Hnrnpu Cas9-KO Strategy

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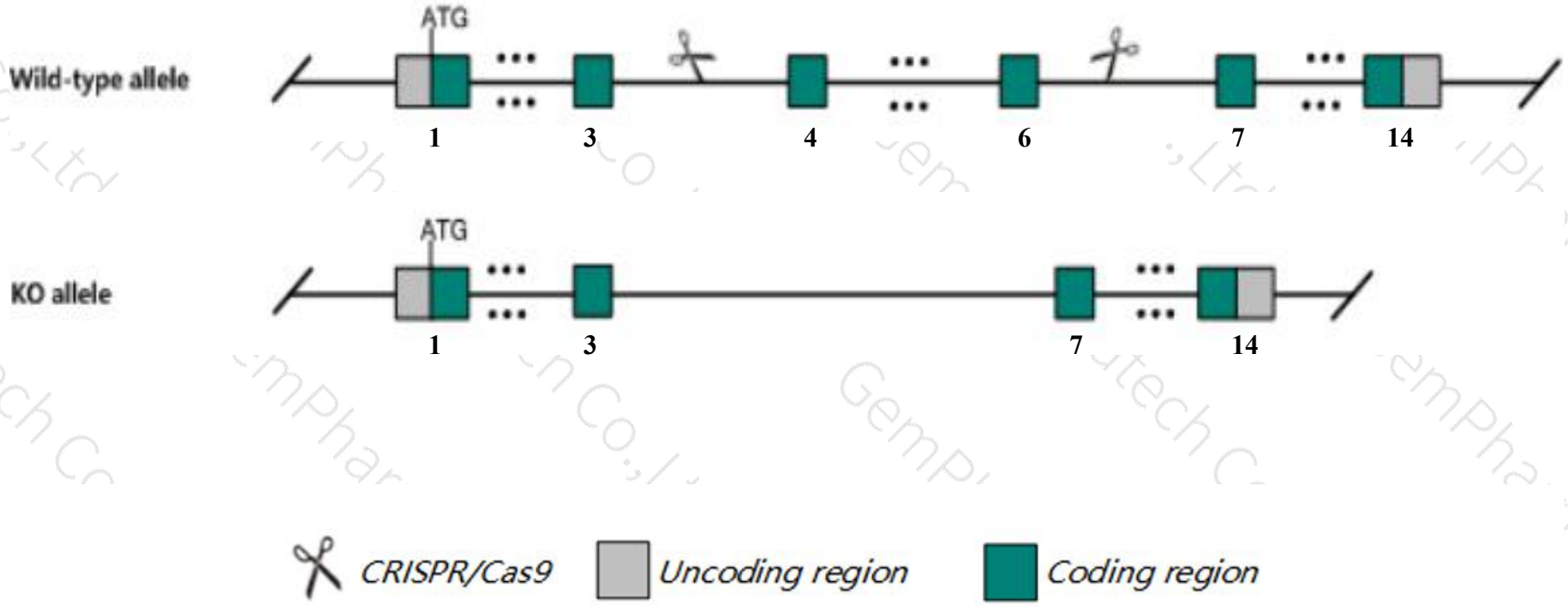
Project Overview

Project Name	***Hnrnpu***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Hnrnpu* gene has 9 transcripts. According to the structure of *Hnrnpu* gene, exon4-exon6 of *Hnrnpu-201*(ENSMUST00000037748.8) transcript is recommended as the knockout region.The region contains 353bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hnrnpu* 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.

Notice

➢ According to the existing MGI data,mice homozygous for a gene trap allele display embryonic lethality, delayed embryonic development, and failure of chorioallantoic fusion.

➢ The *Hnrnpu* gene is located on the Chr1. 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）

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Hnrnpu heterogeneous nuclear ribonucleoprotein U [*Mus musculus* (house mouse)]

Gene ID: 51810, updated on 26-Jun-2020

Summary

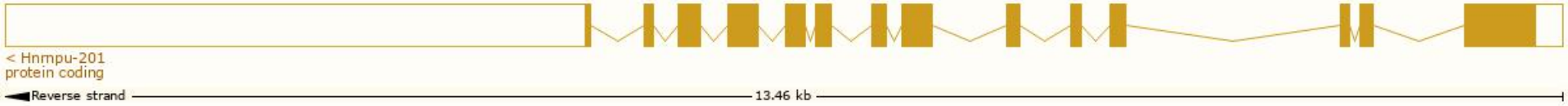
Official Symbol	Hnrnpu provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein U provided by MGI
Primary source	MGI:MGI:1858195
See related	Ensembl:ENSMUSG00000039630
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SAFA; Hnrpu; Sp120; C86794; hnRNP U; AA408410; AI256620; AL024194; AL024437; AW557595
Expression	Broad expression in CNS E11.5 (RPKM 88.9), CNS E14 (RPKM 47.2) and 25 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

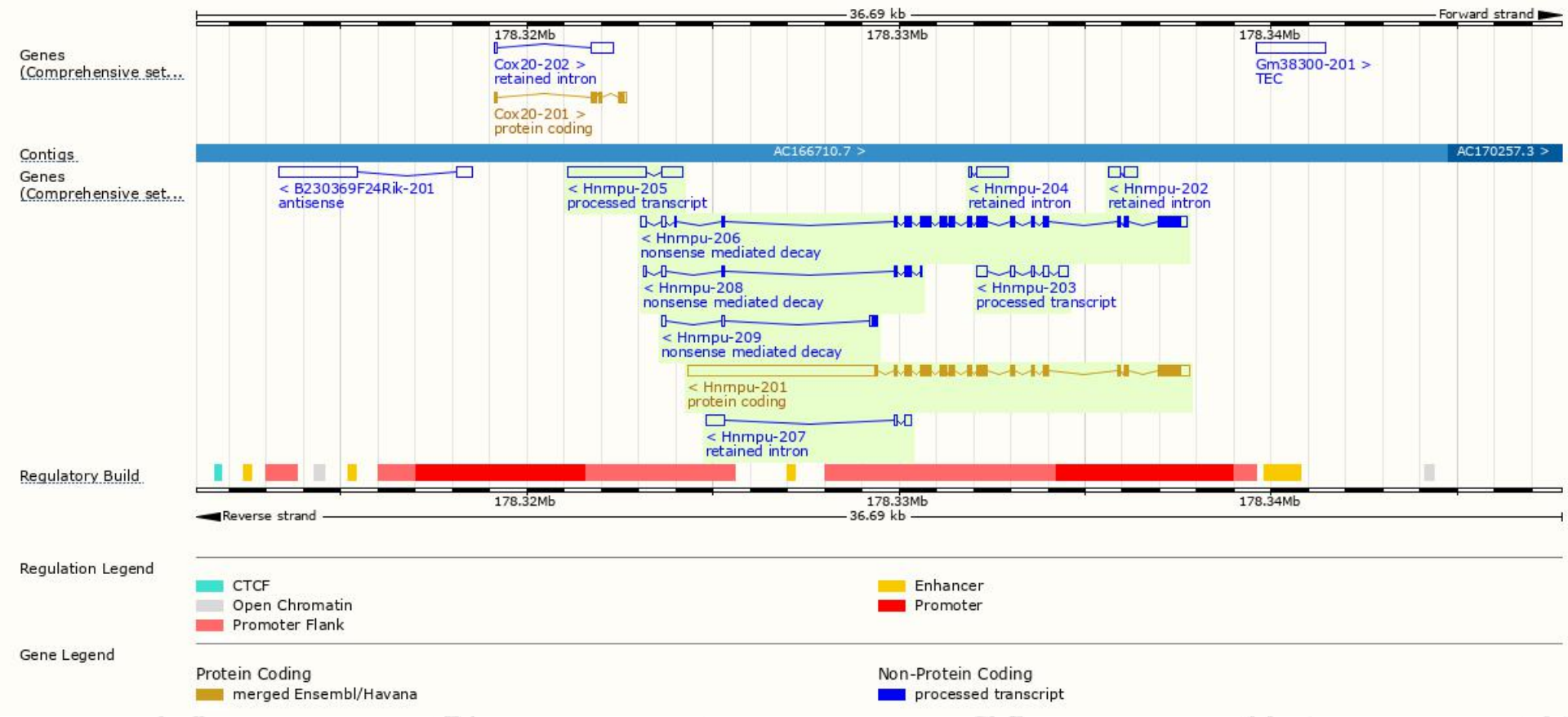
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpu-209	ENSMUST00000189450.1	351	43aa	Nonsense mediated decay	-	A0A087WPF1	CDS 5' incomplete TSL:5
Hnrnpu-208	ENSMUST00000188044.6	511	105aa	Nonsense mediated decay	-	A0A087WPX7	CDS 5' incomplete TSL:5
Hnrnpu-206	ENSMUST00000161769.7	2844	793aa	Nonsense mediated decay	-	Q8VEK3	TSL:1
Hnrnpu-201	ENSMUST00000037748.8	7640	800aa	Protein coding	CCDS35804	Q8VEK3	TSL:1 GENCODE basic APPRIS P1
Hnrnpu-205	ENSMUST00000159117.1	2640	No protein	Processed transcript	-	-	TSL:1
Hnrnpu-203	ENSMUST00000146362.1	869	No protein	Processed transcript	-	-	TSL:5
Hnrnpu-204	ENSMUST00000150825.1	923	No protein	Retained intron	-	-	TSL:2
Hnrnpu-207	ENSMUST00000162916.1	710	No protein	Retained intron	-	-	TSL:3
Hnrnpu-202	ENSMUST00000134291.1	673	No protein	Retained intron	-	-	TSL:2

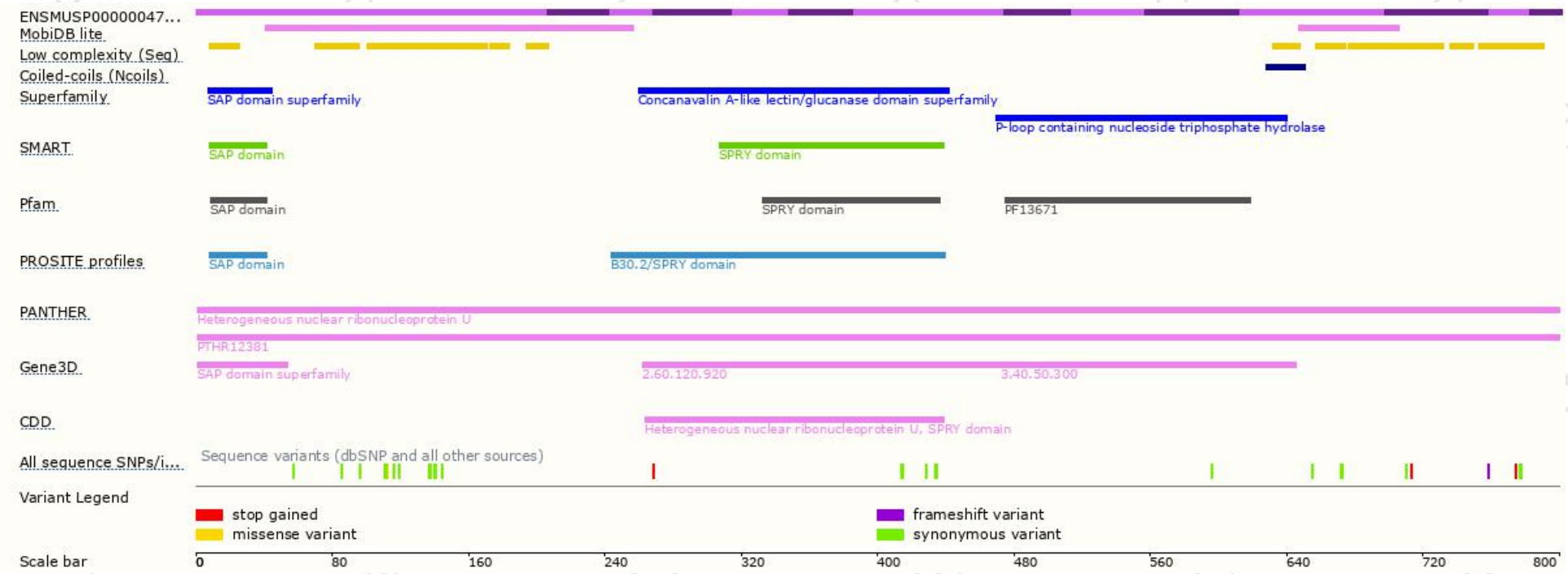
The strategy is based on the design of *Hnrnpu-201* transcript,the transcription is shown below:



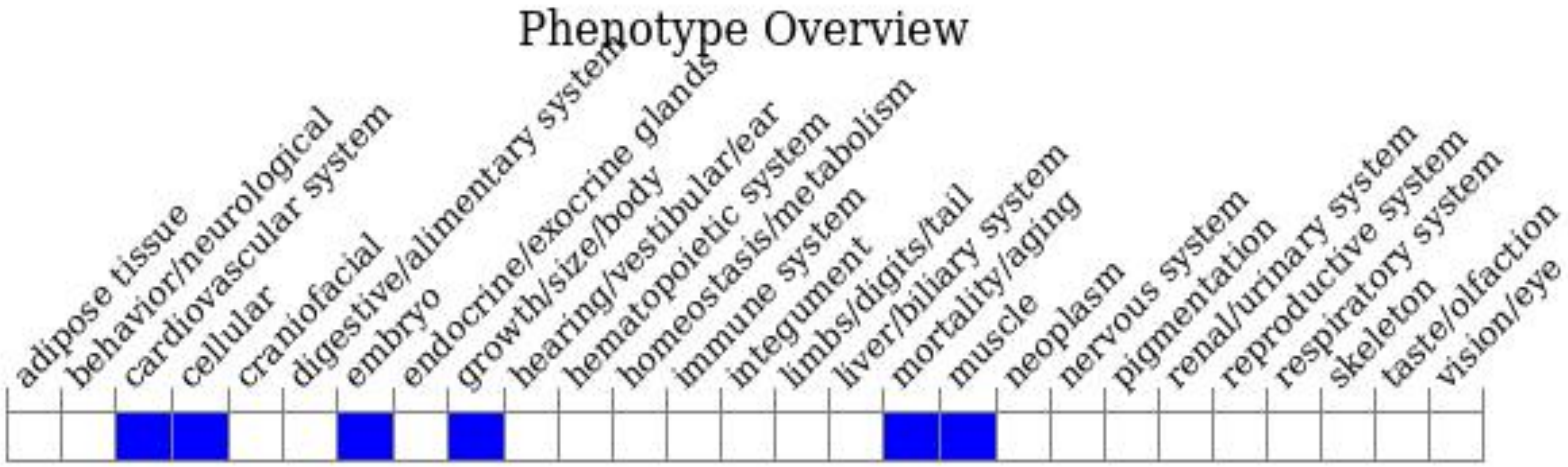
Genomic location distribution



Protein domain



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 gene trap allele display embryonic lethality, delayed embryonic development, and failure of chorioallantoic fusion.

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