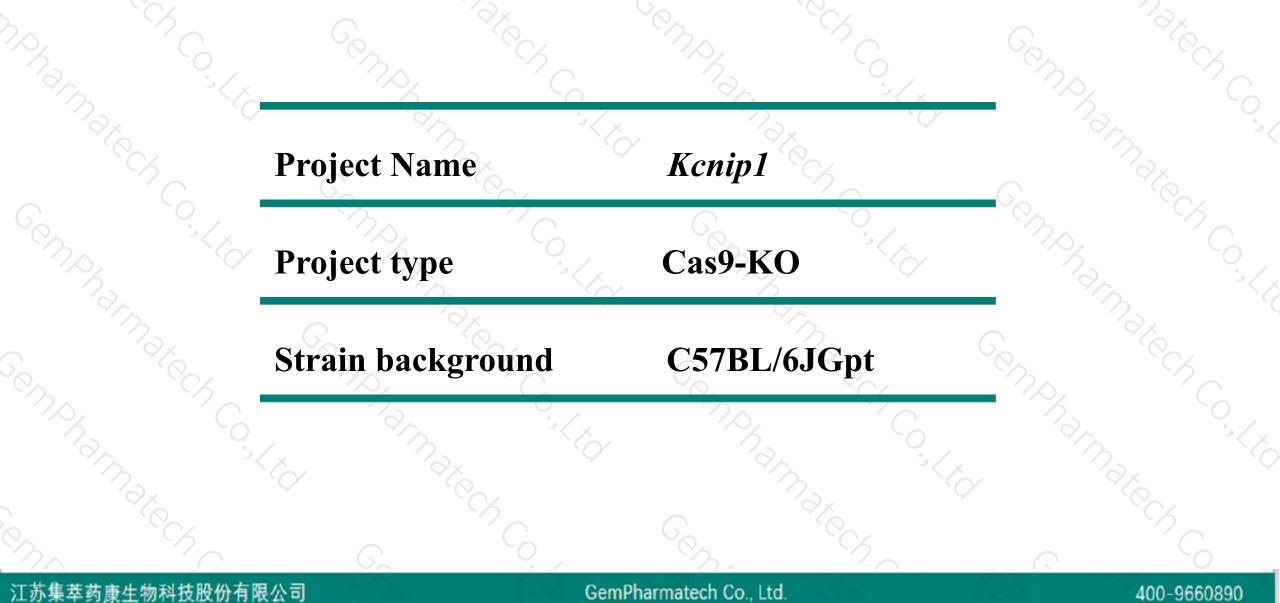


Kcnip1 Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-2-18

Project Overview

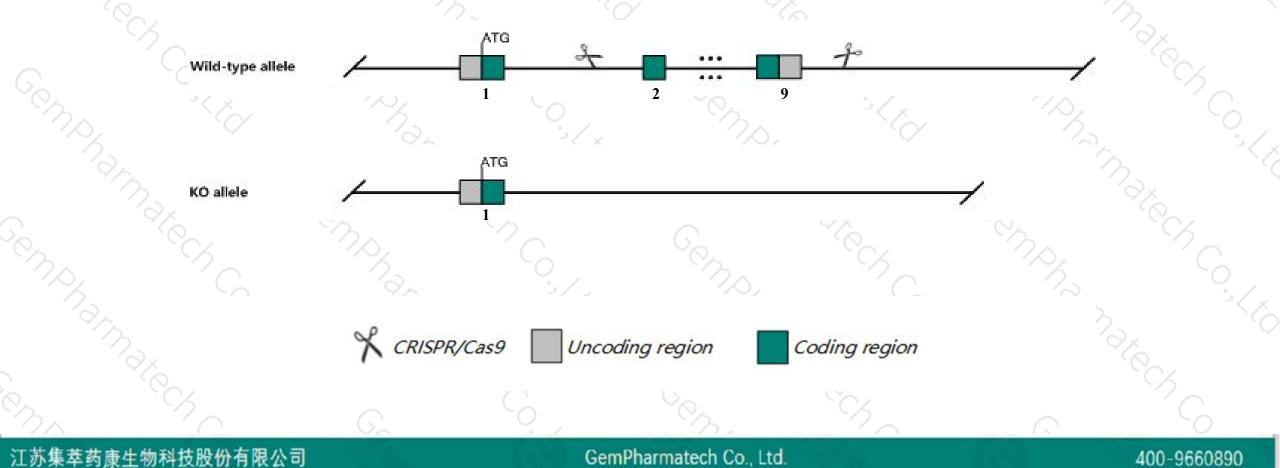




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Kcnip1 gene. The schematic diagram is as follows:





- The Kcnip1 gene has 6 transcripts. According to the structure of Kcnip1 gene, exon3-exon8 of Kcnip1-203 (ENSMUST00000109340.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Kcnip1 gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increase susceptibility to pentylenetetrazole-induced seizures.
- The Kcnip1 gene is located on the Chr11. 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)



\$?

Kcnip1 Kv channel-interacting protein 1 [Mus musculus (house mouse)]

Gene ID: 70357, updated on 5-Mar-2019

Summary

Official Symbol	Kcnip1 provided by MGI
Official Full Name	Kv channel-interacting protein 1 provided by MGI
Primary source	MGI:MGI:1917607
See related	Ensembl:ENSMUSG0000053519
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	KCHIP1, Kchip1.2
Expression	Biased expression in cerebellum adult (RPKM 12.1), CNS E18 (RPKM 11.7) and 8 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



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

Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000101368.8	2322	<u>188aa</u>	Protein coding	CCDS70160	<u>Q9JJ57</u>	TSL:2 GENCODE basic
ENSMUST00000109340.8	1840	<u>227aa</u>	Protein coding	CCDS56766	<u>Q9JJ57</u>	TSL:1 GENCODE basic APPRIS ALT1
ENSMUST0000065970.5	1749	<u>216aa</u>	Protein coding	CCDS24537	Q3YAB6 Q9JJ57	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000238436.1	699	<u>232aa</u>	Protein coding	in the second	20	GENCODE basic
ENSMUST00000154760.1	4095	No protein	IncRNA	65	7.0	TSL:1
ENSMUST00000135034.1	2475	No protein	IncRNA	. e	-	TSL:1
	ENSMUST00000101368.8 ENSMUST00000109340.8 ENSMUST0000065970.5 ENSMUST00000238436.1 ENSMUST00000154760.1	ENSMUST00000101368.8 2322 ENSMUST00000109340.8 1840 ENSMUST0000065970.5 1749 ENSMUST00000238436.1 699 ENSMUST00000154760.1 4095	ENSMUST00000101368.8 2322 188aa ENSMUST00000109340.8 1840 227aa ENSMUST0000065970.5 1749 216aa ENSMUST00000238436.1 699 232aa ENSMUST00000154760.1 4095 No protein	ENSMUST00000101368.82322188aaProtein codingENSMUST00000109340.81840227aaProtein codingENSMUST0000065970.51749216aaProtein codingENSMUST00000238436.1699232aaProtein codingENSMUST00000154760.14095No proteinIncRNA	ENSMUST00000101368.82322188aaProtein codingCCDS70160ENSMUST00000109340.81840227aaProtein codingCCDS56766ENSMUST0000065970.51749216aaProtein codingCCDS24537ENSMUST00000238436.1699232aaProtein coding-ENSMUST00000154760.14095No proteinIncRNA-	ENSMUST0000101368.82322188aaProtein codingCCDS70160Q9JJ57ENSMUST00000109340.81840227aaProtein codingCCDS56766Q9JJ57ENSMUST0000065970.51749216aaProtein codingCCDS24537Q3YAB6 Q9JJ57ENSMUST0000238436.1699232aaProtein codingCENSMUST0000154760.14095No proteinIncRNA

The strategy is based on the design of Kcnip1-203 transcript, The transcription is shown below

< Kcnip1-203
protein coding
</pre>

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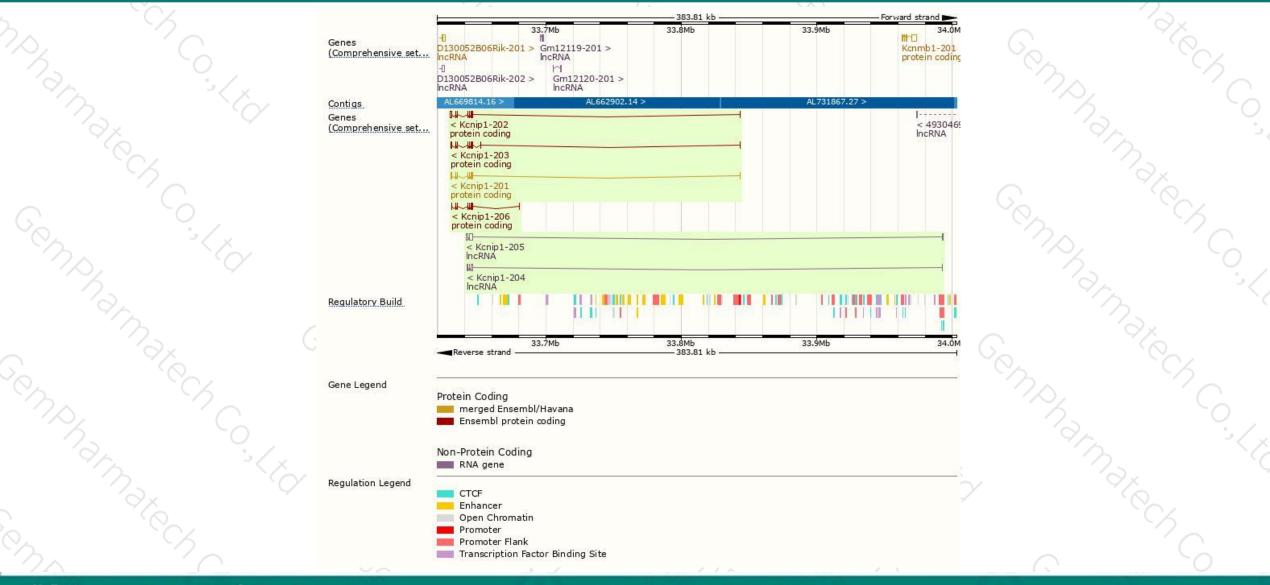
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Genomic location distribution



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Protein domain



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	Prints		PR004	50						-			
	<u>Pfam</u>				PF13833			EF-hand dom	ain				
	PROSITE profiles PROSITE patterns					EF-hand dom	nain	EF-H	and 1, calcium-bin	ding site		· Xo	
	PANTHER	PTHR23055:SF82											
	Gene3D	Recoverin family	-										
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	CDD	-				EF-hand d	domain						
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	Variant Legend	synonymous va	riant									5	
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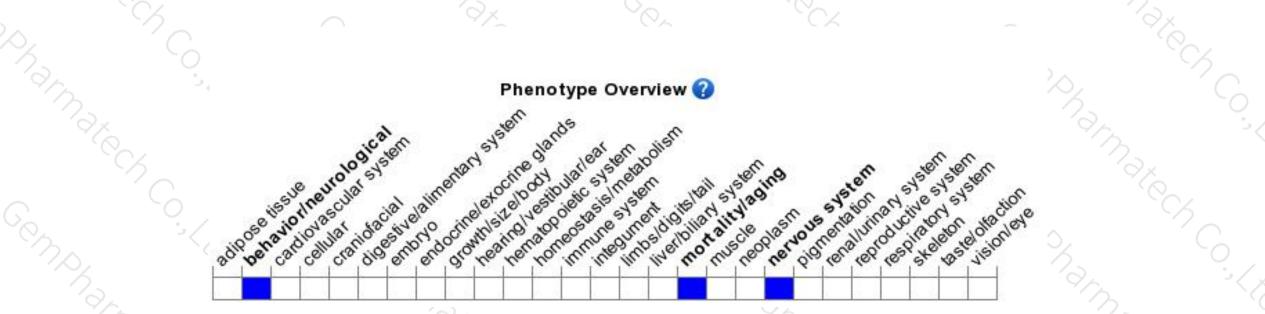
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Mouse phenotype description(MGI)





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, Mice homozygous for a knock-out allele exhibit increase susceptibility to pentylenetetrazole-induced seizures.



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



