

Ephb1 Cas9-KO Strategy

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Project Overview



Project Name

Ephb1

Project type

Cas9-KO

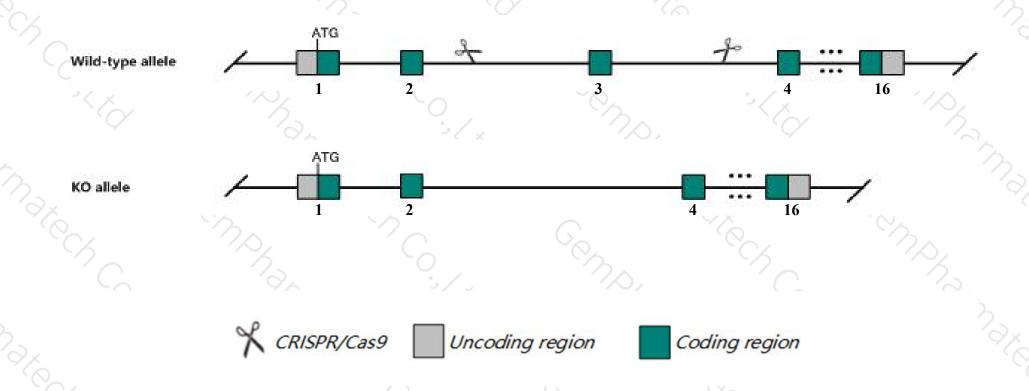
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Ephb1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Ephb1* gene has 6 transcripts. According to the structure of *Ephb1* gene, exon3 of *Ephb1-201*(ENSMUST00000035129.13) transcript is recommended as the knockout region. The region contains 682bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ephb1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for disruptions of this gene display marked reductions of the ipsilateral optic tract. Homozygotes for one null allele show reduced corticospinal tract and abnormal anterior commissure axon crossing.
- > The *Ephb1* gene is located on the Chr9. 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)



Ephb1 Eph receptor B1 [Mus musculus (house mouse)]

Gene ID: 270190, updated on 10-Oct-2019

Summary

Official Symbol Ephb1 provided by MGI

Official Full Name Eph receptor B1 provided by MGI

Primary source MGI:MGI:1096337

See related Ensembl: ENSMUSG00000032537

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 Elk; Net; Cek6; Elkh; Hek6; AW488255; 9330129L11; C130099E04Rik

Expression Biased expression in whole brain E14.5 (RPKM 16.5), CNS E18 (RPKM 12.9) and 7 other tissues See more

Orthologs human all

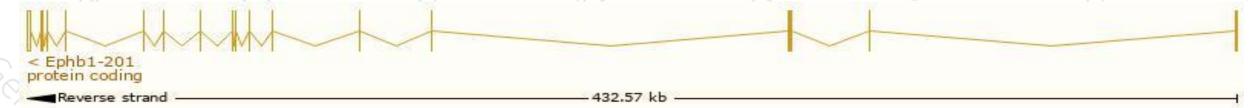
Transcript information (Ensembl)



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

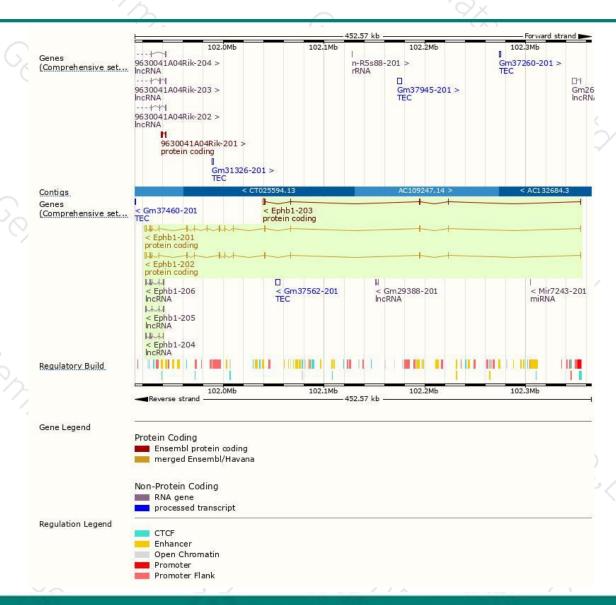
TIGATION AND AND AND AND AND AND AND AND AND AN	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			1200	0.0000000000000000000000000000000000000		`(/
Name A	Transcript ID	pb 👙	Protein	Biotype	CCDS	UniProt #	Flags
Ephb1-201	ENSMUST00000035129.13	4667	984aa	Protein coding	CCDS40742 ₽	Q8CBF3₽	TSL:1 GENCODE basic APPRIS P1
Ephb1-202	ENSMUST00000085169.11	4101	943aa	Protein coding	CCDS52901 ₽	Q8CBF3₽	TSL:1 GENCODE basic
Ephb1-203	ENSMUST00000149800.2	3471	456aa	Protein coding	Ī:	Q8CA63₽	TSL:1 GENCODE basic
Ephb1-204	ENSMUST00000215514.1	1366	No protein	IncRNA	ī.		TSL:5
Ephb1-205	ENSMUST00000217014.1	1263	No protein	IncRNA	ā.	-	TSL:5
Ephb1-206	ENSMUST00000217184.1	1419	No protein	IncRNA	-	5	TSL:5
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The strategy is based on the design of *Ephb1-201* transcript, The transcription is shown below



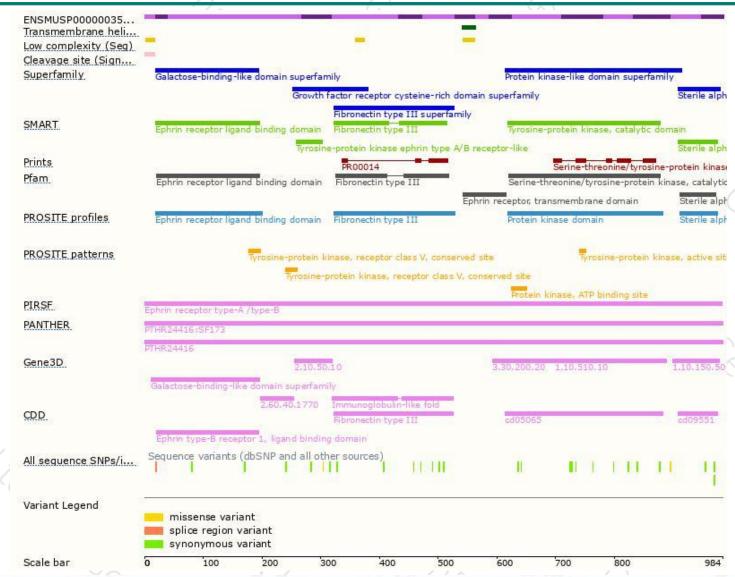
Genomic location distribution





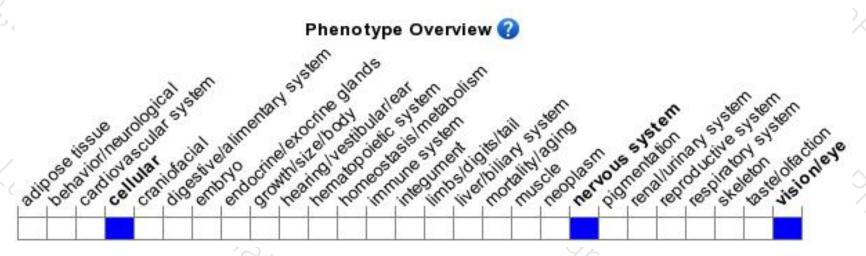
Protein domain





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 of this gene display marked reductions of the ipsilateral optic tract. Homozygotes for one null allele show reduced corticospinal tract and abnormal anterior commissure axon crossing.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





