Epor Cas9-KO Strategy Ronald Stock Co.

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Project Overview



Project Name

Epor

Project type

Cas9-KO

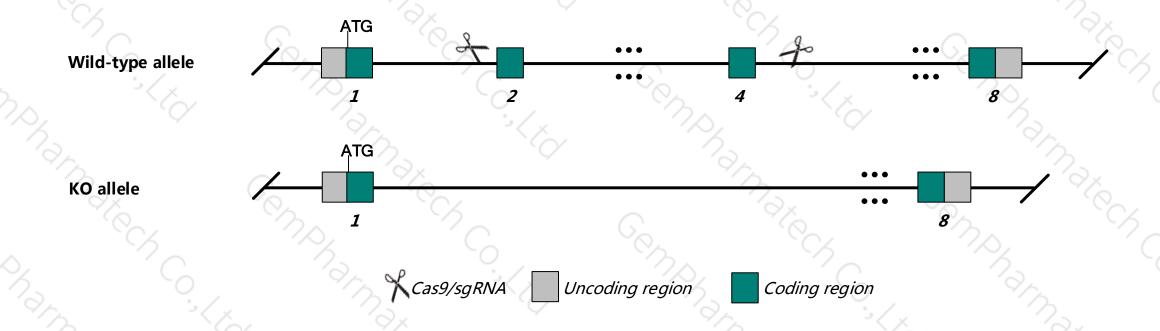
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Epor* gene has 2 transcripts. According to the structure of *Epor* gene, exon2-exon4 of *Epor*-201 (
- ➤ ENSMUST00000006397.6) transcript is recommended as the knockout region. The region contains 467bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Epor* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice



- According to the existing MGI data, Mutations in this locus affect erythropoiesis. Targeted null mutants die at embryonic day 11-12.5 with severe anemia. Mutants with truncated alleles are viable with mild changes in erythropoiesis. A human mutation replacement allele produces polycythemia.
- The *Epor* gene is located on the Chr9. 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,, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



Epor erythropoietin receptor [Mus musculus (house mouse)]

Gene ID: 13857, updated on 11-Jun-2019

Summary

☆ ?

Official Symbol Epor provided by MGI

Official Full Name erythropoietin receptor provided by MGI

Primary source MGI:MGI:95408

See related Ensembl:ENSMUSG00000006235

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

Expression Biased expression in liver E14.5 (RPKM 73.4), liver E14 (RPKM 57.8) and 5 other tissues See more

Orthologs human all

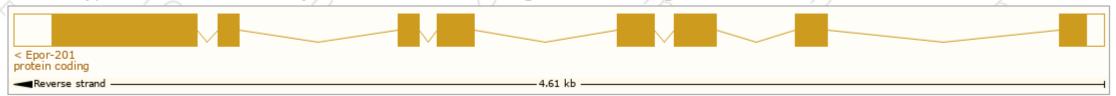
Transcript information (Ensembl)



The gene has 2 transcripts, and all transcripts are shown below:

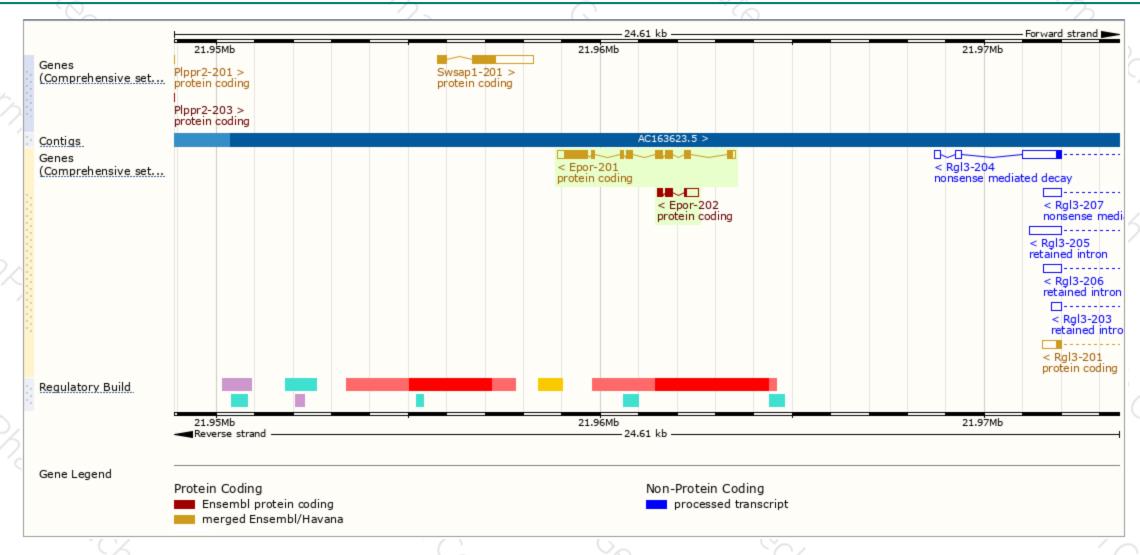
Show/hide columns (1 hidden)							Filter	III
Name 🍦	Transcript ID	bp 🌲	Protein 🍦	Biotype	CCDS 🍦	UniProt	Flags	
Epor-201	ENSMUST00000006397.6	1761	<u>507aa</u>	Protein coding	CCDS22915 ₽	<u>P14753</u> ₽ <u>Q3UTV9</u> ₽	TSL:1 GENCODE basic	APPRIS P1
Epor-202	ENSMUST00000213181.1	659	<u>111aa</u>	Protein coding	-	A0A1L1SRC0 ₽	CDS 3' incomplete	TSL:2

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



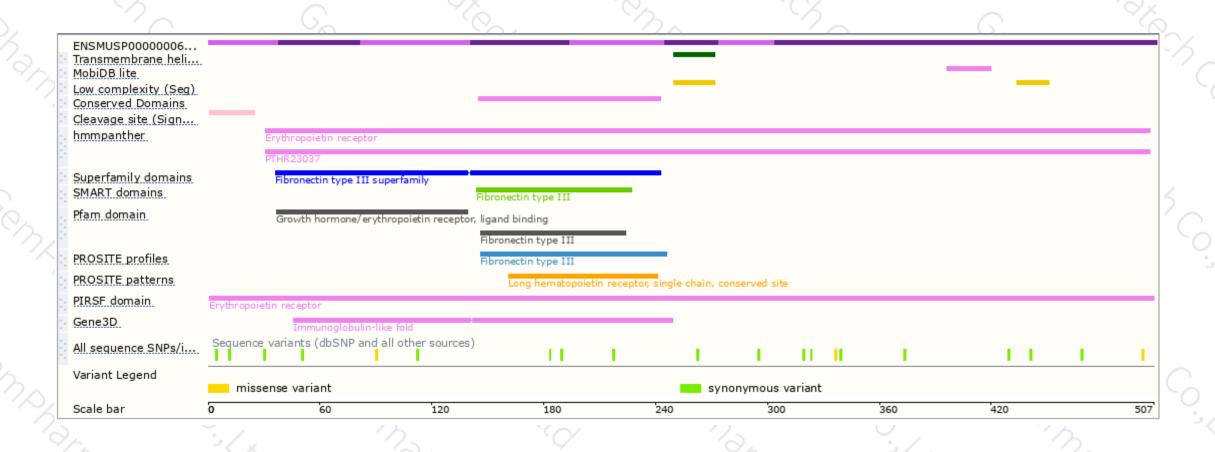
Genomic location distribution





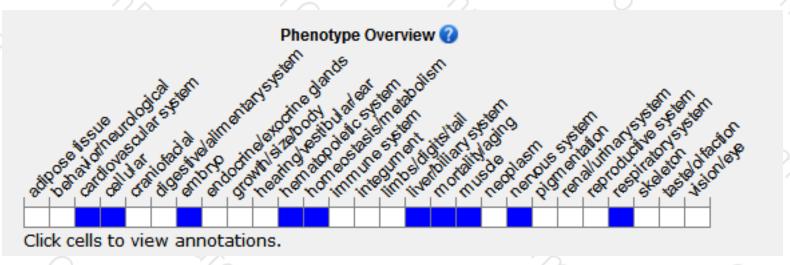
Protein domain





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, Mutations in this locus affect erythropoiesis. Targeted null mutants die at embryonic day 11-12.5 with severe anemia. Mutants with truncated alleles are viable with mild changes in erythropoiesis. A human mutation replacement allele produces polycythemia.

If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





