

Unc13c Cas9-CKO Strategy

Designer:

Daohua Xu

Project Overview



Project Name

Unc13c

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

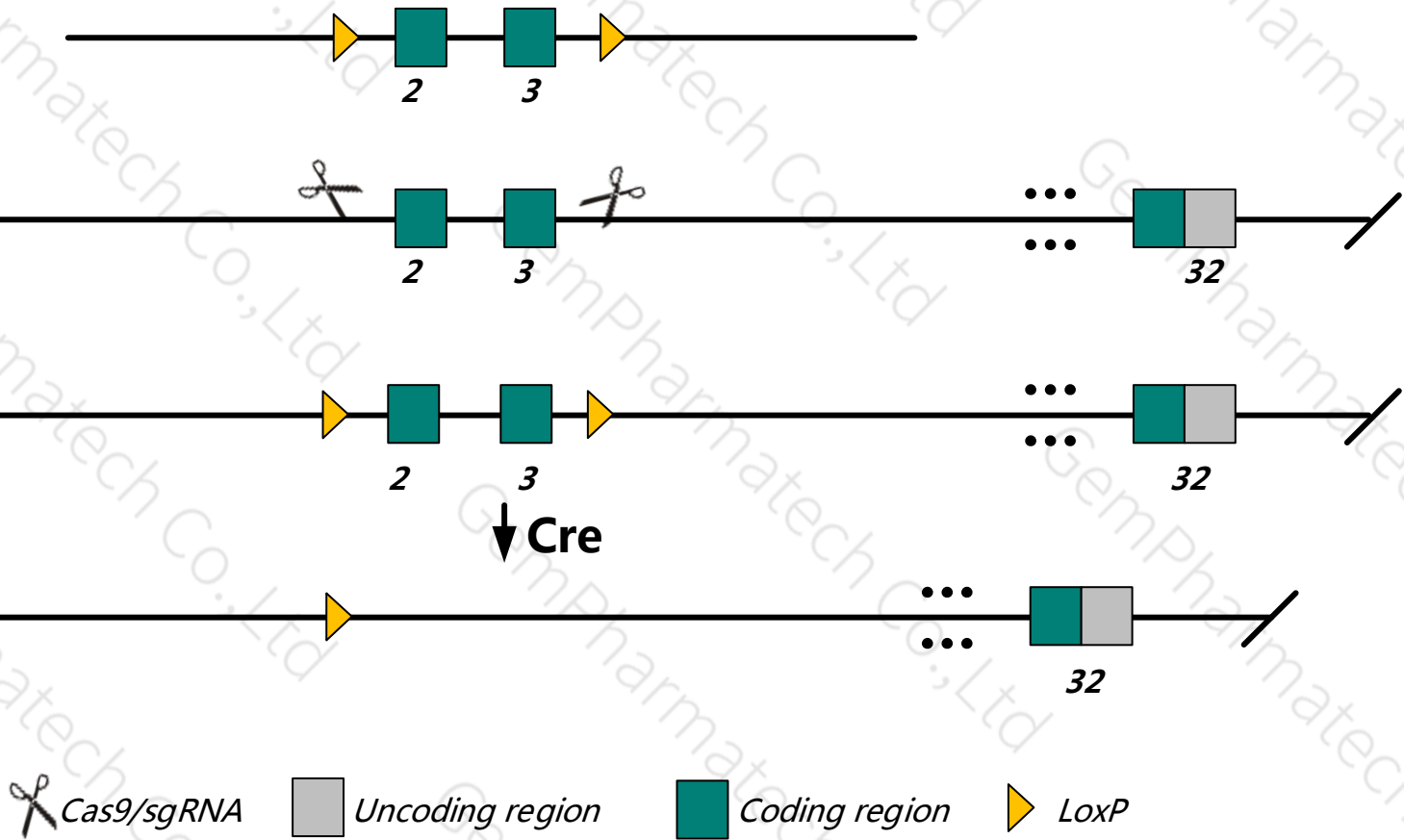
This model will use CRISPR/Cas9 technology to edit the *Unc13c* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Conditional KO allele

KO allele



- 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 region. The region contains 88bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Unc13c* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- 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 *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 biological processes, all risk of the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

Gene ID: 208898, updated on 9-Sep-2018

Summary

Official Symbol Unc13c provided by [MGI](#)

Official Full Name unc-13 homolog C provided by [MGI](#)

Primary source [MGI:MGI:2149021](#)

See related [Ensembl:ENSMUSG000000062151](#) [Vega:OTTMUSG000000044794](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus


Also known as Unc13h3; AU019458; Munc13-3; D9Ert414e; 1500037O19Rik

Expression Biased expression in cerebellum adult (RPKM 10.0), cortex adult (RPKM 1.5) and 3 other tissues [See more](#)

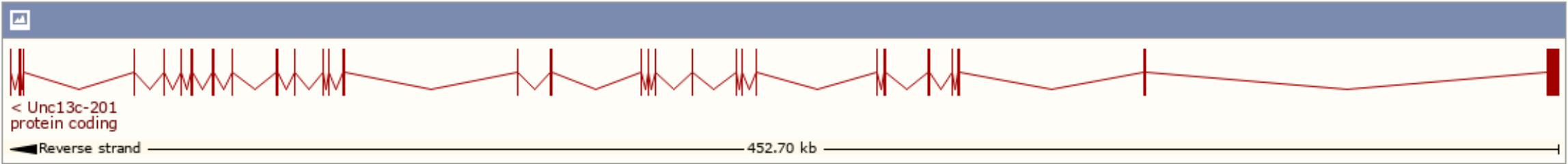
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

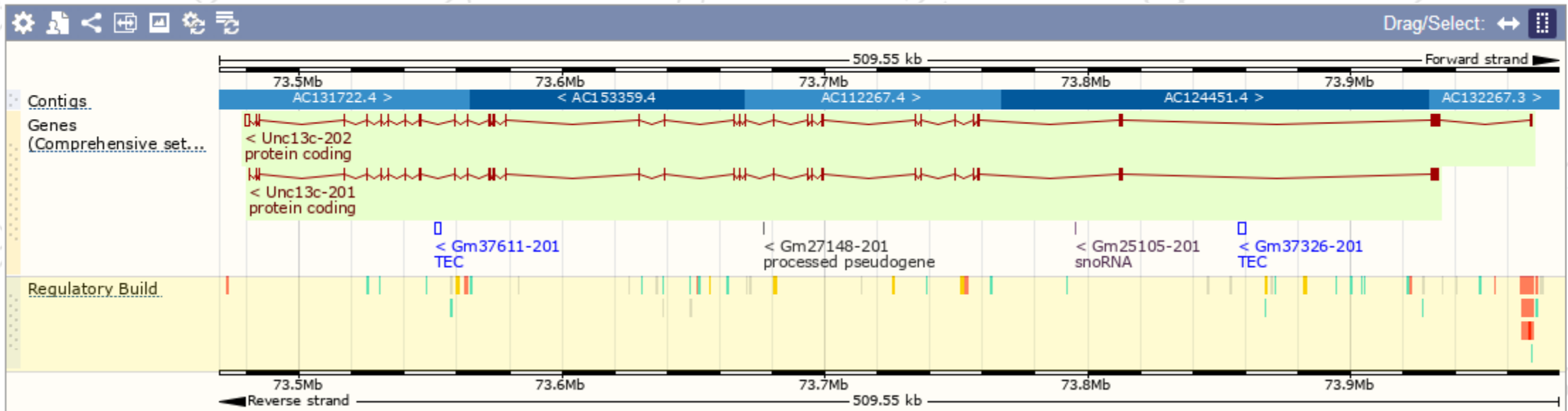
The gene has 2 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	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	NM_001081153 NP_001074622	TSL:5	GENCODE basic APPRIS P1

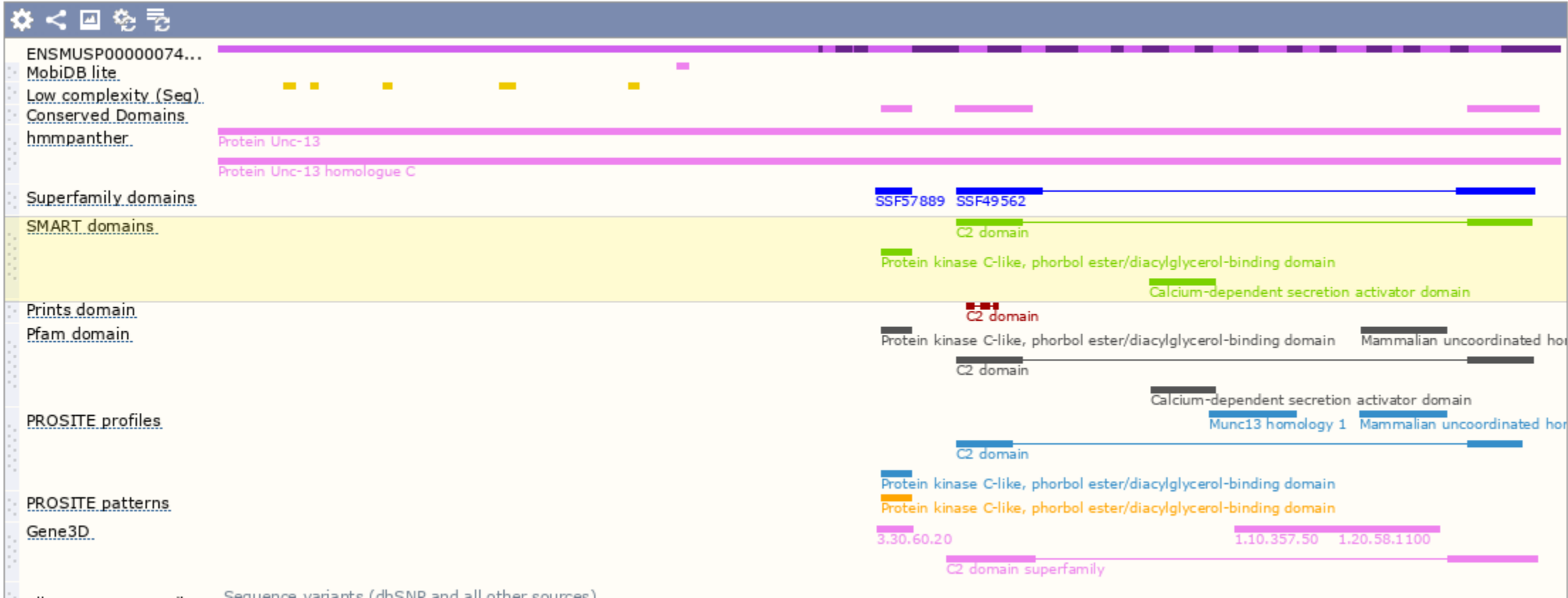
The strategy is based on the design of *Unc13c*-201 transcript, The transcription is shown below



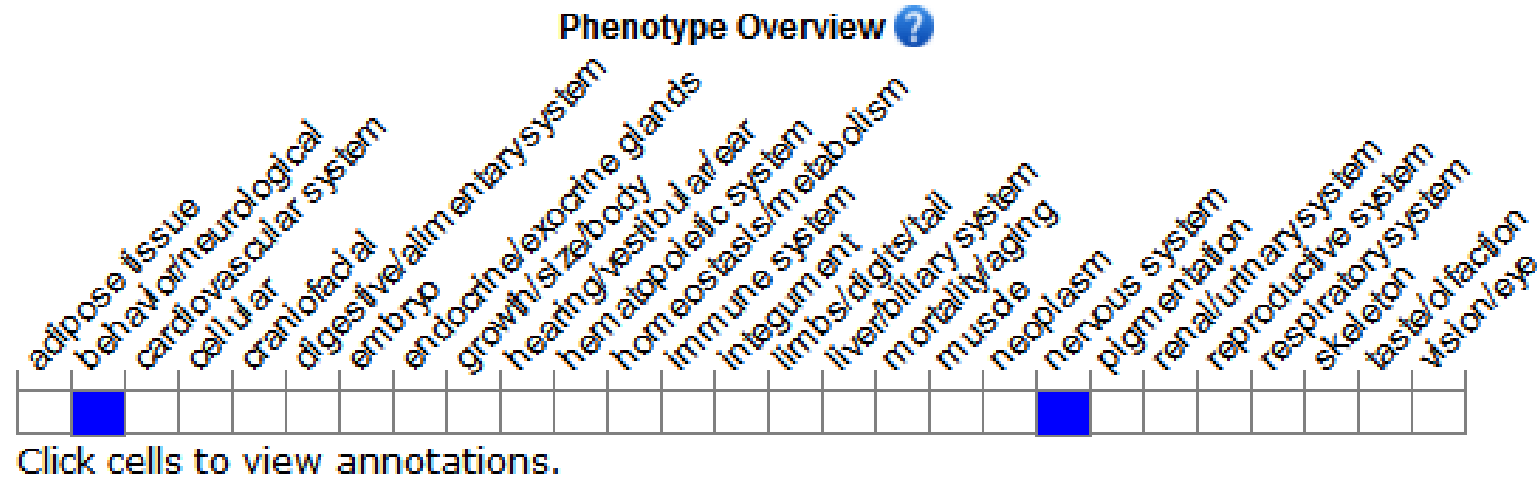
Genomic location distribution



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.

If you have any questions, you are welcome to inquire.
Tel: 025-5864 1534



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