

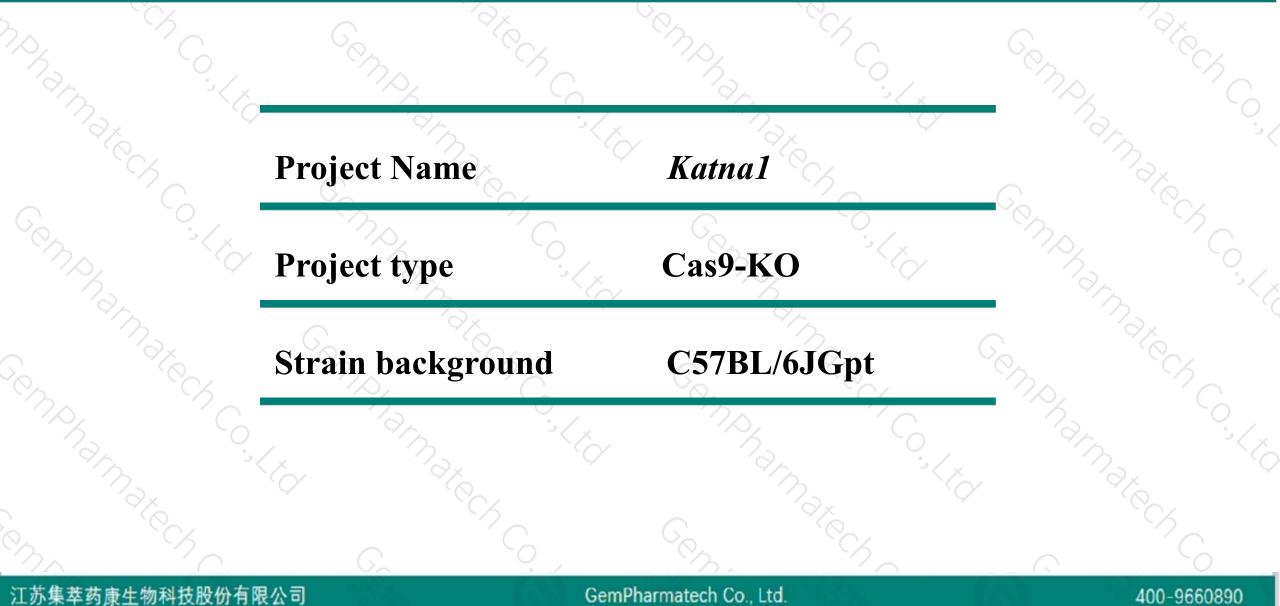
Katnal Cas9-KO Strategy

Designer: Reviewer: Design Date: Ruirui Zhang Huimin Su

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Project Overview

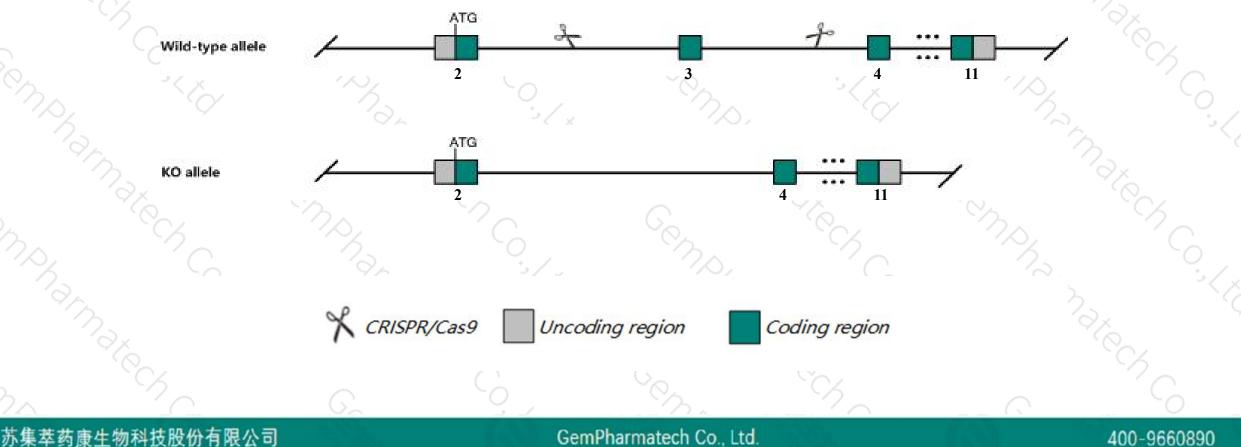




Knockout strategy



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



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- The Katnal gene has 6 transcripts. According to the structure of Katnal gene, exon3 of Katnal-202 (ENSMUST00000165806.7) transcript is recommended as the knockout region. The region contains 158bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Katnal gene. The brief process is as follows: CRISPR/Cas9 system

- The Katnal 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.

Notice

Gene information (NCBI)



Katna1 katanin p60 (ATPase-containing) subunit A1 [Mus musculus (house mouse)]

Gene ID: 23924, updated on 12-Aug-2019

Summary

Official SymbolKatna1 provided by MGIOfficial Full Namekatanin p60 (ATPase-containing) subunit A1 provided by MGIPrimary sourceMGI:MGI:1344353See relatedEnsembl:ENSMUSG0000019794Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
Murinae; Mus; MusExpressionUbiquitous expression in CNS E11.5 (RPKM 6.5), placenta adult (RPKM 5.6) and 27 other tissues See more

Orthologs human all

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Transcript information (Ensembl)



The gene has 6 transcripts, all transcripts are shown below:

Name 🍦	Transcript ID	bp	Protein 🖕 No protein	Biotype 🔺 Retained intron	CCDS 🖕	UniProt 🛊	Flags (TSL:2		
Katna1-203									
Katna1-202	ENSMUST00000165806.7	1775	<u>493aa</u>	Protein coding	<u>CCDS23689</u> @	E9PZI6	TSL:1 GENCODE basic APPRIS P2		
Katna1-201	ENSMUST0000019929.12	1774	<u>491aa</u>	Protein coding	1	E9QKG2@	TSL:1 GENCODE basic APPRIS ALT1		
Katna1-205	ENSMUST00000173511.1	488	<u>54aa</u>	Protein coding		G3UYX0函	CDS 5' incomplete TSL:5		
Katna1-206	ENSMUST00000174007.1	462	<u>66aa</u>	Protein coding	17	<u>G3UWK1</u> @	CDS 5' incomplete TSL:5		
Katna1-204	ENSMUST00000173400.7	683	<u>130aa</u>	Nonsense mediated decay		<u>G3UX83</u> 🖌	TSL:5		

The strategy is based on the design of *Katna1-202* transcript, the transcription is shown below:

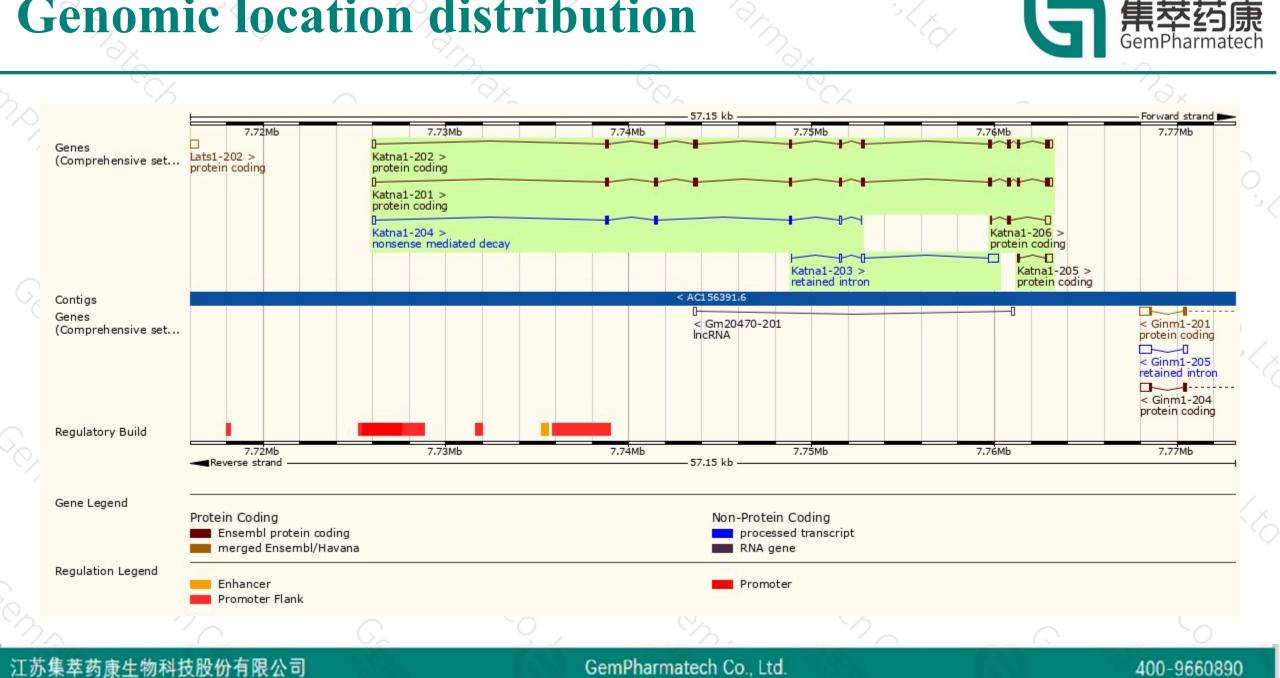
Katna1-202 > protein coding

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37.15 kb

Genomic location distribution



Protein domain



'^					7.Sz			20	°°C	
	ENSMUSP00000132 PDB-ENSP mappings MobiDB lite Low complexity (Seg) Superfamily	MIT domain superfamily		P-loop contai	ning nucleoside triphosphate hy	drolase	_			0.3
	SMART				AAA+ ATPase domain					
	Pfam				ATPase, AAA-type, core				Vps4 oligomerisation	le '
S)	PROSITE patterns PANTHER	PTHR23074					ATPase, AAA-type, co	AAA ATPase, AAA+ I onserved site	id domain.	•3
	НАМАР	PTHR23074;SF71								
	Gene3D	Katanin p60 subunit A1 1.20.58.280		3.40.50.300						
	CDD				cd00009		1,10.8	<i>.</i> 60		
	All sequence SNPs/i	Sequence variants (dbSNP and all othe	r sources)		1	0.1.11	1	E E E E E E	0.1	_
	Variant Legend	start lost synonymous variant		missense variant		spl	ice region variant			
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S)		10			\sim	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~				
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



