

Eeflaknmt Cas9-KO Strategy

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Project Overview

Project Name

Eef1aknmt

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Eeflaknmt* gene has 8 transcripts. According to the structure of *Eeflaknmt* gene, exon2-exon6 of *Eeflaknmt*-201 (ENSMUST00000028017.15) transcript is recommended as the knockout region. The region contains 1537bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eeflaknmt* gene. The brief process is as follows: CRISPR/Cas9 sys

- The *Eef1aknmt* gene is located on the Chr1. 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)

Eef1aknmt EEF1A lysine and N-terminal methyltransferase [Mus musculus (house mouse)]

Gene ID: 71449, updated on 19-Mar-2019

Summary



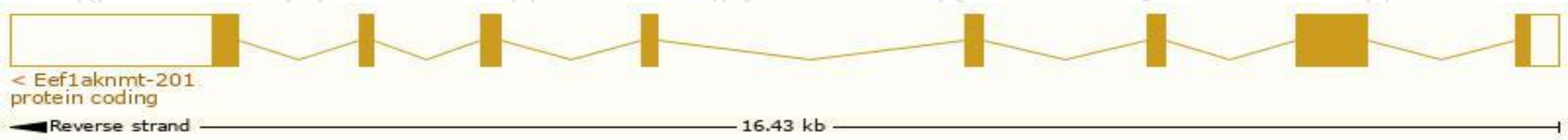
Official Symbol	Eef1aknmt provided by MGI
Official Full Name	EEF1A lysine and N-terminal methyltransferase provided by MGI
Primary source	MGI:MGI:1918699
See related	Ensembl:ENSMUSG00000026694
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5630401D24Rik, Mettl13
Expression	Ubiquitous expression in CNS E11.5 (RPKM 6.1), limb E14.5 (RPKM 5.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

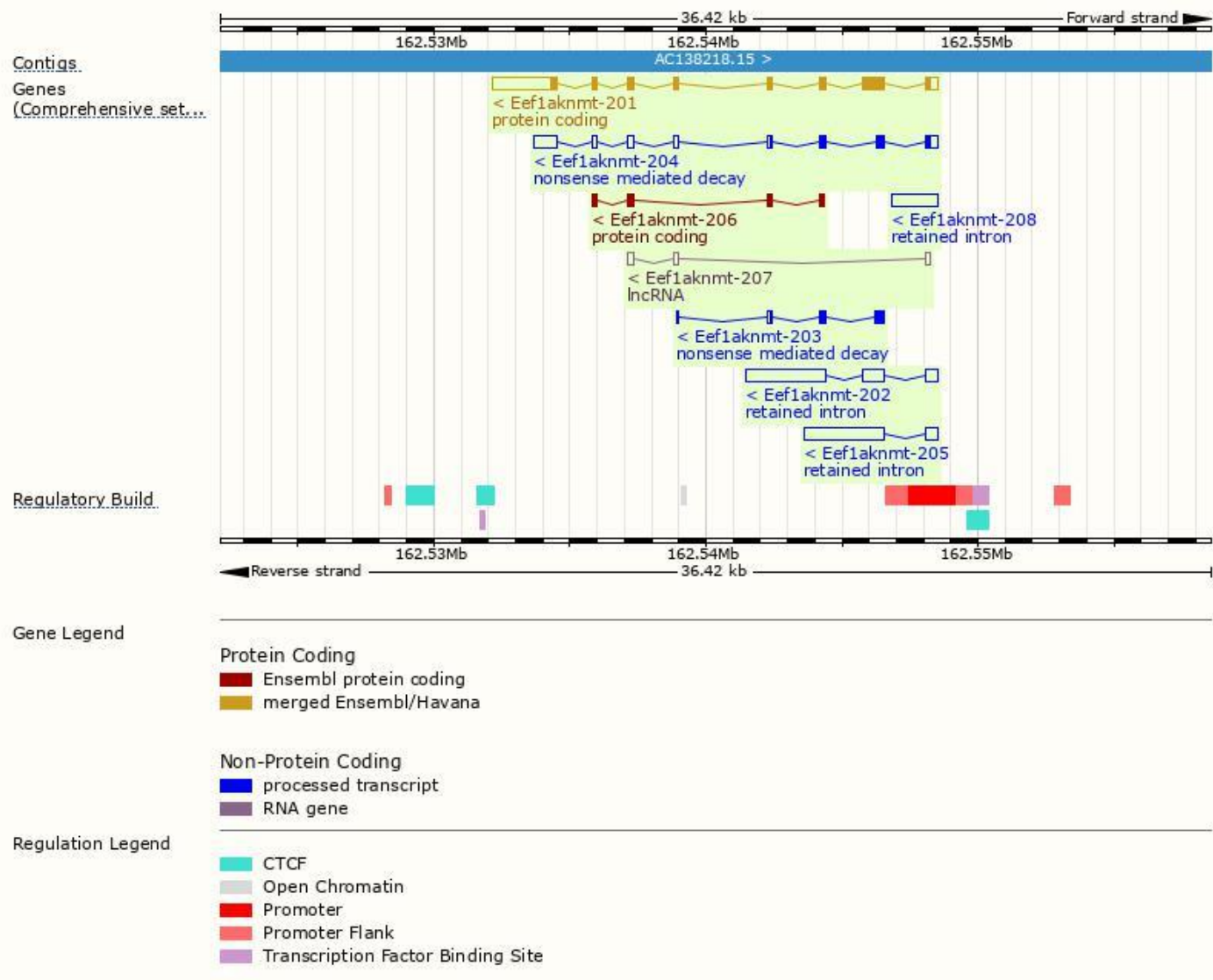
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eef1aknmt-201	ENSMUST00000028017.15	4541	698aa	Protein coding	CCDS15420	Q91YR5	TSL:1 GENCODE basic APPRIS P1
Eef1aknmt-206	ENSMUST00000176220.2	718	239aa	Protein coding	-	H3BLQ8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Eef1aknmt-204	ENSMUST00000159817.8	2482	234aa	Nonsense mediated decay	-	E9PYK1	TSL:5
Eef1aknmt-203	ENSMUST00000159316.2	776	189aa	Nonsense mediated decay	-	H3BLK3	CDS 5' incomplete TSL:3
Eef1aknmt-202	ENSMUST00000159255.1	4132	No protein	Retained intron	-	-	TSL:1
Eef1aknmt-205	ENSMUST00000161760.1	3317	No protein	Retained intron	-	-	TSL:1
Eef1aknmt-208	ENSMUST00000195027.1	1702	No protein	Retained intron	-	-	TSL:NA
Eef1aknmt-207	ENSMUST00000176689.1	510	No protein	lncRNA	-	-	TSL:5

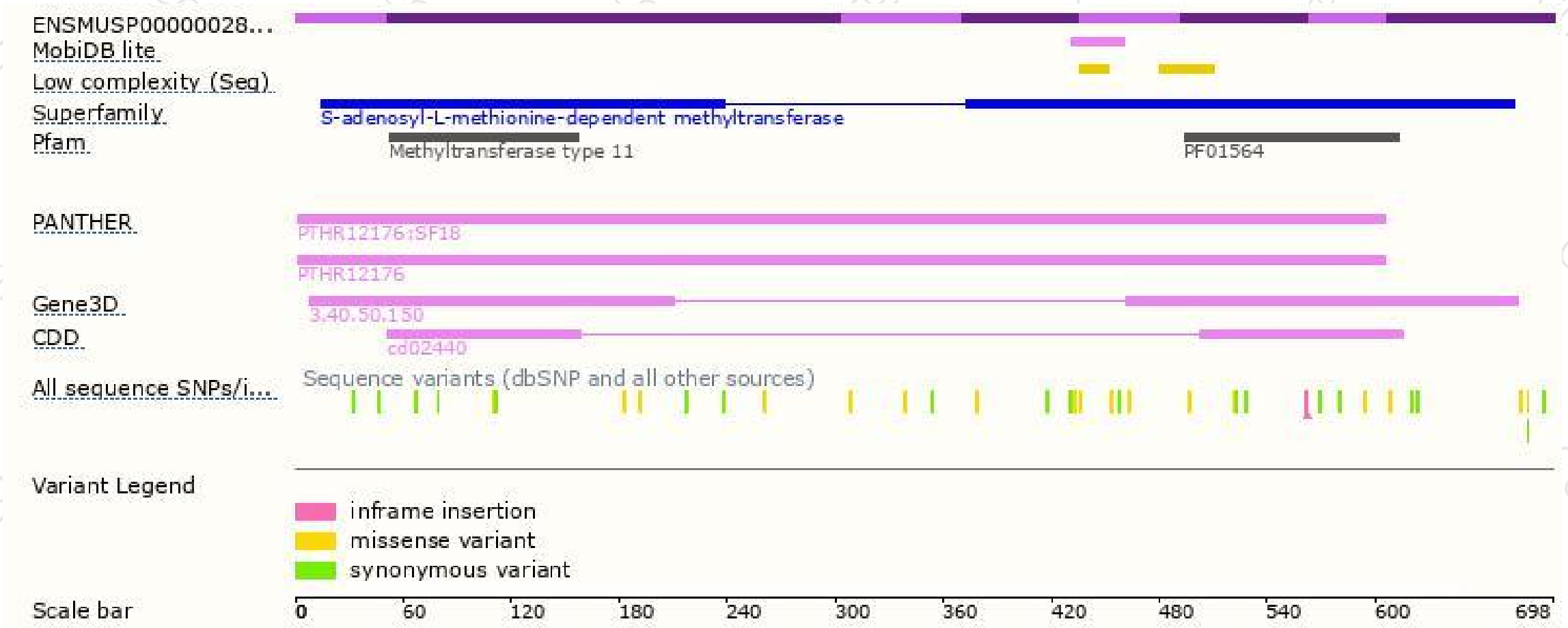
The strategy is based on the design of *Eef1aknmt-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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