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Atic Cas9-CKO Strategy

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Reviewer: Jinling Wang

Design Date: 2023-5-18

Overview

Target Gene Name

- Atic

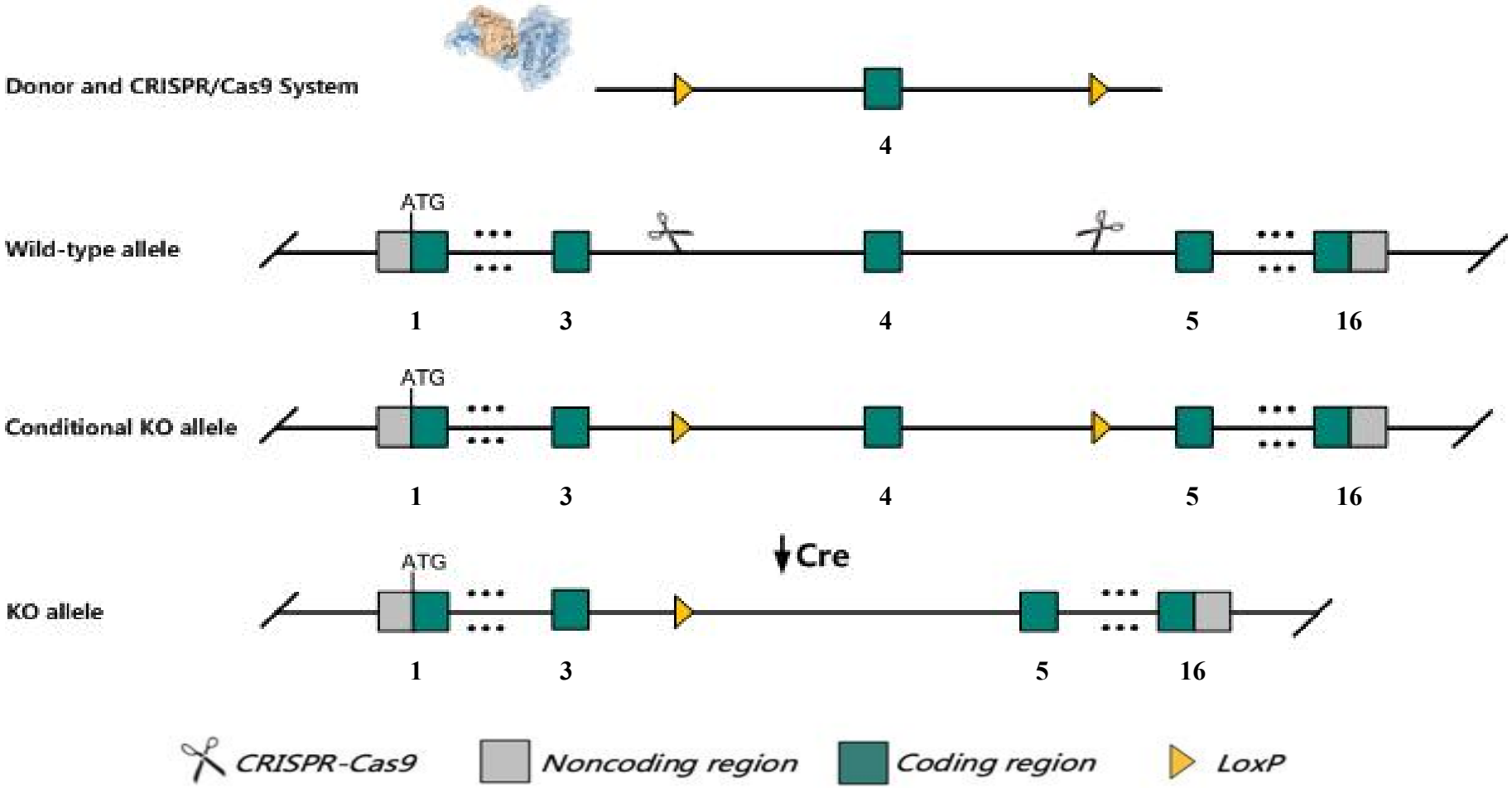
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Atic* gene.

Technical Information

- The *Atic* gene has 6 transcripts. According to the structure of *Atic* gene, exon4 of *Atic*-201 (ENSMUST00000027384.6) transcript is recommended as the knockout region. The region contains 67bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Atic* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Atic 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus (house mouse)]

Gene ID: 108147, updated on 13-Mar-2020

Summary

Official Symbol	Atic provided by MGI
Official Full Name	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase provided by MGI
Primary source	MGI:MGI:1351352
See related	Ensembl:ENSMUSG00000026192
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	2610509C24Rik, AA536954, AW212393
Expression	Ubiquitous expression in liver E14 (RPKM 26.0), limb E14.5 (RPKM 25.0) and 28 other tissues See more
Orthologs	human all

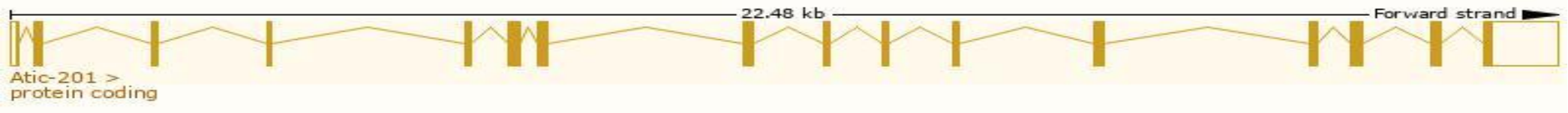
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

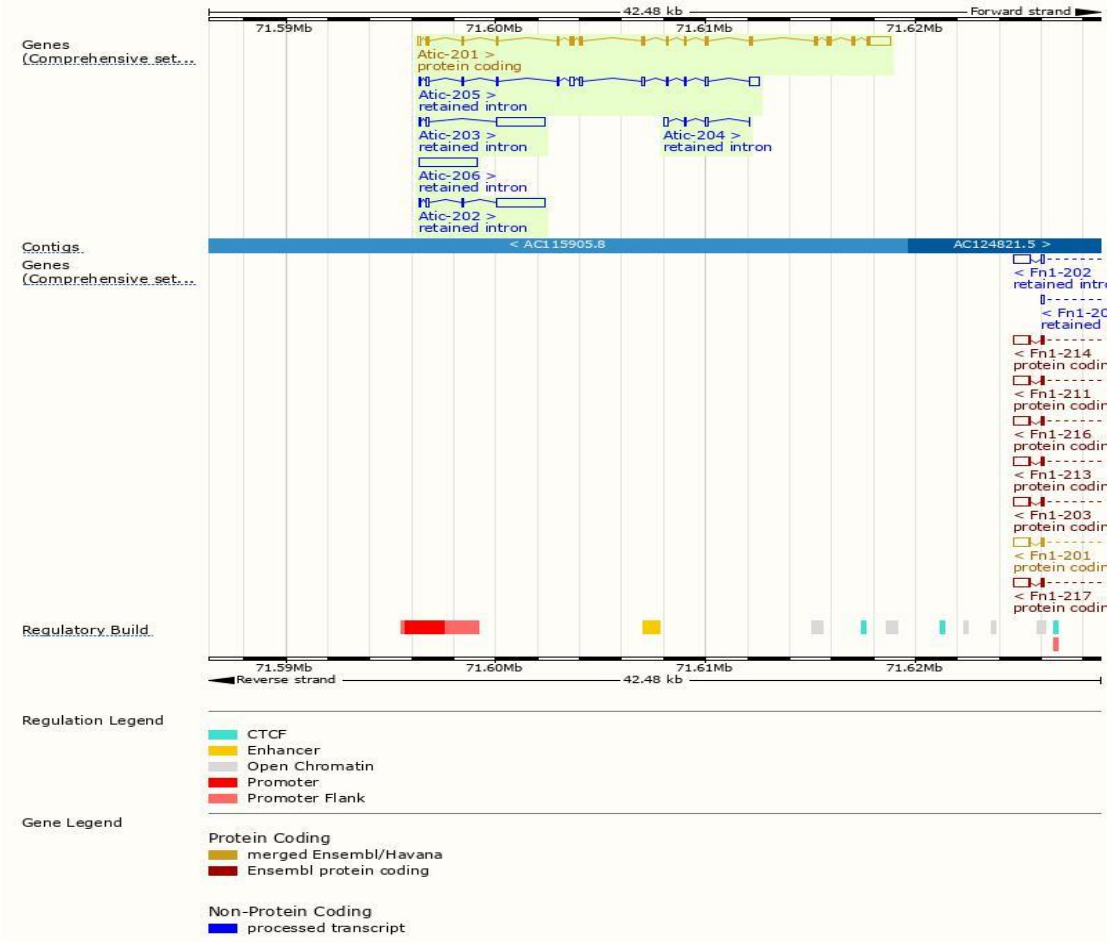
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atic-201	ENSMUST00000027384.5	2845	592aa	Protein coding	CCDS15030	Q9CWJ9	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Atic-206	ENSMUST00000187982.1	2773	No protein	Retained intron	-	-	TSL:NA
Atic-202	ENSMUST00000136443.1	2576	No protein	Retained intron	-	-	TSL:1
Atic-203	ENSMUST00000148077.7	2533	No protein	Retained intron	-	-	TSL:1
Atic-205	ENSMUST00000155769.7	1631	No protein	Retained intron	-	-	TSL:1
Atic-204	ENSMUST00000154855.1	434	No protein	Retained intron	-	-	TSL:3

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



Source: https://www.ensembl.org

Genomic Information



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Source: : https://www.ensembl.org

Protein Information

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Source: : https://www.ensembl.org

Important Information

- This strategy may destroy *Atic*-202&203.
- *Atic* is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.