

Katnal2 Cas9-KO Strategy

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Overview

Target Gene Name

• Katnal2

Project Type

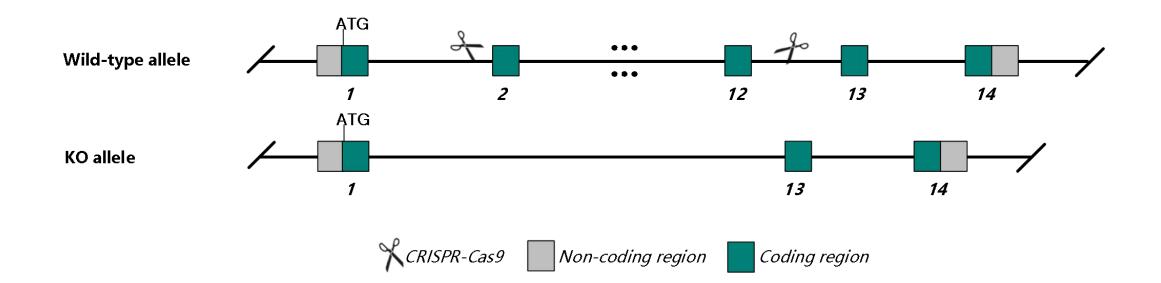
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Katnal2 gene.



Technical Information

- The *Katnal2* gene has 11 transcripts. According to the structure of *Katnal2* gene, exon2-exon12 of *Katnal2*-201 (ENSMUST0000026486.13) transcript is recommended as the knockout region. The region contains 1052bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Katnal2* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

Gene Information

Katnal2 katanin p60 subunit A-like 2 [Mus musculus (house mouse)]

Gene ID: 71206, updated on 26-Sep-2022

. Summary ☆ ? Official Symbol Katnal2 provided by MGI Official Full Name katanin p60 subunit A-like 2 provided by MGI Primary source MGI:MGI:1924234 See related Ensembl: ENSMUSG0000025420 AllianceGenome: MGI: 1924234 Gene type protein coding RefSeg status VALIDATED Organism Mus musculus Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Muriae; Mus; Mus Also known as 3110023G01Rik; 4933439B08Rik Summary Predicted to enable several functions, including ATP binding activity; ATP hydrolysis activity; and microtubule-severing ATPase activity. Predicted to be located in cytoplasm; microtubule; and spindle pole. Orthologous to human KATNAL2 (katanin catalytic subunit A1 like 2). [provided by Alliance of Genome Resources, Apr 2022] Expression Biased expression in testis adult (RPKM 8.9), CNS E11.5 (RPKM 2.5) and 5 other tissues See more Orthologs human all NEW Try the new Gene table Try the new Transcript table -Genomic context < ? See Katnal2 in Genome Data Viewer Location: 18: 18 E3

Exon count: 18

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

L Download Datasets



Transcript Information

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

Transcript ID	Name 🖕	bp 🖕	Protein 💧	Biotype .	CCDS 🖕	UniProt Match	Flags 🕴
ENSMUST00000126153.8	Katnal2-205	1942	<u>539aa</u>	Protein coding		Q9D3R6-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000137498.8	Katnal2-208	1824	<u>495aa</u>	Protein coding		D3Z4J2	GENCODE basic TSL:5
ENSMUST0000026486.13	Katnal2-201	1674	<u>409aa</u>	Protein coding	CCDS37865	Q9D3R6-3 @	GENCODE basic TSL:1
ENSMUST00000154665.2	Katnal2-211	1515	<u>217aa</u>	Protein coding		Q9D3R6-2	GENCODE basic TSL:1
ENSMUST00000137354.8	Katnal2-207	1482	<u>277aa</u>	Protein coding		D3Z0U5 P	GENCODE basic TSL:5
ENSMUST00000123650.2	Katnal2-203	638	<u>85aa</u>	Protein coding		<u>D3Z087</u> @	GENCODE basic TSL:1
ENSMUST00000122984.8	Katnal2-202	2039	<u>39aa</u>	Nonsense mediated decay		D6R139	TSL:5
ENSMUST00000135029.8	Katnal2-206	2003	<u>372aa</u>	Nonsense mediated decay		D6RGM7 团	TSL:2
ENSMUST00000154053.8	Katnal2-210	792	No protein	Protein coding CDS not defined		ie.	TSL:3
ENSMUST00000125744.8	Katnal2-204	768	No protein	Protein coding CDS not defined		. 	TSL:5
ENSMUST00000138336.2	Katnal2-209	668	No protein	Retained intron			TSL:2

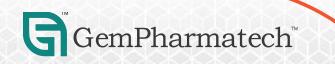
The strategy is based on the design of *Katnal2*-201 transcript, the transcription is shown below:



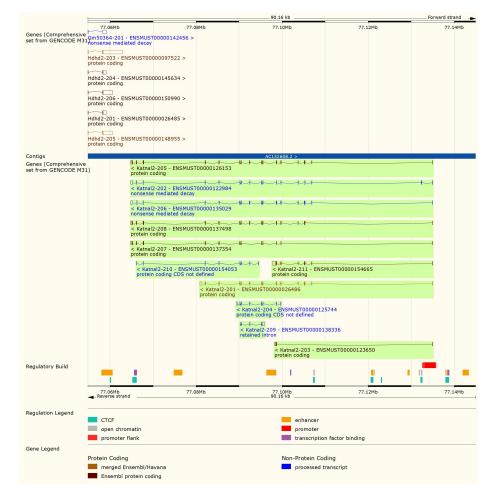
Reverse stran

__ 54.10 kb

Source: https://www.ensembl.org



Genomic Information



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

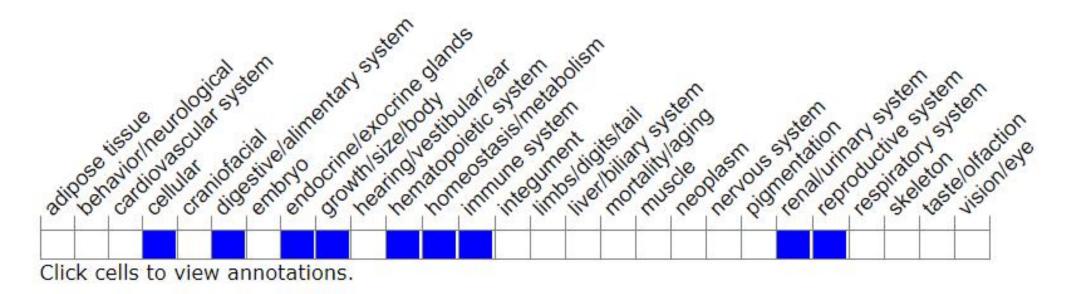
Protein Information

ENSMUSP0000002648 MobiDB lite Superfamily	36.7							aining nucleo	oside triphos	sphate hy	drolase					
SMART	LIS1 homology motif	P-loop containing nucleoside triphosphate hydrolase AAA+ ATPase domain														
Pfam	LIS1 homology motif		ATPase, AAA-type, core									-				
PROSITE profiles	LIS1 homology motif															
PANTHER	PTHR23074:5F78 PTHR23074															
НАМАР	Katanin p60 ATPase-containing subunit A-like 2															
Gene3D							P-loop containing	nucleoside ti	riphosphate	hydrolas	e					
CDD							c	d00009								_
All sequence SNPs/	Sequence variants (dbSNP and all other source	es)	с. с. I	0.0	1.1			۰.	1	1	•	1	•1	ind i	ŧ.	1
Variant Legend																
	stop gained			frameshift variant			stop lost									
	inframe insertion		missense variant				synonymous variant									
Scale bar	0 40	80	120	160		200	240		280		320			360		409

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

Mouse Phenotype Information (MGI)



• Homozygous mutations in this gene result in male sterility associated with multiple anomalies in spermatogenesis, including defects in sperm tail growth, sperm head shaping, acrosome attachment, and sperm release. Males homozygous for a null allele are sterile and show oligoasthenoteratozoospermia.

Source: https://www.informatics.jax.org

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Important Information

- According to the existing MGI data, homozygous null mutations in this gene result in male sterilityassociated with defects in several aspects of spermatogenesis, including abnormalities in the initiation of spermtail growth from the basal body, sperm head shaping, manchette movement and dissolution, acrosome attachmentto the nucleus, and sperm release via spermiation.
- According to breeding data, homozygotes with *Katnal2* gene knockout have lethal phenotype.
- *Katnal2* is located on Chr18. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

