

Eprs Cas9-KO Strategy

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Project Overview

Project Name

Eprs

Project type

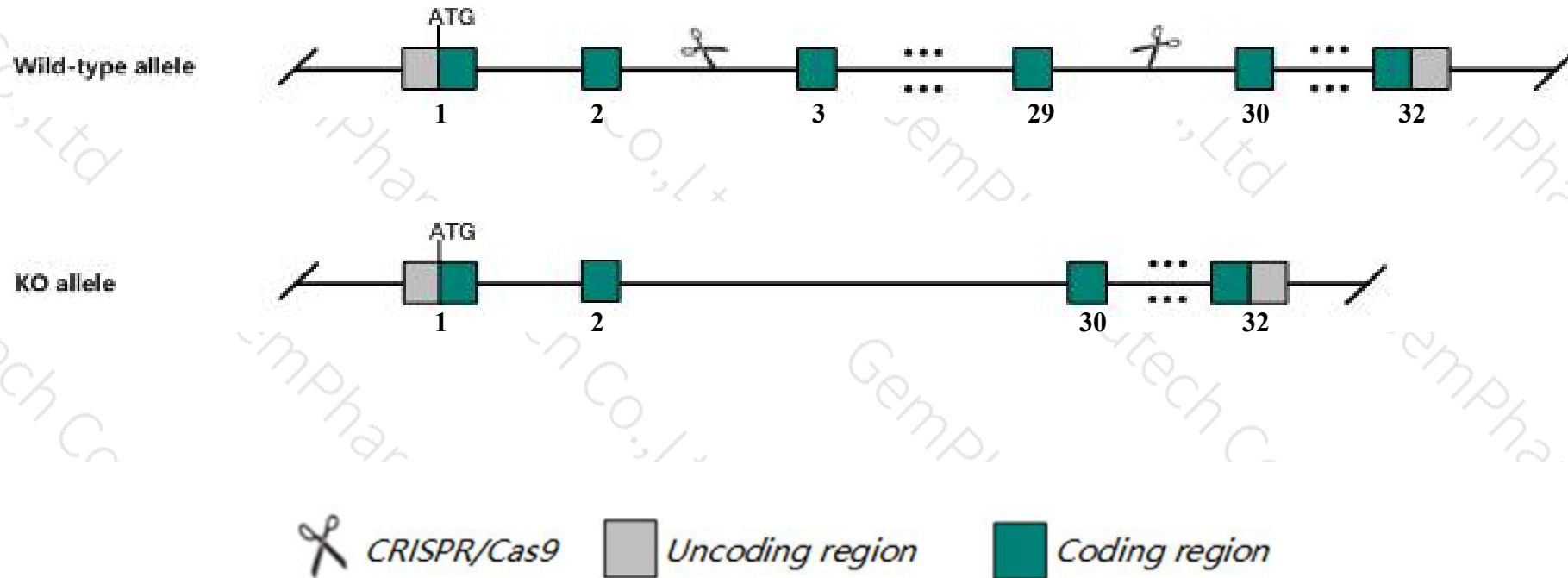
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Eprs* gene has 9 transcripts. According to the structure of *Eprs* gene, exon3-exon29 of *Eprs-201* (ENSMUST00000046514.12) 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 *Eprs* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a phospho-mimetic allele exhibit normal body weight, life span and glucose metabolism. Mice homozygous for a phospho-deficient allele exhibit decrease body weight, enhanced lipolysis, altered glucose metabolism and increased energy expenditure.
- The *Eprs* gene is located on the Chr1. 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)

Eprs glutamyl-prolyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 107508, updated on 31-Jan-2019

Summary



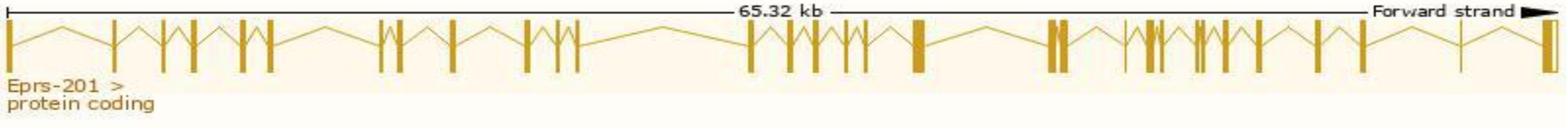
Official Symbol	Eprs provided by MGI
Official Full Name	glutamyl-prolyl-tRNA synthetase provided by MGI
Primary source	MGI:MGI:97838
See related	Ensembl:ENSMUSG00000026615
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410081F06Rik, 3010002K18Rik, C79379, Qprs
Expression	Ubiquitous expression in CNS E11.5 (RPKM 17.5), liver E14 (RPKM 12.9) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

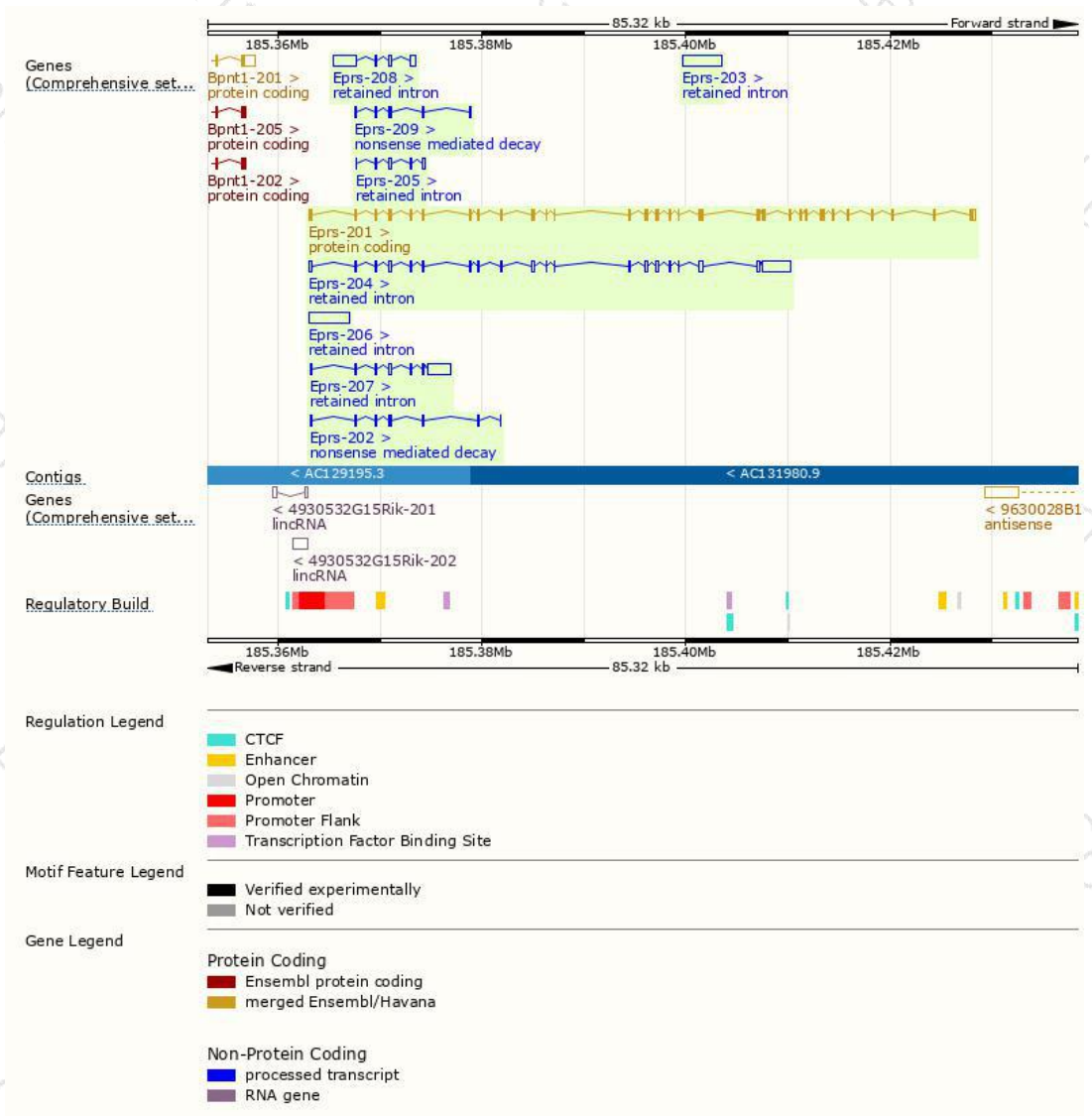
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eprs-201	ENSMUST00000046514.12	4906	1512aa	Protein coding	CCDS35818	Q8CGC7	TSL:1 GENCODE basic APPRIS P1
Eprs-202	ENSMUST00000191900.5	722	131aa	Nonsense mediated decay	-	A0A0A6YWA4	TSL:3
Eprs-209	ENSMUST00000195824.1	487	96aa	Nonsense mediated decay	-	A0A0A6YWH3	CDS 5' incomplete TSL:5
Eprs-204	ENSMUST00000192284.5	5638	No protein	Retained intron	-	-	TSL:1
Eprs-206	ENSMUST00000192588.1	3912	No protein	Retained intron	-	-	TSL:NA
Eprs-203	ENSMUST00000192049.1	3882	No protein	Retained intron	-	-	TSL:NA
Eprs-207	ENSMUST00000193788.5	3034	No protein	Retained intron	-	-	TSL:1
Eprs-208	ENSMUST00000194157.5	2915	No protein	Retained intron	-	-	TSL:1
Eprs-205	ENSMUST00000192324.1	749	No protein	Retained intron	-	-	TSL:1

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



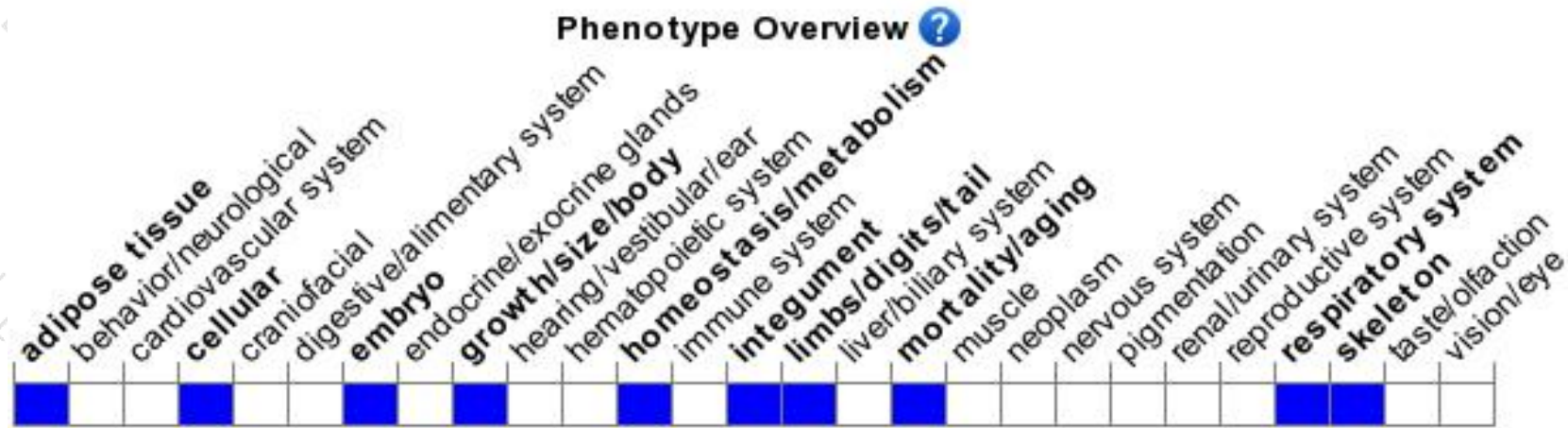
Genomic location distribution



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 phospho-mimetic allele exhibit normal body weight, life span and glucose metabolism. Mice homozygous for a phospho-deficient allele exhibit decrease body weight, enhanced lipolysis, altered glucose metabolism and increased energy expenditure.

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

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