Epha5 Cas9-KO Strategy

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Project Overview

Project Name	***Epha5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epha5* gene. The schematic diagram is as follows:

Technical routes

➢ The *Epha5* gene has 11 transcripts. According to the structure of *Epha5* gene, exon3 of *Epha5-201* (ENSMUST00000053733.14) transcript is recommended as the knockout region.The region contains 664bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Epha5* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Homozygous mutant mice are overtly normal but show abnormal retinal axon mapping.

➢ The *Epha5* gene is located on the Chr5. 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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Epha5 Eph receptor A5 [*Mus musculus* (house mouse)]

Gene ID: 13839, updated on 21-Jan-2020

Summary

Official Symbol	Epha5 provided by MGI
Official Full Name	Eph receptor A5 provided by MGI
Primary source	MGI:MGI:99654
See related	Ensembl:ENSMUSG00000029245
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	bsk; Cek7; Ehk1; Els1; Hek7; Rek7; AI854630; AW125296
Expression	Biased expression in CNS E18 (RPKM 9.2), frontal lobe adult (RPKM 7.7) and 6 other tissues See more
Orthologs	human all

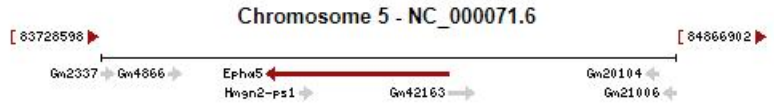
Genomic context

Location: 5 E1; 5 43.0 cM

See Epha5 in Genome Data Viewer

Exon count: 20

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (84054761..84417818, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (84483786..84846407, complement)

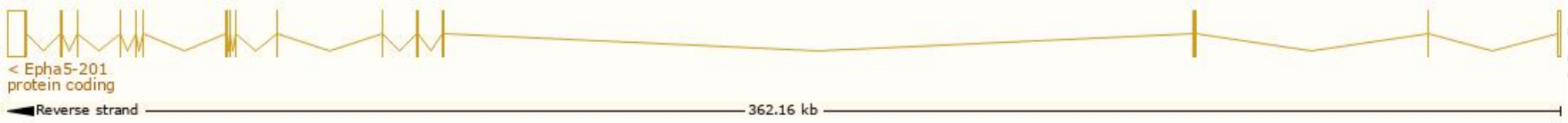


Transcript information（Ensembl）

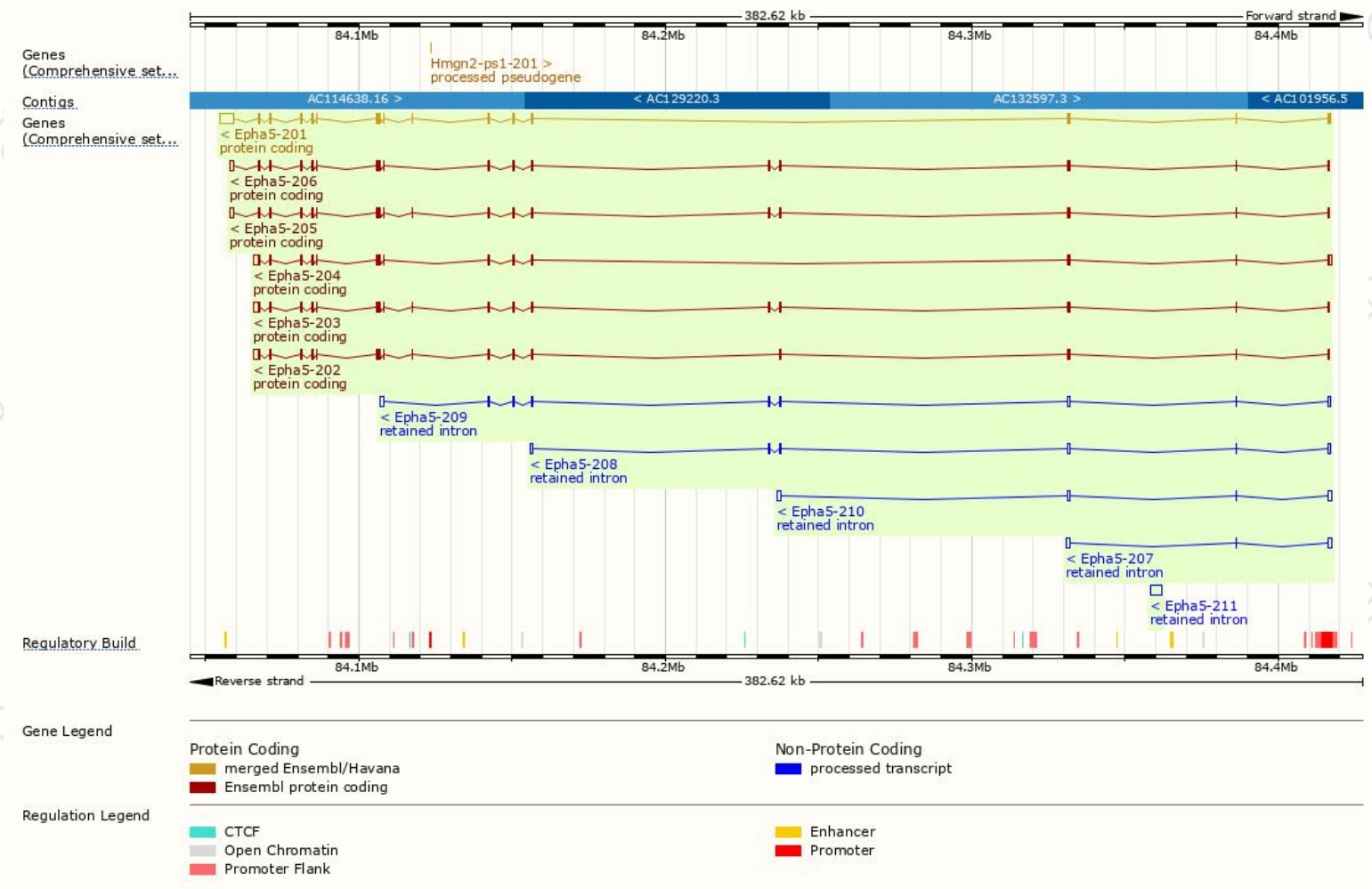
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epha5-201	ENSMUST00000053733.14	7328	876aa	Protein coding	CCDS19376	Q60629	TSL:1 GENCODE basic
Epha5-203	ENSMUST00000113399.5	5166	1006aa	Protein coding	-	E9PUQ2	TSL:5 GENCODE basic APPRIS ALT2
Epha5-204	ENSMUST00000113401.3	5158	819aa	Protein coding	-	Q6PFV6	TSL:1 GENCODE basic
Epha5-202	ENSMUST00000113398.7	4830	894aa	Protein coding	-	E9PUQ4	TSL:5 GENCODE basic
Epha5-205	ENSMUST00000113403.7	4675	1040aa	Protein coding	-	E9PUQ0	TSL:5 GENCODE basic APPRIS P5
Epha5-206	ENSMUST00000113406.7	4606	1017aa	Protein coding	-	E9PUP9	TSL:5 GENCODE basic APPRIS ALT2
Epha5-211	ENSMUST00000200076.1	3677	No protein	Retained intron	-	-	TSL:NA
Epha5-209	ENSMUST00000154804.7	3236	No protein	Retained intron	-	-	TSL:5
Epha5-210	ENSMUST00000155469.7	2933	No protein	Retained intron	-	-	TSL:5
Epha5-208	ENSMUST00000152573.7	2496	No protein	Retained intron	-	-	TSL:5
Epha5-207	ENSMUST00000136775.1	2246	No protein	Retained intron	-	-	TSL:1

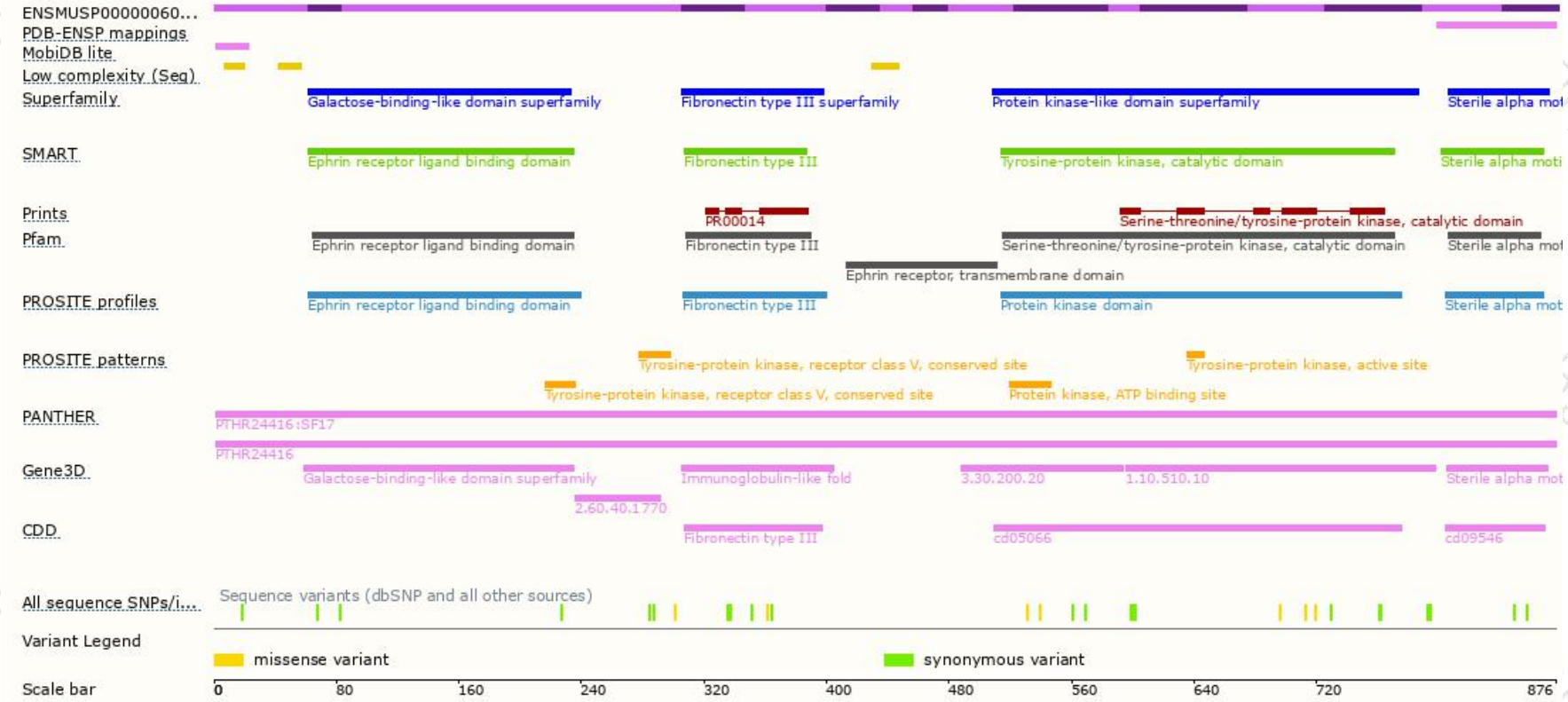
The strategy is based on the design of *Epha5-201* transcript,The transcription is shown below



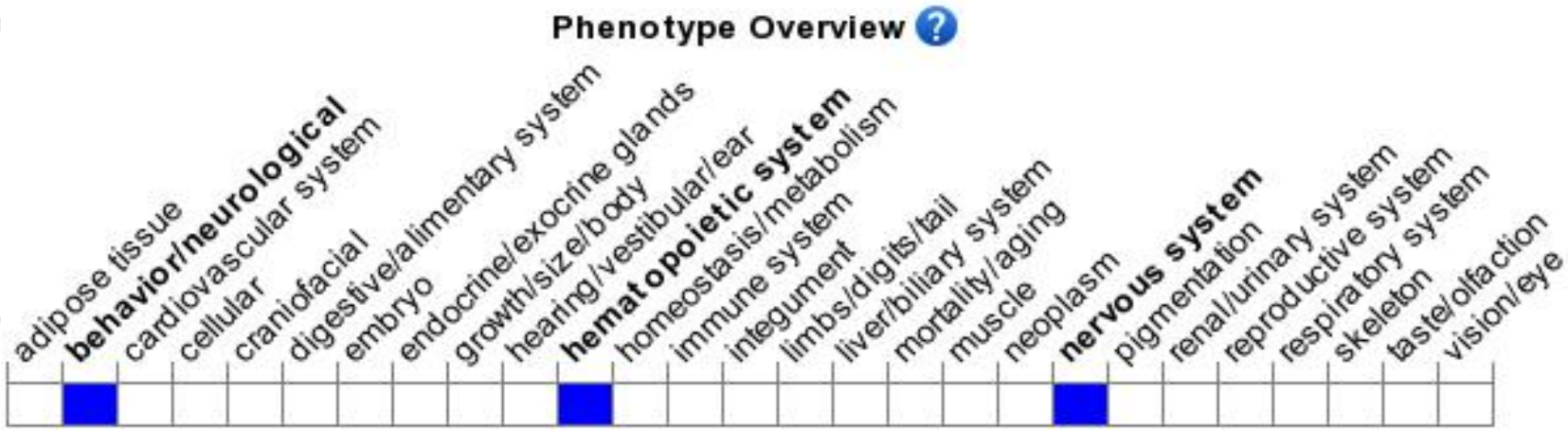
Genomic location distribution



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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