

Atp2a3 Cas9-KO Strategy

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Project Overview

Project Name

Atp2a3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2a3* gene. The schematic diagram is as follows:



- The *Atp2a3* gene has 7 transcripts. According to the structure of *Atp2a3* gene, exon2-exon7 of *Atp2a3-207* (ENSMUST00000163326.7) transcript is recommended as the knockout region. The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutation of this gene results in reduced endothelial-dependent relaxation in the aorta.
- The *Atp2a3* gene is located on the Chr11. 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)

Atp2a3 ATPase, Ca⁺⁺ transporting, ubiquitous [Mus musculus (house mouse)]

Gene ID: 53313, updated on 19-Mar-2019

Summary



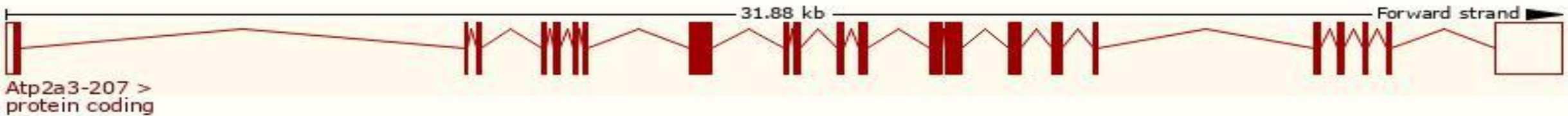
Official Symbol	Atp2a3 provided by MGI
Official Full Name	ATPase, Ca ⁺⁺ transporting, ubiquitous provided by MGI
Primary source	MGI:MGI:1194503
See related	Ensembl:ENSMUSG00000020788
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SERCA3b, Serca3
Expression	Biased expression in colon adult (RPKM 314.1), thymus adult (RPKM 123.3) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2a3-207	ENSMUST00000163326.7	4606	1026aa	Protein coding	CCDS48842	E9Q559	TSL:5 GENCODE basic
Atp2a3-201	ENSMUST00000021142.7	4593	1038aa	Protein coding	CCDS24991	Q64518	TSL:1 GENCODE basic
Atp2a3-203	ENSMUST00000108485.8	4520	999aa	Protein coding	CCDS48843	Q64518 Q8R0X5	TSL:1 GENCODE basic APPRIS P1
Atp2a3-204	ENSMUST00000108486.7	4540	1020aa	Protein coding	-	B1ATS5	TSL:5 GENCODE basic
Atp2a3-202	ENSMUST00000108484.7	4467	981aa	Protein coding	-	B1ATS4	TSL:5 GENCODE basic
Atp2a3-206	ENSMUST00000149493.1	347	No protein	Retained intron	-	-	TSL:3
Atp2a3-205	ENSMUST00000135234.1	816	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Atp2a3-207* transcript,The transcription is shown below



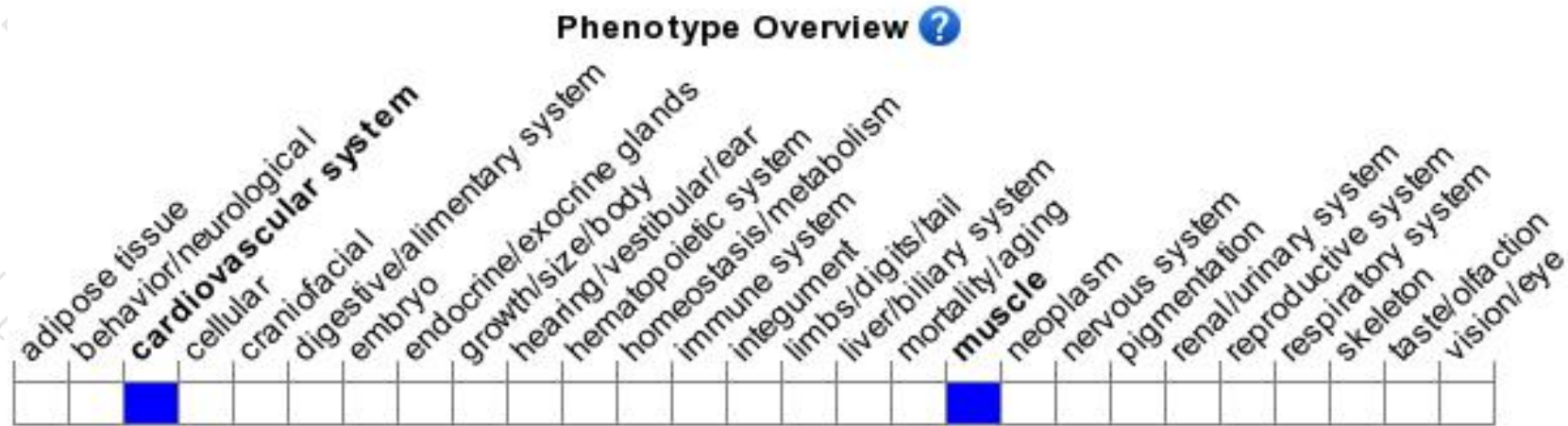
Genomic location distribution



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 mutation of this gene results in reduced endothelial-dependent relaxation in the aorta.

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

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