

Atp2c1 Cas9-KO Strategy

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Project Overview

Project Name

Atp2c1

Project type

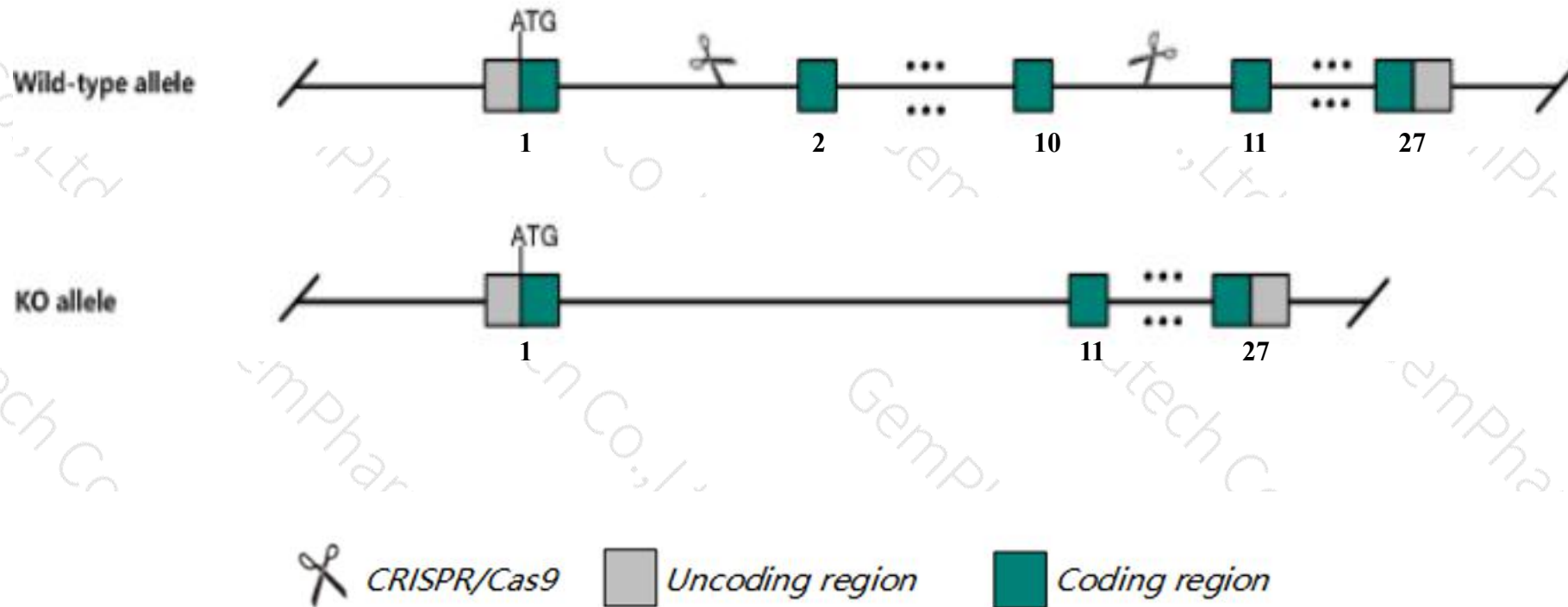
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2c1* gene. The schematic diagram is as follows:



- The *Atp2c1* gene has 21 transcripts. According to the structure of *Atp2c1* gene, exon2-exon10 of *Atp2c1-202* (ENSMUST00000085133.12) transcript is recommended as the knockout region. The region contains 823bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2c1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele show embryonic growth retardation, failure of rostral neural tube closure, golgi and endoplasmic reticulum stress, increased apoptosis, accumulation of intracellular lipid droplets and midgestational lethality. aged heterozygotes develop squamous cell tumors.
- The *Atp2c1* gene is located on the Chr9. 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)

Atp2c1 ATPase, Ca⁺⁺-sequestering [Mus musculus (house mouse)]

Gene ID: 235574, updated on 13-Mar-2020

Summary



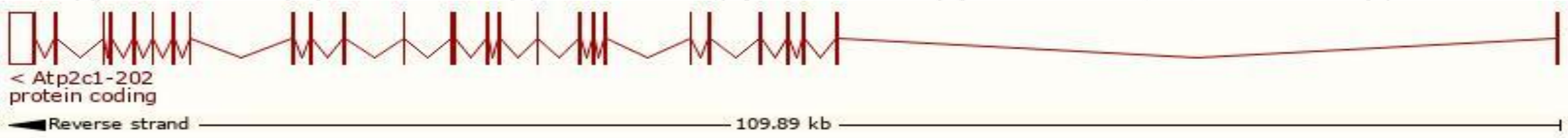
Official Symbol	Atp2c1 provided by MGI
Official Full Name	ATPase, Ca ⁺⁺ -sequestering provided by MGI
Primary source	MGI:MGI:1889008
See related	Ensembl:ENSMUSG00000032570
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700121J11Rik, ATP2C1A, AW061228, BCPM, D930003G21Rik, HHD, SPCA, pmr1
Expression	Ubiquitous expression in CNS E18 (RPKM 19.7), frontal lobe adult (RPKM 16.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

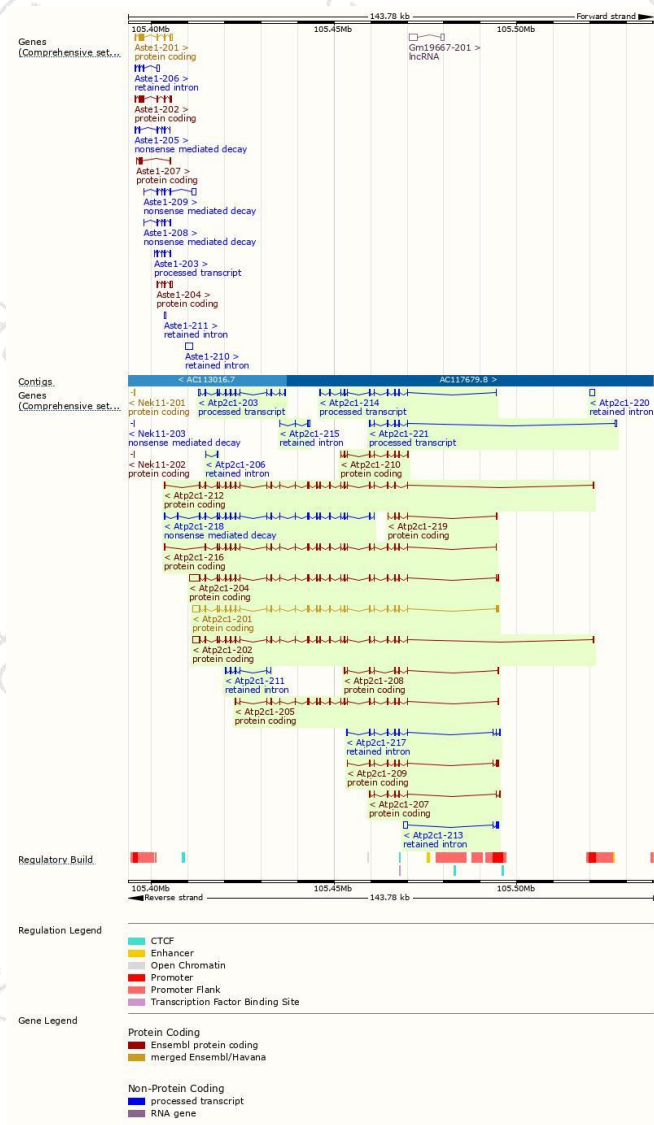
The gene has 21 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2c1-204	ENSMUST00000112558.9	5642	918aa	Protein coding	CCDS40752	Q80XR2	TSL:1 GENCODE basic APPRIS P3
Atp2c1-201	ENSMUST00000038118.14	4876	918aa	Protein coding	CCDS40752	Q80XR2	TSL:1 GENCODE basic APPRIS P3
Atp2c1-202	ENSMUST00000085133.12	4665	952aa	Protein coding	CCDS57698	Q3UZR5	TSL:1 GENCODE basic APPRIS ALT2
Atp2c1-205	ENSMUST00000163879.8	2408	669aa	Protein coding	CCDS57697	Q8BMS7	TSL:1 GENCODE basic
Atp2c1-212	ENSMUST00000176770.7	2781	926aa	Protein coding	-	H3BIX7	TSL:5 GENCODE basic
Atp2c1-216	ENSMUST00000177074.7	2664	887aa	Protein coding	-	H3BL44	TSL:5 GENCODE basic APPRIS ALT2
Atp2c1-209	ENSMUST00000176363.8	1082	230aa	Protein coding	-	H3BJY0	CDS 3' incomplete TSL:5
Atp2c1-210	ENSMUST00000176651.7	899	253aa	Protein coding	-	H3BLC2	CDS 3' incomplete TSL:5
Atp2c1-208	ENSMUST00000176190.7	823	208aa	Protein coding	-	H3BKB1	CDS 3' incomplete TSL:5
Atp2c1-207	ENSMUST00000176036.7	710	177aa	Protein coding	-	H3BJJ5	CDS 3' incomplete TSL:5
Atp2c1-219	ENSMUST00000177334.1	578	111aa	Protein coding	-	H3BJ99	CDS 3' incomplete TSL:5
Atp2c1-218	ENSMUST00000177293.7	2476	786aa	Nonsense mediated decay	-	H3BLI6	CDS 5' incomplete TSL:5
Atp2c1-203	ENSMUST00000112557.8	1514	No protein	Processed transcript	-	-	TSL:1
Atp2c1-214	ENSMUST00000176960.7	1072	No protein	Processed transcript	-	-	TSL:5
Atp2c1-221	ENSMUST00000190802.1	833	No protein	Processed transcript	-	-	TSL:5
Atp2c1-213	ENSMUST00000176787.1	1449	No protein	Retained intron	-	-	TSL:1
Atp2c1-220	ENSMUST00000186495.1	1413	No protein	Retained intron	-	-	TSL:NA
Atp2c1-217	ENSMUST00000177189.7	939	No protein	Retained intron	-	-	TSL:1
Atp2c1-211	ENSMUST00000176656.1	691	No protein	Retained intron	-	-	TSL:3
Atp2c1-215	ENSMUST00000177000.1	642	No protein	Retained intron	-	-	TSL:3
Atp2c1-206	ENSMUST00000175697.1	255	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Atp2c1-202* transcript,the transcription is shown below:



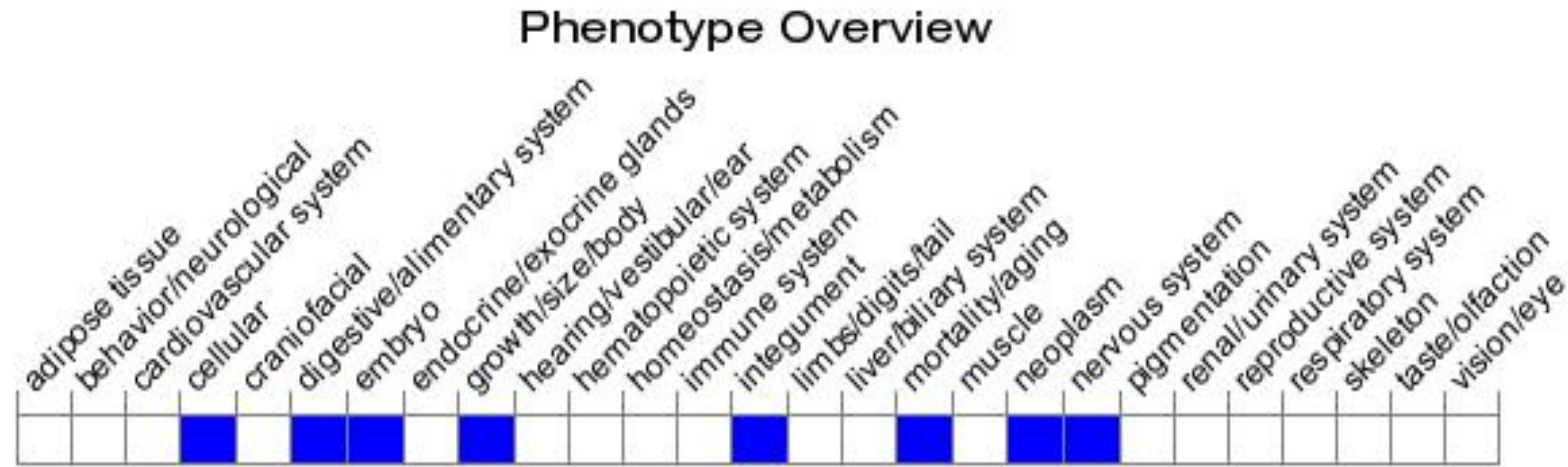
Genomic location distribution



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 show embryonic growth retardation, failure of rostral neural tube closure, Golgi and endoplasmic reticulum stress, increased apoptosis, accumulation of intracellular lipid droplets and midgestational lethality. Aged heterozygotes develop squamous cell tumors.

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

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