

# *Efna5* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Efna5*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Efna5* gene. The schematic diagram is as follows:



- The *Efna5* gene has 2 transcripts. According to the structure of *Efna5* gene, exon2 of *Efna5-201* (ENSMUST00000076840.11) transcript is recommended as the knockout region. The region contains 293bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Efna5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit abnormalities in establishing correct axonal connections involving the retinal, motor, vomeronasal, and tactile axons to their respective targets. Some mutants develop neural tube defects.
- The *Efna5* gene is located on the Chr17. 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)

## Efna5 ephrin A5 [ *Mus musculus* (house mouse) ]

Gene ID: 13640, updated on 14-Dec-2019

### Summary

**Official Symbol** Efna5 provided by [MGI](#)  
**Official Full Name** ephrin A5 provided by [MGI](#)  
**Primary source** [MGI:MGI:107444](#)  
**See related** [Ensembl:ENSMUSG00000048915](#)  
**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** AL-1; Epl7; RAGS; EFL-5; LERK-7; AV158822; Ephrin-A5  
**Expression** Broad expression in CNS E11.5 (RPKM 7.2), limb E14.5 (RPKM 6.9) and 21 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)

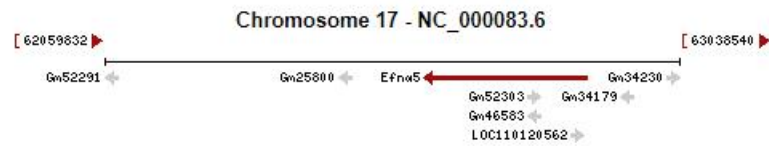
### Genomic context

Location: 17 E1.1; 17 32.57 cM

[See Efna5 in Genome Data Viewer](#)

Exon count: 8

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	17	NC_000083.6 (62602957..62881317, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	17	NC_000083.5 (62952306..63230666, complement)

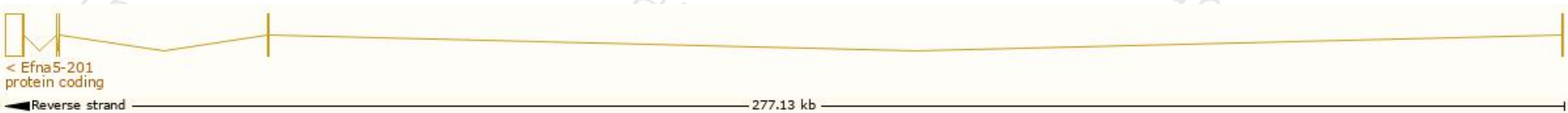


# Transcript information (Ensembl)

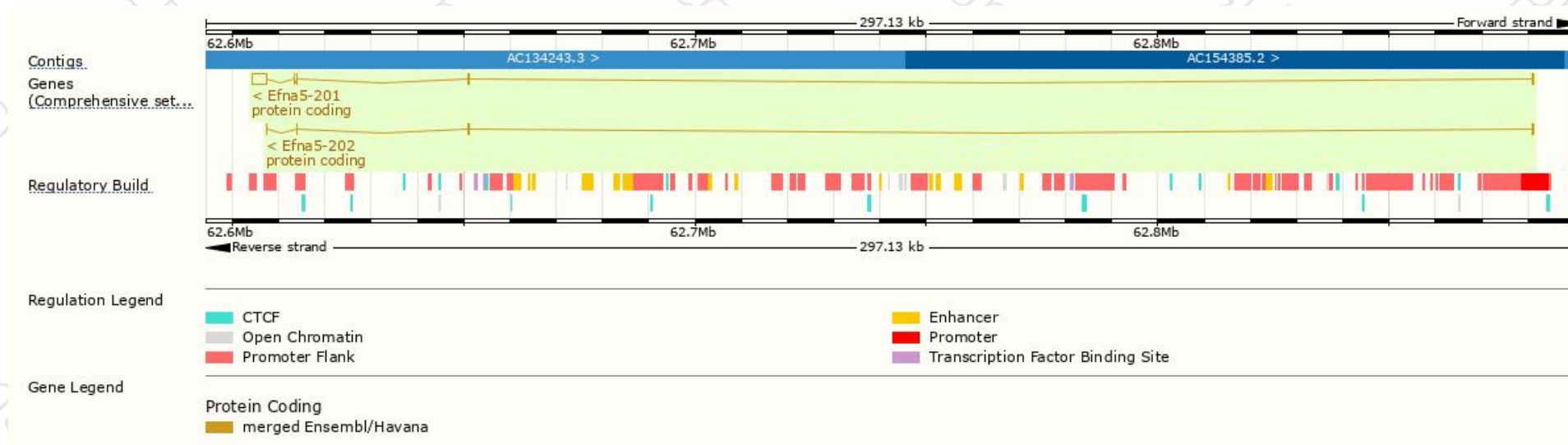
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Efna5-201	<a href="#">ENSMUST00000076840.11</a>	4032	<a href="#">228aa</a>	Protein coding	<a href="#">CCDS28935</a>	<a href="#">O08543</a>	TSL:1 GENCODE basic APPRIS P4
Efna5-202	<a href="#">ENSMUST00000078839.4</a>	643	<a href="#">201aa</a>	Protein coding	<a href="#">CCDS28934</a>	<a href="#">O08543</a>	TSL:1 GENCODE basic APPRIS ALT1

The strategy is based on the design of *Efna5-201* transcript,The transcription is shown below

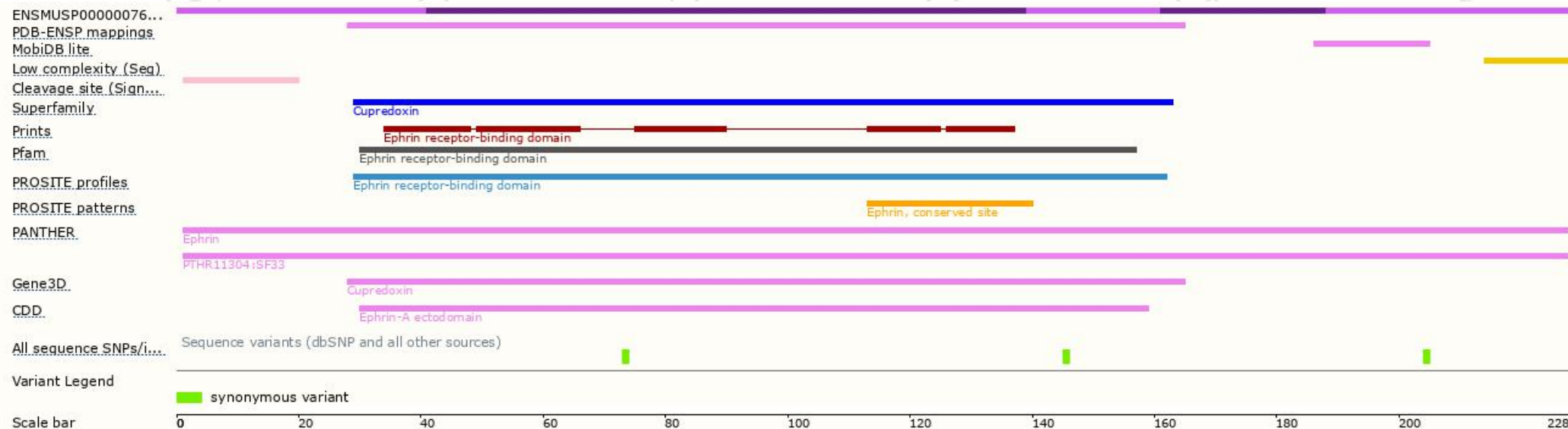


# Genomic location distribution

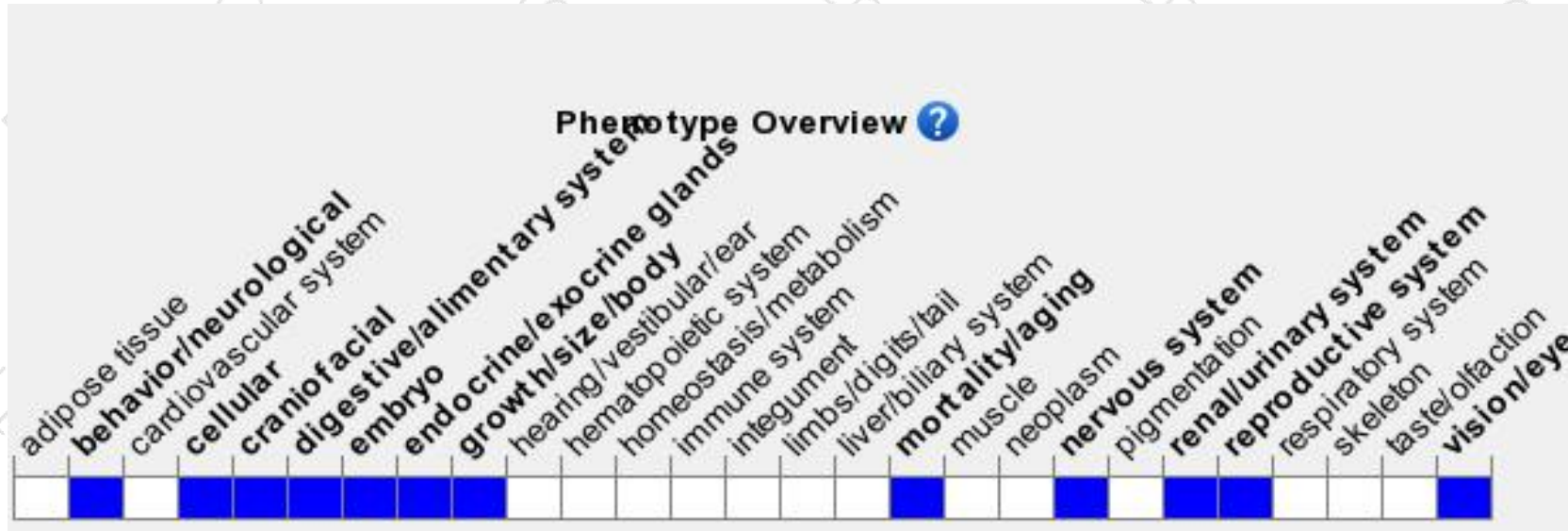




# Protein domain



# 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, Homozygotes for targeted null mutations exhibit abnormalities in establishing correct axonal connections involving the retinal, motor, vomeronasal, and tactile axons to their respective targets. Some mutants develop neural tube defects.

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

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