

Ahnak Cas9-KO Strategy

Designer:

Reviewer:

Design Date:

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2019-11-29

Project Overview



Project Name

Ahnak

Project type

Cas9-KO

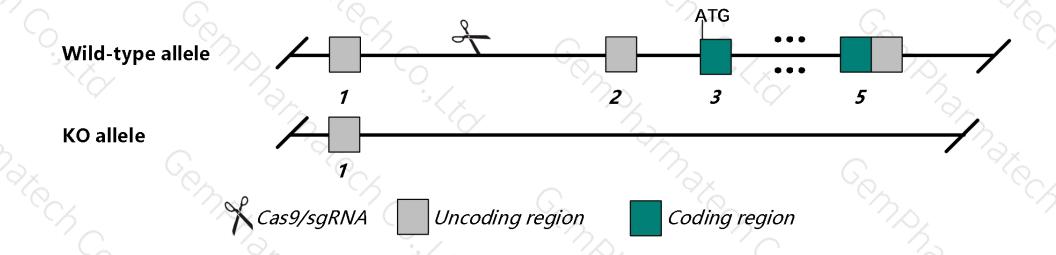
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- The *Ahnak* gene has 5 transcripts. According to the structure of *Ahnak* gene, exon2-exon5 of *Ahnak-202* (ENSMUST00000092956.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ahnak* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for one knock-out allele exhibit decreased T cell proliferation and increased susceptibility to parasitic infection.
- The *Ahnak* 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)



Ahnak AHNAK nucleoprotein (desmoyokin) [Mus musculus (house mouse)]

Gene ID: 66395, updated on 18-Nov-2019

Summary

☆? -

Official Symbol Ahnak provided by MGI

Official Full Name AHNAK nucleoprotein (desmoyokin) provided by MGI

Primary source MGI:MGI:1316648

See related Ensembl:ENSMUSG00000069833

Gene type protein coding
RefSeq status VALIDATED
Organism Mus musculus

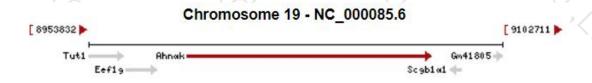
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as DY6

Expression Biased expression in bladder adult (RPKM 56.2), lung adult (RPKM 31.1) and 13 other tissues See more

Orthologs human all

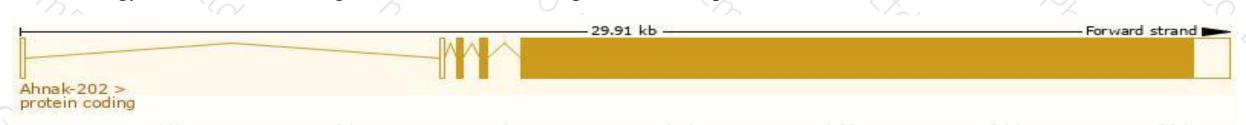


Transcript information (Ensembl)



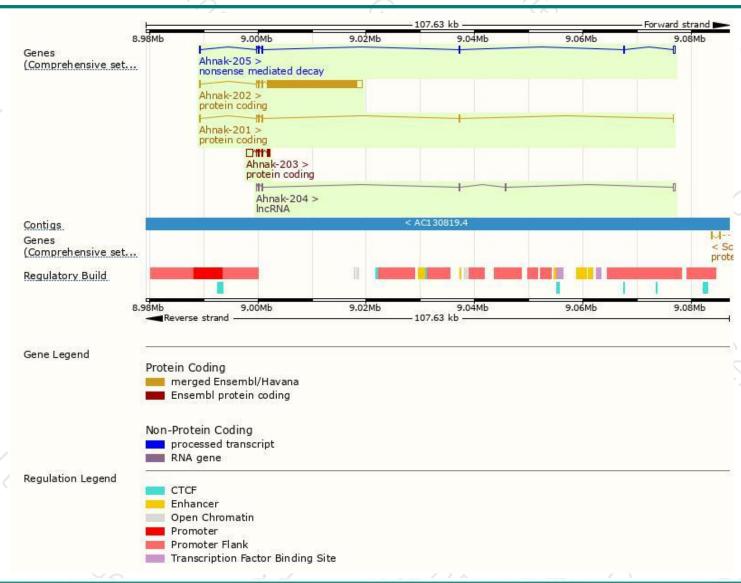
Name 🍦	Transcript ID 🍦	bp 🛊	Protein 🍦	Translation ID 👙	Biotype	CCDS 🍦	UniProt 🍦	Flags
Ahnak-202	ENSMUST00000092956.3	18100	<u>5656aa</u>	ENSMUSP00000090633.2	Protein coding	CCDS29564&	E9Q616광	TSL:1 GENCODE basic
Ahnak-201	ENSMUST00000092955.10	830	<u>150aa</u>	ENSMUSP00000090632.3	Protein coding	CCDS50384@	G5E8K8配	TSL:2 GENCODE basic APPRIS P1
Ahnak-203	ENSMUST00000236390.1	2200	311aa	ENSMUSP00000158470.1	Protein coding	æ	A0A494BBD5₽	CDS 3' incomplete
Ahnak-205	ENSMUST00000237912.1	1188	<u>176aa</u>	ENSMUSP00000157404.1	Nonsense mediated decay		<u>A0A494B8Y7</u> ₽	8 7
Ahnak-204	ENSMUST00000237033.1	989	No protein		IncRNA	ie i	-	le .

The strategy is based on the design of Ahnak-202 transcript, The transcription is shown below



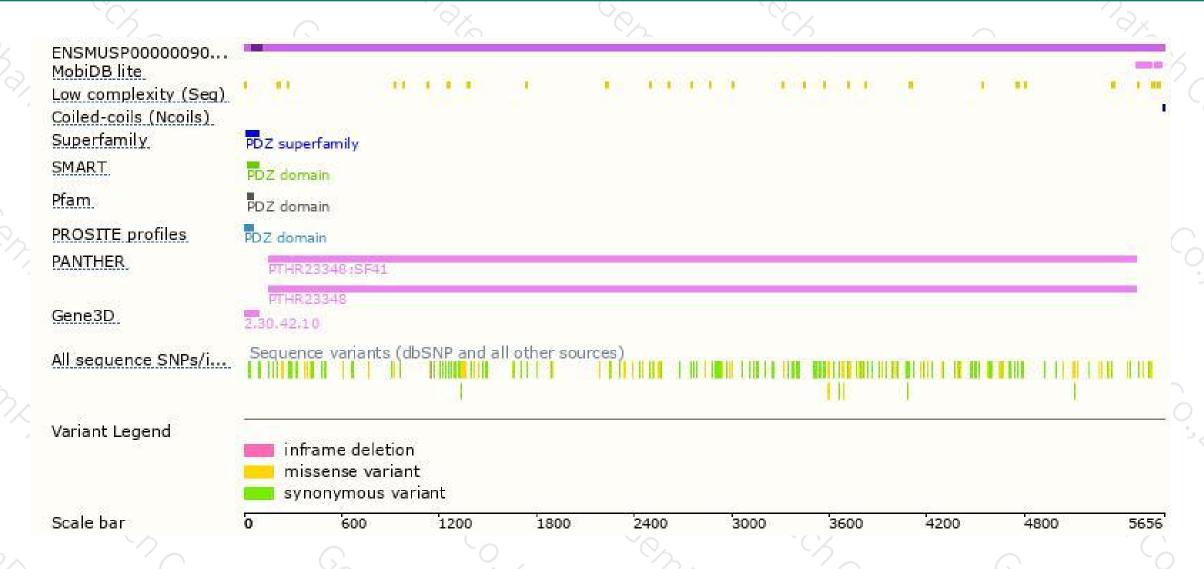
Genomic location distribution





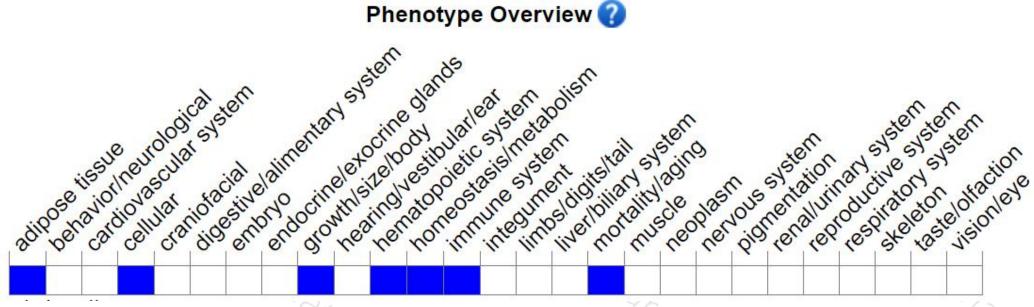
Protein domain





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 one knock-out allele exhibit decreased T cell proliferation and increased susceptibility to parasitic infection.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





