

Epha10 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Jiayuan Yao

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Project Overview

Project Name

Epha10

Project type

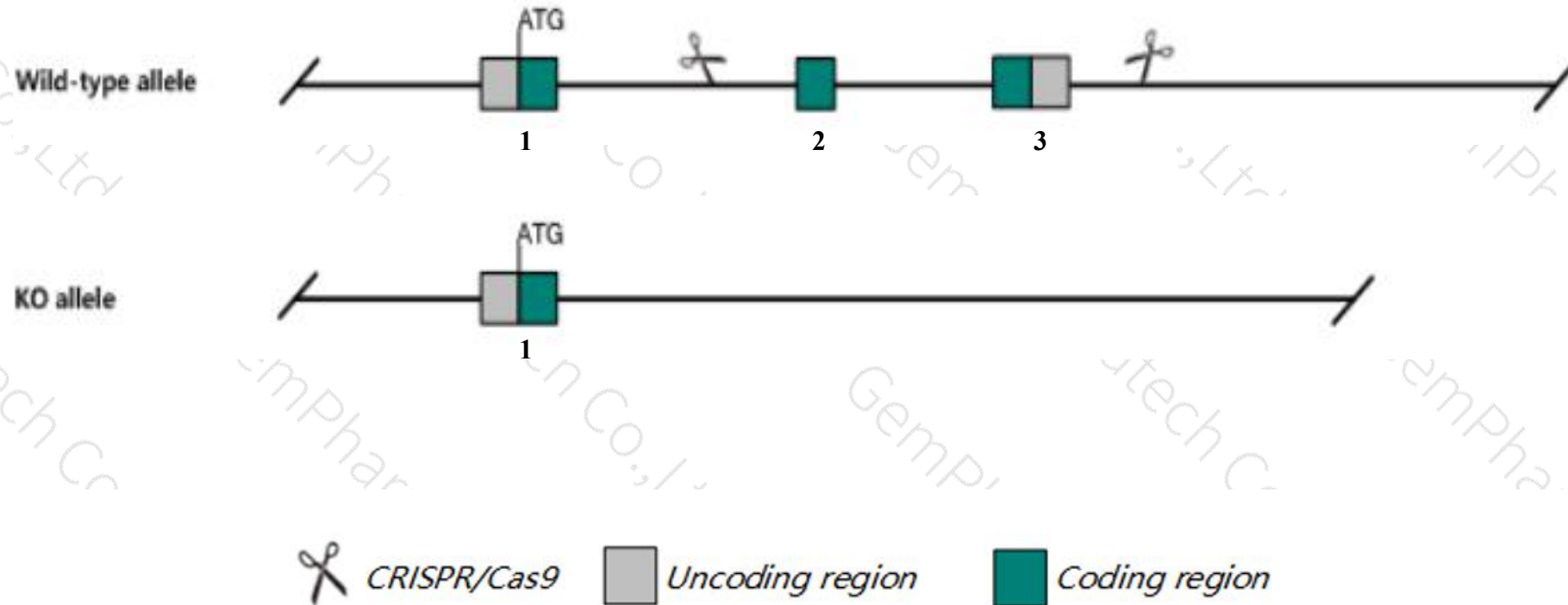
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epha10* gene. The schematic diagram is as follows:



- The *Epha10* gene has 3 transcripts. According to the structure of *Epha10* gene, exon2-exon3 of *Epha10-201* (ENSMUST00000059343.6) transcript is recommended as the knockout region. The region contains 773bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epha10* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Epha10* 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.

Gene information (NCBI)

Epha10 Eph receptor A10 [Mus musculus (house mouse)]

Gene ID: 230735, updated on 13-Mar-2020

Summary



Official Symbol	Epha10 provided by MGI
Official Full Name	Eph receptor A10 provided by MGI
Primary source	MGI:MGI:3586824
See related	Ensembl:ENSMUSG00000028876
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	A330090H18
Expression	Biased expression in cortex adult (RPKM 7.2), frontal lobe adult (RPKM 6.4) and 7 other tissues See more
Orthologs	human all

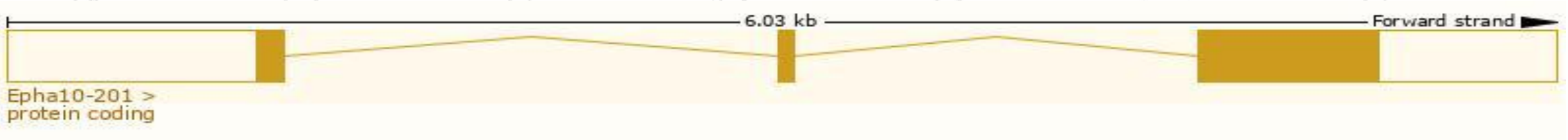
Transcript information（Ensembl）



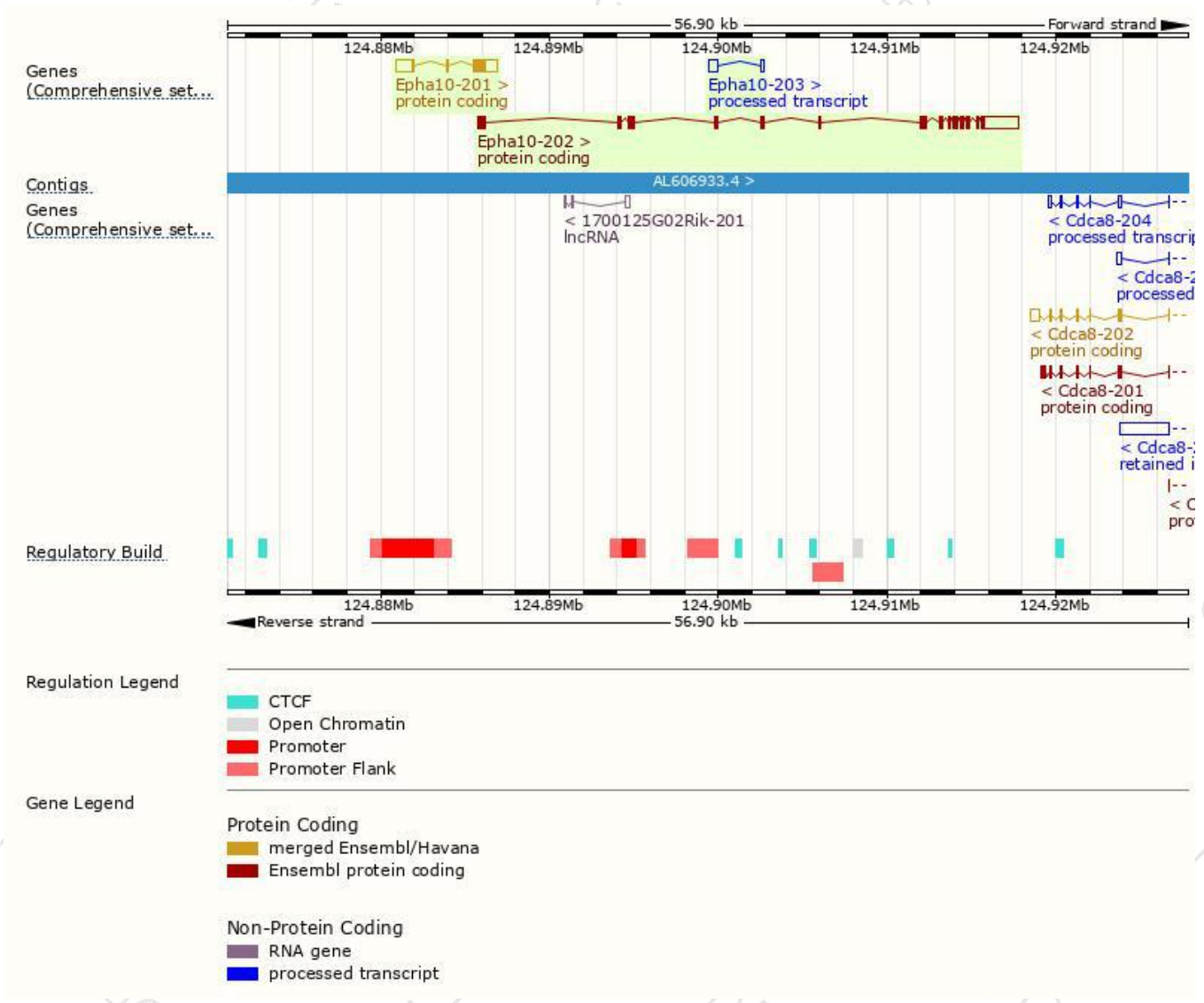
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha10-201	ENSMUST00000059343.6	2544	292aa	Protein coding	CCDS18630	Q8BYG9	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 P1
Epha10-202	ENSMUST00000149146.1	4660	862aa	Protein coding	-	F6WVB0	CDS 5' incomplete TSL:5
Epha10-203	ENSMUST00000151791.1	705	No protein	Processed transcript	-	-	TSL:3

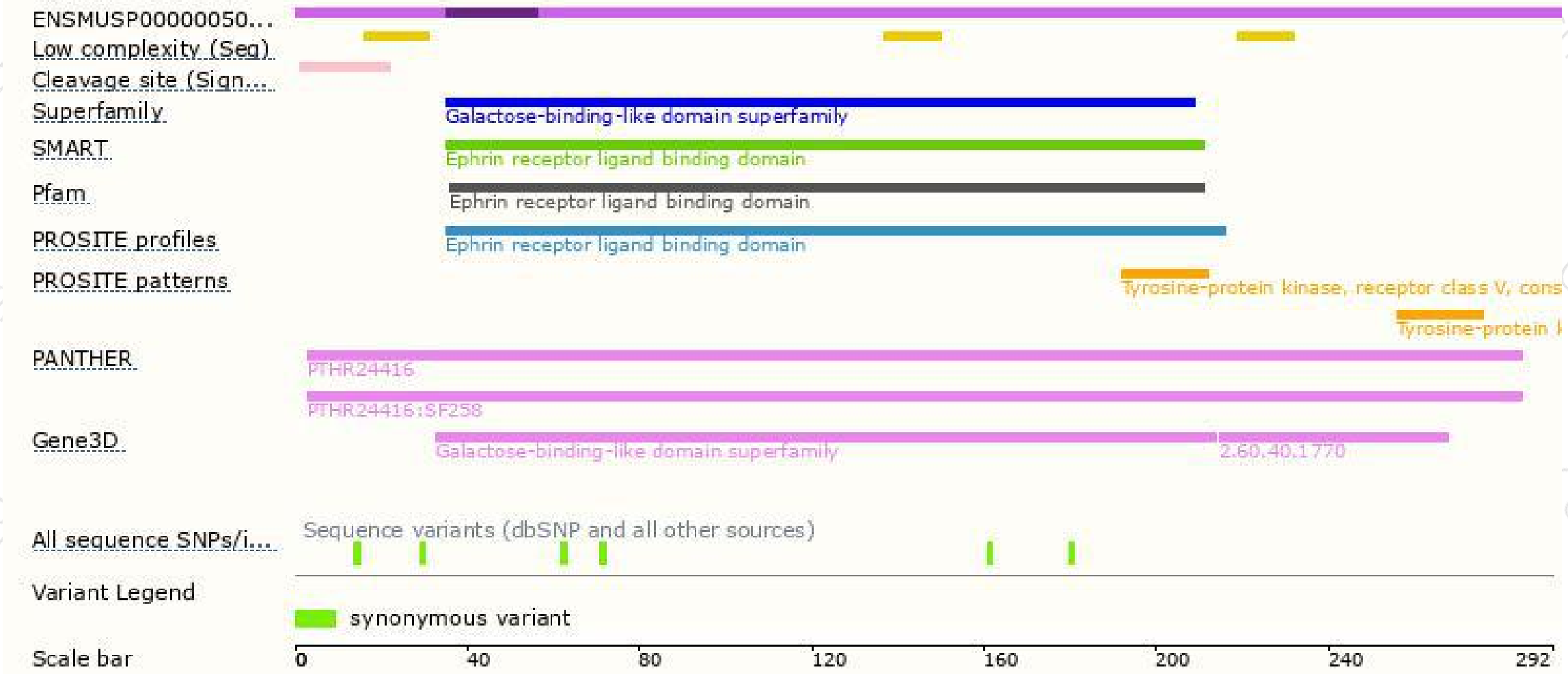
The strategy is based on the design of *Epha10-201* transcript,the transcription is shown below:



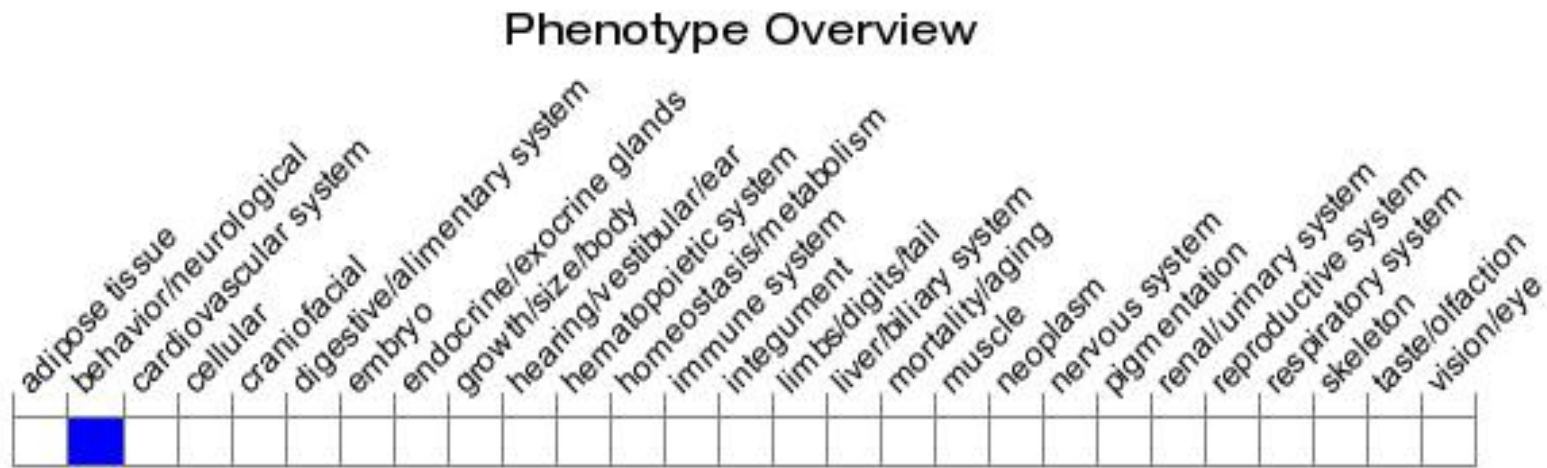
Genomic location distribution



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/>).

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

Tel: 400-9660890

