

# *Gtf3a* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Gtf3a*

**Project type**

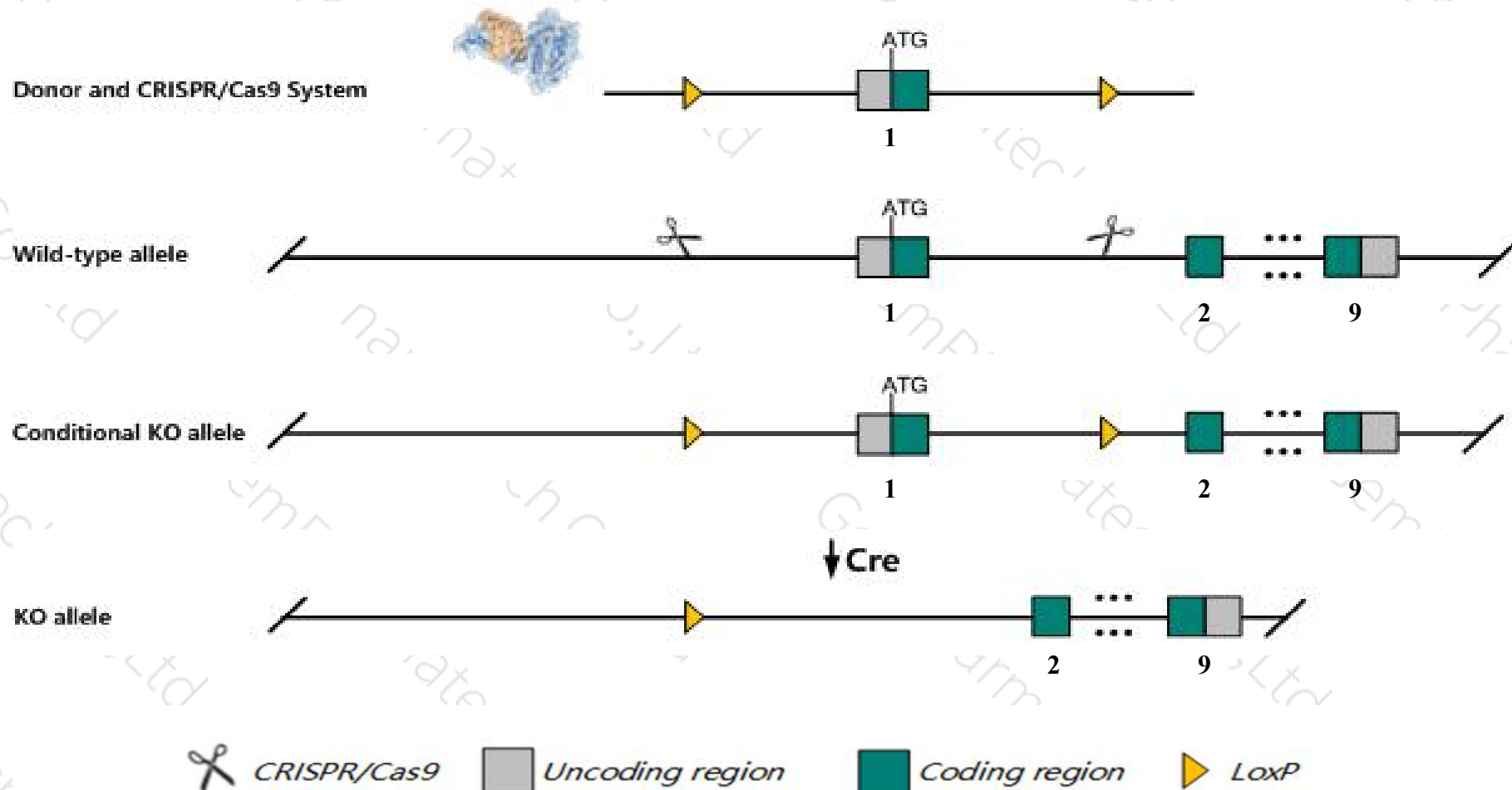
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gtf3a* gene. The schematic diagram is as follows:



# Technical routes

- The *Gtf3a* gene has 5 transcripts. According to the structure of *Gtf3a* gene, exon1 of *Gtf3a-204* (ENSMUST00000146511.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gtf3a* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

# Notice

- The *Gtf3a* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Gtf3a general transcription factor III A [Mus musculus (house mouse)]

Gene ID: 66596, updated on 31-Jan-2019

### Summary



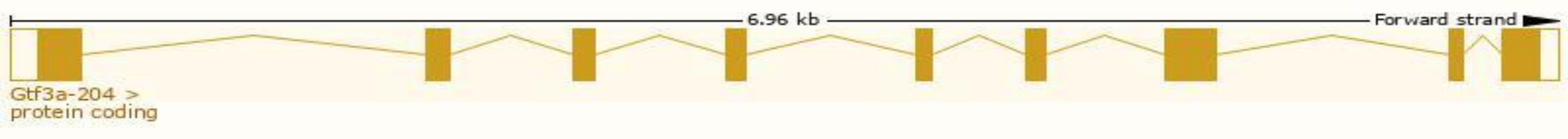
<b>Official Symbol</b>	Gtf3a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	general transcription factor III A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1913846</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000016503</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<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>	2010015D03Rik, 2610111I01Rik, 5330403M05Rik
<b>Summary</b>	The product of this gene is a zinc finger protein with nine Cis[2]-His[2] zinc finger domains. It functions as an RNA polymerase III transcription factor to induce transcription of the 5S rRNA genes. The protein binds to a 50 bp internal promoter in the 5S genes called the internal control region (ICR), and nucleates formation of a stable preinitiation complex. This complex recruits the TFIIC and TFIIIB transcription factors and RNA polymerase III to form the complete transcription complex. The protein is thought to be translated using a non-AUG translation initiation site in mammals based on sequence analysis, protein homology, and the size of the purified protein. [provided by RefSeq, Jul 2008]
<b>Expression</b>	Ubiquitous expression in ovary adult (RPKM 66.8), colon adult (RPKM 54.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

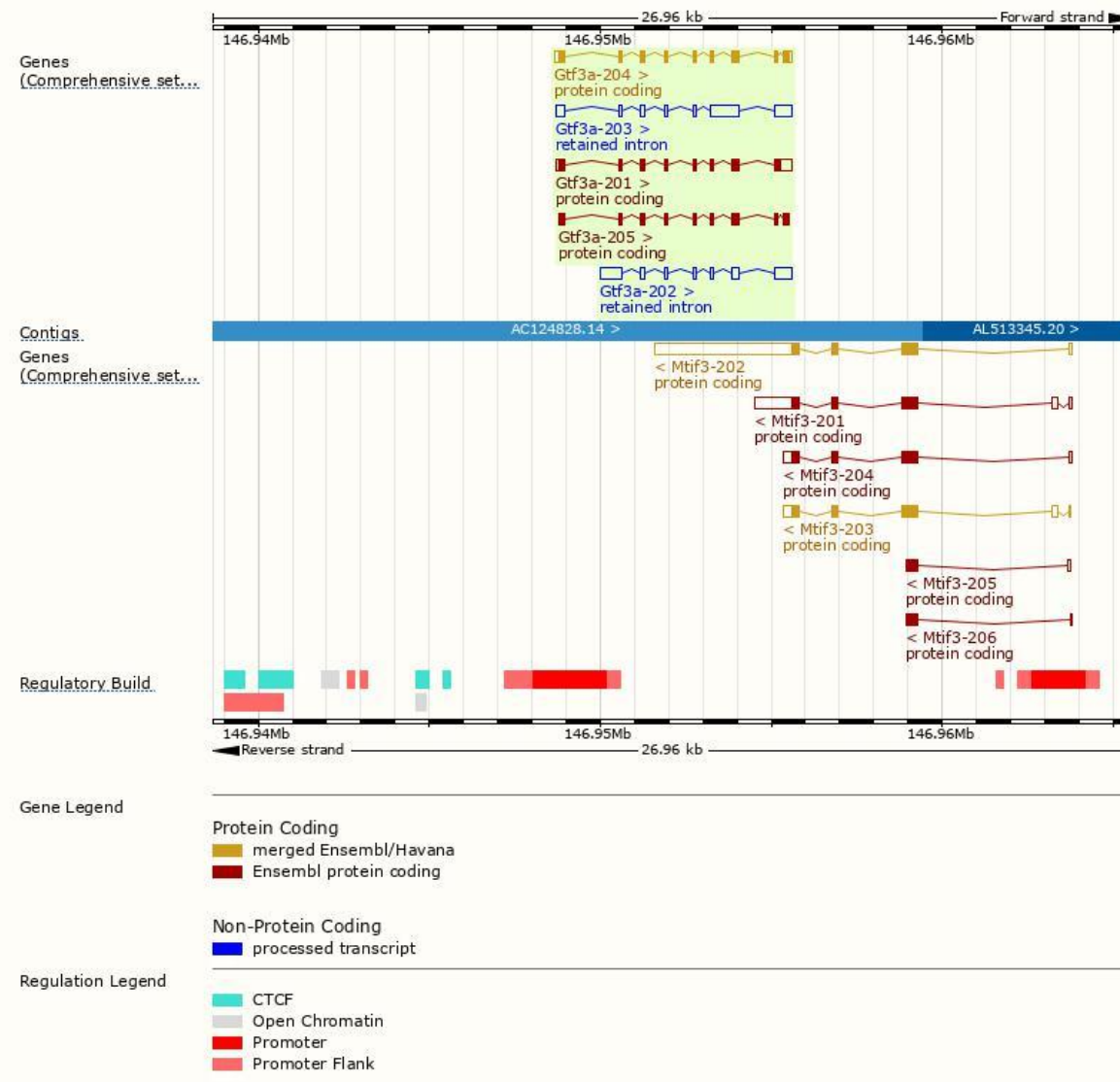
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gtf3a-204	<a href="#">ENSMUST00000146511.7</a>	1298	<a href="#">364aa</a>	Protein coding	<a href="#">CCDS19873</a>	<a href="#">F6RCF6</a>	TSL:1 GENCODE basic APPRIS P5
Gtf3a-205	<a href="#">ENSMUST00000233741.1</a>	1095	<a href="#">364aa</a>	Protein coding	<a href="#">CCDS19873</a>	<a href="#">Q8VHT7</a>	GENCODE basic APPRIS ALT2
Gtf3a-201	<a href="#">ENSMUST00000132102.1</a>	1426	<a href="#">342aa</a>	Protein coding	-	<a href="#">F6SIJ4</a>	TSL:1 GENCODE basic APPRIS ALT2
Gtf3a-203	<a href="#">ENSMUST00000133682.7</a>	1970	No protein	Retained intron	-	-	TSL:1
Gtf3a-202	<a href="#">ENSMUST00000133296.1</a>	1678	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Gtf3a-204* transcript,The transcription is shown below



# Genomic location distribution





# Protein domain

ENSMUSP00000119...

MobiDB lite

Low complexity (Seg)

Superfamily

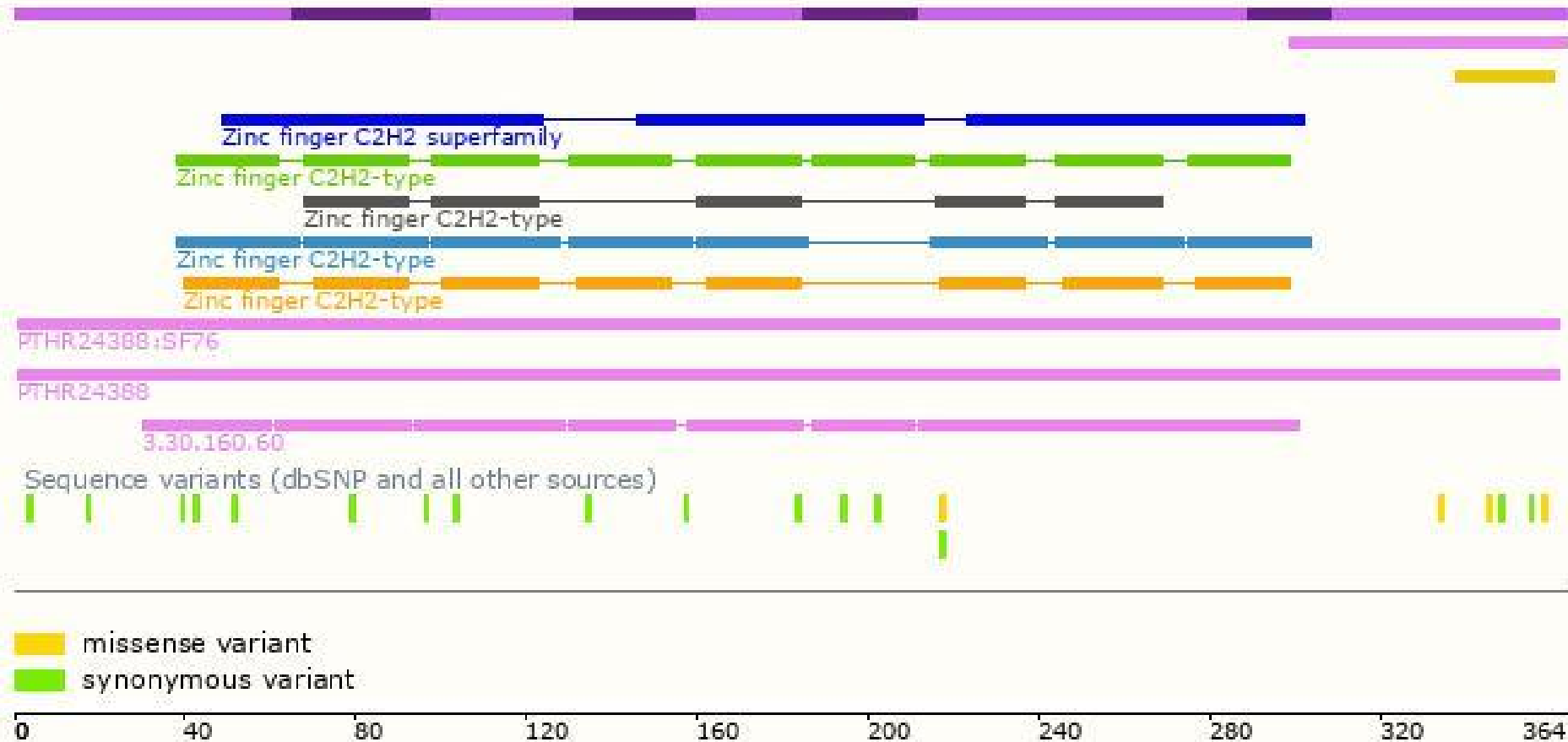
SMART

Pfam

PROSITE profiles

PROSITE patterns

PANTHER



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

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