

# Hnrnpal Cas9-KO Strategy

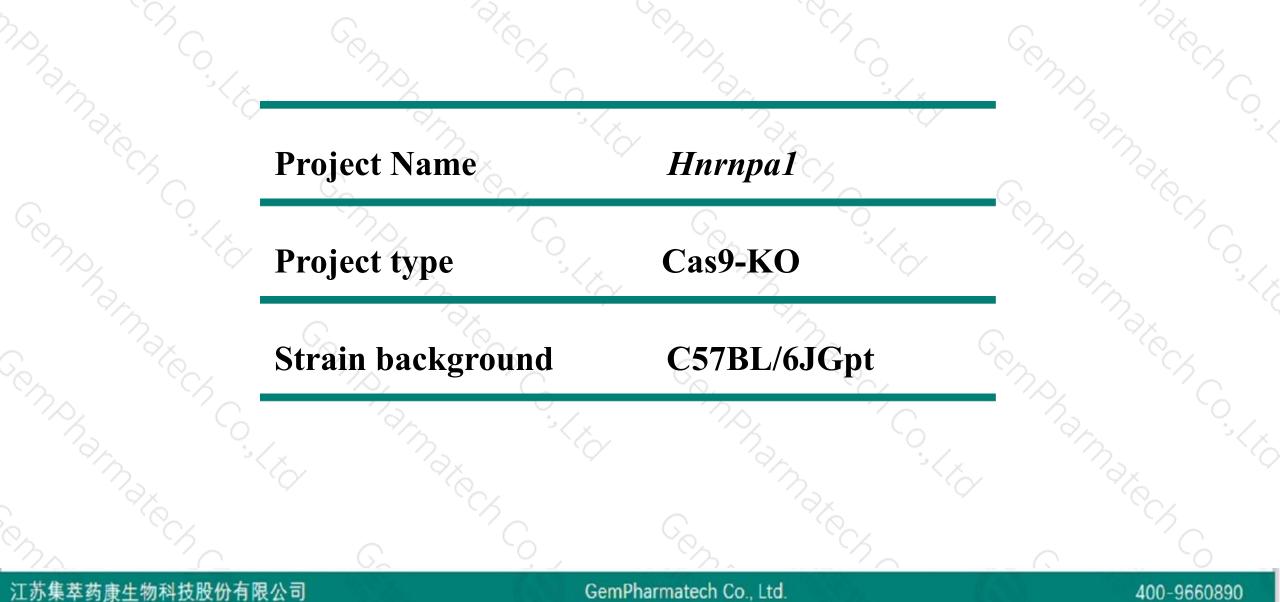
Designer: Reviewer:

**Design Date:** 

Huan Wang Huan Fan 2020-4-28

### **Project Overview**

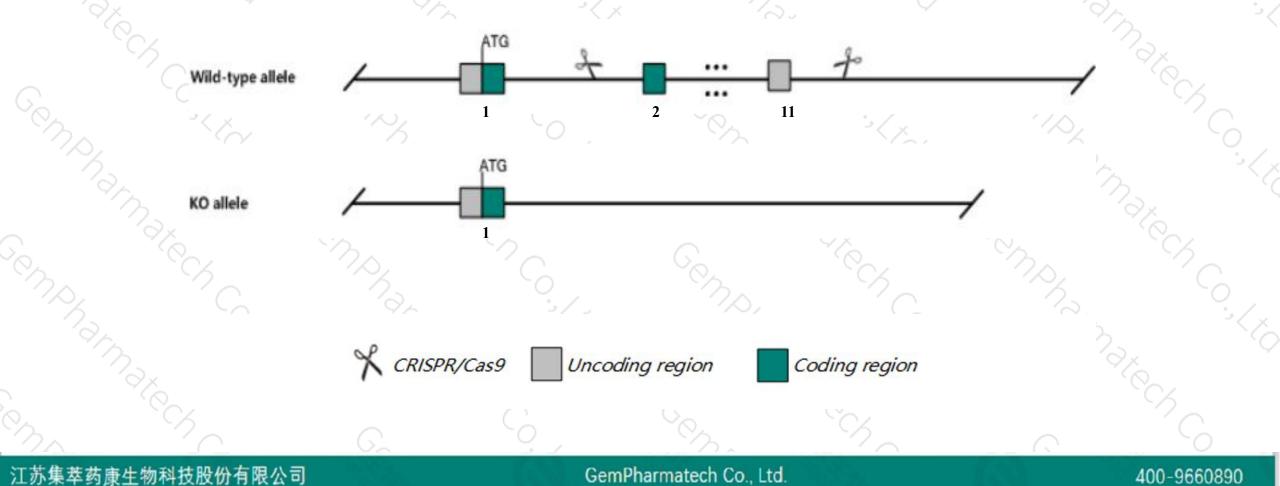




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the *Hnrnpa1* gene. The schematic diagram is as follows:





- The Hnrnpal gene has 5 transcripts. According to the structure of Hnrnpal gene, exon2-exon11 of Hnrnpal-201 (ENSMUST00000036004.15) transcript is recommended as the knockout region. The region contains all 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 *Hnrnpa1* gene. The brief process is as follows: CRISPR/Cas9 syst



- According to the existing MGI data,mice homozygous for a knock-out allele exhibit prenatal and neonatal lethality, dilated cardiacmyopathy, and hypoplastic tongue and intercostal muscles. mice heterozygous for a knock-out allele exhibit altered cardiac signaling, increased heart rate and increased systemic arterial systolic blood pressure.
- > The KO region is about 0.7kb away from the Cbx5 gene.Knockout the region may affect the function of Cbx5 gene.
- The Hnrnpal gene is located on the Chr15. 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)



☆ ?

Hnrnpa1 heterogeneous nuclear ribonucleoprotein A1 [Mus musculus (house mouse)]

Gene ID: 15382, updated on 13-Mar-2020

#### - Summary

 Official Symbol
 Hnrnpa1 provided by MGI

 Official Full Name
 heterogeneous nuclear ribonucleoprotein A1 provided byMGI

 Primary source
 MGI:MGI:104820

 See related
 Ensembi:ENSMUSG0000046434

 Gene type
 protein coding

 RefSeq status
 VALIDATED

 Organism
 Mus musculus

 Lineage
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Murinae; Mus; Mus

 Also known as
 HDP-1, Hdp, Hnrpa1, hnRNP A1, hnrnp-A1

 Expression
 Biased expression in CNS E11.5 (RPKM 643.9), CNS E14 (RPKM 307.8) and 11 other tissues<u>See more</u>

 Orthologs
 human all

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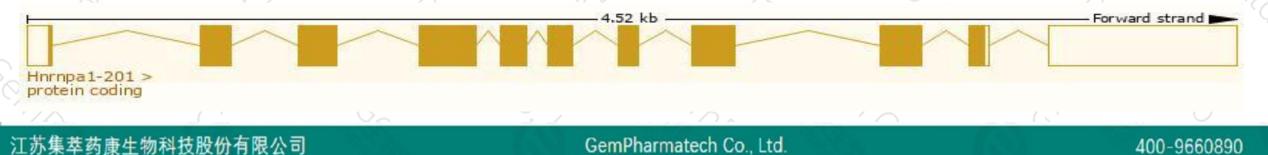
### **Transcript information (Ensembl)**



### The gene has 5 transcripts, all transcripts are shown below:

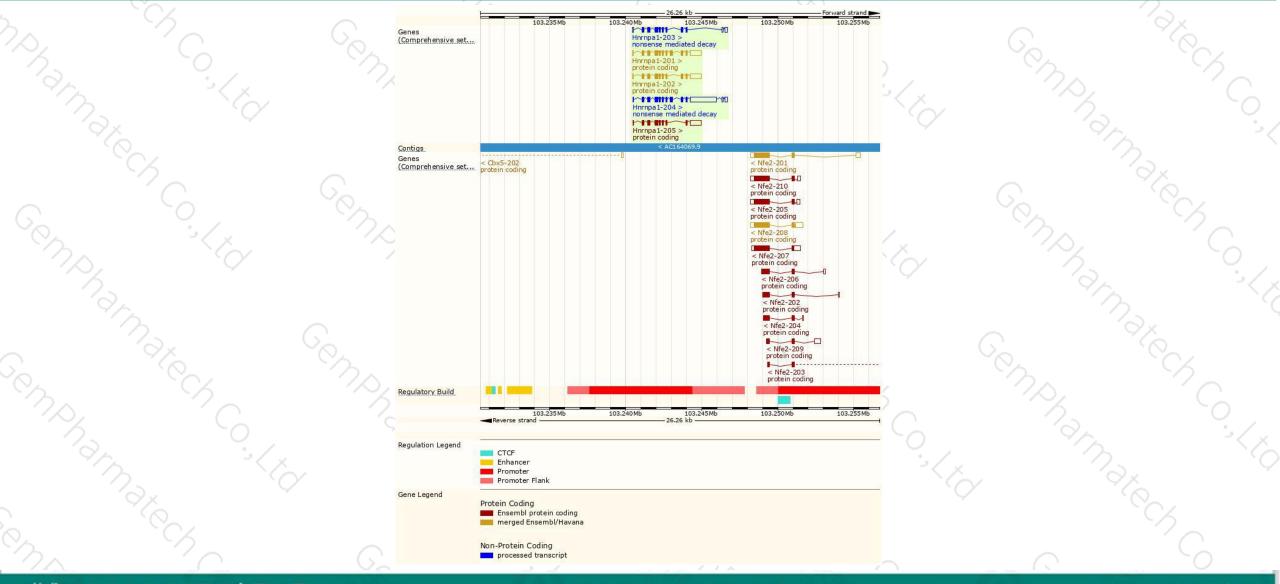
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags					
Hnrnpa1-201	ENSMUST0000036004.15	1918	<u>373aa</u>	Protein coding	CCDS37232	Q5EBP8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P4					
Hnrnpa1-202	ENSMUST0000087351.8	1737	<u>320aa</u>	Protein coding	CCDS37233	P49312	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT					
Hnrnpa1-205	ENSMUST00000231141.1	1541	<u>268aa</u>	Protein coding	(23)	P49312	GENCODE basic					
Hnrnpa1-204	ENSMUST00000230489.1	3118	<u>373aa</u>	Nonsense mediated decay		Q5EBP8						
Hnrnpa1-203	ENSMUST00000230171.1	1283	<u>320aa</u>	Nonsense mediated decay	1.00	P49312						
	· · · · ·	-										

The strategy is based on the design of *Hnrnpa1-201* transcript, the transcription is shown below:



### **Genomic location distribution**





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# **Protein domain**



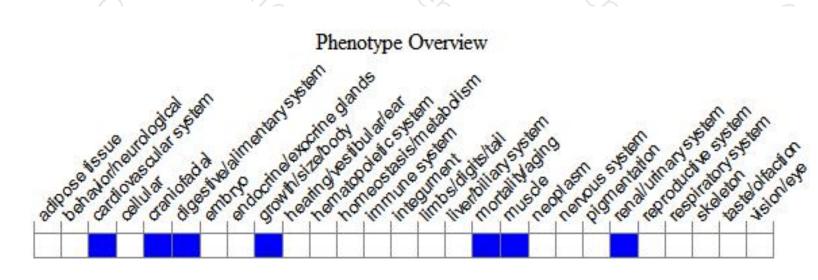
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ENSMUSP00000042 MobiDB lite Low complexity (Seg)						2.			-
Superfamily SMART	RNA-binding dom RNA-recognition								
Pfam.	RNA recognition						1	Nuclear factor	hnRNPA1
PROSITE profiles PANTHER	RNA recognition PTHR15241	motif domain		я-					C
	PTHR15241:SF2	56							
Gene3D CDD	Nucleotide-binding al	F	INRNP A1, RNA	ily recognition mo	tif 2				
All sequence SNPs/i	hnRNP A1, RNA r Sequence variants			s)				14	2
Variant Legend	missense var								sO
Scale bar	0 40	80	120	160	200	240	280	320	373
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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 prenatal and neonatal lethality, dilated cardiacmyopathy, and hypoplastic tongue and intercostal muscles. Mice heterozygous for a knock-out allele exhibit altered cardiac signaling, increased heart rate and increased systemic arterial systolic blood pressure.

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



