

Klf3 Cas9-KO Strategy

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Reviewer: Huimin Su

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Project Overview



Project Name Klf3

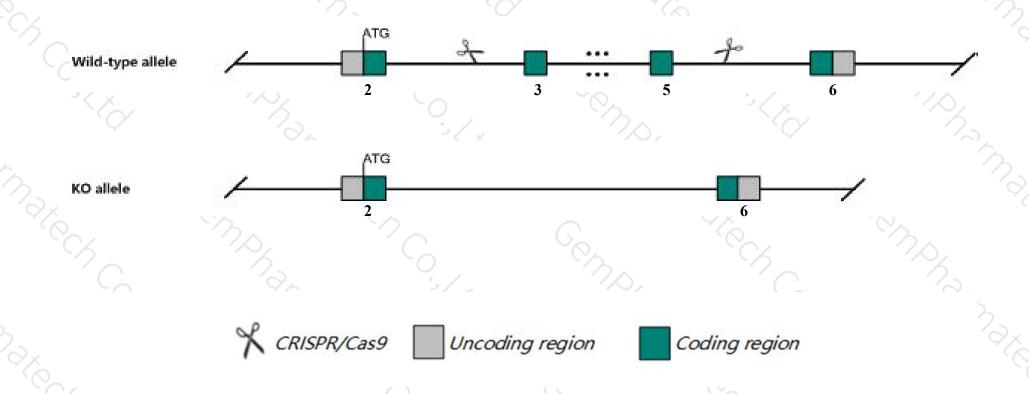
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Klf3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Klf3* gene has 9 transcripts. According to the structure of *Klf3* gene, exon3-exon5 of *Klf3-201* (ENSMUST00000165536.7) transcript is recommended as the knockout region. The region contains 796bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Klf3* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice



- ➤ According to the existing MGI data, Homozygous null mice display reduced viability, body size and white adipose tissue. Mice homozygous for a gene trap allele exhibit cardiac defects, reduced body size and abnormal red blood cells. Mice heterozygous for an ENU-induced allele exhibit lethality with heart defects.
- > The *Klf3* 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)



KIf3 Kruppel-like factor 3 (basic) [Mus musculus (house mouse)]

Gene ID: 16599, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Klf3 provided by MGI

Official Full Name Kruppel-like factor 3 (basic) provided by MGI

Primary source MGI:MGI:1342773

See related Ensembl: ENSMUSG00000029178

Gene type protein coding
RefSeq status PROVISIONAL
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as 9930027G08Rik, AL024007, Bklf, Tef-2

Expression Ubiquitous expression in colon adult (RPKM 33.8), thymus adult (RPKM 20.9) and 27 other tissuesSee more

Orthologs <u>human</u> all

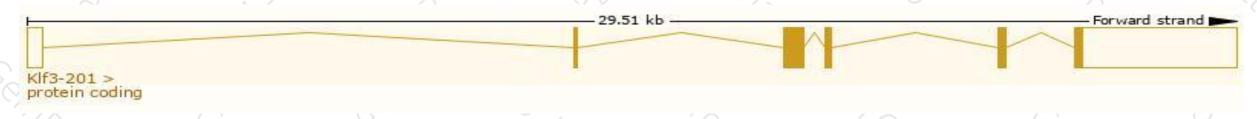
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

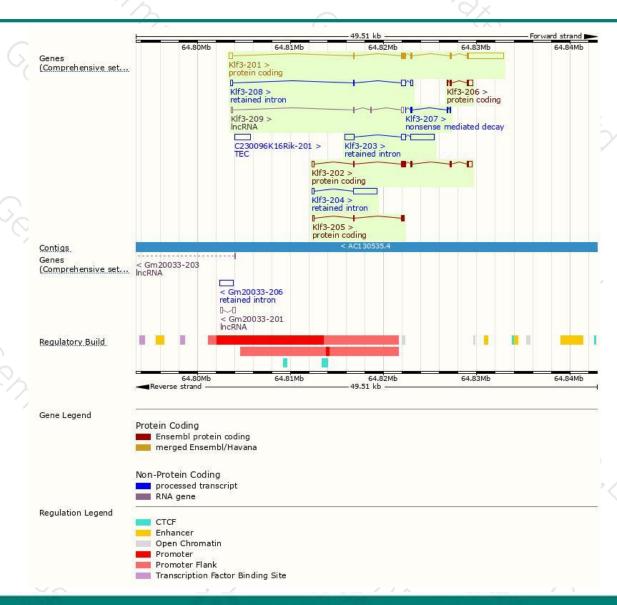
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000165536.7	5221	344aa	Protein coding	CCDS19301	Q545J5 Q60980	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000166409.5	1562	<u>344aa</u>	Protein coding	CCDS19301	Q545J5 Q60980	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000198946.1	809	<u>138aa</u>	Protein coding	49	A0A0G2JE66	CDS 5' incomplete TSL:3
ENSMUST00000197879.1	590	<u>142aa</u>	Protein coding	29	A0A0G2JDH4	CDS 3' incomplete TSL:2
ENSMUST00000200384.1	298	<u>55aa</u>	Nonsense mediated decay	5.6	A0A0G2JE81	CDS 5' incomplete TSL:1
ENSMUST00000196764.1	4016	No protein	Retained intron	#8	6 .0 %	TSL:1
ENSMUST00000197869.1	2749	No protein	Retained intron	10	12	TSL:1
ENSMUST00000200587.4	1026	No protein	Retained intron	29	8 <u>-</u> 8	TSL:1
ENSMUST00000200677.1	648	No protein	IncRNA	ēá	(154)	TSL:3
	ENSMUST00000165536.7 ENSMUST00000166409.5 ENSMUST00000198946.1 ENSMUST00000197879.1 ENSMUST00000200384.1 ENSMUST00000196764.1 ENSMUST00000197869.1 ENSMUST00000197869.1	ENSMUST00000165536.7 5221 ENSMUST00000166409.5 1562 ENSMUST00000198946.1 809 ENSMUST00000197879.1 590 ENSMUST00000200384.1 298 ENSMUST00000196764.1 4016 ENSMUST00000197869.1 2749 ENSMUST00000197869.1 2749	ENSMUST00000165536.7 5221 344aa ENSMUST00000166409.5 1562 344aa ENSMUST00000198946.1 809 138aa ENSMUST00000197879.1 590 142aa ENSMUST00000200384.1 298 55aa ENSMUST00000196764.1 4016 No protein ENSMUST00000197869.1 2749 No protein ENSMUST00000200587.4 1026 No protein	ENSMUST00000165536.7 5221 344aa Protein coding ENSMUST00000166409.5 1562 344aa Protein coding ENSMUST00000198946.1 809 138aa Protein coding ENSMUST00000197879.1 590 142aa Protein coding ENSMUST00000200384.1 298 55aa Nonsense mediated decay ENSMUST00000196764.1 4016 No protein Retained intron ENSMUST00000197869.1 2749 No protein Retained intron ENSMUST00000200587.4 1026 No protein Retained intron	ENSMUST00000165536.7 5221 344aa Protein coding CCDS19301 ENSMUST00000166409.5 1562 344aa Protein coding CCDS19301 ENSMUST00000198946.1 809 138aa Protein coding - ENSMUST00000197879.1 590 142aa Protein coding - ENSMUST00000200384.1 298 55aa Nonsense mediated decay - ENSMUST00000196764.1 4016 No protein Retained intron - ENSMUST000000197869.1 2749 No protein Retained intron - ENSMUST000000200587.4 1026 No protein Retained intron -	ENSMUST00000165536.7 5221 344aa Protein coding CCDS19301 Q545J5 Q60980 ENSMUST00000166409.5 1562 344aa Protein coding CCDS19301 Q545J5 Q60980 ENSMUST00000198946.1 809 138aa Protein coding - A0A0G2JE66 ENSMUST00000197879.1 590 142aa Protein coding - A0A0G2JDH4 ENSMUST00000200384.1 298 55aa Nonsense mediated decay - A0A0G2JE81 ENSMUST00000196764.1 4016 No protein Retained intron - - ENSMUST00000197869.1 2749 No protein Retained intron - - ENSMUST000000200587.4 1026 No protein Retained intron - -

The strategy is based on the design of *Klf3-201* transcript, The transcription is shown below



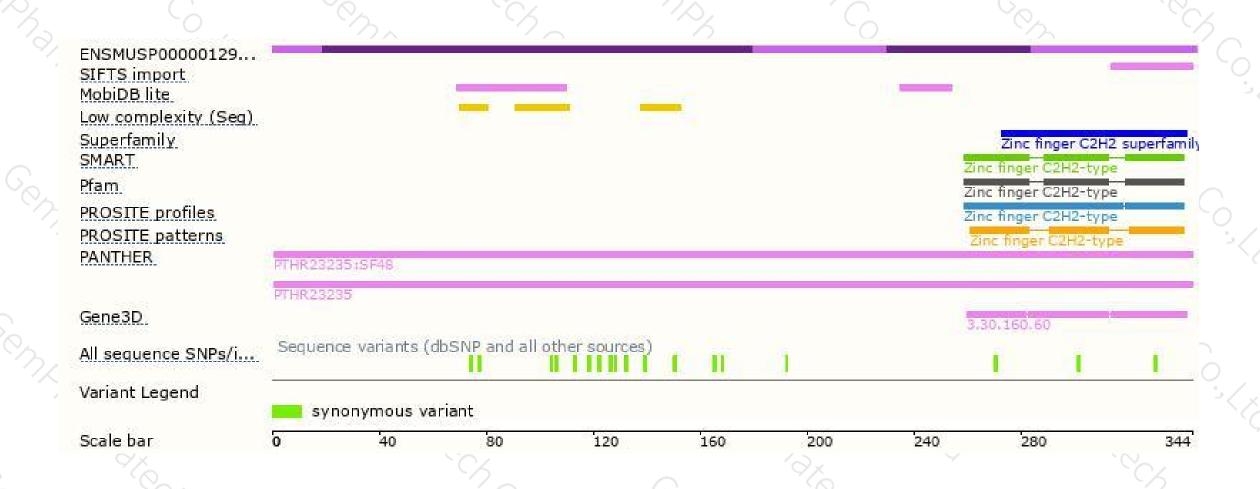
Genomic location distribution





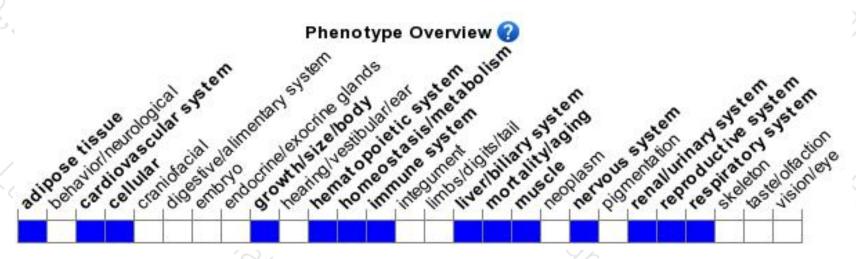
Protein domain





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, Homozygous null mice display reduced viability, body size and white adipose tissue. Mice homozygous for a gene trap allele exhibit cardiac defects, reduced body size and abnormal red blood cells. Mice heterozygous for an ENU-induced allele exhibit lethality with heart defects.



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





