

Epha3 Cas9-CKO Strategy

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Project Overview

Project Name

Epha3

Project type

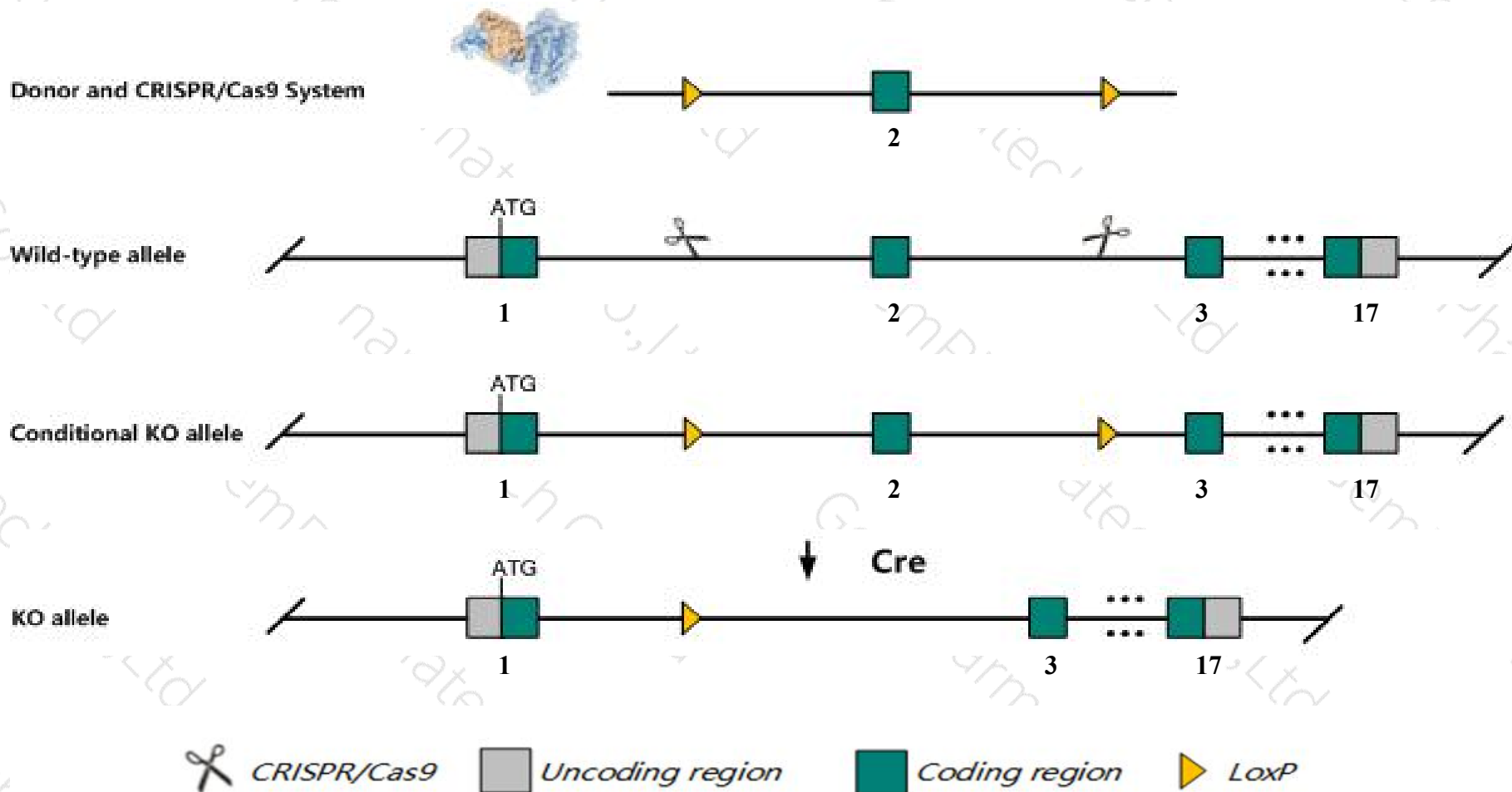
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epha3* gene. The schematic diagram is as follows:



Technical routes

- The *Epha3* gene has 6 transcripts. According to the structure of *Epha3* gene, exon2 of *Epha3-201* (ENSMUST00000064405.7) transcript is recommended as the knockout region. The region contains 65bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epha3* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.
- 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.

- According to the existing MGI data, mice homozygous for disruptions in this gene usually die within 48 hours of birth of cardiac failure. survivors develop normally with no indications of cardiac abnormalities.
- The *Epha3* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Epha3 Eph receptor A3 [Mus musculus (house mouse)]

Gene ID: 13837, updated on 13-Mar-2020

Summary



Official Symbol Epha3 provided by [MGI](#)

Official Full Name Eph receptor A3 provided by [MGI](#)

Primary source [MGI:MGI:99612](#)

See related [Ensembl:ENSMUSG00000052504](#)

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 AW492086, Cek4, EK4, ETK1, End3, Hek, Hek4, Mek4, Tyro4

Expression Biased expression in CNS E11.5 (RPKM 8.7), CNS E14 (RPKM 8.4) and 11 other tissues [See more](#)

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

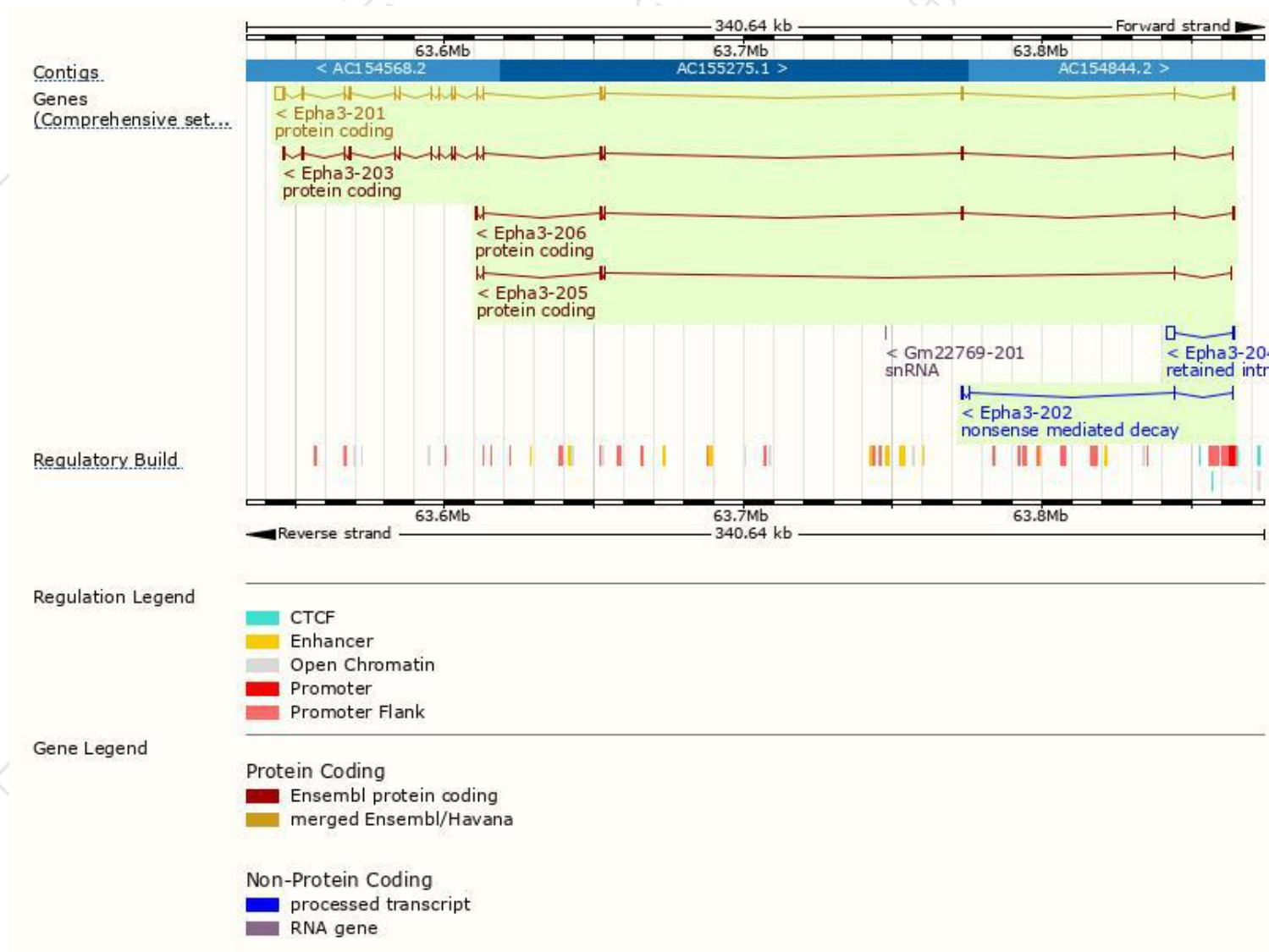
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha3-201	ENSMUST0000064405.7	5663	984aa	Protein coding	CCDS28264	Q8BRB1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Epha3-203	ENSMUST00000232049.1	3011	983aa	Protein coding	-	B7ZNN5	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Epha3-206	ENSMUST00000232654.1	2338	538aa	Protein coding	-	Q8C9K6	GENCODE basic
Epha3-205	ENSMUST00000232461.1	811	204aa	Protein coding	-	A0A338P6A7	CDS 3' incomplete
Epha3-202	ENSMUST00000231270.1	762	83aa	Nonsense mediated decay	-	A0A338P7J9	
Epha3-204	ENSMUST00000232370.1	2466	No protein	Retained intron	-	-	

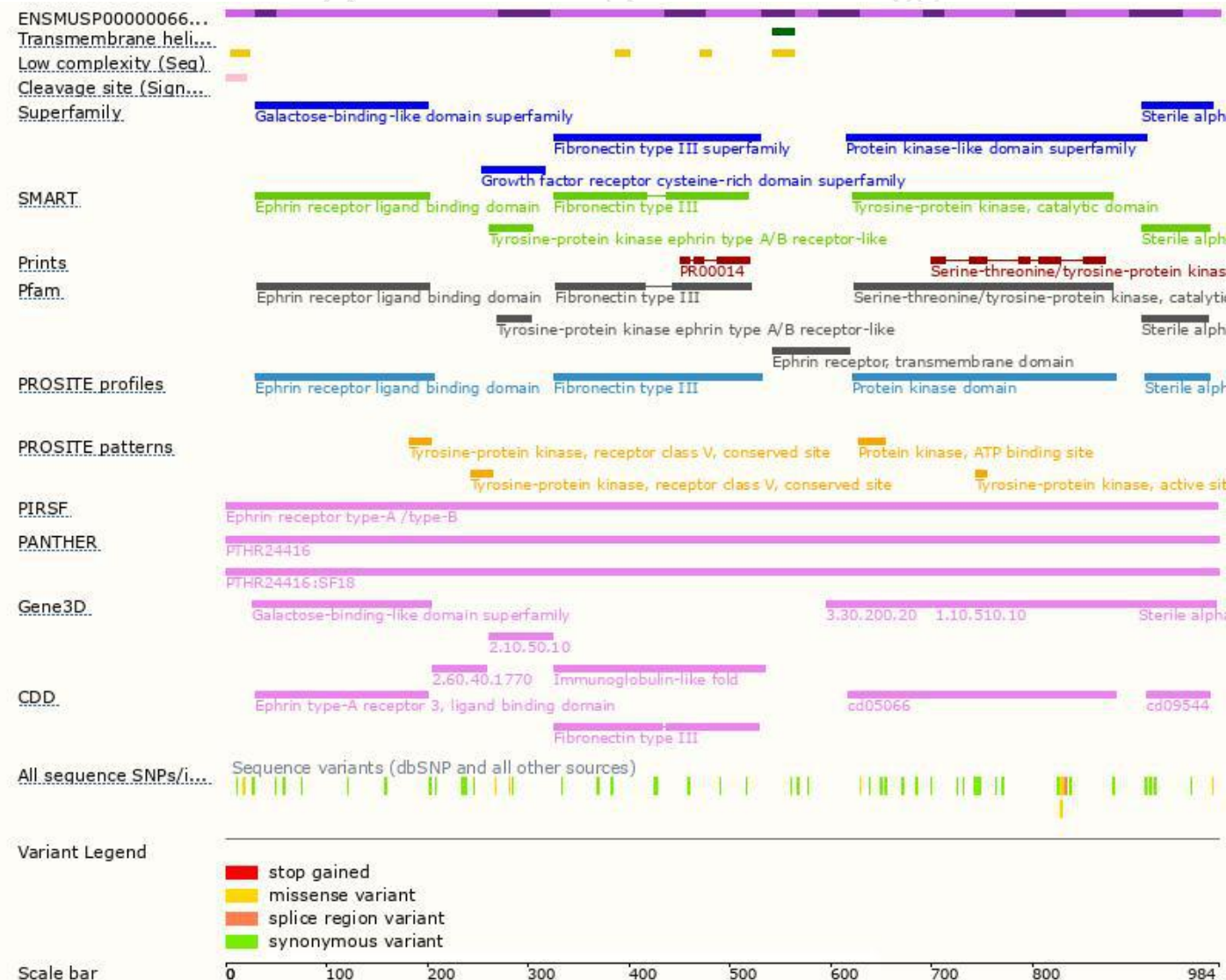
The strategy is based on the design of *Epha3-201* transcript,the transcription is shown below:



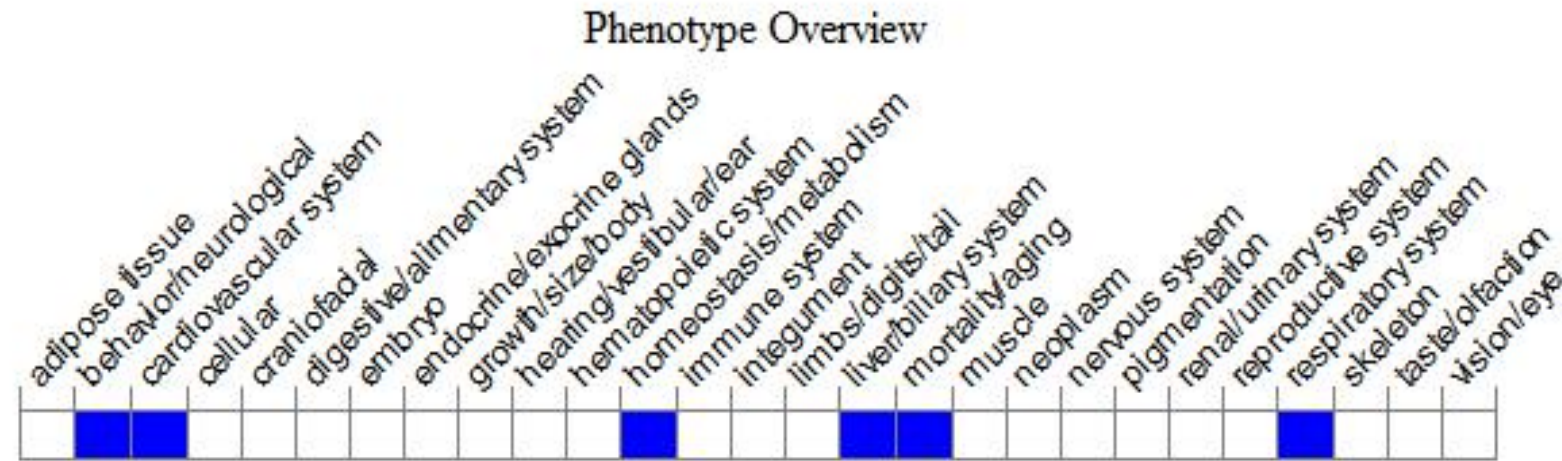
Genomic location distribution



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 disruptions in this gene usually die within 48 hours of birth of cardiac failure. Survivors develop normally with no indications of cardiac abnormalities.

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

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