

Arhgef1 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Arhgef1

Project type

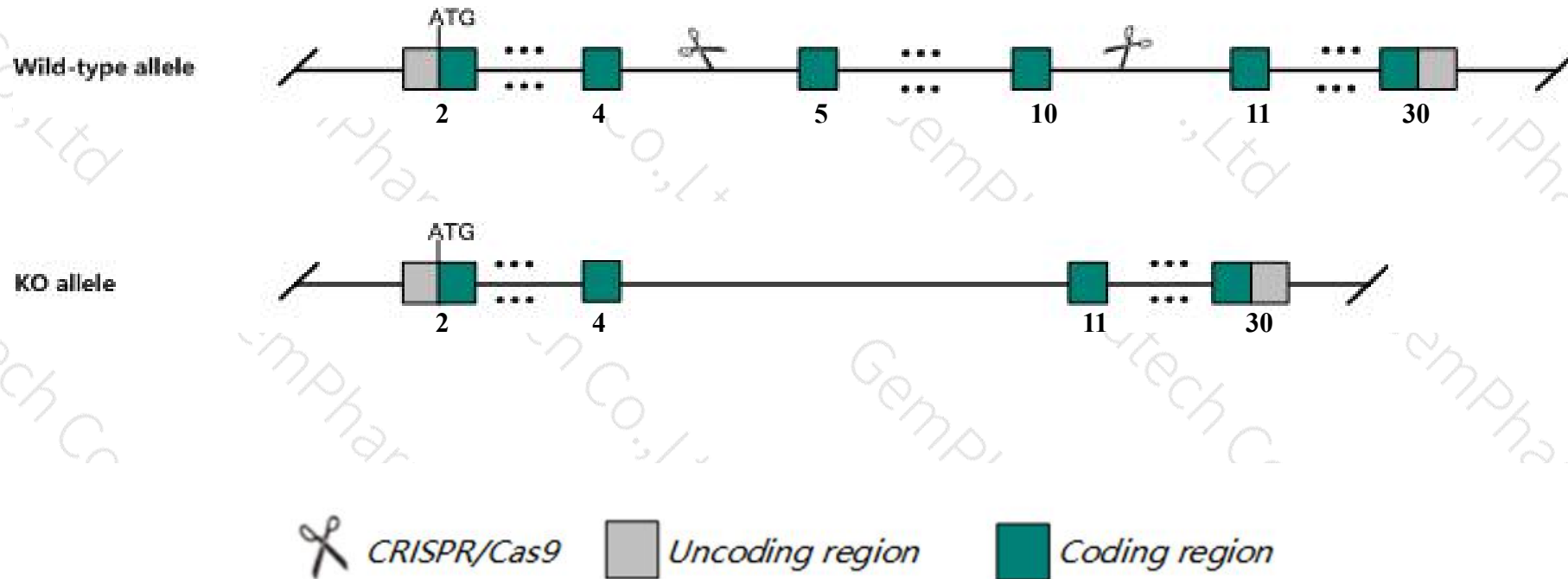
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgef1* gene. The schematic diagram is as follows:



- The *Arhgef1* gene has 19 transcripts. According to the structure of *Arhgef1* gene, exon5-exon10 of *Arhgef1*-204 (ENSMUST00000117796.7) transcript is recommended as the knockout region. The region contains 616bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgef1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous mutation of this gene results in impaired humeral immunity, reduced numbers of marginal zone B (MZB) cells, decreased basal T cell proliferation, and reduced basal motility of lymphocytes but enhanced migration of MZB cells after serum activation, part of null homozygous die before weaning.
- Transcript *Arhgef1-210* and *Arhgef1-217* may not be affected.
- The *Arhgef1* 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.
- 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)

Arhgef1 Rho guanine nucleotide exchange factor (GEF) 1 [*Mus musculus* (house mouse)]

Gene ID: 16801, updated on 5-Jan-2020

Summary

Official Symbol Arhgef1 provided by [MGI](#)

Official Full Name Rho guanine nucleotide exchange factor (GEF) 1 provided by [MGI](#)

Primary source [MGI:MGI:1353510](#)

See related [Ensembl:ENSMUSG00000040940](#)

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 Lsc; Lbcl2

Expression Broad expression in thymus adult (RPKM 202.0), spleen adult (RPKM 157.1) and 26 other tissues [See more](#)

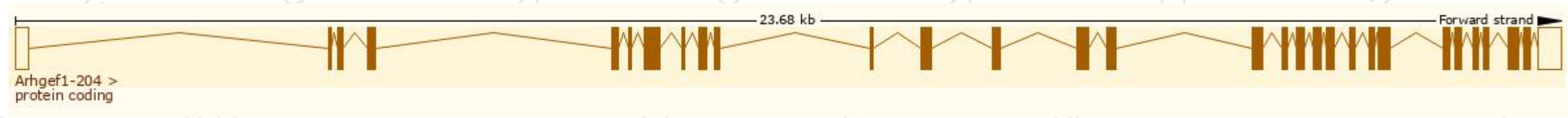
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

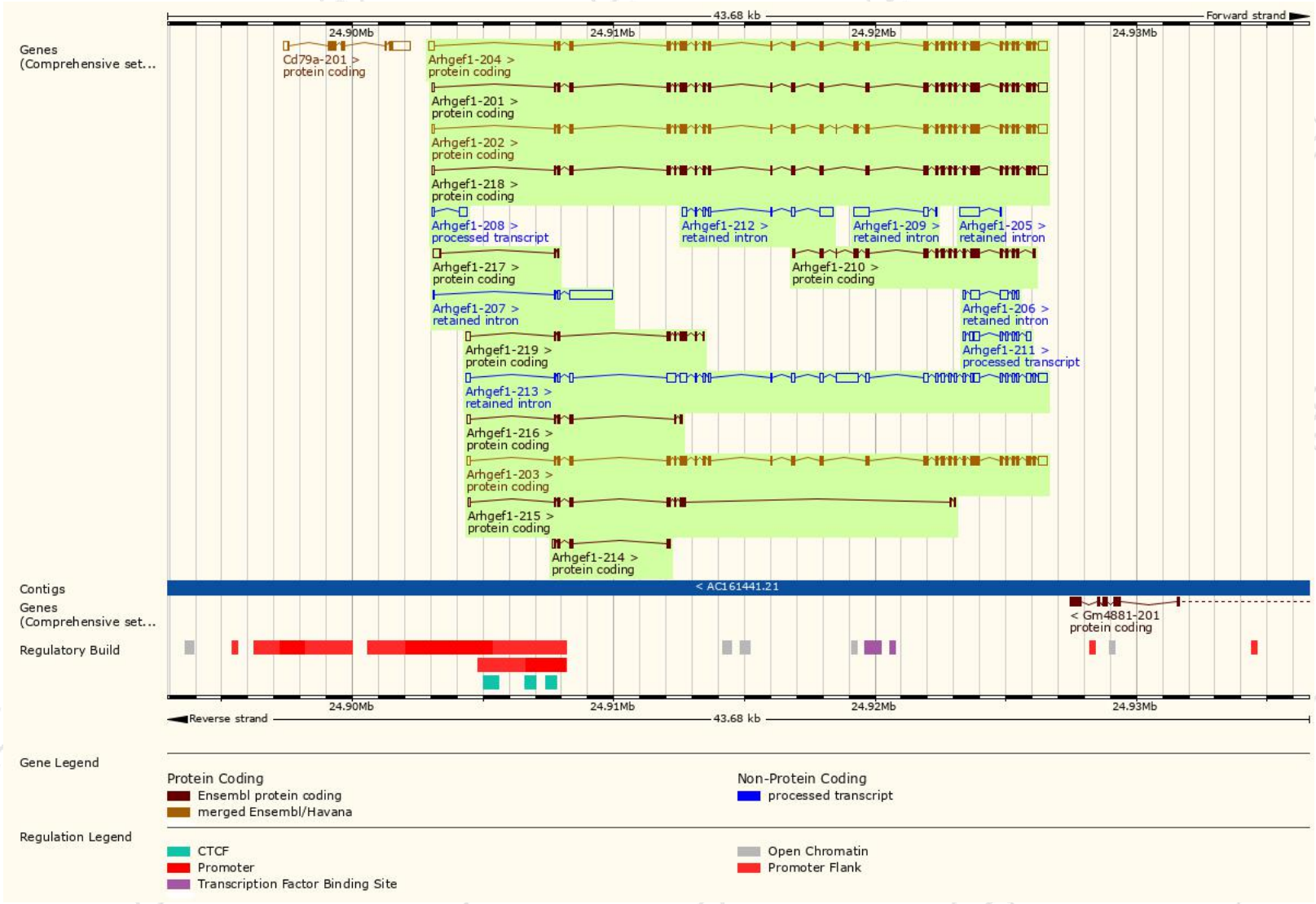
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgef1-204	ENSMUST00000117796.7	3508	976aa	Protein coding	CCDS52140	E9PUF7	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-202	ENSMUST00000098683.10	3375	979aa	Protein coding	CCDS52142	Q61210	TSL:1 GENCODE basic APPRIS P4
Arhgef1-203	ENSMUST00000117419.7	3214	920aa	Protein coding	CCDS52141	Q61210	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-201	ENSMUST00000047873.15	3212	920aa	Protein coding	CCDS52141	Q61210	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-218	ENSMUST00000206508.1	3195	919aa	Protein coding	CCDS85239	Q61210	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-210	ENSMUST00000132751.1	1851	616aa	Protein coding	-	F6ZN61	CDS 5' incomplete TSL:5
Arhgef1-215	ENSMUST00000205295.1	777	233aa	Protein coding	-	A0A0U1RPN7	CDS 3' incomplete TSL:5
Arhgef1-219	ENSMUST00000206906.1	737	192aa	Protein coding	-	A0A0U1RPP2	CDS 3' incomplete TSL:5
Arhgef1-216	ENSMUST00000206011.1	419	102aa	Protein coding	-	A0A0U1RPH2	CDS 3' incomplete TSL:2
Arhgef1-214	ENSMUST00000151121.1	390	101aa	Protein coding	-	D3YVJ9	CDS 3' incomplete TSL:3
Arhgef1-217	ENSMUST00000206028.1	374	30aa	Protein coding	-	A0A0U1RNQ2	CDS 3' incomplete TSL:3
Arhgef1-211	ENSMUST00000132786.1	832	No protein	Processed transcript	-	-	TSL:5
Arhgef1-208	ENSMUST00000129383.1	351	No protein	Processed transcript	-	-	TSL:2
Arhgef1-213	ENSMUST00000145783.7	4243	No protein	Retained intron	-	-	TSL:5
Arhgef1-207	ENSMUST00000127761.7	1827	No protein	Retained intron	-	-	TSL:2
Arhgef1-212	ENSMUST00000144714.1	1087	No protein	Retained intron	-	-	TSL:3
Arhgef1-206	ENSMUST00000126918.7	821	No protein	Retained intron	-	-	TSL:5
Arhgef1-209	ENSMUST00000129928.1	777	No protein	Retained intron	-	-	TSL:2
Arhgef1-205	ENSMUST00000126484.1	775	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Arhgef1-204* transcript, the transcription is shown below:



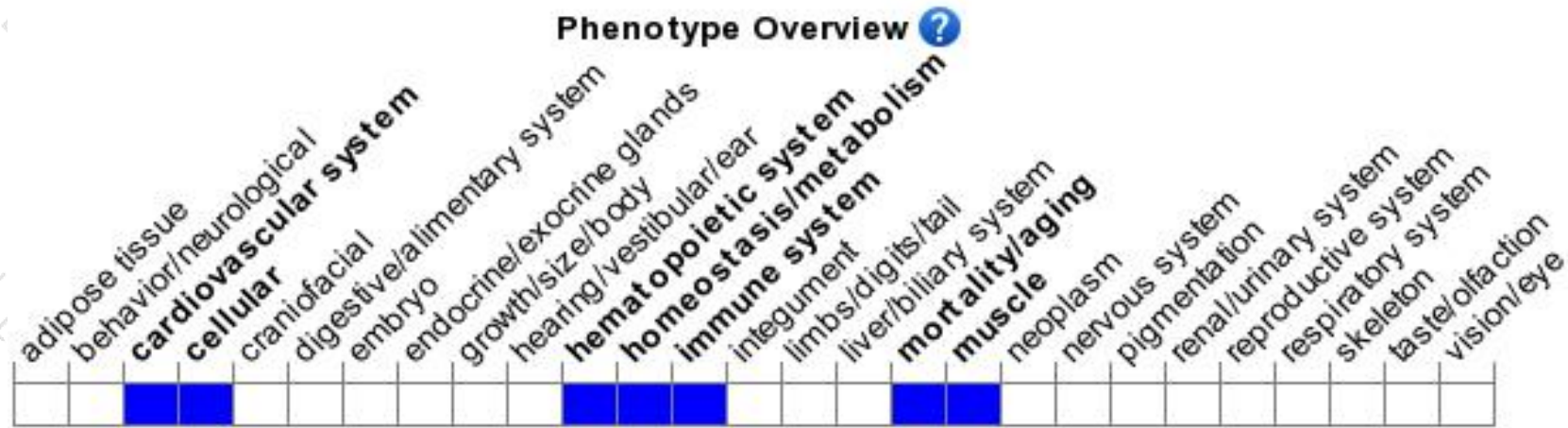
Genomic location distribution



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/>).

According to the existing MGI data, homozygous mutation of this gene results in impaired humeral immunity, reduced numbers of marginal zone B (MZB) cells, decreased basal T cell proliferation, and reduced basal motility of lymphocytes but enhanced migration of MZB cells after serum activation, part of null homozygous die before weaning.

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

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