

Hnrnpa3 Cas9-KO Strategy

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Project Overview

Project Name

Hnrnpa3

Project type

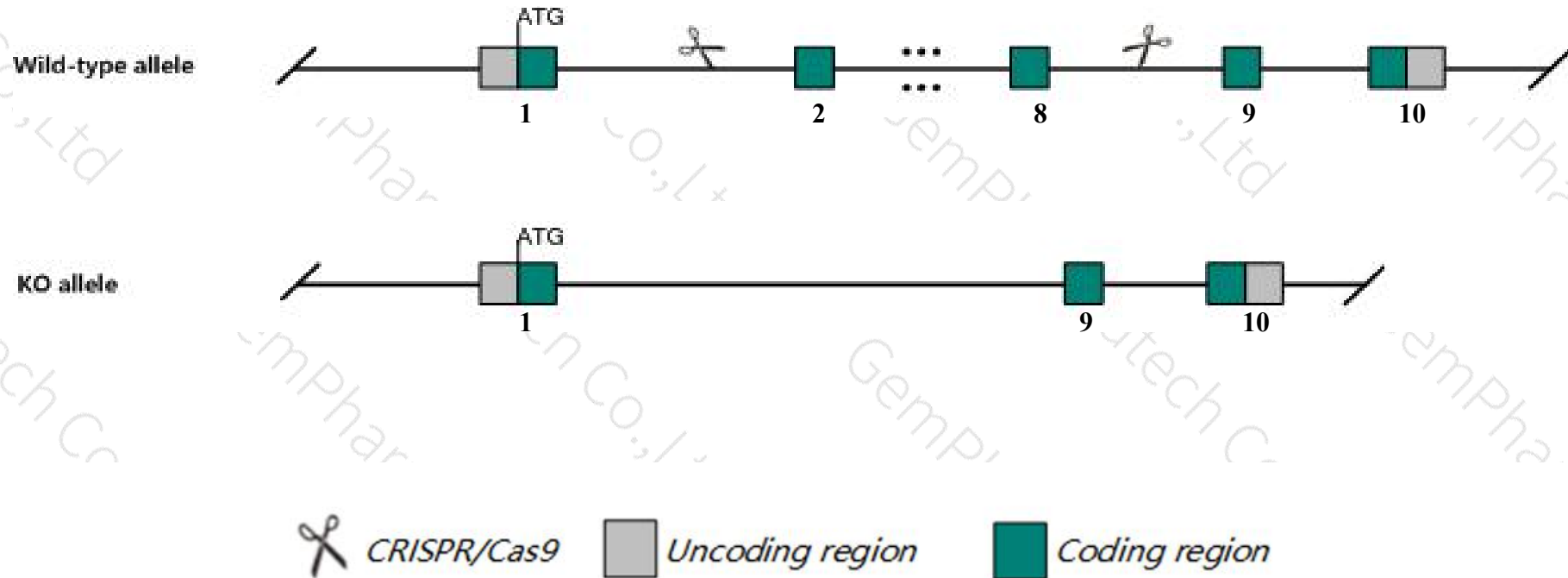
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hnrnpa3* gene. The schematic diagram is as follows:



- The *Hnrnpa3* gene has 7 transcripts. According to the structure of *Hnrnpa3* gene, exon2-exon8 of *Hnrnpa3*-204 (ENSMUST00000111964.7) transcript is recommended as the knockout region. The region contains 892bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hnrnpa3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Hnrnpa3* gene is located on the Chr2. 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)

Hnrnpa3 heterogeneous nuclear ribonucleoprotein A3 [Mus musculus (house mouse)]

Gene ID: 229279, updated on 31-Jan-2019

Summary



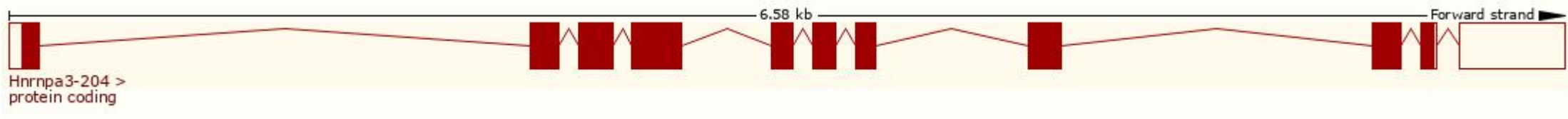
Official Symbol	Hnrnpa3 provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein A3 provided by MGI
Primary source	MGI:MGI:1917171
See related	Ensembl:ENSMUSG00000059005
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410013L13Rik, 2610209F03Rik, 2610510D13Rik, Hnrpa3
Expression	Broad expression in CNS E11.5 (RPKM 167.7), liver E14 (RPKM 103.2) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

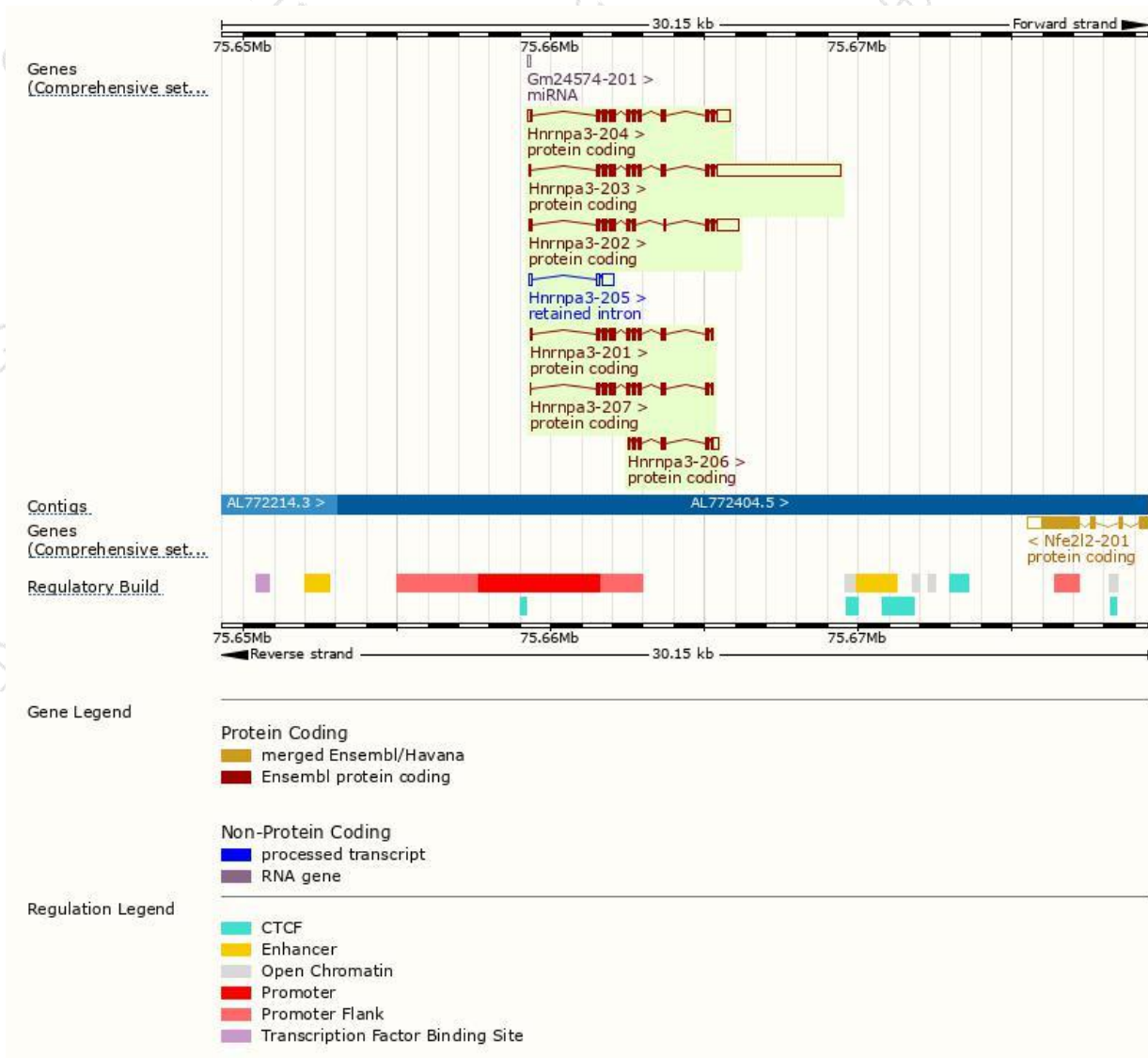
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpa3-203	ENSMUST00000111962.7	5150	357aa	Protein coding	CCDS50610	Q0VG47 Q8BG05	TSL:1 GENCODE basic APPRIS ALT2
Hnrnpa3-204	ENSMUST00000111964.7	1654	379aa	Protein coding	CCDS16149	Q5FB19 Q8BG05	TSL:1 GENCODE basic APPRIS P3
Hnrnpa3-201	ENSMUST00000090792.10	1140	379aa	Protein coding	CCDS16149	Q5FB19 Q8BG05	TSL:5 GENCODE basic APPRIS P3
Hnrnpa3-207	ENSMUST00000164947.8	1074	357aa	Protein coding	CCDS50610	Q0VG47 Q8BG05	TSL:5 GENCODE basic APPRIS ALT2
Hnrnpa3-202	ENSMUST00000111961.7	1734	318aa	Protein coding	-	A2AL12	TSL:1 GENCODE basic APPRIS ALT2
Hnrnpa3-206	ENSMUST00000141974.1	754	194aa	Protein coding	-	A2AL13	CDS 5' incomplete TSL:2
Hnrnpa3-205	ENSMUST00000132392.1	596	No protein	Retained intron	-	-	TSL:2

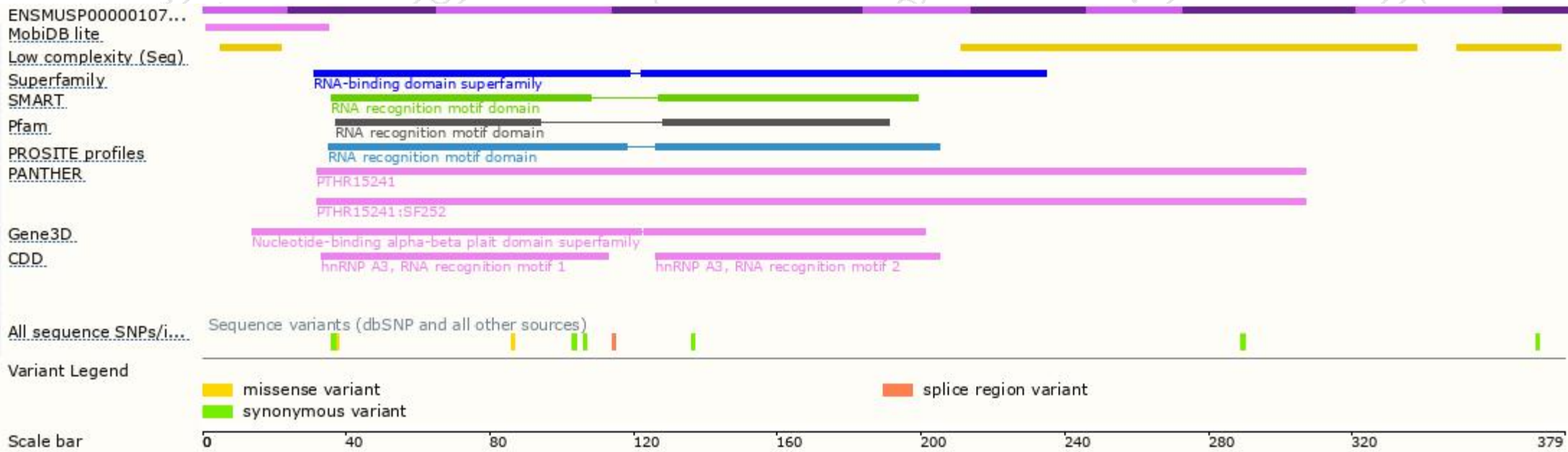
The strategy is based on the design of *Hnrnpa3-204* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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