

Arap1 Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

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Project Overview

Project Name

Arap1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arap1* gene. The schematic diagram is as follows:



- The *Arap1* gene has 20 transcripts. According to the structure of *Arap1* gene, exon4-exon16 of *Arap1*-204 (ENSMUST00000107010.8) transcript is recommended as the knockout region. The region contains 1799bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arap1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Arap1* gene is located on the Chr7. 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.
- The 3-terminal of *Arap1-209*, *Arap1-211* and *Arap1-212* transcripts are incomplete, so the effect on them are unknown.
- 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)

Arap1 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [*Mus musculus* (house mouse)]

Gene ID: 69710, updated on 12-Aug-2019

Summary



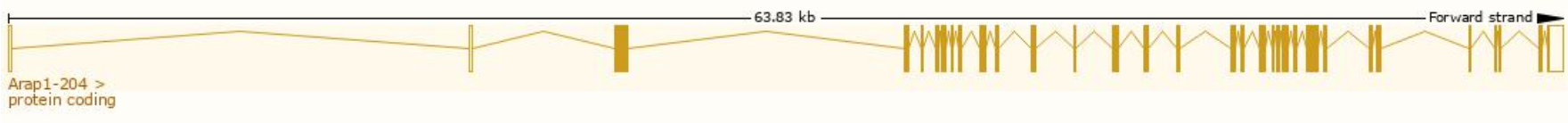
Official Symbol	Arap1 provided by MGI
Official Full Name	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 provided by MGI
Primary source	MGI:MGI:1916960
See related	Ensembl:ENSMUSG00000032812
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Centd2; mKIAA0782; 2410002L19Rik
Expression	Ubiquitous expression in spleen adult (RPKM 27.7), subcutaneous fat pad adult (RPKM 20.3) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

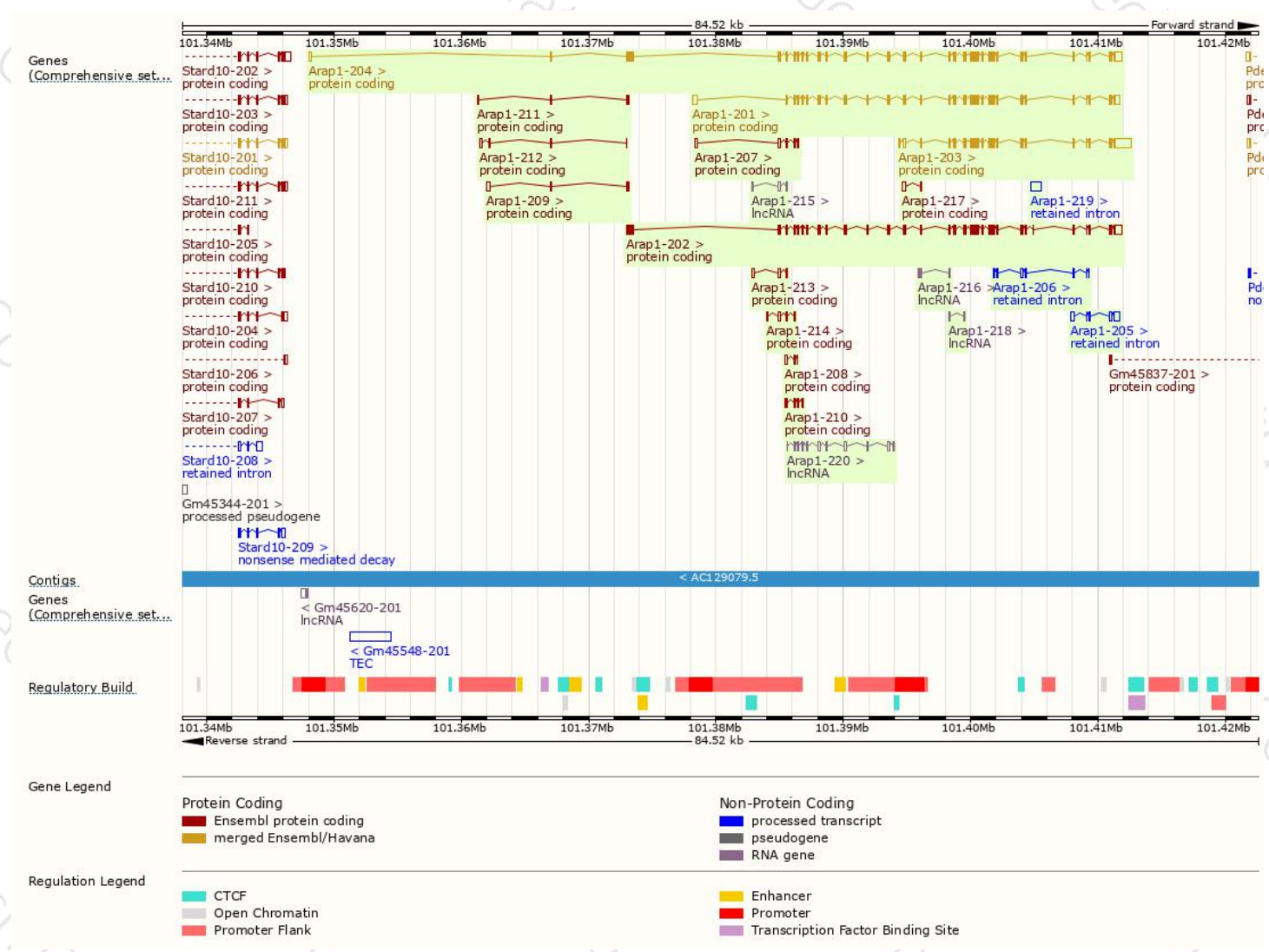
The gene has 20 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arap1-204	ENSMUST00000107010.8	5147	1441aa	Protein coding	CCDS40041	Q4LDD4	TSL:1 GENCODE basic APPRIS ALT2
Arap1-201	ENSMUST00000084895.11	4404	1193aa	Protein coding	CCDS21510	Q4LDD4	TSL:1 GENCODE basic APPRIS P3
Arap1-203	ENSMUST00000098243.3	3693	727aa	Protein coding	CCDS40042	E9PUB0	TSL:1 GENCODE basic
Arap1-202	ENSMUST00000084896.9	4926	1452aa	Protein coding	-	Q4LDD4	TSL:1 GENCODE basic APPRIS ALT2
Arap1-207	ENSMUST00000127873.7	628	76aa	Protein coding	-	D3Z2X3	CDS 3' incomplete TSL:3
Arap1-209	ENSMUST00000133423.1	521	57aa	Protein coding	-	D3Z2S2	CDS 3' incomplete TSL:2
Arap1-210	ENSMUST00000134143.1	412	111aa	Protein coding	-	D3YWW7	CDS 3' incomplete TSL:3
Arap1-213	ENSMUST00000141083.8	401	3aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Arap1-208	ENSMUST00000130016.7	400	63aa	Protein coding	-	D3YY40	CDS 3' incomplete TSL:2
Arap1-214	ENSMUST00000148902.7	381	19aa	Protein coding	-	D3YYF5	CDS 3' incomplete TSL:2
Arap1-212	ENSMUST00000138628.7	363	12aa	Protein coding	-	D3YVS8	CDS 3' incomplete TSL:3
Arap1-211	ENSMUST00000137384.7	356	54aa	Protein coding	-	D3YZJ7	CDS 3' incomplete TSL:3
Arap1-217	ENSMUST00000155754.1	325	34aa	Protein coding	-	A0A1B0GSK4	CDS 3' incomplete TSL:3
Arap1-205	ENSMUST00000124637.1	882	No protein	Retained intron	-	-	TSL:1
Arap1-219	ENSMUST00000210162.1	801	No protein	Retained intron	-	-	TSL:NA
Arap1-206	ENSMUST00000125284.7	621	No protein	Retained intron	-	-	TSL:3
Arap1-220	ENSMUST00000213314.1	1356	No protein	lncRNA	-	-	TSL:5
Arap1-215	ENSMUST00000152082.7	351	No protein	lncRNA	-	-	TSL:3
Arap1-216	ENSMUST00000153340.1	328	No protein	lncRNA	-	-	TSL:3
Arap1-218	ENSMUST00000156017.1	157	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Arap1-204* transcript,The transcription is shown below



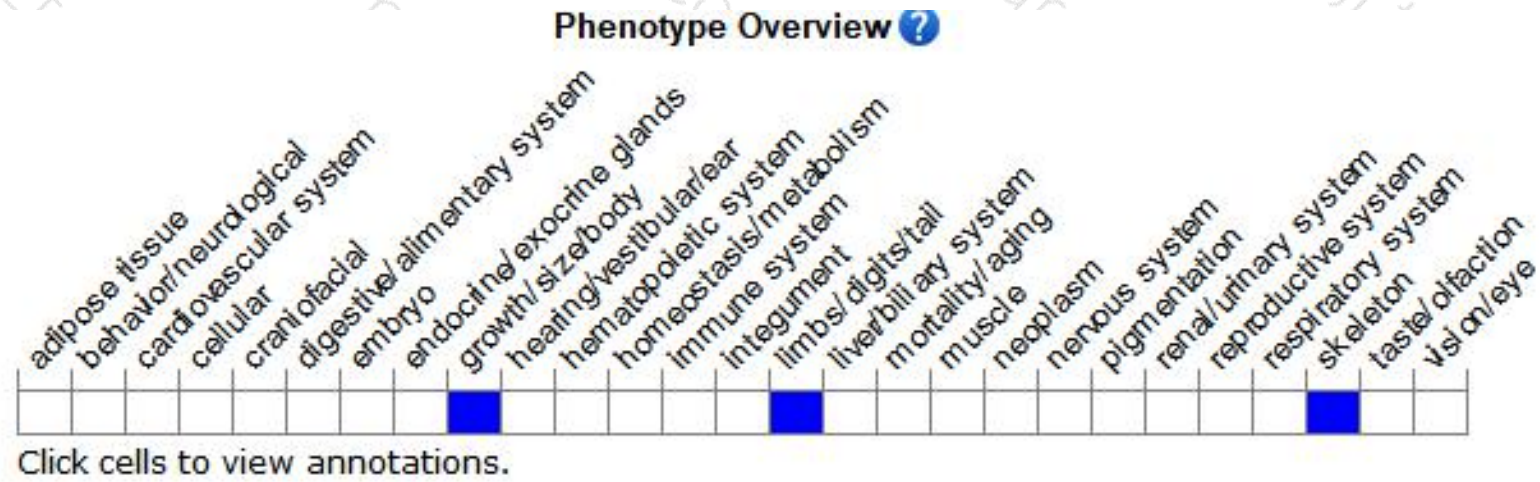
Genomic location distribution



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/>).

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

Tel: 400-9660890

