

Aatk Cas9-KO Strategy

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Project Overview

Project Name

Aatk

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Aatk* gene has 9 transcripts. According to the structure of *Aatk* gene, exon3-exon7 of *Aatk*-201(ENSMUST00000064307.9) transcript is recommended as the knockout region. The region contains 569bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Aatk* gene. The brief process is as follows: CRISPR/Cas9 system 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 decreased brain size, longer axons and fewer neurites.
- The flox region is about 300bp away from the 5th end of the Mir338 gene, which may affect the regulation of this gene or delete it directly.
- The flox region is about 300bp away from the 3th end of the Mir3065 gene, which may affect the regulation of this gene or delete it directly.
- The *Aatk* gene is located on the Chr11. 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)

Aatk apoptosis-associated tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 11302, updated on 20-Mar-2020

Summary



Official Symbol Aatk provided by [MGI](#)

Official Full Name apoptosis-associated tyrosine kinase provided by [MGI](#)

Primary source [MGI:MGI:1197518](#)

See related [Ensembl:ENSMUSG00000025375](#)

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 AATYK, aatyk1, mKIAA0641

Expression Broad expression in cerebellum adult (RPKM 51.8), cortex adult (RPKM 38.4) and 15 other tissues [See more](#)

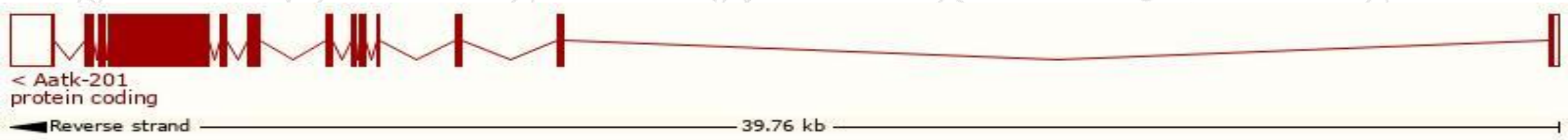
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

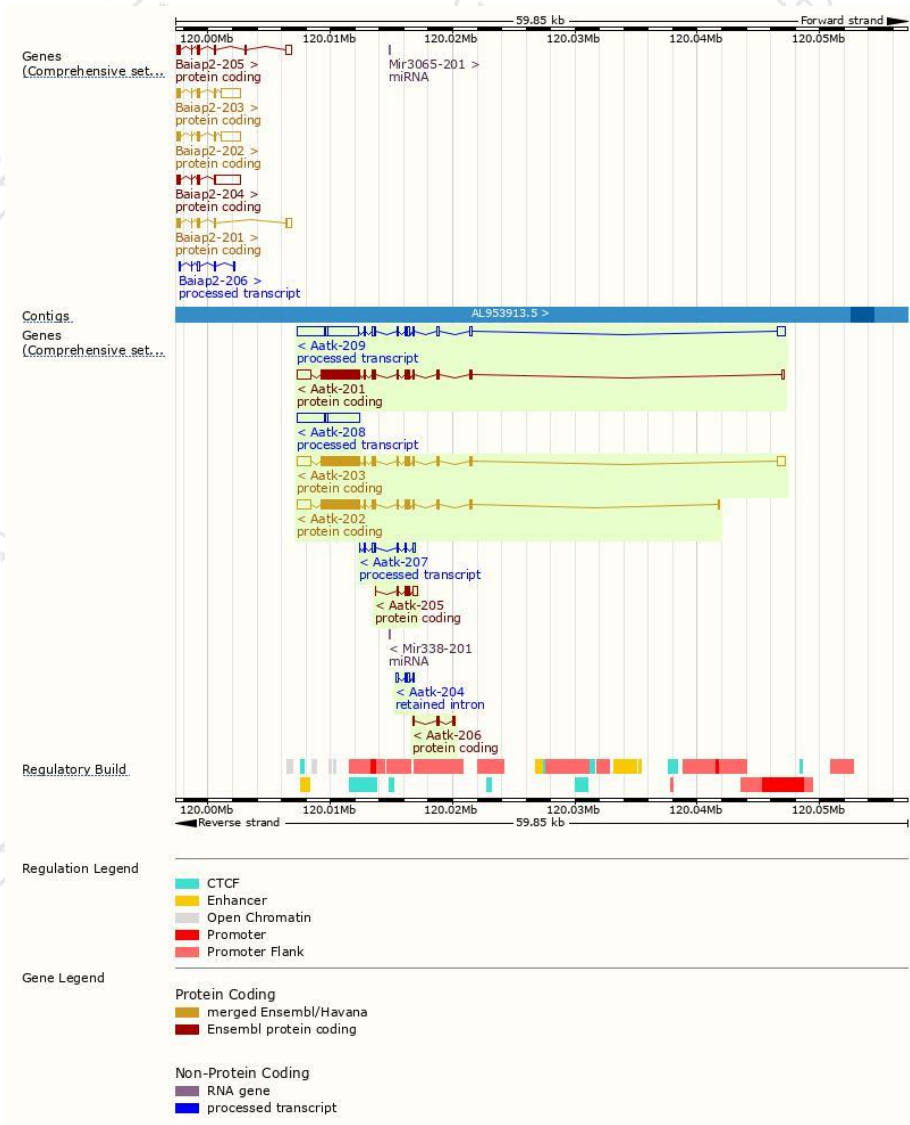
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aatk-203	ENSMUST00000103020.7	5687	1317aa	Protein coding	CCDS25725	B1AZF9	TSL:1 GENCODE basic APPRIS P3
Aatk-201	ENSMUST00000064307.9	5336	1374aa	Protein coding	CCDS56826	B1AZF3	TSL:1 GENCODE basic APPRIS ALT2
Aatk-202	ENSMUST00000103019.1	5177	1317aa	Protein coding	CCDS25725	B1AZF9	TSL:1 GENCODE basic APPRIS P3
Aatk-205	ENSMUST00000132575.7	815	99aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Aatk-206	ENSMUST00000134319.1	365	95aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Aatk-209	ENSMUST00000150730.7	6455	No protein	Processed transcript	-	-	TSL:1
Aatk-208	ENSMUST00000142959.1	4886	No protein	Processed transcript	-	-	TSL:2
Aatk-207	ENSMUST00000136386.7	781	No protein	Processed transcript	-	-	TSL:3
Aatk-204	ENSMUST00000128836.1	553	No protein	Retained intron	-	-	TSL:3

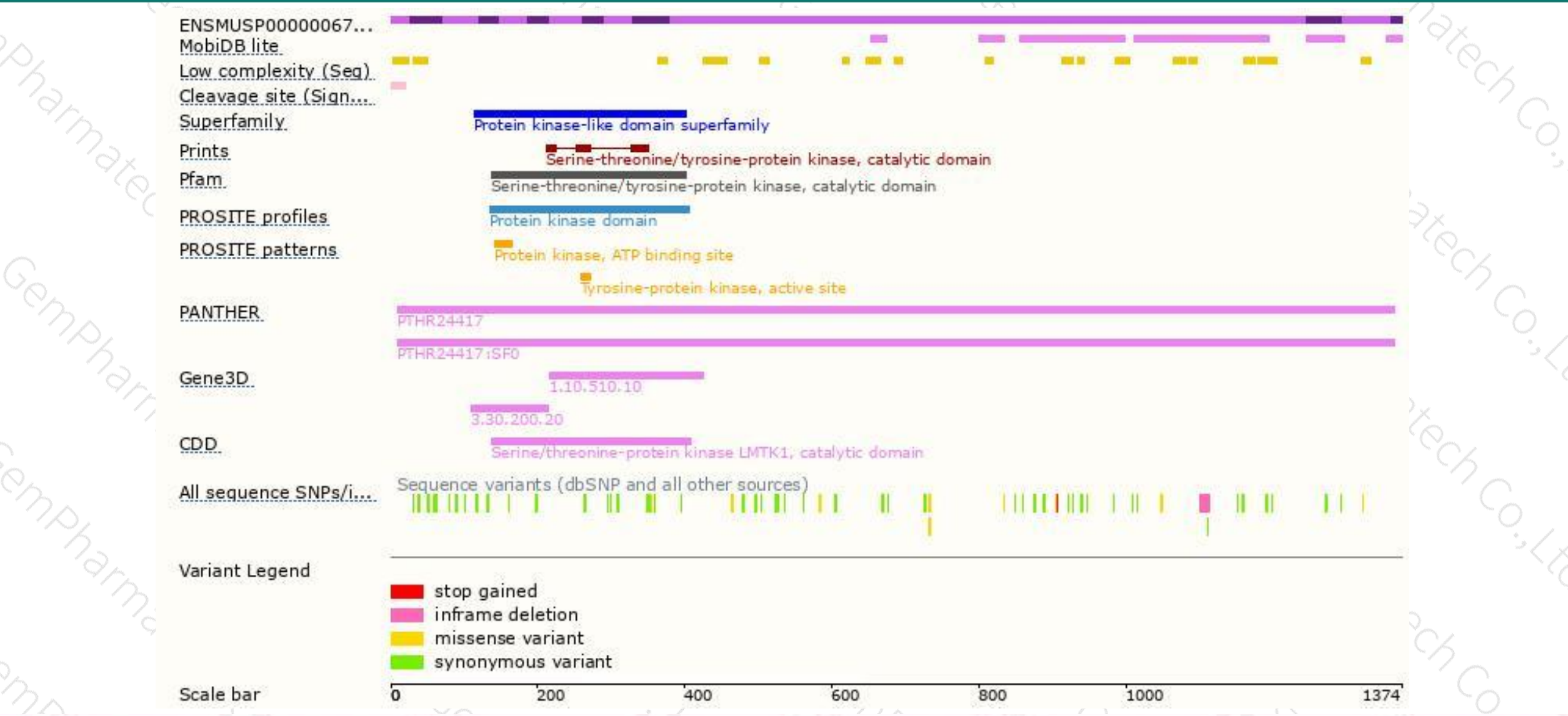
The strategy is based on the design of *Aatk-201* transcript,the transcription is shown below:



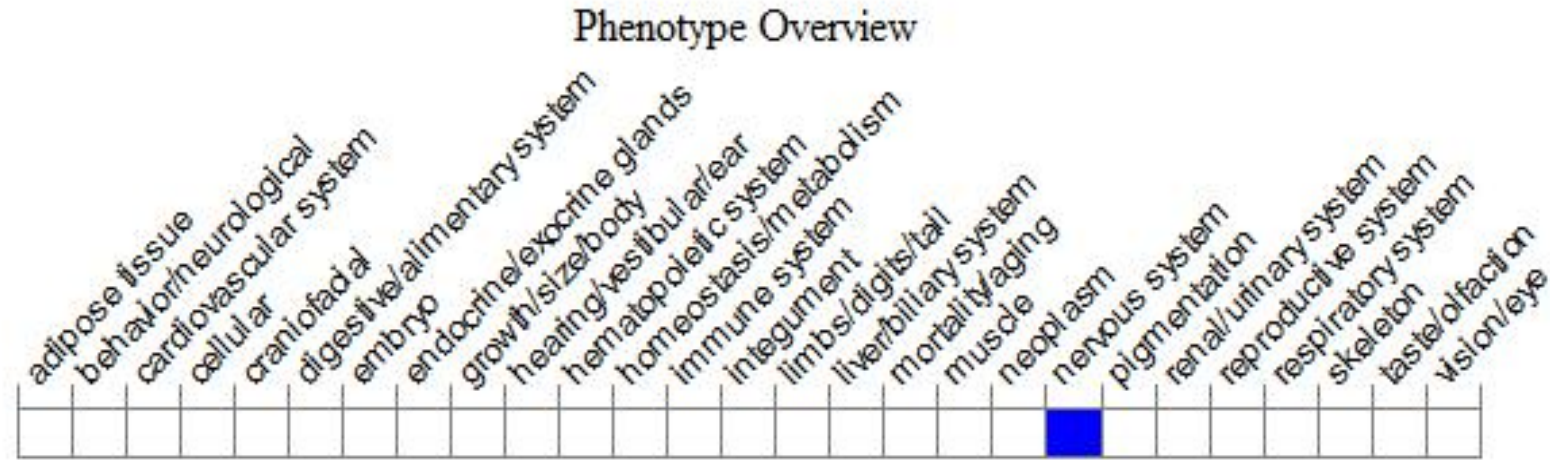
Genomic location distribution



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 decreased brain size, longer axons and fewer neurites.

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

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