

A1cf Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

A1cf

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Alcf* gene has 5 transcripts. According to the structure of *Alcf* gene, exon3-exon4 of *Alcf*-201 (ENSMUST00000075838.7) transcript is recommended as the knockout region. The region contains 266bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Alcf* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Embryos homozygous for a targeted deletion of this gene are detectable only until the blastocyst stage (E3.5) and isolated mutant blastocysts fail to proliferate in vitro.
- The distance between exon4 of *A1cf* and *Gm19241* is about 2.4kb, and the knockout of *A1cf* may affect the 5-terminal regulation of *Gm19241*.
- The *A1cf* gene is located on the Chr19. 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)

A1cf APOBEC1 complementation factor [*Mus musculus* (house mouse)]

Gene ID: 69865, updated on 22-Oct-2019

Summary

Official Symbol A1cf provided by [MGI](#)

Official Full Name APOBEC1 complementation factor provided by [MGI](#)

Primary source [MGI:MGI:1917115](#)

See related [Ensembl:ENSMUSG00000052595](#)

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 ASP; Acf; MCM; mer; ACF64; ACF65; MerCreMer; 1810073H04Rik; 9130016M20Rik; alpha-MHC-MerCreMer; alphaMHC-Cre-Mer-Cre; Tg(Myh6-cre/Esr1*)1Jmk

Expression Biased expression in liver adult (RPKM 13.0), liver E18 (RPKM 9.1) and 8 other tissues [See more](#)

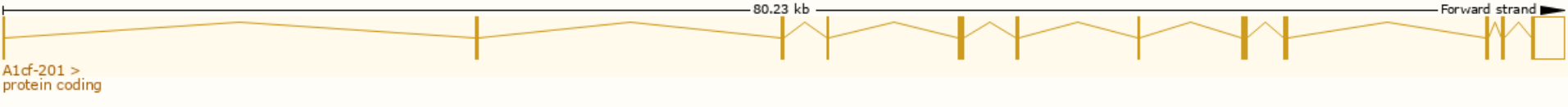
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

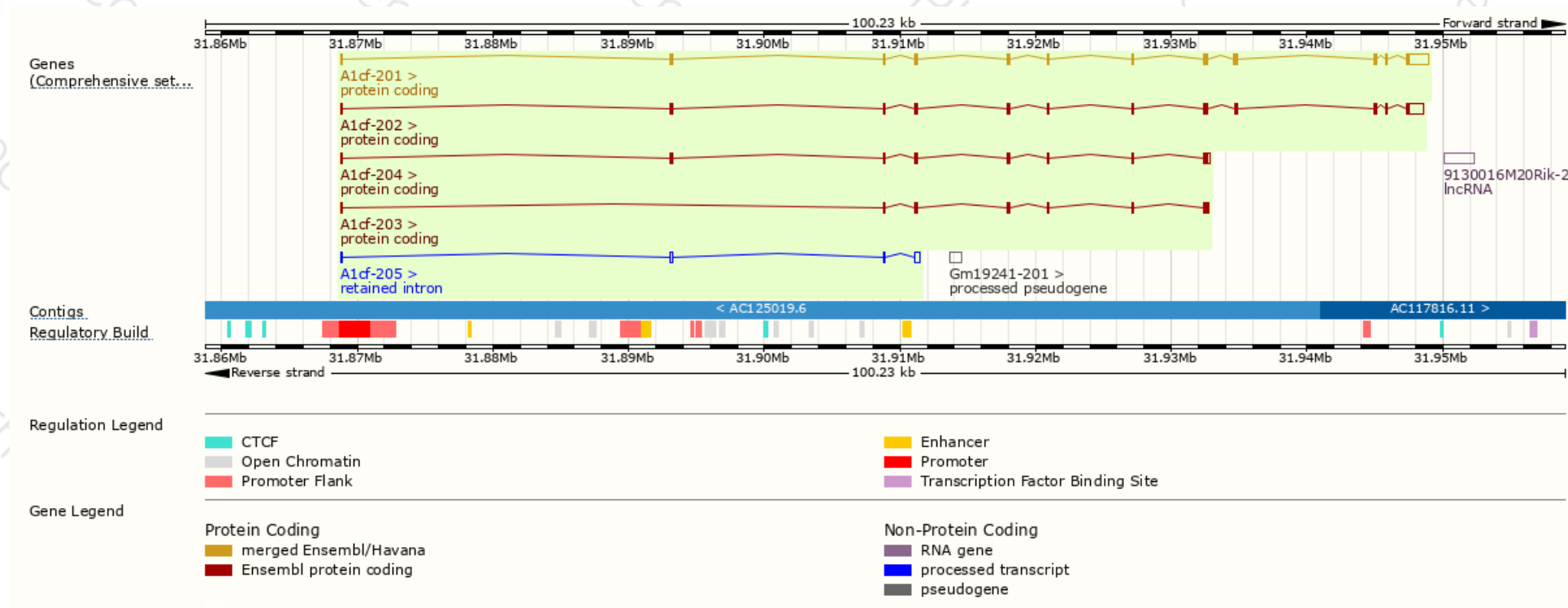
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
A1cf-201	ENSMUST00000075838.7	3414	595aa	Protein coding	CCDS37959	Q5YD48	TSL:1 GENCODE basic APPRIS P2
A1cf-202	ENSMUST00000224304.1	2968	587aa	Protein coding	-	Q5YD48	GENCODE basic APPRIS ALT1
A1cf-204	ENSMUST00000224564.1	1432	384aa	Protein coding	-	Q5YD48	GENCODE basic
A1cf-203	ENSMUST00000224400.1	1204	300aa	Protein coding	-	A0A286YDF7	GENCODE basic
A1cf-205	ENSMUST00000225165.1	696	No protein	Retained intron	-	-	-

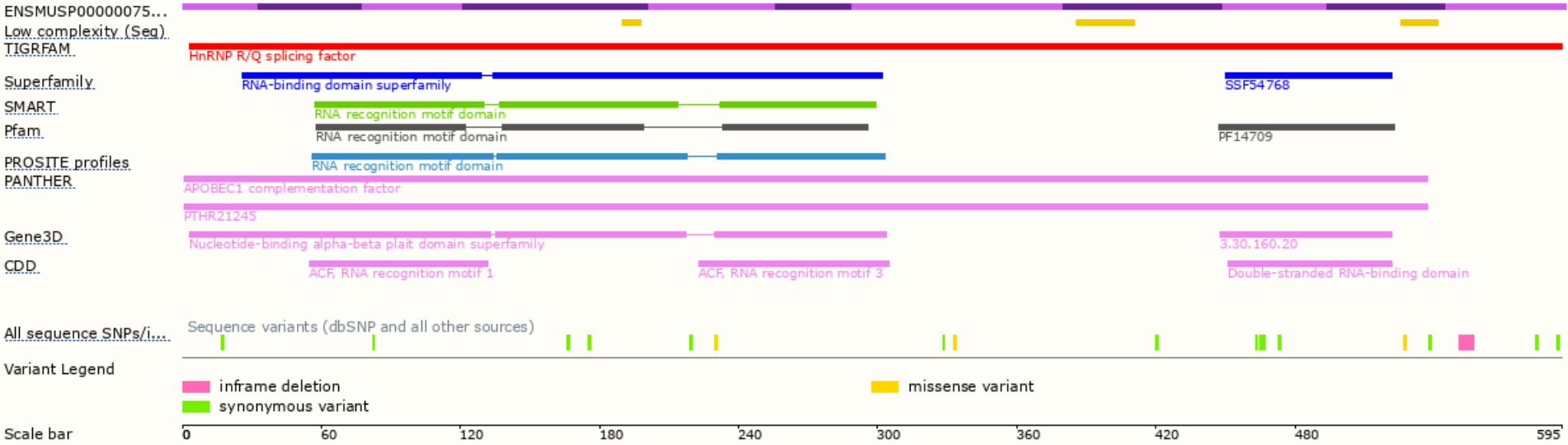
The strategy is based on the design of *A1cf-201* transcript,The transcription is shown below



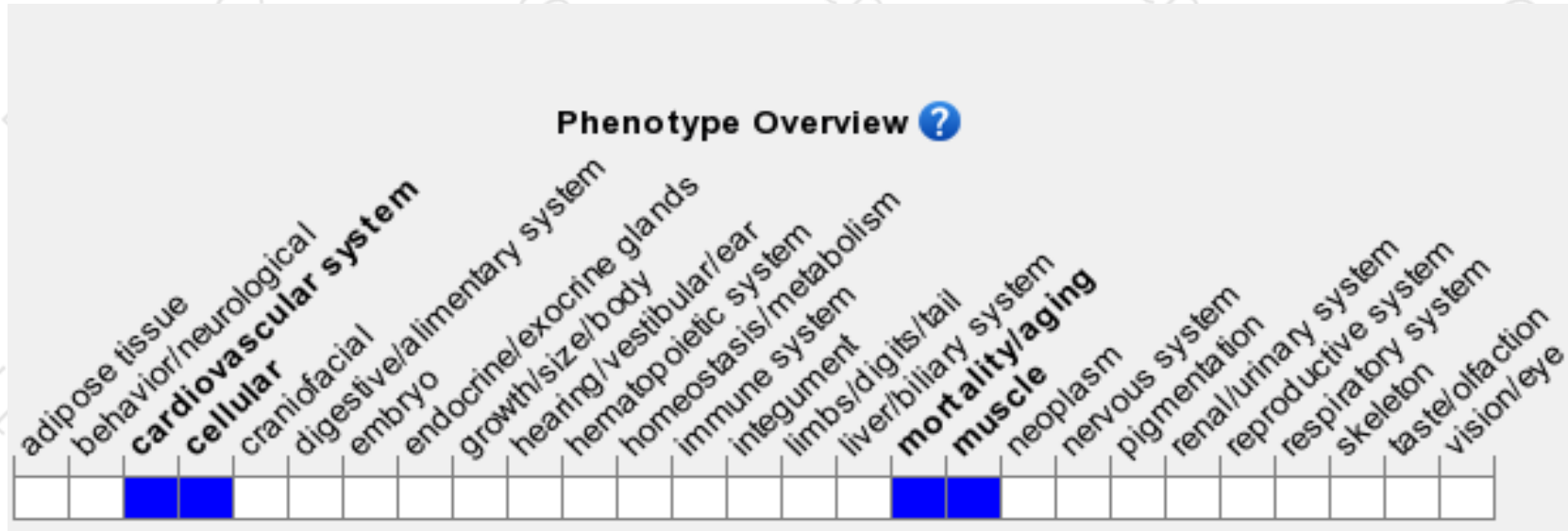
Genomic location distribution



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, Embryos homozygous for a targeted deletion of this gene are detectable only until the blastocyst stage (E3.5) and isolated mutant blastocysts fail to proliferate in vitro.

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

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