

Smarch1 Cas9-KO Strategy

Designer:

Ruirui Zhang

Reviewer:

Huimin Su

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Project Overview



Project Name

Smarcb1

Project type

Cas9-KO

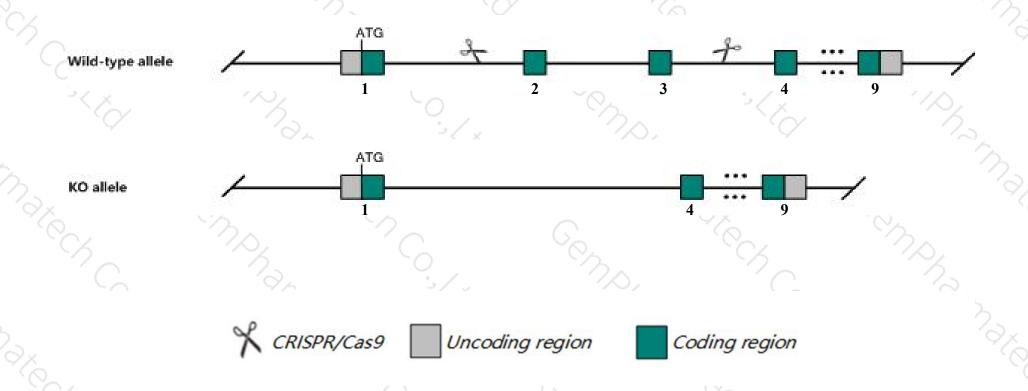
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Smarcb1 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Smarcb1* gene has 6 transcripts. According to the structure of *Smarcb1* gene, exon2-exon3 of *Smarcb1-201* (ENSMUST0000000925.9) transcript is recommended as the knockout region. The region contains 269bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Smarcb1* gene. The brief process is as follows: CRISPR/Cas9 systematically system

Notice



- ➤ According to the existing MGI data, Homozygous inactivation of this gene leads to peri-implantation lethality, likely due to an inability of the blastocysts to hatch and implant in the uterus. A subset of heterozygous null mice develop a variety of tumors in the soft tissues of the head and neck.
- The *Smarcb1* gene is located on the Chr10. 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)



Smarcb1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 [Mus musculus (house mouse)]

Gene ID: 20587, updated on 12-Aug-2019

Summary



Official Symbol Smarcb1 provided by MGI

Official Full Name SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 provided by MGI

Primary source MGI:MGI:1328366

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 Ini1; Snf5; Baf47; AU020204; SNF5/INI1

Expression Ubiquitous expression in adrenal adult (RPKM 44.4), CNS E11.5 (RPKM 42.9) and 28 other tissues See more

Orthologs <u>human</u> all

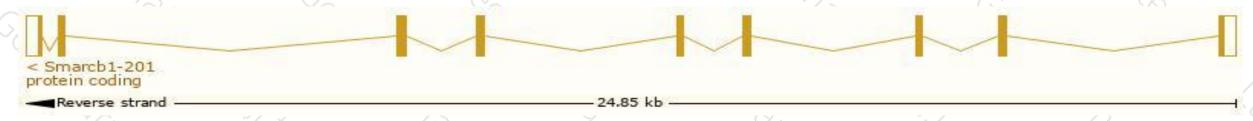
Transcript information (Ensembl)



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

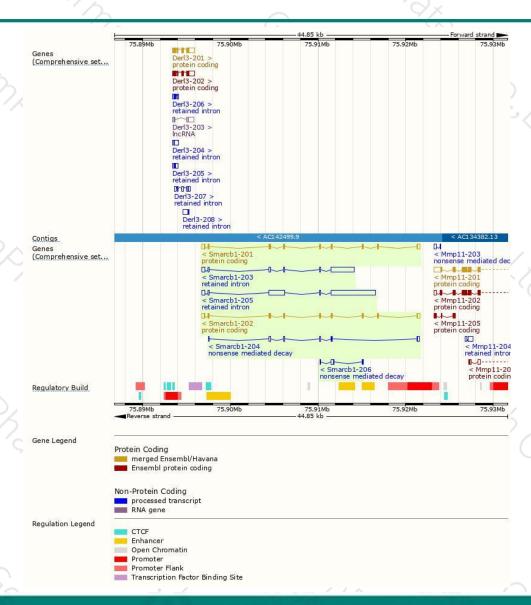
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smarcb1-201	ENSMUST00000000925.9	1660	385aa	Protein coding	CCDS23936₽	Q6ZWP4@ Q9Z0H3@	TSL:1 GENCODE basic APPRIS P3
Smarcb1-202	ENSMUST00000121304.1	1622	376aa	Protein coding	CCDS48602@	Q3UDA4 @ Q9Z0H3 @	TSL:1 GENCODE basic APPRIS ALT1
Smarcb1-204	ENSMUST00000140388.1	960	<u>78aa</u>	Nonsense mediated decay	-	D6RDC4 Ø	TSL:5
Smarcb1-206	ENSMUST00000146555.1	427	<u>55aa</u>	Nonsense mediated decay	2	<u>F6U415</u> ₽	CDS 5' incomplete TSL:5
Smarcb1-205	ENSMUST00000140408.1	7441	No protein	Retained intron	-	-	TSL:1
Smarcb1-203	ENSMUST00000133189.7	3607	No protein	Retained intron	2	2	TSL:5

The strategy is based on the design of Smarcb1-201 transcript, The transcription is shown below



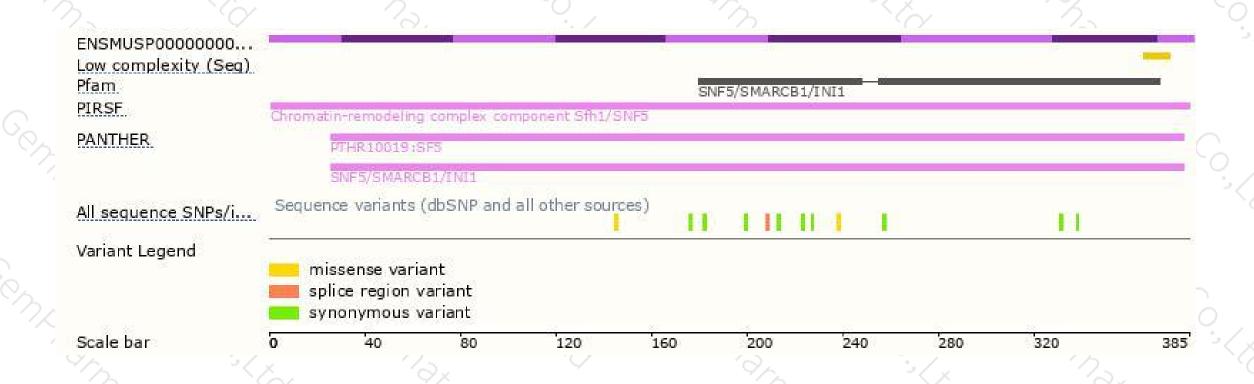
Genomic location distribution





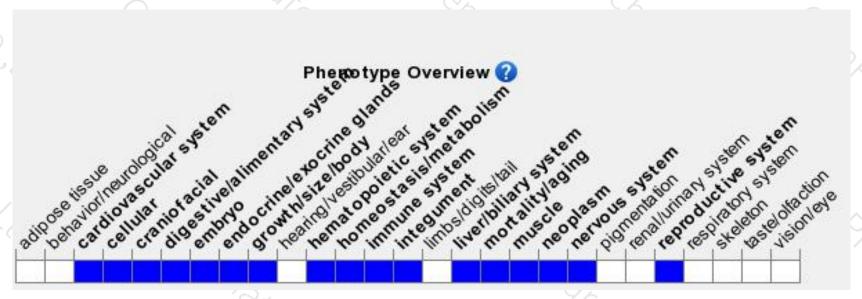
Protein domain





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 inactivation of this gene leads to peri-implantation lethality, likely due to an inability of the blastocysts to hatch and implant in the uterus. A subset of heterozygous null mice develop a variety of tumors in the soft tissues of the head and neck.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





