

Epha10 Cas9-KO Strategy

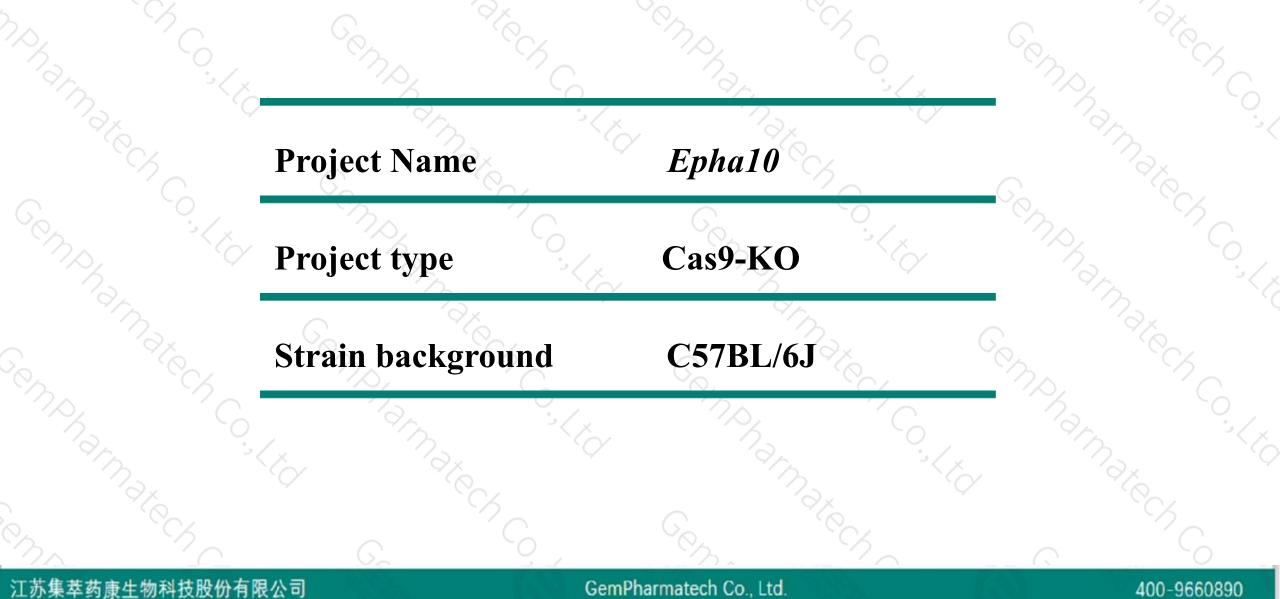
Designer: Lingyan Wu

Reviewer: Jiayuan Yao

Design Date: 2020-4-24

Project Overview

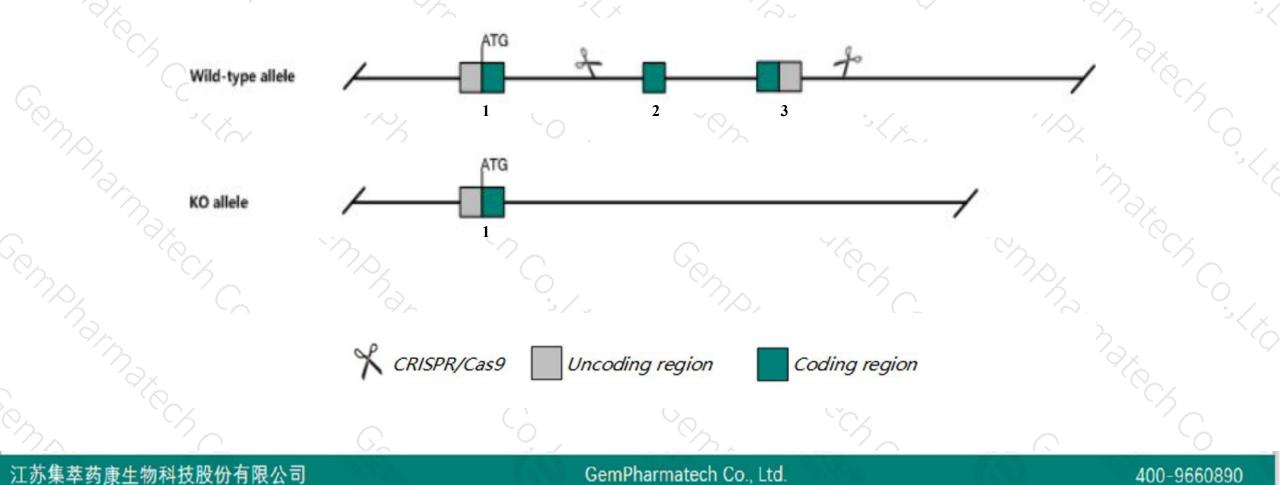




Knockout strategy



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.

Notice

Gene information (NCBI)



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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:ENSMUSG0000028876
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

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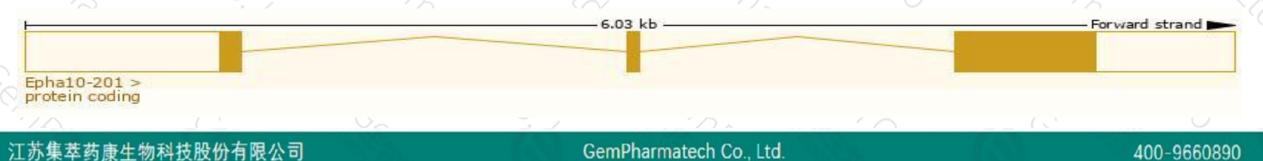
Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha10-201	ENSMUST00000059343.6	2544	<u>292aa</u>	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	<u>862aa</u>	Protein coding	-	F6WVB0	CDS 5' incomplete TSL:5
Epha10-203	ENSMUST00000151791.1	705	No protein	Processed transcript	-	120	TSL:3

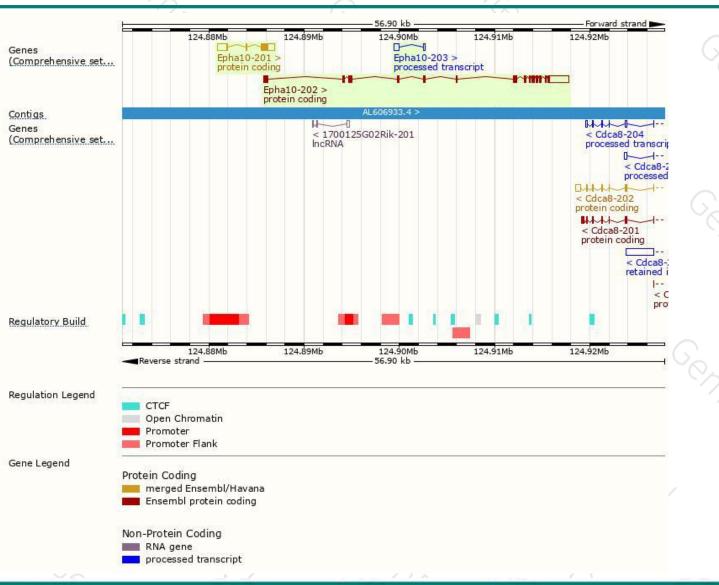
The strategy is based on the design of *Epha10-201* transcript, the transcription is shown below:



Genomic location distribution







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Protein domain



200									
ENSMUSP00000050 Low complexity (Seg) Cleavage site (Sign				-	æ.				× C
Superfamily		Galactose-b	binding-like doma	ain superfamily					
SMART		Ephrin rece	eptor ligand bindir	ng domain					
<u>Pfam</u>		Ephrin rece	eptor ligand bindi	ng domain					
PROSITE profiles		Ephrin rece	eptor ligand bindir	ng domain			-		
PROSITE patterns						Tyros	ine-protein k	inase, recept	or class V, cons
								Ty	rosine-protein I 🔍
PANTHER	PTHR24416								
PANTHER	PTHR24416 PTHR24416:S	F258							
PANTHER Gene3D	PTHR24416:S		inding-like domai	n superfamily			2.60.40	0,1770	
	PTHR24416:S		inding-like domai	n superfamily			2.60.40	.1770	
	PTHR24416:S	Galactose-bi	inding-like domai				2.60.40	.1770	
<u>Gene3D</u>	PTHR244151S	Galactose-bi riants (dbS	NP and all othe			j)	^a 2.60,40	.1770	
Gene3D All sequence SNPs/i Variant Legend	PTHR24416:S Sequence va	Galactose-bi riants (dbS nous varia	iNP and all othe	r sources)	ļį.				
Gene3D All sequence SNPs/i	PTHR244151S	Galactose-bi riants (dbS	NP and all othe		160	2	2.60,40	240	292

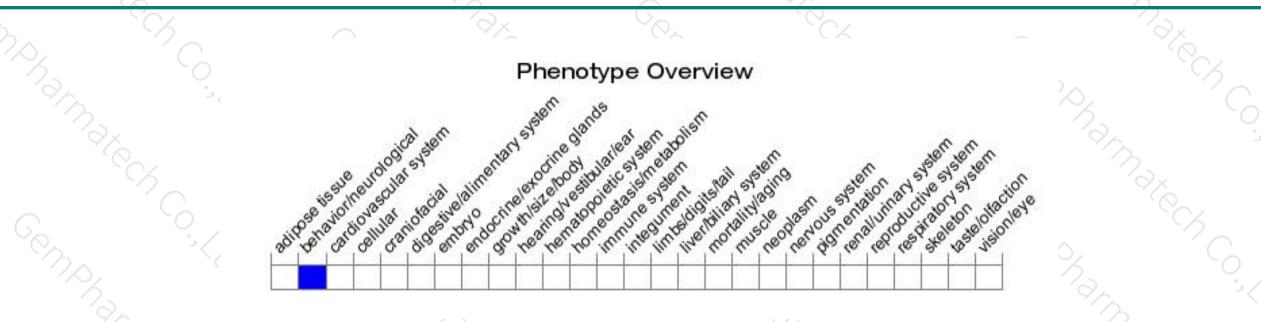
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Mouse phenotype description(MGI)





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



