

# *Dtx3l* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- *Dtx3l*

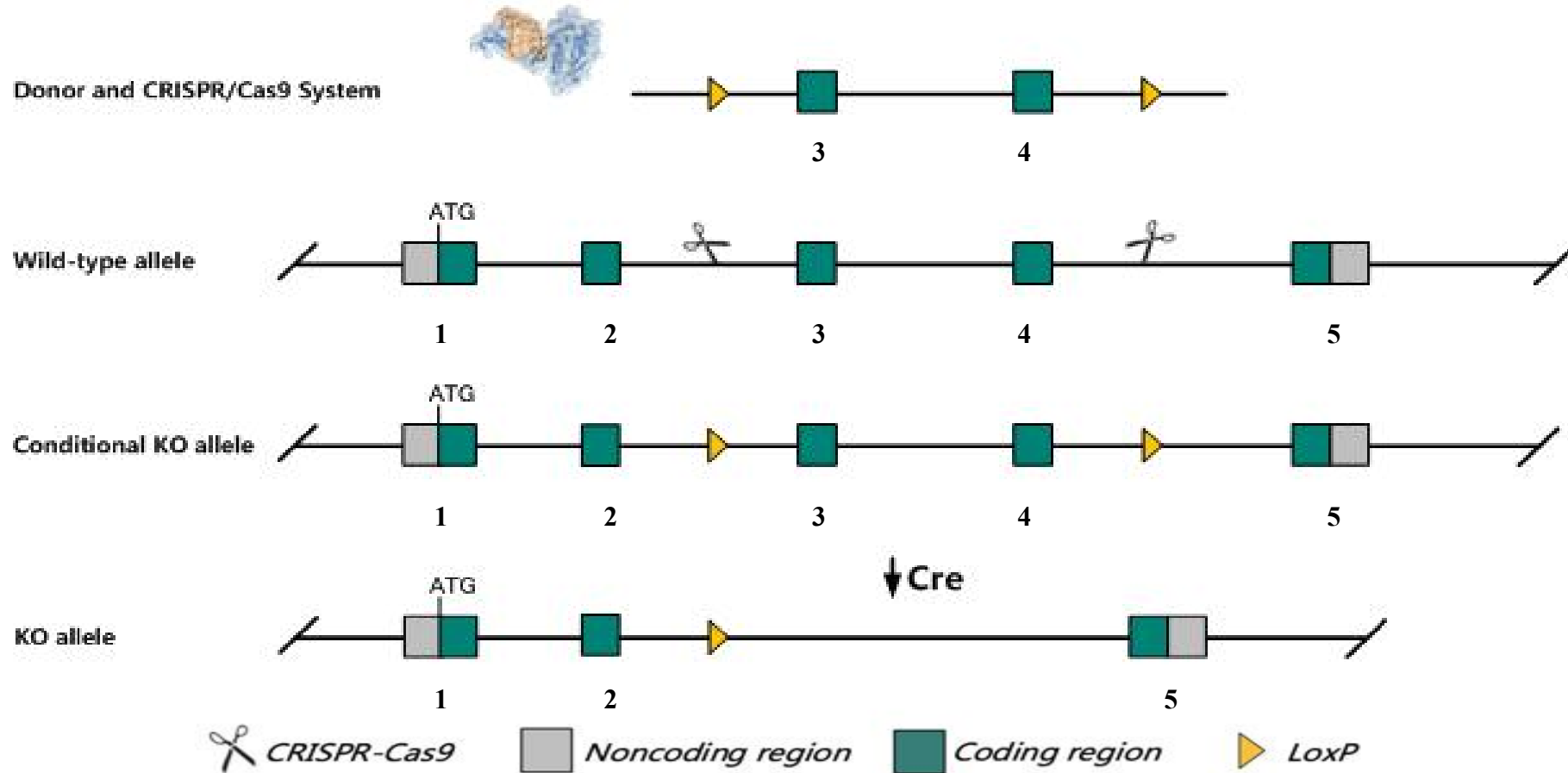
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Dtx3l* gene.

# Technical Information

- The *Dtx3l* gene has 2 transcripts. According to the structure of *Dtx3l* gene, exon 3-exon 4 of *Dtx3l* -201 (ENSMUST00000081933.14) transcript is recommended as the knockout region. Knocking out the region will result in disruption of its function.
- In this project we use CRISPR-Cas9 technology to modify *Dtx3l* gene. The brief process is as follows: gRNAs and Donor were transcribed in vitro. Cas9 and gRNAs 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

**Dtx3l** **deltex 3-like, E3 ubiquitin ligase** [ *Mus musculus* (house mouse) ]

Gene ID: 209200, updated on 26-Sep-2022

[Download Datasets](#)

## Summary

|                    |   |
|--------------------|---|
| Official Symbol    | Dtx3l provided by <a href="#">MGI</a>   |
| Official Full Name | deltex 3-like, E3 ubiquitin ligase provided by <a href="#">MGI</a>  |
| Primary source     | <a href="#">MGI:MGI:2656973</a>   |
| See related        | <a href="#">Ensembl:ENSMUSG00000049502</a> <a href="#">AllianceGenome:MGI:2656973</a>   |
| Gene type          | protein coding  |
| RefSeq status      | VALIDATED   |
| Organism           | <a href="#">Mus musculus</a>  |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus   |
| Summary            | Predicted to enable several functions, including STAT family protein binding activity; ubiquitin protein ligase activity; and ubiquitin-like protein ligase binding activity. Predicted to be involved in several processes, including positive regulation of macromolecule metabolic process; positive regulation of protein localization; and protein ubiquitination. Predicted to act upstream of or within several processes, including DNA repair; chromatin organization; and defense response to other organism. Predicted to be located in cytosol; lysosome; and nucleus. Predicted to be part of protein-containing complex. Predicted to be active in nucleoplasm. Predicted to colocalize with early endosome. Is expressed in several structures, including brain; genitourinary system; gut; immune system; and oral cavity. Orthologous to human DTX3L (deltex E3 ubiquitin ligase 3L). [provided by Alliance of Genome Resources, Apr 2022] |
| Expression         | Broad expression in large intestine adult (RPKM 10.6), thymus adult (RPKM 6.4) and 25 other tissues <a href="#">See more</a>  |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>   |
| <b>NEW</b>         | Try the new <a href="#">Gene table</a><br>Try the new <a href="#">Transcript table</a>  |

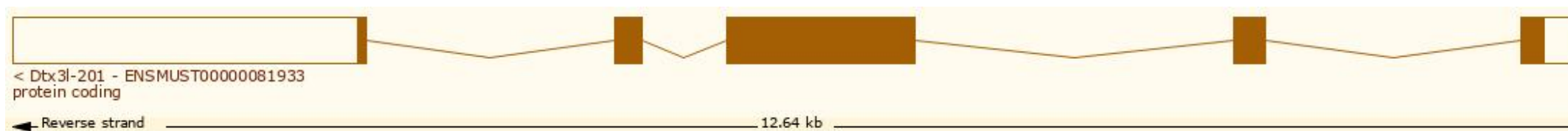
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

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

| Transcript ID                         | Name      | bp   | Protein               | Biotype        | CCDS                      | UniProt Match            | Flags   |
|---------------------------------------|-----------|------|-----------------------|----------------|---------------------------|--------------------------|---|
| <a href="#">ENSMUST00000081933.14</a> | Dtx3l-201 | 5309 | <a href="#">748aa</a> | Protein coding | <a href="#">CCDS37325</a> | <a href="#">Q3UIR3-1</a> | Ensembl Canonical GENCODE basic APPRIS P1 TSL:1 |
| <a href="#">ENSMUST00000114885.3</a>  | Dtx3l-202 | 2649 | <a href="#">691aa</a> | Protein coding |                           | <a href="#">Q3UIR3-2</a> | GENCODE basic TSL:1                             |

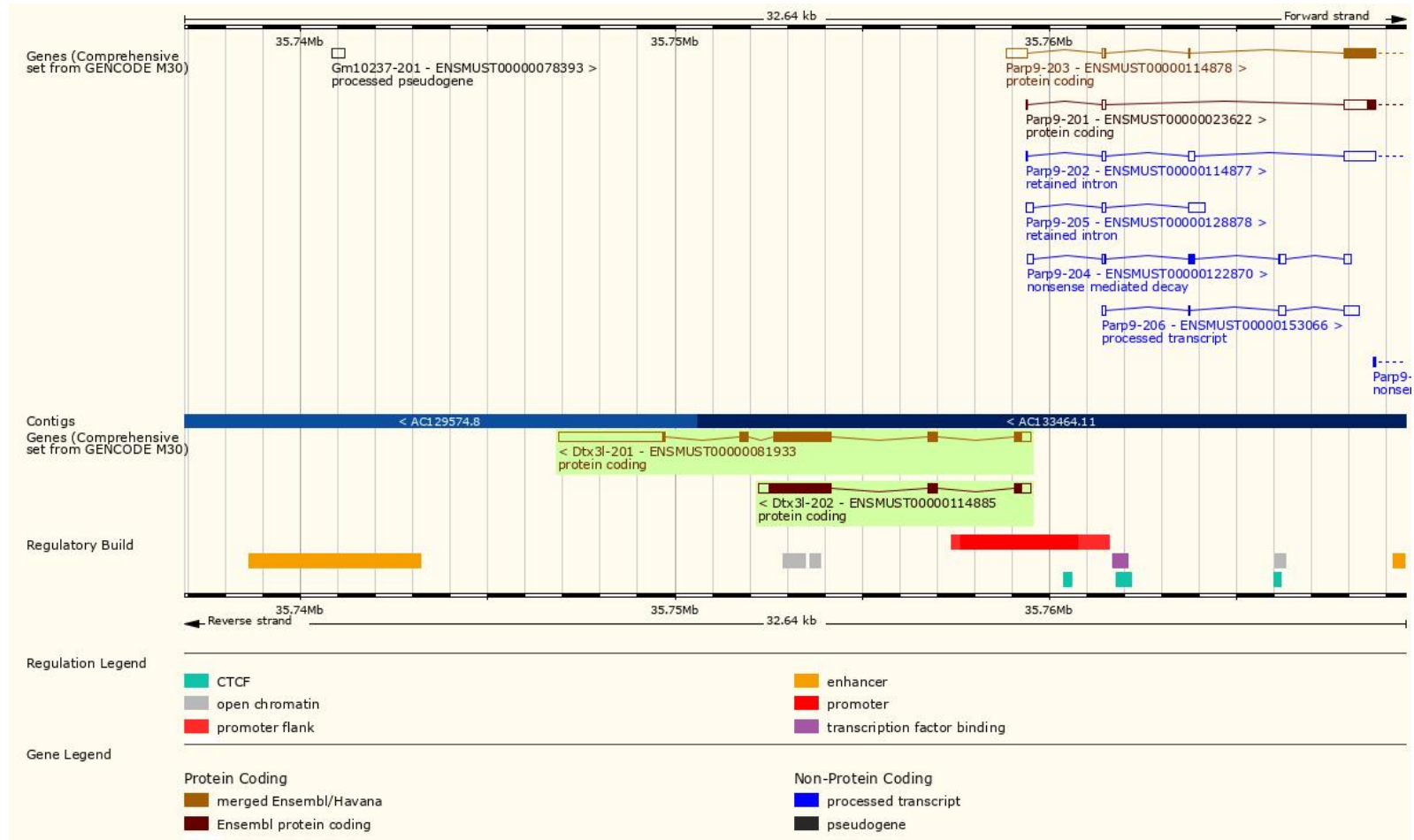
The strategy is based on the design of *Dtx3l-201* transcript, the transcription is shown below:



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



# Genomic Information



# Important Information

- *Dtx3l* is located on Chr 16. 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.
- The flox region is about 4.5 kb away from the 5th end of the *Parp9* gene, which may affect the regulation of this gene.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.