

Eef2-T57M cas9-ki(PM) Mouse Model Strategy

-CRISPR/Cas9 technology

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Design Date: 2021-4-27

Project Overview

Project Name

Eef2-T57M

Project type

cas9-ki(PM)

Strain background

C57BL/6JGpt

A comparison of the aa homology of human and mouse *Eef2* gene

	57	60	70	80	90	100	110	120	130	140
Human EEF2-201 protein	57	TDTRKDEQERCITIKSTAISLFYELSENDLNFIKQSKDGAGFLINLIDSPGHVDFSSEVTAALRVTDGALVVVDCVSGVCVQTETVLR								
Mouse Eef2-201 protein	57	TDTRKDEQERCITIKSTAISLFYELSENDLNFIKQSKDGSGLINLIDSPGHVDFSSEVTAALRVTDGALVVVDCVSGVCVQTETVLR								
Consensus	57	TDTRKDEQERCITIKSTAISLFYELSENDLNFIKQSKDGAGFLINLIDSPGHVDFSSEVTAALRVTDGALVVVDCVSGVCVQTETVLR								
Ready consensus positions: 99.5% identity positions: 99.1% aln: 57										

The 57th amino acid(T) of human *EEF2* gene corresponds to the 57th amino acid(T) of mouse *Eef2* gene after comparing homology of mouse *Eef2* gene and human *EEF2* gene.

Technical Description

- The mouse *Eef2* gene has 3 transcripts. The human *EEF2* gene has 7 transcripts.
- According to the structure of *Eef2* gene and requirements of customer, the 57th amino acid(T) of human *EEF2*(NM_001961.4) gene corresponds to the 57th amino acid(T) of mouse *Eef2* gene after comparing homology of mouse *Eef2* gene and human *EEF2* gene. This project produced *Eef2*-T57A point mutation on exon2 of the transcript of *Eef2*-201(ENSMUST00000047864.11, NM_007907.2). The 57th amino acids will be mutated from T to M, and the corresponding codon will be mutated to ATG by the ACT.
- The mouse *Eef2*-201 transcript contains 14 exons. The translation initiation site ATG is located at exon1, and the translation termination site TAG is located at exon14, encoding 858aa.
- In this project, *Eef2* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, sgRNA and donor vectors were constructed. Cas9, sgRNA and donor were injected into the fertilized eggs of C57BL/6JGpt mice for homologous recombination, and obtained positive F0 mice identified by PCR and sequencing analysis. The stable inheritable positive F1 mice model was obtained by mating F0 mice with C57BL/6JGpt mice.

Mutation Site

Before mutation

+2	V N F T V D Q I R A I M D K K A N I R N M S																					
3001	AGAATCAGCC	TGGCTGCCCA	TCCCCCACC	ACAGGTGAAC	TTCACAGTAG	ATCAGATCCG	TGCCATCATG	GACAAGAAAG	CCAACATCCG	GAACATGTCA	TCTTAGTCGG	ACCGACGGGT	AGGGGGGTGG	TGTCCACTTG	AAGTGTCA TC	TAGTCTAGGC	ACGGTAGTAC	CTGTTCTTTC	GGTTGTAGGC	CTTGACAGT		
+2	V I A H V D H G K S T L T D S L V C K A G I I A S A R A G E T R F T																					
3101	GTCATCGCCC	ATGTGGACCA	CGGCAAGTCC	ACGCTGACCG	ACTCCCTTGT	GTGCAAGGCT	GGCATCATTG	CCTCTGCCCG	AGCTGGGGAG	ACGCGCTTCA	CAGTAGCGGG	TACACCTGGT	GCCGTTTCAAG	TGCGACTGGC	TGAGGGAACA	CACGTTCCGA	CCGTAGTAAC	GGAGACGGGC	TCGACCCCTC	TGCGCGAAGT		
+2	? T D T R K D E Q E R C I T I K S																					
3201	CTGACACTCG	CAAGGATGAG	CAGGAGCGCT	GCATCACAAT	CAAATCCACG	TGAGTGAGGG	GACAGCCCCG	AGGGGTTGTG	CTCTGGGTGT	CACTCGGGTG	GACTGTGAGC	GTTTCTACTC	GTCCTCGCGA	CGTAGTGTTA	GTTTAGGTGC	ACTCACTCCC	CTGTCGGGGC	TCCCCAACAC	GAGACCCACA	GTGAGCCCAC		

After mutation

+2							V	N	F	T	V	D	Q	I	R	A	I	M	D	K	K	A	N	I	R	N	M	S							
3001	AGAATCAGCC	TGGCTGCCCA	TCCCCCACC	ACAGGTGAAC	TTCACAGTAG	ATCAGATCCG	TGCCATCATG	GACAAGAAAG	CCAACATCCG	GAACATGTCA	TCTTAGTCGG	ACCGACGGGT	AGGGGGGTGG	TGTCCACTTG	AAGTGTCTATC	TAGTCTAGGC	ACGGTAGTAC	CTGTTCTTTC	GGTTGTAGGC	CTTGACAGT															
+2	V	I	A	H	V	D	H	G	K	S	T	L	T	D	S	L	V	C	K	A	G	I	I	A	S	A	R	A	G	E	T	R	F	M	?
3101	GTCATCGCCC	ATGTGGACCA	CGGCAAGTCC	ACGCTGACCG	ACTCCCTTGT	GTGCAAGGCT	GGCATCATTG	CCTCTGCCCG	AGCTGGGGAG	ACGCGCTTCA	CAGTAGCGGG	TACACCTGGT	GCCGTTTCAAG	TGCGACTGGC	TGAGGGAACA	CACGTTCCGA	CCGTAGTAAC	GGAGACGGGC	TCGACCCCTC	TGCGCGAAGT															
+2	?M	D	T	R	K	D	E	Q	E	R	C	I	T	I	K	S																			
3201	TG	GACACTCG	CAAGGATGAG	CAGGAGCGCT	GCATCACAAT	CAAATCCACG	TGAGTGAGGG	GACAGCCCCG	AGGGGTTGTG	CTCTGGGTGT	CACTCGGGTG	AC	CTGTGAGC	GTTTCTACTC	GTCCTCGCGA	CGTAGTGTTA	GTTTAGGTGC	ACTCACTCCC	CTGTCGGGGC	TCCCCAACAC	GAGACCCACA	GTGAGCCCAC													

The yellow region is exon2 of *Eef2-201*, the red region represents the mutation site.

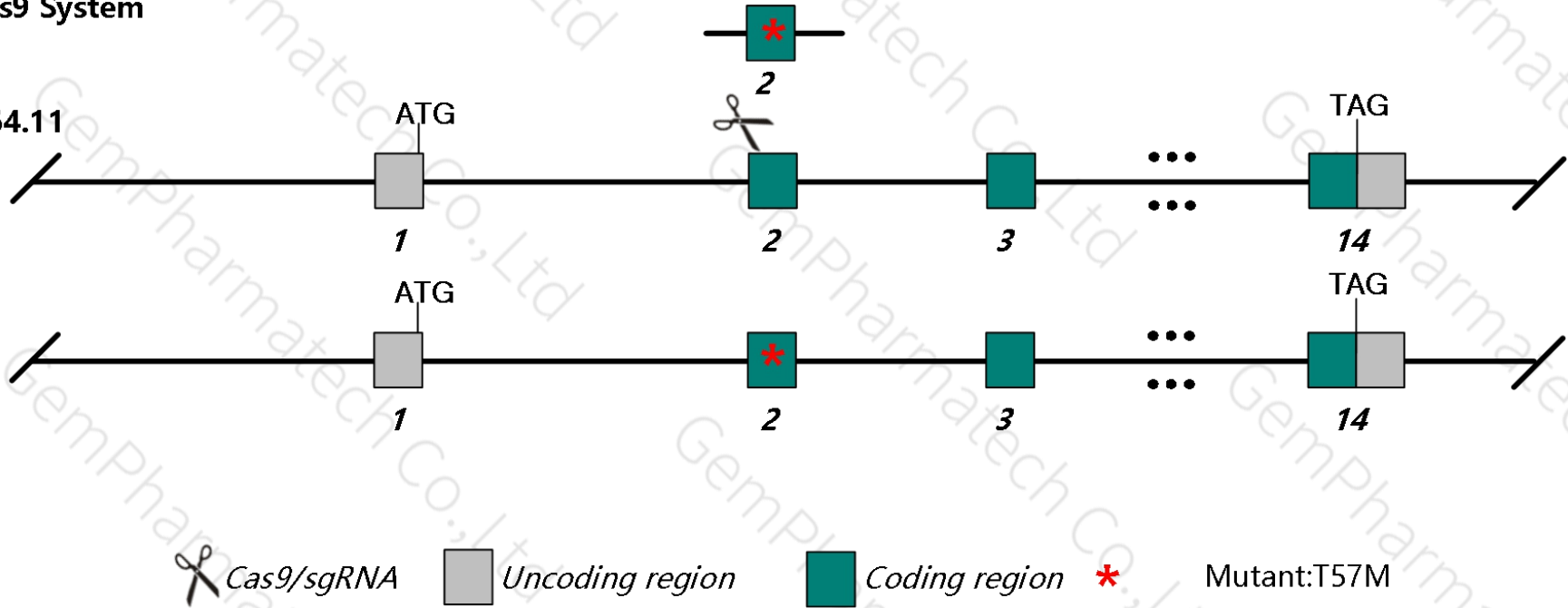
This model uses CRISPR/Cas9 technology to edit the *Eef2* gene and the schematic diagram is as follow:

Donor and CRISPR/Cas9 System

ENSMUST00000047864.11

Wild-type allele

Targeted allele



- According to the data of MGI, mice homozygous for a mutation removing the diphthamide modification display partial neonatal lethality, fetal growth retardation and abnormal cell physiology. Most of the homozygous mice with *Eef2*-G717R point mutation died shortly after birth.
- One or Two synonymous mutations of amino acids will be introduced on exon2 of *Eef2*.
- The mutation site is about 5.2kb away from the 5-terminal of *Dapk3* gene, which may affect its 5-terminal regulation.
- Mouse *Eef2* gene is located on Chr10. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr10, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

Gene name and location (NCBI)

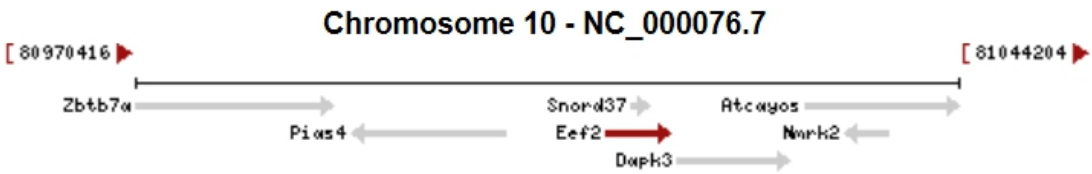
Eef2 eukaryotic translation elongation factor 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 13629, updated on 3-Jan-2021

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
Expression	Ubiquitous expression in ovary adult (RPKM 1248.0), colon adult (RPKM 810.0) and 28 other tissues See more
Orthologs	human all

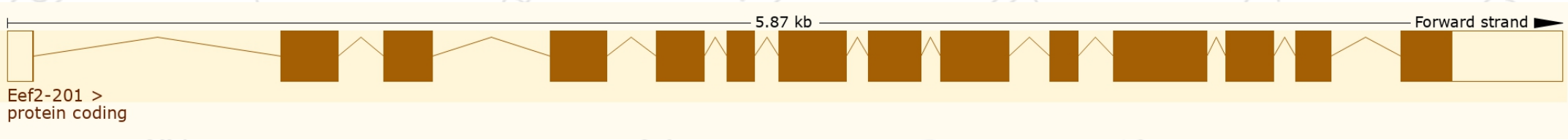


Transcript information (Ensembl)

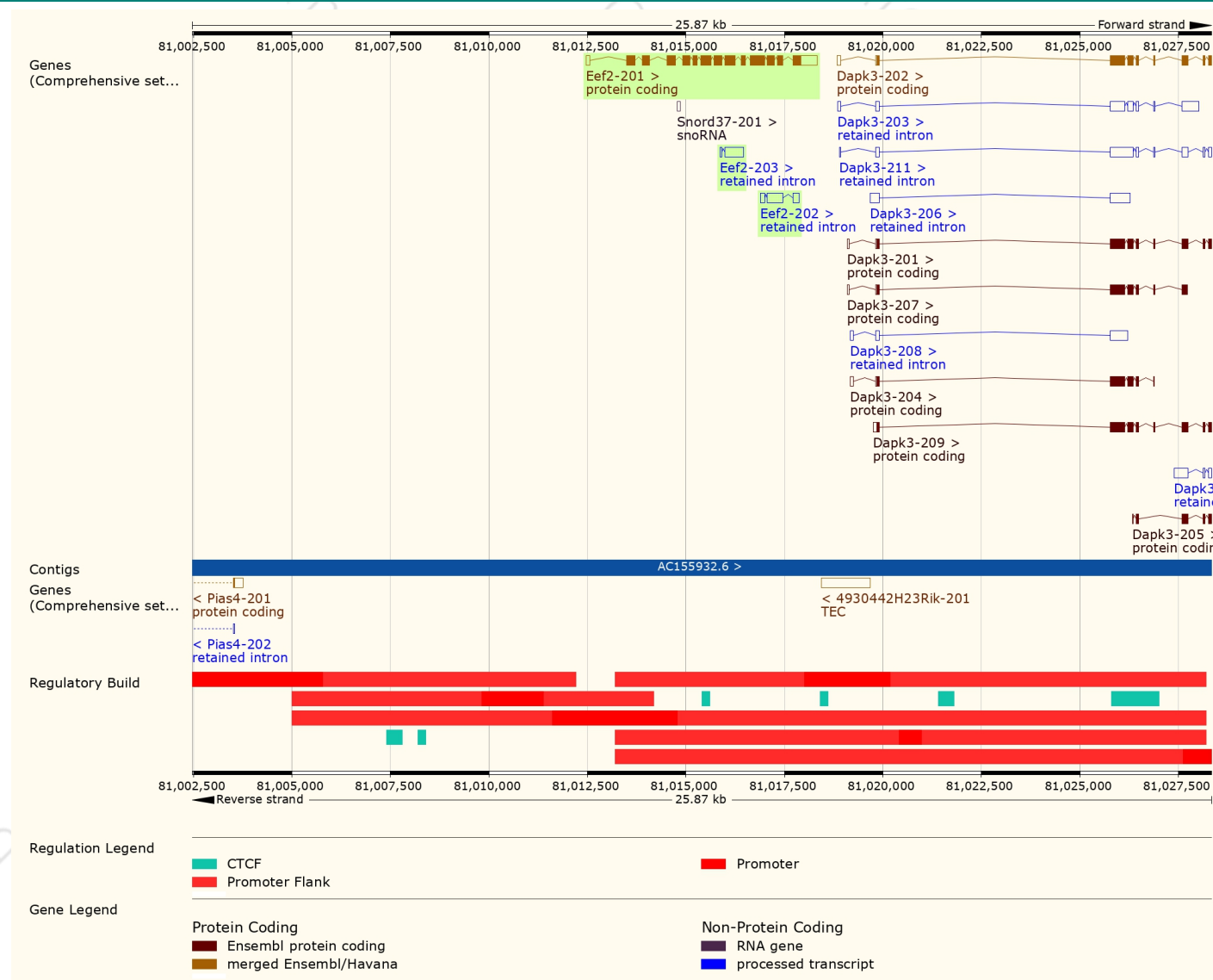
The gene has 3 transcripts, and all transcripts are shown below:

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

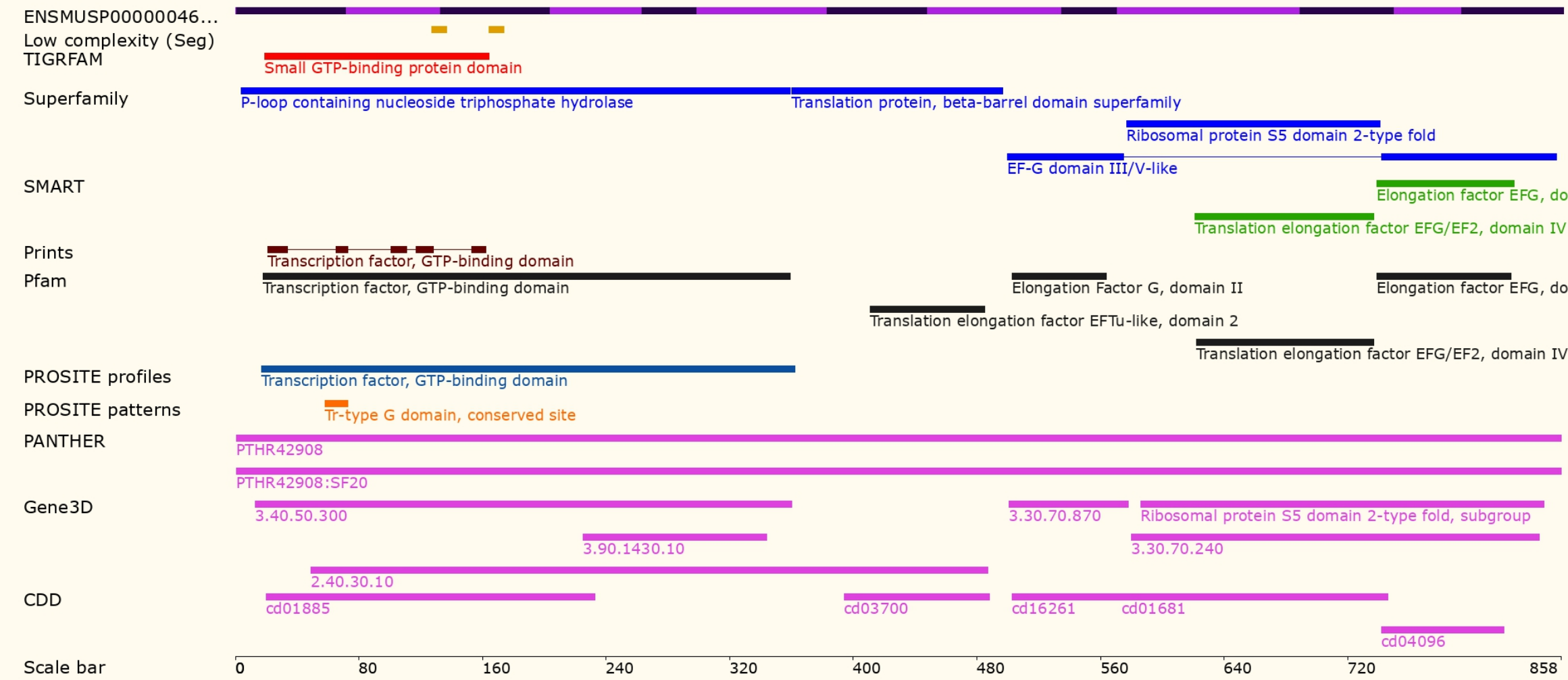
The strategy is based on the design of *Eef2*-201 transcript, the transcription is shown below:



Genomic location distribution



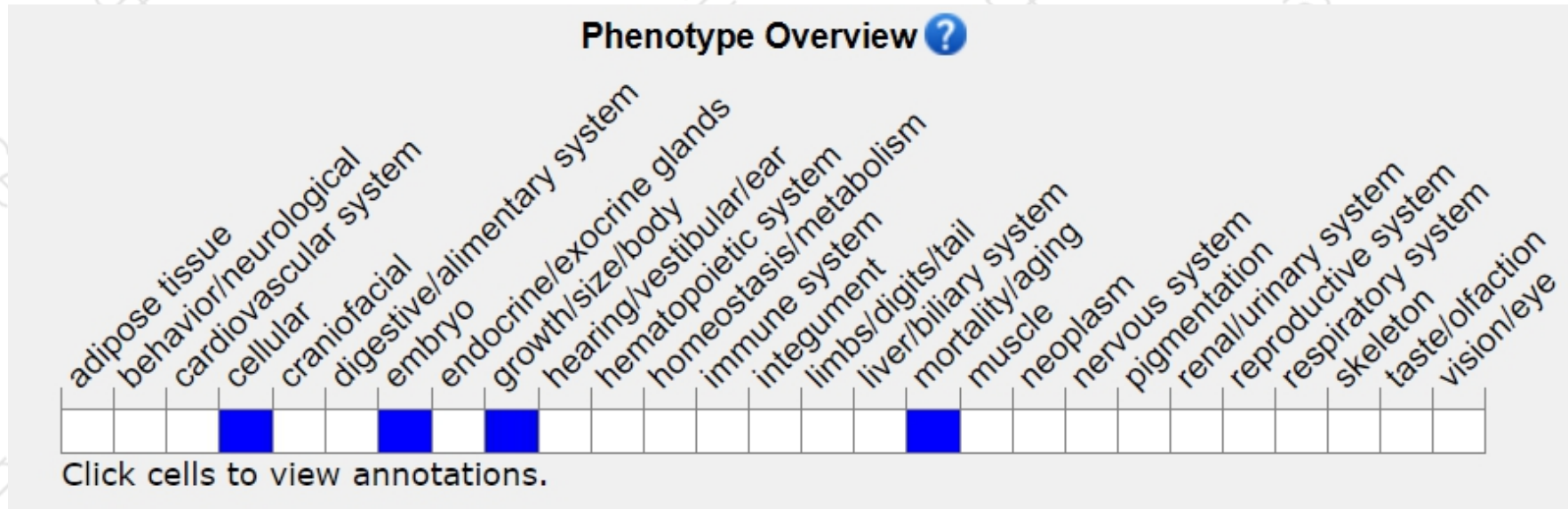
Protein domain



Mouse phenotype description(MGI)

URL link is as follows:

<http://www.informatics.jax.org/marker/MGI:95288>



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

If you have any questions, please feel free to contact us.
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