

Dock8 Cas9-KO Strategy

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Project Overview

Project Name

Dock8

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dock8* gene. The schematic diagram is as follows:



- The *Dock8* gene has 6 transcripts. According to the structure of *Dock8* gene, exon2 of *Dock8-201* (ENSMUST00000025831.7) transcript is recommended as the knockout region. The region contains 103bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dock8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for inactivating mutations of this gene exhibit loss of marginal zone B cells, decrease in peritoneal B1 cells and peripheral naive T cells, failure of sustained antibody response after immunization, failure of germinal center persistence, and failure of B cell affinity maturation.
- The *Dock8* 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.

Gene information (NCBI)

Dock8 dedicator of cytokinesis 8 [Mus musculus (house mouse)]

Gene ID: 76088, updated on 31-Jan-2019

Summary



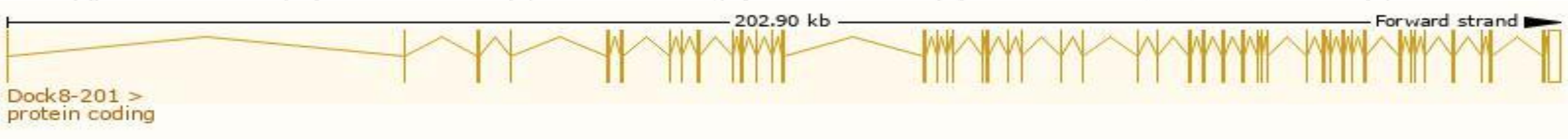
Official Symbol	Dock8 provided by MGI
Official Full Name	dedicator of cytokinesis 8 provided by MGI
Primary source	MGI:MGI:1921396
See related	Ensembl:ENSMUSG00000052085
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200017A24Rik, 5830472H07Rik, A130095G14Rik, AI461977
Expression	Broad expression in thymus adult (RPKM 25.8), spleen adult (RPKM 17.9) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

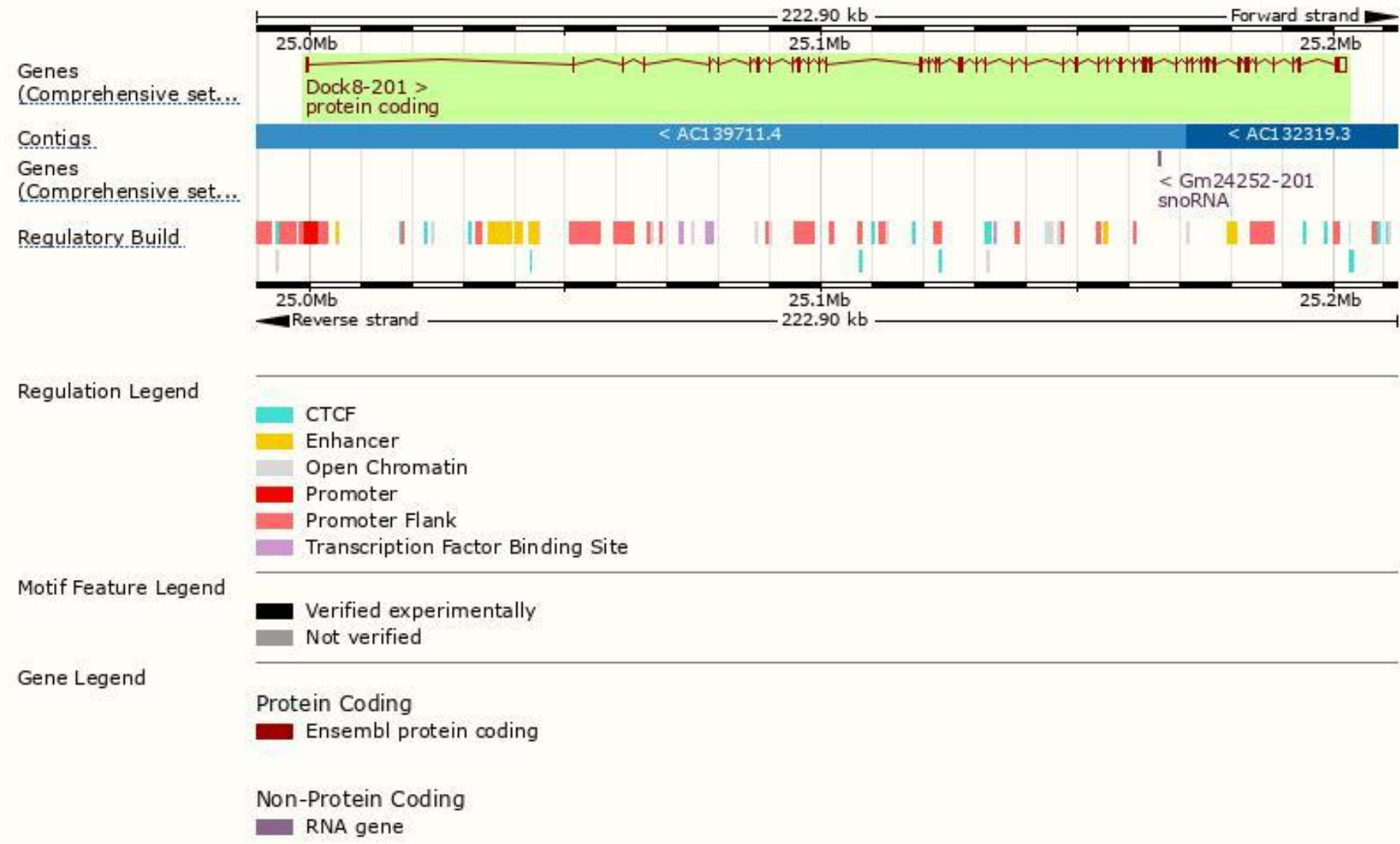
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dock8-201	ENSMUST00000025831.7	7805	2100aa	Protein coding	CCDS37943	Q8C147	TSL:1 GENCODE basic APPRIS P1
Dock8-206	ENSMUST00000237705.1	566	No protein	Processed transcript	-	-	
Dock8-202	ENSMUST00000235722.1	2158	No protein	Retained intron	-	-	
Dock8-205	ENSMUST00000237532.1	624	No protein	Retained intron	-	-	
Dock8-204	ENSMUST00000236576.1	436	No protein	Retained intron	-	-	
Dock8-203	ENSMUST00000236471.1	434	No protein	Retained intron	-	-	

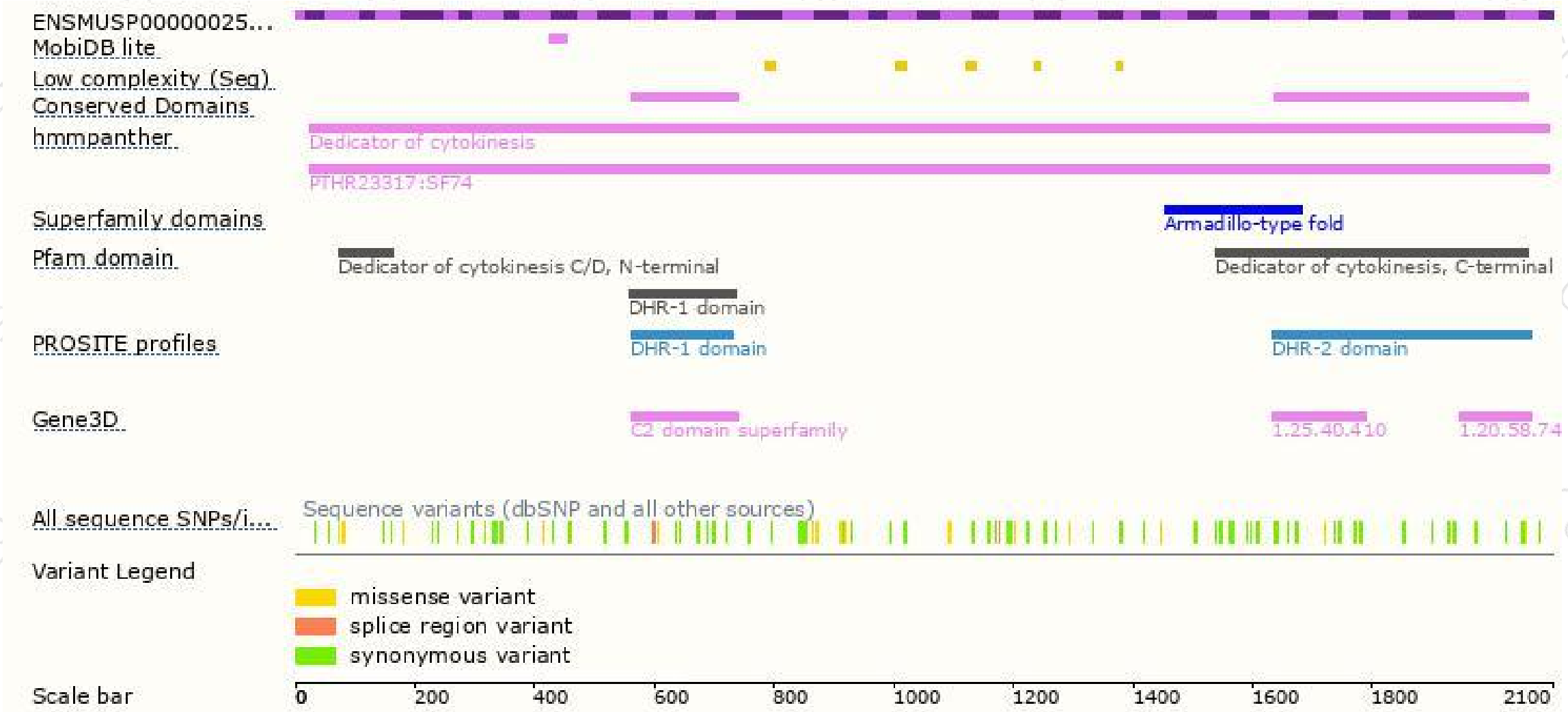
The strategy is based on the design of *Dock8-201* transcript,The transcription is shown below



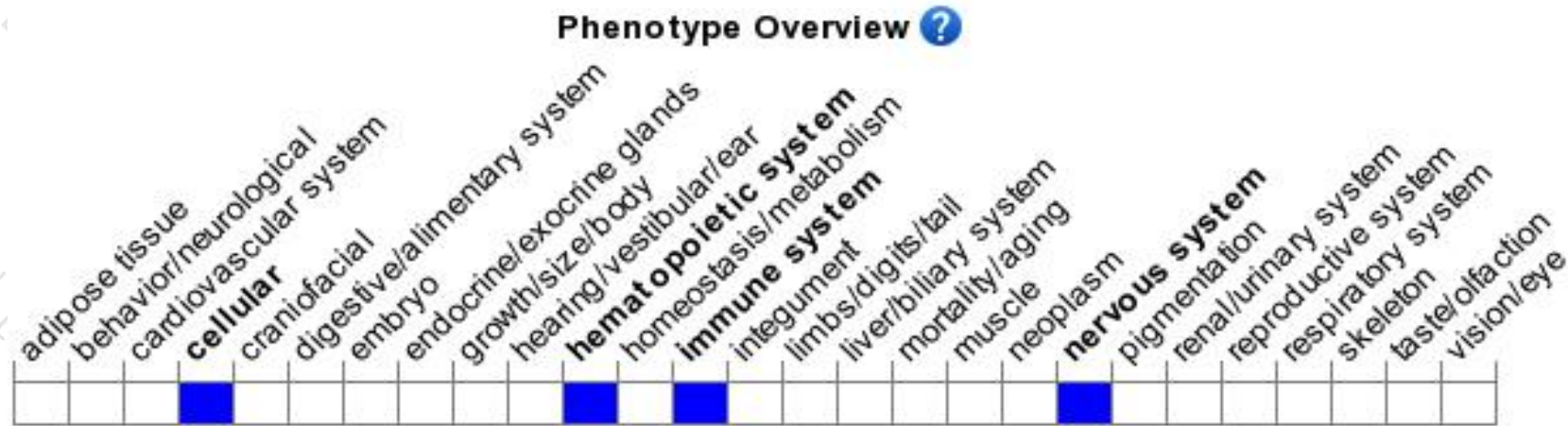
Genomic location distribution



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 inactivating mutations of this gene exhibit loss of marginal zone B cells, decrease in peritoneal B1 cells and peripheral naive T cells, failure of sustained antibody response after immunization, failure of germinal center persistence, and failure of B cell affinity maturation.

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

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