

Suv39h1 Cas9-KO Strategy

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Project Overview



Project Name

Suv39h1

Project type

Cas9-KO

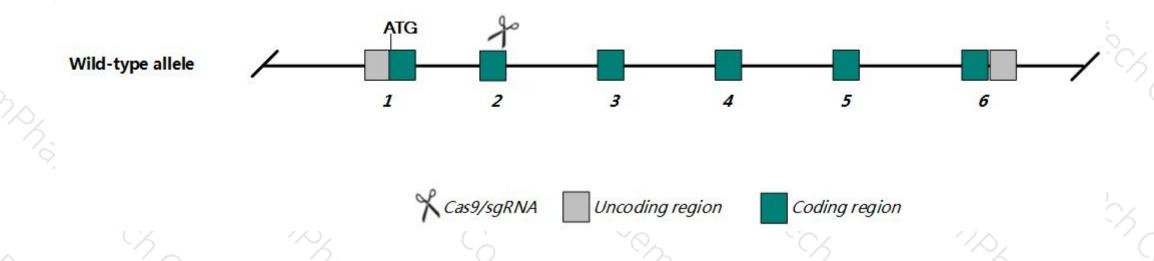
Strain background

C57BL/6N

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Suv39h1 gene. The schematic diagram is as follows:



Technical routes



➤ In this project we use CRISPR/Cas9 technology to modify *Suv39h1* 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.

Notice



- ➤ According to MGI, About one third of mice either heterozygous or homozygous for a reporter/null allele develop late-onset B cell lymphomas.
- ➤ The Suv39h1 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)



Suv39h1 suppressor of variegation 3-9 1 [Mus musculus (house mouse)]

Gene ID: 20937, updated on 12-Aug-2019

Summary

Official Symbol Suv39h1 provided by MGI

Official Full Name suppressor of variegation 3-9 1 provided by MGI

Primary source MGI:MGI:1099440

See related Ensembl: ENSMUSG00000039231

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 mIS6; KMT1A; AI852103; AL022883; DXHXS7466e; H3-K9-HMTase 1

Expression Ubiquitous expression in thymus adult (RPKM 16.1), CNS E11.5 (RPKM 15.8) and 28 other tissues See more

Orthologs <u>human</u> all

Transcript information (Ensembl)

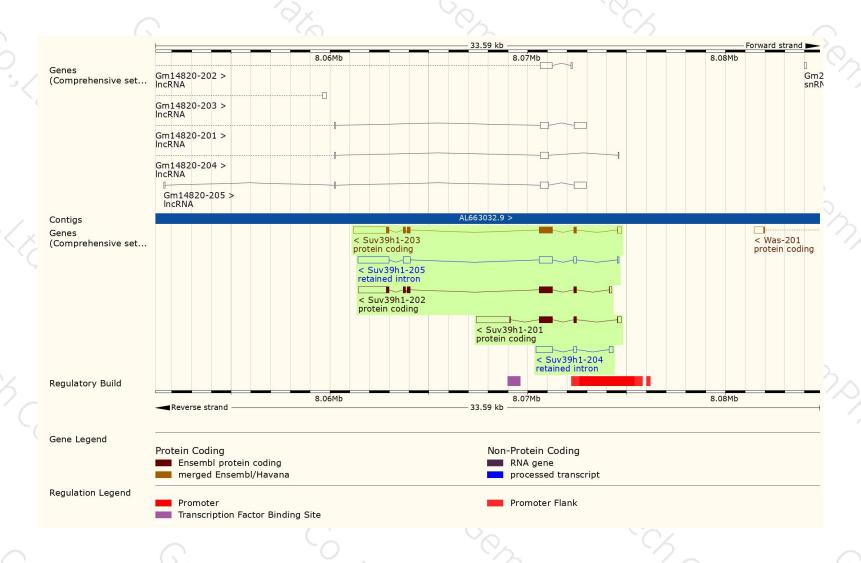


The gene has 5 transcripts, all transcripts are shown below:

Name A	Transcript ID 👙	bp 🍦	Protein	Biotype	CCDS 🍦	UniProt 🍦	Flags
Suv39h1-201	ENSMUST00000115636.3	2707	286aa	Protein coding	(-)	<u>054864</u> ₽	TSL:1 GENCODE basic
Suv39h1-202	ENSMUST00000115637.7	2778	413aa	Protein coding	CCDS72337 ₽	A2AC19₽	TSL:2 GENCODE basic
Suv39h1-203	ENSMUST00000115638.9	3116	412aa	Protein coding	CCDS40846₽	<u>054864</u> 굡	TSL:1 GENCODE basic APPRIS P1
Suv39h1-204	ENSMUST00000127617.1	1166	No protein	Retained intron	10-11	-	TSL:2
Suv39h1-205	ENSMUST00000150095.7	2807	No protein	Retained intron	-	-	TSL:2

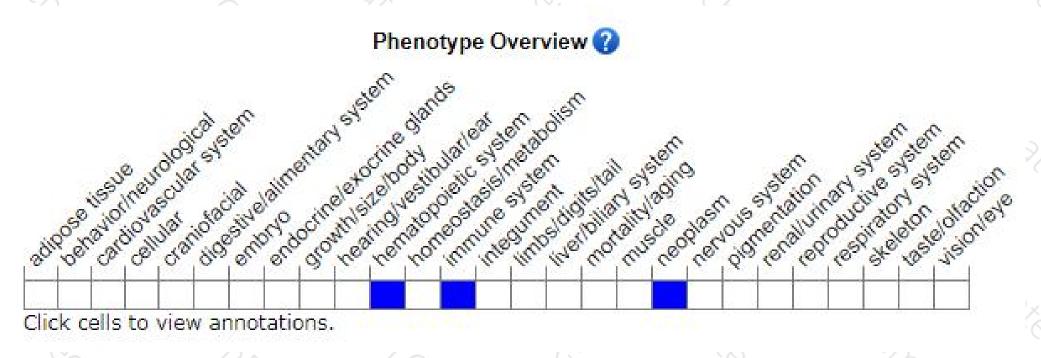
Genomic location distribution





Mouse phenotype description(MGI)





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

About one third 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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