

***Kdm3a* Cas9-KO Strategy**

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Project Overview

Project Name

Kdm3a

Project type

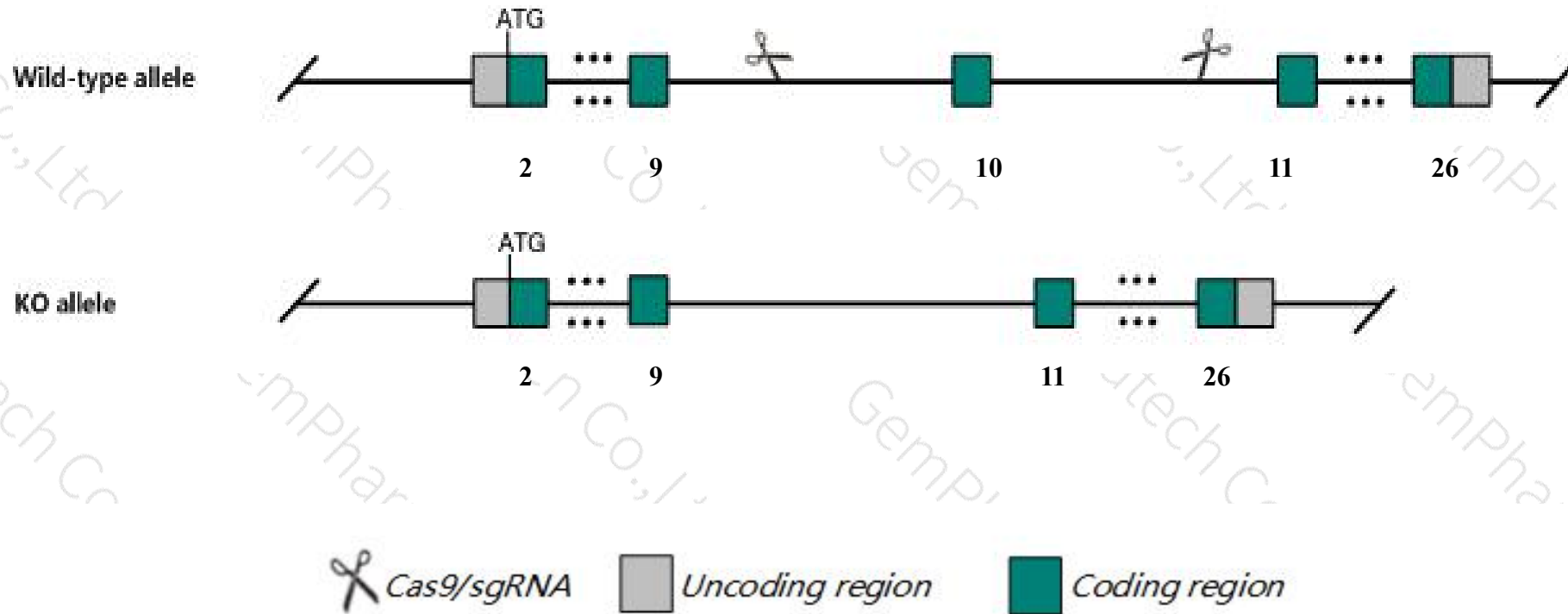
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kdm3a* gene. The schematic diagram is as follows:



- The *Kdm3a* gene has 14 transcripts. According to the structure of *Kdm3a* gene, exon10 of *Kdm3a-202* (ENSMUST00000167220.3) transcript is recommended as the knockout region. The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kdm3a* 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, Male mice homozygous for a hypomorphic allele display infertility, oligoasthenoteratozoospermia, small testis, and impaired spermiogenesis. Mice homozygous for a null allele exhibit abnormal spermatogenesis and obesity associated with hyperlipidemia.
- The *Kdm3a* gene is located on the Chr6. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Kdm3a lysine (K)-specific demethylase 3A [Mus musculus (house mouse)]

Gene ID: 104263, updated on 19-Feb-2019

Summary



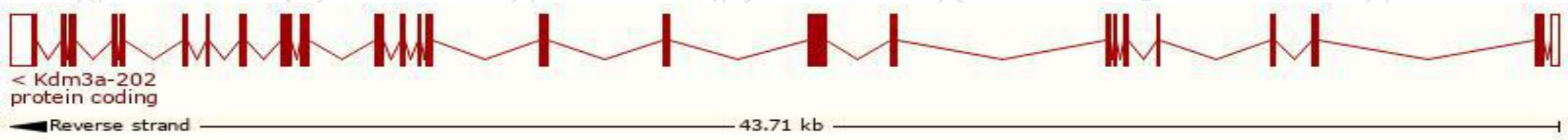
Official Symbol	Kdm3a provided by MGI
Official Full Name	lysine (K)-specific demethylase 3A provided by MGI
Primary source	MGI:MGI:98847
See related	Ensembl:ENSMUSG00000053470
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700105C21Rik, C230043E16Rik, JHDM2a, Jmjd1, Jmjd1a, KDM2A, TGSA, Tsga
Expression	Ubiquitous expression in CNS E11.5 (RPKM 18.6), testis adult (RPKM 15.8) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

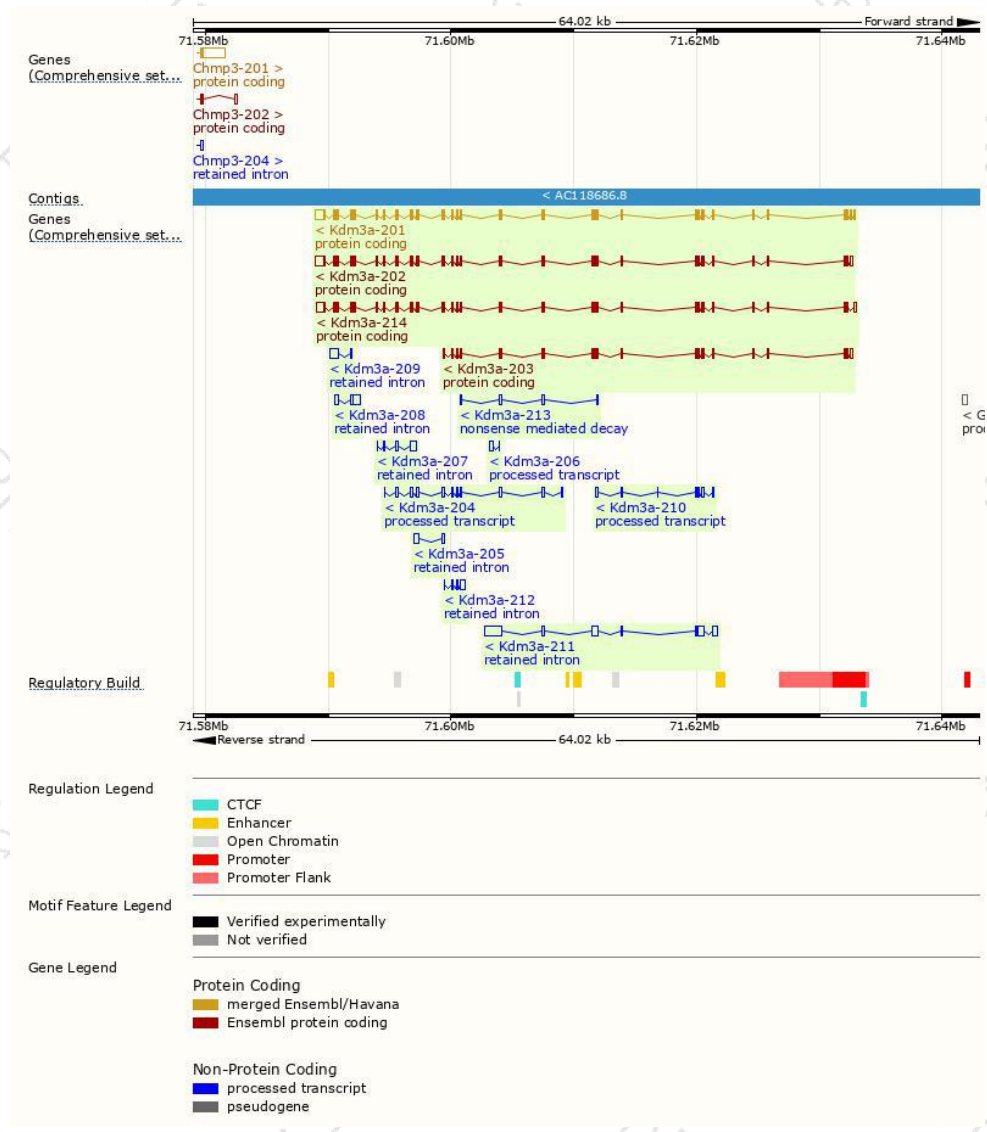
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kdm3a-202	ENSMUST00000167220.3	4853	1323aa	Protein coding	CCDS20233	Q6PCM1	TSL:1 GENCODE basic APPRIS P1
Kdm3a-201	ENSMUST00000065509.10	4816	1323aa	Protein coding	CCDS20233	Q6PCM1	TSL:1 GENCODE basic APPRIS P1
Kdm3a-214	ENSMUST00000207023.1	4753	1323aa	Protein coding	CCDS20233	Q6PCM1	TSL:5 GENCODE basic APPRIS P1
Kdm3a-203	ENSMUST00000205289.1	2723	834aa	Protein coding	-	A0A0U1RNV6	CDS 3' incomplete TSL:1
Kdm3a-213	ENSMUST00000206916.1	679	43aa	Nonsense mediated decay	-	A0A0U1RPI3	CDS 5' incomplete TSL:3
Kdm3a-204	ENSMUST00000205470.1	1718	No protein	Processed transcript	-	-	TSL:5
Kdm3a-210	ENSMUST00000206597.1	828	No protein	Processed transcript	-	-	TSL:3
Kdm3a-206	ENSMUST00000206050.1	341	No protein	Processed transcript	-	-	TSL:3
Kdm3a-211	ENSMUST00000206704.1	3137	No protein	Retained intron	-	-	TSL:1
Kdm3a-208	ENSMUST00000206357.1	917	No protein	Retained intron	-	-	TSL:2
Kdm3a-207	ENSMUST00000206339.1	815	No protein	Retained intron	-	-	TSL:2
Kdm3a-209	ENSMUST00000206582.1	785	No protein	Retained intron	-	-	TSL:3
Kdm3a-212	ENSMUST00000206798.1	743	No protein	Retained intron	-	-	TSL:2
Kdm3a-205	ENSMUST00000205505.1	541	No protein	Retained intron	-	-	TSL:2

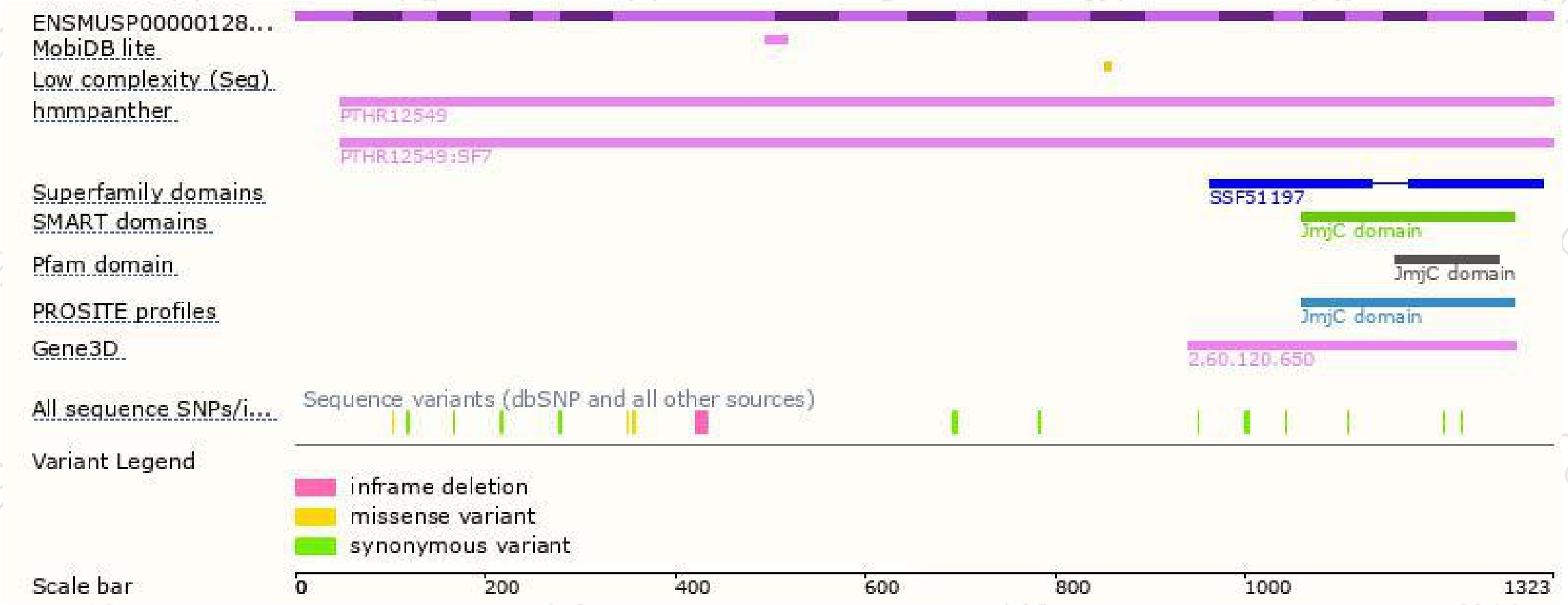
The strategy is based on the design of *Kdm3a-202* transcript,The transcription is shown below



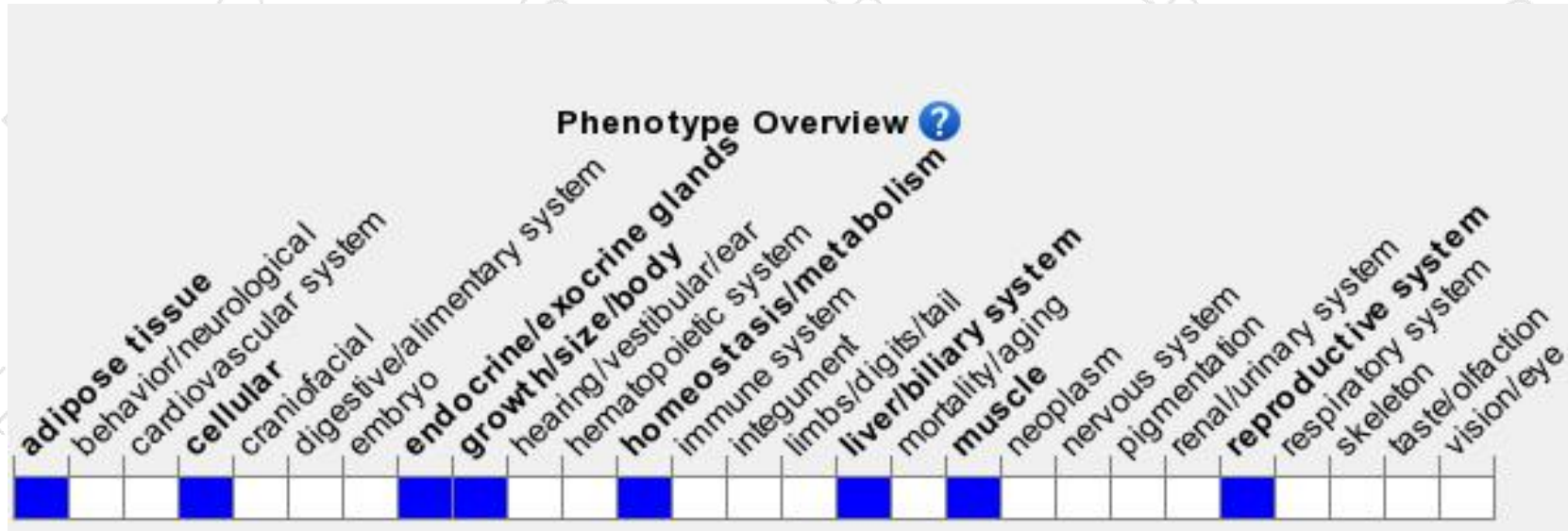
Genomic location distribution



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, Male mice homozygous for a hypomorphic allele display infertility, oligoasthenoteratozoospermia, small testis, and impaired spermiogenesis. Mice homozygous for a null allele exhibit abnormal spermatogenesis and obesity associated with hyperlipidemia.

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

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