

Eif3m Cas9-KO Strategy

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Project Overview

Project Name

Eif3m

Project type

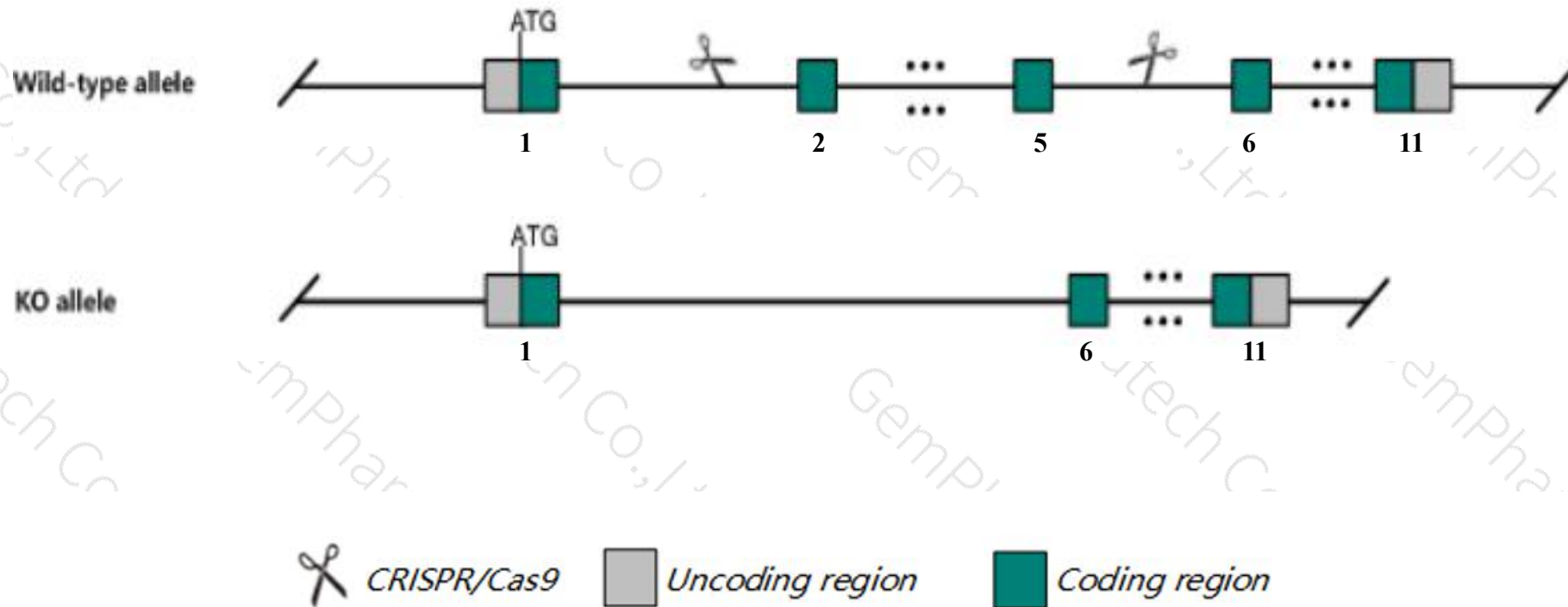
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif3m* gene. The schematic diagram is as follows:



- The *Eif3m* gene has 4 transcripts. According to the structure of *Eif3m* gene, exon2-exon5 of *Eif3m*-201(ENSMUST00000028592.11) transcript is recommended as the knockout region. The region contains 491bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif3m* gene. The brief process is as follows: CRISPR/Cas9 system 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 targeted allele exhibit embryonic lethality. Mice heterozygous for this allele exhibit decreased body weight and altered organ weights.
- The KO region contains intron of the *Ccdc73-204* gene. The effect of *Ccdc73-204* gene is unknown after knockout the region .
- Transcripts 203,204 may not be affected.
- The *Eif3m* gene is located on the Chr2. 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)

Eif3m eukaryotic translation initiation factor 3, subunit M [Mus musculus (house mouse)]

Gene ID: 98221, updated on 13-Mar-2020

Summary



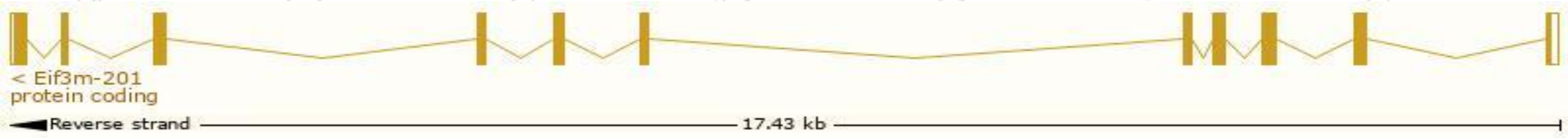
Official Symbol	Eif3m provided by MGI
Official Full Name	eukaryotic translation initiation factor 3, subunit M provided by MGI
Primary source	MGI:MGI:1351744
See related	Ensembl:ENSMUSG00000027170
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ga17, Pcid1, Tango7
Expression	Ubiquitous expression in CNS E11.5 (RPKM 56.9), placenta adult (RPKM 55.1) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

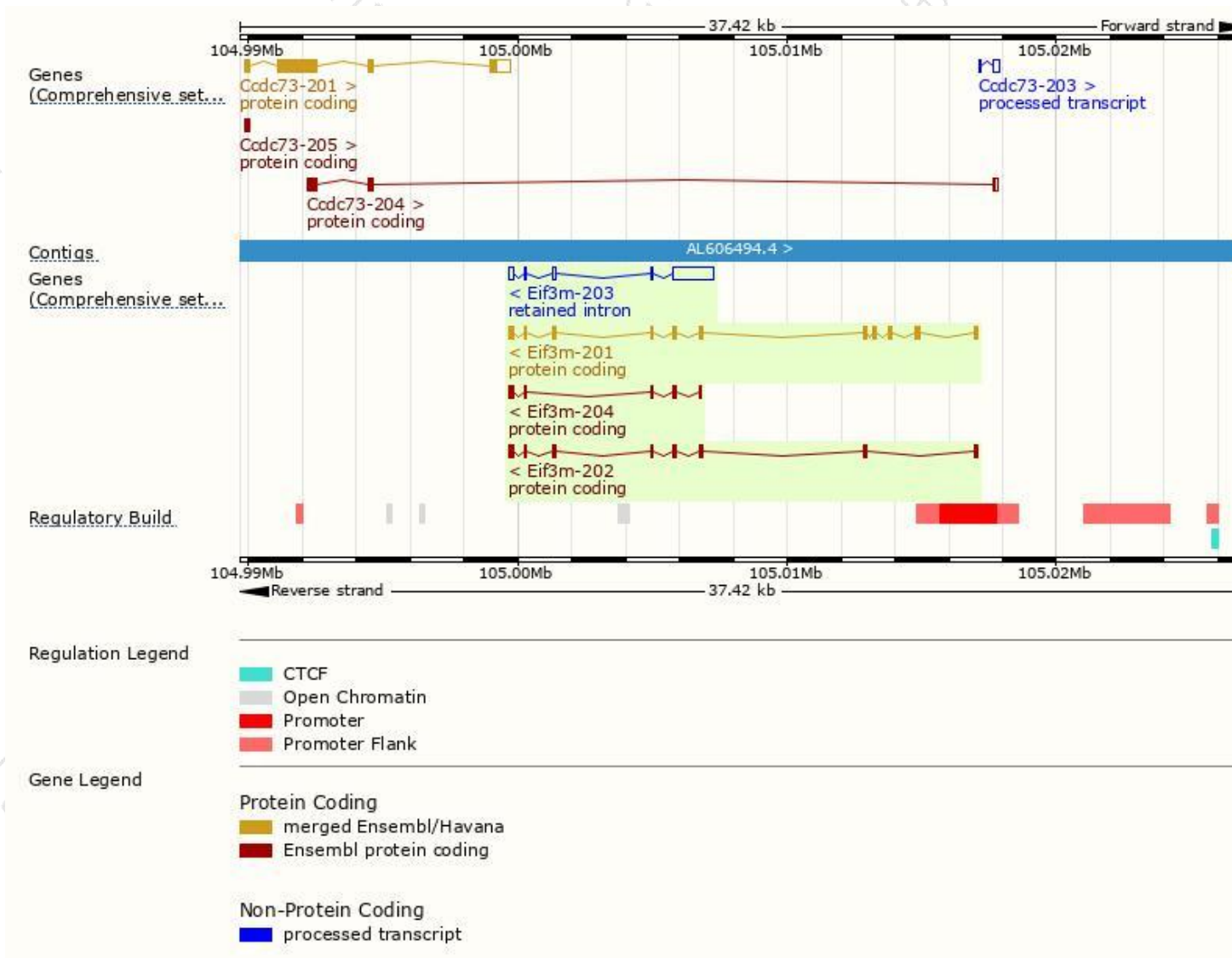
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif3m-201	ENSMUST00000028592.11	1283	374aa	Protein coding	CCDS16495	Q99JX4	TSL:1 GENCODE basic APPRIS P1
Eif3m-202	ENSMUST00000111110.2	817	242aa	Protein coding	-	A2A702	TSL:5 GENCODE basic
Eif3m-204	ENSMUST00000148476.7	494	143aa	Protein coding	-	A2A701	CDS 5' incomplete TSL:3
Eif3m-203	ENSMUST00000131266.1	1964	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Eif3m-201* transcript,the transcription is shown below:



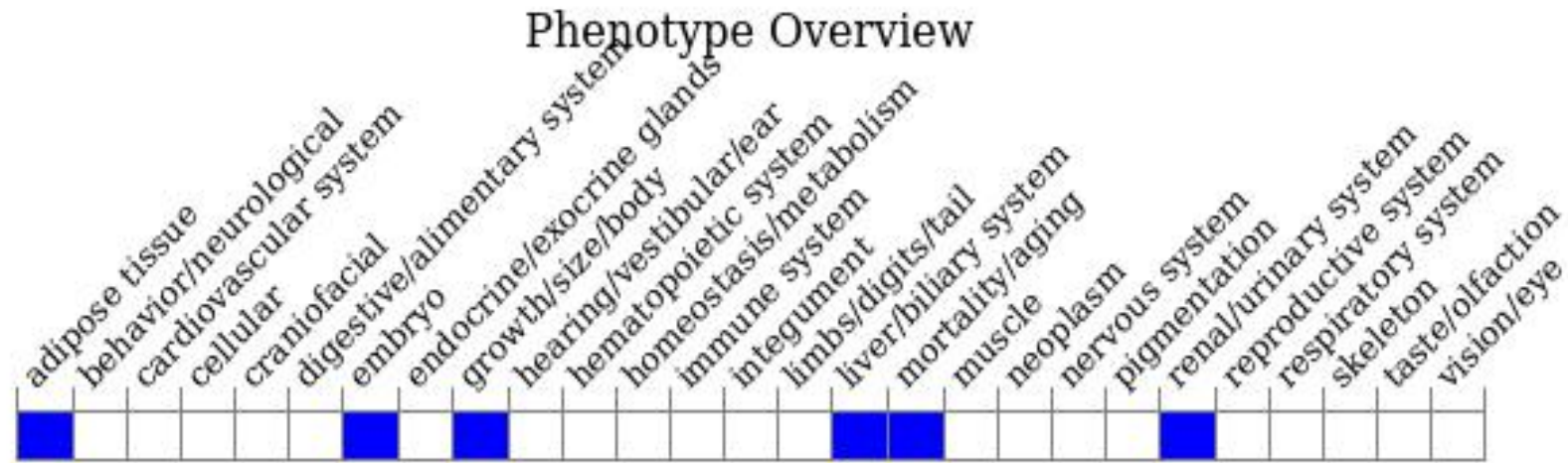
Genomic location distribution



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, mice homozygous for a targeted allele exhibit embryonic lethality. Mice heterozygous for this allele exhibit decreased body weight and altered organ weights.

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

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