

Hfm1 Cas9-KO Strategy

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Project Overview

Project Name

Hfm1

Project type

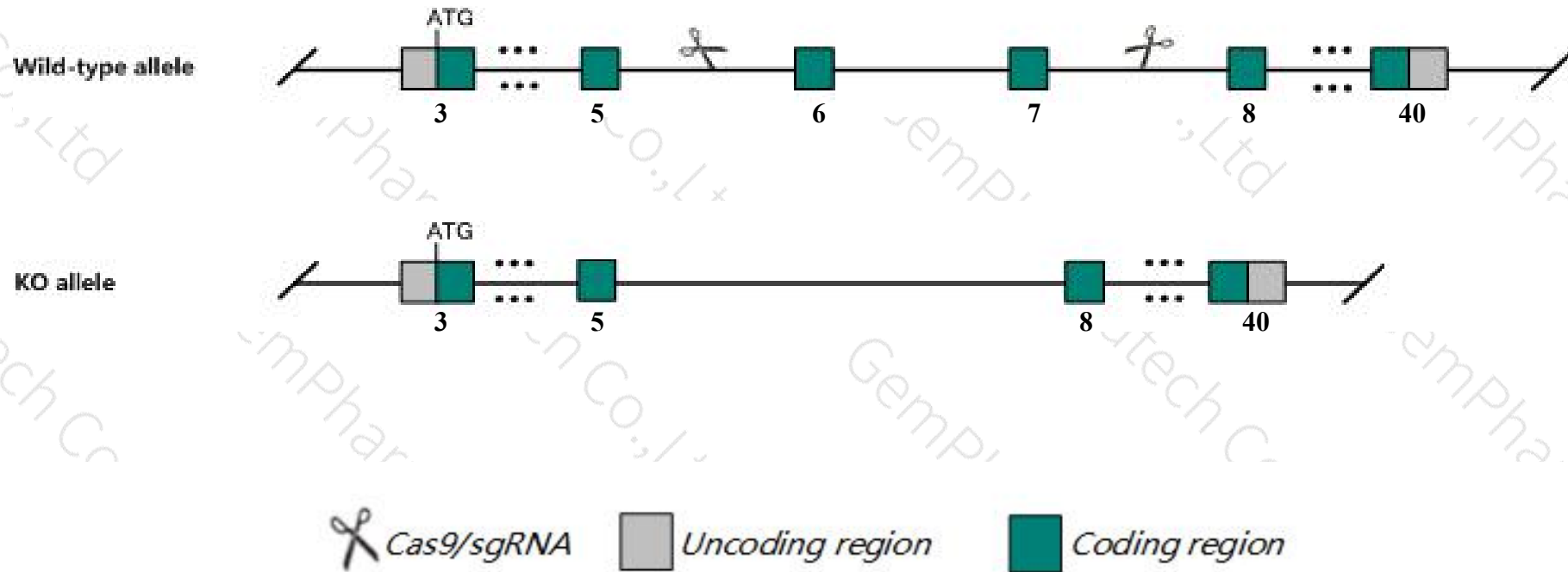
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hfm1* gene. The schematic diagram is as follows:



- The *Hfm1* gene has 7 transcripts. According to the structure of *Hfm1* gene, exon6-exon7 of *Hfm1-201* (ENSMUST00000112690.9) transcript is recommended as the knockout region. The region contains 311bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hfm1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

- According to the existing MGI data, Meiosis is disrupted in homozygotes and both sexes are sterile
- The *Hfm1* gene is located on the Chr5. 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)

Hfm1 HFM1, ATP-dependent DNA helicase homolog [Mus musculus (house mouse)]

Gene ID: 330149, updated on 31-Jan-2019

Summary

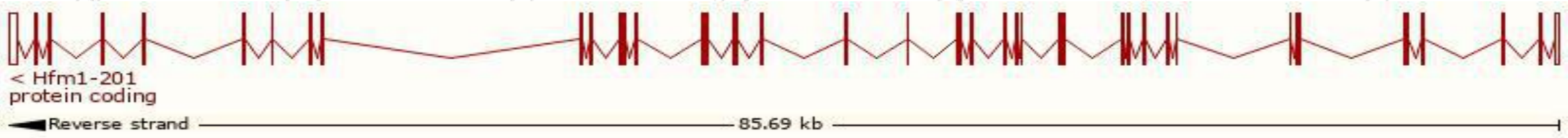
Official Symbol	Hfm1 provided by MGI
Official Full Name	HFM1, ATP-dependent DNA helicase homolog provided by MGI
Primary source	MGI:MGI:3036246
See related	Ensembl:ENSMUSG00000043410
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A330009G12Rik, Gm1046, Mer3, Sec63d1
Expression	Biased expression in testis adult (RPKM 2.8), CNS E18 (RPKM 1.6) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

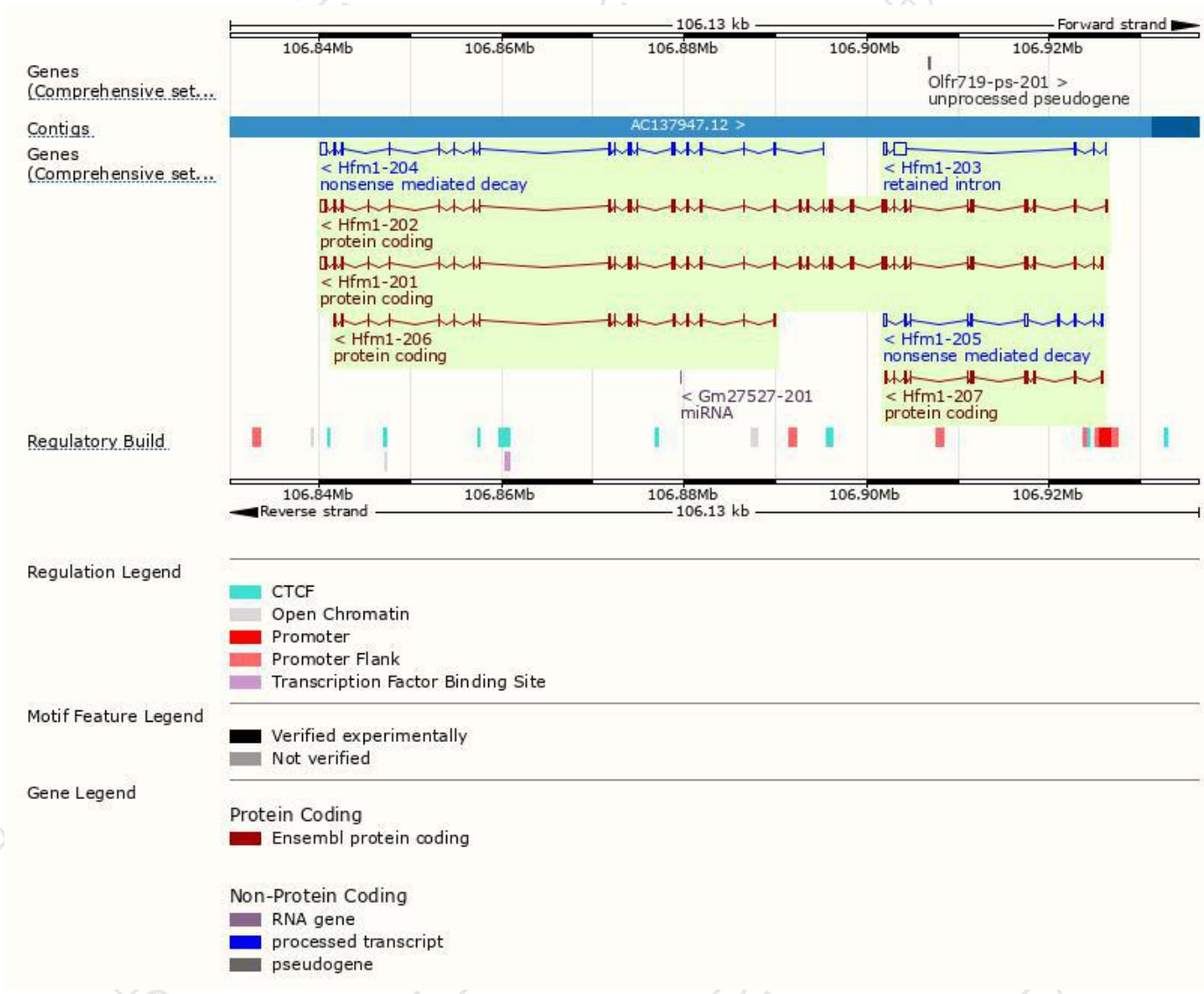
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hfm1-201	ENSMUST00000112690.9	5018	1434aa	Protein coding	CCDS51582	D3Z4R1	TSL:5 GENCODE basic APPRIS P1
Hfm1-202	ENSMUST00000117588.7	4870	1434aa	Protein coding	CCDS51582	D3Z4R1	TSL:5 GENCODE basic APPRIS P1
Hfm1-206	ENSMUST00000155171.1	1928	626aa	Protein coding	-	F6XQ35	CDS 5' incomplete TSL:5
Hfm1-207	ENSMUST00000200249.1	1381	410aa	Protein coding	-	A0A0G2JED3	CDS 3' incomplete TSL:1
Hfm1-204	ENSMUST00000148495.1	2613	49aa	Nonsense mediated decay	-	F7C082	CDS 5' incomplete TSL:5
Hfm1-205	ENSMUST00000148686.7	1440	57aa	Nonsense mediated decay	-	D6RJK3	TSL:1
Hfm1-203	ENSMUST00000134292.1	1959	No protein	Retained intron	-	-	TSL:1

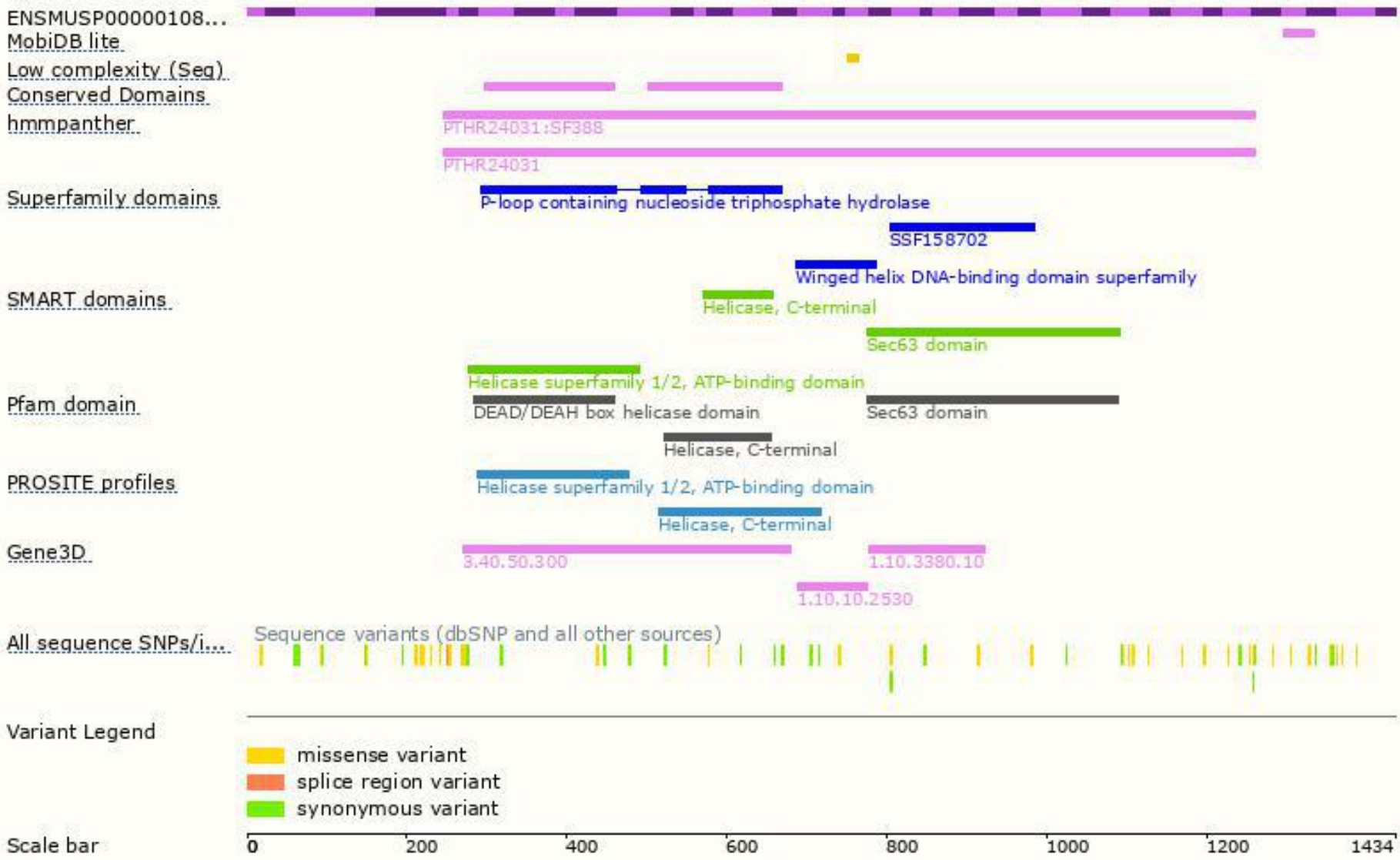
The strategy is based on the design of *Hfm1-201* transcript,The transcription is shown below



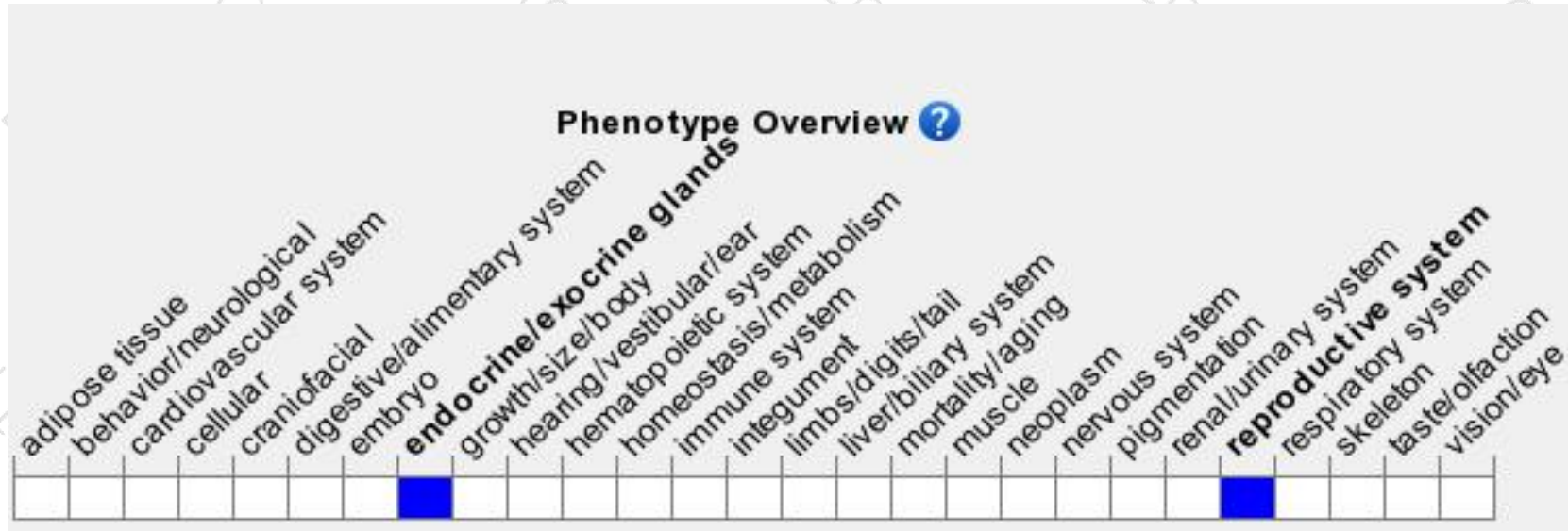
Genomic location distribution



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, Meiosis is disrupted in homozygotes and both sexes are sterile

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

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