

# ***Dhh* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Dhh*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Dhh* gene has 2 transcripts. According to the structure of *Dhh* gene, exon1 of *Dhh-201* (ENSMUST00000023737.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dhh* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mutants are male sterile, failing to produce mature spermatozoa; peripheral nerves are abnormal, with thin and disorganized perineurial sheaths. High penetrance of pseudohermaphroditism observed on some mixed backgrounds.
- The insertion of 3-terminal loxp may affect the activation of the *Rheb11* gene
- The *Dhh* gene is located on the Chr15. 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)

## Dhh desert hedgehog [Mus musculus (house mouse)]

Gene ID: 13363, updated on 9-Apr-2019

### Summary



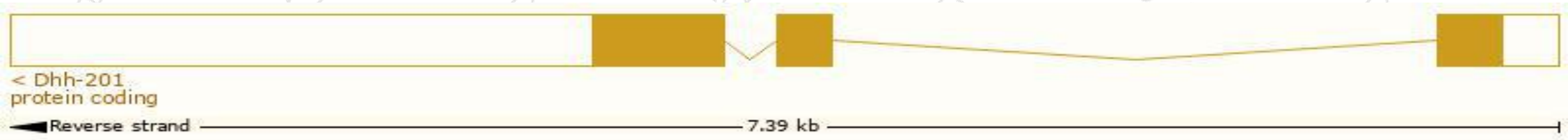
<b>Official Symbol</b>	Dhh provided by <a href="#">MGI</a>
<b>Official Full Name</b>	desert hedgehog provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:94891</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000023000</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	C78960
<b>Expression</b>	Biased expression in ovary adult (RPKM 10.4), testis adult (RPKM 4.0) and 7 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

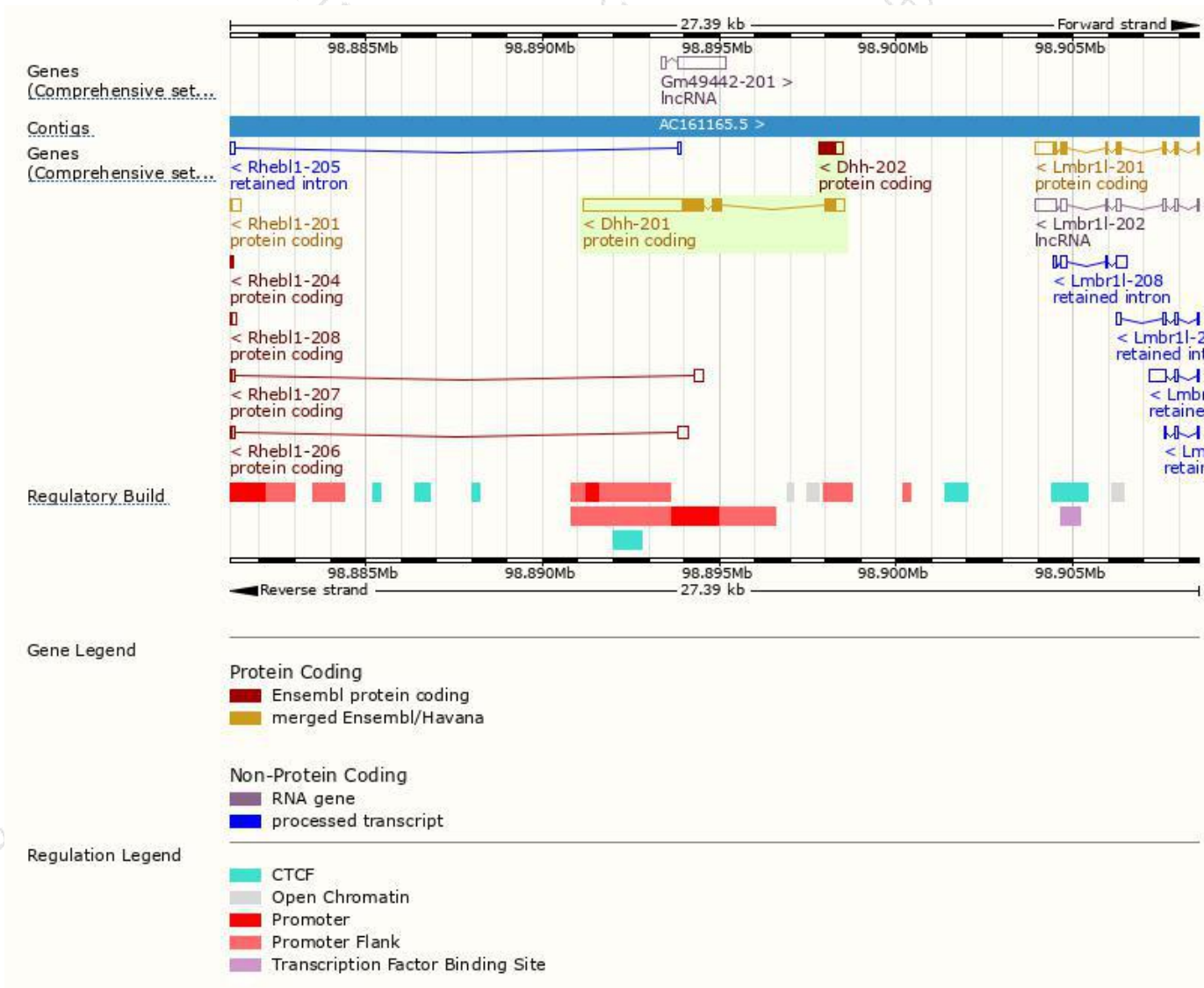
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dhh-201	<a href="#">ENSMUST00000023737.5</a>	4242	<a href="#">396aa</a>	Protein coding	<a href="#">CCDS27810</a>	<a href="#">Q544P6</a> <a href="#">Q61488</a>	TSL:1 GENCODE basic APPRIS P1
Dhh-202	<a href="#">ENSMUST00000229775.1</a>	694	<a href="#">138aa</a>	Protein coding	-	<a href="#">A0A2R8VI43</a>	GENCODE basic

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



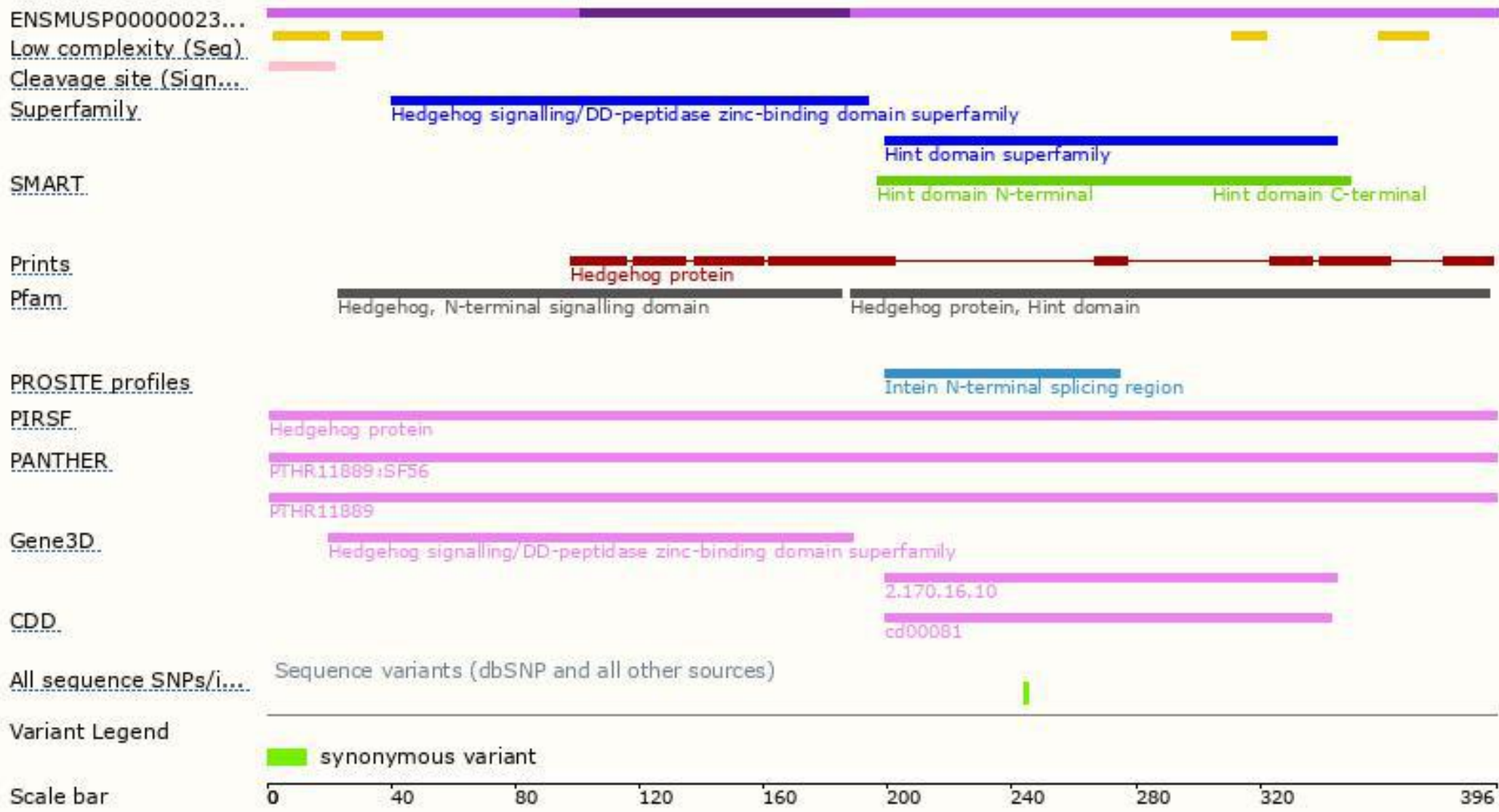
# Genomic location distribution



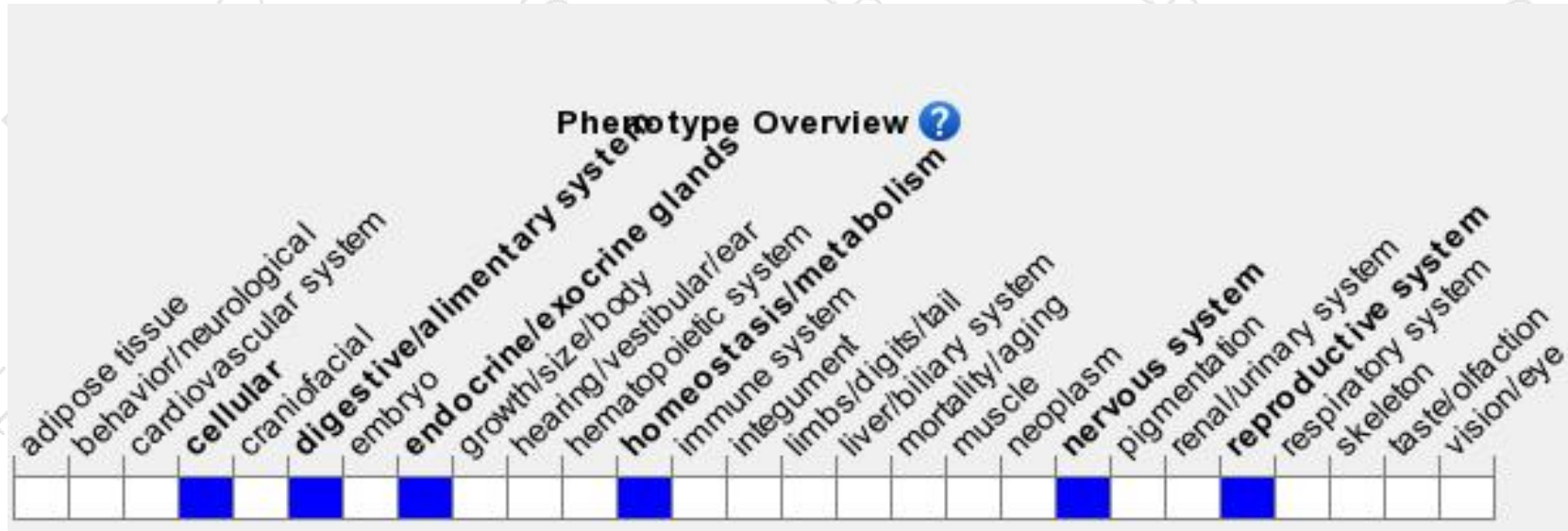
# Protein domain



集萃药康  
GemPharmatech



# 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 null mutants are male sterile, failing to produce mature spermatozoa; peripheral nerves are abnormal, with thin and disorganized perineurial sheaths. High penetrance of pseudohermaphroditism observed on some mixed backgrounds.

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

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