

# *Suv39h2* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Suv39h2***

**Project type**

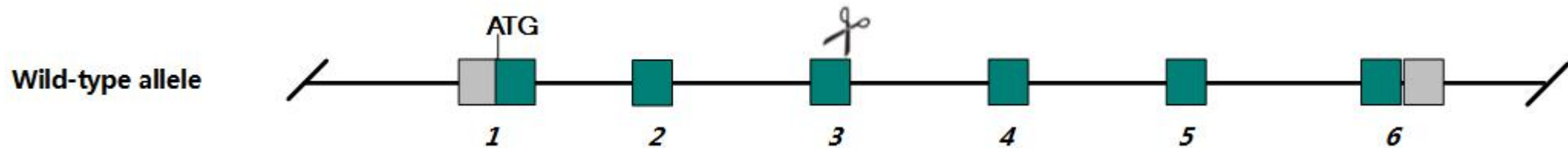
**Cas9-KO**

**Strain background**

**C57BL/6N**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Suv39h2* gene. The schematic diagram is as follows:



- In this project we use CRISPR/Cas9 technology to modify *Suv39h2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N 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/6N mice.

- According to MGI, Less than 5% of mice either heterozygous or homozygous for a reporter/null allele develop late-onset B cell lymphomas.
- The *Suv39h2* gene is located on the Chr2, 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)

## Suv39h2 suppressor of variegation 3-9 2 [ *Mus musculus* (house mouse) ]

Gene ID: 64707, updated on 12-Aug-2019

### Summary

**Official Symbol** Suv39h2 provided by [MGI](#)

**Official Full Name** suppressor of variegation 3-9 2 provided by [MGI](#)

**Primary source** [MGI:MGI:1890396](#)

**See related** [Ensembl:ENSMUSG00000026646](#)

**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** KMT1B; AA536750; D2Ertd544e; 4930507K23Rik; D030054H19Rik

**Expression** Broad expression in CNS E11.5 (RPKM 5.6), placenta adult (RPKM 3.1) and 21 other tissues [See more](#)

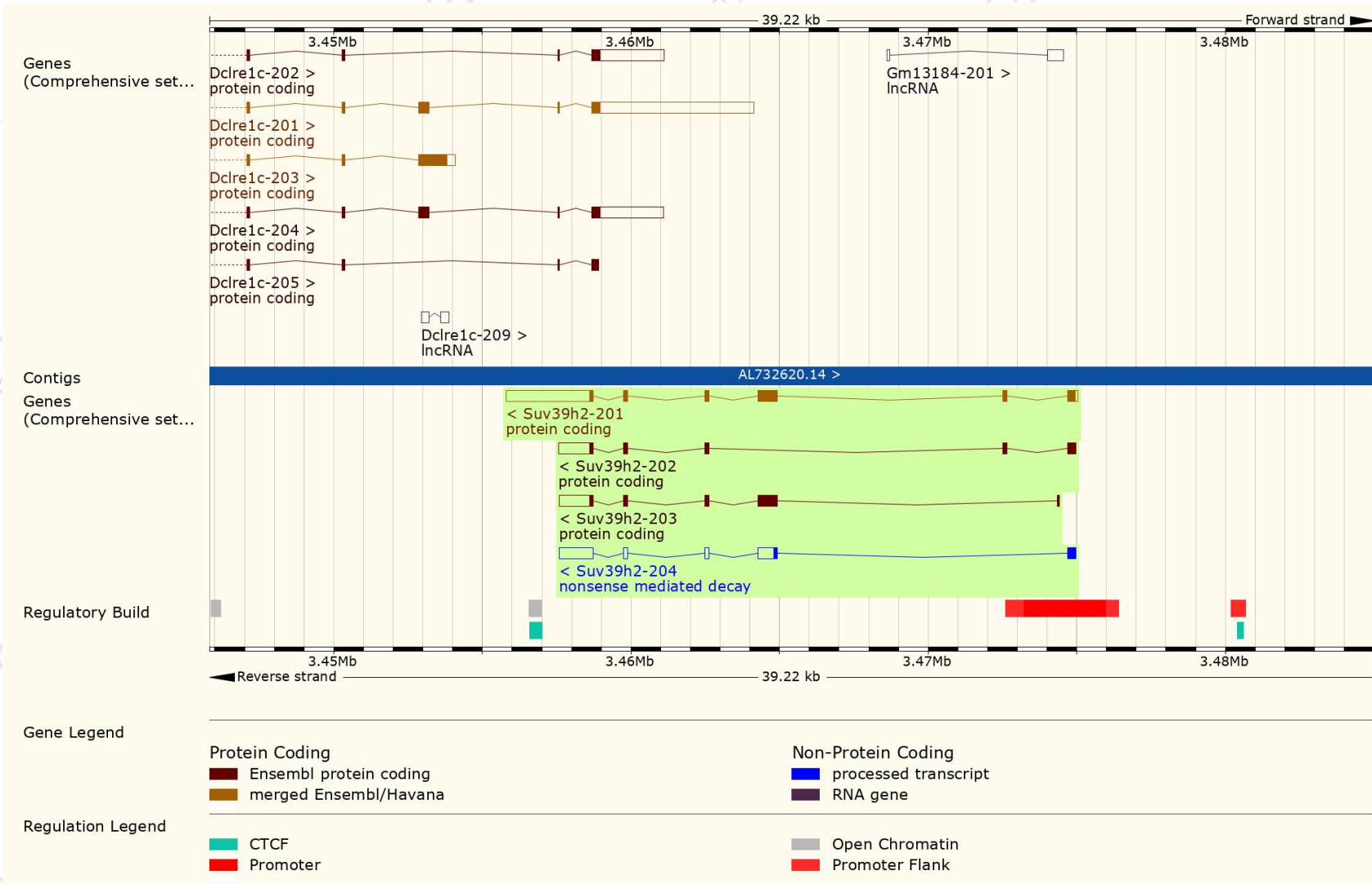
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

The gene has 4 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Suv39h2-201	<a href="#">ENSMUST00000027956.8</a>	4327	<a href="#">477aa</a>	 Protein coding	<a href="#">CCDS15652</a>	<a href="#">A0A0R4J074</a>	TSL:1 GENCODE basic APPRIS P1
Suv39h2-202	<a href="#">ENSMUST00000060618.12</a>	1831	<a href="#">257aa</a>	 Protein coding	-	<a href="#">Q8K085</a>	TSL:1 GENCODE basic
Suv39h2-203	<a href="#">ENSMUST00000100458.3</a>	2169	<a href="#">375aa</a>	 Protein coding	-	<a href="#">F6WB49</a>	CDS 5' incomplete TSL:1
Suv39h2-204	<a href="#">ENSMUST00000127540.1</a>	2331	<a href="#">116aa</a>	 Nonsense mediated decay	-	<a href="#">E0CZC9</a>	TSL:1

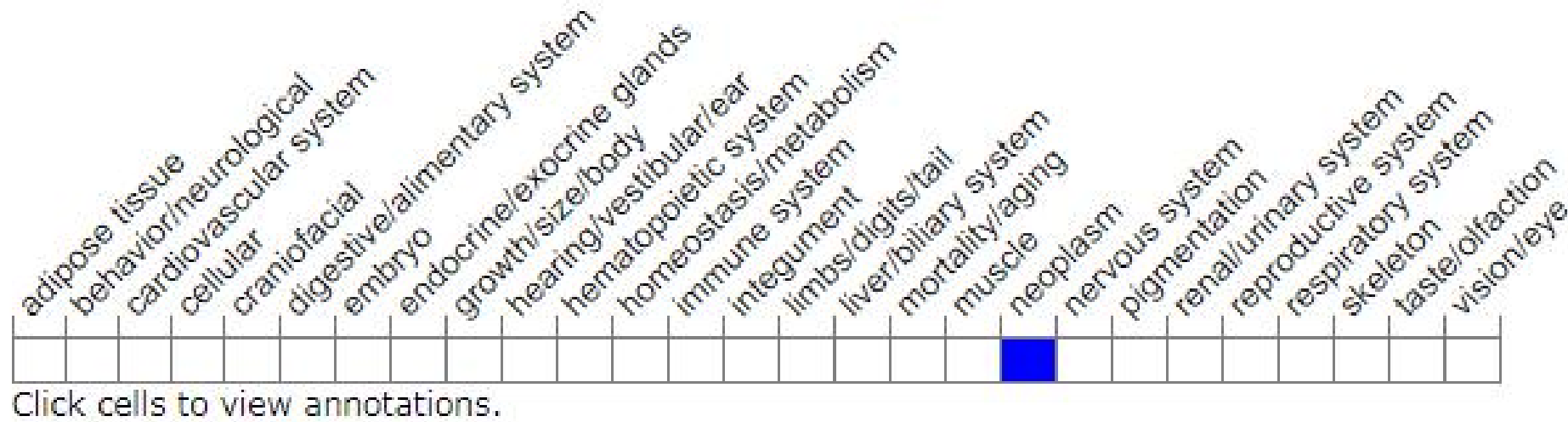
# Genomic location distribution





# Mouse phenotype description(MGI)

## Phenotype Overview ?



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

Less than 5% of mice either heterozygous or homozygous for a reporter/null allele develop late-onset B cell lymphomas.

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

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