

# *Nsdhl* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Nsdhl*

**Project type**

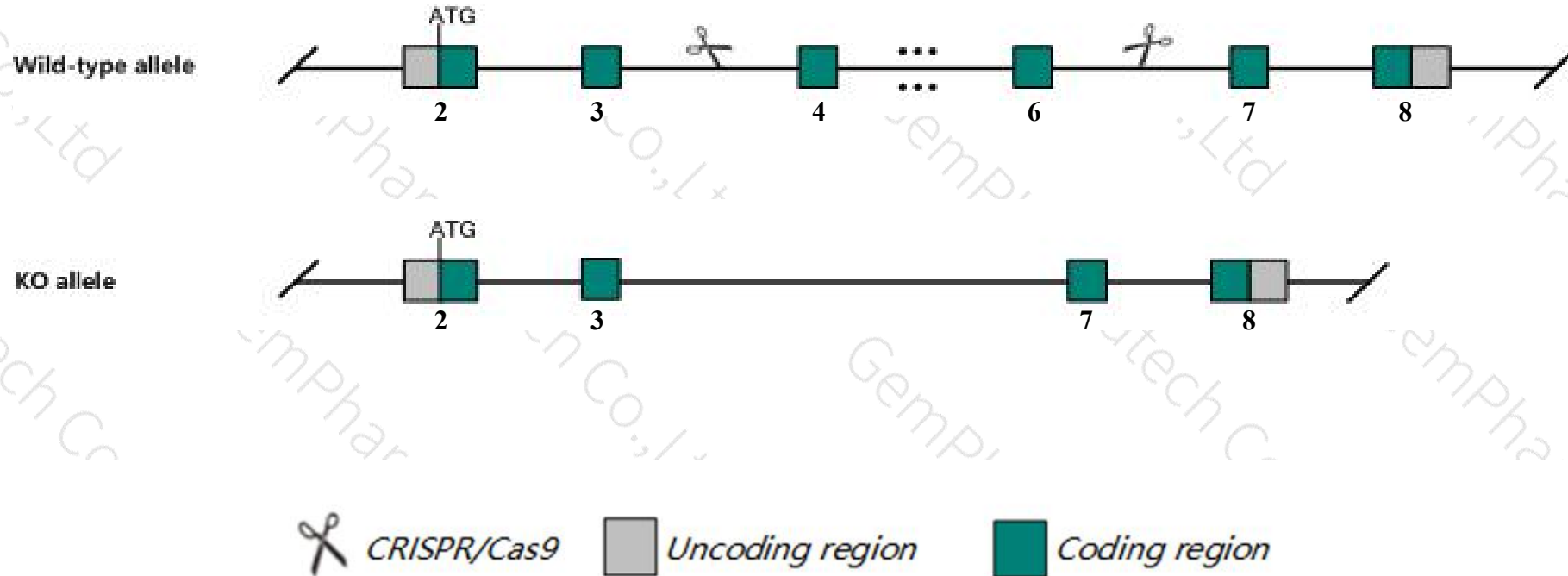
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Nsdhl* gene has 2 transcripts. According to the structure of *Nsdhl* gene, exon4-exon6 of *Nsdhl-201* (ENSMUST00000033715.4) transcript is recommended as the knockout region. The region contains 419bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nsdhl* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Heterozygous females exhibit a striped coat or skin hyperkeratotic lesions leaving bare patches on the coat, with some mutations also resulting in skeletal dysplasia and eye defects. Hemizygous male and homozygous female mice die before birth, presumably due to placental defects.
- The N-terminal of *Nsdhl* gene will remain 78aa, it may remain the partial function of *Nsdhl* gene.
- The *Nsdhl* gene is located on the ChrX. 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)

## Nsdhl NAD(P) dependent steroid dehydrogenase-like [ *Mus musculus* (house mouse) ]

Gene ID: 18194, updated on 20-Aug-2019

### Summary

Official Symbol	Nsdhl provided by <a href="#">MGI</a>
Official Full Name	NAD(P) dependent steroid dehydrogenase-like provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1099438</a>
See related	<a href="#">Ensembl:ENSMUSG000000031349</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	Bpa; Str, H105E3; XAP104; AI747449
Expression	Ubiquitous expression in genital fat pad adult (RPKM 30.5), liver E18 (RPKM 28.4) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: X A7.3; X 37.29 cM

[See Nsdhl in Genome Data Viewer](#)

Exon count: 8

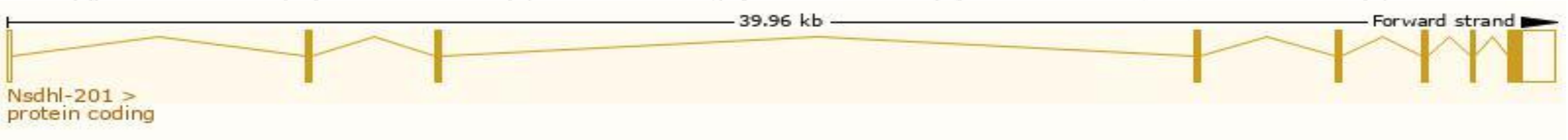
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	X	NC_000086.7 (72918521..72958528)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	X	NC_000086.6 (70163860..70203867)

# Transcript information (Ensembl)

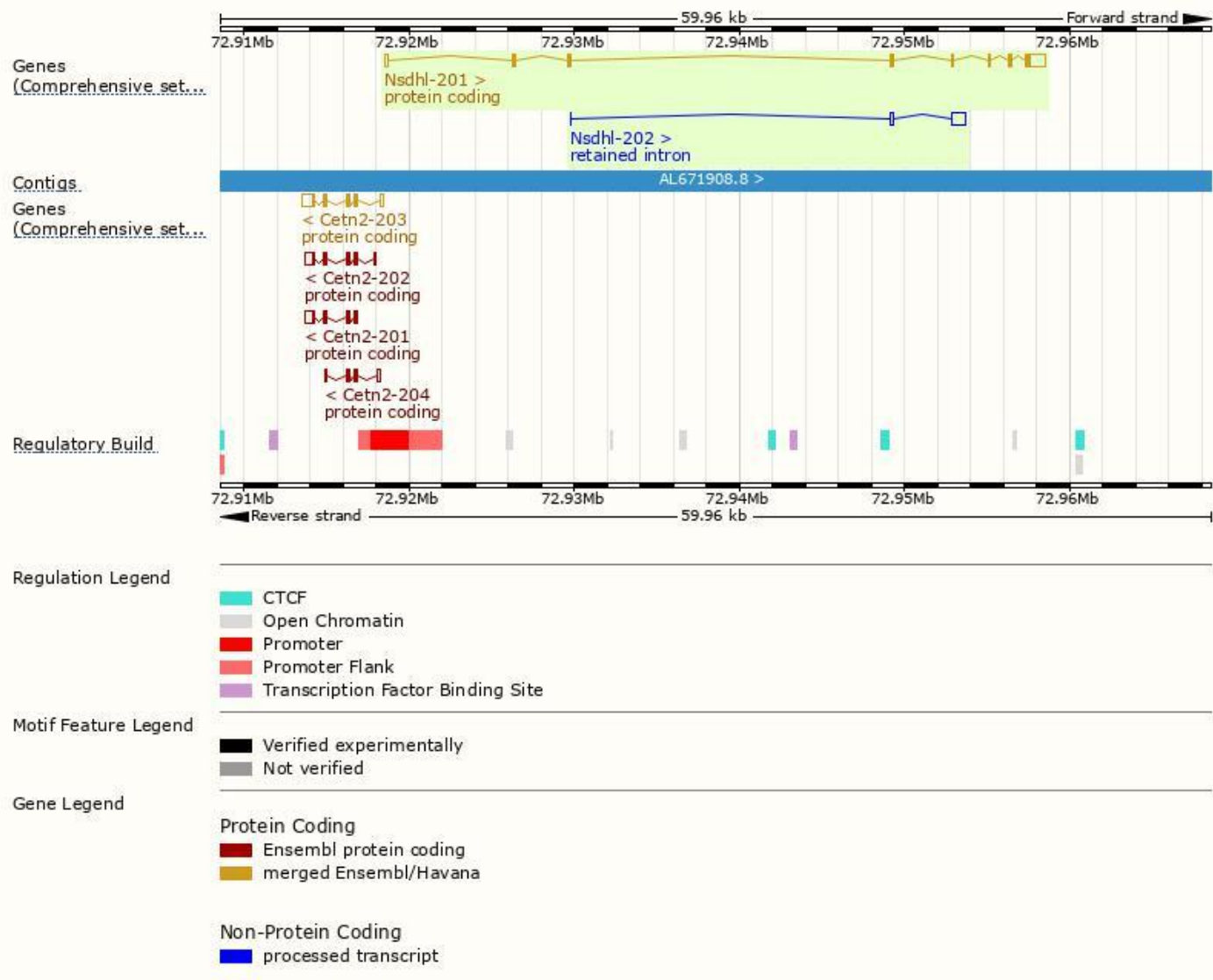
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nsdhl-201	<a href="#">ENSMUST00000033715.4</a>	2168	<a href="#">362aa</a>	Protein coding	<a href="#">CCDS30190</a>	<a href="#">Q3US15 Q9R1J0</a>	TSL:1 GENCODE basic APPRIS P1
Nsdhl-202	<a href="#">ENSMUST00000155663.1</a>	992	No protein	Retained intron	-	-	TSL:3

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



# Genomic location distribution

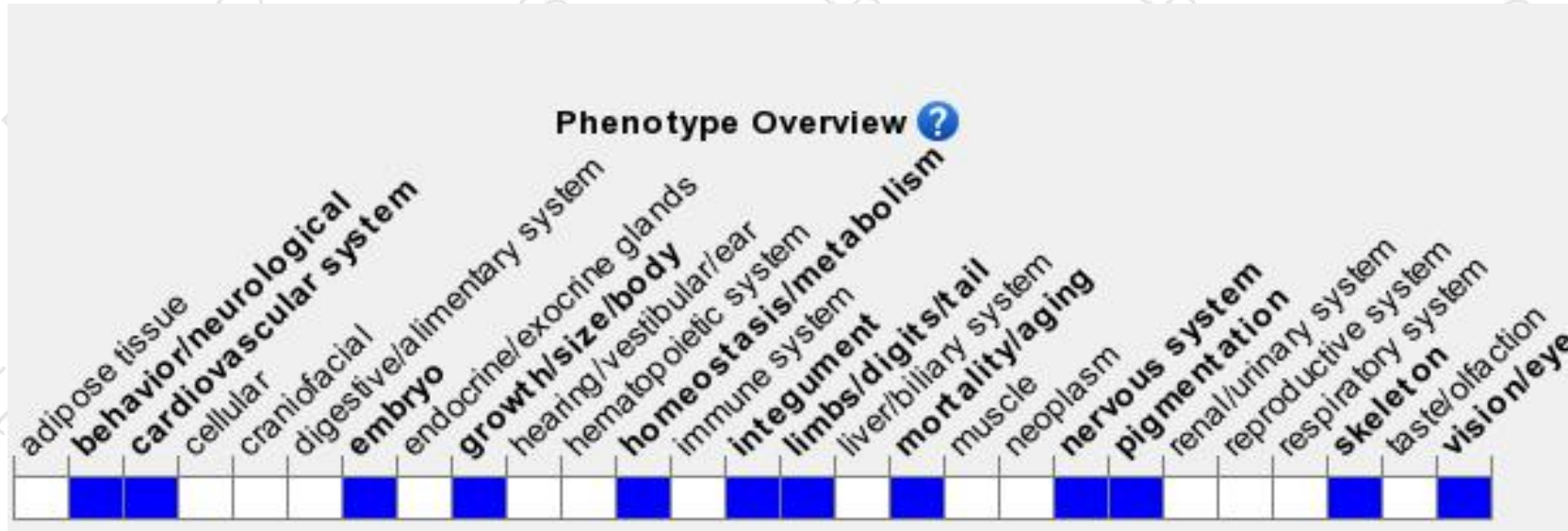




# Protein domain



# 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, Heterozygous females exhibit a striped coat or skin hyperkeratotic lesions leaving bare patches on the coat, with some mutations also resulting in skeletal dysplasia and eye defects. Hemizygous male and homozygous female mice die before birth, presumably due to placental defects.

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

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