Epha1 Cas9-KO Strategy

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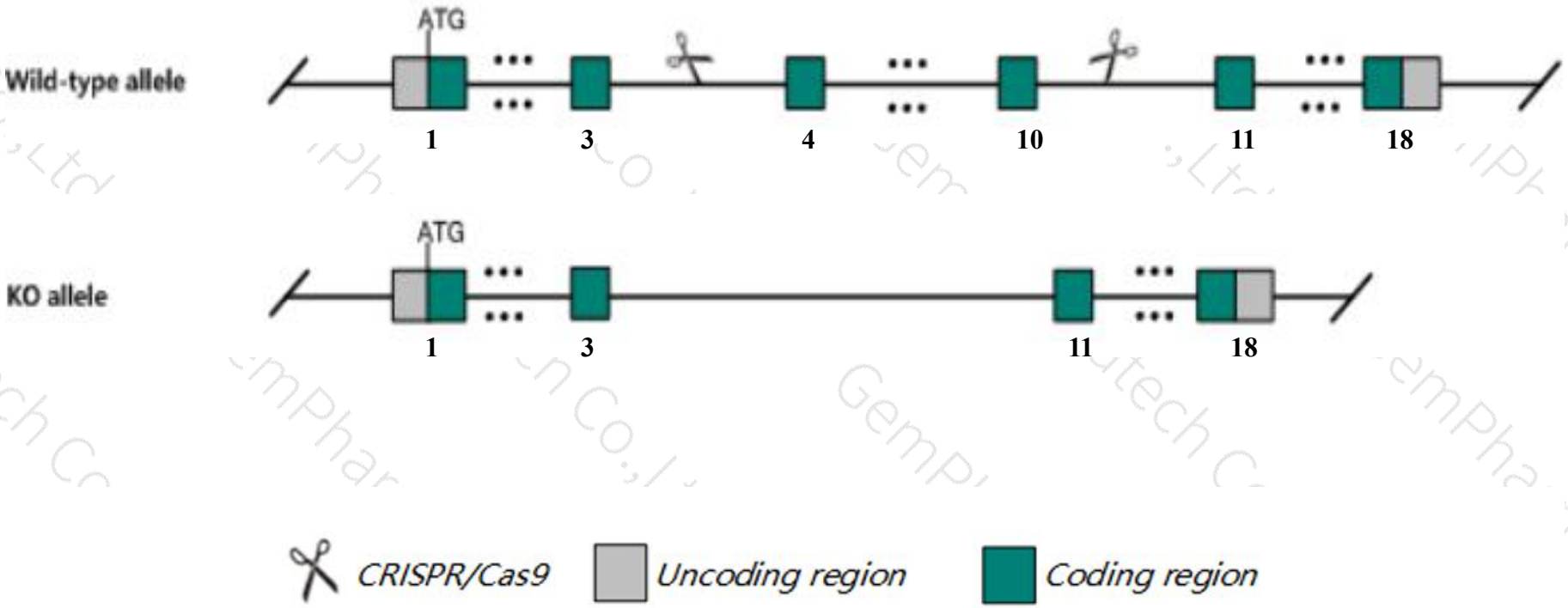
Project Overview

Project Name	***Epha1***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epha1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Epha1* gene has 3 transcripts. According to the structure of *Epha1* gene, exon4-exon10 of *Epha1-201* (ENSMUST00000073387.4) transcript is recommended as the knockout region.The region contains 1339bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Epha1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,most mice homozygous for a null allele exhibit a kinked tail while 18% of mice exhibit vagina atresia with hydrometrocolops and infertility.
- The *Epha1* gene is located on the Chr6. 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）

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Epha1 Eph receptor A1 [Mus musculus (house mouse)]

Gene ID: 13835, updated on 13-Mar-2020

Summary

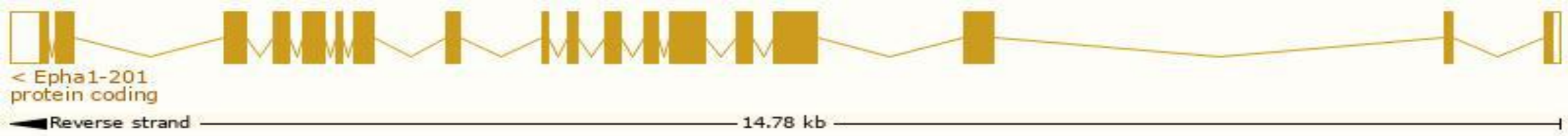
Official Symbol	Epha1 provided by MGI
Official Full Name	Eph receptor A1 provided byMGI
Primary source	MGI:MGI:107381
See related	Ensembl:ENSMUSG00000029859
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730453L17Rik, AL033318, Eph, Esk
Expression	Broad expression in duodenum adult (RPKM 22.5), small intestine adult (RPKM 20.3) and 17 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

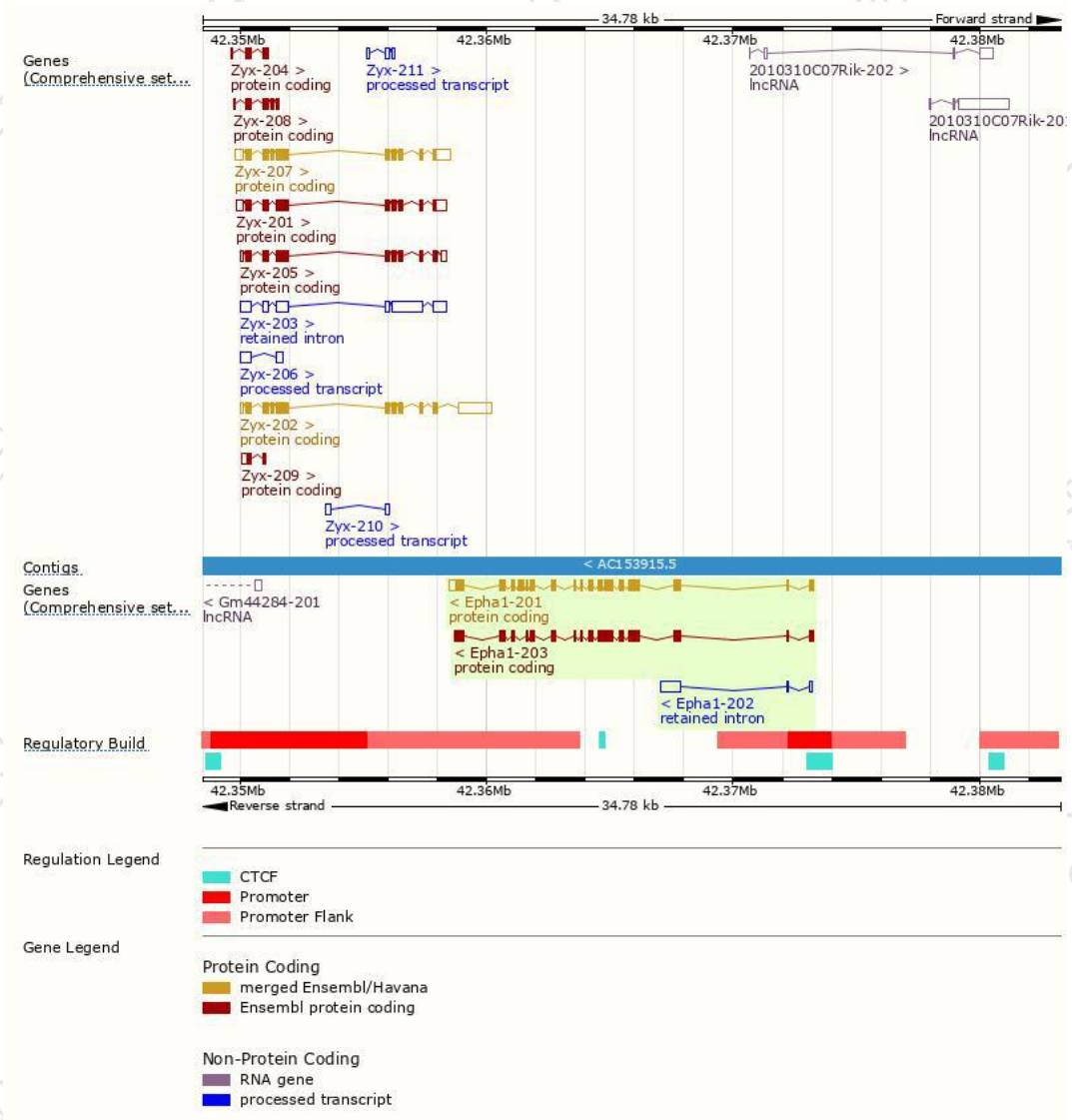
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha1-201	ENSMUST00000073387.4	3273	977aa	Protein coding	CCDS20067	Q60750	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
Epha1-203	ENSMUST00000204357.1	2948	945aa	Protein coding	-	A0A0N4SUP4	TSL:5 GENCODE basic
Epha1-202	ENSMUST00000204238.1	1004	No protein	Retained intron	-	-	TSL:1

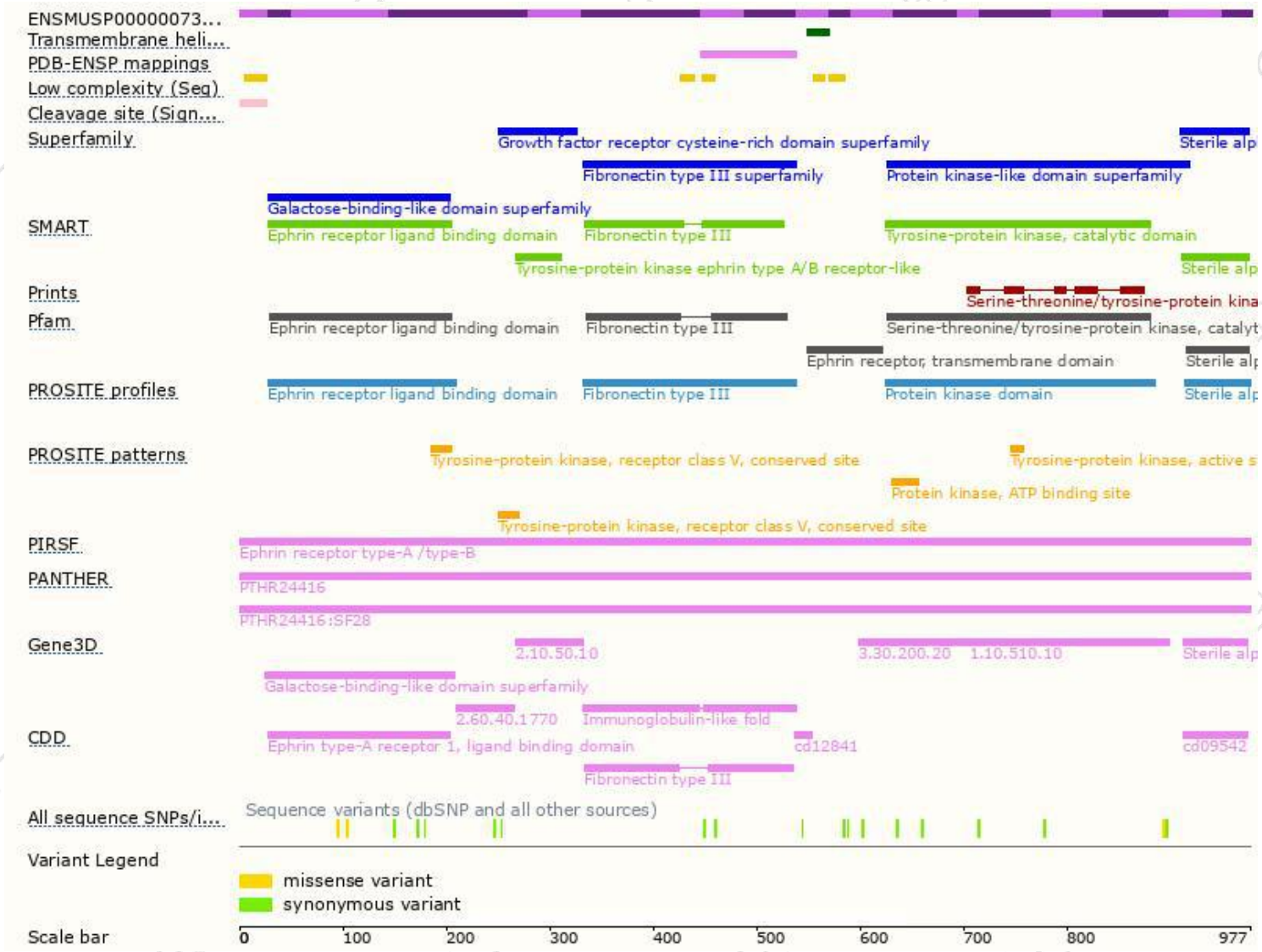
The strategy is based on the design of *Epha1-201* transcript,the transcription is shown below:



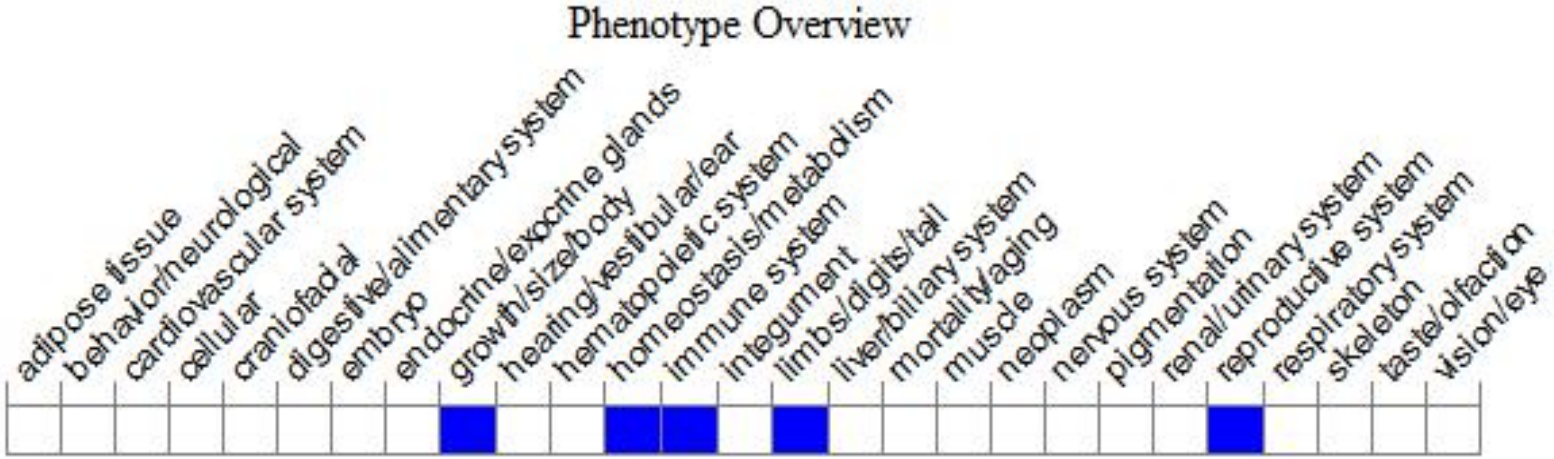
Genomic location distribution



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/).

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

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