

Hmga2 Cas9-KO Strategy

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Reviewer:JiaYu

Project Overview



Project Name

Hmga2

Project type

Cas9-KO

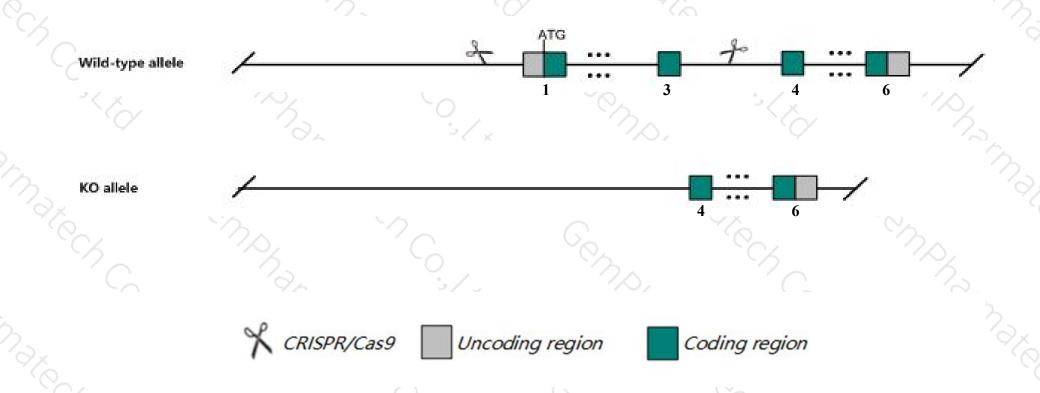
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Hmga2* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Hmga2* gene has 3 transcripts. According to the structure of *Hmga2* gene, exon1-exon3 of *Hmga2-203* (ENSMUST00000159699.1) 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 *Hmga2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Homozygotes for null mutations exhibit proportionate dwarfing with a significant reduction in body weight, reduced amounts of fat tissue, and infertility in both sexes. Mutants have normal growth hormone levels.
- ➤ In this strategy, the exon1-exon3 code is deleted and the starting codon ATG is deleted, which may generate new ATG translation unknown protein
- > The *Hmga2* gene is located on the Chr10. 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)



Hmga2 high mobility group AT-hook 2 [Mus musculus (house mouse)]

Gene ID: 15364, updated on 12-Nov-2019

Summary

Official Symbol Hmga2 provided by MGI

Official Full Name high mobility group AT-hook 2 provided by MGI

Primary source MGI:MGI:101761

See related Ensembl: ENSMUSG00000056758

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 pg; Hmgic; pygmy; HMGI-C; 9430083A20Rik

Expression Biased expression in CNS E11.5 (RPKM 40.3), limb E14.5 (RPKM 26.9) and 5 other tissues See more

Orthologs human all

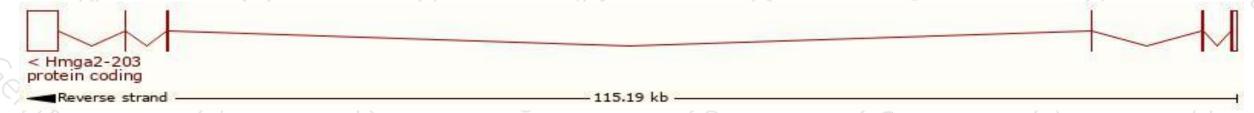
Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

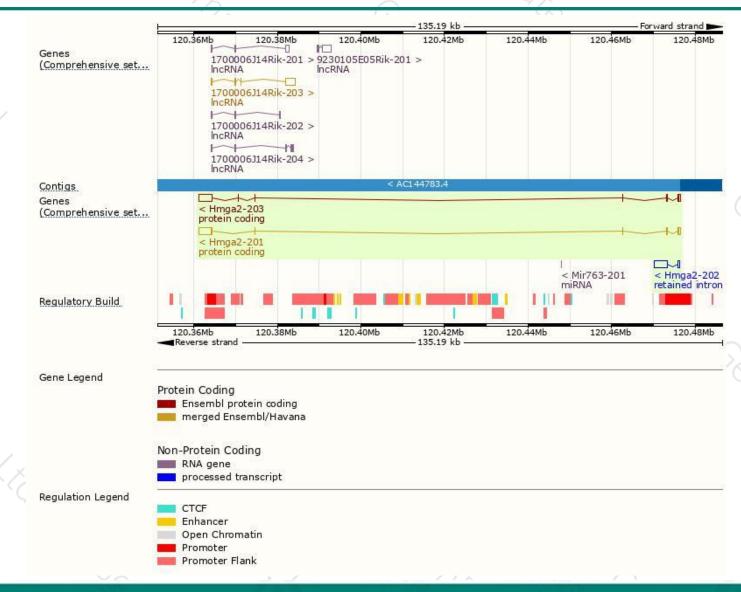
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmga2-203	ENSMUST00000159699.1	3810	<u>129aa</u>	Protein coding	CCDS83758	Q6NSP9	TSL:1 GENCODE basic
Hmga2-201	ENSMUST00000072777.13	3710	<u>108aa</u>	Protein coding	CCDS36073	P52927	TSL:1 GENCODE basic APPRIS P1
Hmga2-202	ENSMUST00000159310.1	3389	No protein	Retained intron	120	-	TSL:1

The strategy is based on the design of *Hmga2-203* transcript, The transcription is shown below



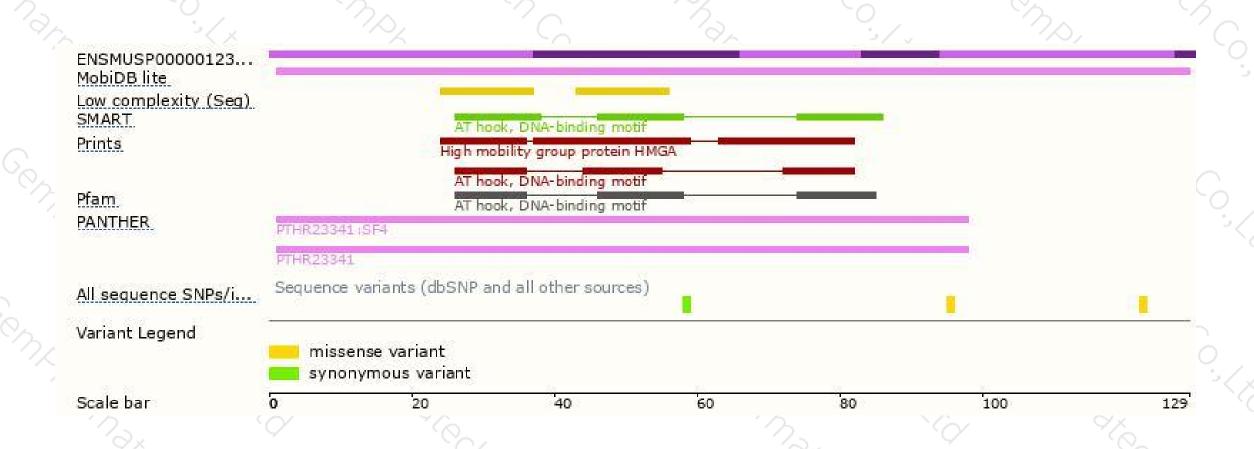
Genomic location distribution





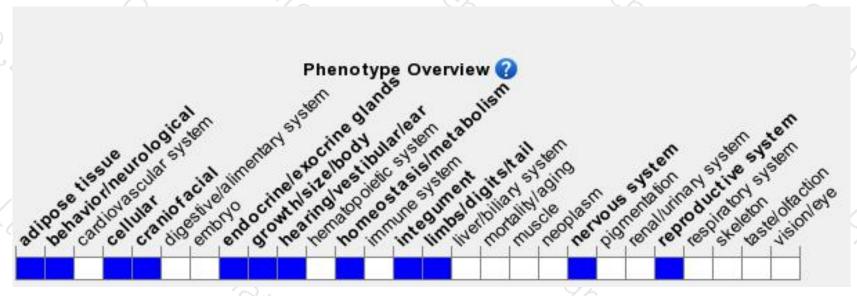
Protein domain





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, Homozygotes for null mutations exhibit proportionate dwarfing with a significant reduction in body weight, reduced amounts of fat tissue, and infertility in both sexes. Mutants have normal growth hormone levels.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





