

Hnrnpk Cas9-KO Strategy

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Project Overview

Project Name

Hnrnpk

Project type

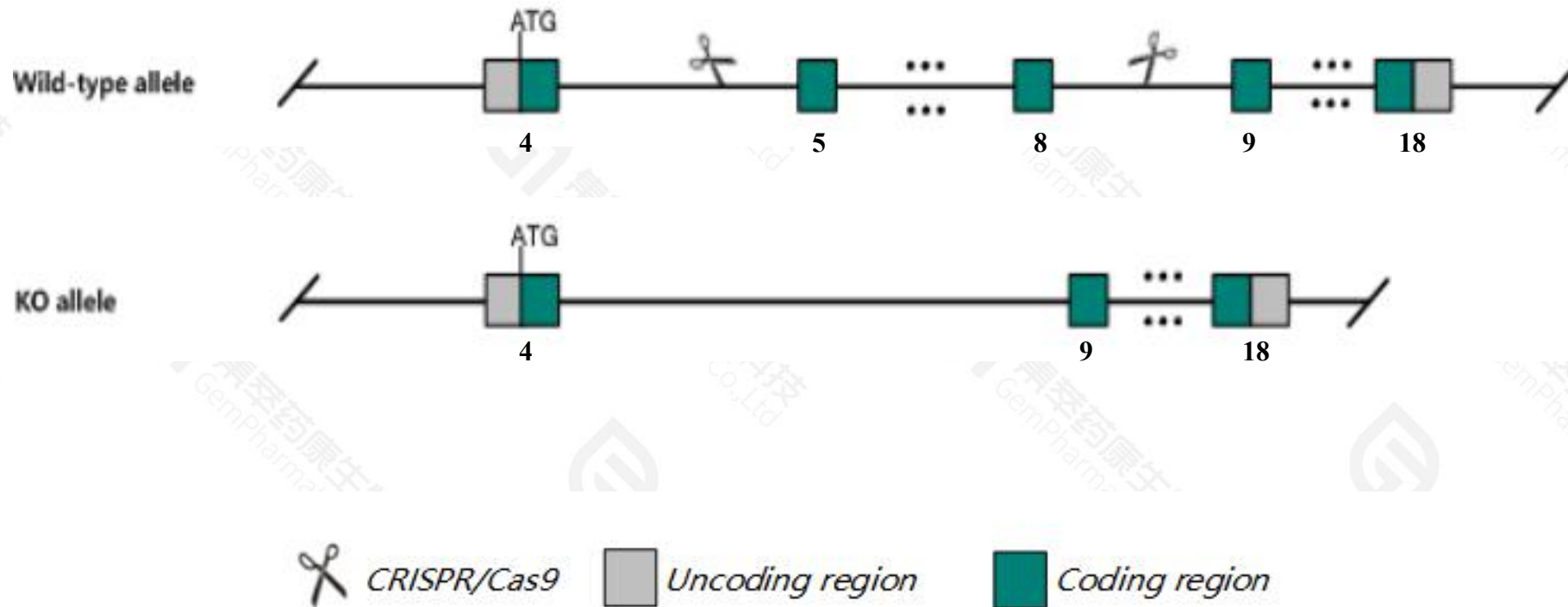
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hnrnpk* gene has 34 transcripts. According to the structure of *Hnrnpk* gene, exon5-exon8 of *Hnrnpk*-202(ENSMUST00000116403.9) transcript is recommended as the knockout region. The region contains 272bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hnrnpk* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The *Hnrnpk* gene is located on the Chr13. 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)

Hnrnpk heterogeneous nuclear ribonucleoprotein K [Mus musculus (house mouse)]

Gene ID: 15387, updated on 13-Mar-2020

Summary

Official Symbol Hnrnpk provided by [MGI](#)

Official Full Name heterogeneous nuclear ribonucleoprotein K provided by [MGI](#)

Primary source [MGI:MGI:99894](#)

See related [Ensembl:ENSMUSG00000021546](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

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

Also known as Hnrpk, KBBP, NOVA

Summary The protein encoded by this gene is a component of the heterogeneous nuclear ribonucleoprotein (hnRNP) complex, and is a poly-cytosine binding protein (PCBP). It is found in multiple subcellular compartments including the nucleus, cytoplasm and mitochondria. This gene product is thought to interact with RNA, DNA, and protein, and is involved in multiple cellular processes, including transcription, chromatin remodeling, DNA damage response, signal transduction, mRNA splicing, export, and translation. Multiple transcript variants and protein isoforms exist, with some isoforms containing a unique C-terminus. There are four pseudogenes of this gene, found on chromosomes 2, 3, 7 and 13. [provided by RefSeq, Aug 2014]

Expression Ubiquitous expression in CNS E11.5 (RPKM 240.5), CNS E14 (RPKM 167.5) and 25 other tissues [See more](#)

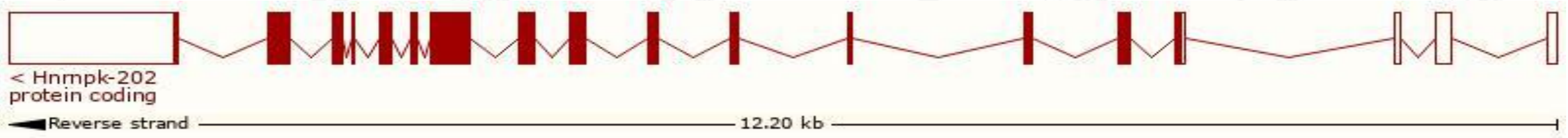
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

The gene has 34 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpk-202	ENSMUST00000116403.8	2970	464aa	Protein coding	CCDS79199	P61979_Q6FWJ5	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 ALT1
Hnrnpk-224	ENSMUST00000224182.1	2754	464aa	Protein coding	CCDS79199	P61979_Q6FWJ5	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 ALT1
Hnrnpk-232	ENSMUST00000225674.1	2704	464aa	Protein coding	CCDS79199	P61979_Q6FWJ5	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 ALT1
Hnrnpk-201	ENSMUST0000043269.3	2676	463aa	Protein coding	CCDS49283	P61979	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 P3
Hnrnpk-205	ENSMUST00000176207.7	2653	439aa	Protein coding	CCDS79197	P61979	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 ALT1
Hnrnpk-216	ENSMUST00000177019.7	2626	440aa	Protein coding	CCDS79198	B2M1R6	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 ALT1
Hnrnpk-221	ENSMUST00000177497.7	2585	394aa	Protein coding	-	H3BLI4	TSL-1 GENCODE basic
Hnrnpk-210	ENSMUST00000176568.1	1053	97aa	Protein coding	-	Q8RT23	TSL-2 GENCODE basic
Hnrnpk-214	ENSMUST00000176849.7	1004	299aa	Protein coding	-	H3BKQ0	CDS 3' incomplete TSL-5
Hnrnpk-208	ENSMUST00000176305.7	900	256aa	Protein coding	-	H3BKQ6	CDS 3' incomplete TSL-5
Hnrnpk-231	ENSMUST00000225176.1	839	230aa	Protein coding	-	AA028EY0M3	CDS 3' incomplete
Hnrnpk-213	ENSMUST00000176797.7	810	210aa	Protein coding	-	H3BLP7	CDS 5' incomplete TSL-3
Hnrnpk-226	ENSMUST00000224524.1	761	192aa	Protein coding	-	AA028EYCM2	CDS 3' incomplete
Hnrnpk-218	ENSMUST00000177060.7	676	178aa	Protein coding	-	H3BKQ8	CDS 3' incomplete TSL-5
Hnrnpk-225	ENSMUST00000224342.1	515	150aa	Protein coding	-	AA028EYEC4	CDS 3' incomplete
Hnrnpk-223	ENSMUST00000224030.1	485	143aa	Protein coding	-	AA028EYDH1	CDS 3' incomplete
Hnrnpk-219	ENSMUST00000177117.1	476	87aa	Protein coding	-	H3BUS9	CDS 3' incomplete TSL-3
Hnrnpk-222	ENSMUST00000223822.1	379	52aa	Protein coding	-	AA028EYEA1	CDS 3' incomplete
Hnrnpk-203	ENSMUST00000175847.7	723	77aa	Nonsense mediated decay	-	H3BJ43	TSL-3
Hnrnpk-230	ENSMUST00000225031.1	708	77aa	Nonsense mediated decay	-	H3BJ43	
Hnrnpk-229	ENSMUST00000224636.1	452	77aa	Nonsense mediated decay	-	H3BJ43	
Hnrnpk-206	ENSMUST00000176267.7	1380	No protein	Retained intron	-	-	TSL-5
Hnrnpk-217	ENSMUST00000177061.7	874	No protein	Retained intron	-	-	TSL-2
Hnrnpk-207	ENSMUST00000176269.7	833	No protein	Retained intron	-	-	TSL-5
Hnrnpk-204	ENSMUST00000175939.1	780	No protein	Retained intron	-	-	TSL-2
Hnrnpk-220	ENSMUST00000177377.7	775	No protein	Retained intron	-	-	TSL-2
Hnrnpk-228	ENSMUST00000224782.1	743	No protein	Retained intron	-	-	
Hnrnpk-211	ENSMUST00000176609.7	737	No protein	Retained intron	-	-	TSL-2
Hnrnpk-209	ENSMUST00000176359.1	731	No protein	Retained intron	-	-	TSL-2
Hnrnpk-234	ENSMUST00000226015.1	692	No protein	Retained intron	-	-	
Hnrnpk-233	ENSMUST00000225866.1	566	No protein	Retained intron	-	-	
Hnrnpk-215	ENSMUST00000176888.7	522	No protein	Retained intron	-	-	TSL-2
Hnrnpk-227	ENSMUST00000224531.1	514	No protein	Retained intron	-	-	
Hnrnpk-212	ENSMUST00000176745.7	459	No protein	Retained intron	-	-	TSL-2

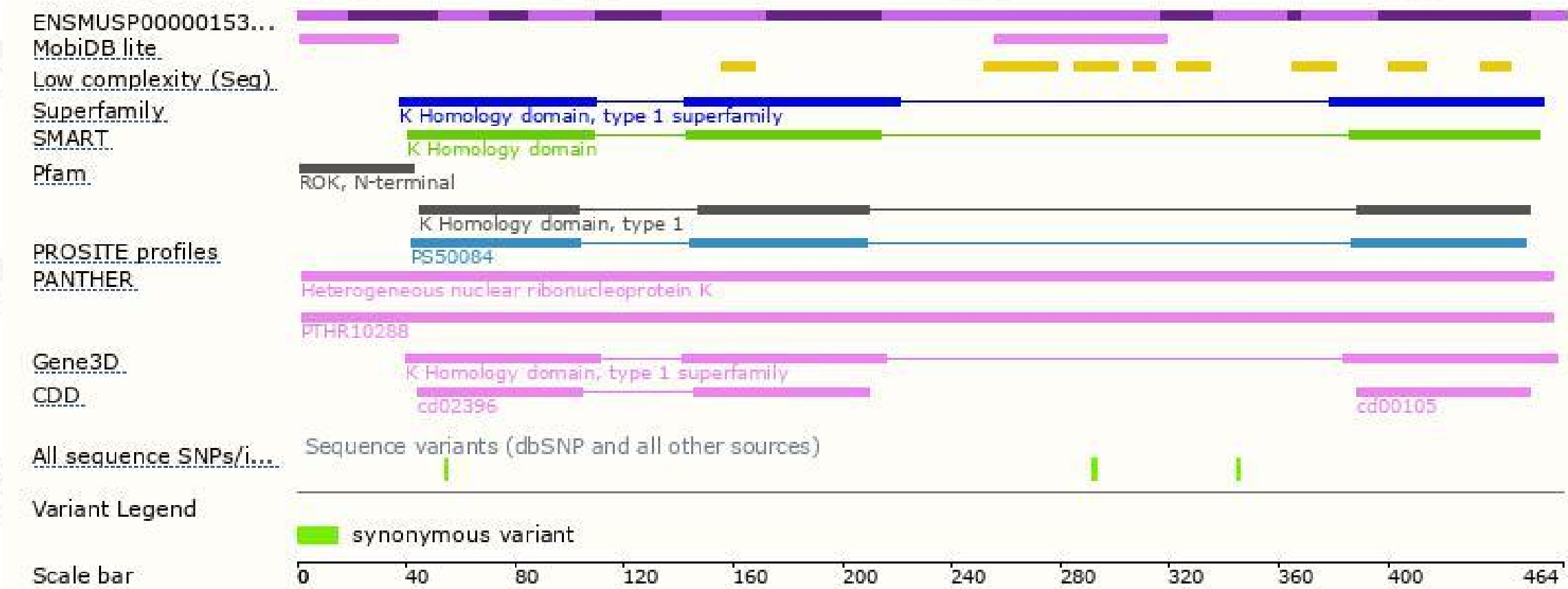
The strategy is based on the design of *Hnrnpk-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.
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