

Arfgap2 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-3-6

Project Overview

Project Name

Arfgap2

Project type

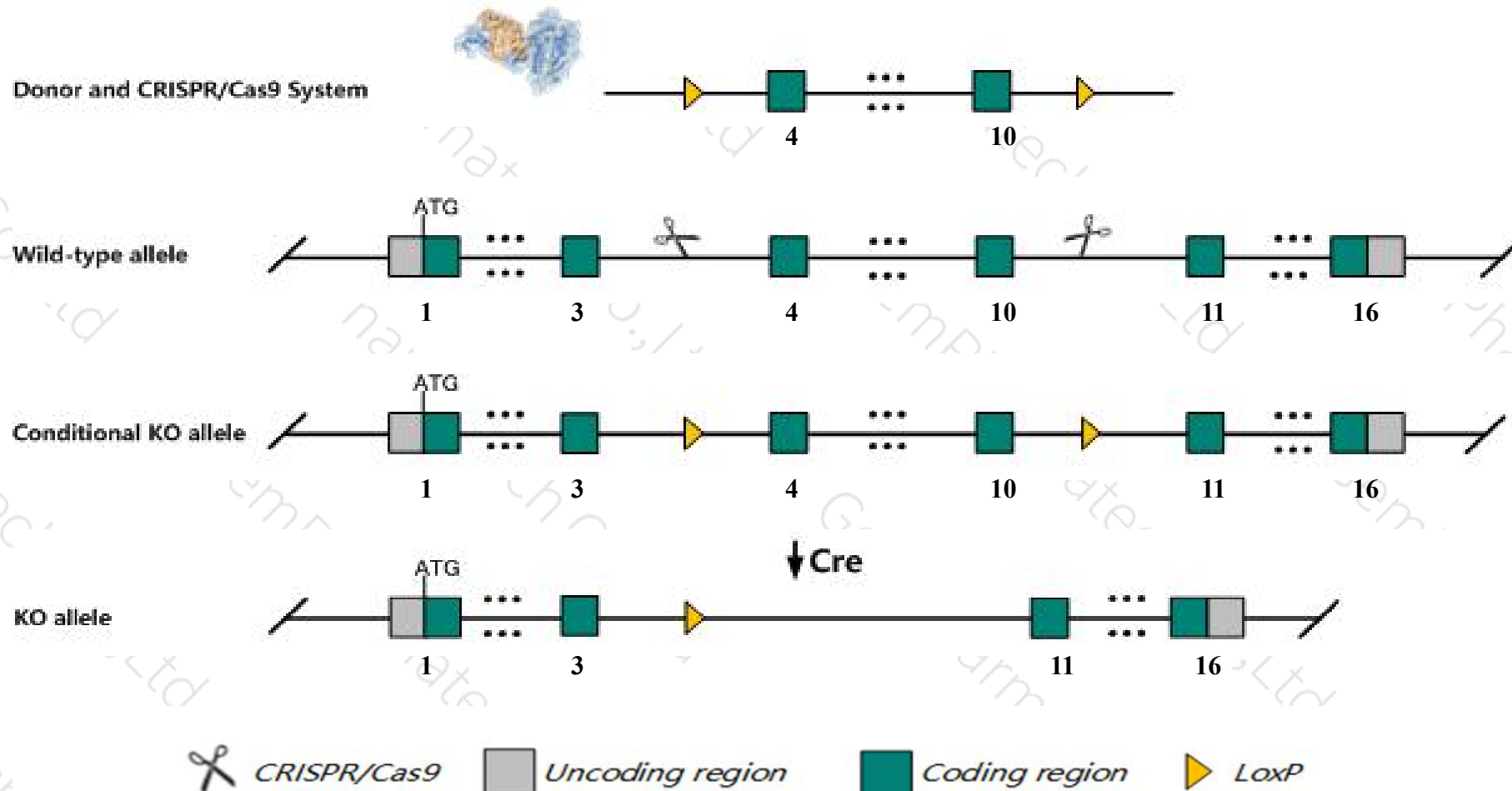
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arfgap2* gene. The schematic diagram is as follows:



- The *Arfgap2* gene has 7 transcripts. According to the structure of *Arfgap2* gene, exon4-exon10 of *Arfgap2*-202 (ENSMUST00000080008.12) transcript is recommended as the knockout region. The region contains 674bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arfgap2* 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.

Notice

- The *Arfgap2* gene is located on the Chr2. 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)

Arfgap2 ADP-ribosylation factor GTPase activating protein 2 [Mus musculus (house mouse)]

Gene ID: 77038, updated on 31-Jan-2019

Summary



Official Symbol Arfgap2 provided by [MGI](#)

Official Full Name ADP-ribosylation factor GTPase activating protein 2 provided by [MGI](#)

Primary source [MGI:MGI:1924288](#)

See related [Ensembl:ENSMUSG00000027255](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 2310032E02Rik, Zfp289

Summary This gene encodes a zinc-finger-containing GTPase-activating protein for ADP ribosylation factor 1 (ARF1), a small GTPase that plays a role in coatamer-mediated vesicular trafficking. This gene product stimulates the hydrolysis of ARF1-bound GTP, which may lead to dissociation of coatamer from Golgi-derived membranes to allow fusion with target membranes. It may regulate the retrograde transport from the Golgi complex to the endoplasmic reticulum. Expression of this gene has been shown to be controlled by inhibitor of DNA binding 1 (Id1). Alternatively spliced transcript variants encoding different isoforms have been found for this gene. A pseudogene of this gene was identified on chromosome 6. [provided by RefSeq, Oct 2009]

Expression Ubiquitous expression in thymus adult (RPKM 21.9), liver adult (RPKM 21.6) and 28 other tissues [See more](#)

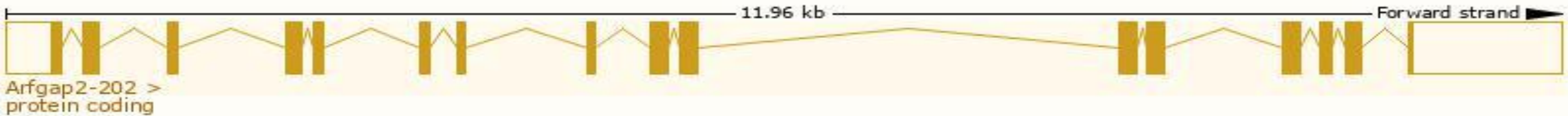
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

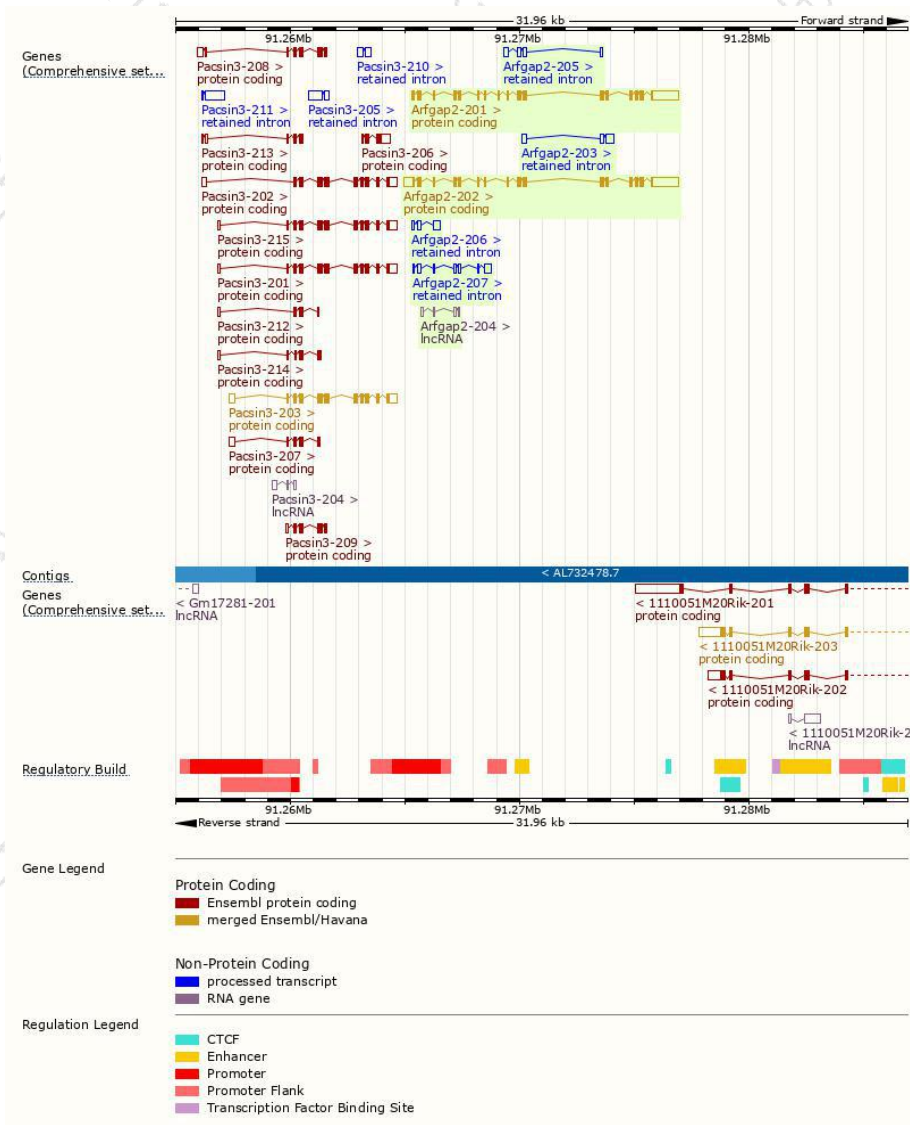
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arfgap2-202	ENSMUST00000080008.12	3068	520aa	Protein coding	CCDS16430	Q99K28	TSL:1 GENCODE basic APPRIS P3
Arfgap2-201	ENSMUST00000028691.6	2791	534aa	Protein coding	CCDS50639	Q99K28	TSL:1 GENCODE basic APPRIS ALT1
Arfgap2-207	ENSMUST00000150753.7	859	No protein	Retained intron	-	-	TSL:2
Arfgap2-203	ENSMUST00000127895.2	700	No protein	Retained intron	-	-	TSL:3
Arfgap2-206	ENSMUST00000150701.7	520	No protein	Retained intron	-	-	TSL:2
Arfgap2-205	ENSMUST00000146228.1	499	No protein	Retained intron	-	-	TSL:3
Arfgap2-204	ENSMUST00000128296.1	373	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Arfgap2-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP000000078...

[MobiDB lite](#)

[Low complexity \(Seg\)](#)

[Coiled-coils \(Ncoils\)](#)

[Superfamily](#)

[SMART](#)

[Prints](#)

[Pfam](#)

[PROSITE profiles](#)

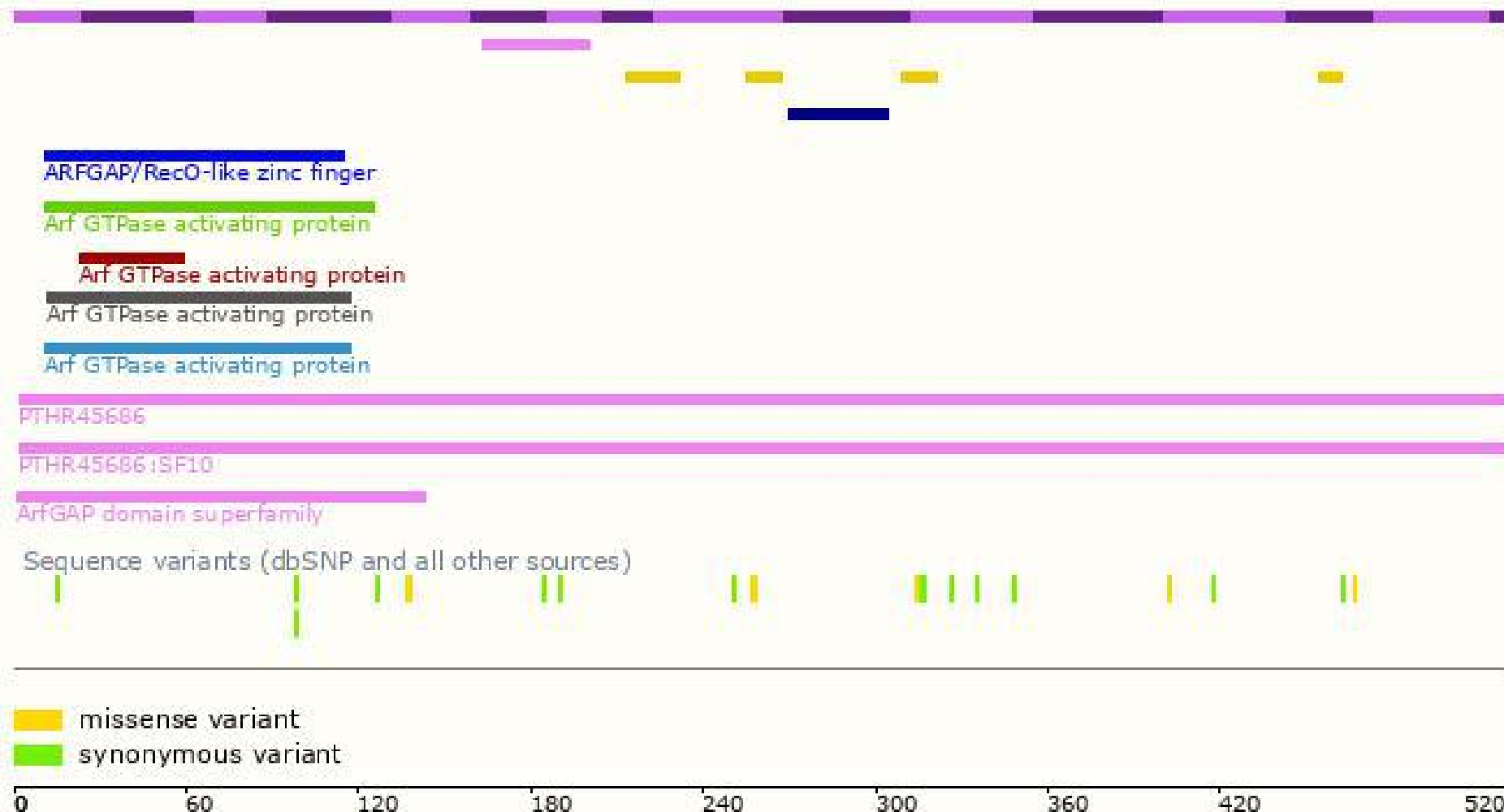
[PANTHER](#)

[Gene3D](#)

[All sequence SNPs/i...](#)

Variant Legend

Scale bar



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

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