

Paics Cas9-CKO Strategy

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Design Date: 2023-10-07

Overview

Target Gene Name

• Paics

Project Type

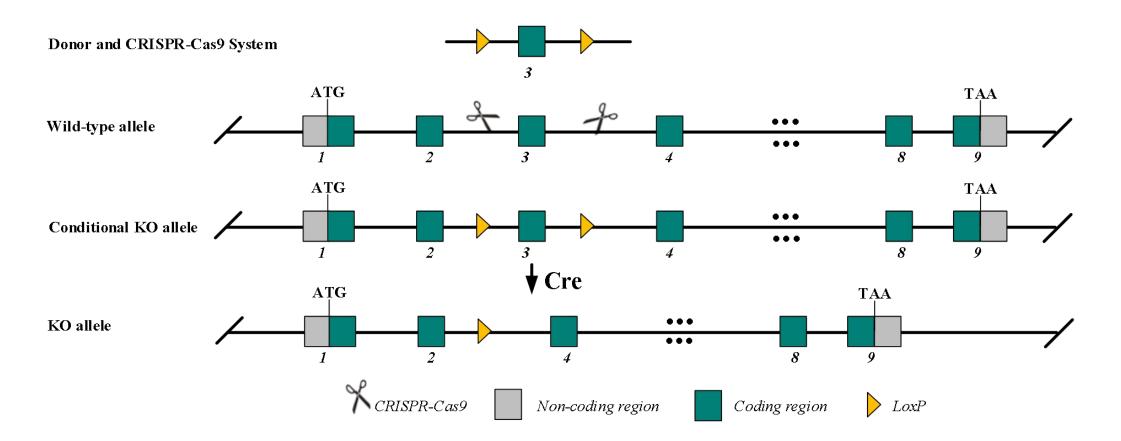
• Cas9-CKO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Paics gene.

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Technical Information

- The *Paics* gene has 7 transcripts. According to the structure of *Paics* gene, exon3 of *Paics*-201 (ENSMUST00000031160.16) transcript is recommended as the knockout region. The region contains 179bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Paics* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.



Gene Information

Paics phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoibosylaminoimidazole, succinocarboxamide synthetase [*Mus musculus* (house mouse)]

Gene ID: 67054, updated on 7-Sep-2023

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Summary

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Official Symbol	Paics provided by MGI						
Official Full Name	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase provided by MGI						
Primary source	MGI:MGI:1914304						
See related	Ensembl:ENSMUSG00000029247 AllianceGenome:MGI:1914304						
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	AIRC; PAIS; ADE2H1; 2610511109Rik						
Summary Expression	Predicted to enable identical protein binding activity; phosphoribosylaminoimidazole carboxylase activity; and phosphoribosylaminoimidazolesuccinocarboxamide synthase activity. Predicted to be involved in purine ribonucleoside monophosphate biosynthetic process. Predicted to act upstream of or within purine nucleotide biosynthetic process. Predicted to be located in cytoplasm. Predicted to be active in cytosol. Is expressed in several structures, including alimentary system; genitourinary system; nervous system; respiratory system; and sensory organ. Human ortholog(s) of this gene implicated in schizophrenia. Orthologous to human PAICS (phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinocarboxamide synthase). [provided by Alliance of Genome Resources, Apr 2022] Ubiquitous expression in CNS E11.5 (RPKM 67.7), placenta adult (RPKM 55.6) and 26 other tissues <u>See more</u>						
NEW	Try the new Gene table Try the new Transcript table						

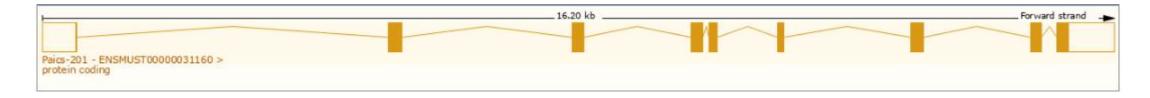
Source: https://www.ncbi.nlm.nih.gov/gene/67054

Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

Transcript ID	Name 💧	bp 🛊	Protein 💧	Biotype	CCDS 🛊	UniProt Match	Flags
ENSMUST0000031160.16	Paics-201	2482	<u>425aa</u>	Protein coding	CCDS19367	<u>Q9DCL9</u> &	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000120912.8	Paics-203	2345	<u>425aa</u>	Protein coding	CCDS19367@	<u>Q9DCL9</u> &	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000117536.8	Paics-202	1862	<u>425aa</u>	Protein coding	<u>CCDS19367</u> 교	<u>Q9DCL9</u> &	GENCODE basic APPRIS P1 TSL:5
ENSMUST00000141687.2	Paics-205	422	<u>83aa</u>	Protein coding		D3Z6P1@	TSL:5 CDS 3' incomplete
ENSMUST00000153648.2	Paics-206	886	<u>103aa</u>	Nonsense mediated decay		D6RCU8	TSL:5
ENSMUST00000140051.2	Paics-204	575	No protein	Retained intron		-	TSL:5
ENSMUST00000154688.2	Paics-207	443	No protein	Retained intron			TSL:2

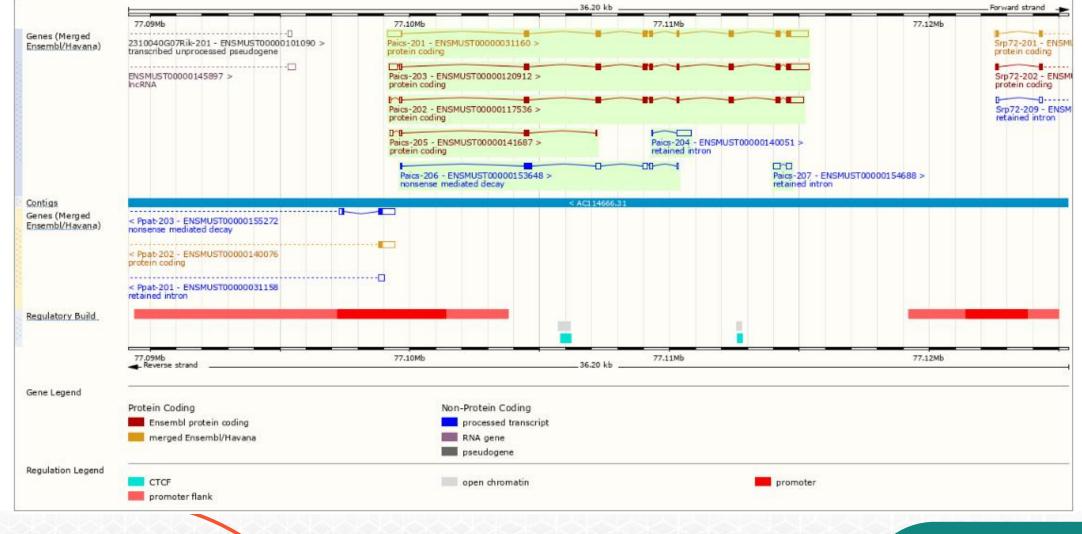
The strategy is based on the design of *Paics*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



Genomic Information



Source: : https://www.ensembl.org

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Protein Information

ENSMUSP0000031160 AFDB-ENSP mappings		
Superfamily	SSF56104	SSF52255
SMART		Pure domain
Pfam	SAICAR synthetase/ADE2, N-terminal	Purte domain
PROSITE patterns	SAICAR synthetase, conserved site SAICAR synthetase, co	onserved site
PANTHER	PTRR43599	
HAMAP	SAICAR synthetase/ADE2, N-terminal	Class II Purb
Gene3D	3.30.200.20	3.40.50.1970
CDD	Cd01416	
All sequence SNPs/	Sequence variants (EVA and all other sources)	a nagrani arara na ningara a
		a manana ana ana amin'ny fiana amin'ny fiana amin'ny fiana amin'ny fiana amin'ny fiana amin'ny fiana amin'ny fi
Variant Legend		
		neshift variant
	inframe insertion miss	sense variant
Scale bar	o 40 80 120 160 200	240 280 320 360 425

Source: : https://www.ensembl.org

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Important Information

- The impact on the *Paics*-205 transcript is unknown.
- The knockout region is about 6.7 kb away from the 5' of *Ppat*, which may affect the regulation of this gene.
- *Paics* is located on Chr5. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

