

Sdhb Cas9-KO Strategy

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Project Overview



Project Name

Sdhb

Project type

Cas9-KO

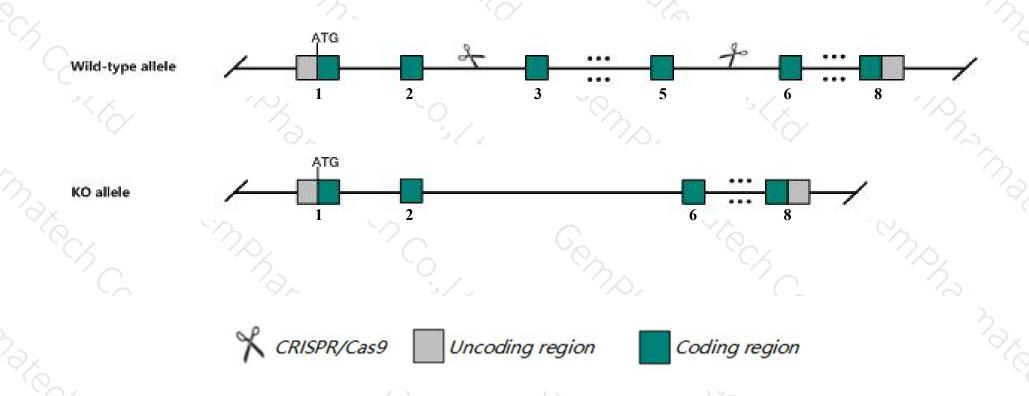
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Sdhb* gene has 3 transcripts. According to the structure of *Sdhb* gene, exon3-exon5 of *Sdhb-201* (ENSMUST0000010007.8) transcript is recommended as the knockout region. The region contains 340bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Sdhb* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- ➤ According to the existing MGI data, The gene is involved in the hypoxia-induced RNA editing pathway in monocytes. Heterozygous compound KOs show reduced increase in blood hemoglobin under hypoxic conditions. Homozygous inactivation of this gene results in complete embryonic lethality.
- > The *Sdhb* gene is located on the Chr4. 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)



Sdhb succinate dehydrogenase complex, subunit B, iron sulfur (lp) [Mus musculus (house mouse)]

Gene ID: 67680, updated on 5-Jan-2020

Summary



Official Symbol Sdhb provided by MGI

Official Full Name succinate dehydrogenase complex, subunit B, iron sulfur (lp) provided by MGI

Primary source MGI:MGI:1914930

See related Ensembl: ENSMUSG00000009863

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 0710008N11Rik

Expression Ubiquitous expression in heart adult (RPKM 390.1), kidney adult (RPKM 243.7) and 28 other tissues See more

Orthologs human all

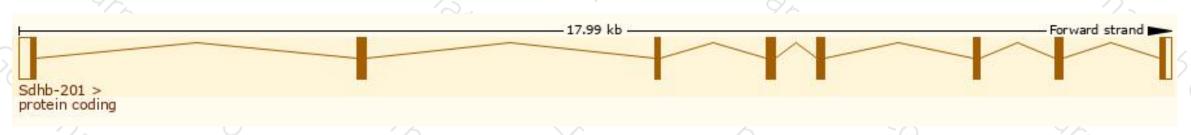
Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

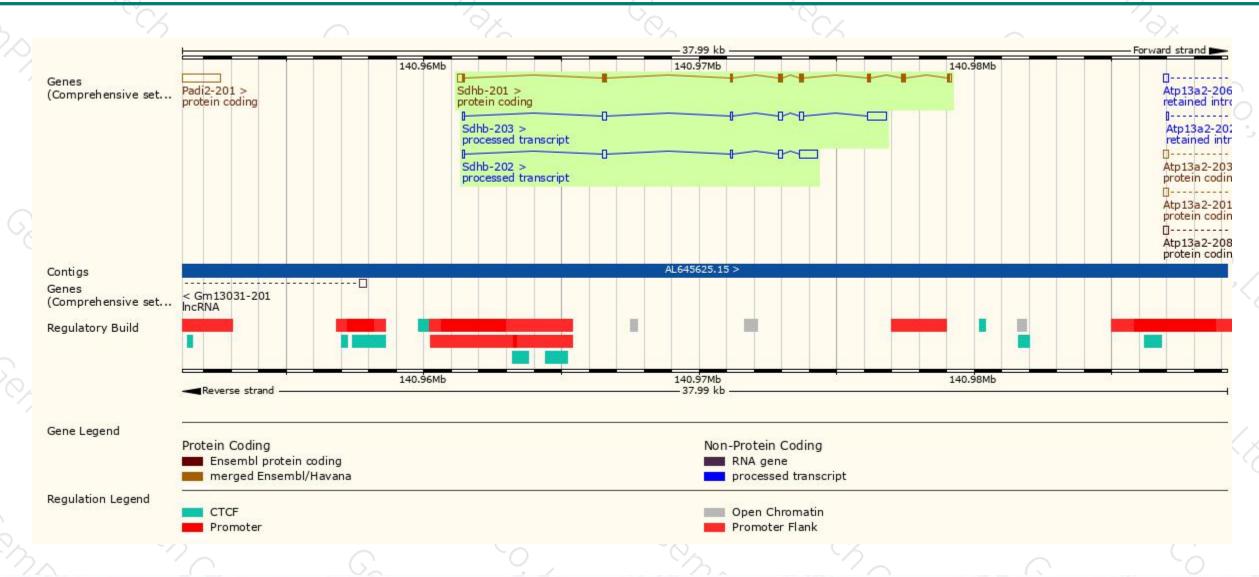
Name 🍦	Transcript ID	bp 🛊	Protein	Biotype A	CCDS .	UniProt	Flags
Sdhb-201	ENSMUST00000010007.8	1142	282aa	Protein coding	CCDS18858 €	Q9CQA3₽	TSL:1 GENCODE basic APPRIS P1
Sdhb-203	ENSMUST00000129181.7	1232	No protein	Processed transcript	=	-	TSL:2
Sdhb-202	ENSMUST00000125780.1	1065	No protein	Processed transcript	9		TSL:2

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



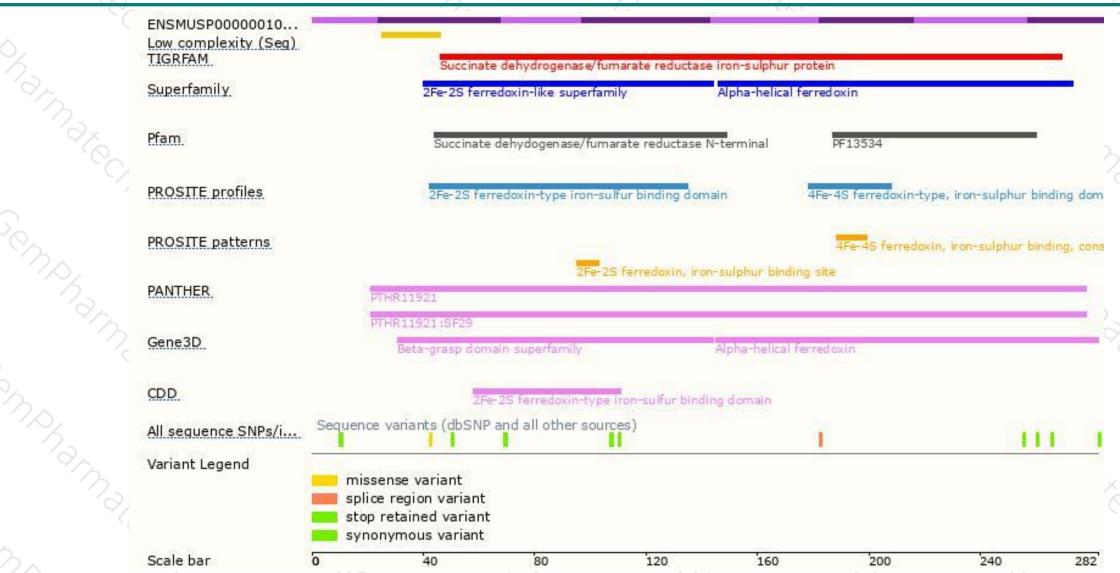
Genomic location distribution





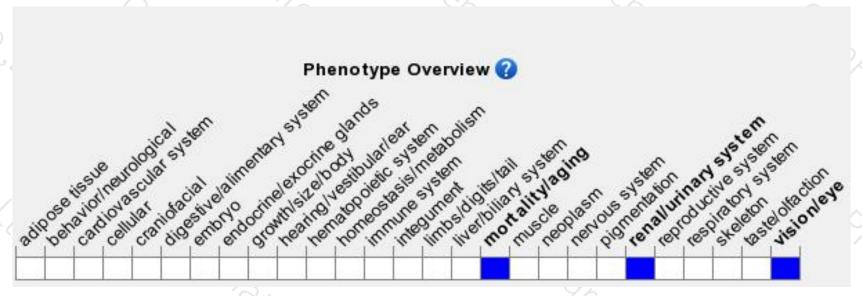
Protein domain





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, The gene is involved in the hypoxia-induced RNA editing pathway in monocytes.

Heterozygous compound KOs show reduced increase in blood hemoglobin under hypoxic conditions. Homozygous inactivati gene results in complete embryonic lethality.



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





