

# Ache Cas9-KO Strategy

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**Reviewer: Xueting Zhang** 

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# **Project Overview**



**Project Name** 

Ache

**Project type** 

Cas9-KO

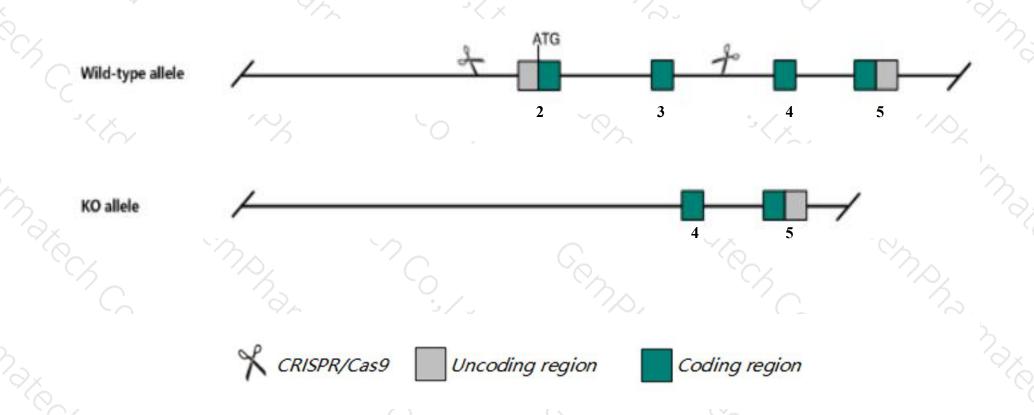
Strain background

C57BL/6JGpt

# **Knockout strategy**



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



### **Technical routes**



- > The *Ache* gene has 9 transcripts. According to the structure of *Ache* gene, exon2-exon3 of *Ache-*201(ENSMUST00000024099.10) transcript is recommended as the knockout region. The region contains start codon
  ATG.Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ache* 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.

### **Notice**



- > According to the existing MGI data, homozygous mutants show retarded postnatal development, tremors, impaired righting response, delayed maturation of external ear, failure of eyelids to open, and die by 3-wk. of age. Mutants are highly sensitive to butyrylcholinesterase inhibitor toxicity.
- The KO region contains functional region of the *Ufsp1,Mir8116* and *Gm42456* gene.Knockout the region may affect the function of *Ufsp1,Mir8116* and *Gm42456* gene.
- > The *Ache* gene is located on the Chr5. 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)



#### Ache acetylcholinesterase [Mus musculus (house mouse)]

Gene ID: 11423, updated on 13-Mar-2020

#### Summary

↑ ?

Official Symbol Ache provided by MGI

Official Full Name acetylcholinesterase provided by MGI

Primary source MGI:MGI:87876

See related Ensembl: ENSMUSG00000023328

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

Expression Broad expression in cerebellum adult (RPKM 25.6), thymus adult (RPKM 23.5) and 19 other tissuesSee more

Orthologs human all

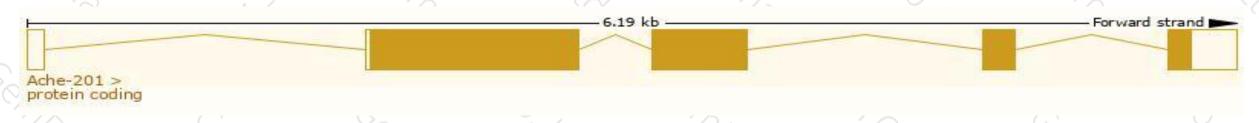
# Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

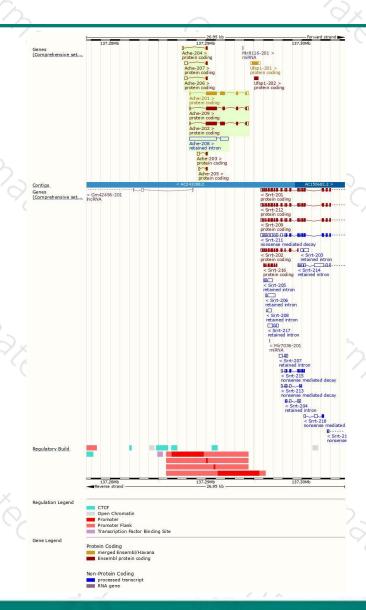
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ache-201	ENSMUST00000024099.10	2186	614aa	Protein coding	CCDS19763	P21836 Q543Z1	TSL:1 GENCODE basic APPRIS P1
Ache-202	ENSMUST00000085934.3	2176	614aa	Protein coding	CCDS19763	P21836 Q543Z1	TSL:1 GENCODE basic APPRIS P1
Ache-209	ENSMUST00000196208.4	1911	<u>526aa</u>	Protein coding	10-2	A0A0G2JDM6	TSL:5 GENCODE basic
Ache-207	ENSMUST00000141123.7	438	40aa	Protein coding		<u>D3Z064</u>	CDS 3' incomplete TSL:1
Ache-206	ENSMUST00000138591.7	409	<u>40aa</u>	Protein coding	100	<u>D3Z064</u>	CDS 3' incomplete TSL:1
Ache-203	ENSMUST00000125195.7	360	<u>40aa</u>	Protein coding		<u>D3Z064</u>	CDS 3' incomplete TSL:1
Ache-204	ENSMUST00000132191.7	262	40aa	Protein coding	323	D3Z064	CDS 3' incomplete TSL:1
Ache-205	ENSMUST00000137126.1	254	40aa	Protein coding		<u>D3Z064</u>	CDS 3' incomplete TSL:1
Ache-208	ENSMUST00000150983.1	3687	No protein	Retained intron	1.0	N-1	TSL:1
		7 7 7			V 2		

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



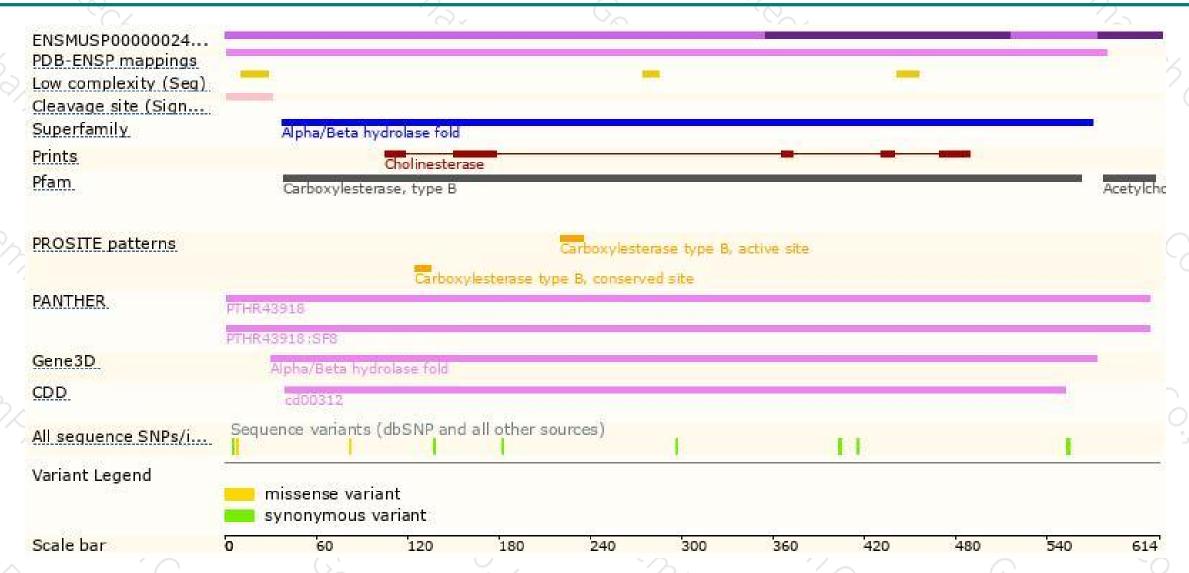
### Genomic location distribution





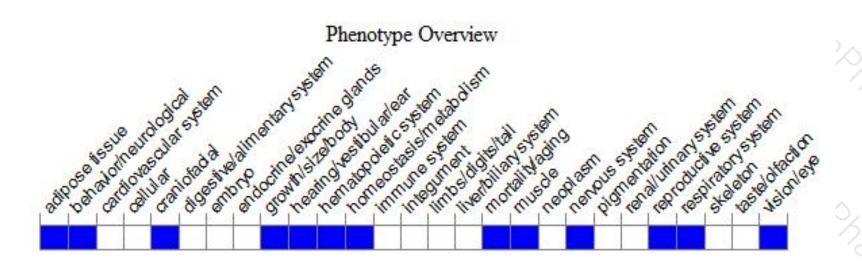
### Protein domain





### Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,homozygous mutants show retarded postnatal development, tremors, impaired righting response, delayed maturation of external ear, failure of eyelids to open, and die by 3-wk. of age. Mutants are highly sensitive to butyrylcholinesterase inhibitor toxicity.



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





