

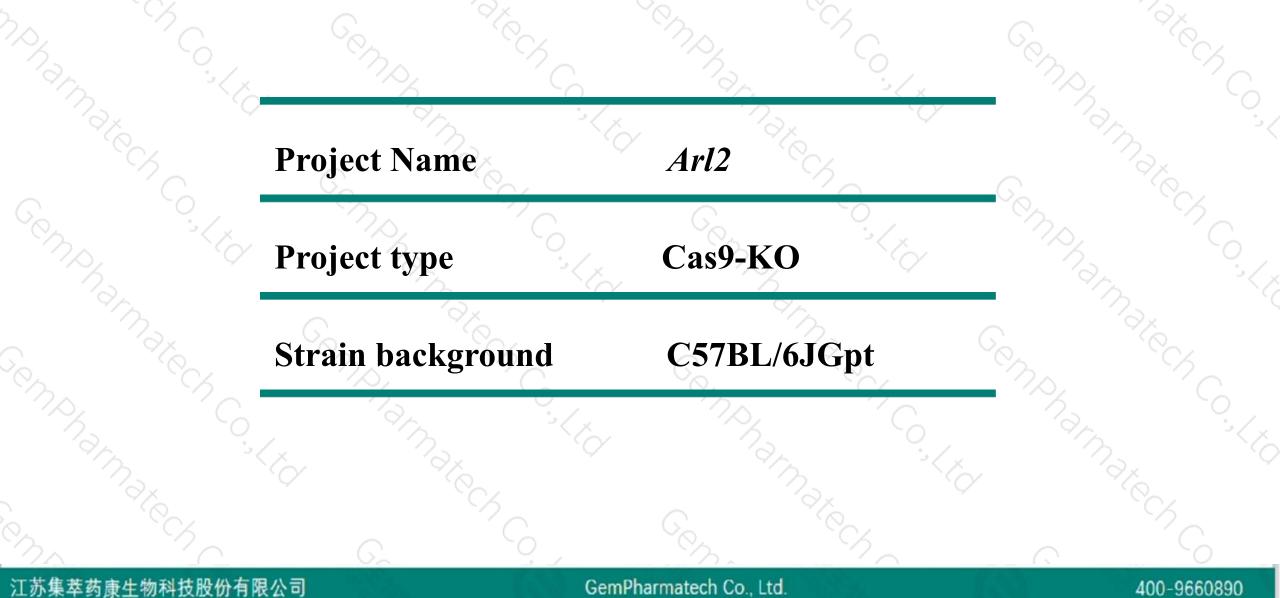
Arl2 Cas9-KO Strategy

Designer: Reviewer: Design Date: Huimin Su Ruirui Zhang

2020/2/17

Project Overview

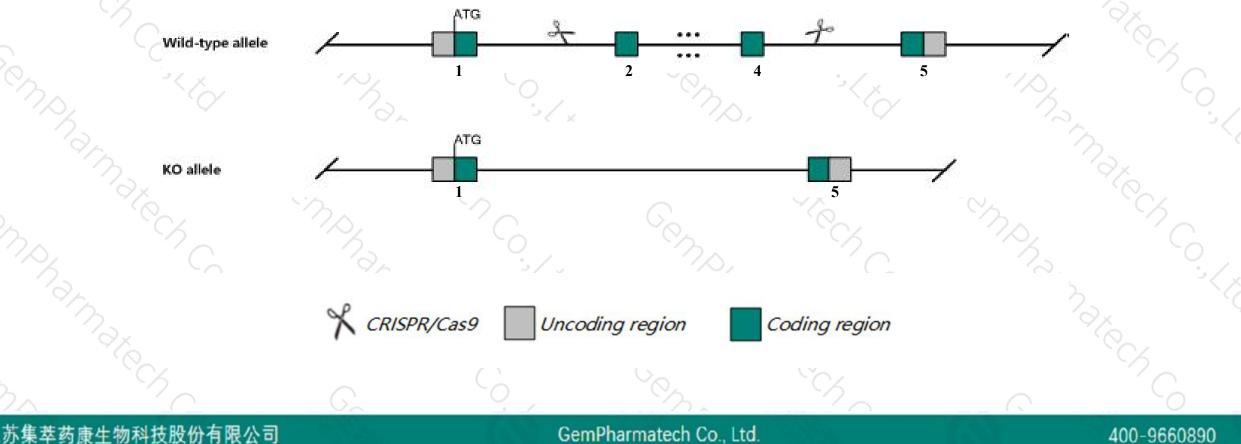




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Arl2 gene. The schematic diagram is as follows:



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- The Arl2 gene has 5 transcripts. According to the structure of Arl2 gene, exon2-exon4 of Arl2-201 (ENSMUST00000025893.6) transcript is recommended as the knockout region. The region contains 355bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Arl2 gene. The brief process is as follows: CRISPR/Cas9 system v

- The Arl2 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.

Notice

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Gene information (NCBI)

Arl2 ADP-ribosylation factor-like 2 [Mus musculus (house mouse)]

Gene ID: 56327, updated on 10-Dec-2019

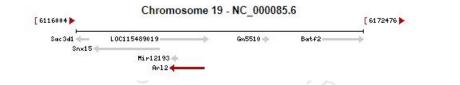
 Summary 	(\$)
Official Symbol	Arl2 provided by MGI
Official Full Name	ADP-ribosylation factor-like 2 provided by MGI
Primary source	MGI:MGI:1928393
See related	Ensembl:ENSMUSG0000024944
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
	Murinae; Mus; Mus
Also known as	AI115441; AW553335; 2610009M23Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 136.8), mammary gland adult (RPKM 70.2) and 27 other tissues See more
Orthologs	human all

- Genomic context

Location: 19; 19 A

Exon count: 5

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (61343896141137, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (61343896141137, complement)



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See Arl2 in Genome Data Viewer

Transcript information (Ensembl)



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

3 /							
Transcript ID 🖕	bp 🖕 Protein		Biotype 🖕	CCDS 🍦	UniProt 🖕	Flags	
ENSMUST0000025893.6	1286	<u>184aa</u>	Protein coding	<u>CCDS29496</u> 교	Q9D0J4@	TSL:1 GENCODE basic APPRIS P1	
ENSMUST00000235200.1	1153	No protein	Processed transcript	1	5		
ENSMUST00000236138.1	954	No protein	Processed transcript	-	-	(5)	
ENSMUST00000134821.1	2305	No protein	Retained intron	1	5	TSL:1	
ENSMUST00000123193.1	602	No protein	Retained intron	-		TSL:3	
	ENSMUST0000025893.6 ENSMUST00000235200.1 ENSMUST00000236138.1 ENSMUST00000134821.1	ENSMUST0000025893.6 1286 ENSMUST00000235200.1 1153 ENSMUST00000236138.1 954 ENSMUST00000134821.1 2305	ENSMUST0000025893.6 1286 184aa ENSMUST00000235200.1 1153 No protein ENSMUST00000236138.1 954 No protein ENSMUST00000134821.1 2305 No protein	ENSMUST0000025893.61286184aaProtein codingENSMUST00000235200.11153No proteinProcessed transcriptENSMUST00000236138.1954No proteinProcessed transcriptENSMUST0000134821.12305No proteinRetained intron	ENSMUST0000025893.61286184aaProtein codingCCDS29496 PENSMUST00000235200.11153No proteinProcessed transcript-ENSMUST00000236138.1954No proteinProcessed transcript-ENSMUST00000134821.12305No proteinRetained intron-	ENSMUST0000025893.61286184aaProtein codingCCDS29496Q9D0J4ENSMUST0000235200.11153No proteinProcessed transcriptENSMUST0000236138.1954No proteinProcessed transcriptENSMUST0000134821.12305No proteinRetained intron	

The strategy is based on the design of Arl2-201 transcript, The transcription is shown below

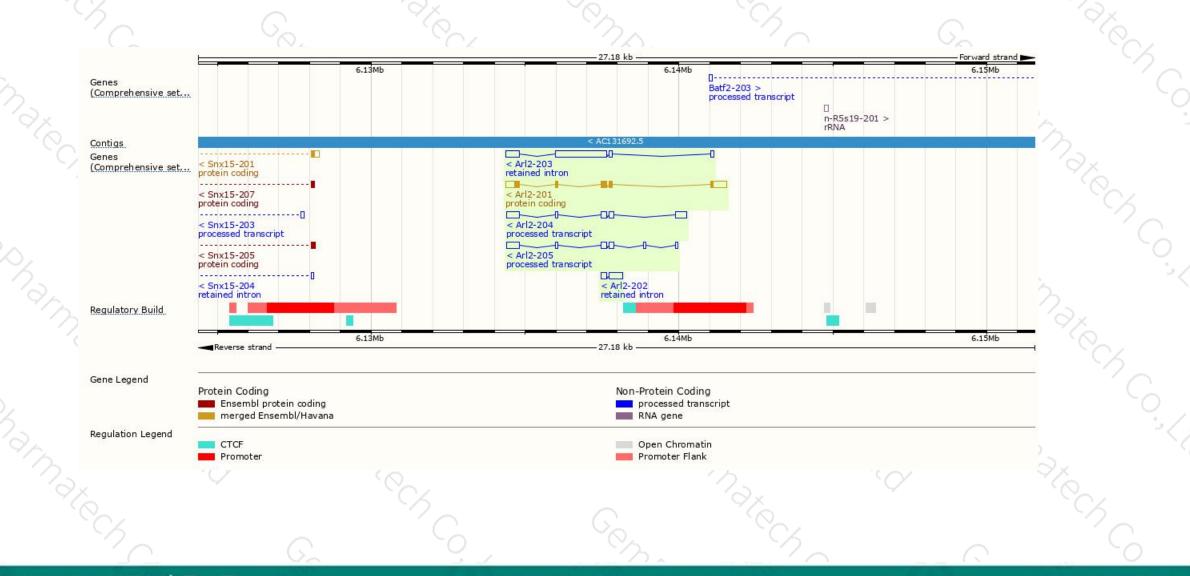
< Arl2-201 protein coding

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Genomic location distribution





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Protein domain



	G S (x		N CA			Cho,	[°] [°] [°]
	ENSMUSP00000025 PDB-ENSP mappings TIGRFAM Superfamily	Small GTP-binding protein (~~~ ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3	SMART	P-loop containing nucleoside tr SM00177 SM00178	ipnosphate hydrolase				
	Prints Pfam PROSITE profiles	SM00175 Small GTPase superfamil Small GTPase superfamily, ARF/SAR type PS51417	y, ARF/SAR type				~~~~
	PANTHER Gene3D	PTHR45697:SF2 PTHR45697					
5.	CDD. All sequence SNPs/i	3,40,50,300 cd04154 Sequence variants (dbSNP and all other	sources)	1			
9	Variant Legend Scale bar	synonymous variant 0 20	40 60	80 100	120 140	160 184	C'Ch C
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



