

# *Hmgn2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Hmgn2*

**Project type**

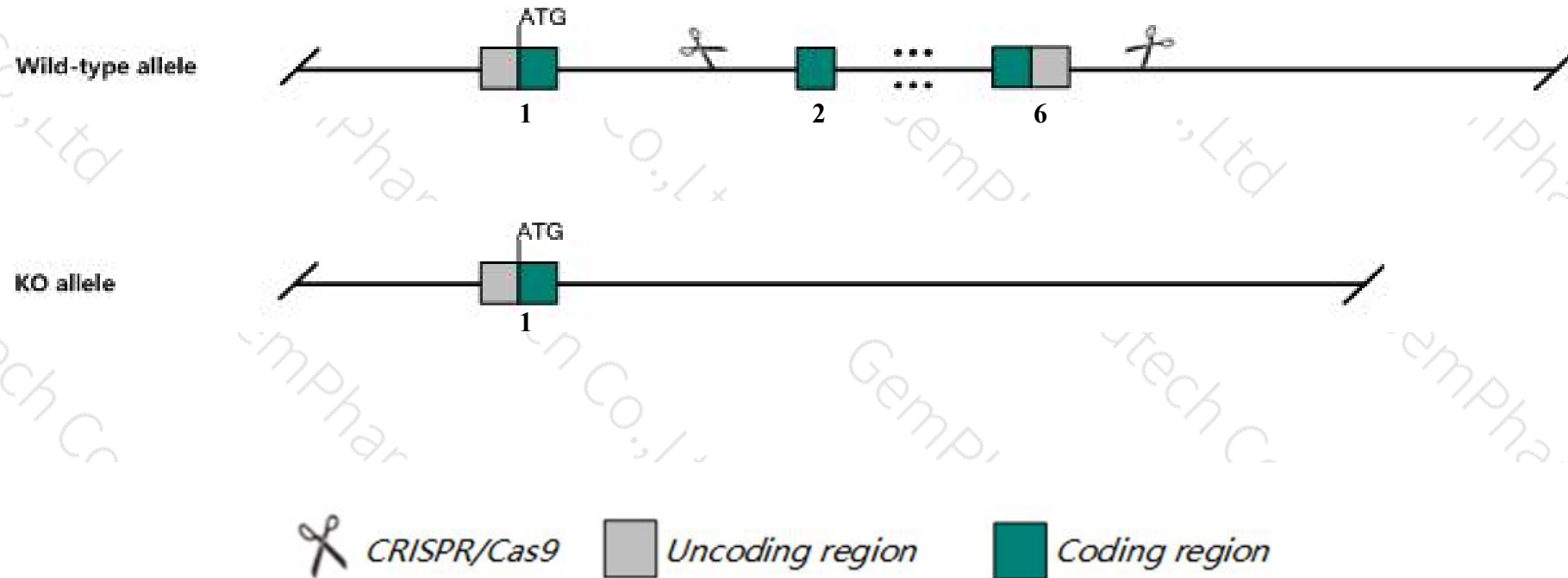
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable.
- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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

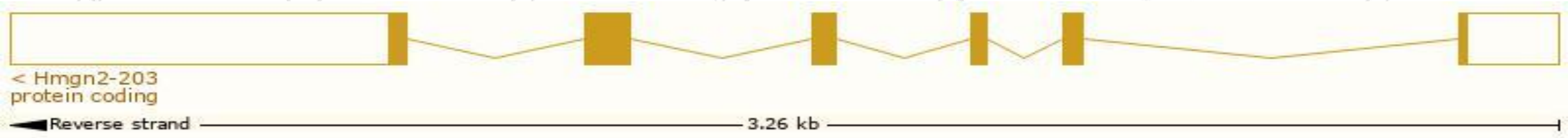
|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Hmgn2 provided by <a href="#">MGI</a>                                                                                                                                     |
| Official Full Name | high mobility group nucleosomal binding domain 2 provided by <a href="#">MGI</a>                                                                                          |
| Primary source     | <a href="#">MGI:MGI:96136</a>                                                                                                                                             |
| See related        | <a href="#">Ensembl:ENSMUSG000000003038</a>                                                                                                                               |
| Gene type          | protein coding                                                                                                                                                            |
| RefSeq status      | VALIDATED                                                                                                                                                                 |
| Organism           | <a href="#">Mus musculus</a>                                                                                                                                              |
| 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 <a href="#">See more</a>                                                        |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

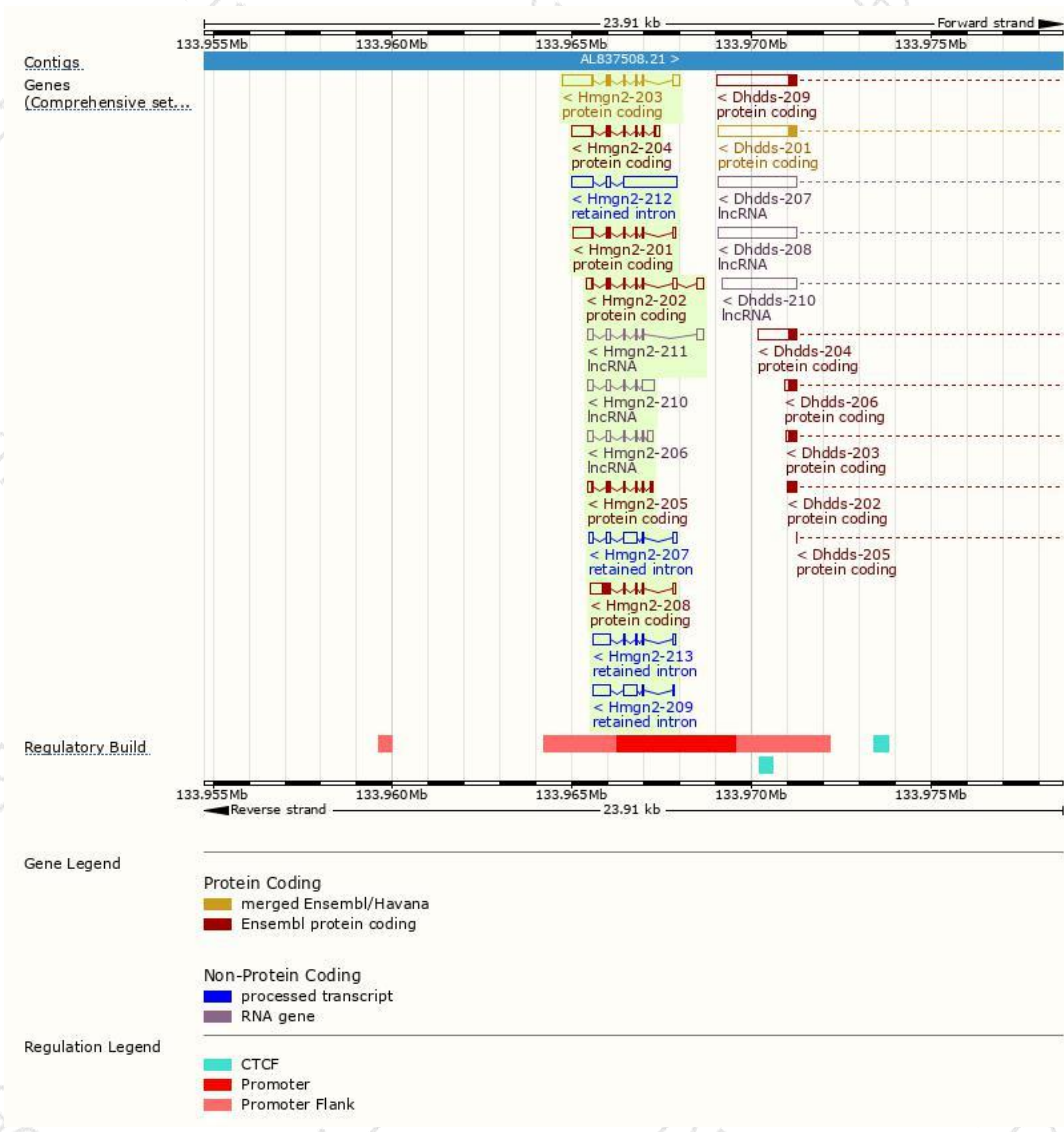
The gene has 13 transcripts,all transcripts are shown below:

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

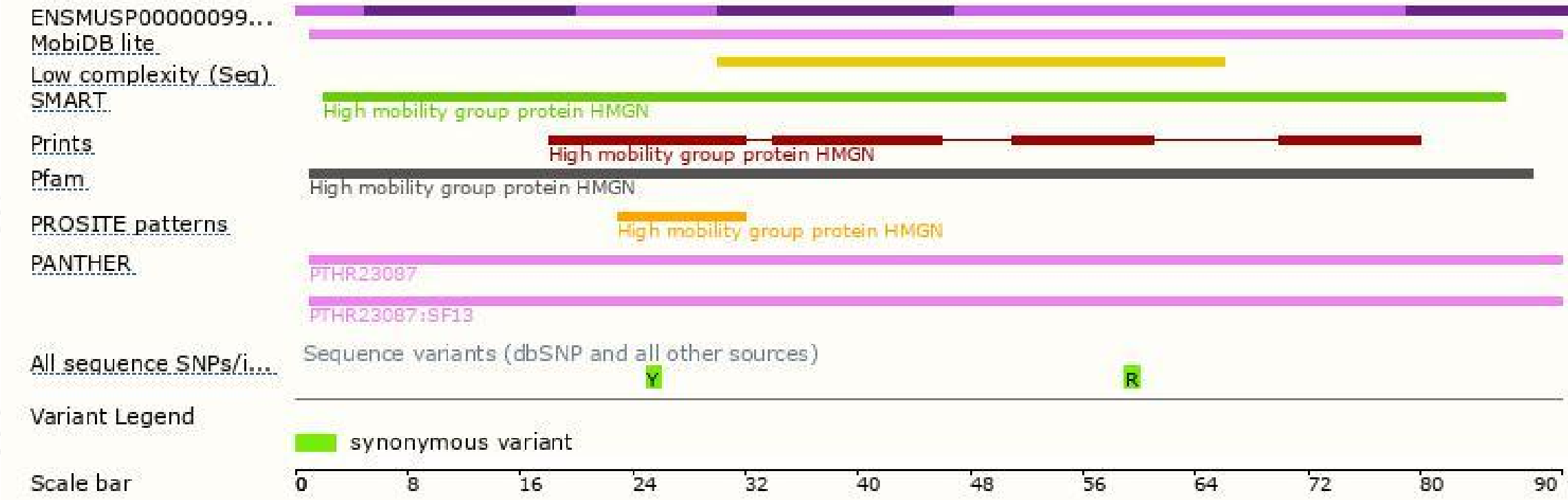
The strategy is based on the design of *Hmgn2-203* transcript,The transcription is shown below



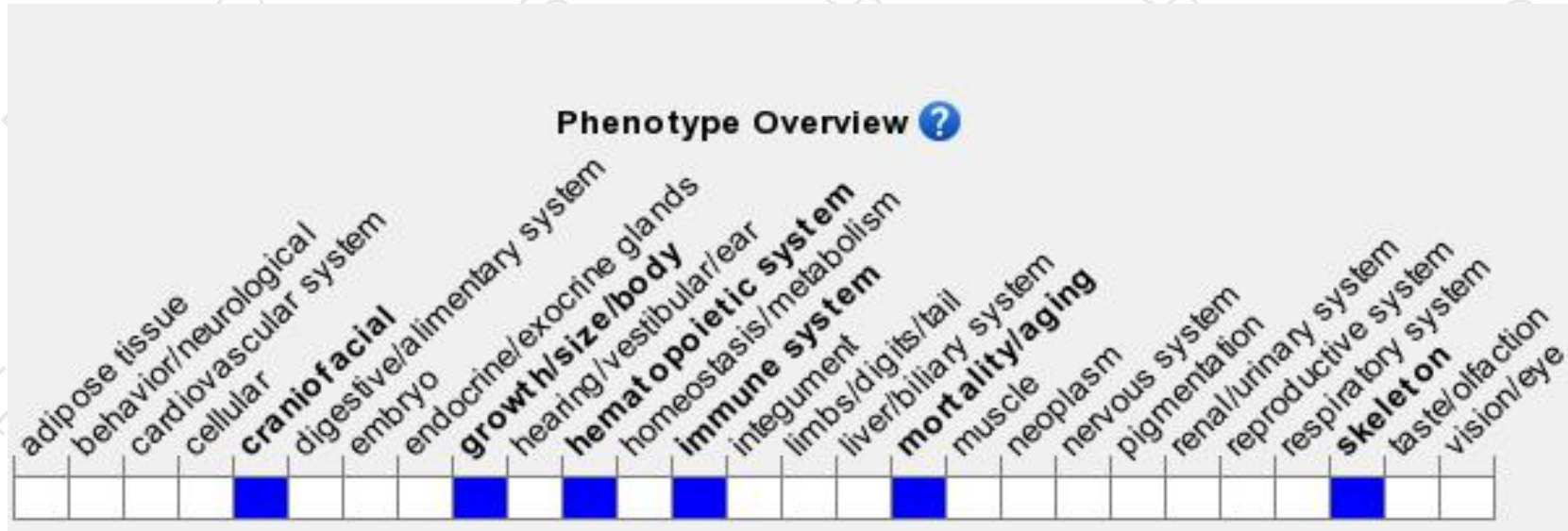
# Genomic location distribution



# Protein domain



# 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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