

Arid3a Cas9-KO Strategy

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Design Date:	2018-10-31

Project Overview

Project Name

Arid3a

Project type

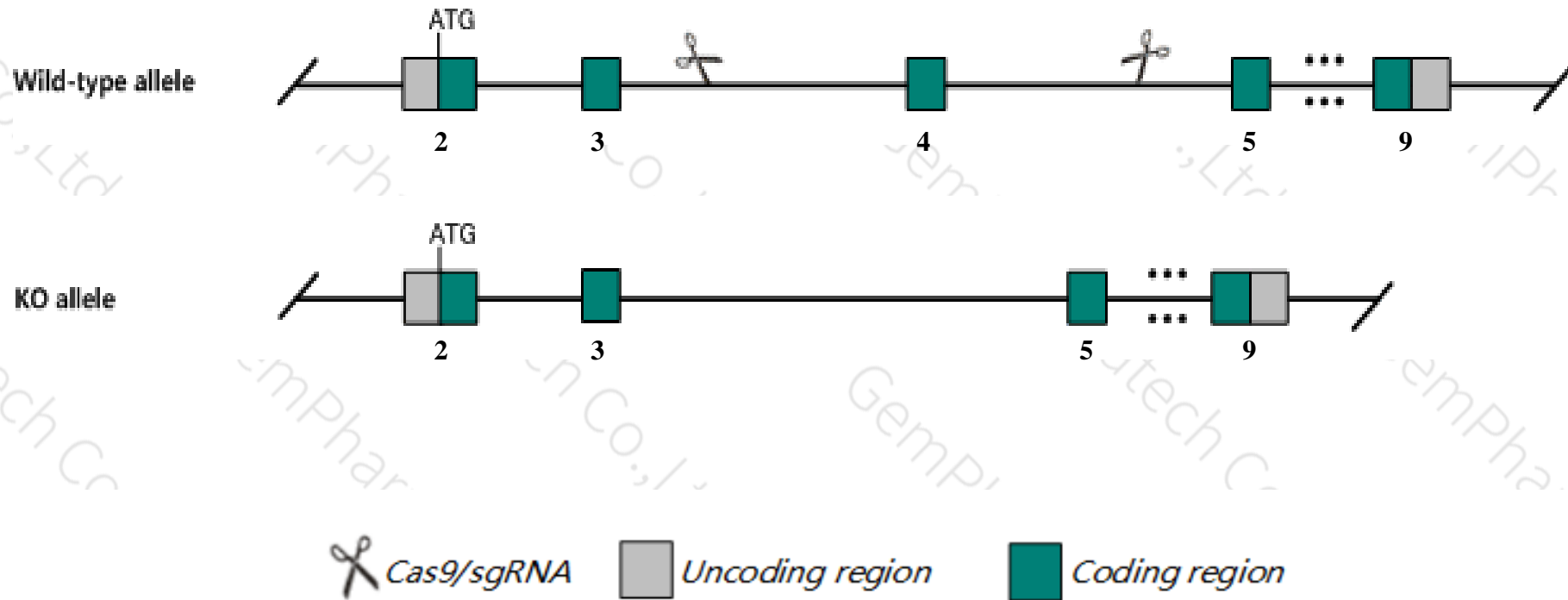
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arid3a* gene. The schematic diagram is as follows:



- The *Arid3a* gene has 5 transcripts. According to the structure of *Arid3a* gene, exon4 of *Arid3a*-201(ENSMUST00000019708.11) transcript is recommended as the knockout region. The region contains 73bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arid3a* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit embryonic lethality between E11.5 and E13.5 due to impaired erythropoiesis.
- Transcript *Arid3a*-204 may not be affected.
- The *Arid3a* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Arid3a AT rich interactive domain 3A (BRIGHT-like) [Mus musculus (house mouse)]

Gene ID: 13496, updated on 13-Mar-2020

Summary

Official Symbol Arid3a provided by [MGI](#)

Official Full Name AT rich interactive domain 3A (BRIGHT-like) provided by [MGI](#)

Primary source [MGI:MGI:1328360](#)

See related [Ensembl:ENSMUSG00000019564](#)

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 Bright, Dri1, Dril1

Expression Ubiquitous expression in placenta adult (RPKM 13.2), testis adult (RPKM 6.1) and 25 other tissues [See more](#)

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

Transcript information (Ensembl)

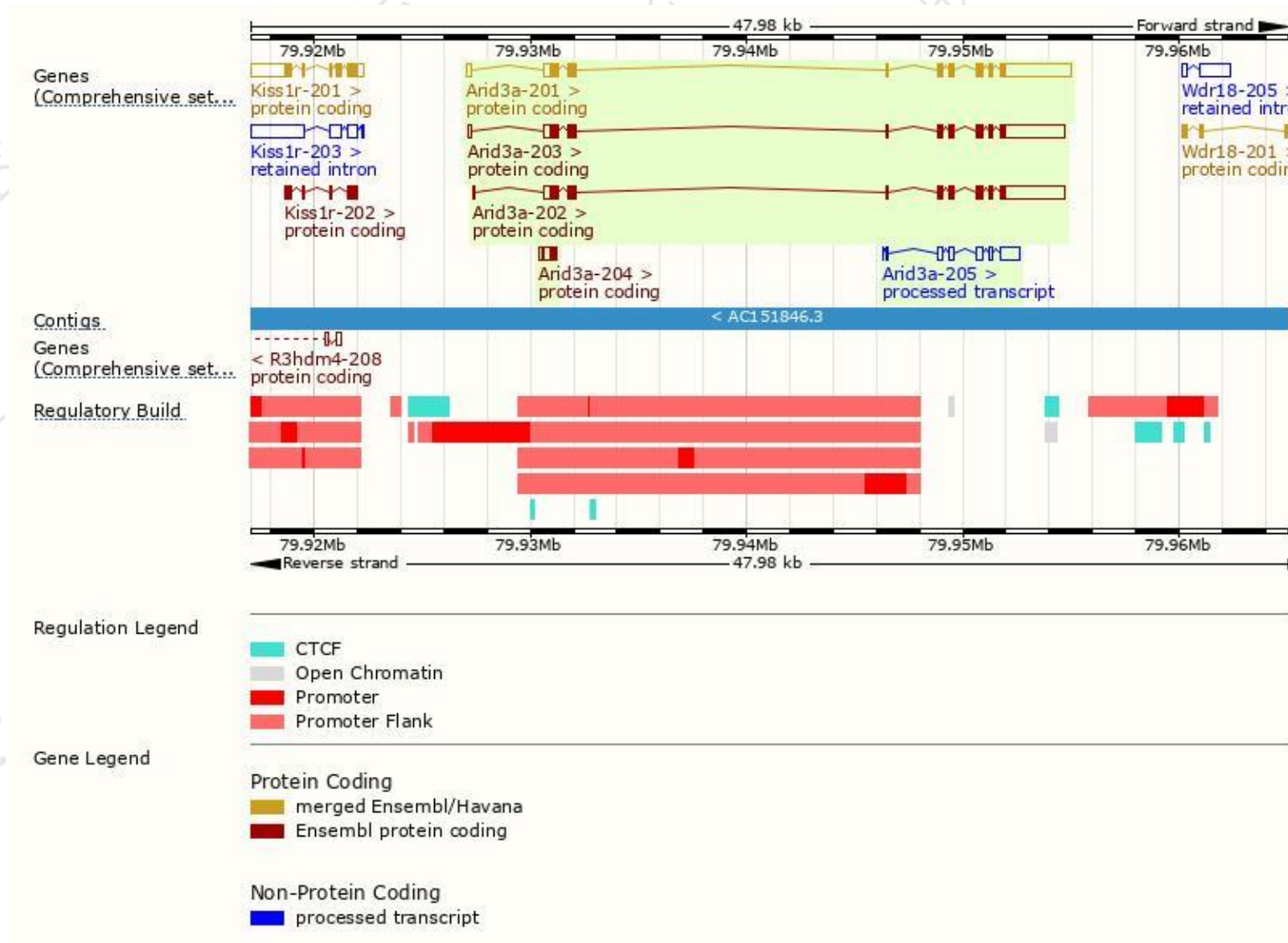
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arid3a-201	ENSMUST00000019708.11	5361	601aa	Protein coding	CCDS23999	Q62431	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Arid3a-203	ENSMUST00000105377.7	4952	599aa	Protein coding	CCDS78851	A0A0R4J1A7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Arid3a-202	ENSMUST00000105376.1	4892	601aa	Protein coding	CCDS23999	Q62431	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Arid3a-204	ENSMUST00000131118.1	691	108aa	Protein coding	-	D3YVQ2	CDS 3' incomplete TSL:3
Arid3a-205	ENSMUST00000135005.1	1839	No protein	Processed transcript	-	-	TSL:1

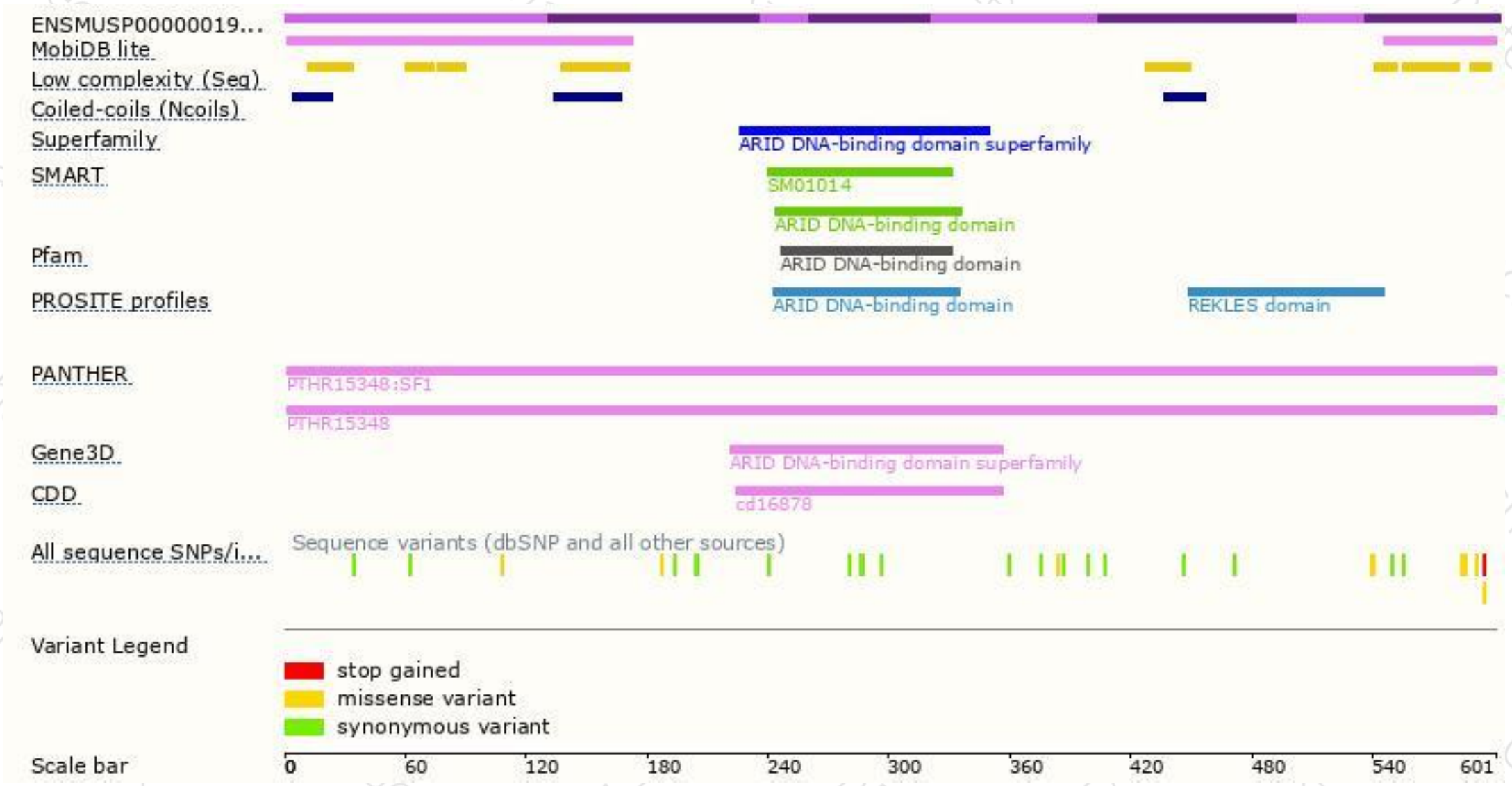
The strategy is based on the design of *Arid3a-201* transcript,the transcription is shown below:



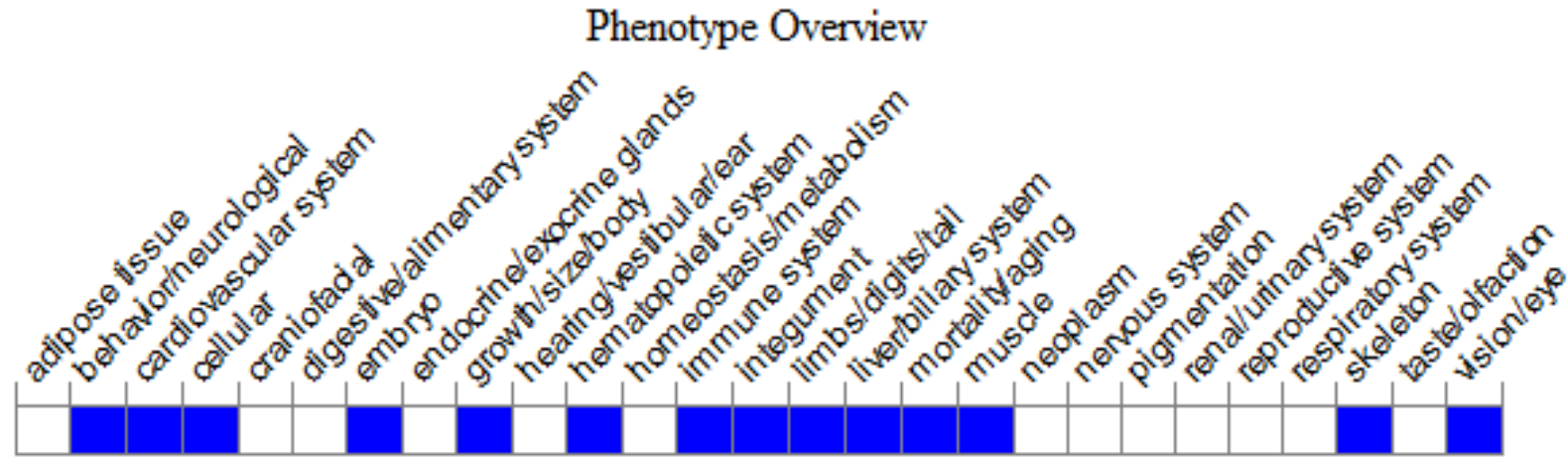
Genomic location distribution



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, mice homozygous for a knock-out allele exhibit embryonic lethality between E11.5 and E13.5 due to impaired erythropoiesis.

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

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