

Kat6a Cas9-KO Strategy

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Design Date: 2019-7-31

Project Overview

Project Name

Kat6a

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kat6a* gene. The schematic diagram is as follows:



- The *Kat6a* gene has 3 transcripts. According to the structure of *Kat6a* gene, exon4-exon8 of *Kat6a-201* (ENSMUST00000044331.6) transcript is recommended as the knockout region. The region contains 760bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kat6a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display perinatal lethality, cyanosis, decreased hematopoietic progenitor cell numbers, and severely impaired spleen and thymus development, but are not anemic. Heterozygotes display strain background dependent reductions in fertility.
- The *Kat6a* gene is located on the Chr8. 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)

Kat6a K(lysine) acetyltransferase 6A [Mus musculus (house mouse)]

Gene ID: 244349, updated on 19-Feb-2019

Summary



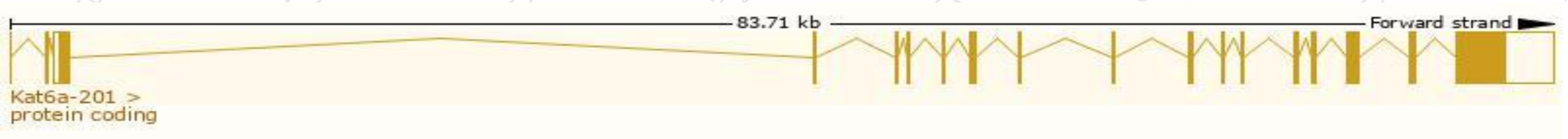
Official Symbol	Kat6a provided by MGI
Official Full Name	K(lysine) acetyltransferase 6A provided by MGI
Primary source	MGI:MGI:2442415
See related	Ensembl:ENSMUSG00000031540
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1500036M03, 9930021N24Rik, MOZ, Myst3, Zfp220
Expression	Ubiquitous expression in thymus adult (RPKM 13.7), CNS E11.5 (RPKM 10.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

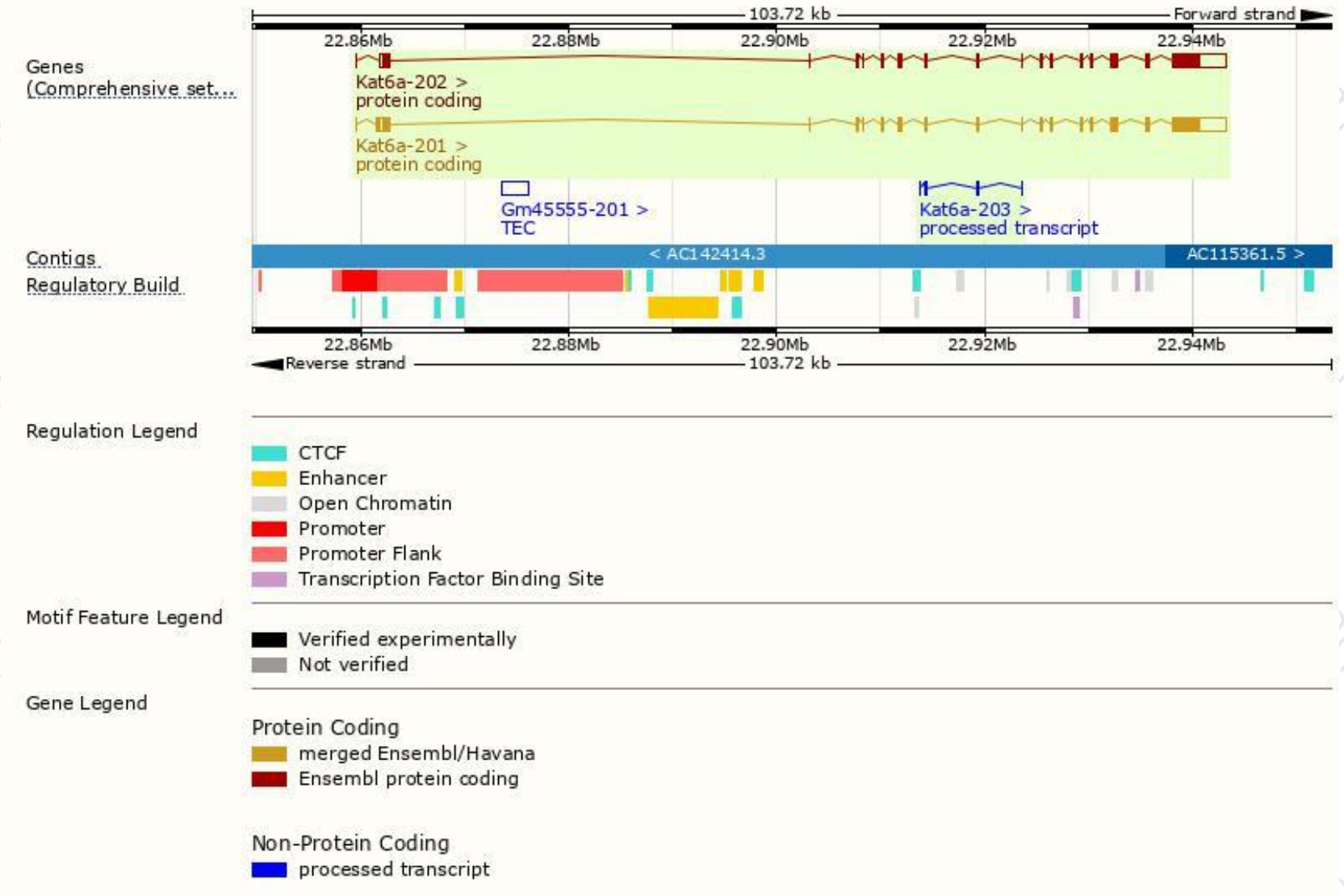
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kat6a-201	ENSMUST00000044331.6	9113	2003aa	Protein coding	CCDS40294	G3X940	TSL:1 GENCODE basic APPRIS P1
Kat6a-202	ENSMUST00000110696.7	9041	2003aa	Protein coding	CCDS40294	G3X940	TSL:1 GENCODE basic APPRIS P1
Kat6a-203	ENSMUST00000130718.1	419	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Kat6a-201* transcript,The transcription is shown below



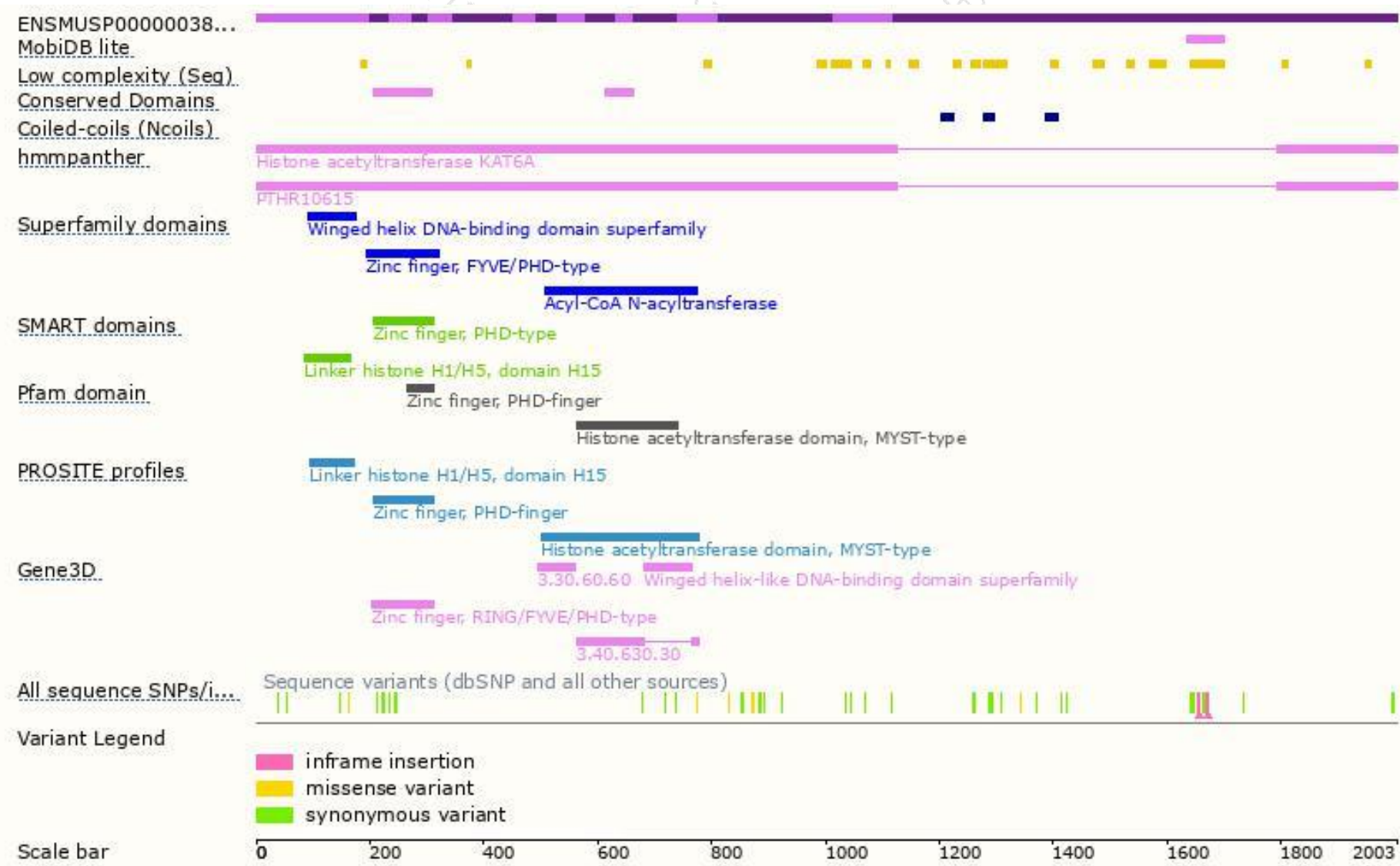
Genomic location distribution



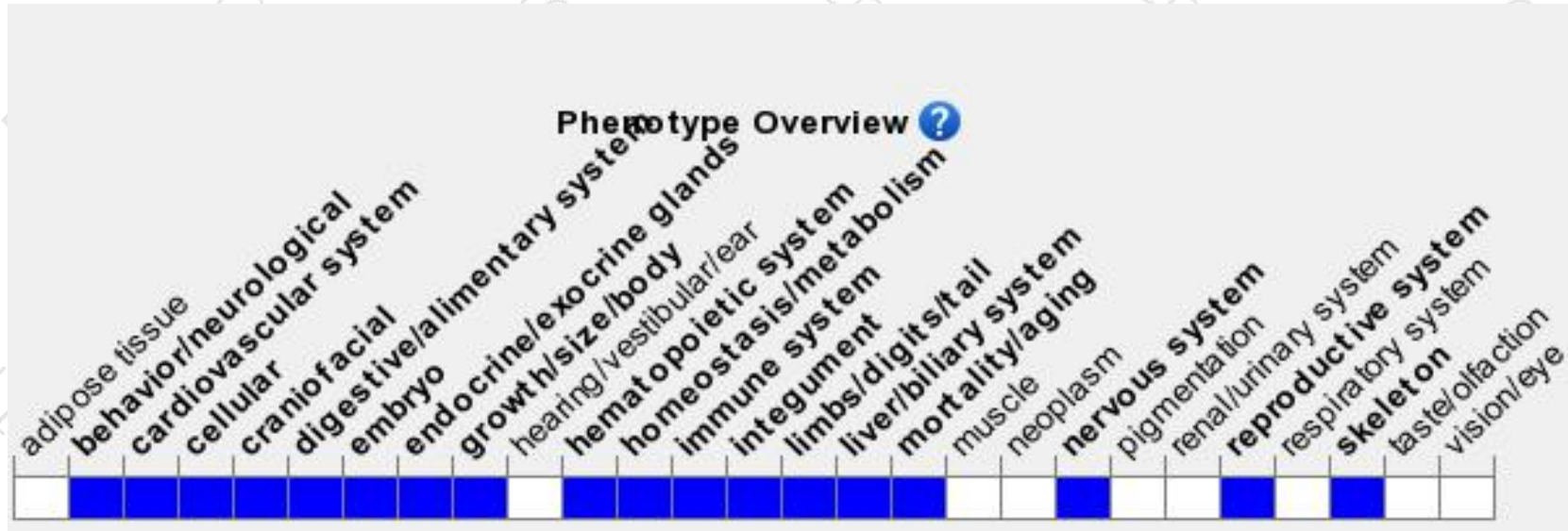
Protein domain



集萃药康
GemPharmatech



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, Homozygous null mice display perinatal lethality, cyanosis, decreased hematopoietic progenitor cell numbers, and severely impaired spleen and thymus development, but are not anemic. Heterozygous mice show strain background dependent reductions in fertility.

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

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