

# ***Zdhhc24* Cas9-CKO Strategy**

Designer:Xiaojing Li

Reviewer:JiaYu

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# Project Overview

**Project Name**

***Zdhhc24***

**Project type**

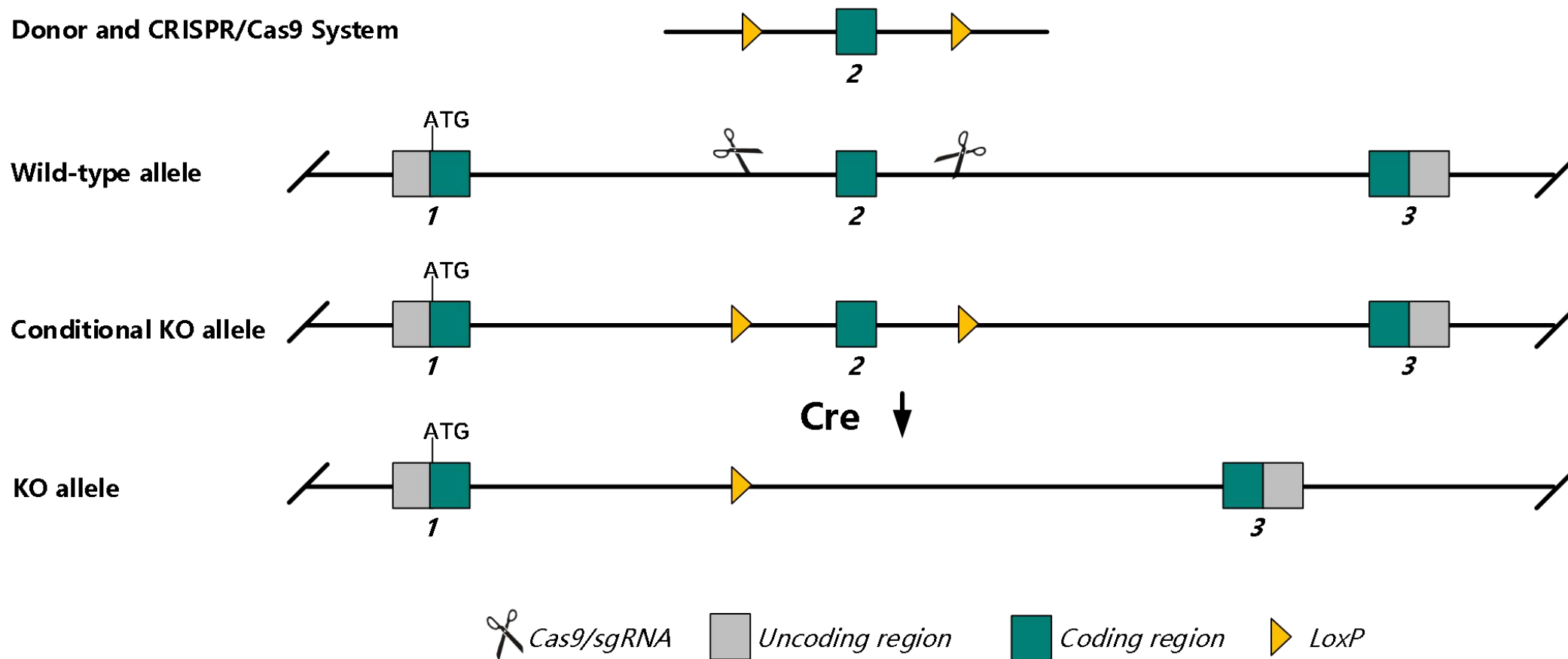
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zdhhc24* gene. The schematic diagram is as follows:



- The *Zdhhc24* gene has 6 transcripts. According to the structure of *Zdhhc24* gene, exon2 of *Zdhhc24-201* (ENSMUST00000006632.7) transcript is recommended as the knockout region. The region contains 278bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zdhhc24* 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.

- According to the existing MGI data, Phenotypic analysis of mice homozygous for a gene trap allele indicates this mutation has no notable phenotype in any parameter tested in a high-throughput screen.
- The flox region is about 1.7 kb away from the N-terminus of the *Actn3* gene, which may affect the regulation of the N-terminus of the gene.
- The *Zdhhc24* gene is located on the Chr19. 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)

## Zdhhc24 zinc finger, DHHC domain containing 24 [ *Mus musculus* (house mouse) ]

Gene ID: 70605, updated on 20-Mar-2020

### Summary

Official Symbol	Zdhhc24 provided by <a href="#">MGI</a>
Official Full Name	zinc finger, DHHC domain containing 24 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1917855</a>
See related	<a href="#">Ensembl:ENSMUSG000000006463</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
Also known as	Leng4; 5730496N17Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 20.6), ovary adult (RPKM 13.3) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

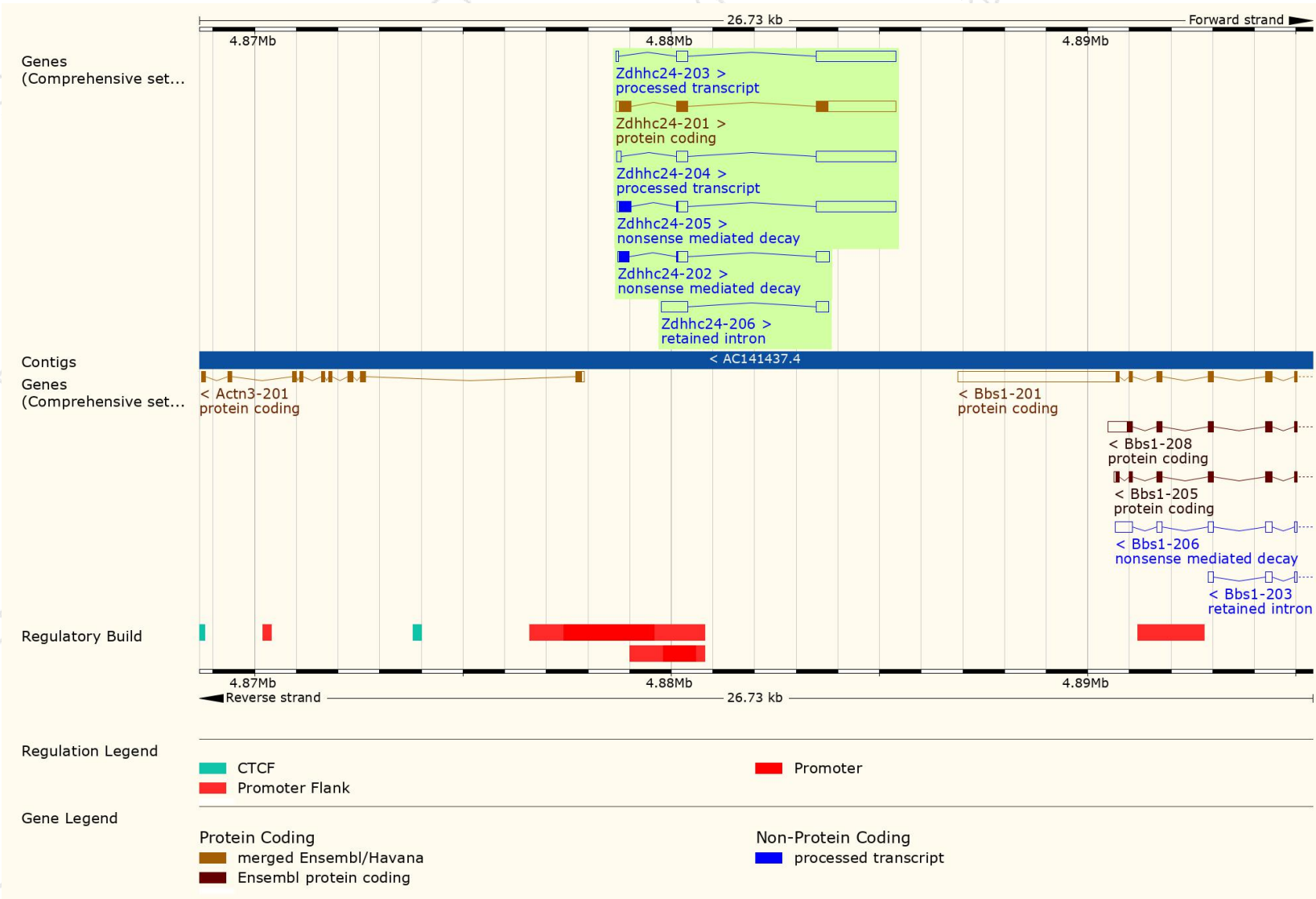
The gene has 6 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Zdhhc24-201	<a href="#">ENSMUST00000006632.7</a>	2558	<a href="#">284aa</a>	Protein coding	<a href="#">CCDS50353</a>	<a href="#">Q6IR37</a>	TSL:1 GENCODE basic APPRIS P1
Zdhhc24-202	<a href="#">ENSMUST00000160014.1</a>	871	<a href="#">93aa</a>	Nonsense mediated decay	-	<a href="#">E0CZ11</a>	TSL:3
Zdhhc24-203	<a href="#">ENSMUST00000162088.7</a>	2269	No protein	Processed transcript	-	-	TSL:2
Zdhhc24-204	<a href="#">ENSMUST00000162134.1</a>	2314	No protein	Processed transcript	-	-	TSL:1
Zdhhc24-205	<a href="#">ENSMUST00000162720.7</a>	2523	<a href="#">105aa</a>	Nonsense mediated decay	-	<a href="#">E0CYB8</a>	TSL:1
Zdhhc24-206	<a href="#">ENSMUST00000162754.1</a>	939	No protein	Retained intron	-	-	TSL:2

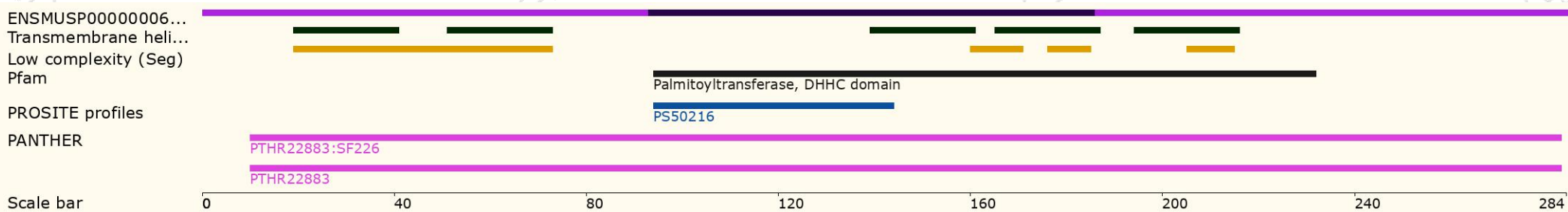
The strategy is based on the design of *Zdhhc24-201* transcript,The transcription is shown below



# Genomic location distribution



# Protein domain



# Mouse phenotype description(MGI)

*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

Phenotypic analysis of mice homozygous for a gene trap allele indicates this mutation has no notable phenotype in any parameter tested in a high-throughput screen

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

Tel: 400-9660890

