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmgn1* gene. The schematic diagram is as follows:



- The *Hmgn1* gene has 4 transcripts. According to the structure of *Hmgn1* gene, exon1-exon4 of *Hmgn1-201* (ENSMUST00000050884.15) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hmgn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele display partial embryonic lethality, increased cellular sensitivity to ultraviolet- and gamma-irradiation, increased tumor incidence and metastatic potential, increased incidence of ionizing radiation-induced tumors, and abnormal cell cycle checkpoint function.
- The *Hmgn1* gene is located on the Chr16. 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)

Hmgn1 high mobility group nucleosomal binding domain 1 [*Mus musculus* (house mouse)]

Gene ID: 15312, updated on 13-Jan-2020

Summary

Official Symbol Hmgn1 provided by [MGI](#)

Official Full Name high mobility group nucleosomal binding domain 1 provided by [MGI](#)

Primary source [MGI:MGI:96120](#)

See related [Ensembl:ENSMUSG00000040681](#)

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 Hmg14; HMG-14

Expression Broad expression in CNS E11.5 (RPKM 270.4), limb E14.5 (RPKM 161.5) and 21 other tissues [See more](#)

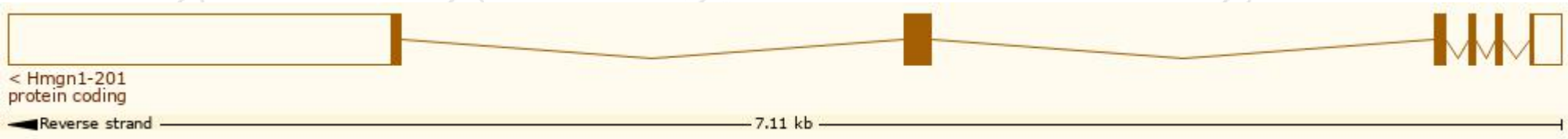
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

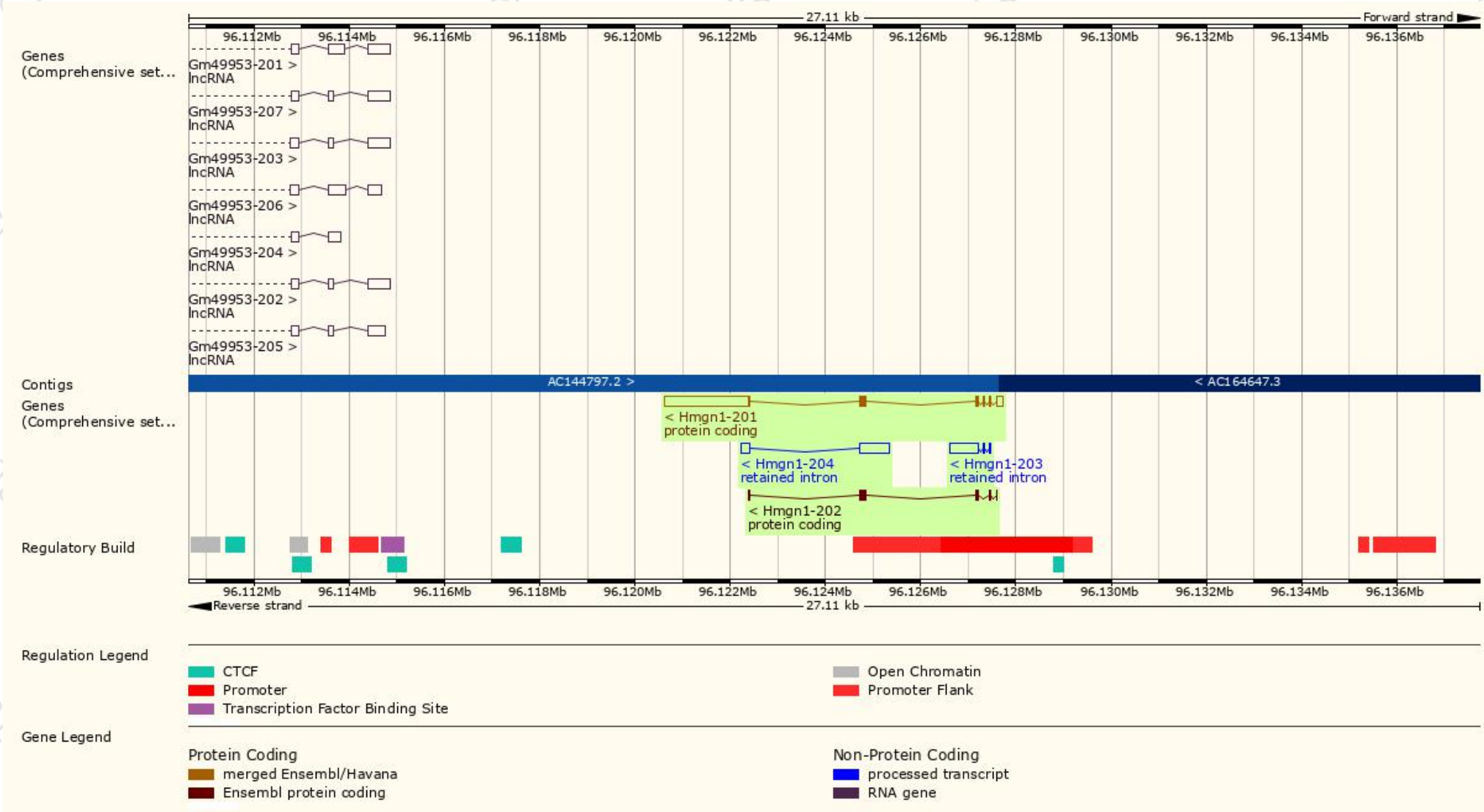
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmgn1-204	ENSMUST00000233638.1	801	No protein	Retained intron	-	-	-
Hmgn1-203	ENSMUST00000233297.1	664	No protein	Retained intron	-	-	-
Hmgn1-201	ENSMUST00000050884.15	2174	96aa	Protein coding	CCDS28353	P18608	TSL:1 GENCODE basic APPRIS P1
Hmgn1-202	ENSMUST00000233292.1	261	86aa	Protein coding	-	A0A3B2W3M7	GENCODE basic

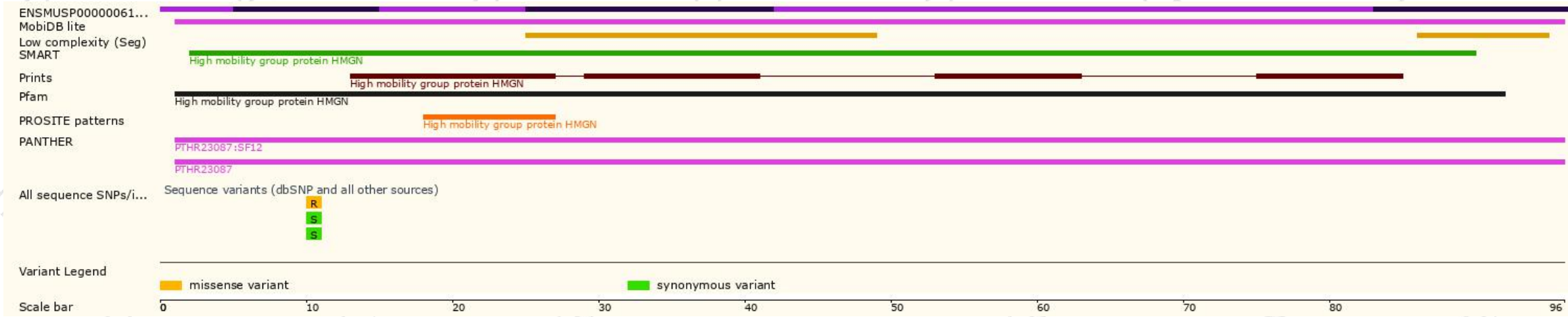
The strategy is based on the design of *Hmgn1-201* transcript, the transcription is shown below:



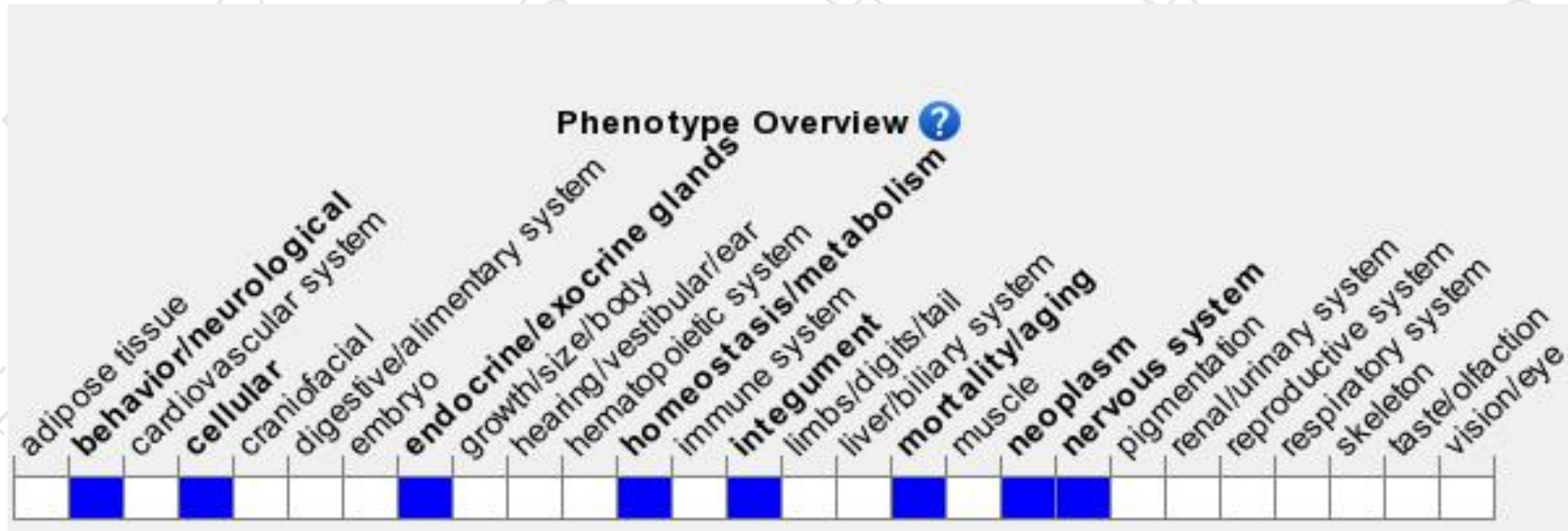
Genomic location distribution



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 knock-out allele display partial embryonic lethality, increased cellular sensitivity to ultraviolet- and gamma-irradiation, increased tumor incidence and metastatic potential, increased incidence of ionizing radiation-induced tumors, and abnormal cell cycle checkpoint function.

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

Tel: 400-9660890

