# *Unc13c* Cas9-KO Strategy

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# Project Overview

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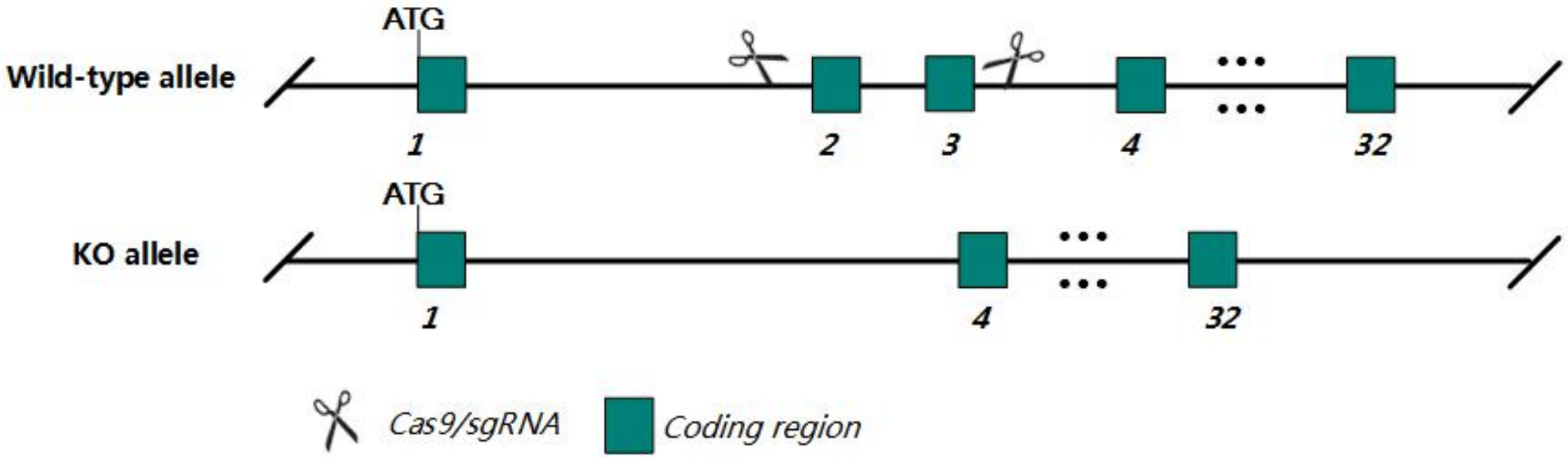
|---|---|
| **Project Name** | ***Unc13c*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6J** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Unc13c* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Unc13c* gene has 2 transcripts. According to the structure of *Unc13c* gene, exon2-exon3 of *Unc13c-201* (ENSMUST00000075245.6) transcript is recommended as the knockout The region contains 88bp coding sequence. Knock out the region will result in disruption of protein function.

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➢ In this project we use CRISPR/Cas9 technology to modify *Unc13c* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

# Notice

- According to the existing MGI data,Homozygous mutant mice demonstrate an impaired ability to learn complex motor tasks, putatively due to an observed increase in paired-pulse facilitation.

- The N-terminal of *Unc13c* gene will remain 990aa,it may remain the partial function of *Unc13c* gene.

- The *Unc13c* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Unc13c unc-13 homolog C [Mus musculus (house mouse)]

Gene ID: 208898, updated on 12-Feb-2019

### Summary

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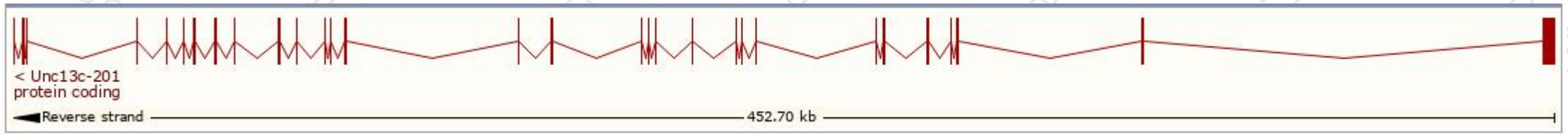
|---|---|
| **Official Symbol** | Unc13c provided by MGI |
| **Official Full Name** | unc-13 homolog C provided byMGI |
| **Primary source** | MGI:MGI:2149021 |
| **See related** | Ensembl:ENSMUSG00000062151 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 1500037O19Rik, D9Ertd414e, Munc13-3, Unc13h3 |
| **Expression** | Biased expression in cerebellum adult (RPKM 10.0), cortex adult (RPKM 1.5) and 3 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

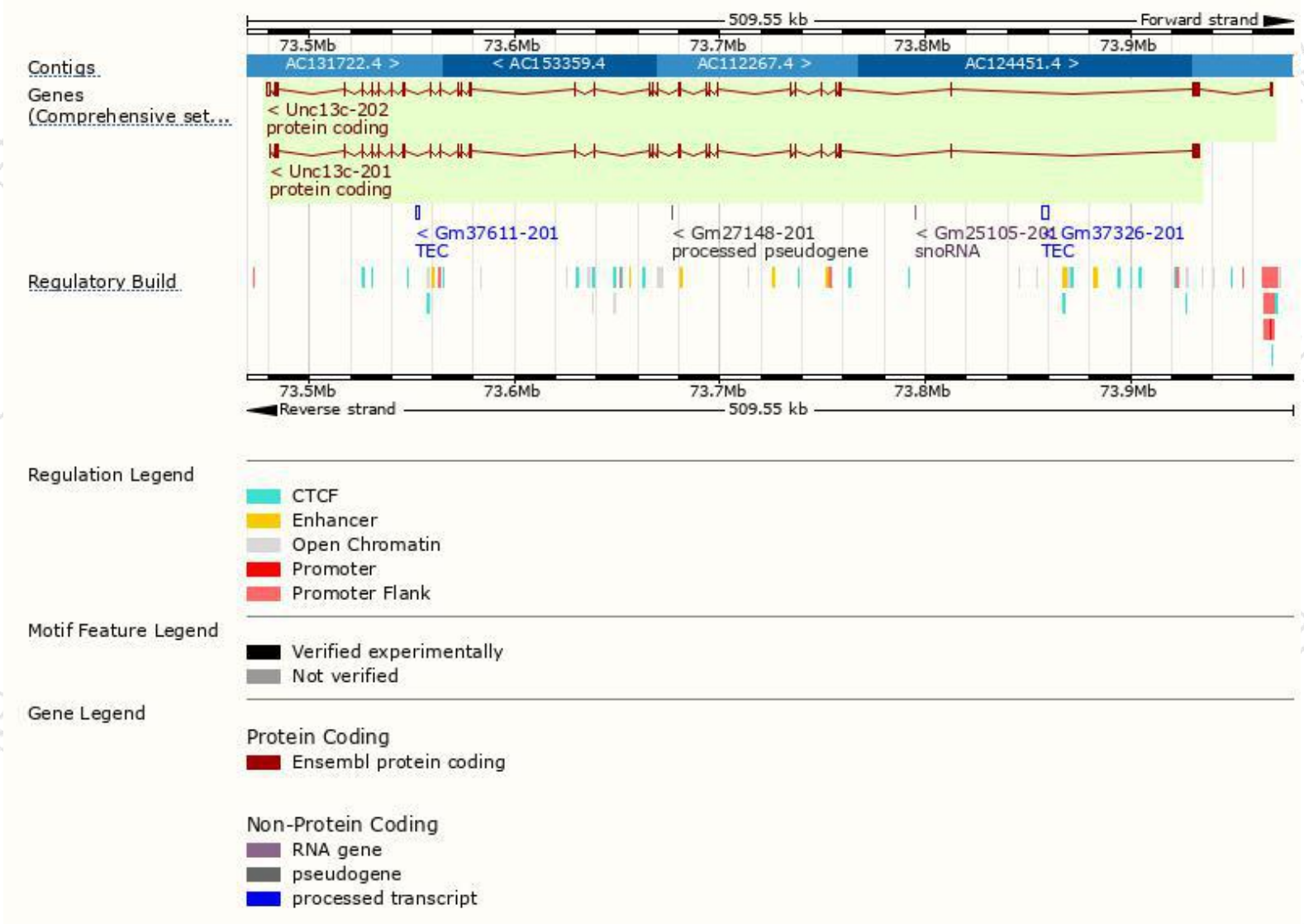
The gene has 2 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Unc13c-202 | ENSMUST00000184666.7 | 8796 | 2210aa | Protein coding | CCDS40690 | Q8K0T7 | TSL:5 GENCODE basic APPRIS P1 |
| Unc13c-201 | ENSMUST00000075245.6 | 6633 | 2210aa | Protein coding | CCDS40690 | Q8K0T7 | TSL:5 GENCODE basic APPRIS P1 |

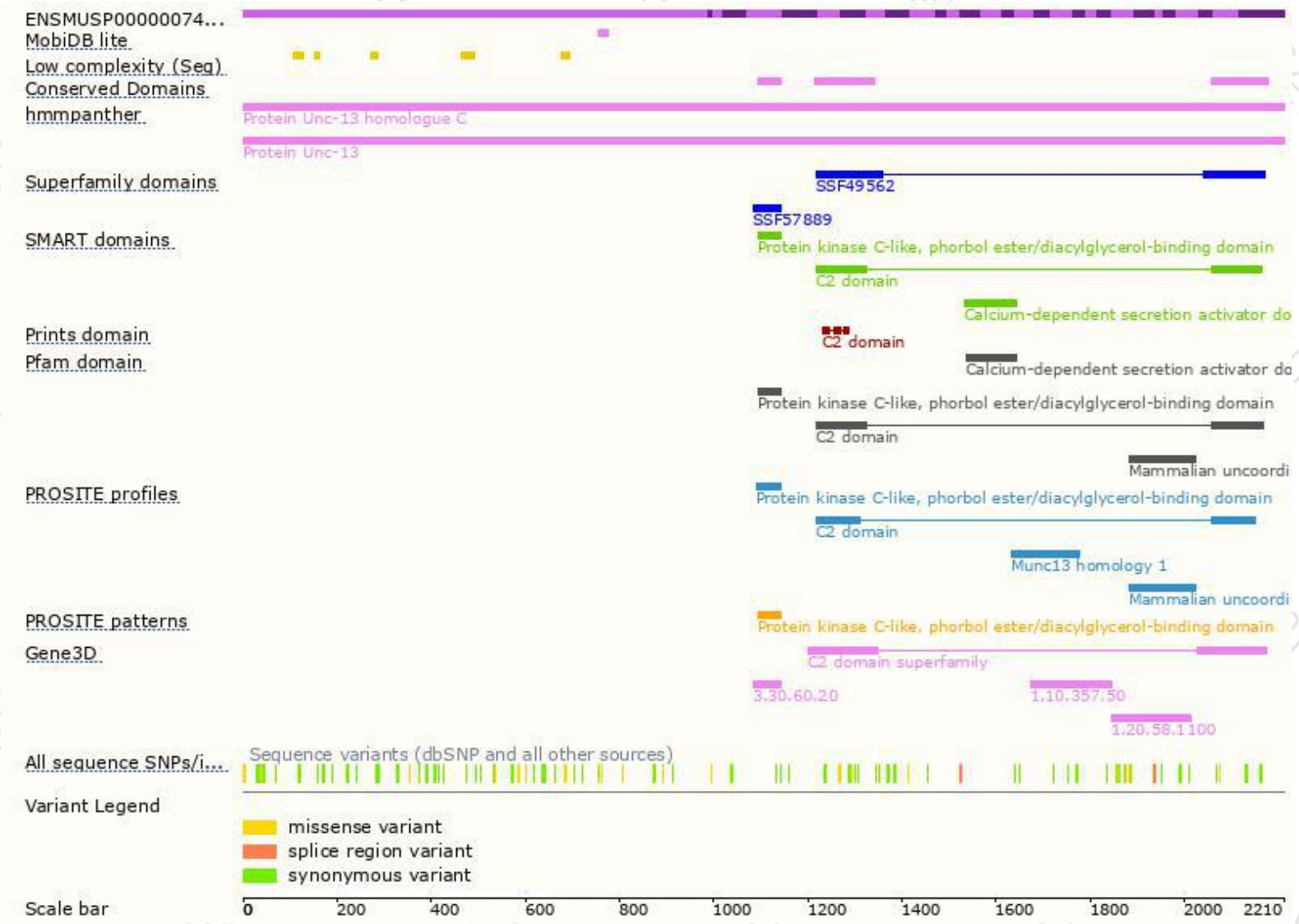
The strategy is based on the design of *Unc13c-201* transcript,The transcription is shown below



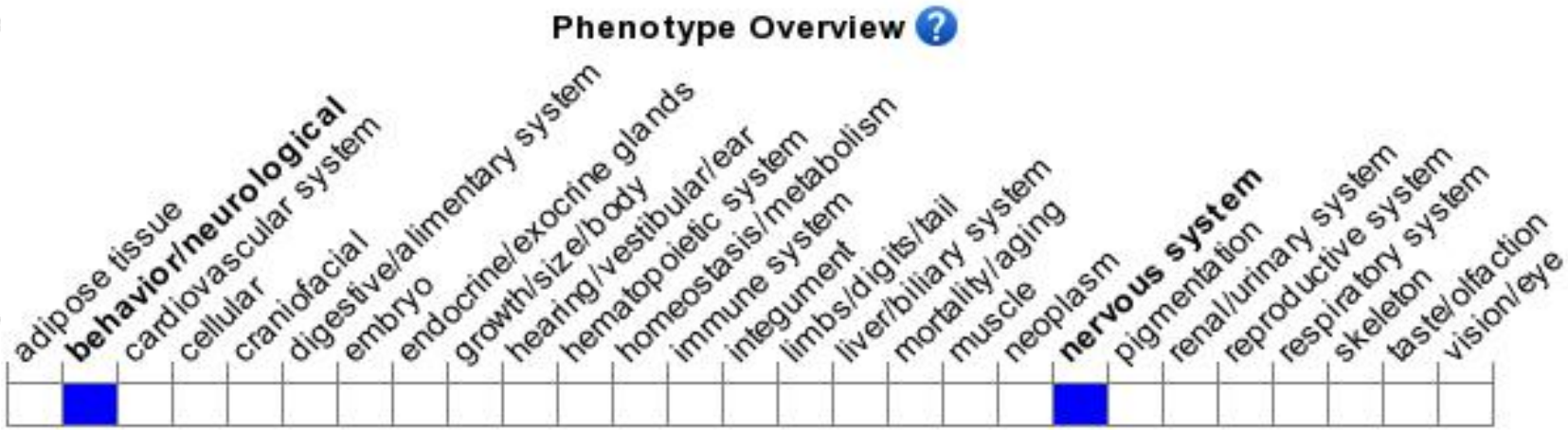
# Genomic location distribution



# 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 demonstrate an impaired ability to learn complex motor tasks, putatively due to an observed increase in paired-pulse facilitation.

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

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