

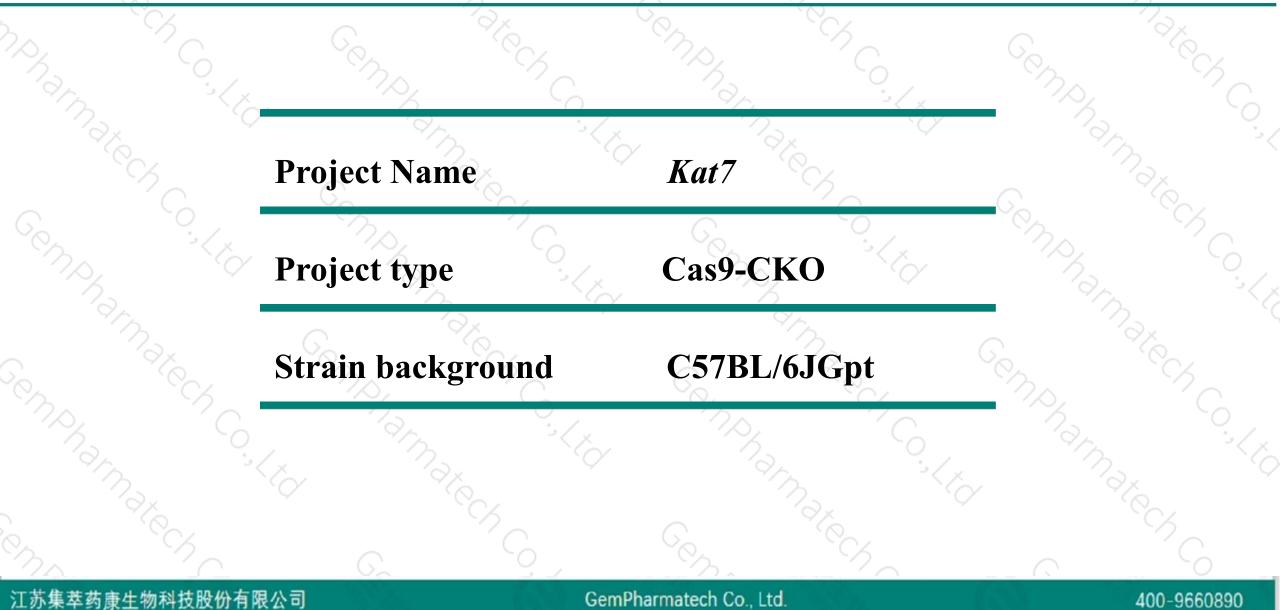
Kat7 Cas9-CKO Strategy

Designer: Xiaojing Li Design Date: 2020-1-8 Reviewer: JiaYu

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Project Overview

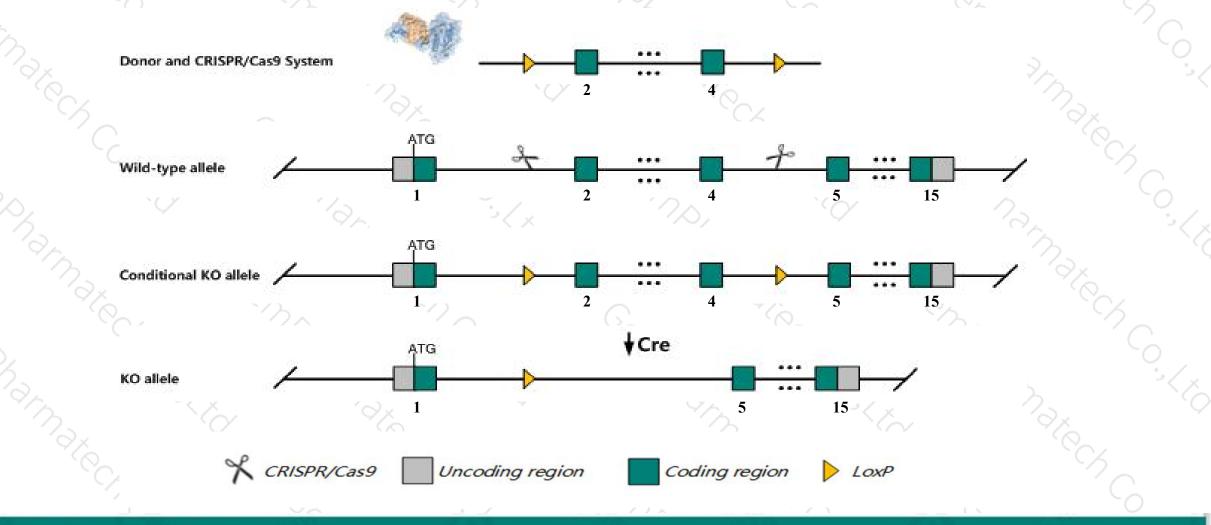




Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Kat7 gene. The schematic diagram is as follows:



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The Kat7 gene has 11 transcripts. According to the structure of Kat7 gene, exon2-exon4 of Kat7-205 (ENSMUST00000107734.9) transcript is recommended as the knockout region. The region contains 565bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Kat7* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit embryonic growth arrest, incomplete embryo turning, disorganized yolk sac vascular plexus, and increased apoptosis.
- > The Kat7 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Kat7 K(lysine) acetyltransferase 7 [Mus musculus (house mouse)]

Gene ID: 217127, updated on 10-Oct-2019

Summary

Official Symbol Kat7 provided by MGI Official Full Name K(lysine) acetyltransferase 7 provided by MGI Primary source MGI:MGI:2182799 See related Ensembl:ENSMUSG0000038909 protein coding Gene type RefSeg 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 Hbo1; Hboa; Myst2 Ubiquitous expression in testis adult (RPKM 20.1), placenta adult (RPKM 13.7) and 28 other tissues See more Expression Orthologs human all

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Transcript information (Ensembl)



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

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Name 🔺	Transcript ID 🖕	bp 🖕	Protein 🖕	Biotype 🖕	CCDS 🍦	UniProt 🖕	Flags
Kat7-201	ENSMUST0000072621.11	3324	<u>583aa</u>	Protein coding	870	Q5SVQ0 &	TSL:5 GENCODE basic
Kat7-202	ENSMUST0000092766.11	3414	<u>613aa</u>	Protein coding	870	Q5SVQ0 &	TSL:5 GENCODE basic
Kat7-203	ENSMUST00000103159.9	3248	<u>522aa</u>	Protein coding	<u>CCDS25275</u> @	<u>Q5SVQ0</u> &	TSL:1 GENCODE basic
Kat7-204	ENSMUST00000107733.9	3470	<u>581aa</u>	Protein coding	CCDS56798 @	<u>Q3TD41ക് Q5SVQ0</u> ക്	TSL:1 GENCODE basic APPRIS ALT1
Kat7-205	ENSMUST00000107734.9	3560	<u>611aa</u>	Protein coding	<u>CCDS56799</u> &	<u>Q1AJD0ക് Q5SVQ0ക്</u>	TSL:1 GENCODE basic APPRIS P4
Kat7-206	ENSMUST00000138671.1	1003	<u>150aa</u>	Protein coding	879	<u>F6S4B9</u> &	CDS 5' incomplete TSL:3
Kat7-207	ENSMUST00000143171.1	305	No protein	IncRNA	870	5	TSL:3
Kat7-208	ENSMUST00000144456.7	657	No protein	IncRNA	870	5	TSL:5
Kat7-209	ENSMUST00000146365.1	1954	No protein	IncRNA	870	5	TSL:2
Kat7-210	ENSMUST00000149356.1	438	No protein	IncRNA	870	5	TSL:3
Kat7-211	ENSMUST00000154327.1	370	No protein	IncRNA			TSL:3
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The strategy is based on the design of *Kat7-205* transcript, The transcription is shown below

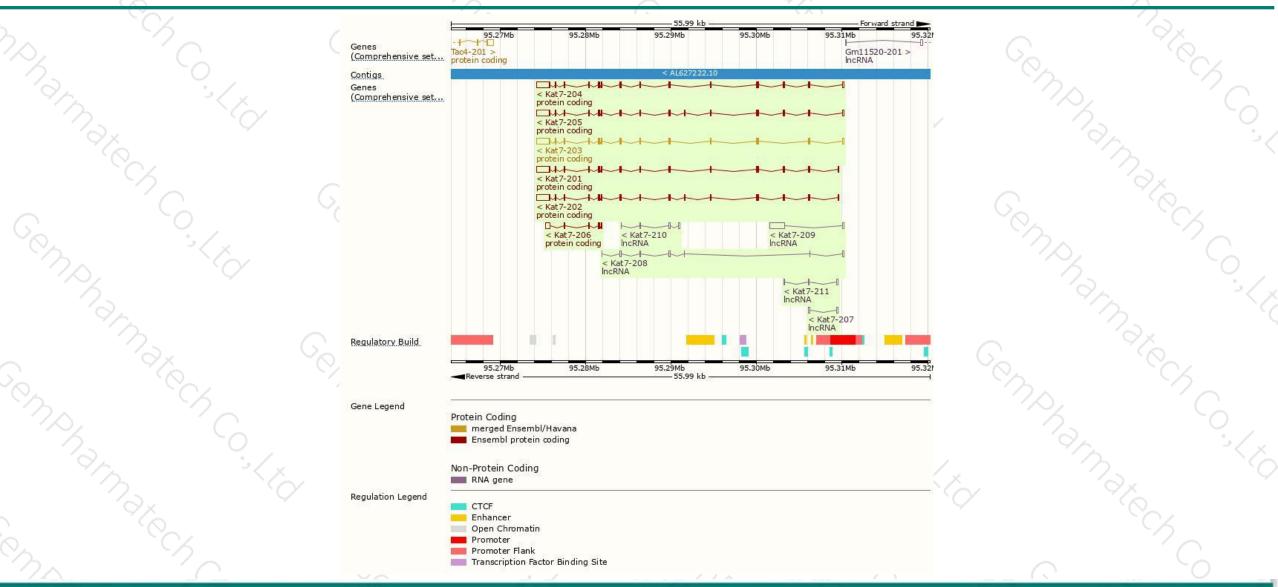
< Kat7-205 protein coding

Reverse strand -

- 35.99 kb -

Genomic location distribution





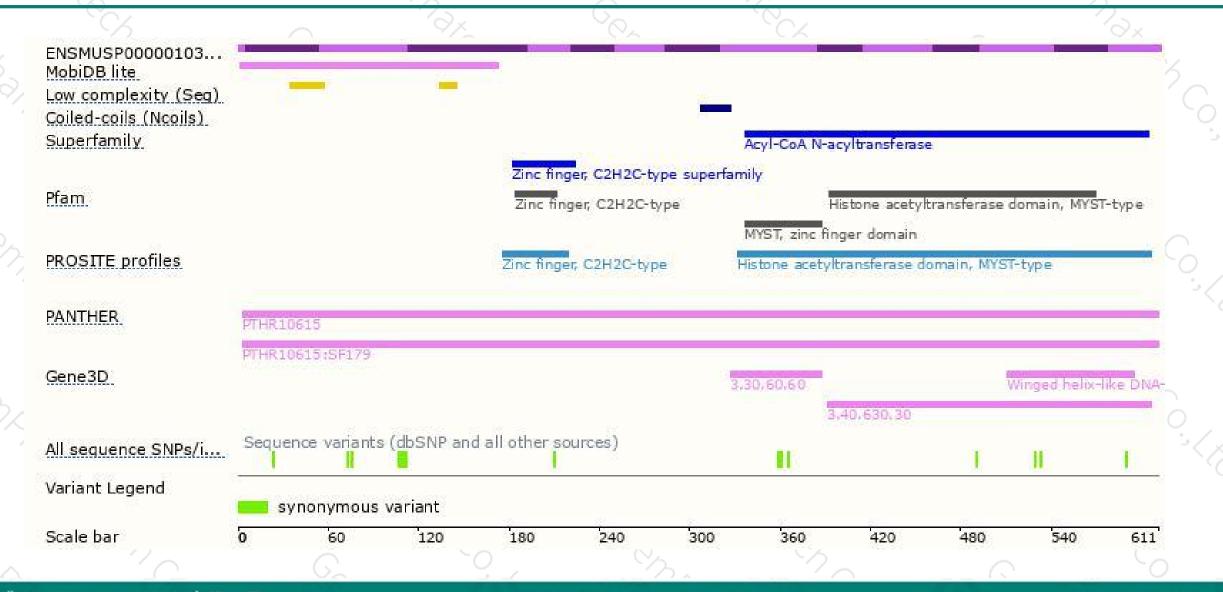
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Protein domain





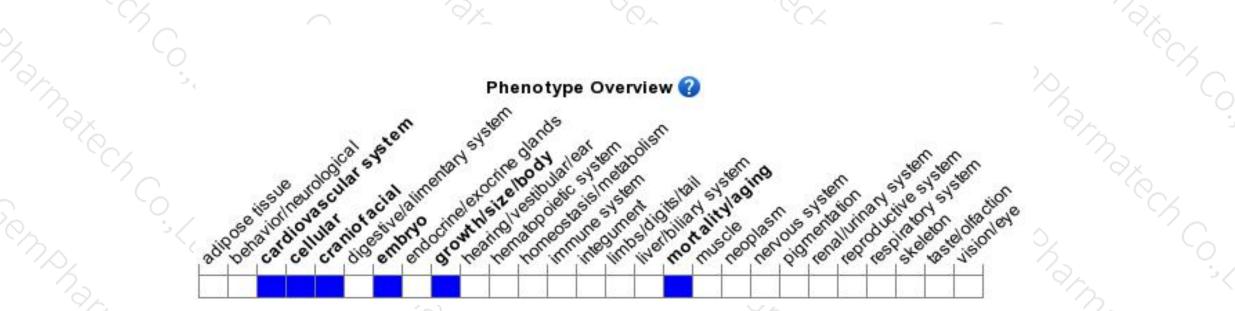
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Mouse phenotype description(MGI)





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 embryonic growth arrest, incomplete embryo turning, disorganized yolk sac vascular plexus, and increased apoptosis.



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



