

# ***Kat14*** Cas9-KO Strategy

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# Project Overview



**Project Name**

***Kat14***

**Project type**

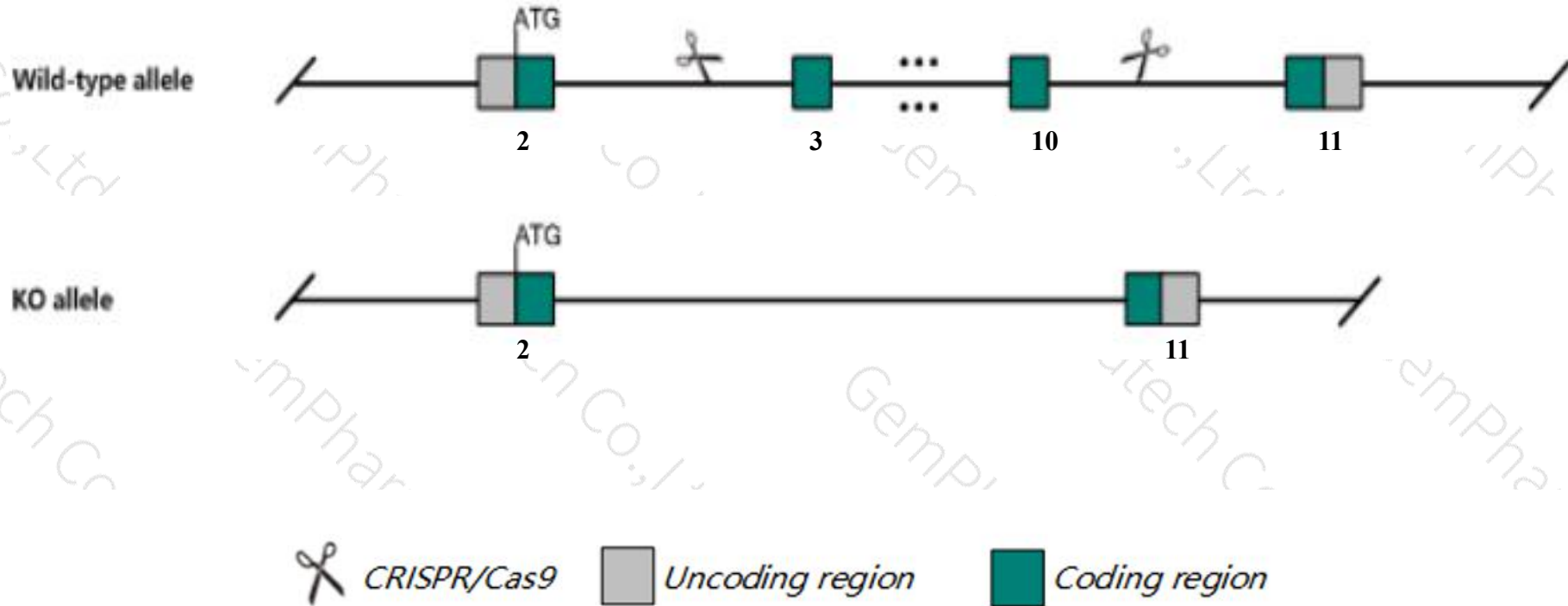
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kat14* gene. The schematic diagram is as follows:



- The *Kat14* gene has 11 transcripts. According to the structure of *Kat14* gene, exon3-exon10 of *Kat14-201*(ENSMUST00000028911.14) transcript is recommended as the knockout region. The region contains 1907bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kat14* 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 null allele exhibit embryonic lethality during organogenesis, decreased size, increased apoptosis, and disrupted cell cycling. Mice heterozygous for one targeted allele exhibit corneal opacity.
- The *Kat14* gene is located on the Chr2. 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)

## Kat14 lysine acetyltransferase 14 [Mus musculus (house mouse)]

Gene ID: 228714, updated on 13-Mar-2020

### Summary



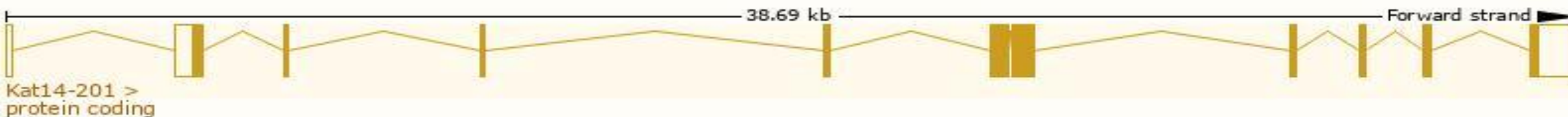
<b>Official Symbol</b>	Kat14 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	lysine acetyltransferase 14 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1917264</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027425</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2510008M08Rik, ATAC2, AU023459, Csrp2bp, D2Ertd473e, D2Wsu131e, E430020F17
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 11.4), placenta adult (RPKM 8.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

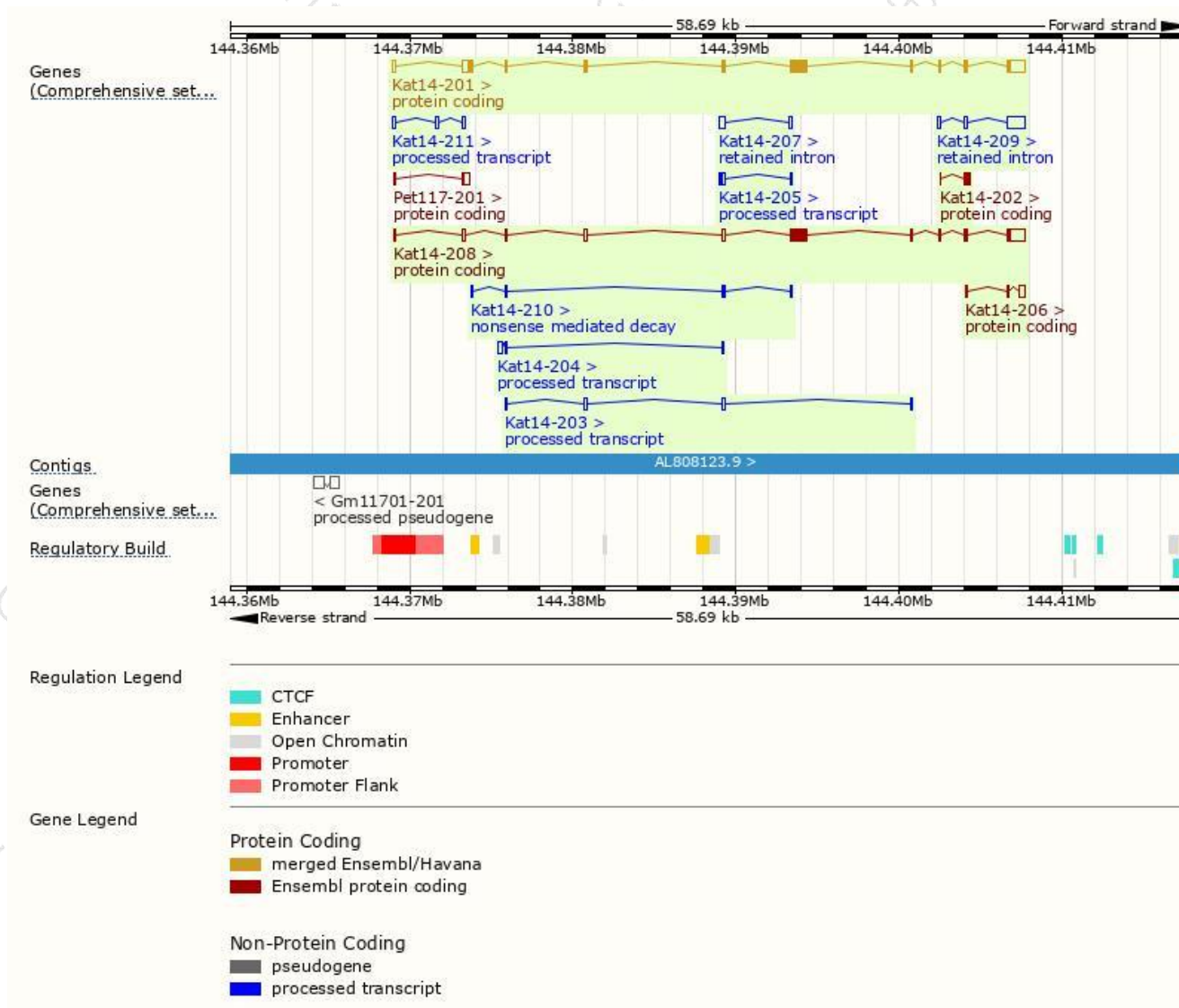
The gene has 11 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kat14-201	<a href="#">ENSMUST00000028911.14</a>	3801	<a href="#">779aa</a>	Protein coding	<a href="#">CCDS16819</a>	<a href="#">Q8CID0</a>	TSL:1 GENCODE basic APPRIS P1
Kat14-208	<a href="#">ENSMUST00000147747.7</a>	3299	<a href="#">568aa</a>	Protein coding	-	<a href="#">E9QA90</a>	TSL:1 GENCODE basic
Kat14-206	<a href="#">ENSMUST00000139812.1</a>	566	<a href="#">92aa</a>	Protein coding	-	<a href="#">F7C4S8</a>	CDS 5' incomplete TSL:3
Kat14-202	<a href="#">ENSMUST00000125398.2</a>	379	<a href="#">83aa</a>	Protein coding	-	<a href="#">E9Q3Q5</a>	CDS 5' incomplete TSL:3
Kat14-210	<a href="#">ENSMUST00000156410.1</a>	453	<a href="#">97aa</a>	Nonsense mediated decay	-	<a href="#">F6S6Z2</a>	CDS 5' incomplete TSL:3
Kat14-211	<a href="#">ENSMUST00000171261.1</a>	562	No protein	Processed transcript	-	-	TSL:3
Kat14-203	<a href="#">ENSMUST00000130654.7</a>	504	No protein	Processed transcript	-	-	TSL:3
Kat14-204	<a href="#">ENSMUST00000131836.1</a>	478	No protein	Processed transcript	-	-	TSL:3
Kat14-205	<a href="#">ENSMUST00000137611.1</a>	435	No protein	Processed transcript	-	-	TSL:3
Kat14-209	<a href="#">ENSMUST00000148500.1</a>	1468	No protein	Retained intron	-	-	TSL:1
Kat14-207	<a href="#">ENSMUST00000143318.1</a>	567	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Kat14-201* transcript, the transcription is shown below:



# Genomic location distribution



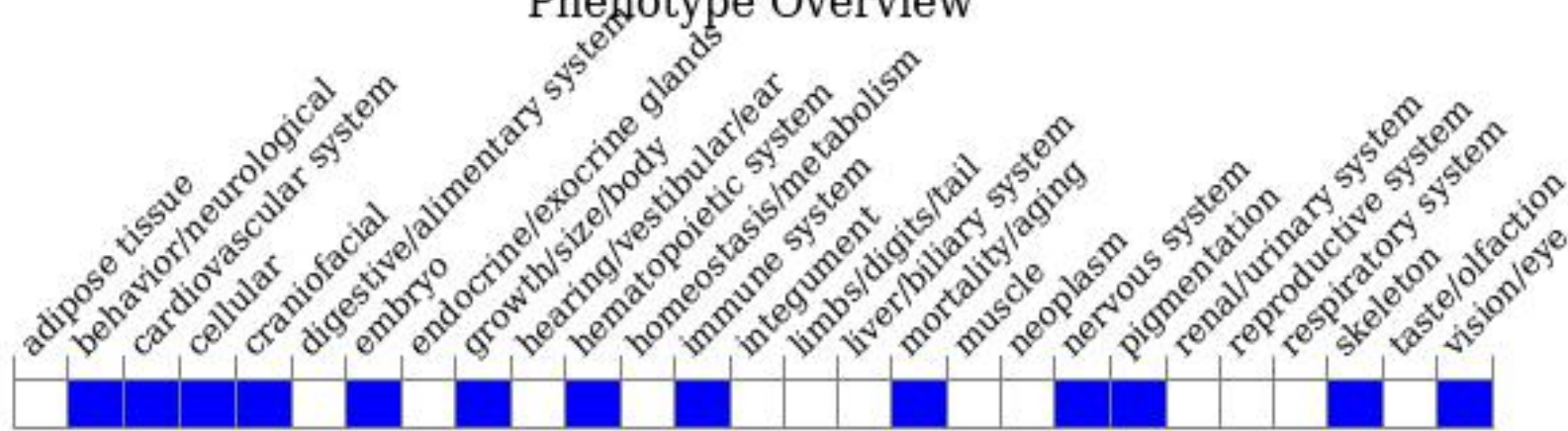


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview



*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 null allele exhibit embryonic lethality during organogenesis, decreased size, increased apoptosis, and disrupted cell cycling. Mice heterozygous for one targeted allele exhibit corneal opacity.

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

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