

# *Zfand3* Cas9-CKO Strategy

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**Design Date: 2020-8-24**

# Project Overview

**Project Name**

***Zfand3***

**Project type**

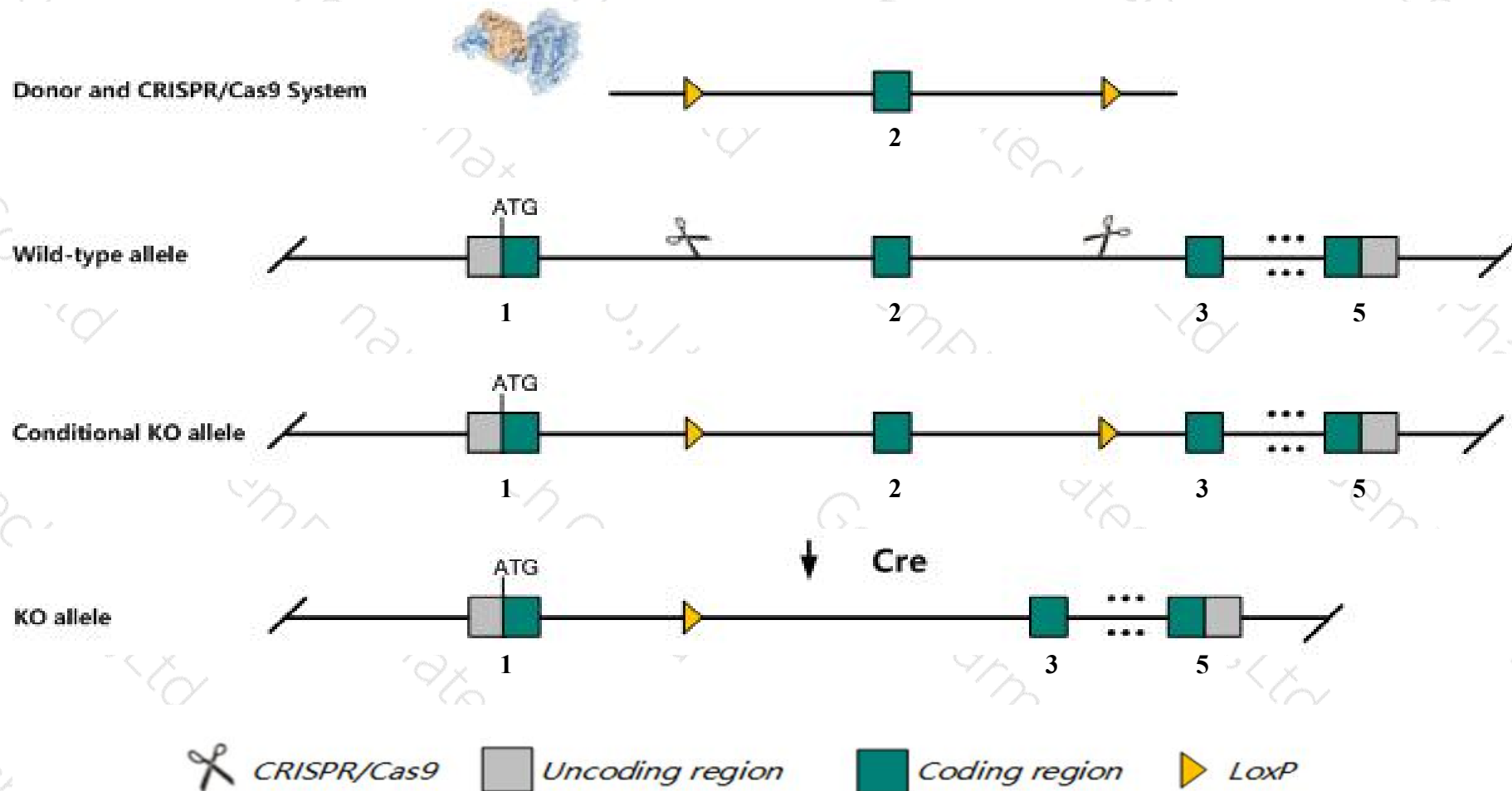
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfand3* gene. The schematic diagram is as follows:



- The *Zfand3* gene has 10 transcripts. According to the structure of *Zfand3* gene, exon2 of *Zfand3*-201(ENSMUST00000057897.9) transcript is recommended as the knockout region. The region contains 41bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfand3* 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.

- The *Zfand3* gene is located on the Chr17. 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)

## Zfand3 zinc finger, AN1-type domain 3 [Mus musculus (house mouse)]

Gene ID: 21769, updated on 13-Mar-2020

### Summary



<b>Official Symbol</b>	Zfand3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	zinc finger, AN1-type domain 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1096572</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000044477</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>	AW539211, TEG-27, Tex27
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 72.1), subcutaneous fat pad adult (RPKM 35.4) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

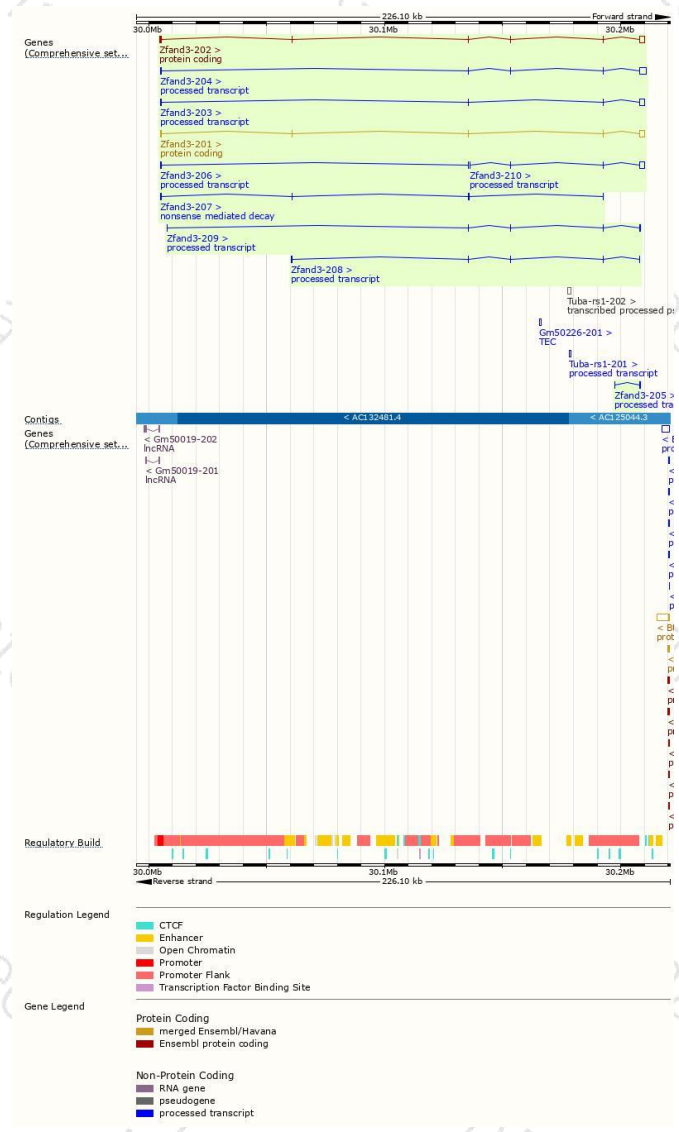
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfand3-201	<a href="#">ENSMUST00000057897.9</a>	2640	<a href="#">205aa</a>	Protein coding	<a href="#">CCDS28598</a>	<a href="#">Q497H0</a>	TSL:1 GENCODE basic
Zfand3-202	<a href="#">ENSMUST00000226208.2</a>	3039	<a href="#">227aa</a>	Protein coding	-	<a href="#">Q497H0</a>	GENCODE basic APPRIS P1
Zfand3-207	<a href="#">ENSMUST00000234671.1</a>	496	<a href="#">121aa</a>	Nonsense mediated decay	-	<a href="#">A0A3Q4EGM4</a>	CDS 5' incomplete
Zfand3-204	<a href="#">ENSMUST00000226421.2</a>	3489	No protein	Processed transcript	-	-	
Zfand3-203	<a href="#">ENSMUST00000226308.1</a>	2565	No protein	Processed transcript	-	-	
Zfand3-210	<a href="#">ENSMUST00000234902.1</a>	2289	No protein	Processed transcript	-	-	
Zfand3-209	<a href="#">ENSMUST00000234866.1</a>	886	No protein	Processed transcript	-	-	
Zfand3-208	<a href="#">ENSMUST00000234790.1</a>	763	No protein	Processed transcript	-	-	
Zfand3-206	<a href="#">ENSMUST00000234238.1</a>	474	No protein	Processed transcript	-	-	
Zfand3-205	<a href="#">ENSMUST00000234091.1</a>	360	No protein	Processed transcript	-	-	

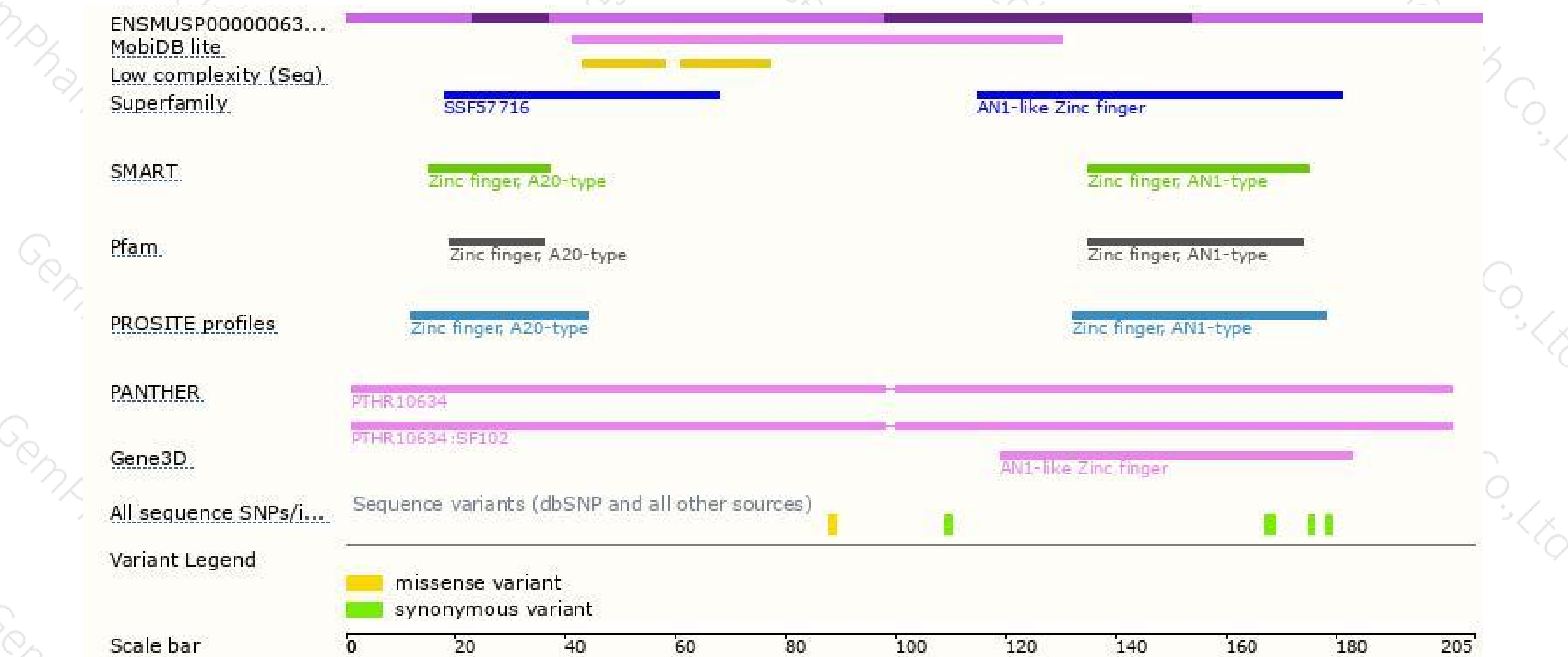
The strategy is based on the design of *Zfand3-201* transcript,the transcription is shown below:



# Genomic location distribution



# Protein domain



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

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