

Epha2 Cas9-KO Strategy

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Reviewer

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Design Date:

2020-1-4

Project Overview

Project Name

Epha2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epha2* gene. The schematic diagram is as follows:



- The *Epha2* gene has 4 transcripts. According to the structure of *Epha2* gene, exon2 of *Epha2-201* (ENSMUST00000006614.2) transcript is recommended as the knockout region. The region contains 68bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epha2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit abnormal angiogenesis. Mice homozygous for a gene trap allele exhibit increased incidence of chemically-induced tumors, increased metastatic potential, and age-related cataracts.
- The *Epha2* gene is located on the Chr4. 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.

Epha2 Eph receptor A2 [Mus musculus (house mouse)]

Gene ID: 13836, updated on 19-Feb-2019

Summary



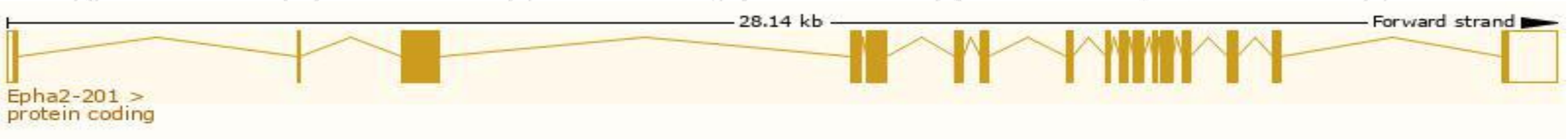
Official Symbol	Epha2 provided by MGI
Official Full Name	Eph receptor A2 provided by MGI
Primary source	MGI:MGI:95278
See related	Ensembl:ENSMUSG00000006445
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW545284, Eck, Myk2, Sek-2, Sek2
Expression	Broad expression in lung adult (RPKM 25.3), small intestine adult (RPKM 22.7) and 19 other tissues See more
Orthologs	human all

Transcript information Ensembl

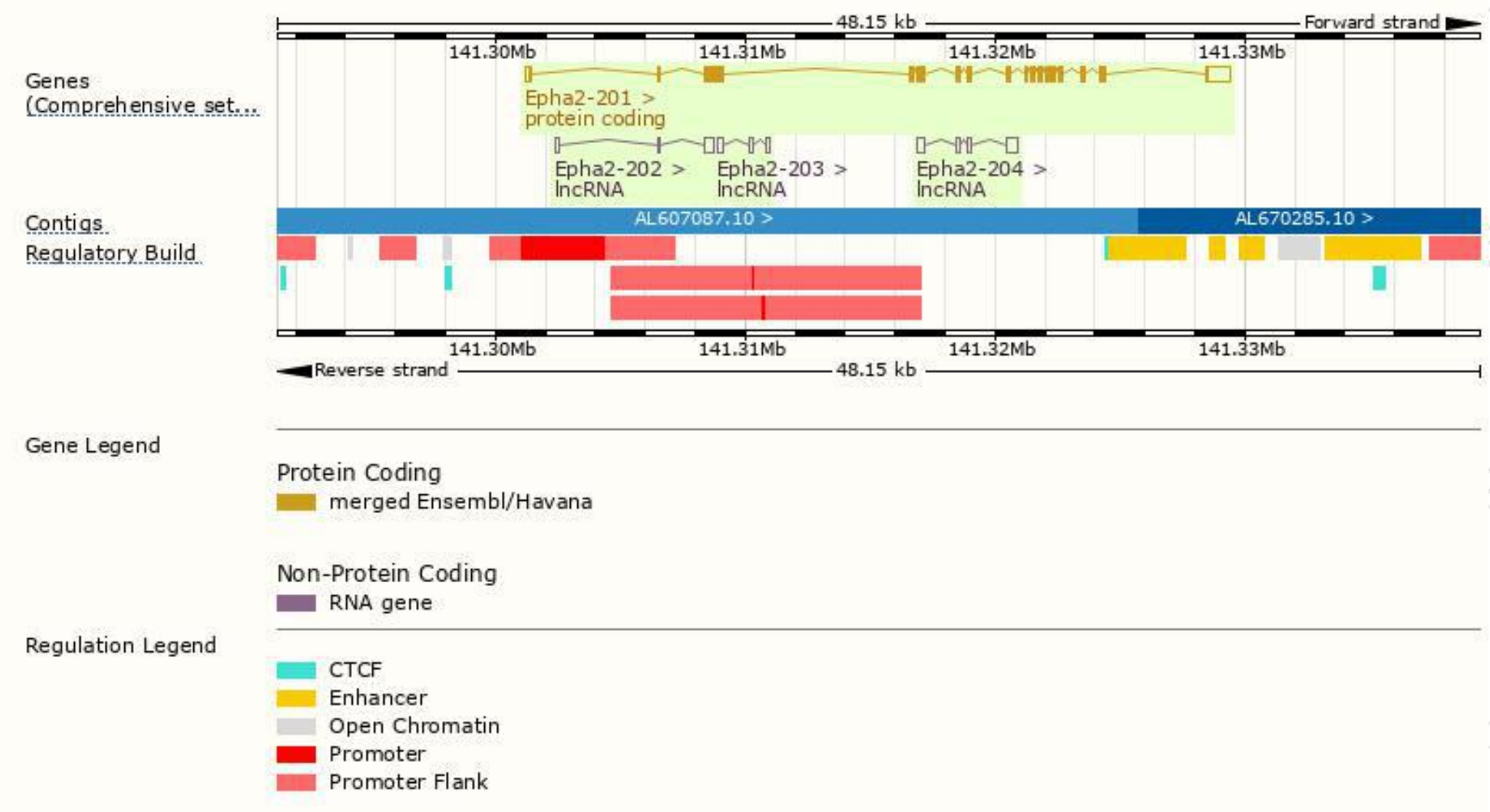
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha2-201	ENSMUST00000006614.2	3913	977aa	Protein coding	CCDS18869	Q03145	TSL:1 GENCODE basic APPRIS P1
Epha2-204	ENSMUST00000149002.1	969	No protein	lncRNA	-	-	TSL:5
Epha2-203	ENSMUST00000145523.1	531	No protein	lncRNA	-	-	TSL:3
Epha2-202	ENSMUST00000131026.1	507	No protein	lncRNA	-	-	TSL:3

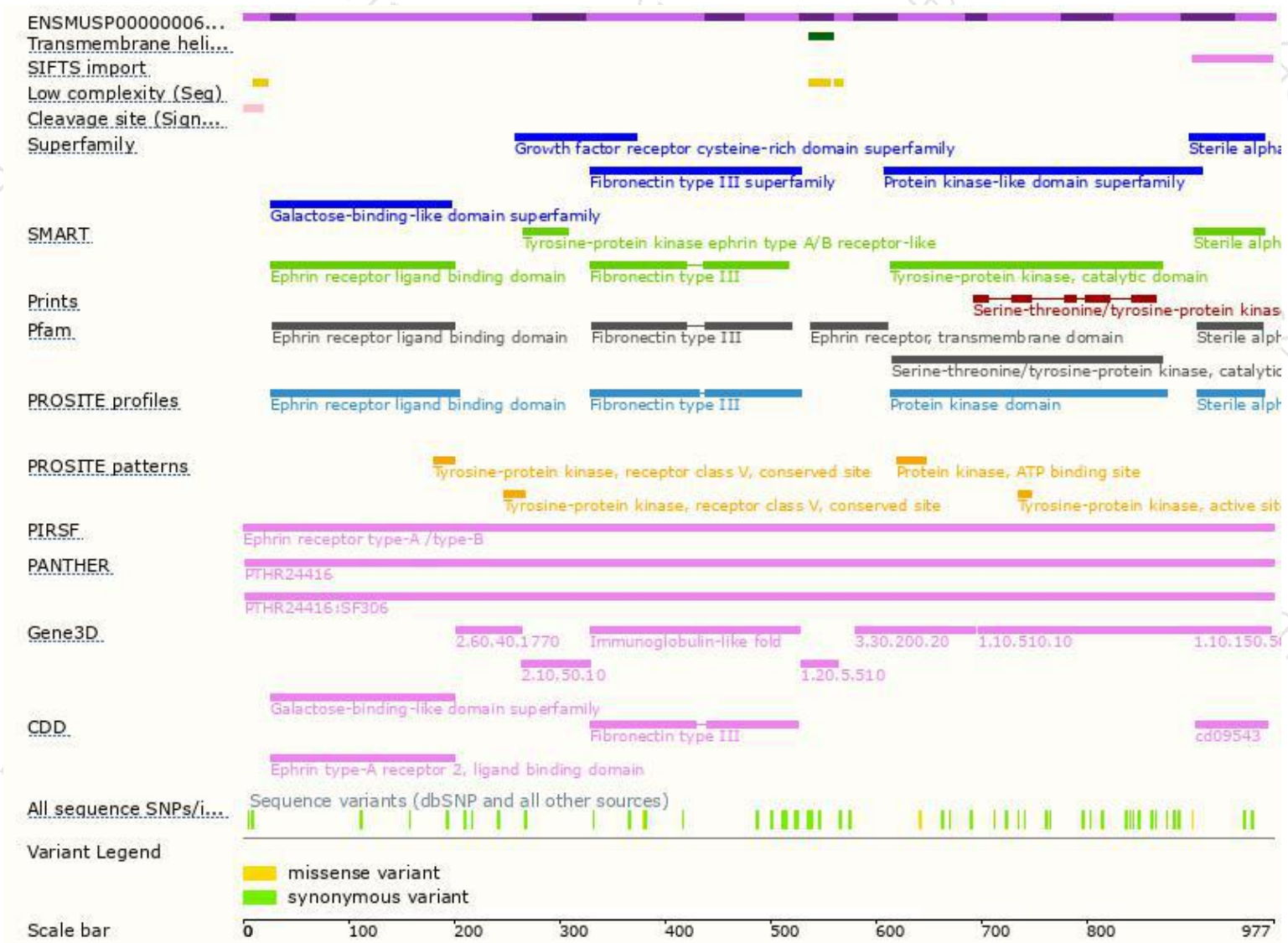
The strategy is based on the design of *Epha2-201* transcript,The transcription is shown below



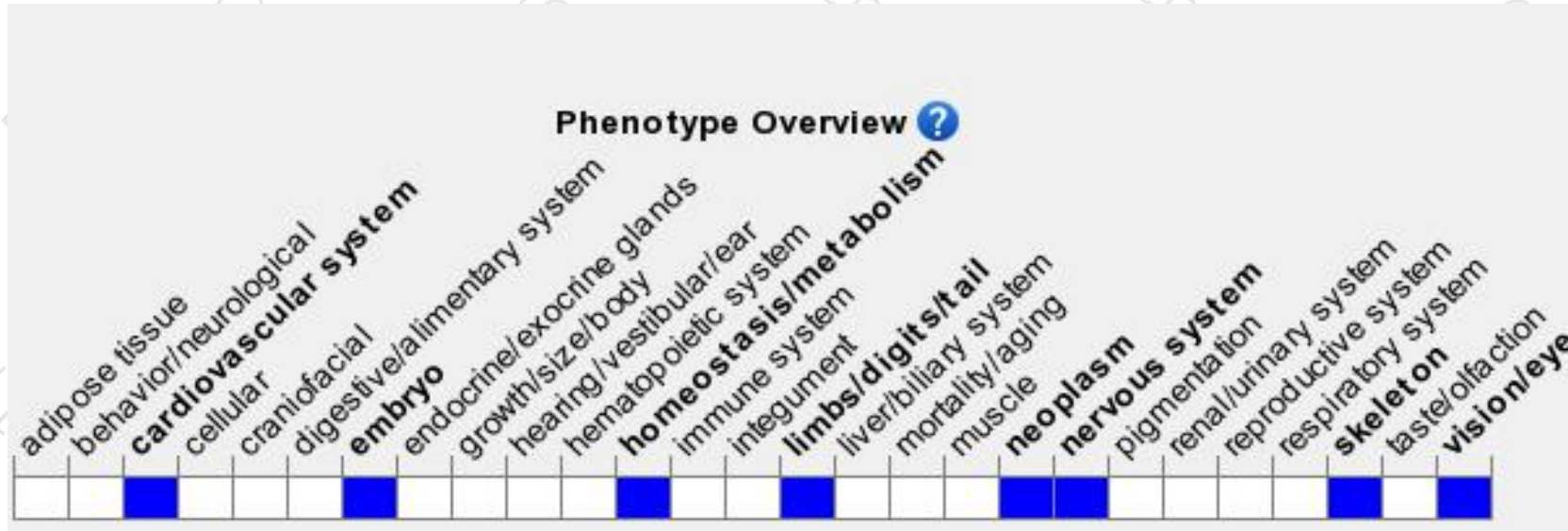
Genomic location distribution



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 null allele exhibit abnormal angiogenesis. Mice homozygous for a gene trap allele exhibit increased incidence of chemically-induced tumors, increased metastatic potential, and age-related cataracts.

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

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