

Kat2a Cas9-KO Strategy

Designer: Yanhua Shen

Reviewer: Zihe Cui

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Project Overview

Project Name

Kat2a

Project type

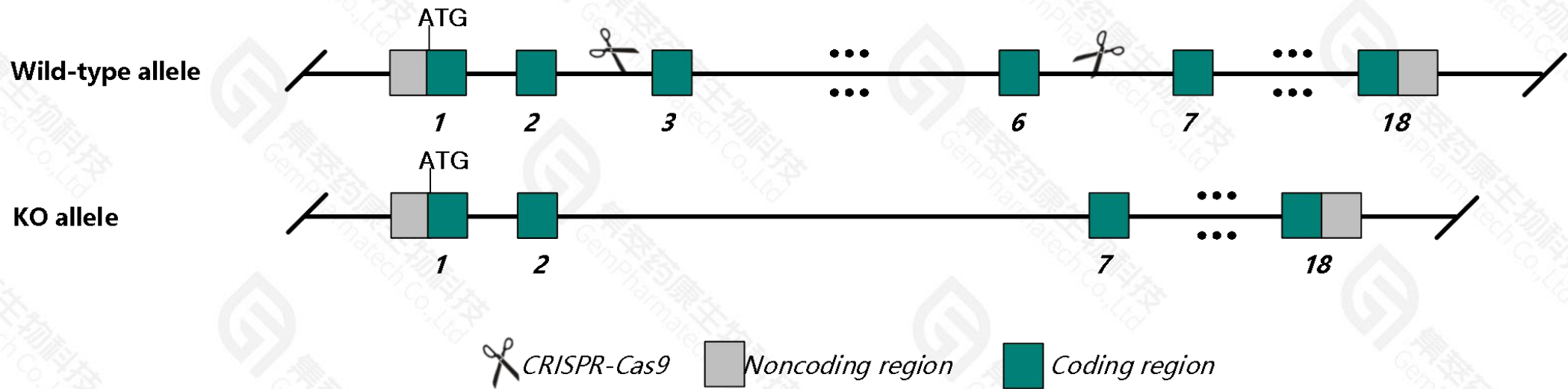
Cas9-KO

Strain background

BALB/cJGpt

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Kat2a* gene. The schematic diagram is as follows:



- The *Kat2a* gene has 4 transcripts. According to the structure of *Kat2a* gene, exon 3-exon 6 of MGP_BALBcJ_T0032341.1 transcript is recommended as the knockout region. The region contains 610 bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Kat2a* gene. The brief process is as follows: CRISPR-Cas9 system were microinjected into the fertilized eggs of BALB/cJGpt 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 BALB/cJGpt mice.

- According to the MGI, homozygotes for targeted null mutations exhibit poorly developed yolk sac blood vessels, retarded growth, absence of dorsal mesoderm lineages, failure to form somites, and lethality between embryonic days 9.5-11.5.
- The effect of *Hspb9* gene is unknown.
- The *Kat2a* 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)

Kat2a K(lysine) acetyltransferase 2A [*Mus musculus* (house mouse)]

Gene ID: 14534, updated on 15-May-2022

[Download Datasets](#)

Summary

Official Symbol	Kat2a provided by MGI
Official Full Name	K(lysine) acetyltransferase 2A provided by MGI
Primary source	MGI:MGI:1343101
See related	Ensembl:ENSMUSG00000020918 AllianceGenome:MGI:1343101
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	Gcn5; Gcn5l2; mmGCN5; AW212720; 1110051E14Rik
Summary	Enables H3 histone acetyltransferase activity; chromatin binding activity; and histone acetyltransferase activity (H4-K12 specific). Involved in several processes, including long-term memory; positive regulation of macromolecule metabolic process; and regulation of regulatory T cell differentiation. Acts upstream of or within several processes, including brain development; chordate embryonic development; and histone acetylation. Located in mitotic spindle and nucleus. Part of ATAC complex and SAGA complex. Is expressed in several structures, including alimentary system; central nervous system; early conceptus; genitourinary system; and hemolymphoid system gland. Orthologous to human KAT2A (lysine acetyltransferase 2A). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 33.5), ovary adult (RPKM 29.4) and 28 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context





Location: 11 D; 11 63.53 cM

See Kat2a in [Genome Data Viewer](#)

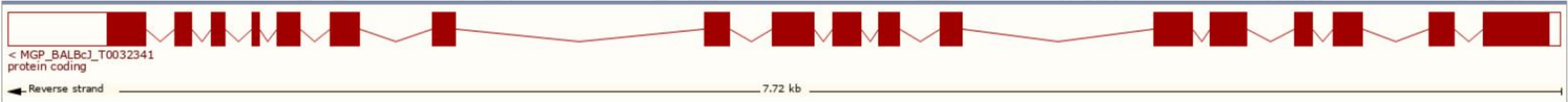
Exon count: 18

Transcript information (Ensembl)

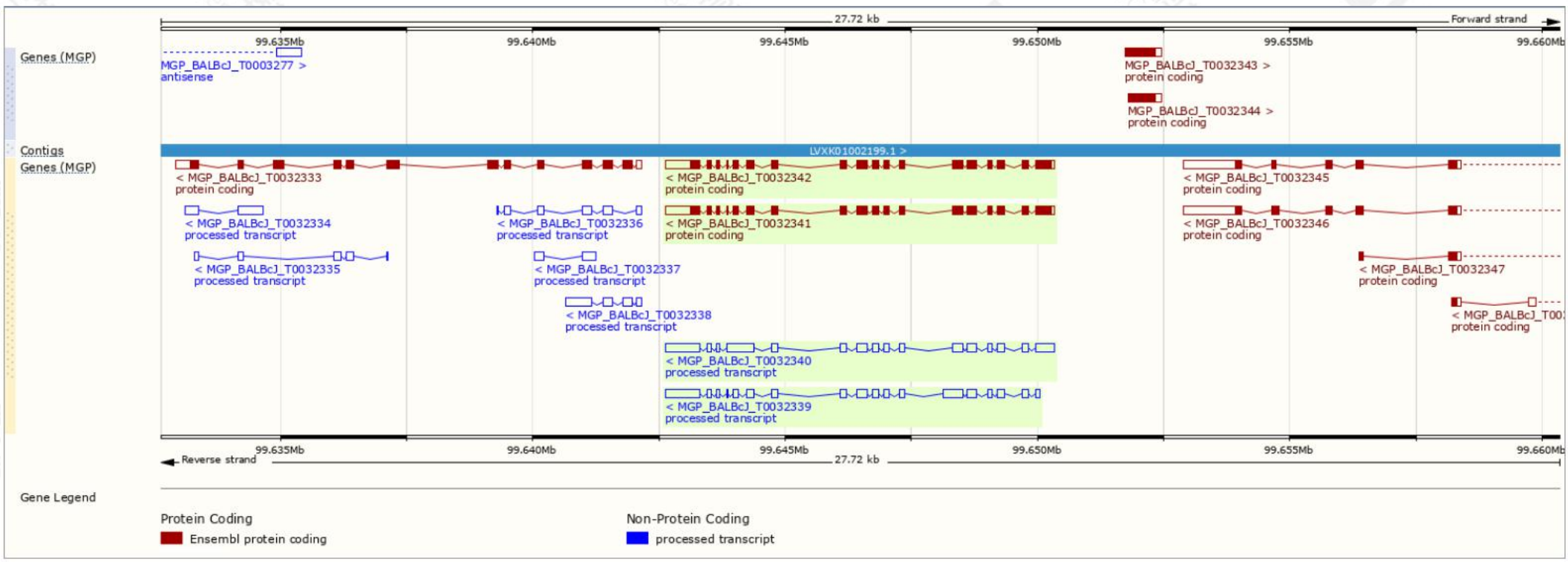
The gene has 4 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	Flags
MGP_BALBcJ_T0032339.1	-	2946	No protein	 Processed transcript	CCDS25432	-
MGP_BALBcJ_T0032341.1	-	3046	830aa	 Protein coding		Ensembl Canonical
MGP_BALBcJ_T0032342.1	-	3043	829aa	 Protein coding		-
MGP_BALBcJ_T0032340.1	-	3269	No protein	 Processed transcript		-

The strategy is based on the design of MGP_BALBcJ_T0032341.1 transcript,the transcription is shown below:



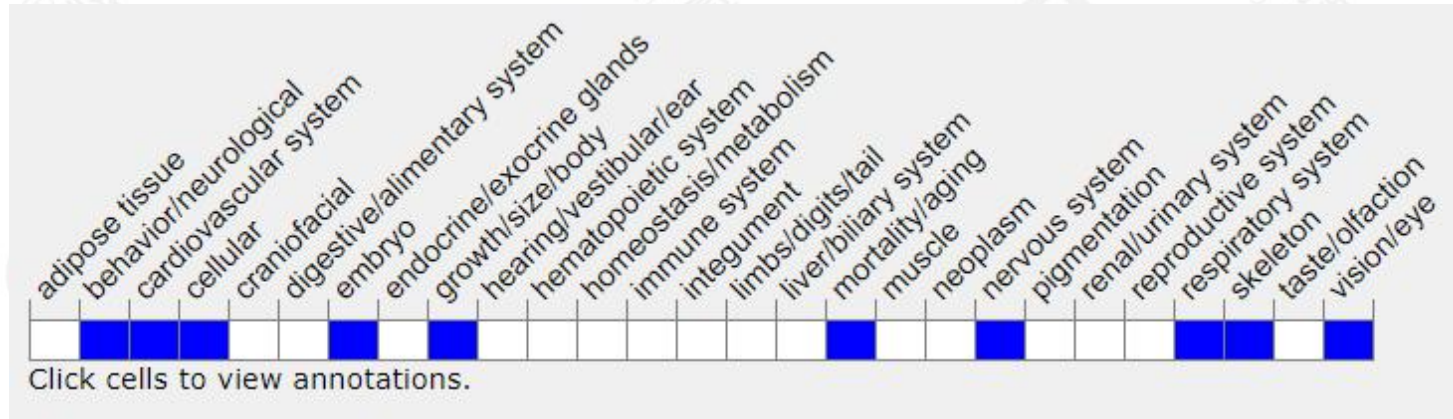
Genomic location distribution



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/>).

Homozygotes for targeted null mutations exhibit poorly developed yolk sac blood vessels, retarded growth, absence of dorsal mesoderm lineages, failure to form somites, and lethality between embryonic days 9.5-11.5.

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

