

Etfbkmt Cas9-KO Strategy

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Design Date: 2021-6-15

Project Overview

Project Name

Etfbkmt

Project type

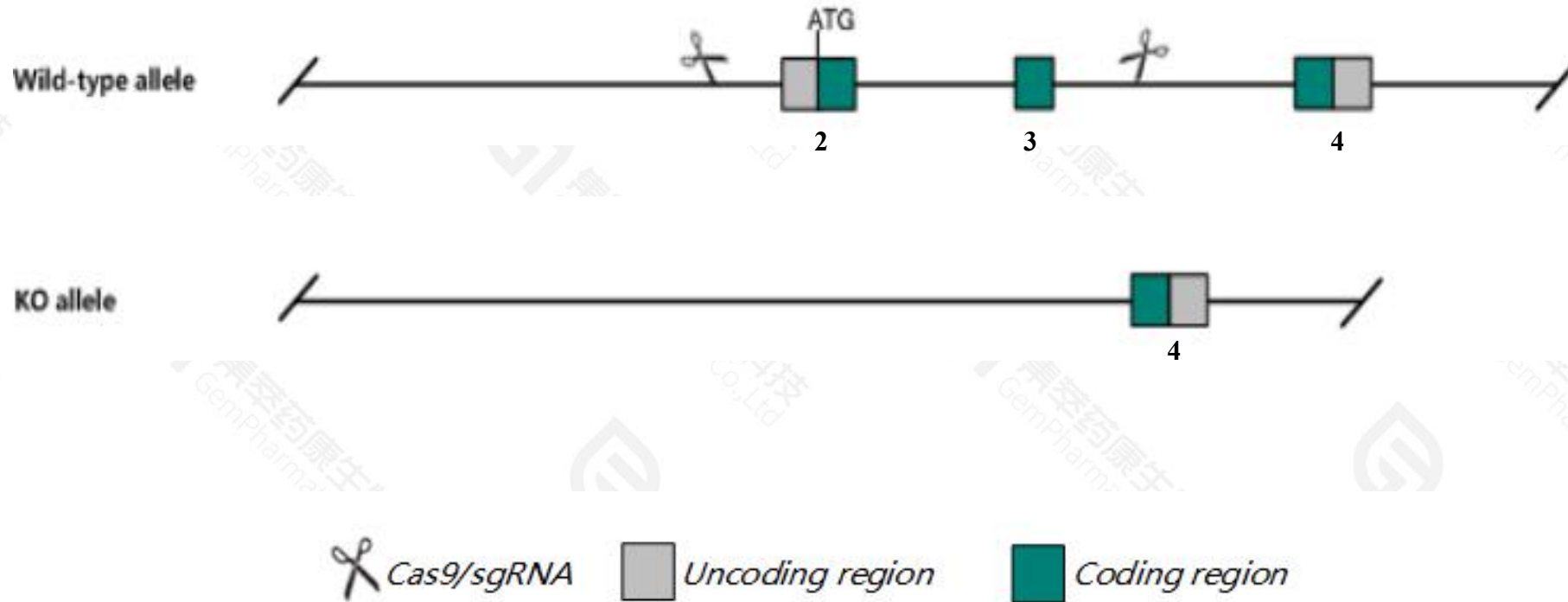
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Etfbkmt* gene has 9 transcripts. According to the structure of *Etfbkmt* gene, exon2-exon3 of *Etfbkmt*-209(ENSMUST00000179873.8) 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 *Etfbkmt* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased oxygen consumption rate and heat production under ketogenic conditions and enhanced cold tolerance during fasting.
- The *Etfbkmt* 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 biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Etfbkmt electron transfer flavoprotein beta subunit lysine methyltransferase [Mus musculus (house mouse)]

Gene ID: 320204, updated on 20-Feb-2021

Summary



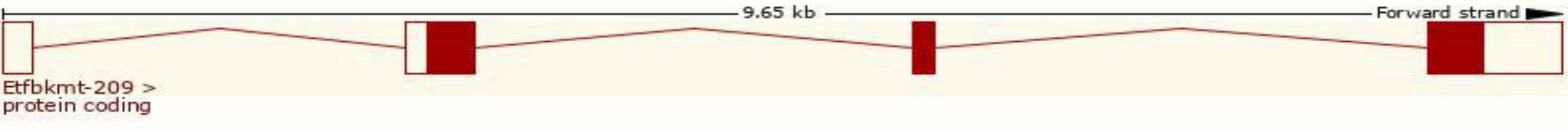
| | |
|---------------------------|---|
| Official Symbol | Etfbkmt provided by MGI |
| Official Full Name | electron transfer flavoprotein beta subunit lysine methyltransferase provided by MGI |
| Primary source | MGI:MGI:2443575 |
| See related | Ensembl:ENSMUSG00000039958 |
| Gene type | protein coding |
| 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 | 4833442J19Rik, AI256744, ETFB-KMT, Mettl2, Mettl20 |
| Expression | Ubiquitous expression in bladder adult (RPKM 13.6), heart adult (RPKM 5.1) and 24 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

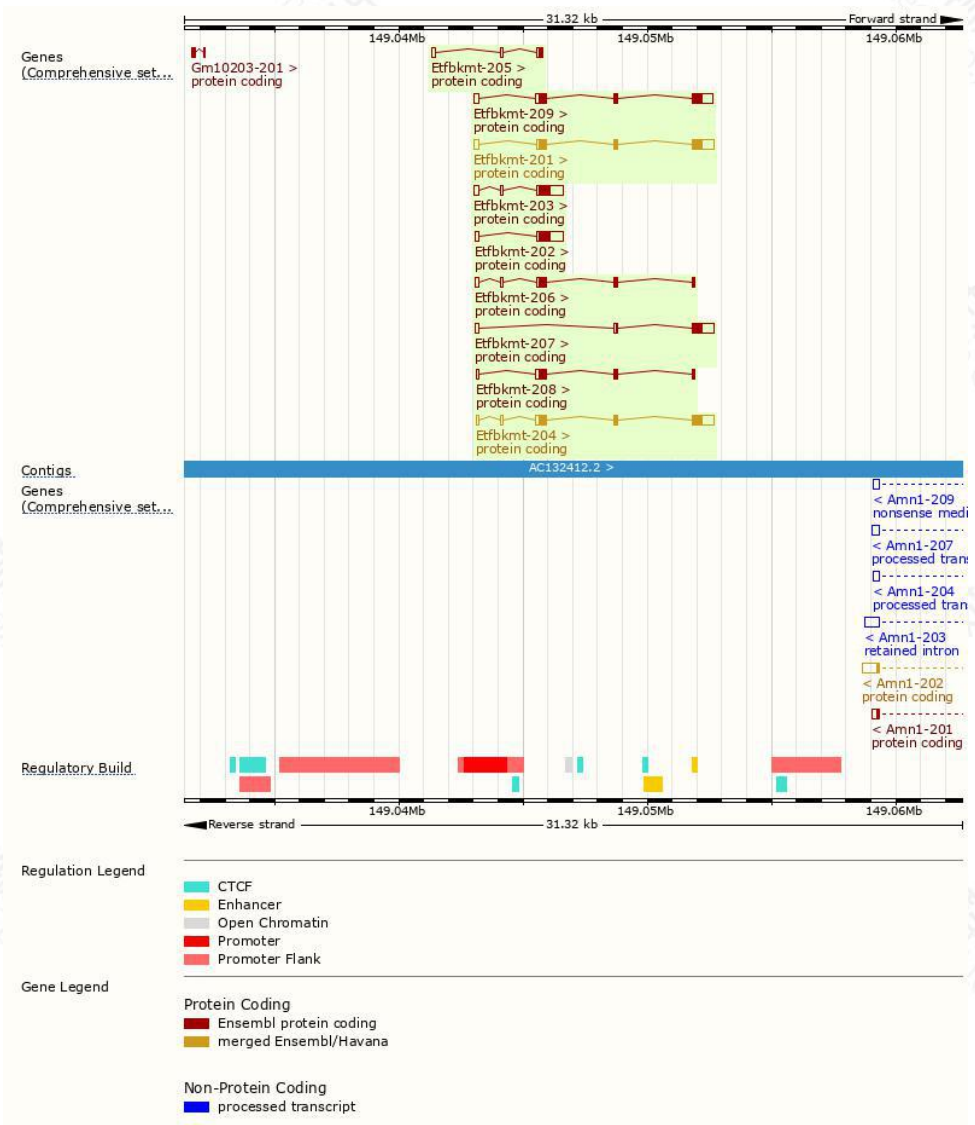
The gene has 9 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|---------------------------------------|------|-----------------------|----------------|---------------------------|---------|-------------------------------------|
| Etfbkmt-209 | ENSMUST00000179873.8 | 1576 | 255aa | Protein coding | CCDS20715 | | TSL:3 , GENCODE basic , APPRIS P1 , |
| Etfbkmt-201 | ENSMUST00000047531.16 | 1562 | 255aa | Protein coding | CCDS20715 | | TSL:1 , GENCODE basic , APPRIS P1 , |
| Etfbkmt-204 | ENSMUST00000111551.2 | 1558 | 255aa | Protein coding | CCDS20715 | | TSL:1 , GENCODE basic , APPRIS P1 , |
| Etfbkmt-207 | ENSMUST00000147934.4 | 1092 | 128aa | Protein coding | CCDS85191 | | TSL:1 , GENCODE basic , |
| Etfbkmt-203 | ENSMUST00000111548.8 | 1398 | 150aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Etfbkmt-202 | ENSMUST00000111547.2 | 1250 | 150aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Etfbkmt-206 | ENSMUST00000134306.8 | 848 | 160aa | Protein coding | - | | CDS 3' incomplete , TSL:5 , |
| Etfbkmt-208 | ENSMUST00000166416.8 | 698 | 165aa | Protein coding | - | | CDS 3' incomplete , TSL:3 , |
| Etfbkmt-205 | ENSMUST00000126406.8 | 478 | 45aa | Protein coding | - | | CDS 3' incomplete , TSL:3 , |

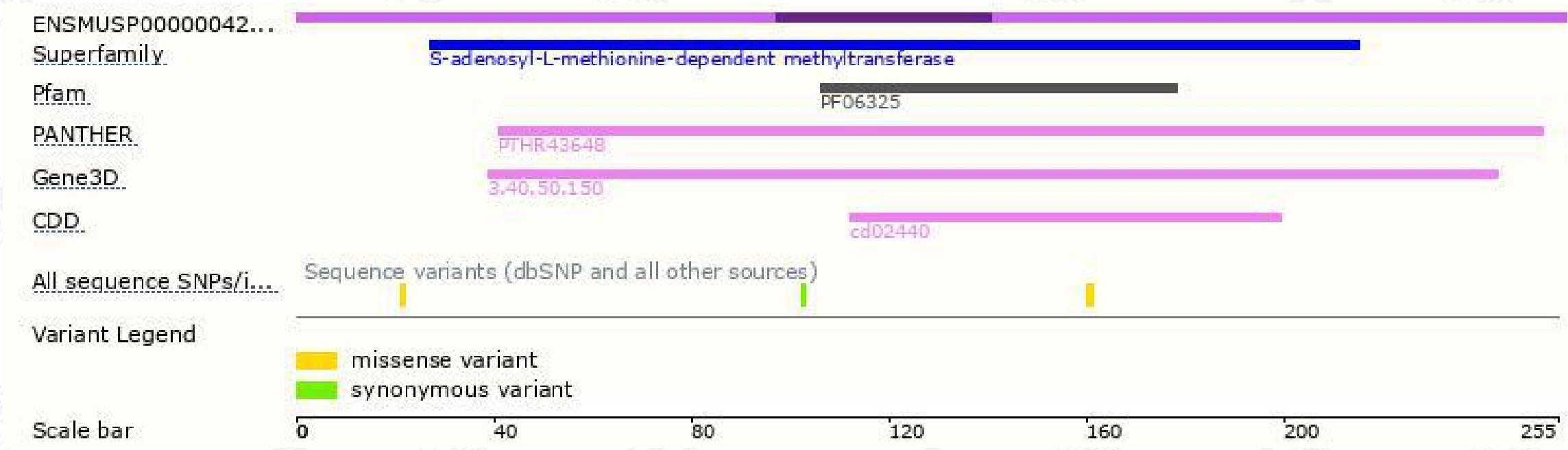
The strategy is based on the design of *Etfbkmt-209* transcript,the transcription is shown below:



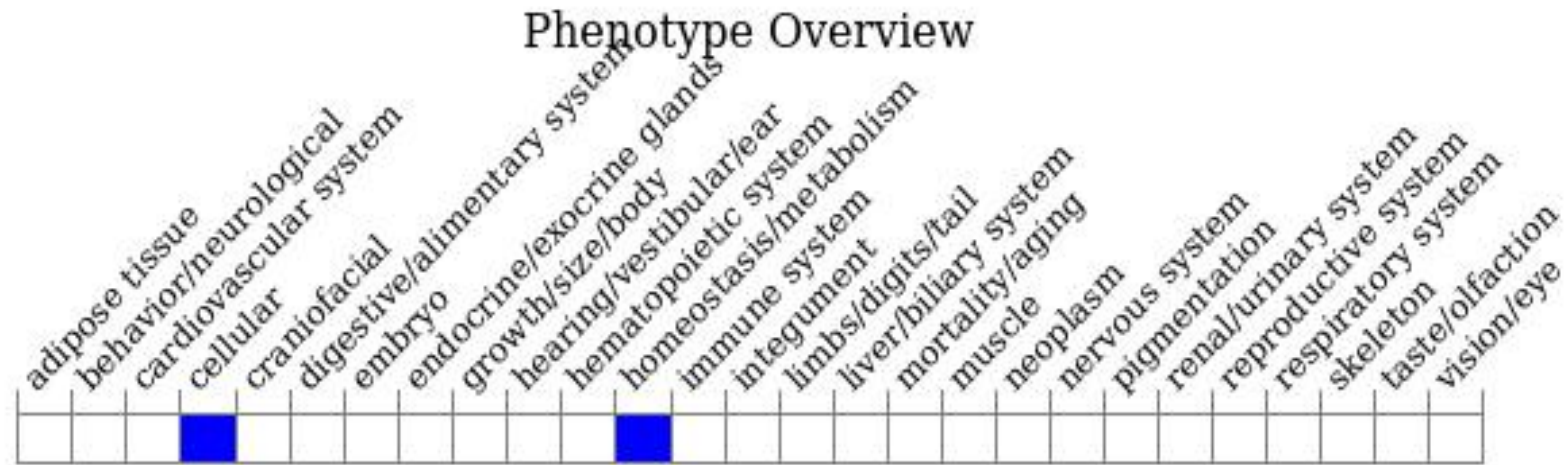
Genomic location distribution



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, mice homozygous for a knock-out allele exhibit increased oxygen consumption rate and heat production under ketogenic conditions and enhanced cold tolerance during fasting.

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

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