

Arhgef25 Cas9-CKO Strategy

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Project Overview

Project Name

Arhgef25

Project type

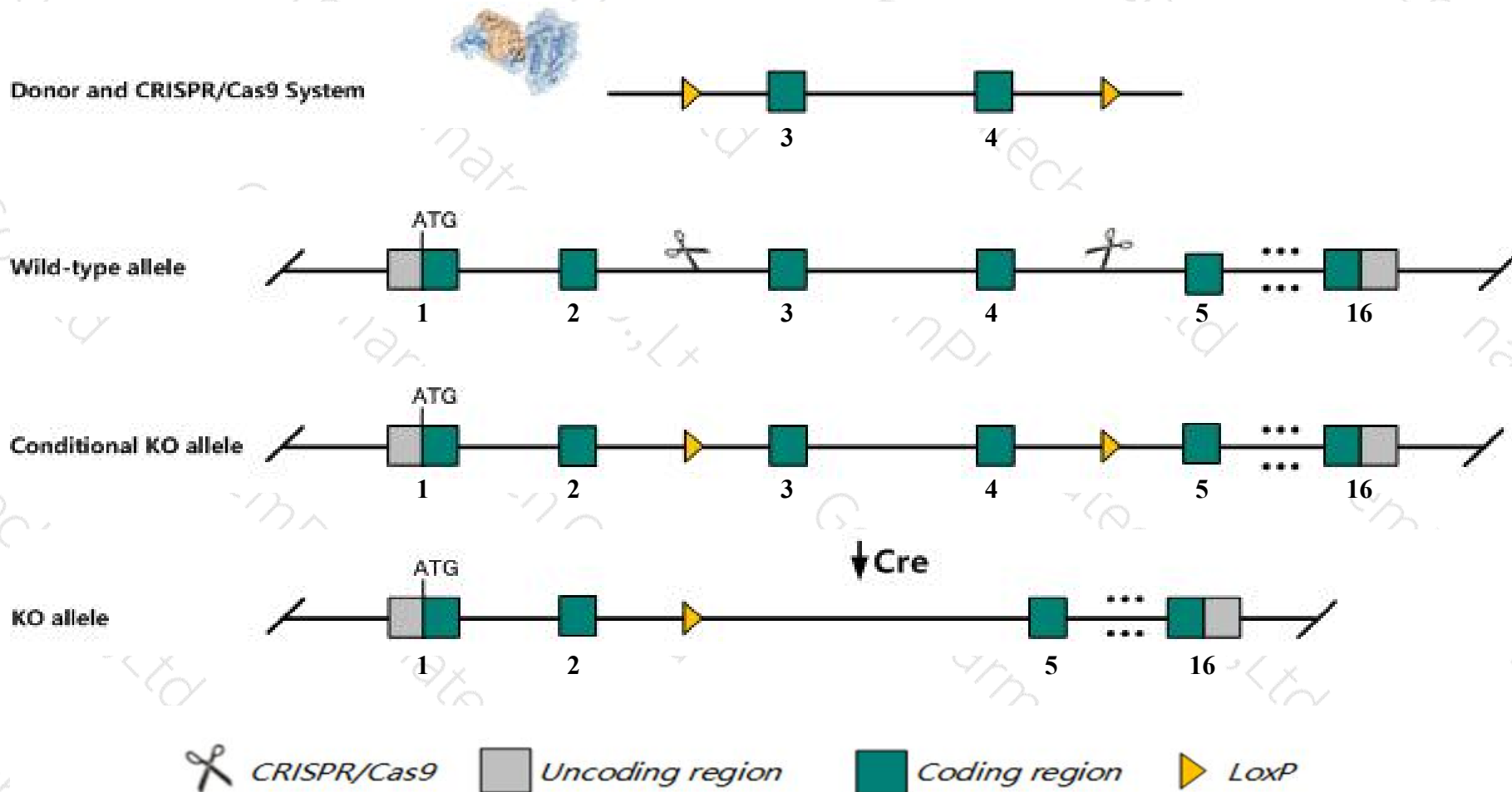
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgef25* gene. The schematic diagram is as follows:



- The *Arhgef25* gene has 12 transcripts. According to the structure of *Arhgef25* gene, exon3-exon4 of *Arhgef25-201* (ENSMUST00000019611.14) transcript is recommended as the knockout region. The region contains 311bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgef25* 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.

- According to the existing MGI data, Mice homozygous for a conditional allele activated in the second heart field exhibit normal cardiac development and prenatal survival.
- The effect on transcript *Arhgef25-207* is unknown.
- Transcript *Arhgef25-208&209&211* may not be affected.
- The floxed region is near to the N-terminal of *F420014N23Rik/Slc26a10* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Arhgef25* gene is located on the Chr10. 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)

Arhgef25 Rho guanine nucleotide exchange factor (GEF) 25 [*Mus musculus* (house mouse)]

Gene ID: 52666, updated on 24-Oct-2019

Summary

- Official Symbol** Arhgef25 provided by [MGI](#)
- Official Full Name** Rho guanine nucleotide exchange factor (GEF) 25 provided by [MGI](#)
- Primary source** [MGI:MGI:1277173](#)
- See related** [Ensembl:ENSMUSG00000019467](#)
- 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** GEFT; D10Ert610e; 2410008H17Rik
- Expression** Broad expression in limb E14.5 (RPKM 49.4), bladder adult (RPKM 39.6) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10 D3; 10 74.5 cM See Arhgef25 in [Genome Data Viewer](#)

Exon count: 19

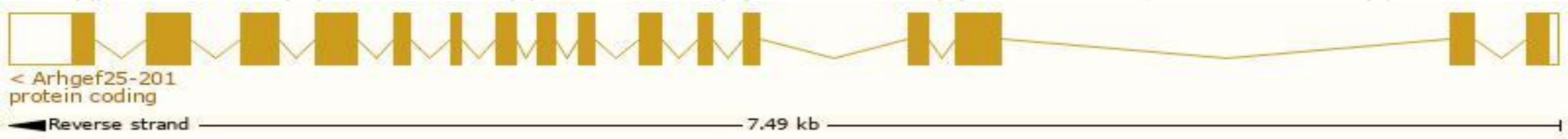
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (127182521..127190083, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (126619577..126627110, complement)

Transcript information (Ensembl)

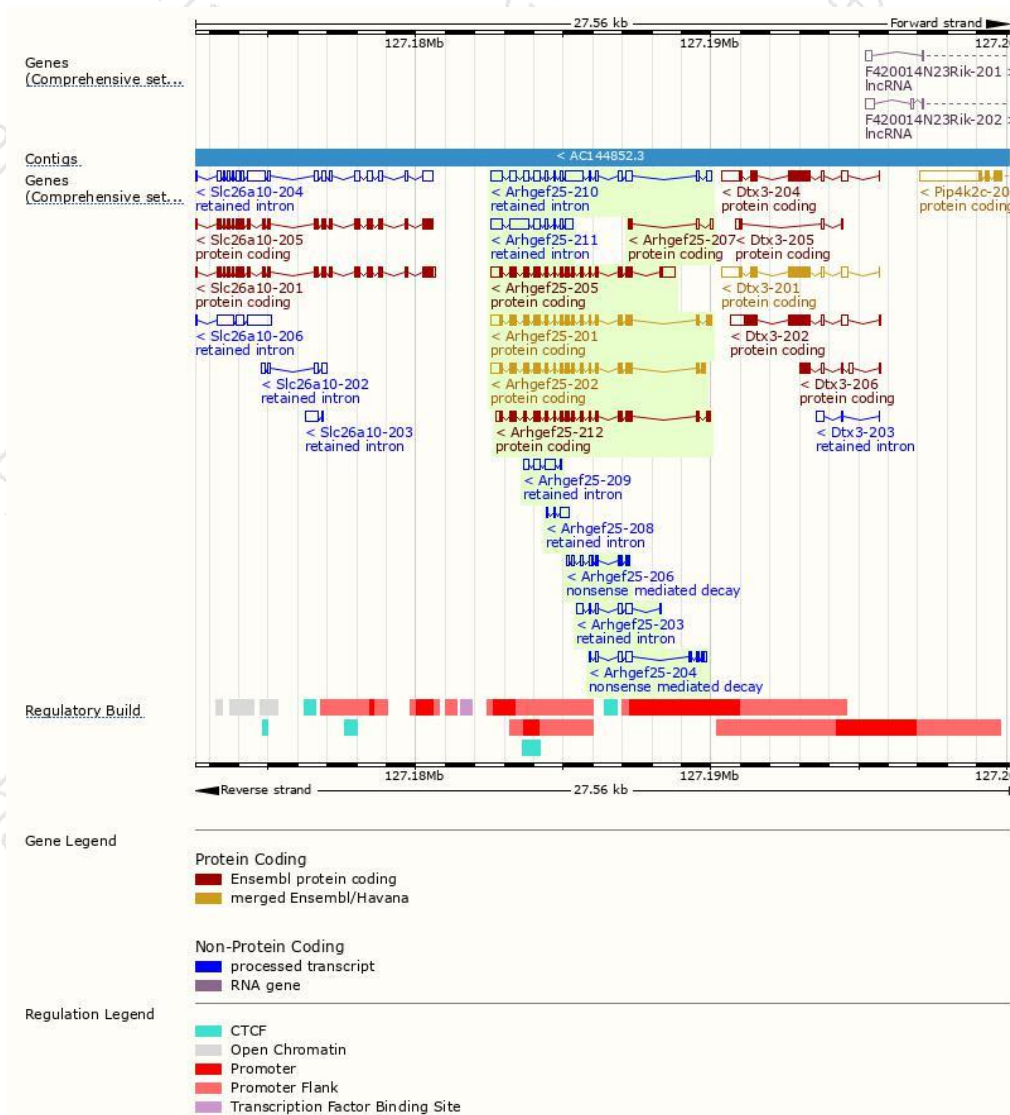
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgef25-201	ENSMUST00000019611.14	2218	618aa	Protein coding	CCDS24231	G5E825	TSL:1 GENCODE basic APPRIS P2
Arhgef25-202	ENSMUST00000167353.2	2189	609aa	Protein coding	CCDS48715	A0A0R4J211	TSL:1 GENCODE basic
Arhgef25-205	ENSMUST00000218654.1	2475	579aa	Protein coding	-	A0A1W2P6R9	TSL:5 GENCODE basic APPRIS ALT 1
Arhgef25-212	ENSMUST00000222006.1	1896	584aa	Protein coding	-	A0A1Y7VNM7	TSL:5 GENCODE basic
Arhgef25-207	ENSMUST00000219245.1	321	23aa	Protein coding	-	A0A1W2P813	CDS 3' incomplete TSL:3
Arhgef25-204	ENSMUST00000218587.1	798	100aa	Nonsense mediated decay	-	A0A1W2P718	TSL:5
Arhgef25-206	ENSMUST00000218864.1	645	102aa	Nonsense mediated decay	-	A0A1W2P7S3	CDS 5' incomplete TSL:3
Arhgef25-210	ENSMUST00000219649.1	2571	No protein	Retained intron	-	-	TSL:1
Arhgef25-211	ENSMUST00000220295.1	1718	No protein	Retained intron	-	-	TSL:2
Arhgef25-209	ENSMUST00000219587.1	738	No protein	Retained intron	-	-	TSL:3
Arhgef25-203	ENSMUST00000218478.1	732	No protein	Retained intron	-	-	TSL:2
Arhgef25-208	ENSMUST00000219428.1	415	No protein	Retained intron	-	-	TSL:2

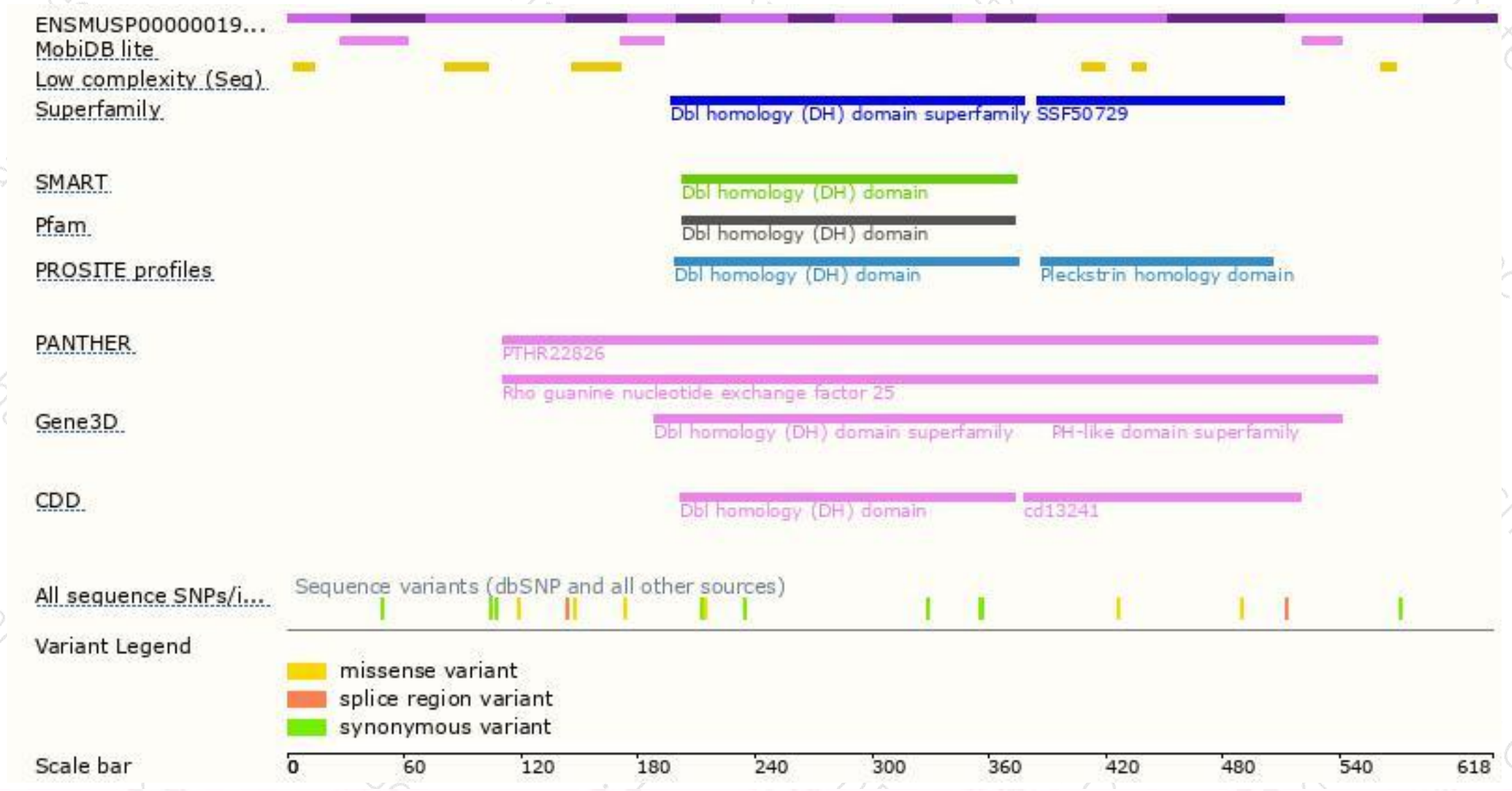
The strategy is based on the design of *Arhgef25-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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