

Eif2a Cas9-KO Strategy

Designer:

Ruirui Zhang

Reviewer:

Huimin Su

Design Date:

2019-9-21

Project Overview

Project Name

Eif2a

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif2a* gene. The schematic diagram is as follows:



- The *Eif2a* gene has 7 transcripts. According to the structure of *Eif2a* gene, exon2 of *Eif2a-201* (ENSMUST00000029387.14) transcript is recommended as the knockout region. The region contains 70bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif2a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele are viable and fertile with no visible phenotypes.
- The *Eif2a* gene is located on the Chr3. 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)

Eif2a eukaryotic translation initiation factor 2A [*Mus musculus* (house mouse)]

Gene ID: 229317, updated on 12-Aug-2019

Summary

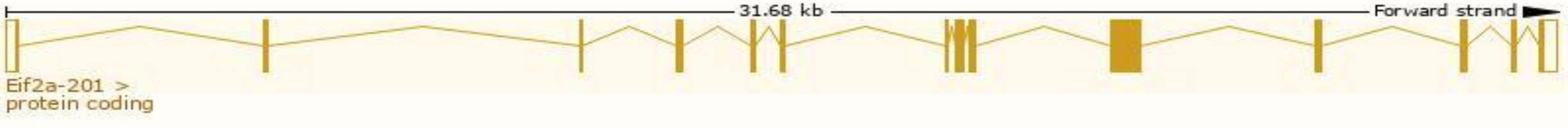
Official Symbol	Eif2a provided by MGI
Official Full Name	eukaryotic translation initiation factor 2A provided by MGI
Primary source	MGI:MGI:1098684
See related	Ensembl:ENSMUSG00000027810
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D030048D22; D3Ert194e
Expression	Broad expression in adrenal adult (RPKM 100.7), duodenum adult (RPKM 76.7) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

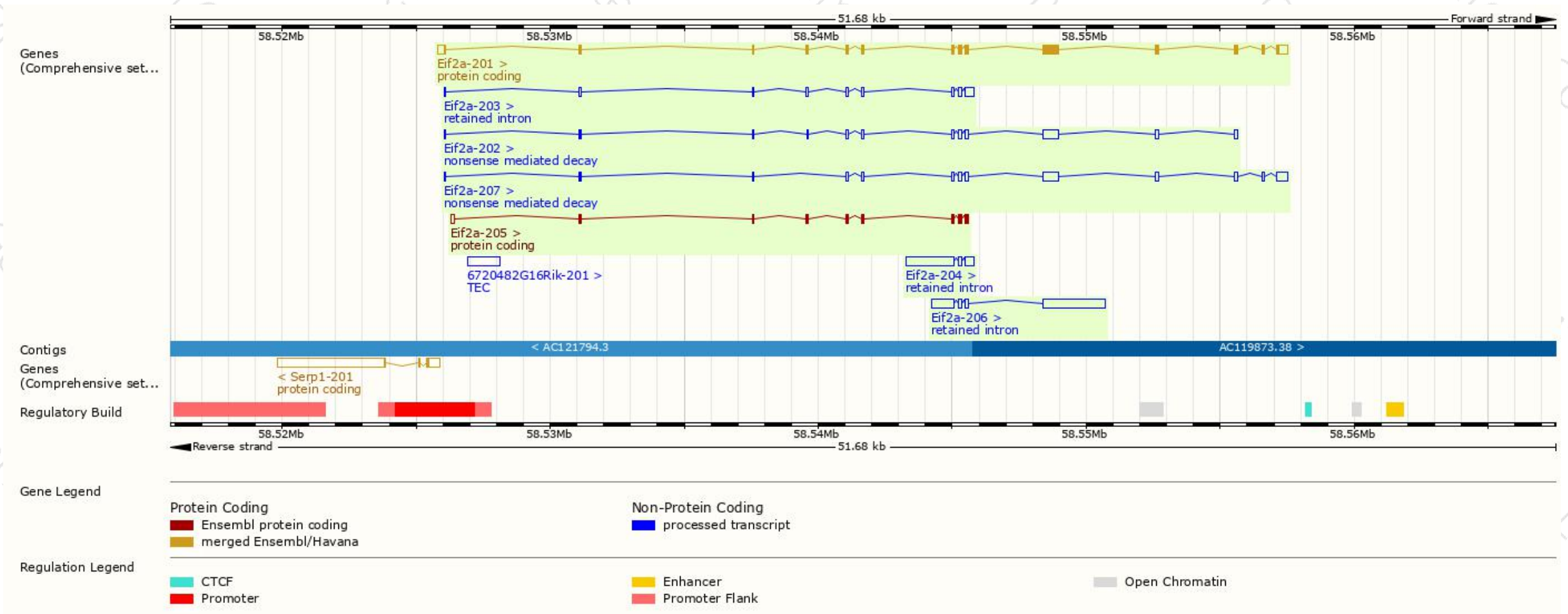
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif2a-201	ENSMUST00000029387.14	2299	581aa	Protein coding	CCDS17367	Q8BJW6	TSL:1 GENCODE basic APPRIS P1
Eif2a-205	ENSMUST00000138848.1	913	251aa	Protein coding	-	D3YZZ6	CDS 3' incomplete TSL:5
Eif2a-207	ENSMUST00000154219.7	1945	59aa	Nonsense mediated decay	-	D6RFN2	TSL:5
Eif2a-202	ENSMUST00000135876.7	1561	60aa	Nonsense mediated decay	-	D6RGA6	TSL:1
Eif2a-206	ENSMUST00000148251.1	3432	No protein	Retained intron	-	-	TSL:1
Eif2a-204	ENSMUST00000138827.7	2258	No protein	Retained intron	-	-	TSL:1
Eif2a-203	ENSMUST00000137469.7	1035	No protein	Retained intron	-	-	TSL:1

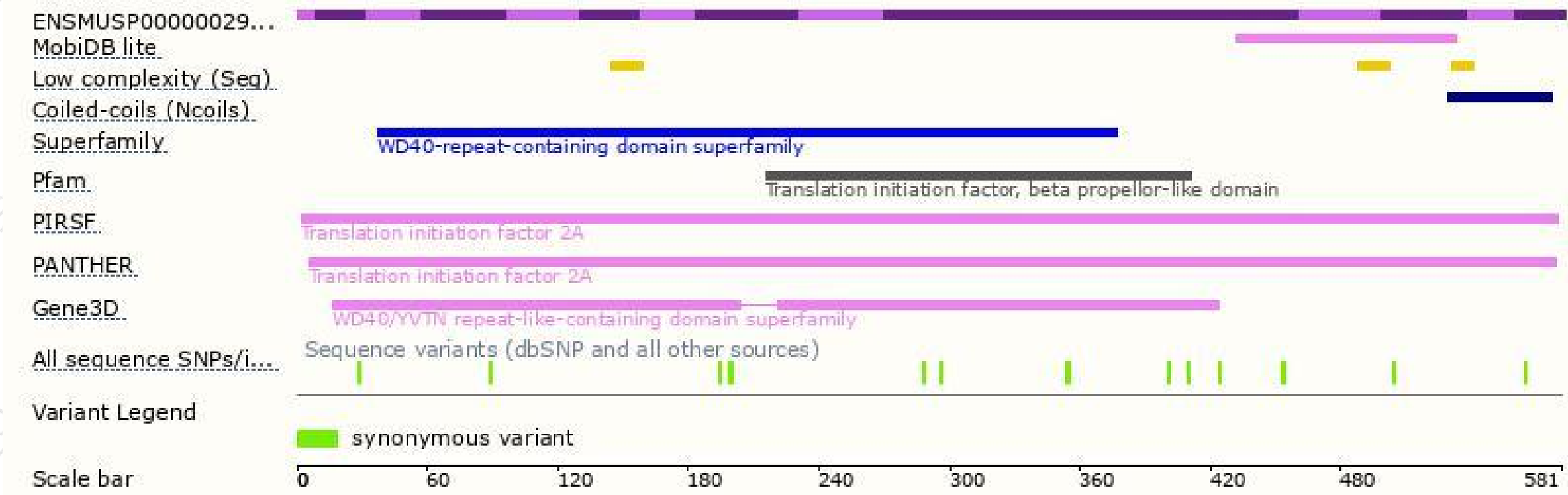
The strategy is based on the design of *Eif2a-201* transcript,The transcription is shown below



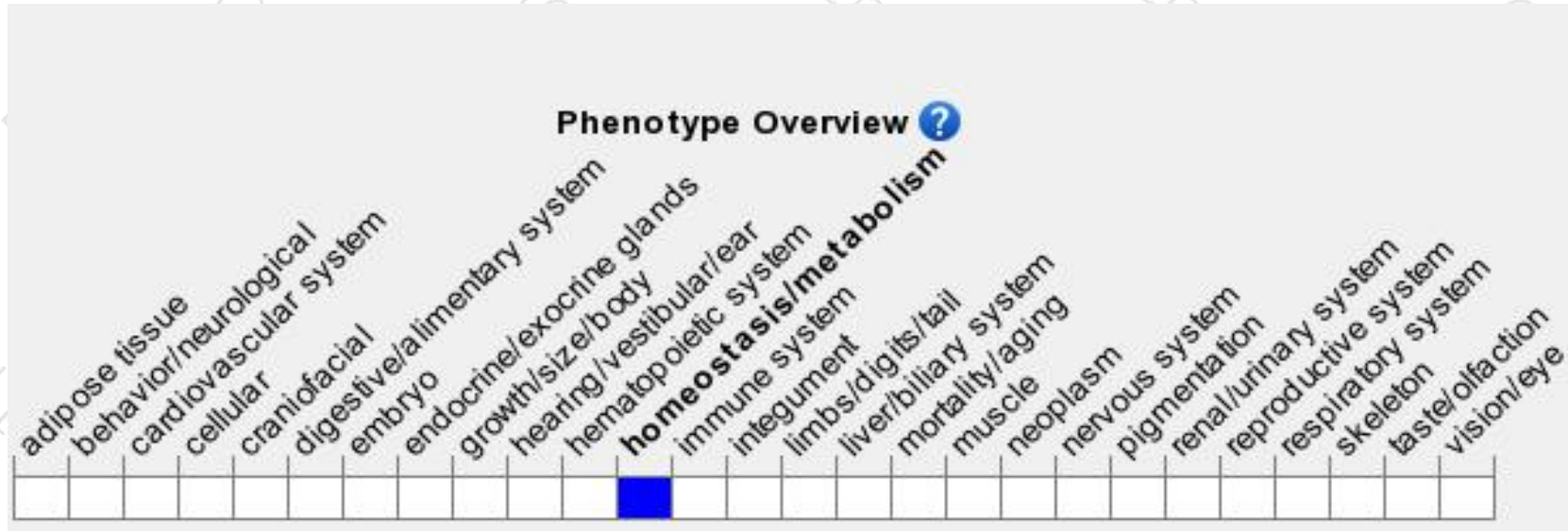
Genomic location distribution



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 null allele are viable and fertile with no visible phenotypes.

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

Tel: 400-9660890

