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Eef2 Cas9-CKO Strategy

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Design Date: 2023-8-7

Overview

Target Gene Name

- Eef2

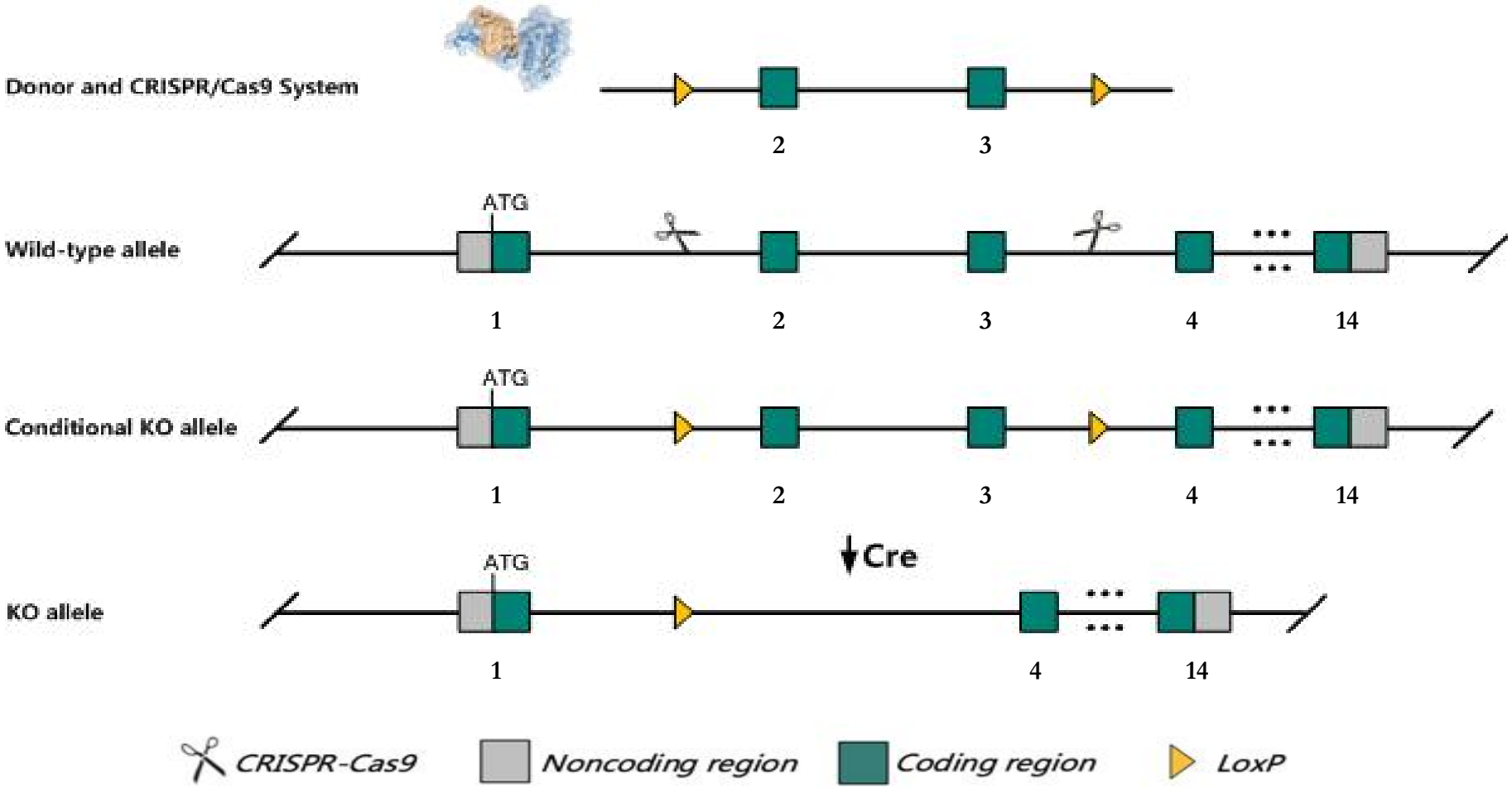
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Eef2* gene.

Technical Information

- The *Eef2* gene has 3 transcripts. According to the structure of *Eef2* gene, exon2-exon3 of *Eef2*-201 (ENSMUST00000047864.11) transcript is recommended as the knockout region. The region contains 397bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Eef2* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Eef2 eukaryotic translation elongation factor 2 [Mus musculus (house mouse)]

Gene ID: 13629, updated on 31-May-2023

Summary

Official Symbol	Eef2 provided by MGI
Official Full Name	eukaryotic translation elongation factor 2 provided by MGI
Primary source	MGI:MGI:95288
See related	Ensembl:ENSMUSG00000034994
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	Ef-2
Summary	Enables GTPase activity. Acts upstream of or within hematopoietic progenitor cell differentiation and translational elongation. Located in cytoplasm. Part of polysome. Is active in synapse. Is expressed in brain. Human ortholog(s) of this gene implicated in glaucoma and spinocerebellar ataxia type 26. Orthologous to human EEF2 (eukaryotic translation elongation factor 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in ovary adult (RPKM 1248.0), colon adult (RPKM 810.0) and 28 other tissues See more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

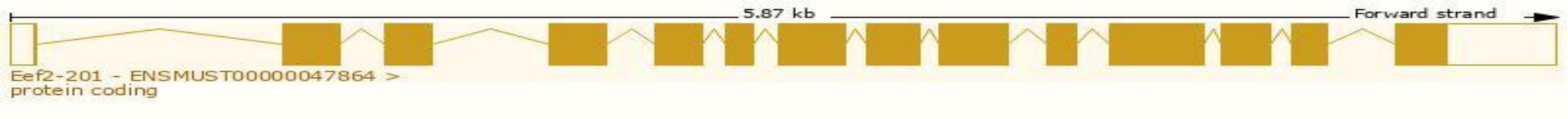
Transcript Information

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

Show/hide columns (1 hidden) Filter

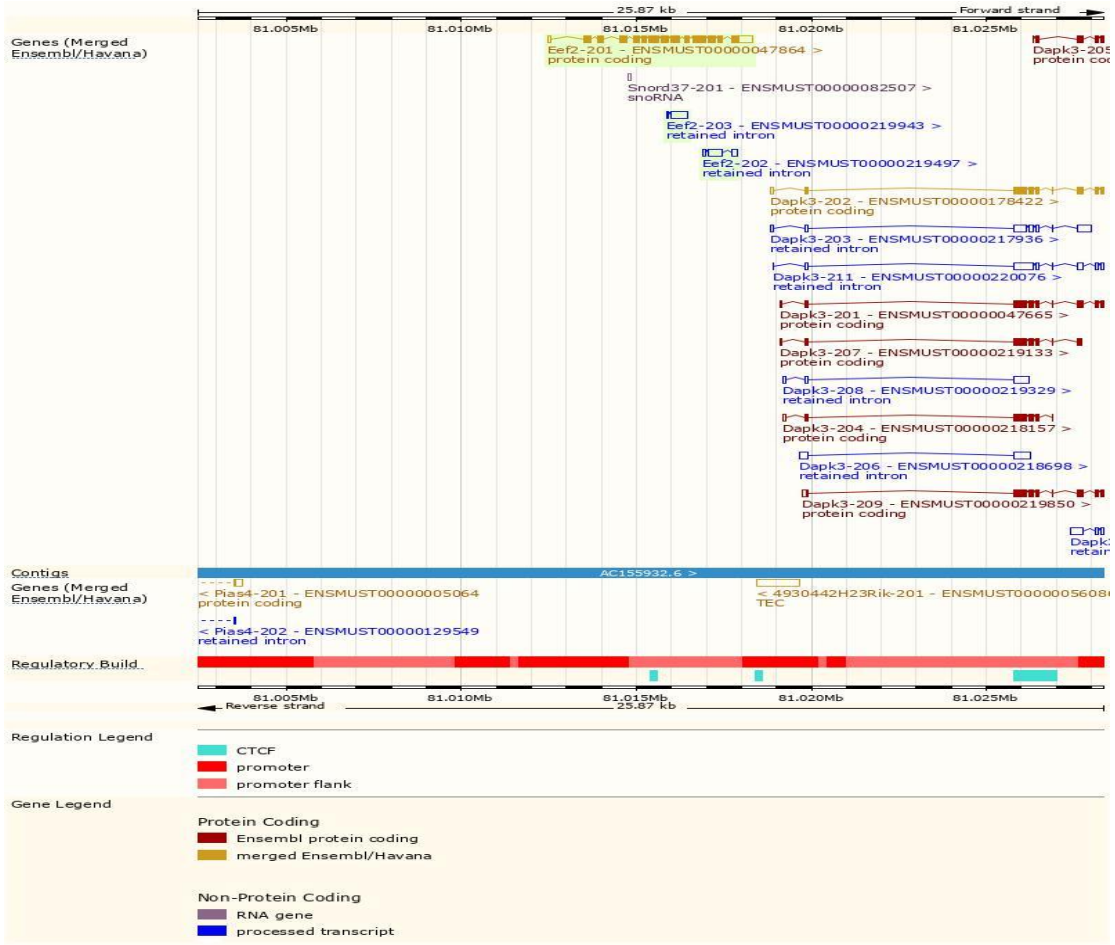
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000047864.11	Eef2-201	3089	858aa	Protein coding	CCDS35993	P58252	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000219497.2	Eef2-202	651	No protein	Retained intron		-	TSL:3
ENSMUST00000219943.2	Eef2-203	519	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Eef2*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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Source: : https://www.ensembl.org

Protein Information

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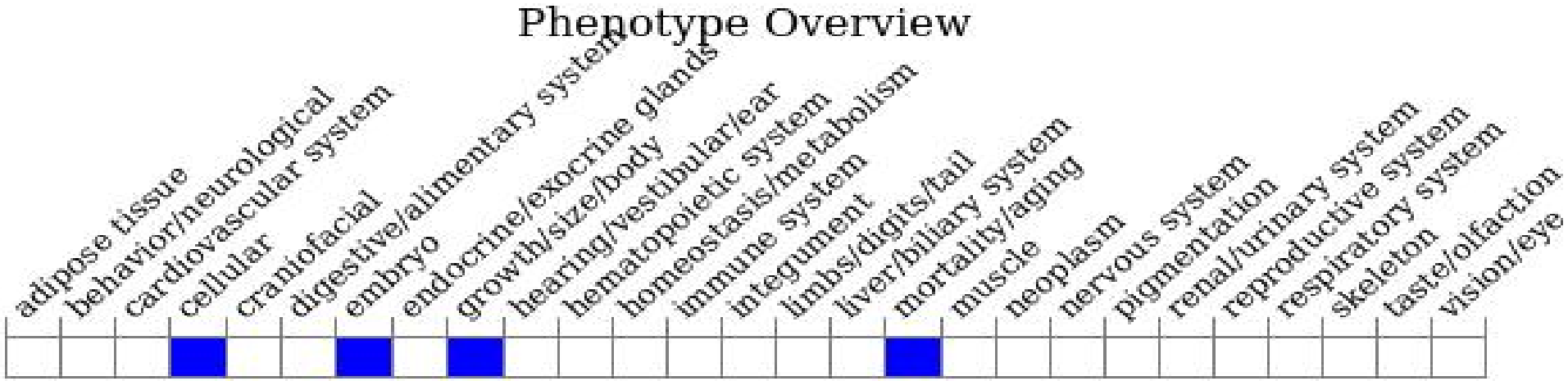
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Mice homozygous for a mutation removing the diphthamide modification display partial neonatal lethality, fetal growth retardation and abnormal cell physiology.

Source: https://www.informatics.jax.org

Important Information

- The effect of *Eef2*-202, *Eef2*-203 is unknown.
- This Strategy may effect the N-terminal regulation of *Snord37* and *Dapk3*.
- The loxp which insert in intron 3-4 may affects the splicing function.
- *Eef2* is located on Chr10. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.