

***Zdhhc21* Cas9-CKO Strategy**

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Reviewer:

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Design Date:

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Project Overview

Project Name

Zdhhc21

Project type

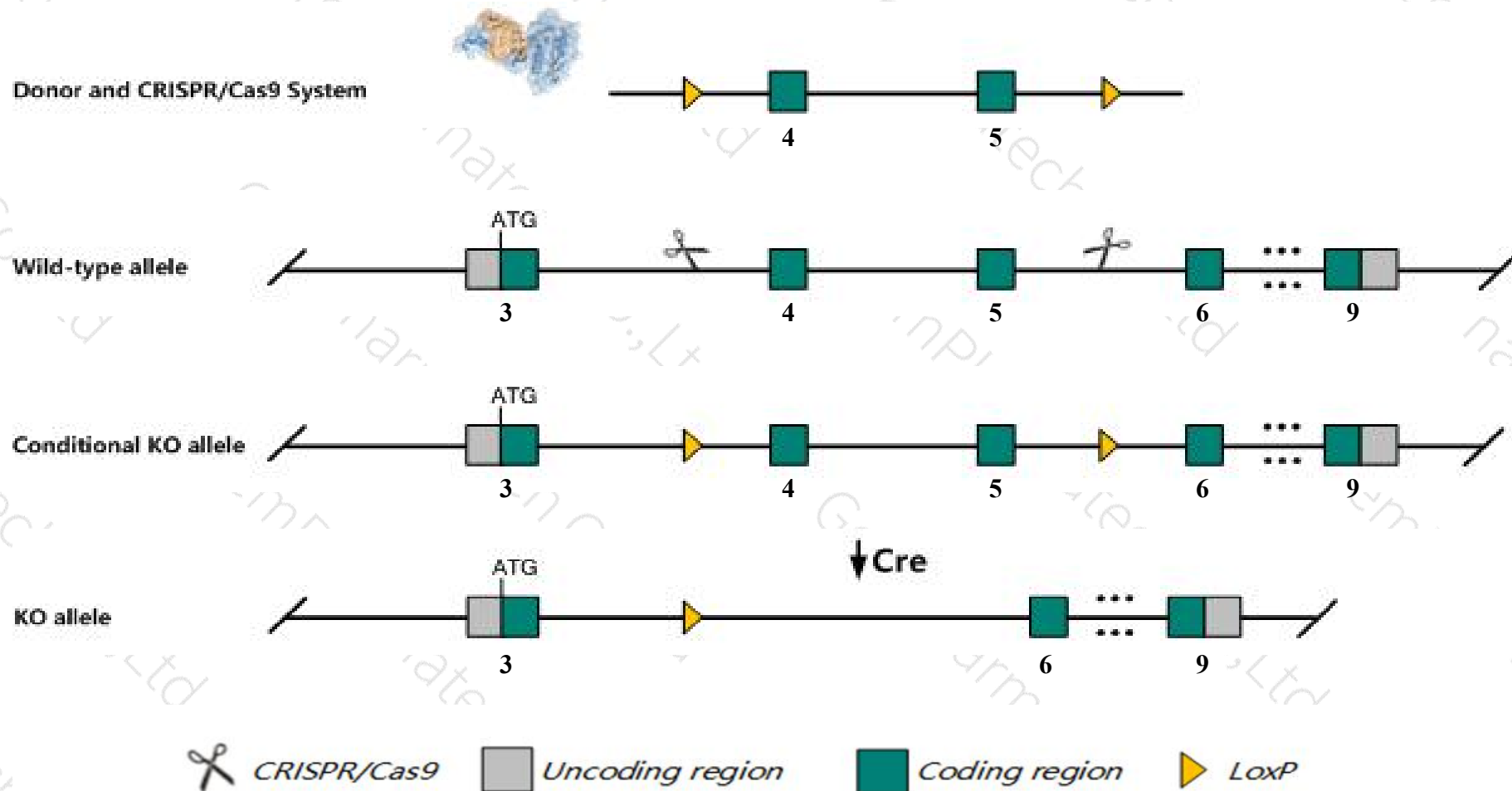
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zdhhc21* gene. The schematic diagram is as follows:



- The *Zdhhc21* gene has 6 transcripts. According to the structure of *Zdhhc21* gene, exon4-exon5 of *Zdhhc21-201* (ENSMUST00000030110.14) transcript is recommended as the knockout region. The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zdhhc21* 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, homozygous mutants of this epidermal acting gene have thin, short hair, many misshapen and disoriented hair follicles, and clumps of pigment reflecting remains of degenerating follicles.
- The *Zdhhc21* gene is located on the Chr4. 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)

Zdhhc21 zinc finger, DHHC domain containing 21 [*Mus musculus* (house mouse)]

Gene ID: 68268, updated on 12-Aug-2019

Summary

Official Symbol Zdhhc21 provided by [MGI](#)
Official Full Name zinc finger, DHHC domain containing 21 provided by [MGI](#)
Primary source [MGI:MGI:1915518](#)
See related [Ensembl:ENSMUSG00000028403](#)
Gene type protein coding
RefSeq status VALIDATED
Organism [Mus musculus](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as dep; AL024349; 9130404H11Rik; D130004H04Rik
Expression Ubiquitous expression in placenta adult (RPKM 3.3), CNS E18 (RPKM 3.0) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

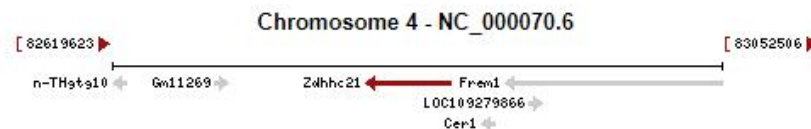
Genomic context

Location: 4 39.4 cM; 4 C3

See Zdhhc21 in [Genome Data Viewer](#)

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p6 (GCF_000001635.26)	4	NC_000070.6 (82798738..82859897, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (82444642..82505565, complement)

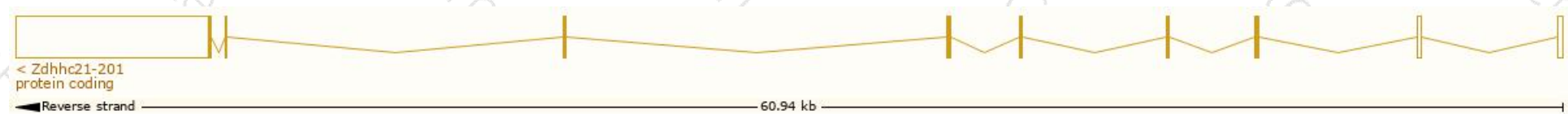


Transcript information (Ensembl)

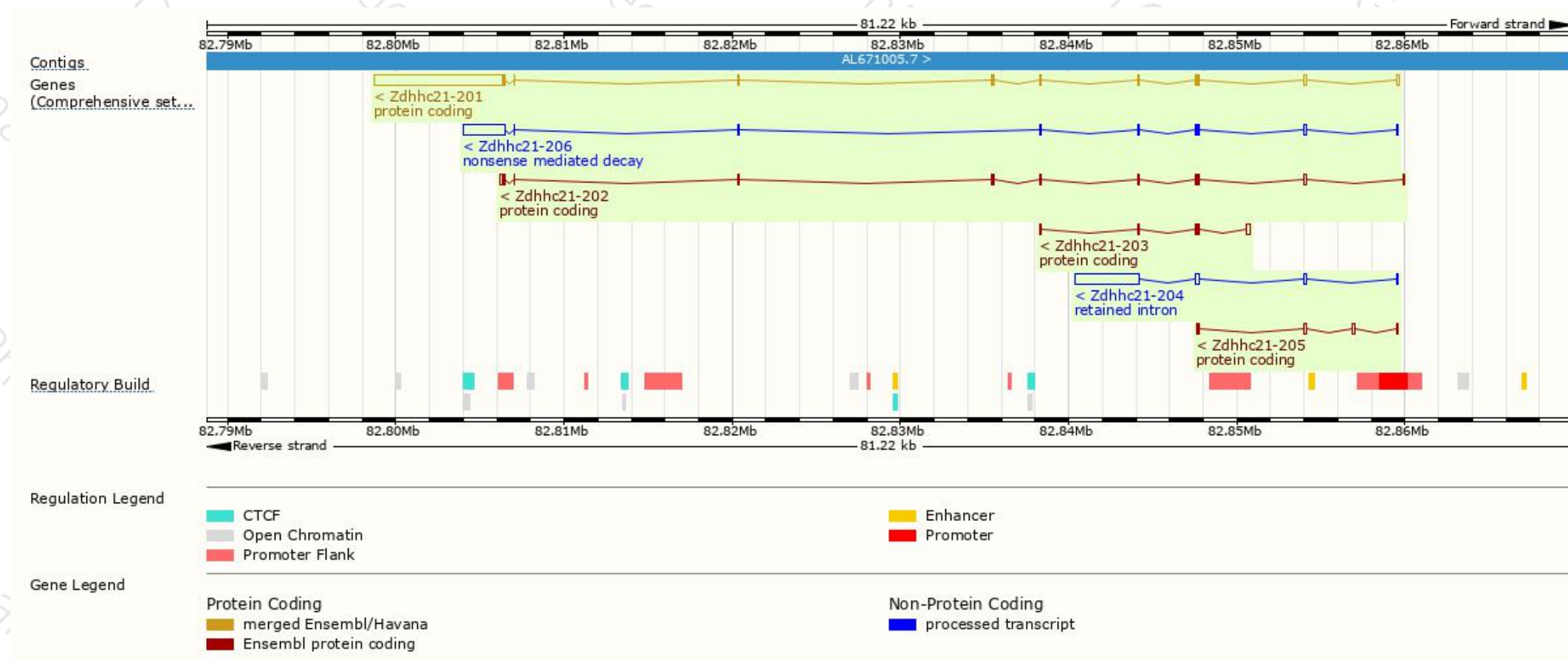
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zdhhc21-201	ENSMUST00000030110.14	8763	265aa	Protein coding	CCDS18294	Q9D270	TSL:1 GENCODE basic APPRIS P1
Zdhhc21-202	ENSMUST00000107239.7	1148	265aa	Protein coding	CCDS18294	Q9D270	TSL:1 GENCODE basic APPRIS P1
Zdhhc21-203	ENSMUST00000139401.1	644	109aa	Protein coding	-	Q5SRN8	CDS 3' incomplete TSL:5
Zdhhc21-205	ENSMUST00000156055.1	515	26aa	Protein coding	-	Q5SRP0	CDS 3' incomplete TSL:2
Zdhhc21-206	ENSMUST00000173741.7	3203	133aa	Nonsense mediated decay	-	G3UXC1	TSL:1
Zdhhc21-204	ENSMUST00000144139.8	4244	No protein	Retained intron	-	-	TSL:1

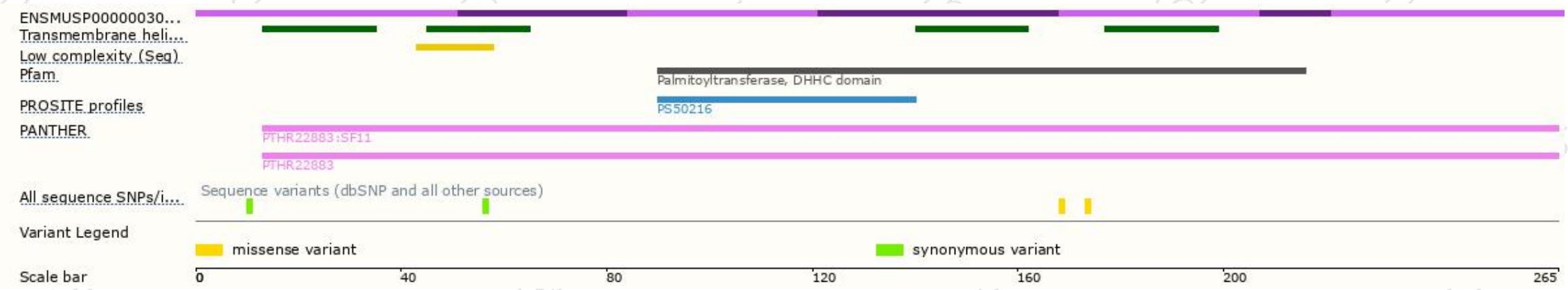
The strategy is based on the design of *Zdhhc21-201* transcript, the transcription is shown below:



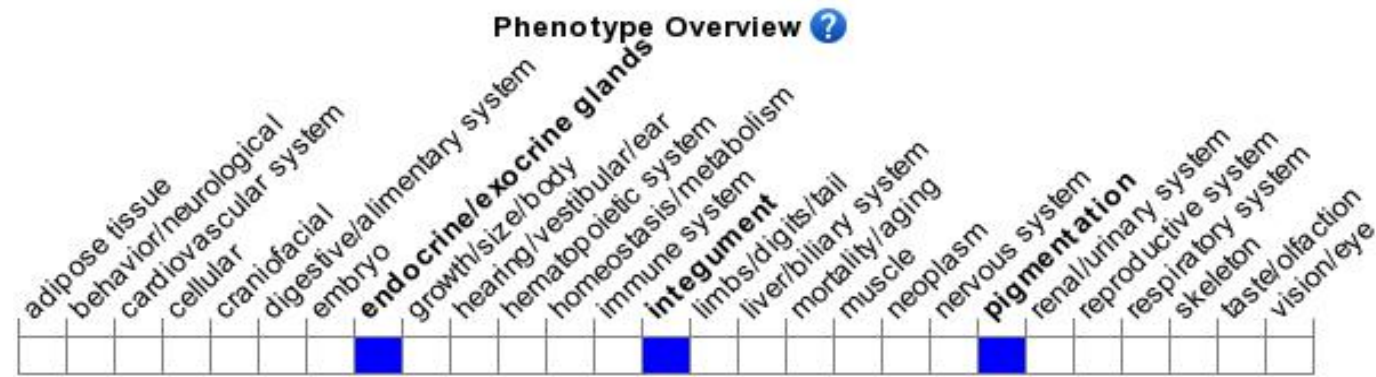
Genomic location distribution



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/>).

According to the existing MGI data, homozygous mutants of this epidermal acting gene have thin, short hair, many misshapen and disoriented hair follicles, and clumps of pigment reflecting remains of degenerating follicles.

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

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