



Eeflakmtl Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-5-6

Project Overview

Project Name

Eeflakmt1

Project type

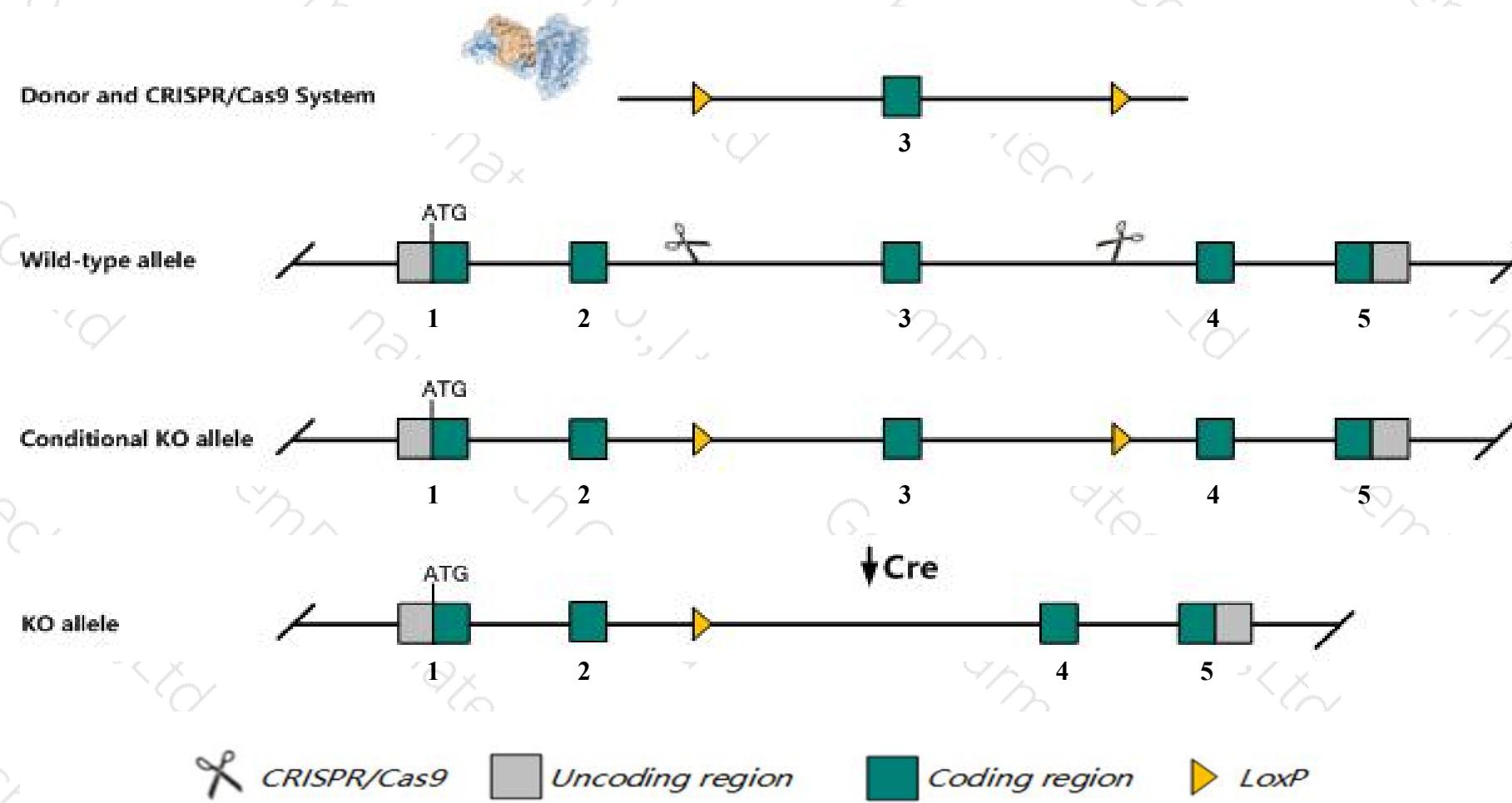
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eeflakmt1* gene. The schematic diagram is as follows:



Technical routes

- The *Eeflakmt1* gene has 3 transcripts. According to the structure of *Eeflakmt1* gene, exon3 of *Eeflakmt1-201* (ENSMUST00000022518.7) transcript is recommended as the knockout region. The region contains 83bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eeflakmt1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



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Notice

- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Eeflakmt1* gene is located on the Chr14. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



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Gene information (NCBI)

Eef1akmt1 EEF1A alpha lysine methyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 68043, updated on 13-Mar-2020

Summary



Official Symbol Eef1akmt1 provided by [MGI](#)

Official Full Name EEF1A alpha lysine methyltransferase 1 provided by [MGI](#)

Primary source [MGI:MGI:1915293](#)

See related [Ensembl:ENSMUSG00000021951](#)

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 2510005D08Rik, AW045965, Ayu21-96, Gt(pU21)96lmeg, GtAyu21-96, N6amt2

Expression Ubiquitous expression in CNS E18 (RPKM 13.2), placenta adult (RPKM 12.2) and 28 other tissues [See more](#)

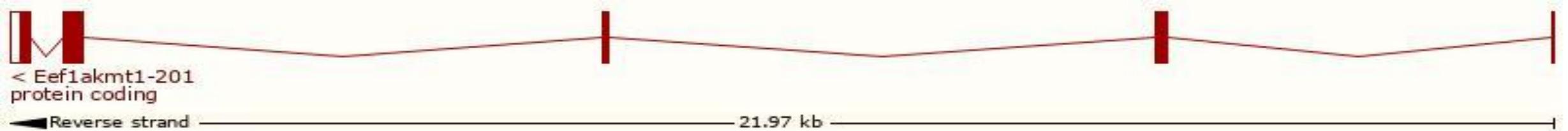
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

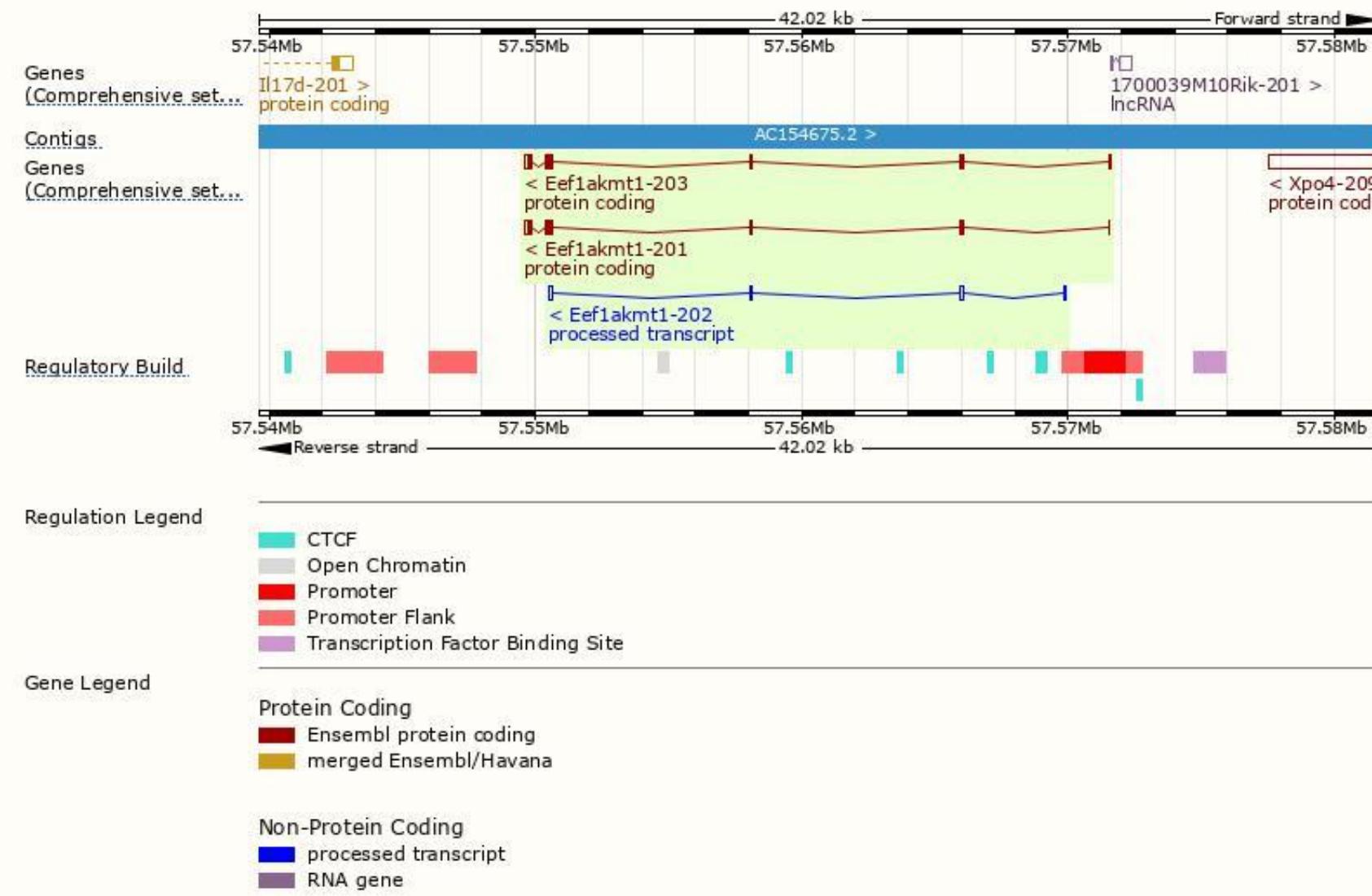
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eef1akmt1-201	ENSMUST0000022518.7	836	224aa	Protein coding	CCDS27157	A0A0D2X7Z2	TSL:1 GENCODE basic
Eef1akmt1-203	ENSMUST00000239099.1	880	214aa	Protein coding	-	Q9CY45	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Eef1akmt1-202	ENSMUST00000225504.1	457	No protein	Processed transcript	-	-	

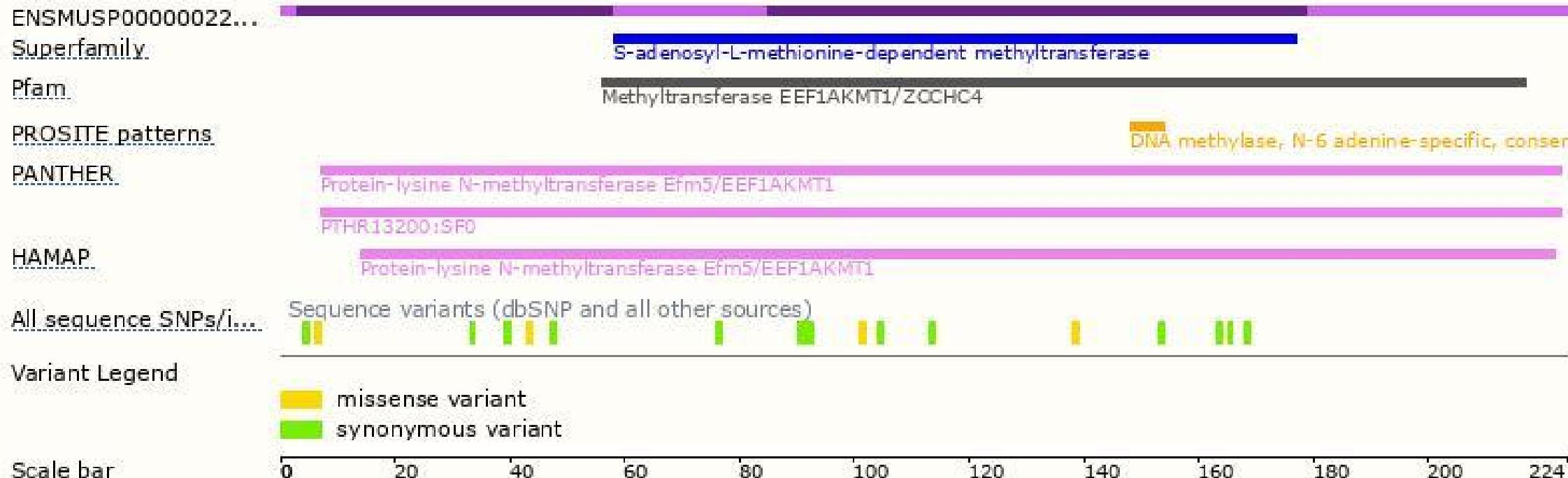
The strategy is based on the design of *Eef1akmt1-201* transcript, the transcription is shown below:



Genomic location distribution



Protein domain





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

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