

# Top2b Cas9-CKO Strategy

Designer: Xingkai Xiao

Reviewer: Yanhua Shen

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### Overview

#### **Target Gene Name**

• *Top2b* 

#### **Project Type**

• Cas9-CKO

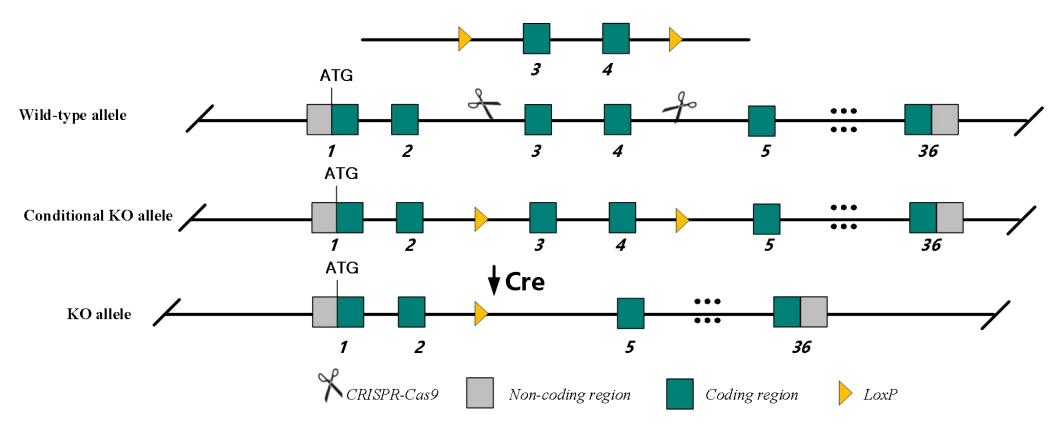
#### Genetic Background

• C57BL/6JGpt

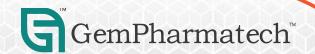


# Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Top2b* gene.



#### **Technical Information**

- The *Top2b* gene has 8 transcripts. According to the structure of *Top2b* gene, exon3-4 of *Top2b*-201 (ENSMUST00000017629.12) transcript is recommended as the knockout region. The region contains 155 bp of coding sequences. Knocking out the region will result in deletion the most coding region of *Top2b*, which may disrupt the function of *Top2b*.
- In this project we use CRISPR-Cas9 technology to modify *Top2b* gene. The brief process is as follows: CRISPR-Cas9 system 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



#### Gene Information

Top2b topoisomerase (DNA) II beta [ Mus musculus (house mouse) ]

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Gene ID: 21974, updated on 7-Sep-2023



Official Symbol Top2b provided by MGI

Official Full Name topoisomerase (DNA) II beta provided by MGI

Primary source MGI:MGI:98791

See related Ensembl: ENSMUSG00000017485 Alliance Genome: MGI:98791

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 Top-2; D230016L12Rik

**Summary** Predicted to enable several functions, including enzyme binding activity; protein C-terminus binding activity; and protein

heterodimerization activity. Acts upstream of or within axonogenesis; forebrain development; and neuron migration. Located in nucleus. Is expressed in central nervous system; genitourinary system; and retina. Orthologous to human TOP2B (DNA

topoisomerase II beta). [provided by Alliance of Genome Resources, Apr 2022]

Expression Broad expression in CNS E11.5 (RPKM 40.7), CNS E14 (RPKM 36.8) and 22 other tissues See more

Orthologs human all

Try the new Gene table

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

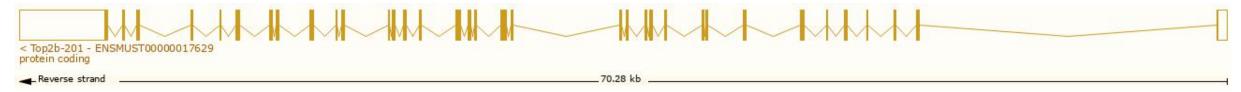


# Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

Transcript ID 🔻	Name 🍦	bp 🍦	Protein 🍦	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000224695.2	Top2b-208	837	No protein	Retained intron		=	÷
ENSMUST00000224460.2	Top2b-207	3401	No protein	Retained intron		-	5
ENSMUST00000163032.2	Top2b-206	634	No protein	Retained intron		=	TSL:3
ENSMUST00000161693.2	Top2b-205	1044	<u>348aa</u>	Protein coding		<u>F6XX57</u> ₺	TSL:5 CDS 5' and 3' incomplete
ENSMUST00000160501.8	Top2b-204	689	230aa	Protein coding		<u>F6U5K2</u> ₽	TSL:3 CDS 5' and 3' incomplete
ENSMUST00000159987.2	Top2b-203	671	No protein	Retained intron		-	TSL:2
ENSMUST00000159302.2	Top2b-202	658	No protein	Protein coding CDS not defined		2	TSL:3
ENSMUST00000017629.12	Top2b-201	10335	1612aa	Protein coding	CCDS26833 ₽	Q64511 ₽	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1

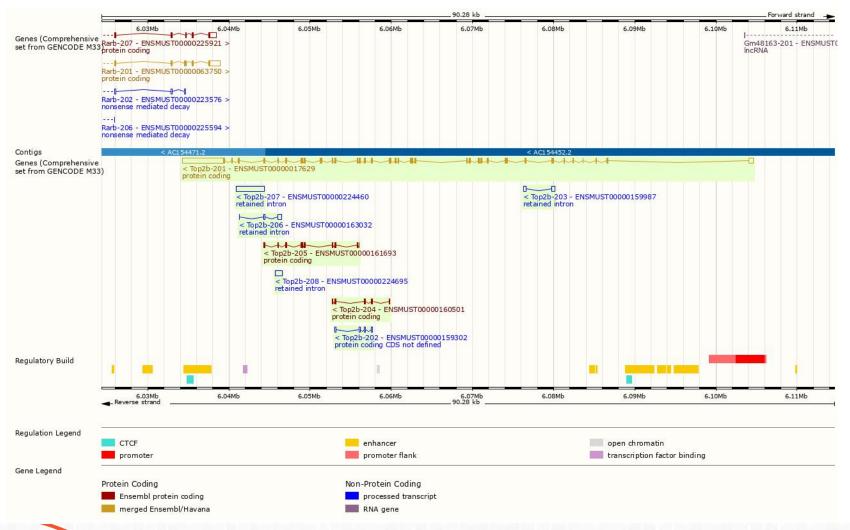
The strategy is based on the design of *Top2b*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



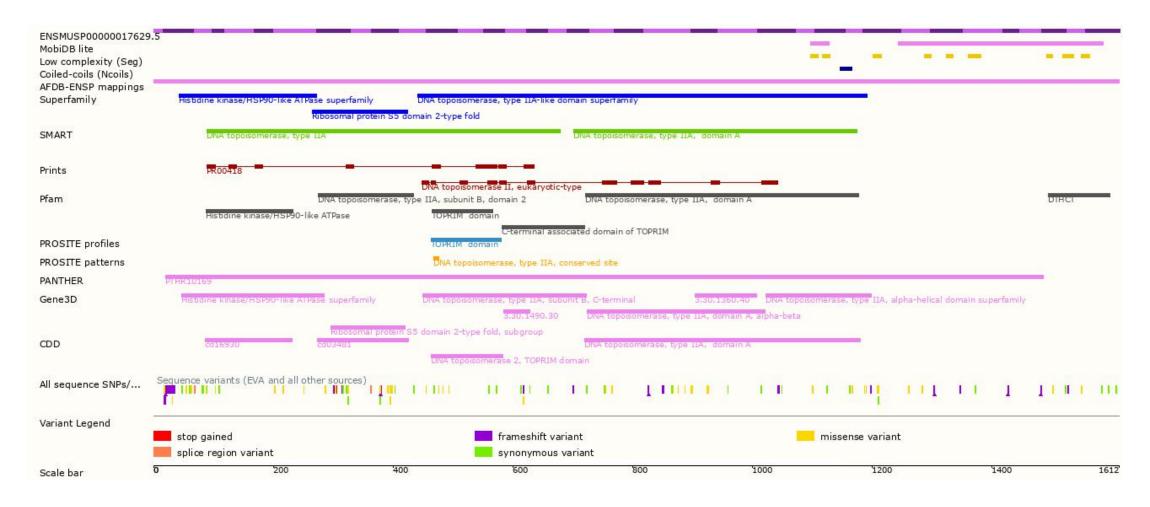
## Genomic Information





Source: : https://www.ensembl.org

#### Protein Information





Source: : https://www.ensembl.org

# Important Information

- Homozygous null mice exhibit abnormal innervation. Offspring die shortly after birth due to respiratory failure. Conditional KO in the retina results in postnatal retinal degeneration.
- The 5' of transcription *Top2b*-204, 205, the effect is unknown.
- This stratergy is not affect the *Top2b*-202, 204, 206, 207 and 208, the risk is unknown.
- *Top2b* is located on Chr14. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



#### Reference

[1]Yang,X. DNA Topoisomerase IIβ and Neural Development [J]. Science, 2000, 287(5450):131-134. DOI:10.1126/science.287.5450.131.

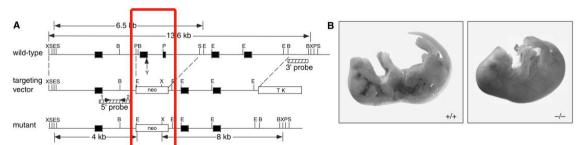


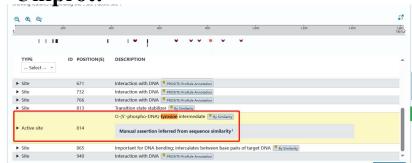
Fig. 1. (A) The relevant regions in the WT murine  $TOP2\beta$  gene (upper), the neo/TK targeting vector (middle), and the mutated  $top2\beta$  allele (lower). Coding stretches are represented by filled boxes; B, E, P, S, and X denote restriction sites of Bam HI, Eco RI, Pst I, Sac I, and Xba I, respectively, and neo and TK denote the neomycin-resistance and thymidine kinase markers. The letter Y (upper) marks the position of the

active-site tyrosine codon. The hatched bars mark the positions of probes used in genotyping; the "5' probe" was prepared by polymerase chain reaction with primers represented by the arrows 1 and 2 [see supplementary Web material (6) for details on the construction of the targeting vector and examples of genotyping and mRNA blot-hybridization results]. (B) Images of E17.5 WT (left) and  $top2\beta^{-/-}$  (right) embryos.

by distinct genes (*I*). The IIα rather than the IIβ isoform appears to unlink DNA during chromosome segregation. Cell lines expressing IIα but not IIβ have been identified, indicating that IIβ is dispensable in cellular processes (*4*). To determine the role of IIβ in vivo, we disrupted the murine *TOP2*β gene according to standard procedures (*5*). Two adjacent exons in one copy of *TOP2*β in embryonic stem cells, one of which contains the active-site tyrosine codon, were replaced by the neomycin-resistance marker (Fig. 1A) [see supplementary Web material (*6*) for details on targeting vector construction]. Germ line chimeras from blastocysts injected with the mutated cells were then used

to obtain heterozygous  $top2\beta^{+/-}$  mice (5).

**Uniprot:** 



https://www.uniprot.org/uniprotkb/Q64511/entry

