

# ***Zdhhc21 Cas9-KO Strategy***

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**Reviewer:**

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**2020-2-24**

# Project Overview

**Project Name**

***Zdhhc21***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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](#)

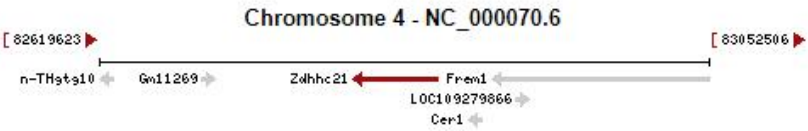
### Genomic context

Location: 4 39.4 cM; 4 C3

See Zdhhc21 in [Genome Data Viewer](#)

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCh38.p6 ( <a href="#">GCF_000001635.26</a> )	4	NC_000070.6 (82798738..82859897, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	4	NC_000070.5 (82444642..82505565, complement)

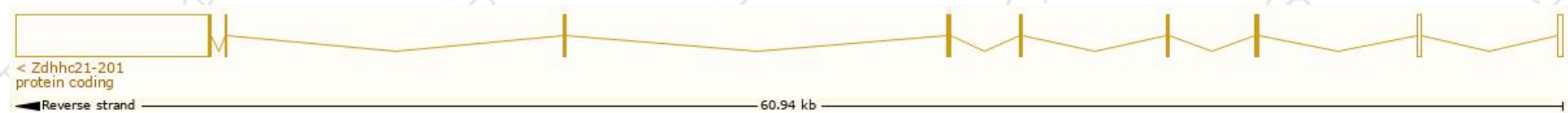


# Transcript information (Ensembl)

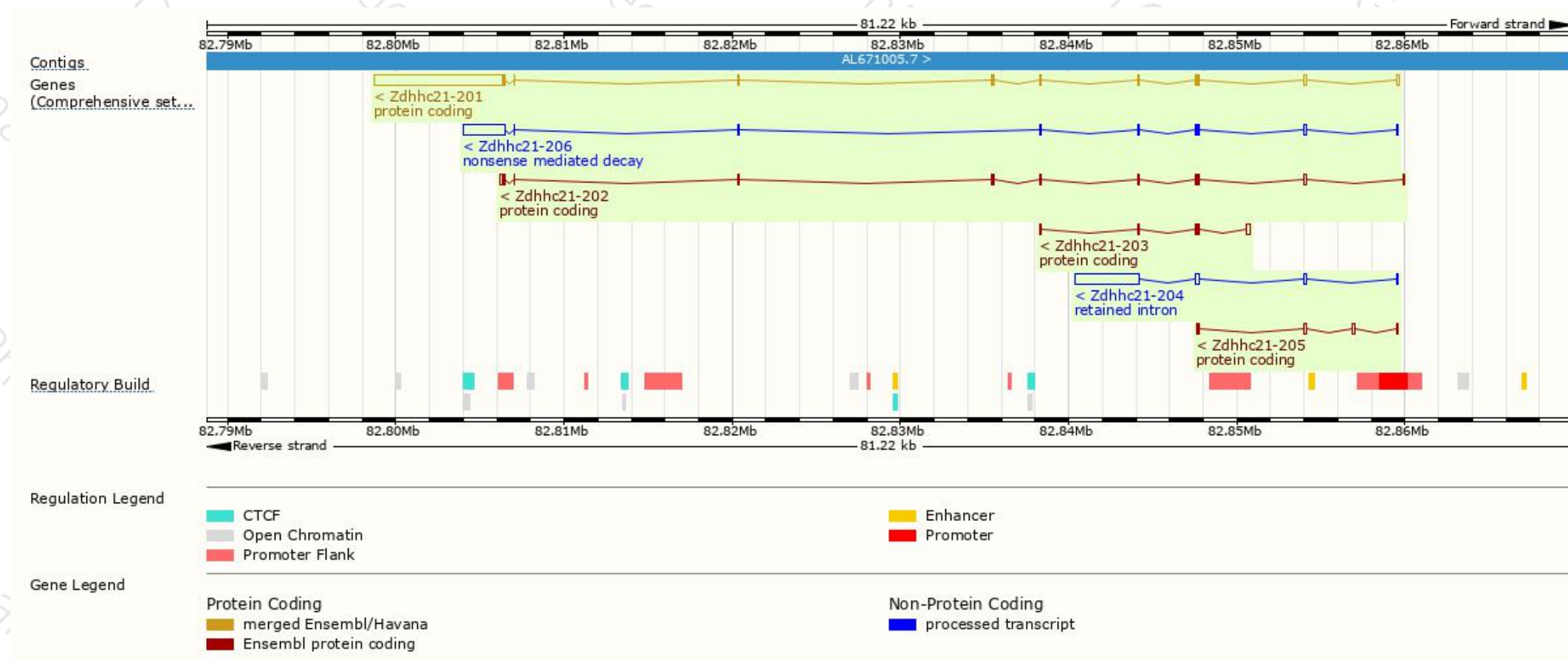
The gene has 6 transcripts,all transcripts are shown below:

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

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

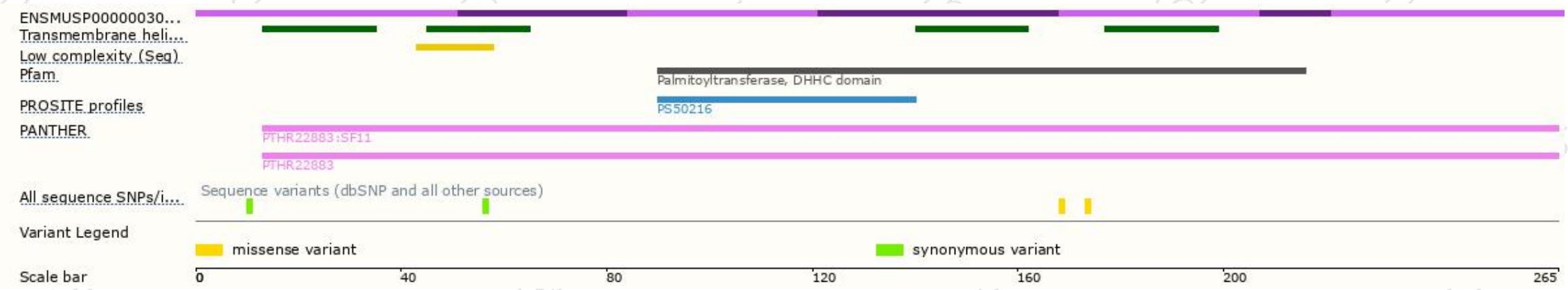


# Genomic location distribution

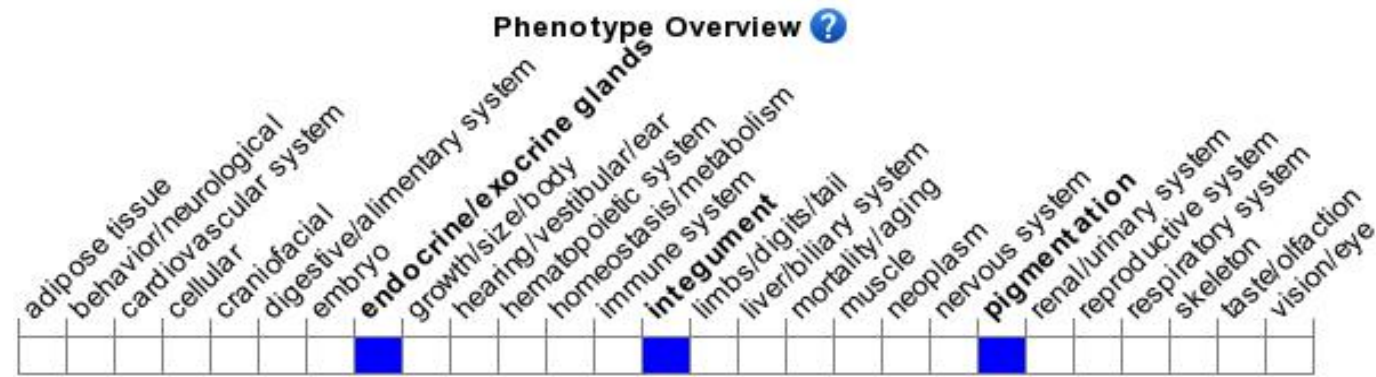




# Protein domain



# 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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