

Eif4g2 Cas9-CKO Strategy

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Project Overview

Project Name

Eif4g2

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif4g2* gene. The schematic diagram is as follows:

- The *Eif4g2* gene has 14 transcripts. According to the structure of *Eif4g2* gene, exon2-21 of *Eif4g2*-213 (ENSMUST00000162415.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif4g2* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 or cell types.

- According to the existing MGI data Mice homozygous for a targeted null mutation fail to undergo gastrulation and die by E11.5.
- The *Eif4g2* gene is located on the Chr7. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Eif4g2 eukaryotic translation initiation factor 4, gamma 2 [*Mus musculus* (house mouse)]

Gene ID: 13690, updated on 2-Jul-2019

Summary

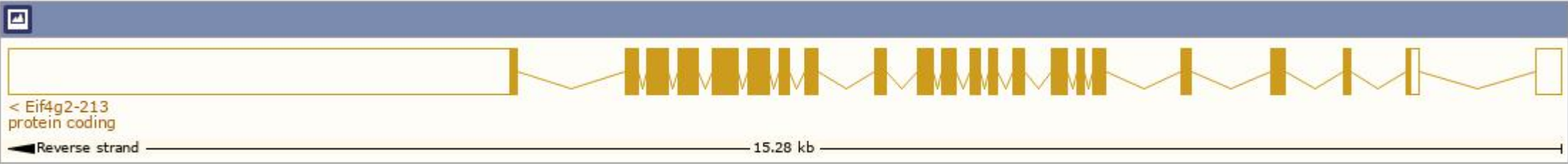
Official Symbol	Eif4g2 provided by MGI
Official Full Name	eukaryotic translation initiation factor 4, gamma 2 provided by MGI
Primary source	MGI:MGI:109207
See related	Ensembl:ENSMUSG000000005610
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	p97; Nat1; DAP-5; Natm1; E130105L11Rik
Summary	Translation initiation is mediated by specific recognition of the cap structure by eukaryotic translation initiation factor 4F (eIF4F), which is a cap binding protein complex that consists of three subunits: eIF4A, eIF4E and eIF4G. The protein encoded by this gene shares similarity with the C-terminal region of eIF4G, that contains the binding sites for eIF4A and eIF3; eIF4G in addition, contains a binding site for eIF4E at the N-terminus. Unlike eIF4G which supports cap-dependent and independent translation, this gene product functions as a general repressor of translation by forming translationally inactive complexes. Transgene expression of the apolipoprotein B mRNA-editing enzyme (APOBEC-1) causes extensive editing of this mRNA, which could contribute to the potent oncogenesis induced by overexpression of APOBEC-1. In vitro and in vivo studies in human indicate that translation of this mRNA initiates exclusively at a non-AUG (GUG) codon. This also appears to be true for mouse. Two alternatively spliced transcript variants that encode different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 106.9), CNS E14 (RPKM 96.1) and 24 other tissues See more
Orthologs	human all

Transcript information Ensembl

The gene has 14 transcripts, and all transcripts are shown below:

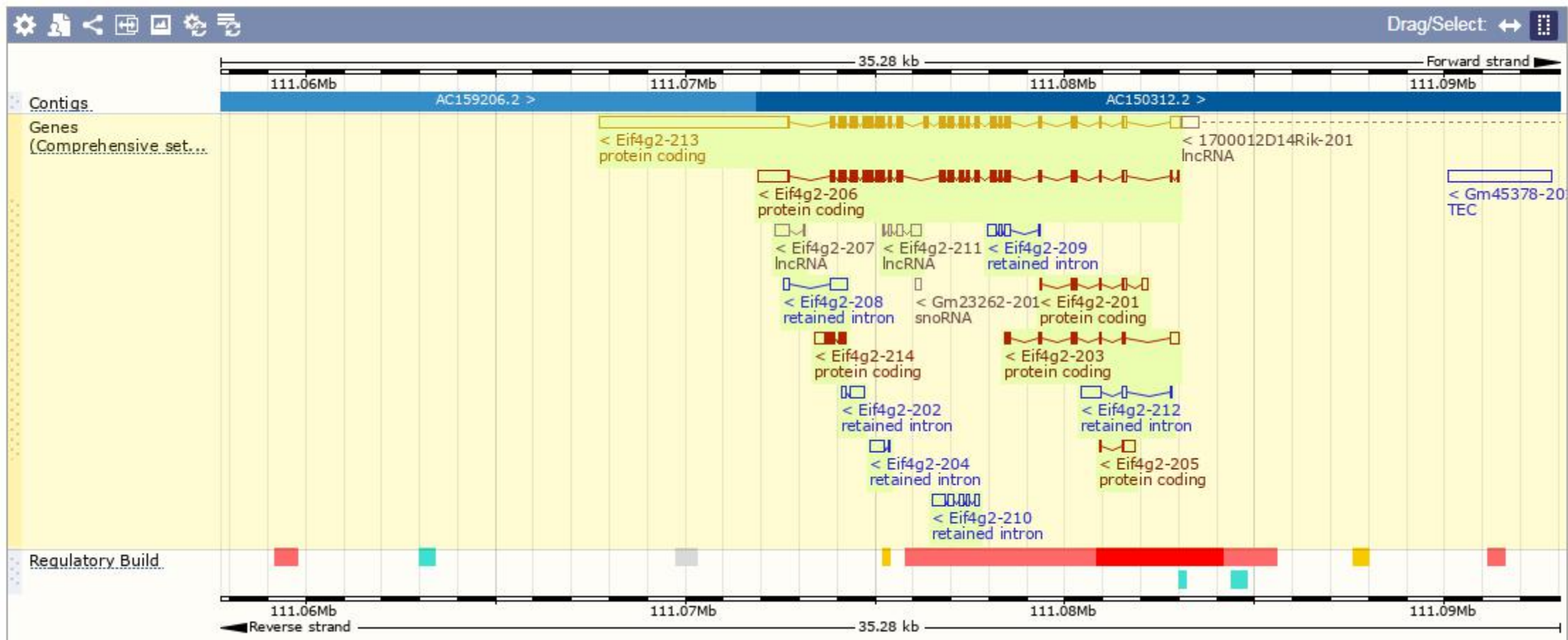
Show/hide columns (1 hidden)		Filter					
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif4g2-213	ENSMUST00000162415.8	7995	906aa	Protein coding	CCDS40088	G3XA17	TSL:1 GENCODE basic
Eif4g2-206	ENSMUST00000161051.7	3548	868aa	Protein coding	CCDS40087	F7CBP1	TSL:1 GENCODE basic
Eif4g2-214	ENSMUST00000163014.1	763	158aa	Protein coding	-	F6UU81	CDS 5' incomplete TSL:2
Eif4g2-203	ENSMUST00000160132.7	742	161aa	Protein coding	-	F6TW20	CDS 3' incomplete TSL:5 APPRIS P1
Eif4g2-201	ENSMUST00000159305.1	560	102aa	Protein coding	-	F7DAB1	CDS 3' incomplete TSL:3
Eif4g2-205	ENSMUST00000160966.1	395	29aa	Protein coding	-	F7CHS2	CDS 3' incomplete TSL:2
Eif4g2-210	ENSMUST00000161736.1	771	No protein	Retained intron	-	-	TSL:2
Eif4g2-212	ENSMUST00000162394.1	716	No protein	Retained intron	-	-	TSL:2
Eif4g2-208	ENSMUST00000161158.1	599	No protein	Retained intron	-	-	TSL:2
Eif4g2-209	ENSMUST00000161682.1	498	No protein	Retained intron	-	-	TSL:2
Eif4g2-202	ENSMUST00000159465.1	472	No protein	Retained intron	-	-	TSL:2
Eif4g2-204	ENSMUST00000160552.1	418	No protein	Retained intron	-	-	TSL:2
Eif4g2-211	ENSMUST00000161790.1	522	No protein	lncRNA	-	-	TSL:3
Eif4g2-207	ENSMUST00000161079.1	429	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Eif4g2-213* transcript, The transcription is shown below

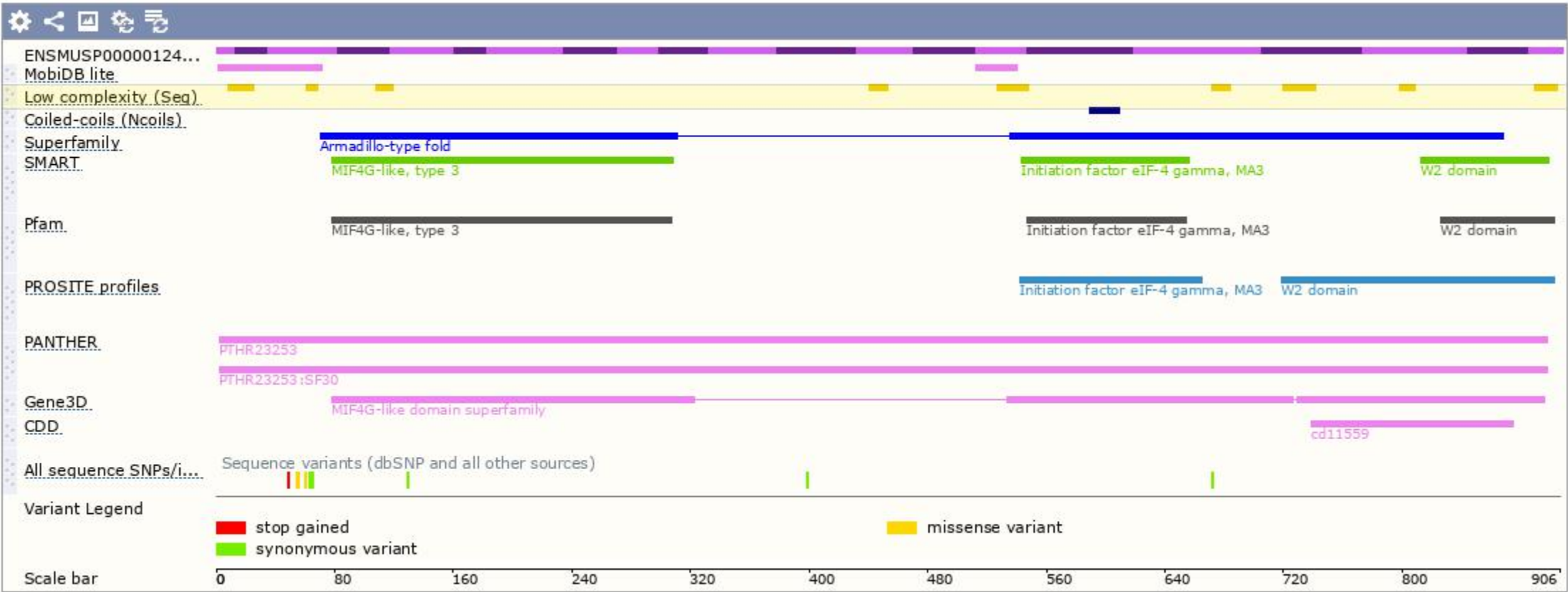


Statistics Exons: 22, Coding exons: 21, Transcript length: 7,995 bps, Translation length: 906 residues

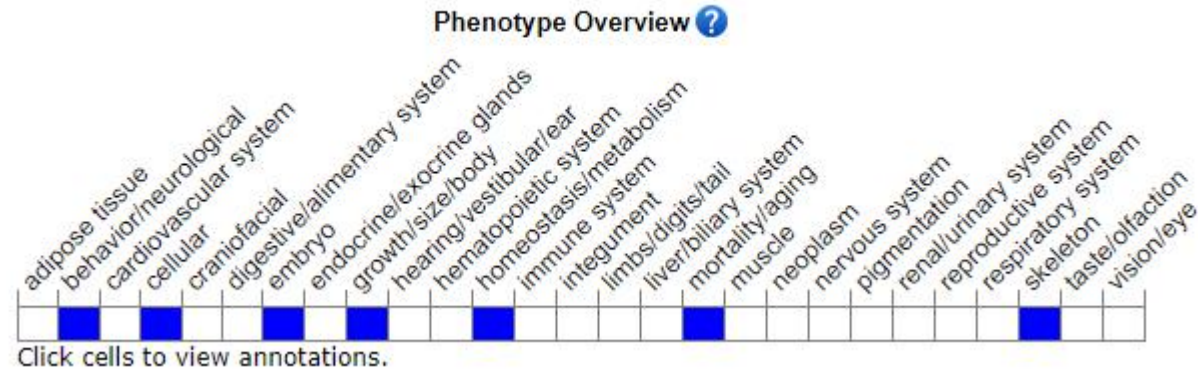
Genomic location distribution



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/>) .

Mice homozygous for a targeted null mutation fail to undergo gastrulation and die by E11.5.

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