

Adat2 Cas9-KO Strategy

Designer:

Reviewer:

Design Date:

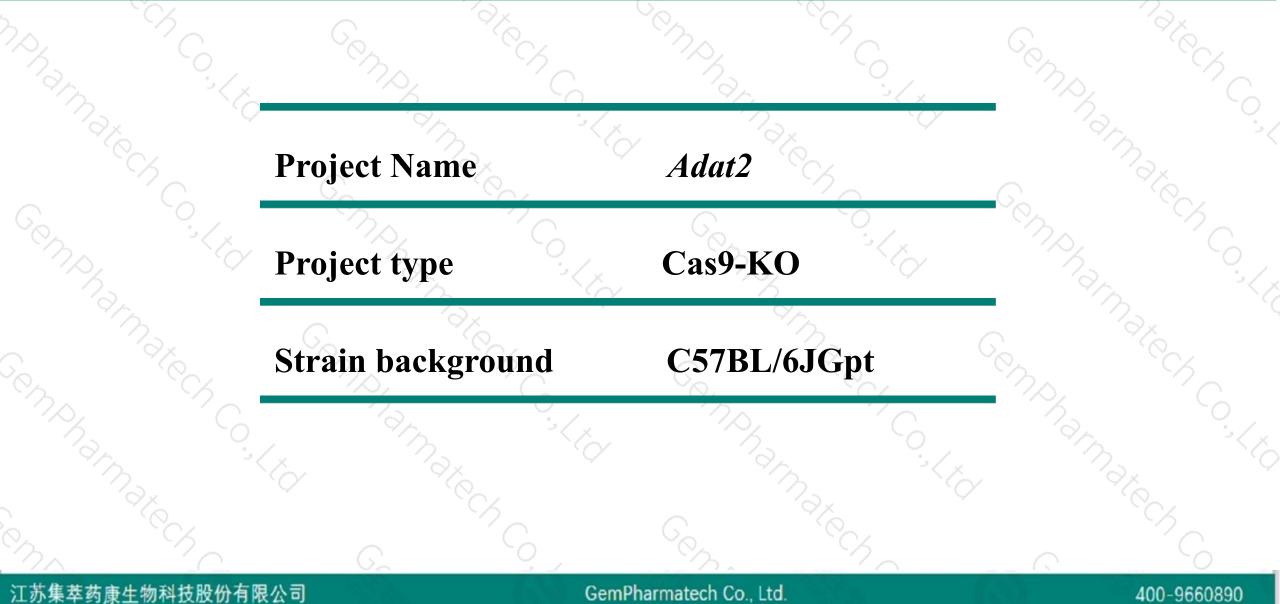
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2020-4-14

Project Overview

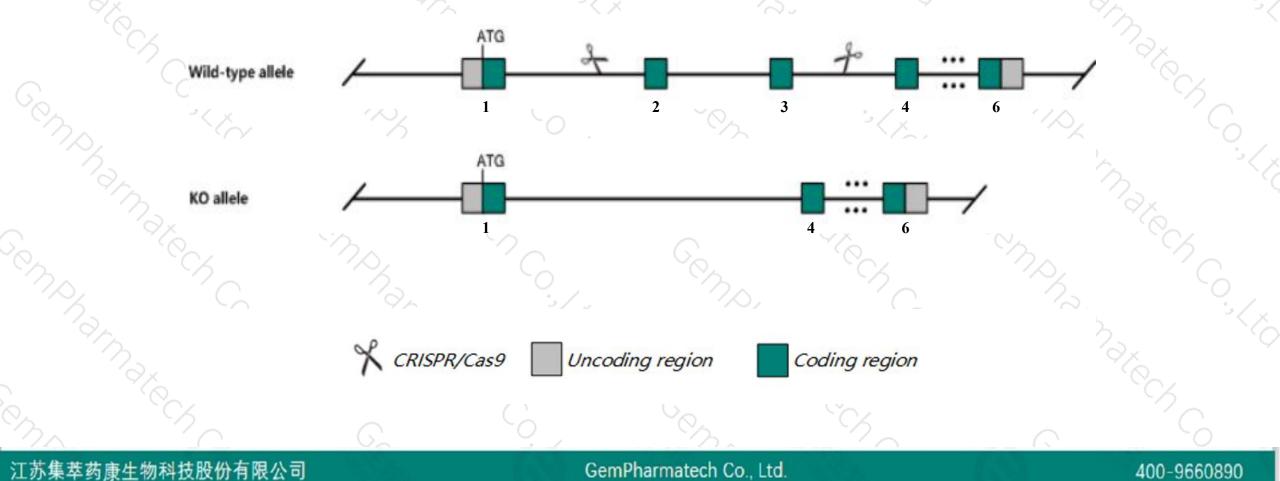




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Adat2 gene. The schematic diagram is as follows:





- The Adat2 gene has 1 transcript. According to the structure of Adat2 gene, exon2-exon3 of Adat2-201 (ENSMUST00000019944.8) transcript is recommended as the knockout region. The region contains 256bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Adat2 gene. The brief process is as follows: CRISPR/Cas9 system



The knockout region is near to the N-terminal of *Pex3* gene, this strategy may influence the regulatory function of the N-terminal of *Pex3* gene.

The Adat2 gene is located on the Chr10. 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)



\$?

Adat2 adenosine deaminase, tRNA-specific 2 [Mus musculus (house mouse)]

Gene ID: 66757, updated on 13-Mar-2020

Summary

Adat2 provided by MGI									
adenosine deaminase, tRNA-specific 2 provided by MGI									
MGI:MGI:1914007									
Ensembl:ENSMUSG0000019808									
protein coding									
VALIDATED									
Mus musculus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;									
Muroidea; Muridae; Murinae; Mus; Mus									
4933426M09Rik, Deadc1									
Ubiquitous expression in testis adult (RPKM 16.0), CNS E11.5 (RPKM 4.4) and 28 other tissues See more									
human all									

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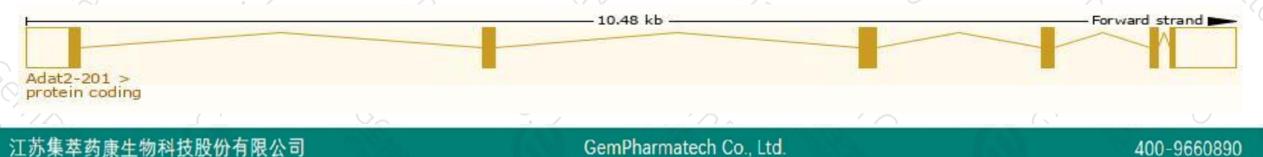
Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

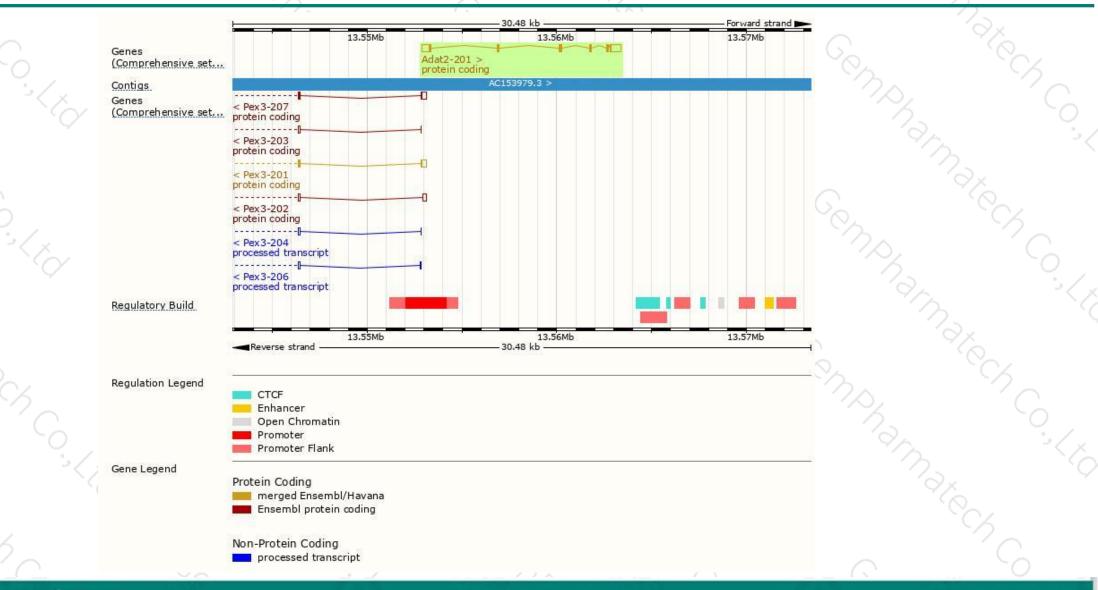
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Adat2-201	ENSMUST00000019944.8	1466	<u>191aa</u>	Protein coding	CCDS35847	<u>Q6P6J0</u>	SL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify th	e most functionally important transcript(s) of a gene. APPRIS P1
	12		$\neg \Diamond$				$\sim 13/3$ ~ 12	

The strategy is based on the design of Adat2-201 transcript, the transcription is shown below



Genomic location distribution





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Protein domain



			Κ						
ENSMUSP00000019 Superfamily	Cytidii	ne deaminase-lik	ke						•
Pfam.	Cytidir	ne and deoxycyt	dylate deam	inase domain					
PROSITE profiles	Cytidin	e and deoxycyt	idylate deami	nase domain					
PROSITE patterns				APOBEC/CMP	leaminase, zin	c-binding			
PANTHER	PTHR1	1079							
	PTHR1	1079:SF149							-
HAMAP	tRI	VA-specific aden	iosine deamin	ase					
Gene3D	3.40.140.1	0							115
CDD	cd	01285							
All sequence SNPs/i	Sequence variants	(dbSNP and a	all other sou	rces)	an in the second		2		wee
/ariant Legend	-								
	missense var								
Scale bar	0 20	40	60	80	100	120	140	160	191
									50
10						~ 2			

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



