

# *Fndc3a* Cas9-KO Strategy

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# Overview

## Target Gene Name

- Fndc3a

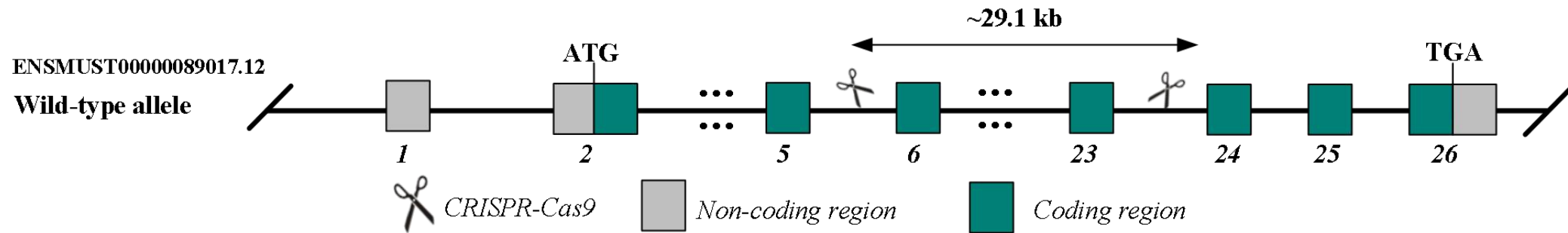
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



# Technical Information

- The *Fndc3a* gene has 7 transcripts. According to the structure of *Fndc3a* gene, exon6-exon23 of *Fndc3a*-201 (ENSMUST00000089017.12) transcript is recommended as the knockout region. The region contains 2497 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fndc3a* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

# Gene Information

## Fndc3a fibronectin type III domain containing 3A [Mus musculus (house mouse)]

Gene ID: 319448, updated on 31-Jan-2019

### Summary

<b>Official Symbol</b>	Fndc3a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	fibronectin type III domain containing 3A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1196463</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033487</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>	1700094E19Rik, D14Ert453e, F730017H24Rik, Fndc3, sys
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 15.1), placenta adult (RPKM 12.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

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

# Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

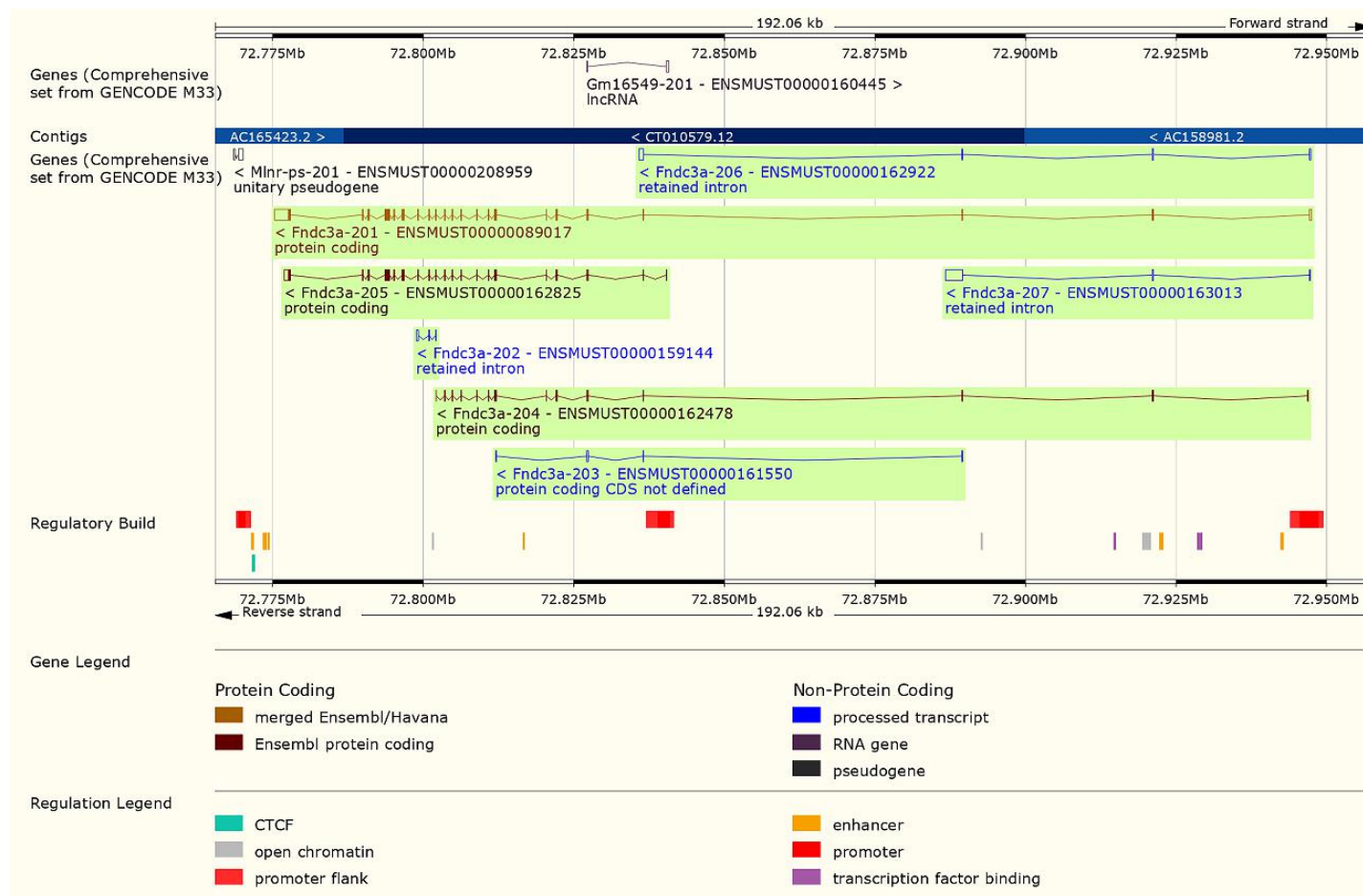
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000089017.12</a>	Fndc3a-201	6143	<a href="#">1198aa</a>	Protein coding	<a href="#">CCDS27264</a>	<a href="#">Q8BX90</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000159144.2</a>	Fndc3a-202	452	No protein	Retained intron		-	TSL:3
<a href="#">ENSMUST00000161550.2</a>	Fndc3a-203	491	No protein	Protein coding CDS not defined		-	TSL:3
<a href="#">ENSMUST00000162478.8</a>	Fndc3a-204	1808	<a href="#">540aa</a>	Protein coding		<a href="#">E0CXY0</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000162825.8</a>	Fndc3a-205	4100	<a href="#">1154aa</a>	Protein coding		<a href="#">F6TLV3</a>	TSL:5 CDS 5' incomplete
<a href="#">ENSMUST00000162922.8</a>	Fndc3a-206	1262	No protein	Retained intron		-	TSL:1
<a href="#">ENSMUST00000163013.2</a>	Fndc3a-207	3109	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Fndc3a*-201 transcript, the transcription is shown below:



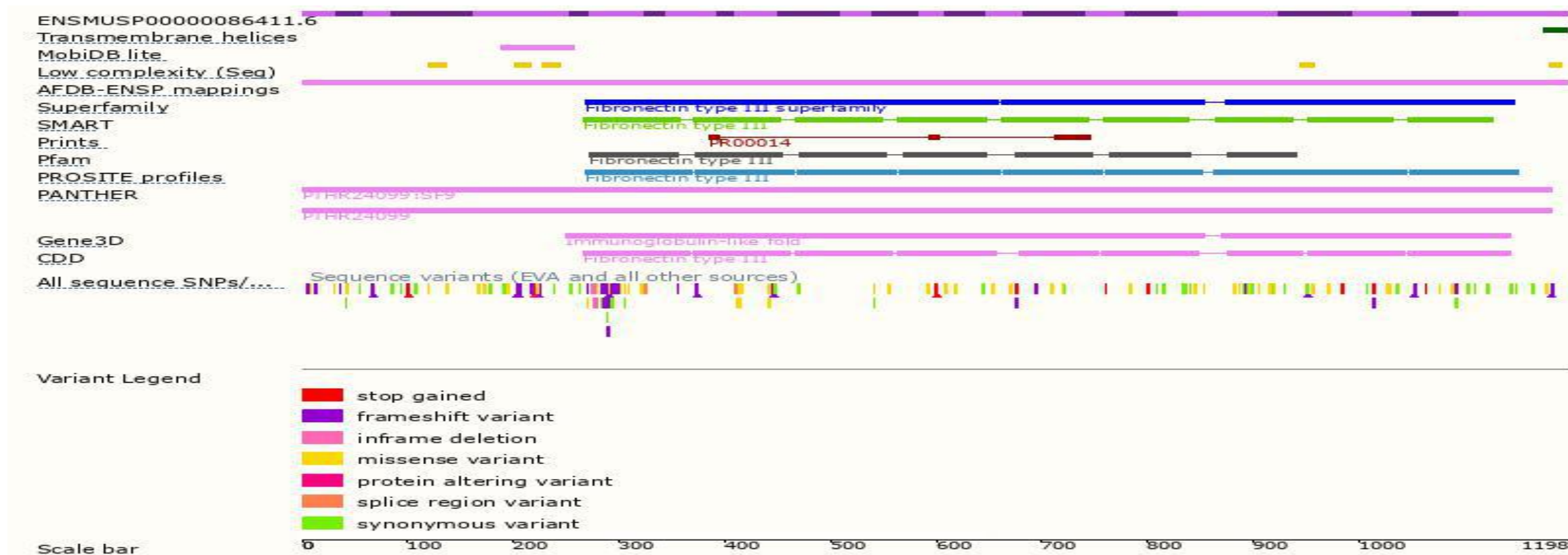
Source: <https://www.ensembl.org>

# Genomic Information



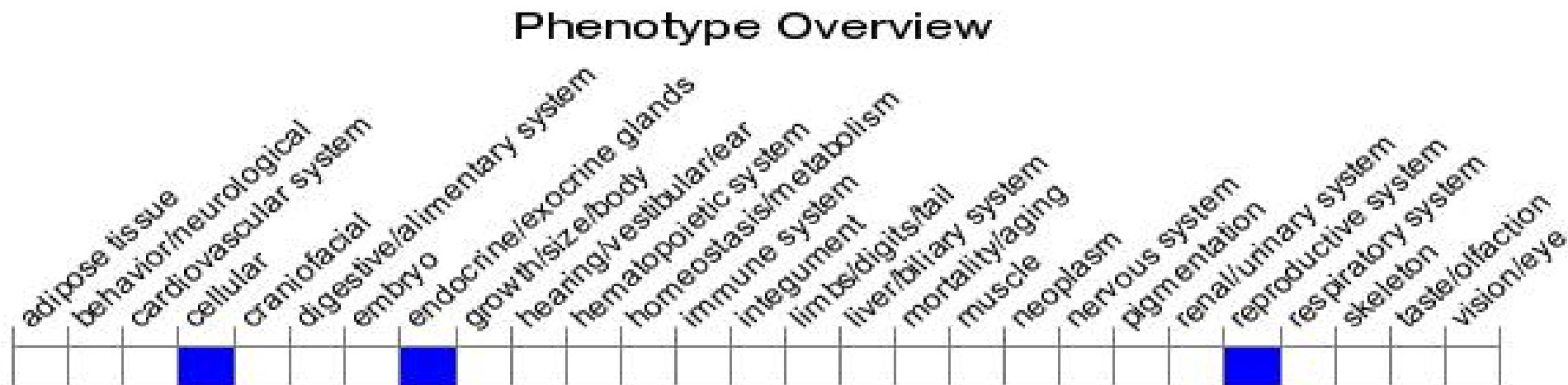


# Protein Information





# Mouse Phenotype Information (MGI)



- Males homozygous for an insertional mutation are sterile; females are fertile. In mutant males, spermatids form multinucleated syncytia and fail to mature, while Sertoli cells exhibit abnormal cytoplasmic vacuoles.

# Important Information

- *Fndc3a* 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.
- The knockout region of this strategy is about 4.2 kb away from the *Gm16549-201* gene, which may affect its 5-terminal regulatory function.
- The *Fndc3a-204* and *Fndc3a-205* transcript is incomplete, and the impact of this strategy on it is unknown.
- 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.