

# *Unc13b* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2019-8-22**

# Project Overview

**Project Name**

***Unc13b***

**Project type**

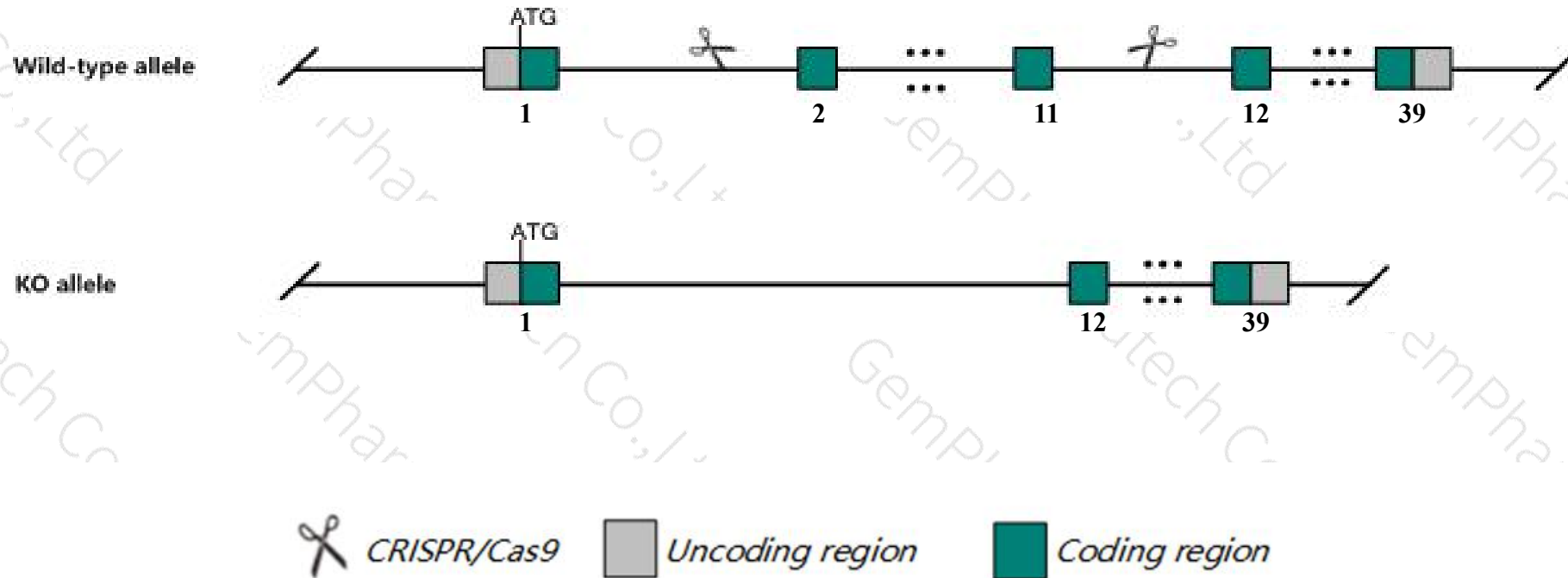
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Unc13b* gene. The schematic diagram is as follows:



- The *Unc13b* gene has 16 transcripts. According to the structure of *Unc13b* gene, exon2-exon11 of *Unc13b-201* (ENSMUST00000079978.12) transcript is recommended as the knockout region. The region contains 1192bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Unc13b* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice are grossly phenotypically normal. Mice older than 12 months will exhibit sporadic seizures.
- The KO region contains *Gm23709* and *Gm25010* gene. Knockout the region will delete them.
- The *Unc13b* 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.



# Gene information (NCBI)

## Unc13b unc-13 homolog B [Mus musculus (house mouse)]

Gene ID: 22249, updated on 19-Mar-2019

### Summary



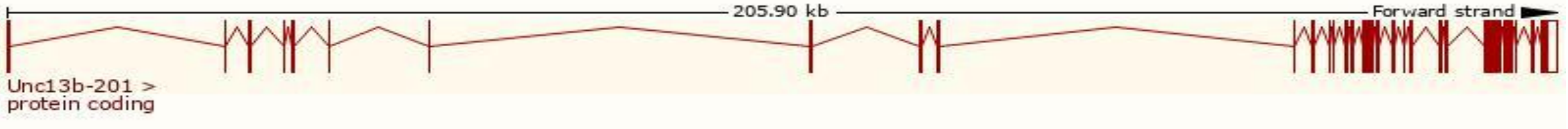
|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Unc13b provided by <a href="#">MGI</a>  |
| <b>Official Full Name</b> | unc-13 homolog B provided by <a href="#">MGI</a>  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1342278</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000028456</a>  |
| <b>Gene type</b>          | protein coding  |
| <b>RefSeq status</b>      | VALIDATED   |
| <b>Organism</b>           | <a href="#">Mus musculus</a>  |
| <b>Lineage</b>            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| <b>Also known as</b>      | Munc13-1, Munc13-2, Unc13a, Unc13h1, Unc13h2  |
| <b>Expression</b>         | Broad expression in CNS E18 (RPKM 6.9), CNS E14 (RPKM 6.8) and 23 other tissues <a href="#">See more</a>  |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>   |

# Transcript information (Ensembl)

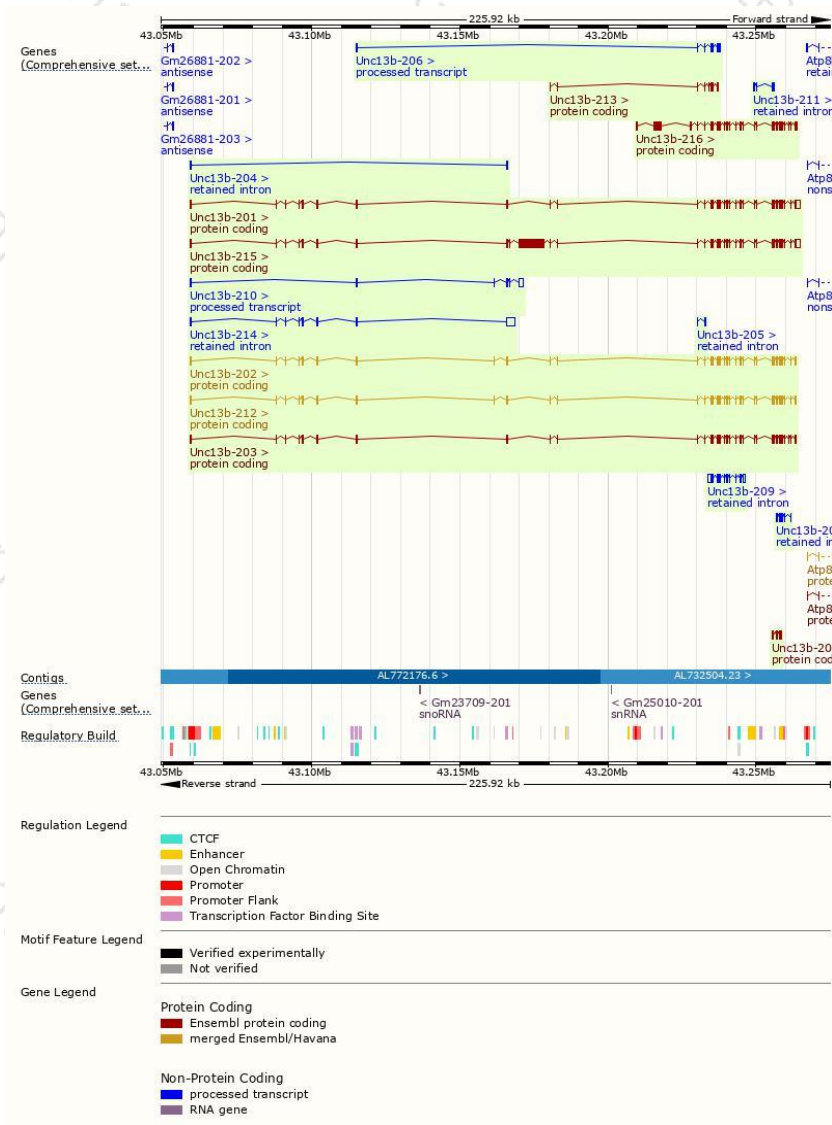
The gene has 16 transcripts,all transcripts are shown below:

| Name       | Transcript ID                         | bp    | Protein                | Biotype              | CCDS                      | UniProt                    | Flags   |
|------------|---------------------------------------|-------|------------------------|----------------------|---------------------------|----------------------------|---|
| Unc13b-201 | <a href="#">ENSMUST00000079978.12</a> | 6354  | <a href="#">1590aa</a> | Protein coding       | <a href="#">CCDS80089</a> | <a href="#">Q9Z1N9</a>     | TSL:5 GENCODE basic APPRIS P2   |
| Unc13b-202 | <a href="#">ENSMUST000000107952.8</a> | 5037  | <a href="#">1602aa</a> | Protein coding       | <a href="#">CCDS51161</a> | <a href="#">Q9Z1N9</a>     | TSL:1   |
| Unc13b-212 | <a href="#">ENSMUST000000163653.7</a> | 5034  | <a href="#">1601aa</a> | Protein coding       | <a href="#">CCDS38738</a> | <a href="#">Q9Z1N9</a>     | TSL:1   |
| Unc13b-215 | <a href="#">ENSMUST000000207569.1</a> | 14754 | <a href="#">4390aa</a> | Protein coding       | -                         | <a href="#">A0A140LJ69</a> | TSL:5 GENCODE basic   |
| Unc13b-216 | <a href="#">ENSMUST000000207708.1</a> | 6574  | <a href="#">1982aa</a> | Protein coding       | -                         | <a href="#">A0A140LHX5</a> | TSL:5 GENCODE basic   |
| Unc13b-203 | <a href="#">ENSMUST000000107953.8</a> | 5034  | <a href="#">1609aa</a> | Protein coding       | -                         | <a href="#">E9Q263</a>     | TSL:5 GENCODE basic APPRIS ALT 1  |
| Unc13b-213 | <a href="#">ENSMUST000000168032.1</a> | 768   | <a href="#">256aa</a>  | Protein coding       | -                         | <a href="#">F6X605</a>     | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Unc13b-208 | <a href="#">ENSMUST000000145899.1</a> | 569   | <a href="#">189aa</a>  | Protein coding       | -                         | <a href="#">F7CEK4</a>     | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Unc13b-210 | <a href="#">ENSMUST000000151611.8</a> | 2173  | No protein             | Processed transcript | -                         | -                          | TSL:1   |
| Unc13b-206 | <a href="#">ENSMUST000000132310.8</a> | 780   | No protein             | Processed transcript | -                         | -                          | TSL:5   |
| Unc13b-214 | <a href="#">ENSMUST000000171234.1</a> | 3617  | No protein             | Retained intron      | -                         | -                          | TSL:1   |
| Unc13b-209 | <a href="#">ENSMUST000000149945.2</a> | 3258  | No protein             | Retained intron      | -                         | -                          | TSL:2   |
| Unc13b-207 | <a href="#">ENSMUST000000143653.2</a> | 1036  | No protein             | Retained intron      | -                         | -                          | TSL:5   |
| Unc13b-211 | <a href="#">ENSMUST000000153168.2</a> | 856   | No protein             | Retained intron      | -                         | -                          | TSL:3   |
| Unc13b-204 | <a href="#">ENSMUST000000126878.1</a> | 712   | No protein             | Retained intron      | -                         | -                          | TSL:3   |
| Unc13b-205 | <a href="#">ENSMUST000000127597.1</a> | 495   | No protein             | Retained intron      | -                         | -                          | TSL:3   |

The strategy is based on the design of *Unc13b-201* transcript,The transcription is shown below



# Genomic location distribution

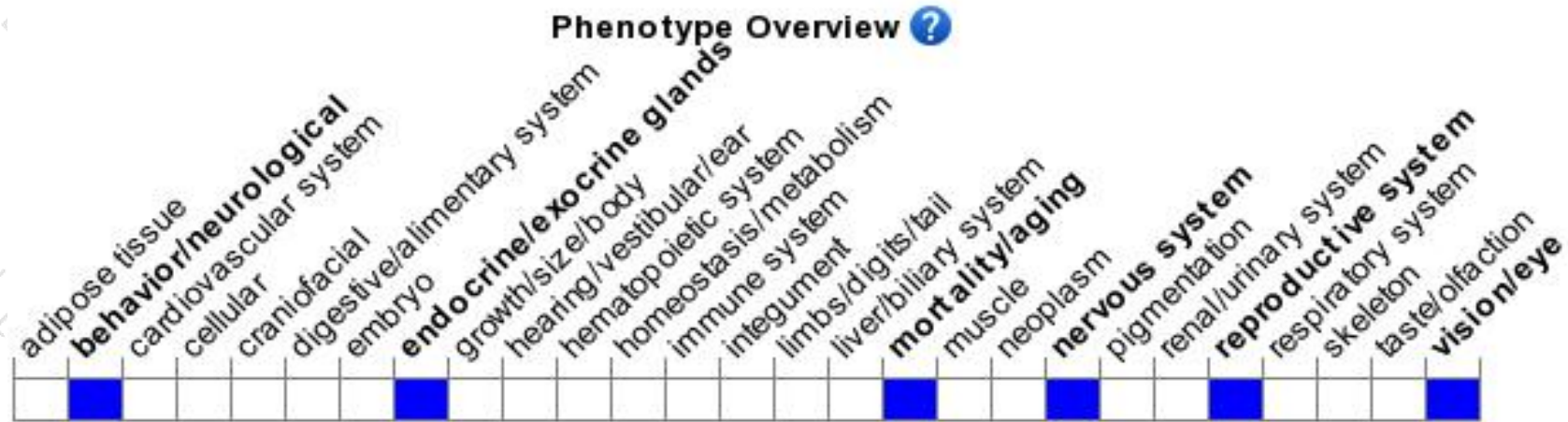




# Protein domain



# 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, Homozygous mutant mice are grossly phenotypically normal. Mice older than 12 months will exhibit sporadic seizures.

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

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