

Arhgef40 Cas9-KO Strategy

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Project Overview

Project Name

Arhgef40

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgef40* gene. The schematic diagram is as follows:



- The *Arhgef40* gene has 26 transcripts. According to the structure of *Arhgef40* gene, exon3-exon4 of *Arhgef40*-201(ENSMUST00000093813.11) transcript is recommended as the knockout region. The region contains 1405bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgef40* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Arhgef40* gene is located on the Chr14. 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.
- Transcript 206,214,218 CDS 5' incomplete the influences is unknown.
- Transcript 205 CDS 3' incomplete the influences is 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)

Arhgef40 Rho guanine nucleotide exchange factor (GEF) 40 [Mus musculus (house mouse)]

Gene ID: 268739, updated on 13-Mar-2020

Summary



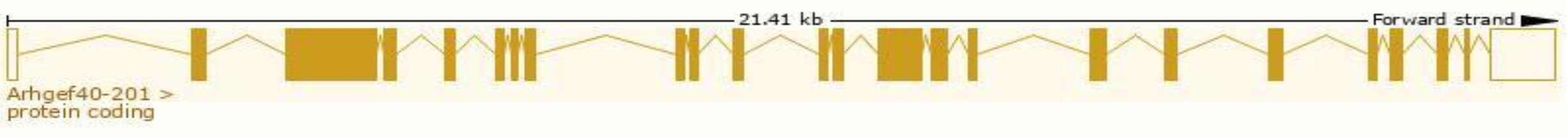
Official Symbol	Arhgef40 provided by MGI
Official Full Name	Rho guanine nucleotide exchange factor (GEF) 40 provided by MGI
Primary source	MGI:MGI:2685515
See related	Ensembl:ENSMUSG00000004562
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E130112L23Rik, Gm669, Solo
Expression	Ubiquitous expression in limb E14.5 (RPKM 18.9), genital fat pad adult (RPKM 11.5) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

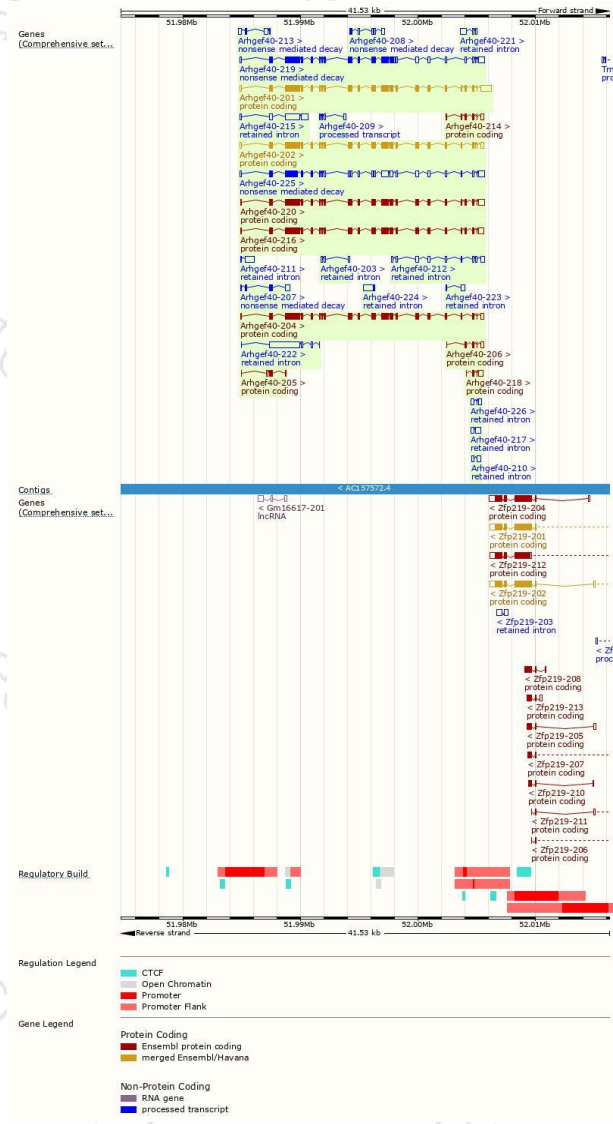
The gene has 26 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgef40-201	ENSMUST00000093813.1	5621	1517aa	Protein coding	CCDS49488	Q3UPH7	TSL:1 GENCODE basic APPRIS P4
Arhgef40-220	ENSMUST00000182909.7	5108	1517aa	Protein coding	CCDS49488	Q3UPH7	TSL:5 GENCODE basic APPRIS P4
Arhgef40-202	ENSMUST00000100639.10	4843	1476aa	Protein coding	CCDS49489	Q3UPH7	TSL:1 GENCODE basic APPRIS ALT2
Arhgef40-204	ENSMUST00000182061.7	4756	1469aa	Protein coding	CCDS59616	Q3UPH7	TSL:1 GENCODE basic APPRIS ALT2
Arhgef40-216	ENSMUST00000182760.7	5130	1526aa	Protein coding	-	S4R189	TSL:5 GENCODE basic APPRIS ALT2
Arhgef40-214	ENSMUST00000182667.7	827	179aa	Protein coding	-	S4R1Y4	CDS 5' incomplete TSL:3
Arhgef40-206	ENSMUST00000182217.7	638	115aa	Protein coding	-	S4R2A6	CDS 5' incomplete TSL:5
Arhgef40-218	ENSMUST00000182828.1	608	73aa	Protein coding	-	S4R1R5	CDS 5' incomplete TSL:3
Arhgef40-205	ENSMUST00000182193.1	393	89aa	Protein coding	-	S4R2B3	CDS 3' incomplete TSL:5
Arhgef40-219	ENSMUST00000182905.7	5320	1191aa	Nonsense mediated decay	-	S4R2U9	TSL:1
Arhgef40-225	ENSMUST00000183208.7	4826	500aa	Nonsense mediated decay	-	S4R156	TSL:5
Arhgef40-208	ENSMUST00000182412.1	822	45aa	Nonsense mediated decay	-	S4R1X0	CDS 5' incomplete TSL:3
Arhgef40-207	ENSMUST00000182338.1	812	85aa	Nonsense mediated decay	-	S4R237	TSL:3
Arhgef40-213	ENSMUST00000182649.7	751	44aa	Nonsense mediated decay	-	S4R2G8	TSL:5
Arhgef40-209	ENSMUST00000182480.7	461	No protein	Processed transcript	-	-	TSL:3
Arhgef40-222	ENSMUST00000182961.1	2903	No protein	Retained intron	-	-	TSL:1
Arhgef40-215	ENSMUST00000182740.1	2191	No protein	Retained intron	-	-	TSL:1
Arhgef40-212	ENSMUST00000182644.7	1429	No protein	Retained intron	-	-	TSL:1
Arhgef40-224	ENSMUST00000183167.1	924	No protein	Retained intron	-	-	TSL:3
Arhgef40-211	ENSMUST00000182609.1	848	No protein	Retained intron	-	-	TSL:3
Arhgef40-221	ENSMUST00000182931.1	820	No protein	Retained intron	-	-	TSL:5
Arhgef40-217	ENSMUST00000182777.1	676	No protein	Retained intron	-	-	TSL:3
Arhgef40-226	ENSMUST00000183213.1	515	No protein	Retained intron	-	-	TSL:2
Arhgef40-210	ENSMUST00000182504.1	478	No protein	Retained intron	-	-	TSL:3
Arhgef40-223	ENSMUST00000183022.1	387	No protein	Retained intron	-	-	TSL:3
Arhgef40-203	ENSMUST00000182019.1	336	No protein	Retained intron	-	-	TSL:3

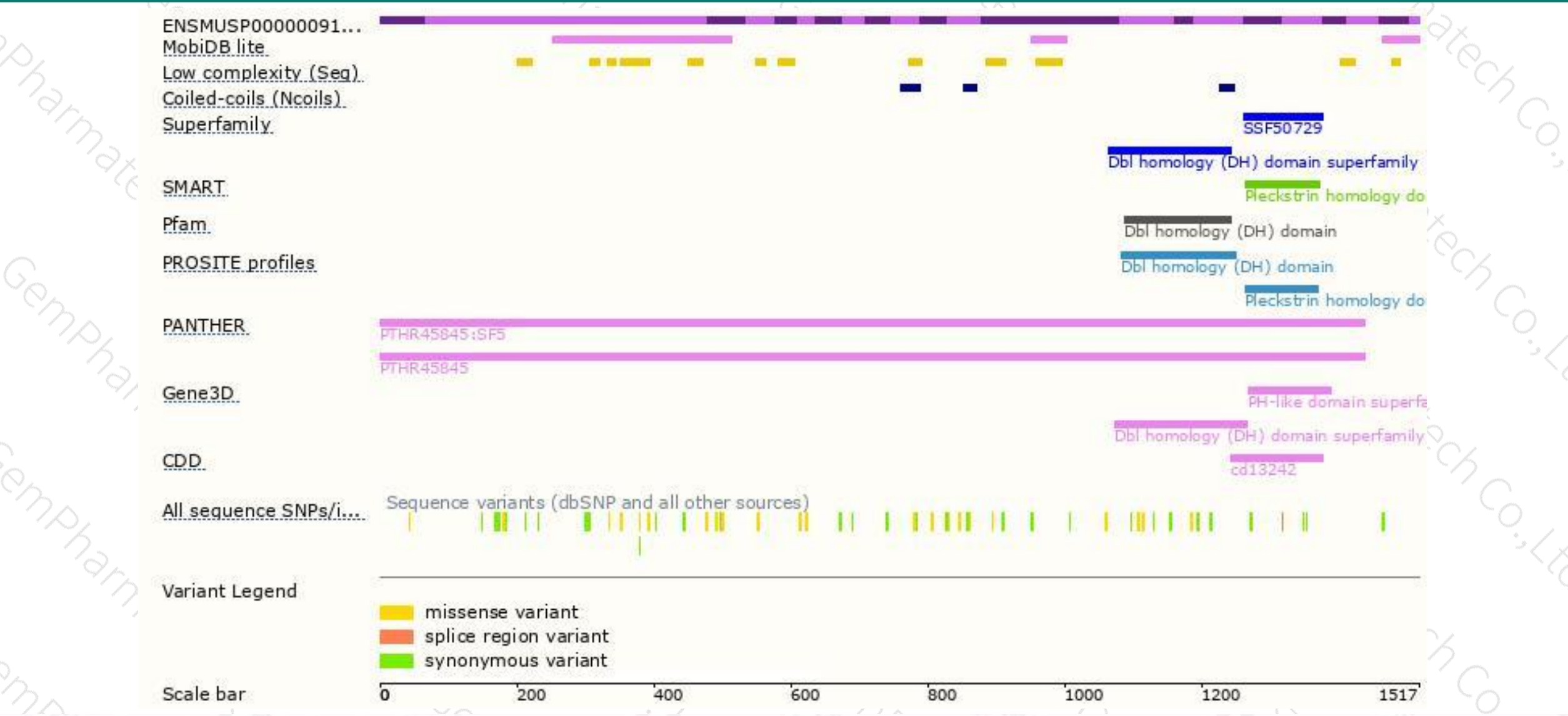
The strategy is based on the design of *Arhgef40-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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