

***Sirt5* Cas9-CKO Strategy**

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Project Overview

Project Name

Sirt5

Project type

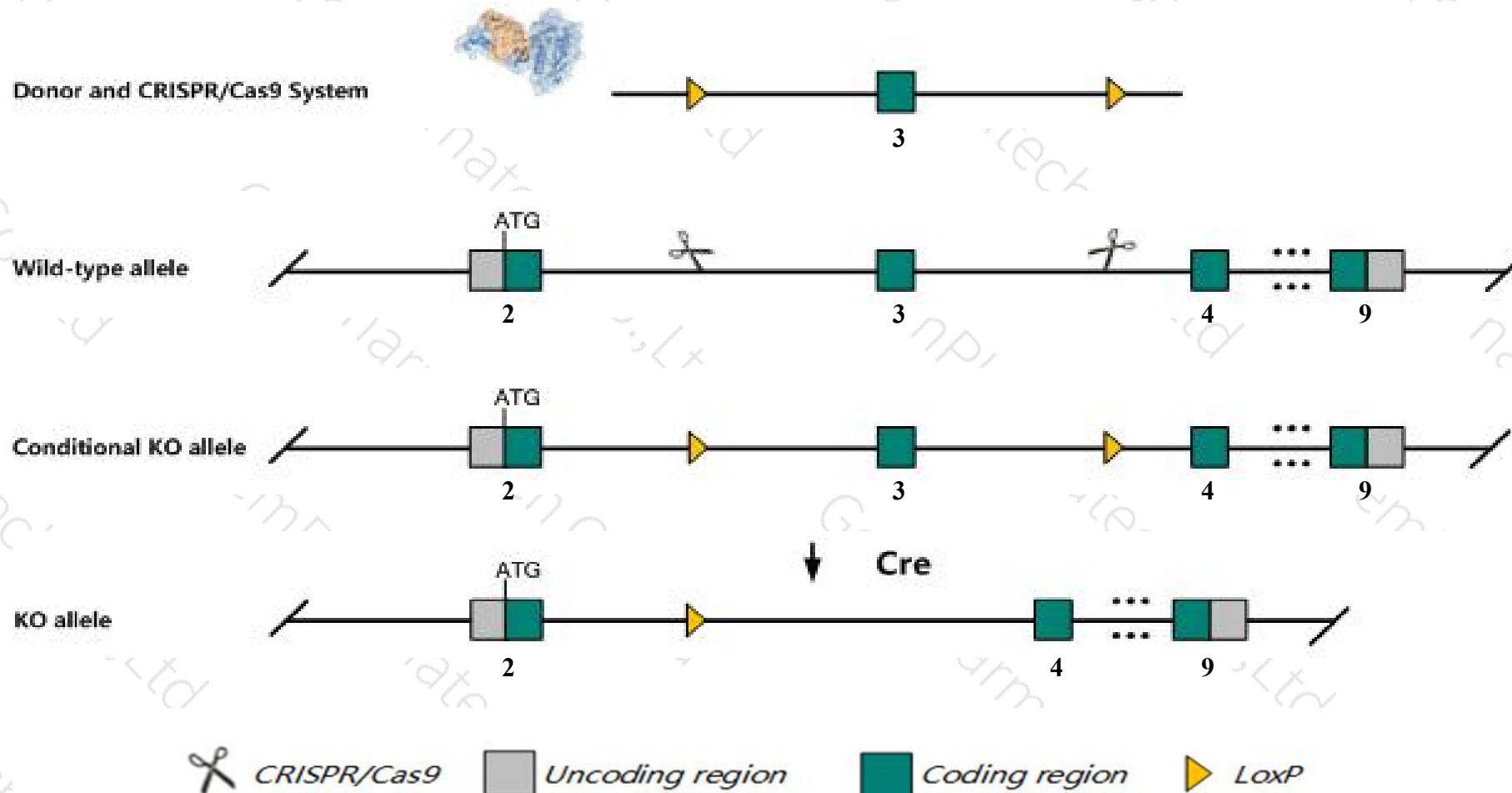
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sirt5* gene. The schematic diagram is as follows:



Technical routes

- The *Sirt5* gene has 11 transcripts. According to the structure of *Sirt5* gene, exon3 of *Sirt5-211* (ENSMUST00000223194.1) transcript is recommended as the knockout region. The region contains 134bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sirt5* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable, fertile and grossly healthy and do not exhibit globally increased mitochondrial protein acetylation levels relative to wild-type controls.
- The *Sirt5* gene is located on the Chr13. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Sirt5 sirtuin 5 [Mus musculus (house mouse)]

Gene ID: 68346, updated on 2-Mar-2019

Summary



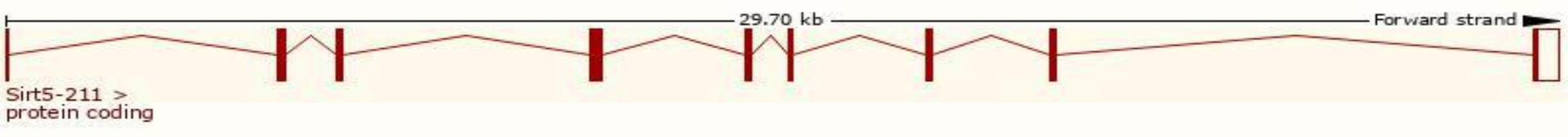
Official Symbol	Sirt5 provided by MGI
Official Full Name	sirtuin 5 provided by MGI
Primary source	MGI:MGI:1915596
See related	Ensembl:ENSMUSG00000054021
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610012J09Rik, 1500032M05Rik, AV001953
Expression	Ubiquitous expression in heart adult (RPKM 3.8), bladder adult (RPKM 2.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

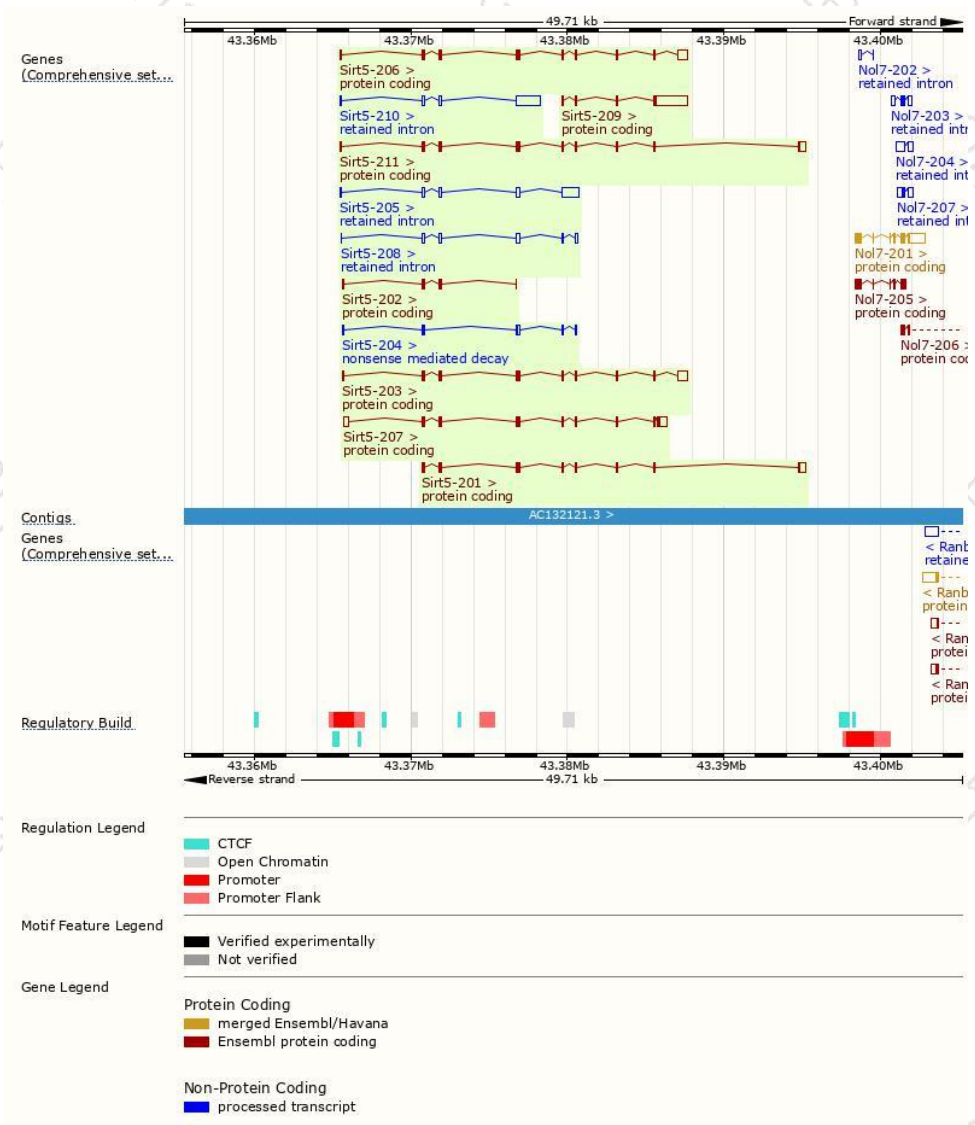
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sirt5-211	ENSMUST00000223194.1	1398	310aa	Protein coding	CCDS26478	Q8K2C6	TSL:1 GENCODE basic APPRIS P1
Sirt5-201	ENSMUST00000066804.4	1367	310aa	Protein coding	CCDS26478	Q8K2C6	TSL:1 GENCODE basic APPRIS P1
Sirt5-209	ENSMUST00000222106.1	2425	135aa	Protein coding	-	A0A1Y7VK33	CDS 5' incomplete TSL:5
Sirt5-207	ENSMUST00000221515.1	1793	350aa	Protein coding	-	A0A1Y7VM56	TSL:5 GENCODE basic
Sirt5-203	ENSMUST00000220576.1	1579	289aa	Protein coding	-	A0A1Y7VJY8	TSL:5 GENCODE basic
Sirt5-206	ENSMUST00000221481.1	1548	289aa	Protein coding	-	A0A1Y7VJY8	TSL:5 GENCODE basic
Sirt5-202	ENSMUST00000220458.1	435	95aa	Protein coding	-	A0A1Y7VNW0	CDS 3' incomplete TSL:3
Sirt5-204	ENSMUST00000220645.1	621	79aa	Nonsense mediated decay	-	A0A1Y7VMJ7	TSL:5
Sirt5-210	ENSMUST00000222489.1	1943	No protein	Retained intron	-	-	TSL:2
Sirt5-205	ENSMUST00000220874.1	1577	No protein	Retained intron	-	-	TSL:3
Sirt5-208	ENSMUST00000221955.1	803	No protein	Retained intron	-	-	TSL:3

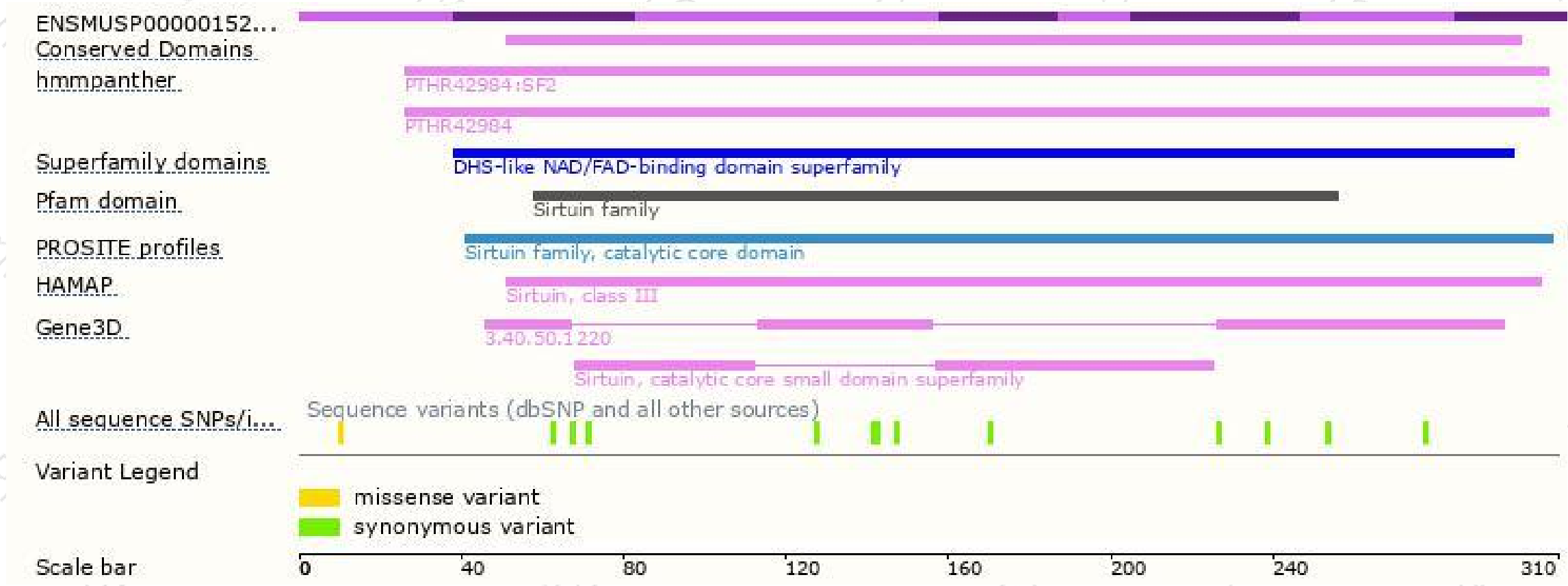
The strategy is based on the design of *Sirt5-211* transcript,The transcription is shown below



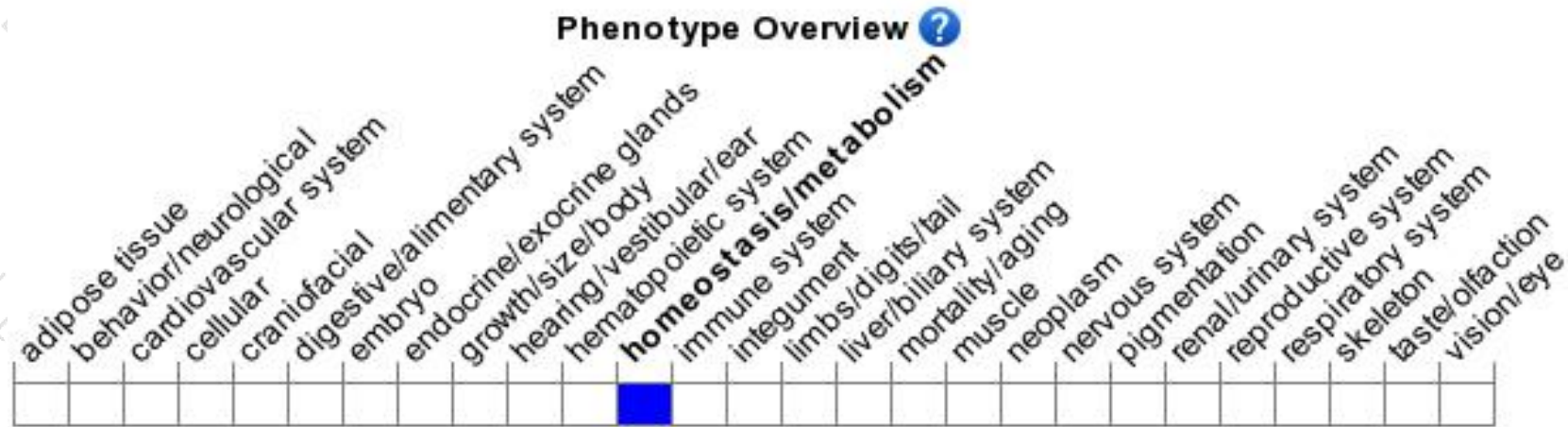
Genomic location distribution



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, Mice homozygous for a knock-out allele are viable, fertile and grossly healthy and do not exhibit globally increased mitochondrial protein acetylation levels relative to wild-type controls.

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

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