

# Hmga1 Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Hmgal

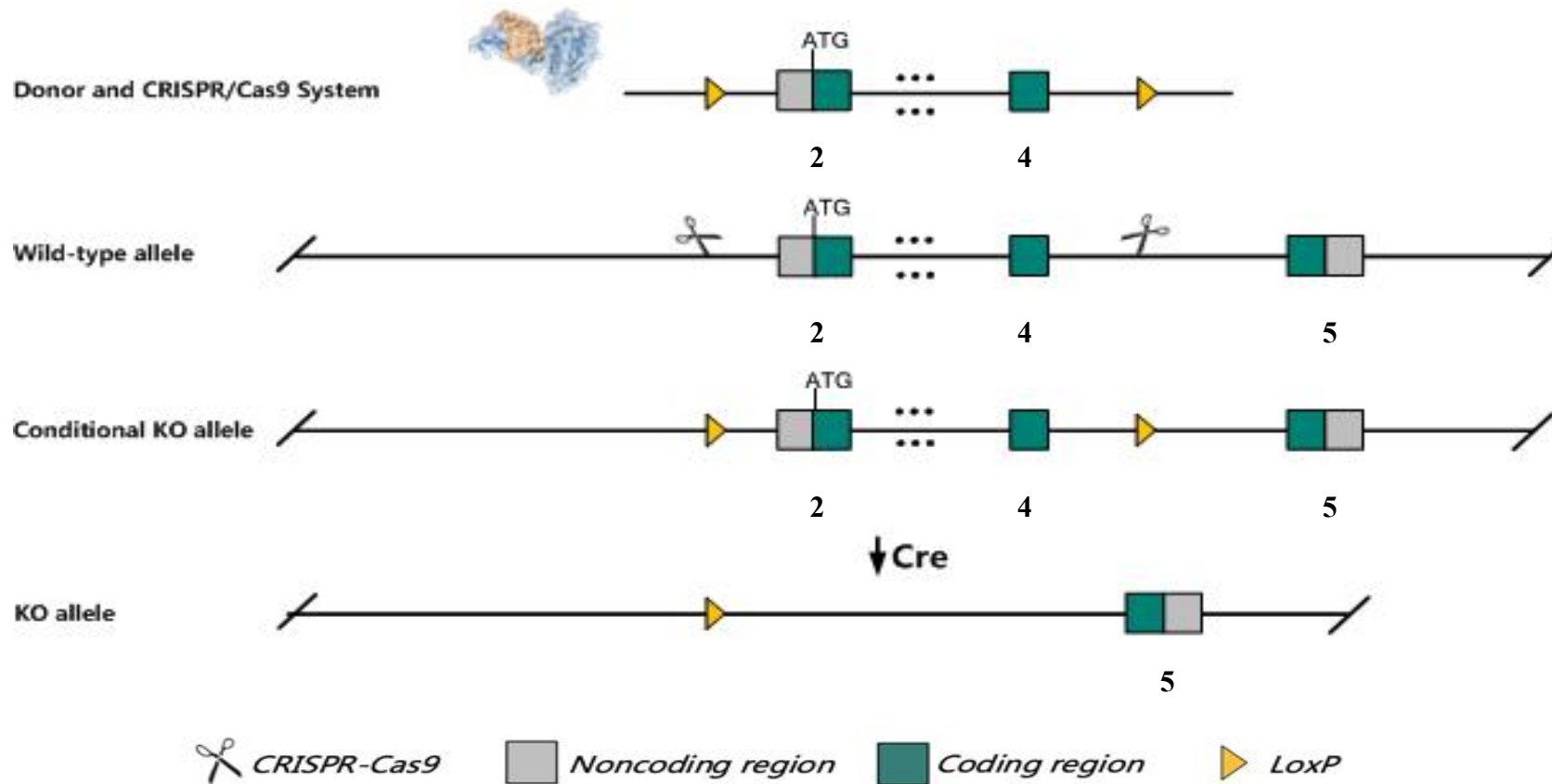
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Hmgal* gene.

# Technical Information

- The *Hmgal* gene has 17 transcripts. According to the structure of *Hmgal* gene, exon2-exon4 of *Hmgal*-213 (ENSMUST00000231874.2) 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 *Hmgal* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

# Gene Information

## Hmga1 high mobility group AT-hook 1 [Mus musculus (house mouse)]

Gene ID: 15361, updated on 12-Jul-2022

Summary	
<b>Official Symbol</b>	Hmga1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	high mobility group AT-hook 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:96160</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000046711</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AL023995, Hmga1a, Hmga1b, Hmgi, Hmgiy, Hmgy
<b>Summary</b>	This locus encodes a member of the nuclear, non-histone high mobility group protein family. This architectural transcription factor binds to A-T rich DNA sequences and participates in enhanceosome formation, chromatin remodeling and regulation of transcription. This protein functions in many cellular processes, including cell growth and differentiation. Alternatively spliced transcript variants have been described. [provided by RefSeq, Oct 2009]
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 119.5), liver E14.5 (RPKM 82.7) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

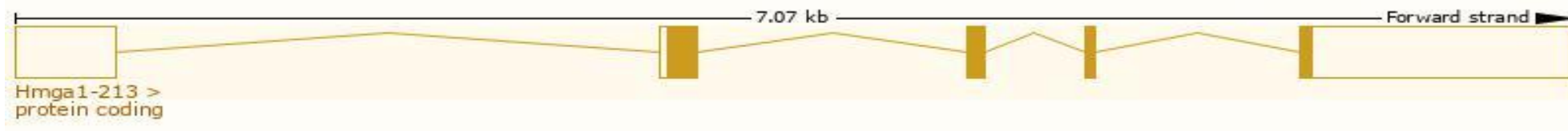
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 17 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmga1-213	<a href="#">ENSMUST00000231874.2</a>	2001	<a href="#">107aa</a>	Protein coding	<a href="#">CCDS28564</a>		GENCODE basic ,
Hmga1-204	<a href="#">ENSMUST00000118570.2</a>	1898	<a href="#">96aa</a>	Protein coding	<a href="#">CCDS50044</a>		TSL:1 , GENCODE basic , APPRIS P2 ,
Hmga1-211	<a href="#">ENSMUST00000231825.2</a>	1717	<a href="#">96aa</a>	Protein coding	<a href="#">CCDS50044</a>		GENCODE basic , APPRIS P2 ,
Hmga1-216	<a href="#">ENSMUST00000232265.2</a>	1681	<a href="#">107aa</a>	Protein coding	<a href="#">CCDS28564</a>		GENCODE basic ,
Hmga1-201	<a href="#">ENSMUST00000114888.11</a>	1631	<a href="#">96aa</a>	Protein coding	<a href="#">CCDS50044</a>		TSL:1 , GENCODE basic , APPRIS P2 ,
Hmga1-205	<a href="#">ENSMUST00000118599.9</a>	1045	<a href="#">107aa</a>	Protein coding	<a href="#">CCDS28564</a>		TSL:3 , GENCODE basic ,
Hmga1-206	<a href="#">ENSMUST00000119486.9</a>	1030	<a href="#">107aa</a>	Protein coding	<a href="#">CCDS28564</a>		TSL:2 , GENCODE basic ,
Hmga1-217	<a href="#">ENSMUST00000232552.2</a>	917	<a href="#">96aa</a>	Protein coding	<a href="#">CCDS50044</a>		GENCODE basic , APPRIS P2 ,
Hmga1-208	<a href="#">ENSMUST00000231358.2</a>	805	<a href="#">96aa</a>	Protein coding	<a href="#">CCDS50044</a>		GENCODE basic , APPRIS P2 ,
Hmga1-214	<a href="#">ENSMUST00000232013.2</a>	805	<a href="#">107aa</a>	Protein coding	<a href="#">CCDS28564</a>		GENCODE basic ,
Hmga1-203	<a href="#">ENSMUST00000117600.9</a>	1595	<a href="#">106aa</a>	Protein coding	-		TSL:1 , GENCODE basic ,
Hmga1-202	<a href="#">ENSMUST00000117254.9</a>	916	<a href="#">95aa</a>	Protein coding	-		TSL:2 , GENCODE basic , APPRIS ALT1 ,
Hmga1-210	<a href="#">ENSMUST00000231796.2</a>	706	<a href="#">111aa</a>	Protein coding	-		GENCODE basic ,
Hmga1-209	<a href="#">ENSMUST00000231780.2</a>	619	<a href="#">87aa</a>	Protein coding	-		GENCODE basic ,
Hmga1-215	<a href="#">ENSMUST00000232253.2</a>	600	<a href="#">106aa</a>	Protein coding	-		GENCODE basic ,
Hmga1-212	<a href="#">ENSMUST00000231866.2</a>	584	<a href="#">118aa</a>	Protein coding	-		GENCODE basic ,
Hmga1-207	<a href="#">ENSMUST00000231243.2</a>	524	<a href="#">118aa</a>	Protein coding	-		GENCODE basic ,

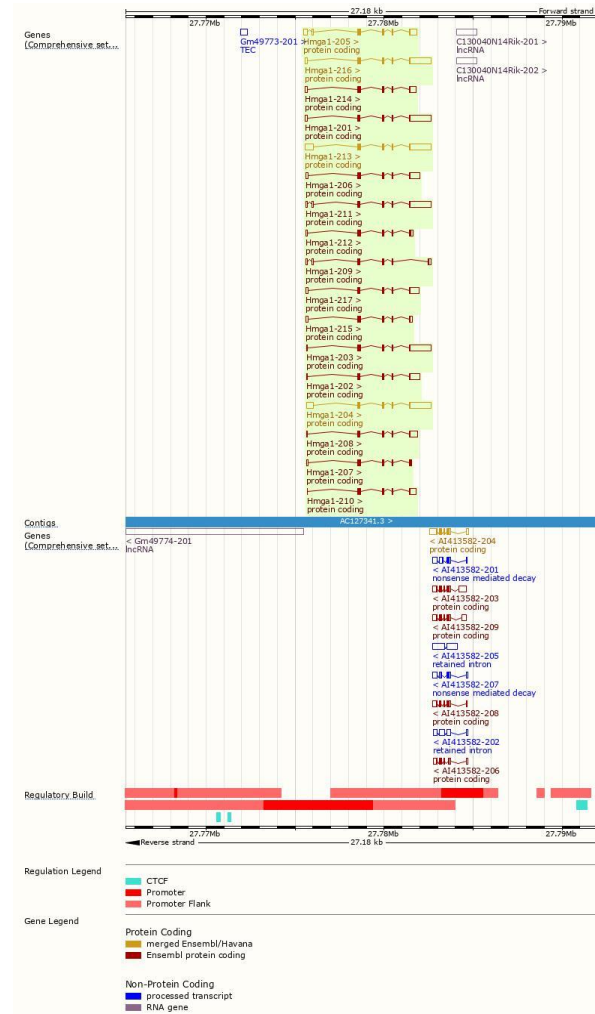
The strategy is based on the design of *Hmga1*-213 transcript, the transcription is shown below:



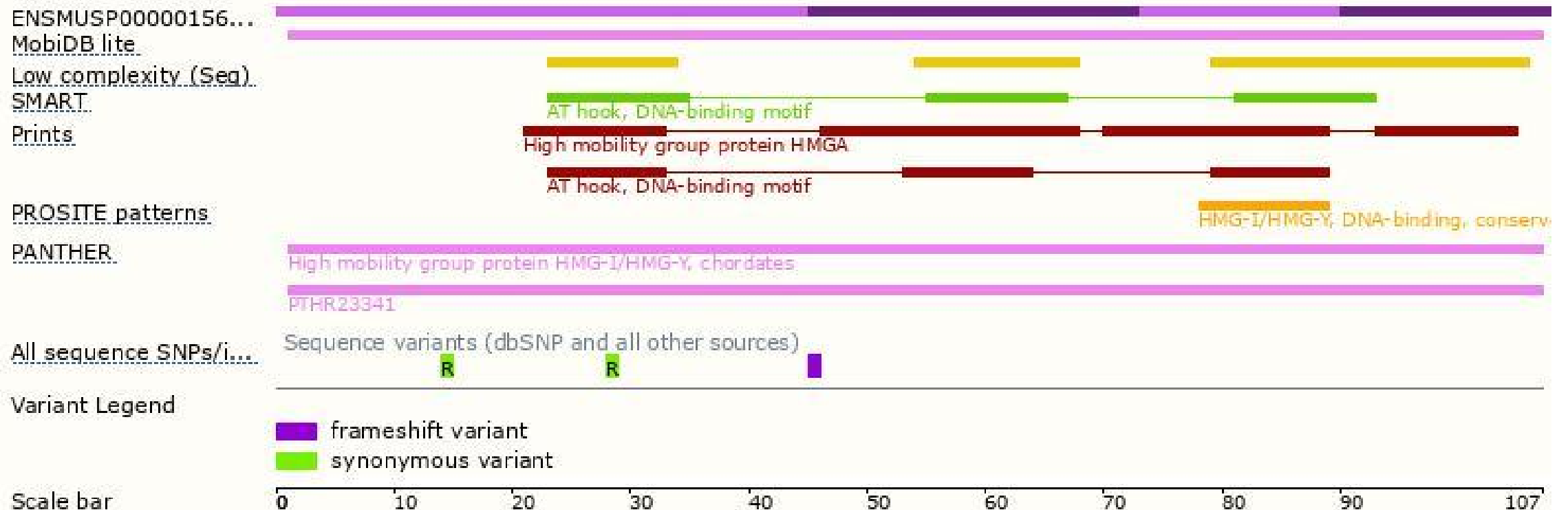
Source: <https://www.ensembl.org>



# Genomic Information

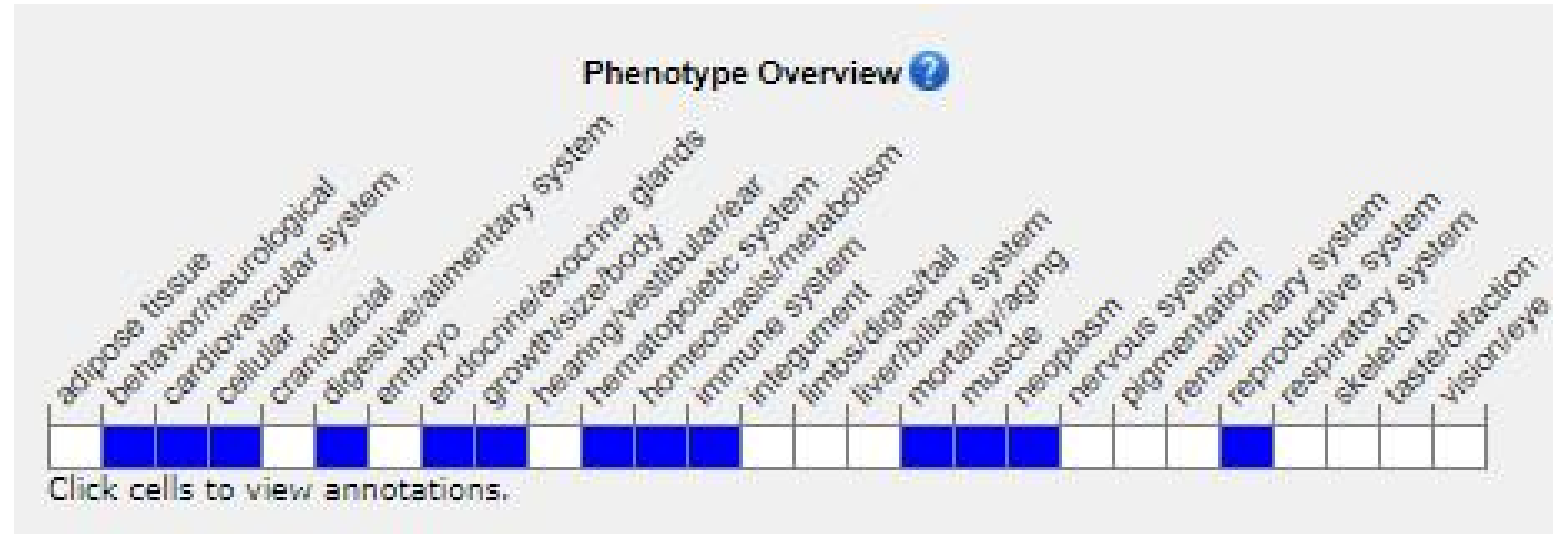


# Protein Information





# Mouse Phenotype Information (MGI)



- According to the existing MGI data, although haploinsufficiency at this locus is not compatible with germline transmission of one allele at this locus, mice homozygous for two other disruptions are fertile. Abnormalities are seen in glucose metabolism and in the cardiovascular system.

# Important Information

- According to the existing MGI data, although haploinsufficiency at this locus is not compatible with germline transmission of one allele at this locus, mice homozygous for two other disruptions are fertile. Abnormalities are seen in glucose metabolism and in the cardiovascular system.
- *Hmgal* & *Hmgalb* express identical proteins, which cannot be distinguished from the protein level.
- The KO region contains functional region of the *Gm49774* gene. Knockout the region may affect the function of *Gm49774* gene.
- *Hmgal* is located on Chr17. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.