

Eif3i Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-3-12

Project Overview

Project Name

Eif3i

Project type

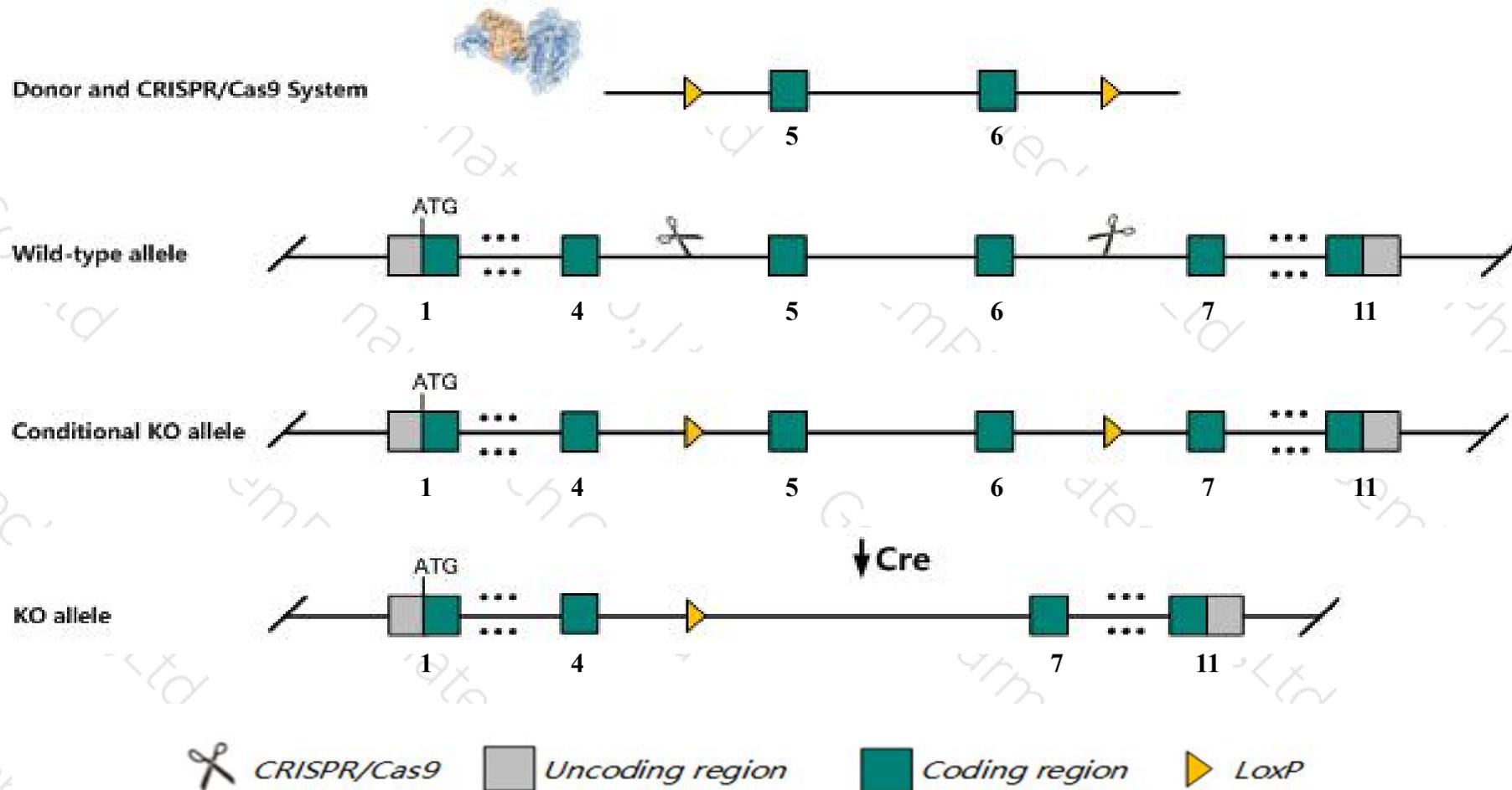
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif3i* gene. The schematic diagram is as follows:



- The *Eif3i* gene has 5 transcripts. According to the structure of *Eif3i* gene, exon5-exon6 of *Eif3i-201* (ENSMUST00000102593.10) transcript is recommended as the knockout region. The region contains 278bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif3i* 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.

Notice

- The *Eif3i* gene is located on the Chr4. 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.

Gene information (NCBI)

Eif3i eukaryotic translation initiation factor 3, subunit I [*Mus musculus* (house mouse)]

Gene ID: 54709, updated on 12-Aug-2019

Summary

Official Symbol Eif3i provided by [MGI](#)
Official Full Name eukaryotic translation initiation factor 3, subunit I provided by [MGI](#)
Primary source [MGI:1860763](#)
See related [Ensembl:ENSMUSG00000028798](#)
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 36kDa; Trip1; Eif3s2; D4Ert632e
Expression Ubiquitous expression in genital fat pad adult (RPKM 152.6), liver E14.5 (RPKM 125.2) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

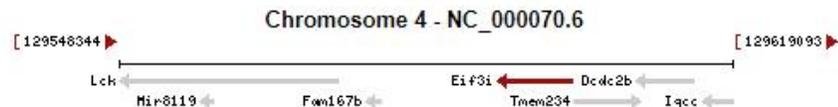
Genomic context

Location: 4 D2.2; 4 63.26 cM

[See Eif3i in Genome Data Viewer](#)

Exon count: 11

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (129591974..129600648, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (129269218..129277892, complement)

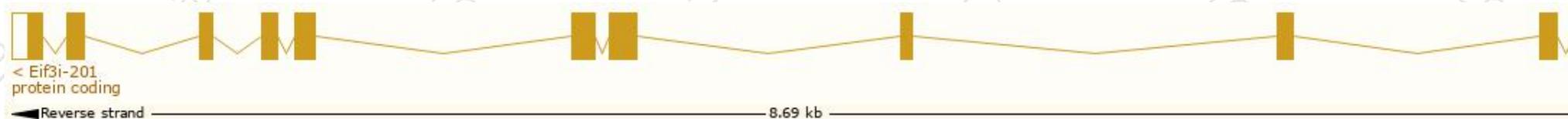


Transcript information (Ensembl)

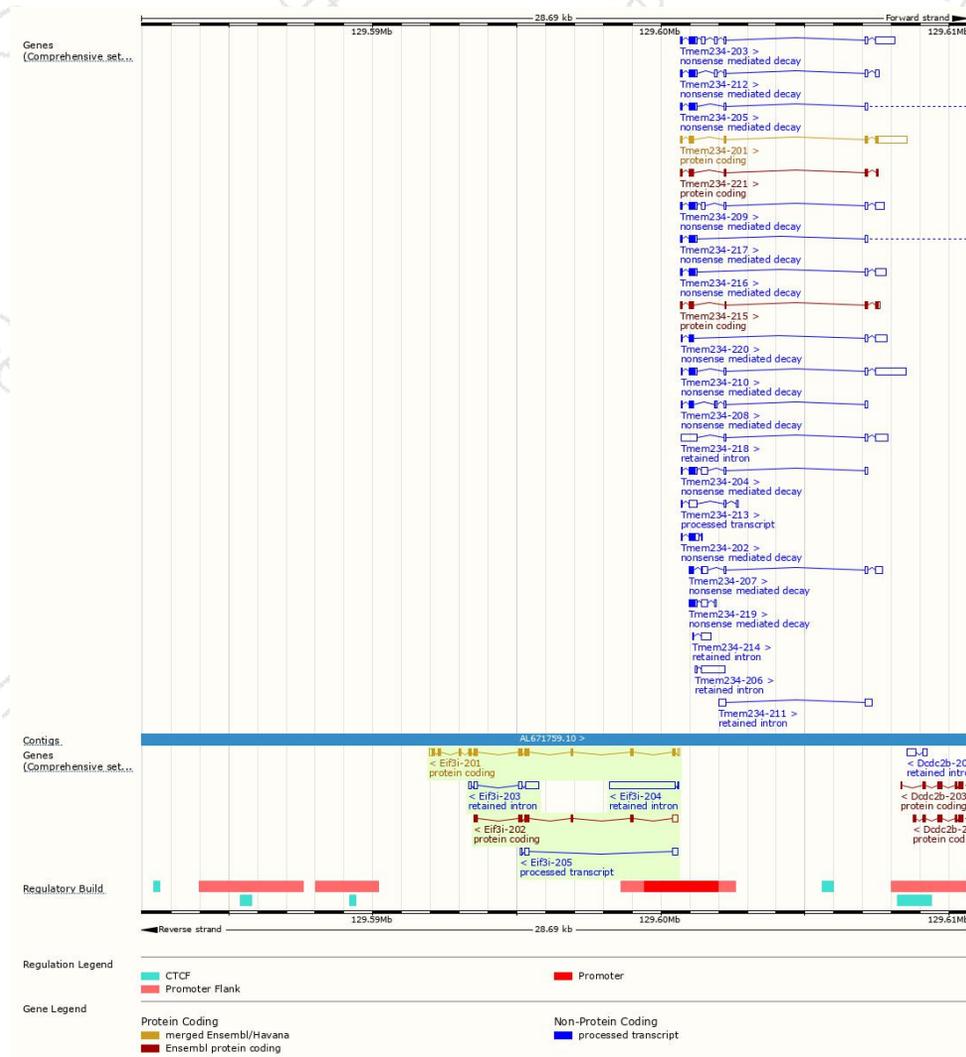
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif3i-201	ENSMUST00000102593.10	1123	325aa	Protein coding	CCDS18698	Q9QZD9	TSL:1 Gencode basic APPRIS P1
Eif3i-202	ENSMUST00000135055.7	734	165aa	Protein coding	-	A2AE03	CDS 3' incomplete TSL:2
Eif3i-205	ENSMUST00000155428.1	401	No protein	Processed transcript	-	-	TSL:3
Eif3i-204	ENSMUST00000143384.1	2323	No protein	Retained intron	-	-	TSL:1
Eif3i-203	ENSMUST00000136843.1	797	No protein	Retained intron	-	-	TSL:3

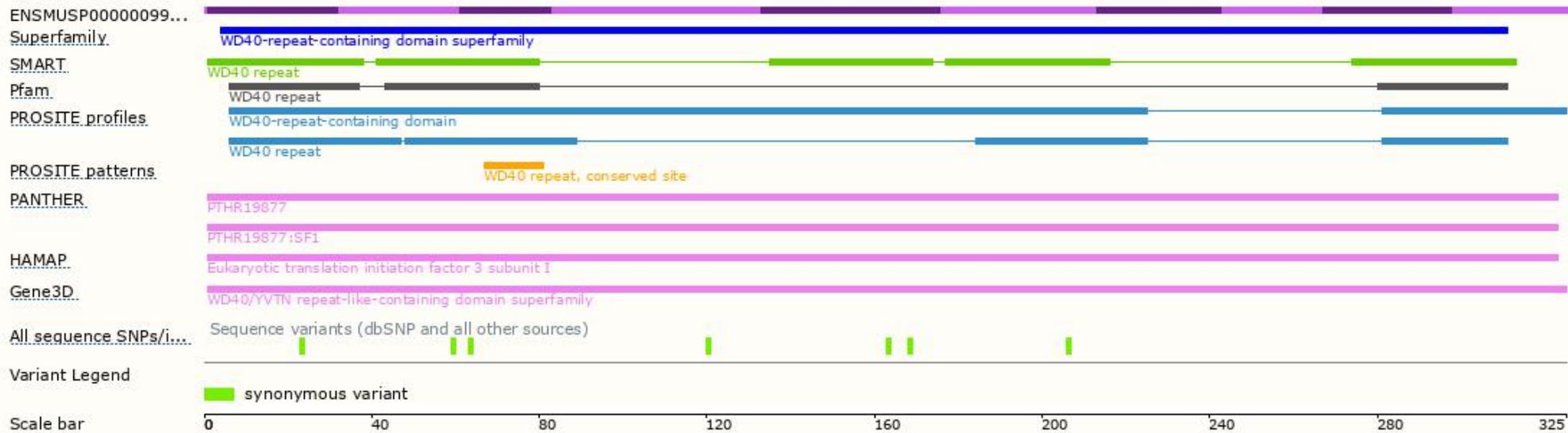
The strategy is based on the design of *Eif3i-201* transcript, the transcription is shown below



Genomic location distribution



Protein domain



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

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