

Eif2s2 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Eif2s2

Project type

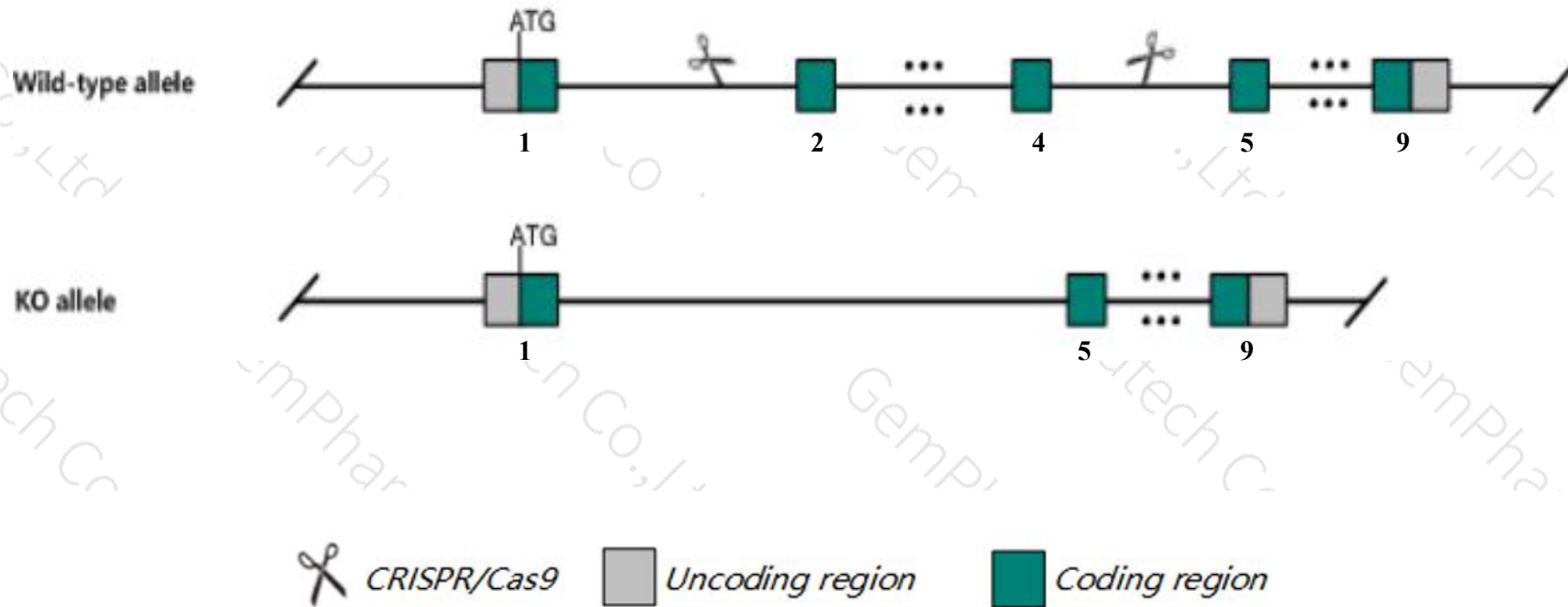
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif2s2* gene. The schematic diagram is as follows:



- The *Eif2s2* gene has 5 transcripts. According to the structure of *Eif2s2* gene, exon2-exon4 of *Eif2s2-201* (ENSMUST00000099173.10) transcript is recommended as the knockout region. The region contains 418bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif2s2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit embryonic lethality prior to E8.5. Mice heterozygous for a gene trap allele exhibit reduced incidence of testicular germ cell tumors.
- The *Eif2s2* gene is located on the Chr2. 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)

Eif2s2 eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus (house mouse)]

Gene ID: 67204, updated on 31-Jan-2019

Summary



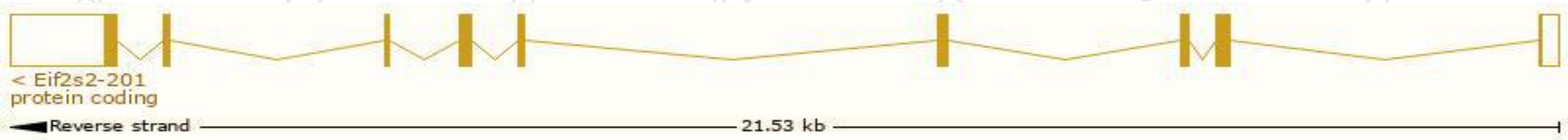
Official Symbol	Eif2s2 provided by MGI
Official Full Name	eukaryotic translation initiation factor 2, subunit 2 (beta) provided by MGI
Primary source	MGI:MGI:1914454
See related	Ensembl:ENSMUSG00000074656
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810026E11Rik, 38kDa, AA408636, AA571381, AA986487, AW822225, D2Erd303e, EIF2, EIF2B
Expression	Broad expression in CNS E11.5 (RPKM 37.7), placenta adult (RPKM 37.6) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

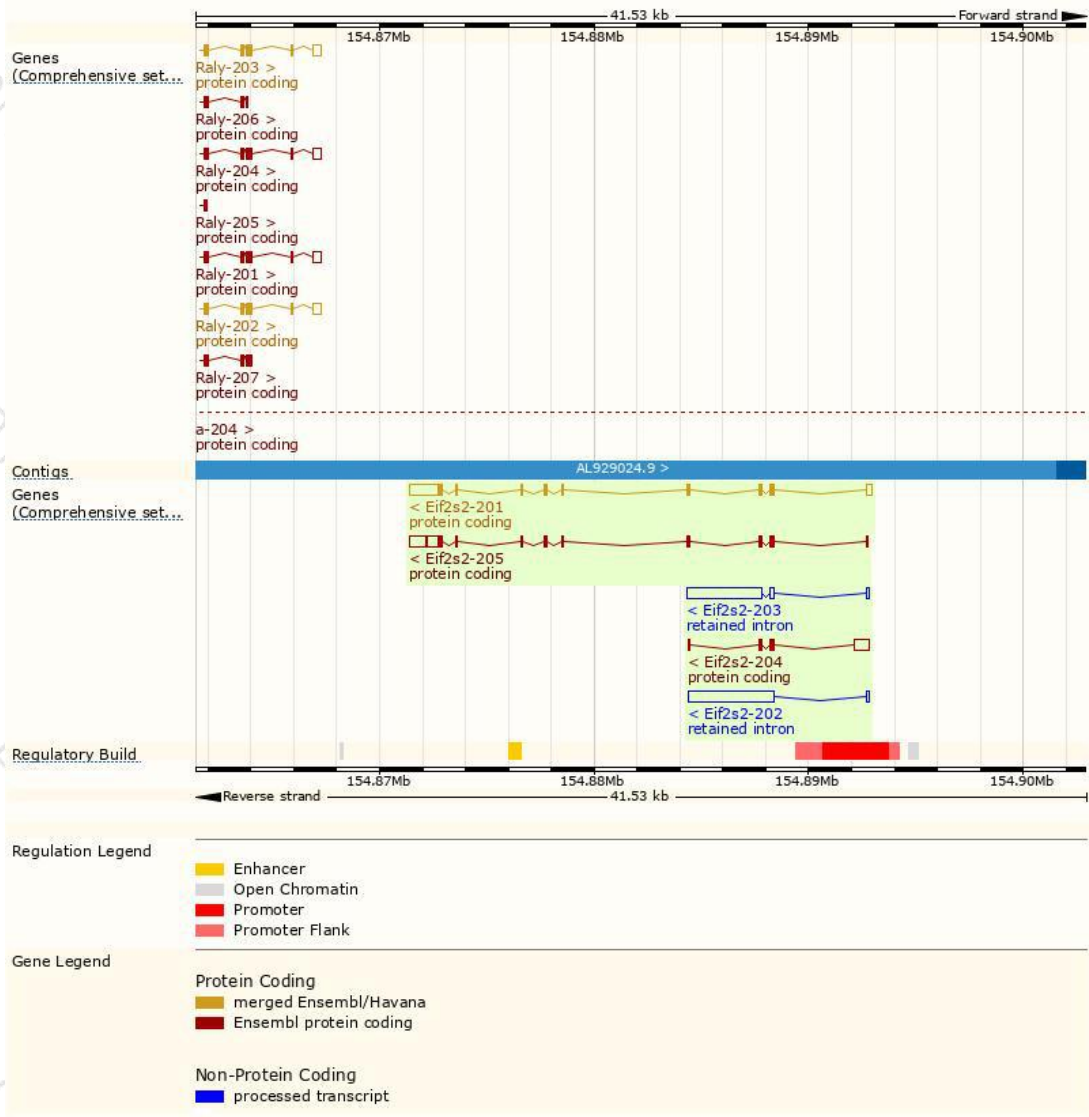
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Elf2s2-201	ENSMUST00000099173.10	2542	331aa	Protein coding	CCDS38292	Q3ULL5 Q99L45	TSL:1 GENCODE basic APPRIS P1
Elf2s2-205	ENSMUST00000166171.7	2312	331aa	Protein coding	CCDS38292	Q3ULL5 Q99L45	TSL:1 GENCODE basic APPRIS P1
Elf2s2-204	ENSMUST00000161172.2	1041	118aa	Protein coding	-	E0CXJ3	CDS 3' incomplete TSL:2
Elf2s2-202	ENSMUST00000135524.1	4102	No protein	Retained intron	-	-	TSL:1
Elf2s2-203	ENSMUST00000147136.1	3785	No protein	Retained intron	-	-	TSL:1

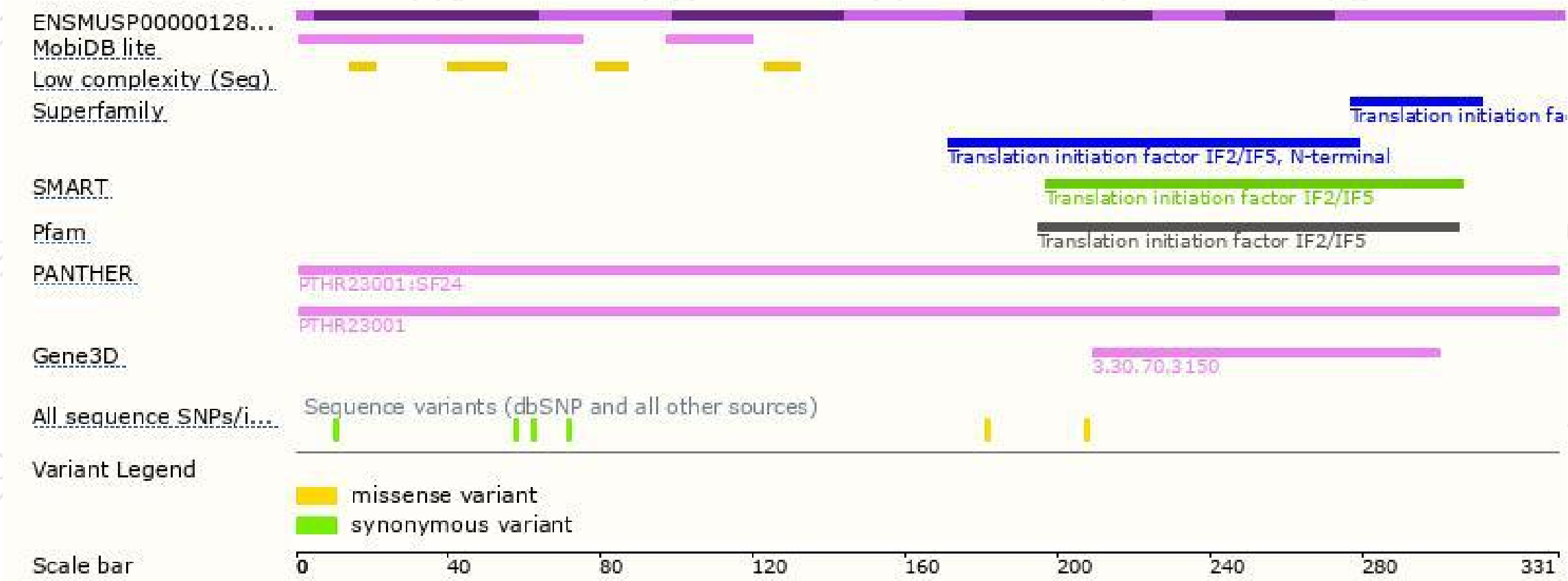
The strategy is based on the design of *Elf2s2-201* transcript,The transcription is shown below



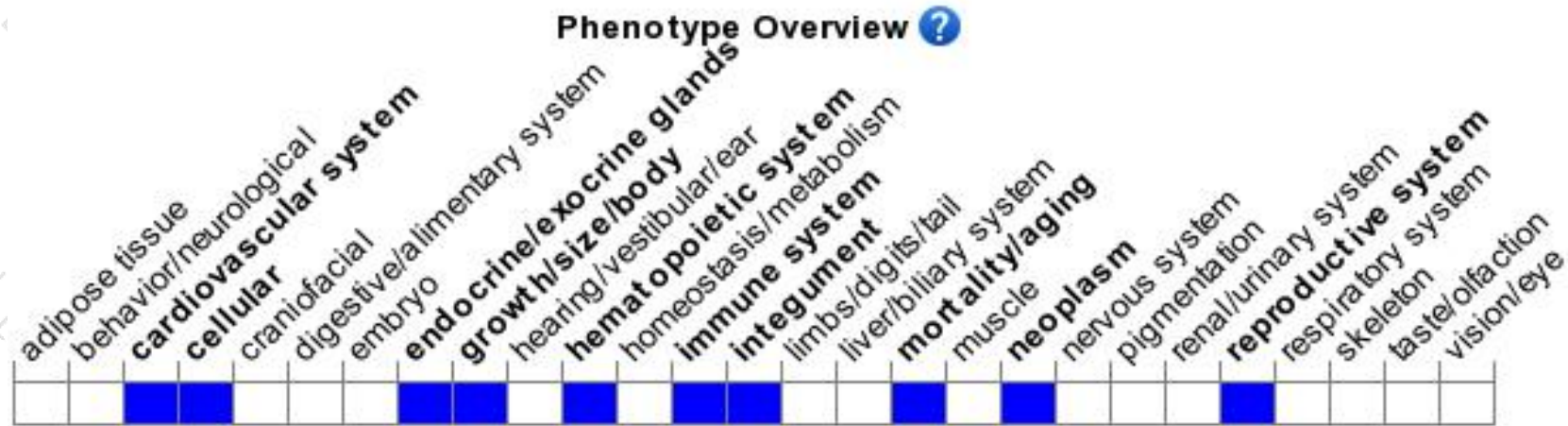
Genomic location distribution



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 gene trap allele exhibit embryonic lethality prior to E8.5.

Mice heterozygous for a gene trap allele exhibit reduced incidence of testicular germ cell tumors.

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

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