

Hmgn5 Cas9-KO Strategy

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Project Overview

Project Name

Hmgn5

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmgn5* gene. The schematic diagram is as follows:



- The *Hmgn5* gene has 1 transcript. According to the structure of *Hmgn5* gene, exon1-exon6 of *Hmgn5-201* (ENSMUST00000033597.8) transcript is recommended as the knockout region. The region contains all 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 *Hmgn5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased prepulse inhibition, abnormal erythrocyte cell number, abnormal glucose tolerance, decreased granulocyte, increased CD8+ T cells, increased IgA, decreased IgE and abnormal respiration.
- *Gm23322* gene may be destroyed directly.
- The *Hmgn5* gene is located on the ChrX. 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)

Hmgn5 high-mobility group nucleosome binding domain 5 [*Mus musculus* (house mouse)]

Gene ID: 50887, updated on 12-Aug-2019

Summary

- Official Symbol** Hmgn5 provided by [MGI](#)
- Official Full Name** high-mobility group nucleosome binding domain 5 provided by [MGI](#)
- Primary source** [MGI:MGI:1355295](#)
- See related** [Ensembl:ENSMUSG00000031245](#)
- 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** Nsbp1; GARP45; NBP-45
- Expression** Biased expression in placenta adult (RPKM 39.8), CNS E11.5 (RPKM 28.7) and 9 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: X; X D

See Hmgn5 in [Genome Data Viewer](#)

Exon count: 6

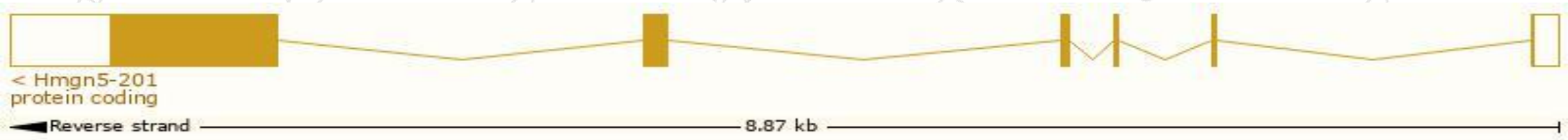
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	X	NC_000086.7 (109004537..109013380, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	X	NC_000086.6 (106199876..106208719, complement)

Transcript information (Ensembl)

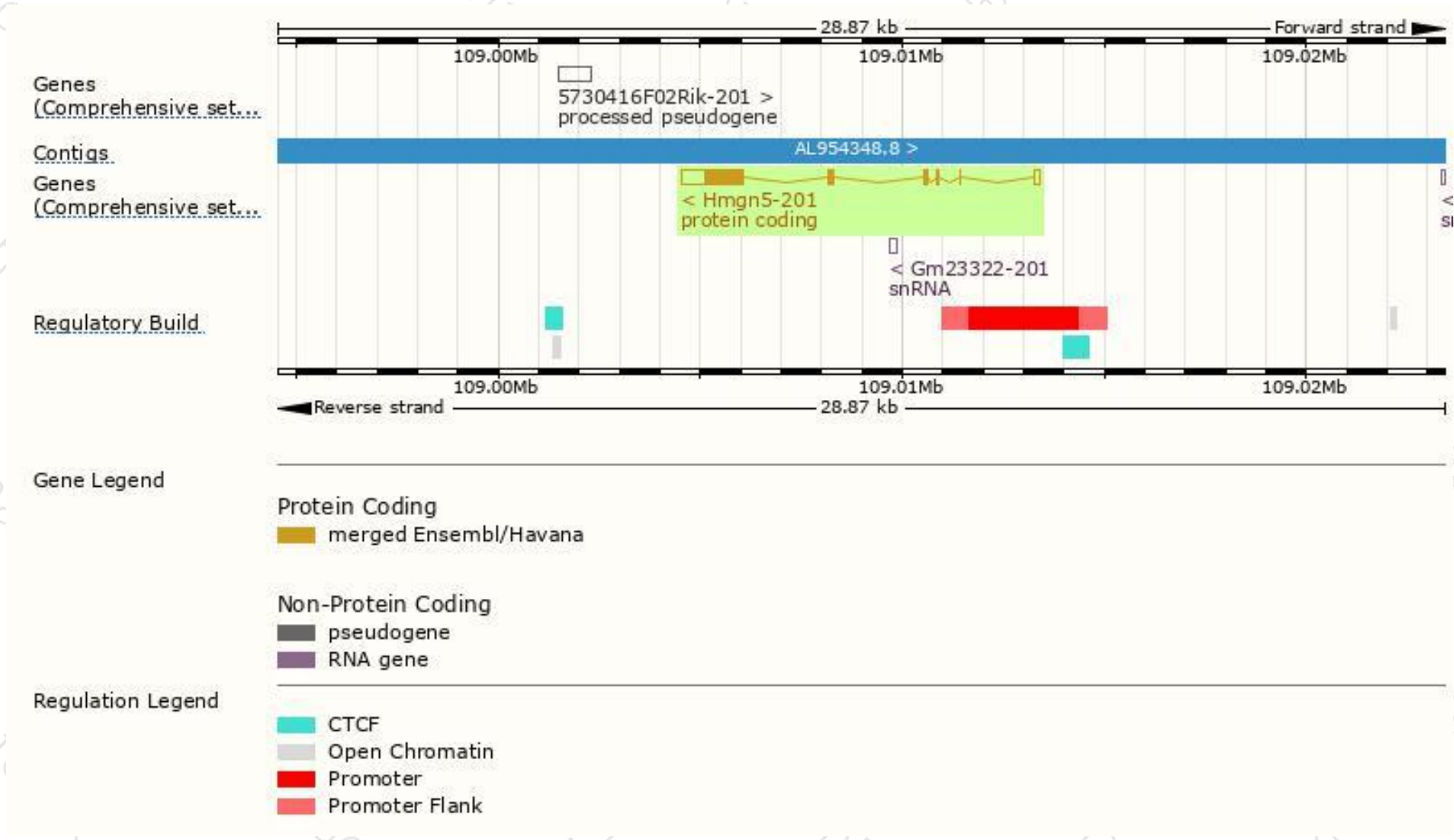
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmgn5-201	ENSMUST00000033597.8	1934	406aa	Protein coding	CCDS41101	Q9JL35	TSL:1 GENCODE basic APPRIS P1

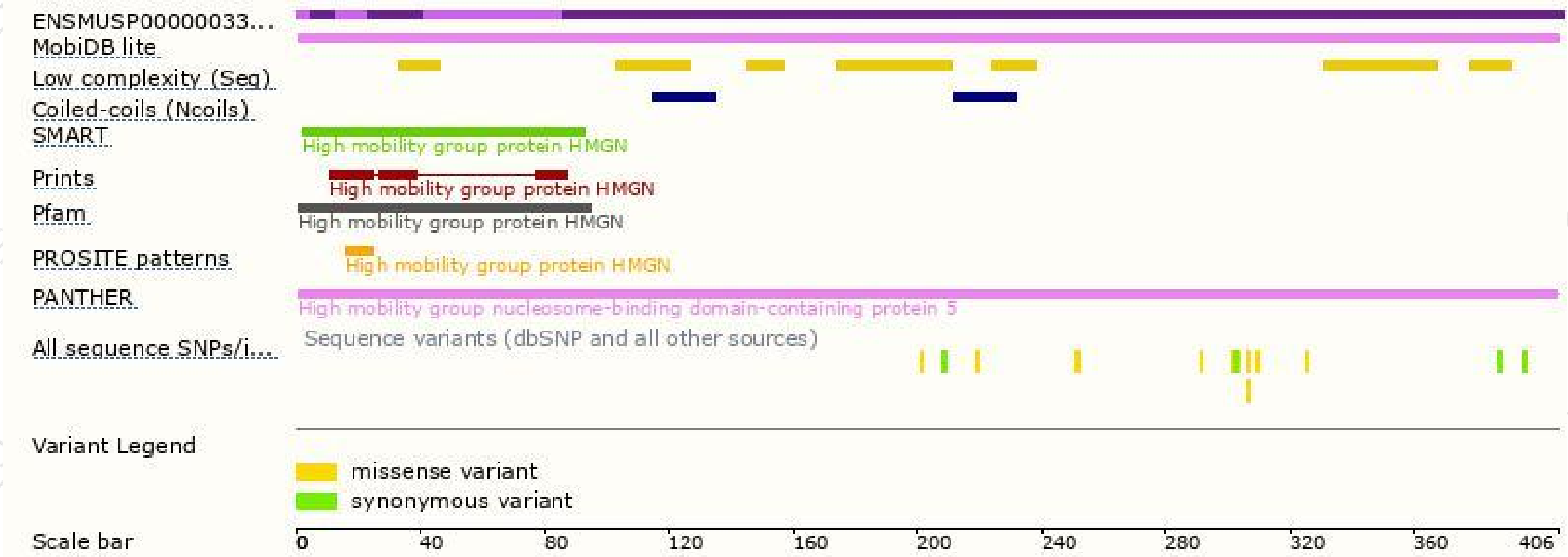
The strategy is based on the design of *Hmgn5-201* transcript, The transcription is shown below



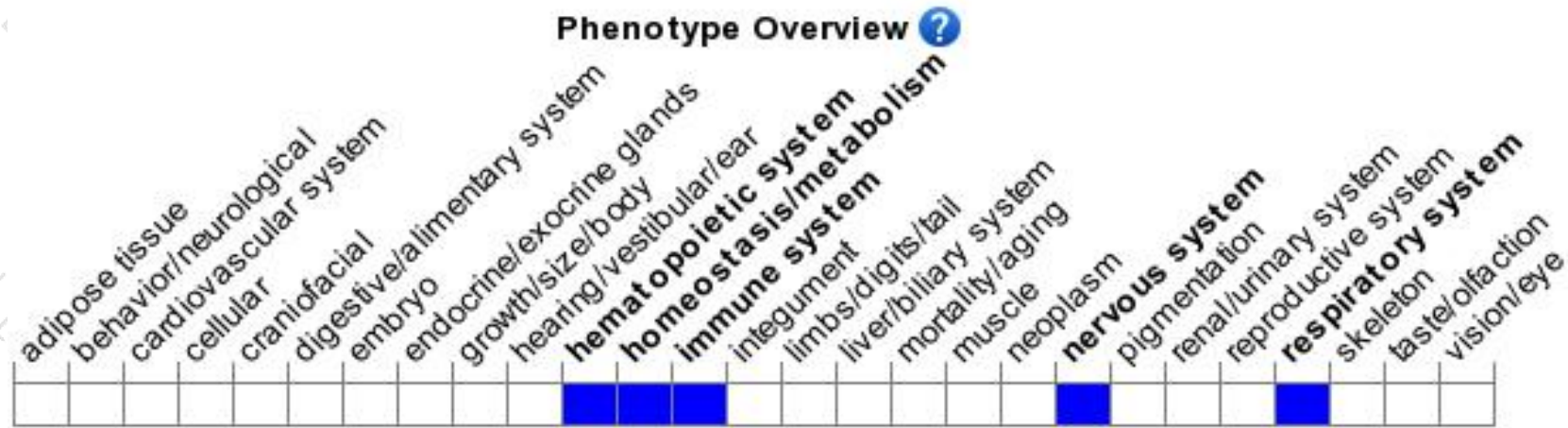
Genomic location distribution



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 exhibit decreased prepulse inhibition, abnormal erythrocyte cell number, abnormal glucose tolerance, decreased granulocyte, increased CD8⁺ T cells, increased IgA, decreased IgE and abnormal respiration.

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

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