

Hnrnpa2b1 Cas9-KO Strategy

Designer:	Huan Wang
Reviewer	Huan Fan
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Project Overview

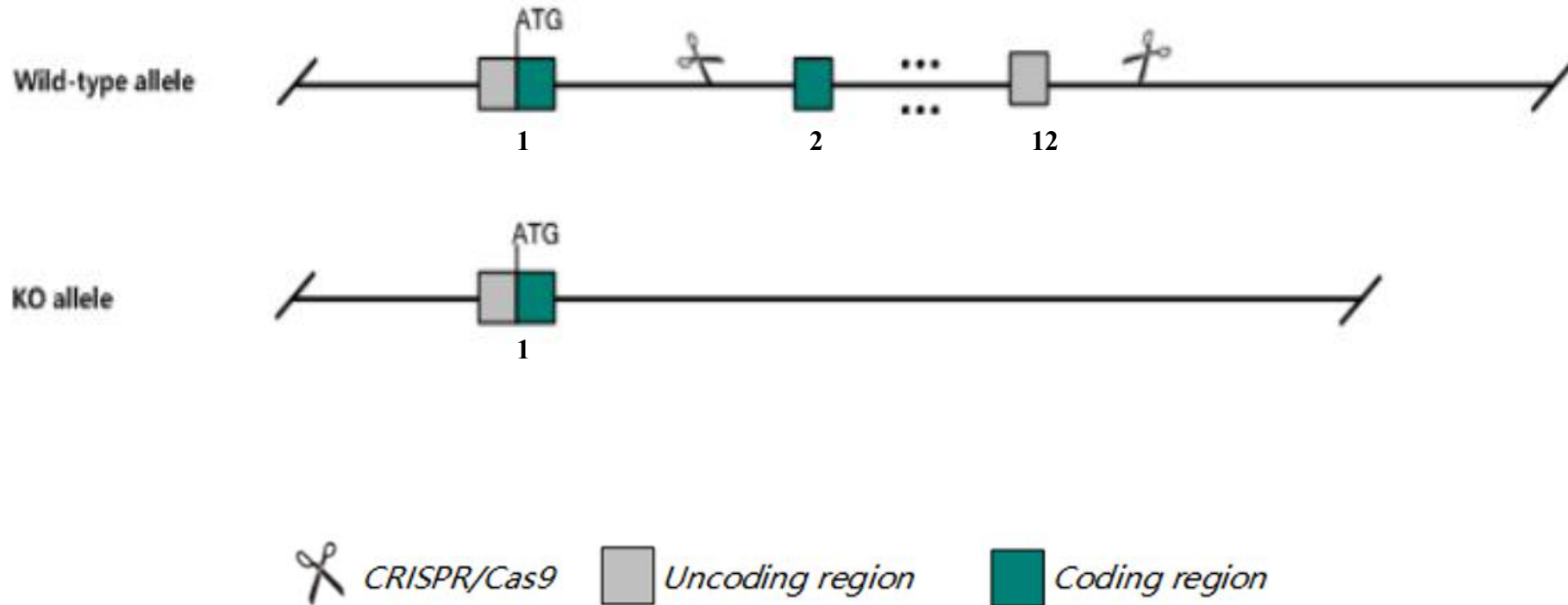
Project Name *Hnrnpa2b1*

Project type **Cas9-KO**

Strain background **C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hnrnpa2b1* gene. The schematic diagram is as follows:



The *Hnrnpa2b1* gene has 13 transcripts. According to the structure of *Hnrnpa2b1* gene, exon2-exon12 of *Hnrnpa2b1-202* (ENSMUST00000090002.9) 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 *Hnrnpa2b1* gene. The brief process is as follows: CRISPR/Cas9 sy

The *Hnrnpa2b1* gene is located on the Chr6. 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.

The KO region is about 2.5kb away from *Cbx3* gene. Knockout the region may affect the function of *Cbx3* gene .

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.

Hnrnpa2b1 heterogeneous nuclear ribonucleoprotein A2/B1 [Mus musculus (house mouse)]

Gene ID: 53379, updated on 13-Mar-2020

Summary



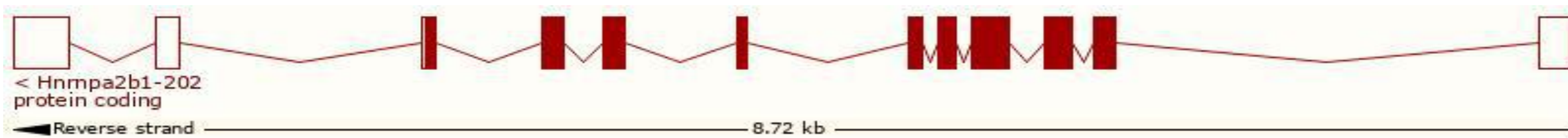
Official Symbol	Hnrnpa2b1 provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein A2/B1 provided by MGI
Primary source	MGI:MGI:104819
See related	Ensembl:ENSMUSG00000004980
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9130414A06Rik, Hnrpa2, Hnrpa2b1, hnmp-A
Expression	Broad expression in CNS E11.5 (RPKM 290.0), liver E14 (RPKM 181.3) and 16 other tissues See more
Orthologs	human all

Transcript information Ensembl

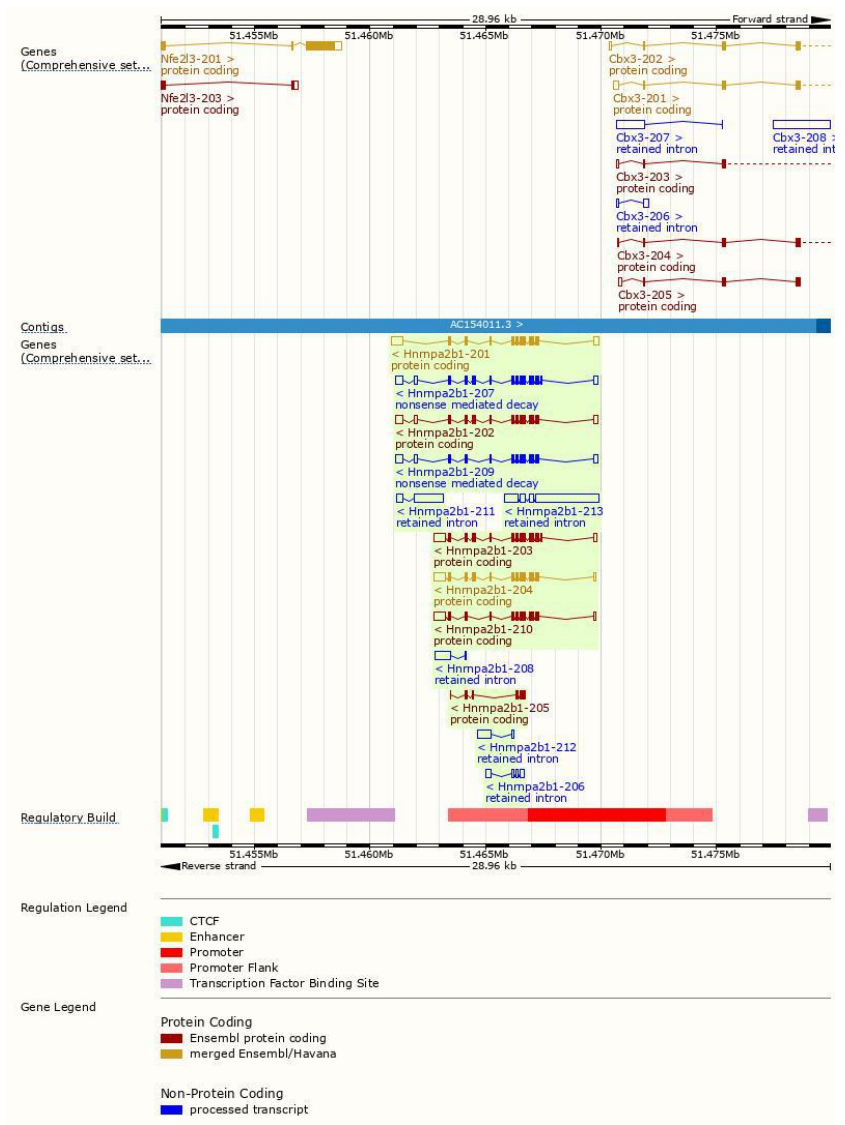
The gene has 13 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpa2b1-202	ENSMUST00000090002.9	1662	341aa	Protein coding	CCDS51774	O88569	TSL:5 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 P2
Hnrnpa2b1-201	ENSMUST00000069949.12	1647	301aa	Protein coding	CCDS51773	O88569	TSL:1 GENCODE basic
Hnrnpa2b1-204	ENSMUST00000203220.2	1638	341aa	Protein coding	CCDS51774	O88569	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 P2
Hnrnpa2b1-210	ENSMUST00000204188.2	1518	301aa	Protein coding	CCDS51773	O88569	TSL:5 GENCODE basic
Hnrnpa2b1-203	ENSMUST00000114459.7	1728	353aa	Protein coding	-	O88569	TSL:5 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 1
Hnrnpa2b1-205	ENSMUST00000203253.1	466	155aa	Protein coding	-	A0A0N4SUM2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Hnrnpa2b1-207	ENSMUST00000203954.2	1703	353aa	Nonsense mediated decay	-	O88569	TSL:5
Hnrnpa2b1-209	ENSMUST00000204158.2	1542	301aa	Nonsense mediated decay	-	O88569	TSL:1
Hnrnpa2b1-213	ENSMUST00000205204.1	3645	No protein	Retained intron	-	-	TSL:1
Hnrnpa2b1-211	ENSMUST00000204885.1	1554	No protein	Retained intron	-	-	TSL:1
Hnrnpa2b1-208	ENSMUST00000204090.1	766	No protein	Retained intron	-	-	TSL:2
Hnrnpa2b1-212	ENSMUST00000204902.1	706	No protein	Retained intron	-	-	TSL:2
Hnrnpa2b1-206	ENSMUST00000203655.1	596	No protein	Retained intron	-	-	TSL:2

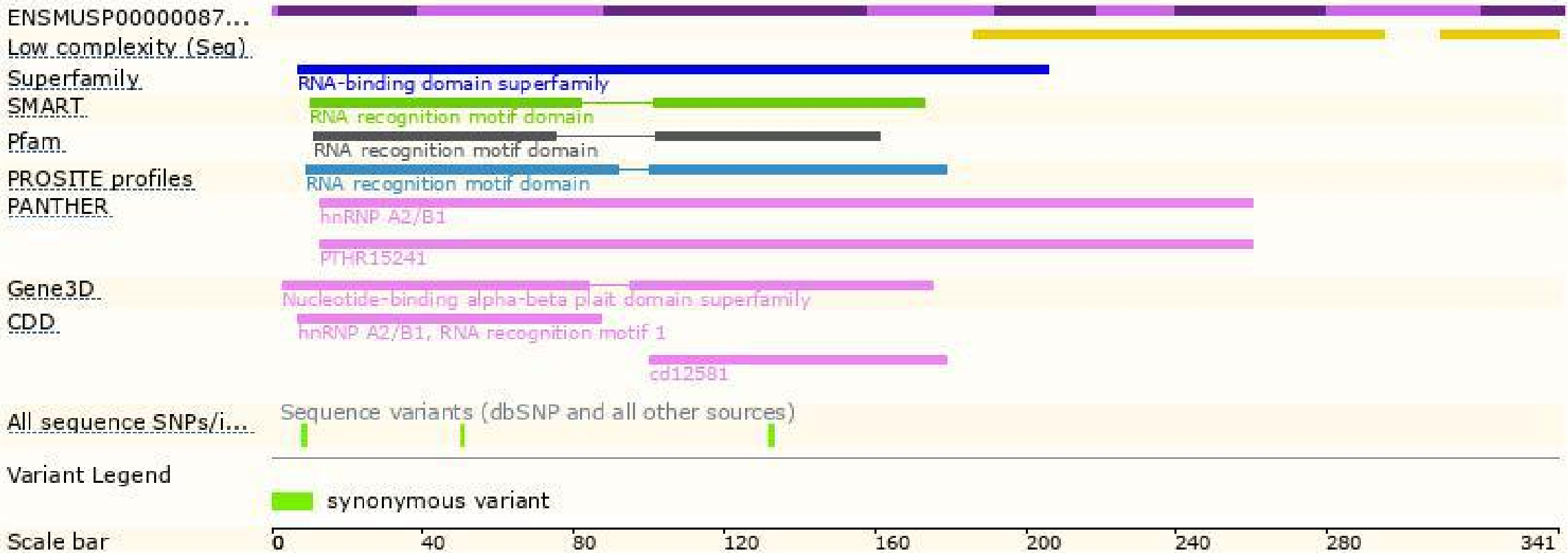
The strategy is based on the design of *Hnrnpa2b1-202* transcript, the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

