

Hnrnpab Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Hnrnpab

Project type

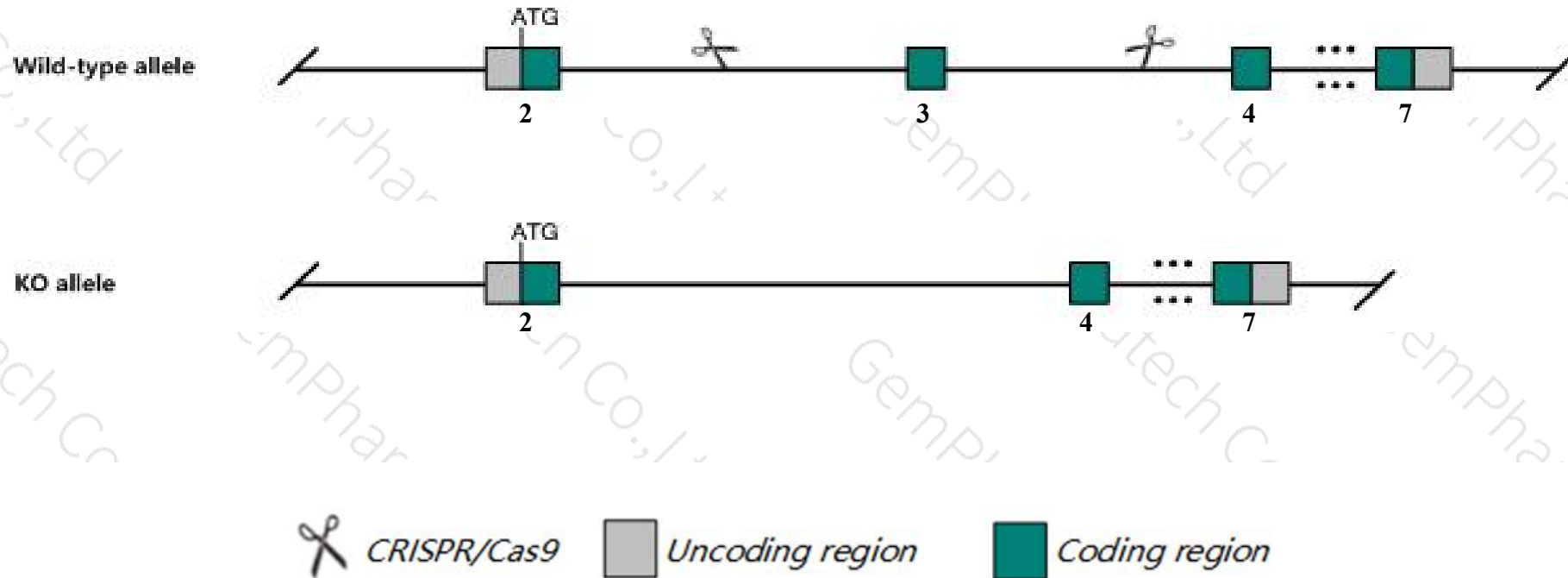
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hnrnpab* gene has 3 transcripts. According to the structure of *Hnrnpab* gene, exon3 of *Hnrnpab-201* (ENSMUST00000074669.9) transcript is recommended as the knockout region. The region contains 169bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hnrnpab* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit abnormal neuron differentiation, increased susceptibility to neuronal excitotoxicity and long neurites.
- The *Hnrnpab* gene is located on the Chr11. 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)

Hnrnpab heterogeneous nuclear ribonucleoprotein A/B [Mus musculus (house mouse)]

Gene ID: 15384, updated on 31-Jan-2019

Summary



Official Symbol Hnrnpab provided by [MGI](#)

Official Full Name heterogeneous nuclear ribonucleoprotein A/B provided by [MGI](#)

Primary source [MGI:MGI:1330294](#)

See related [Ensembl:ENSMUSG00000020358](#)

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 3010025C11Rik, CBF-A, Cgbfa, Hnrpab

Summary This gene encodes a protein with consensus RNA binding domains present in a number of other RNA binding proteins and a glycine-rich C-terminus. This gene overlaps in a tail-to-tail orientation the gene encoding alanine-glyoxylate aminotransferase 2-like 2. Some of the exons of this gene are interspersed with exons of alanine-glyoxylate aminotransferase 2-like 2. Two alternatively spliced transcript variants that encode distinct proteins have been described for this gene. [provided by RefSeq, Jul 2008]

Expression Ubiquitous expression in ovary adult (RPKM 222.6), CNS E11.5 (RPKM 200.6) and 28 other tissues [See more](#)

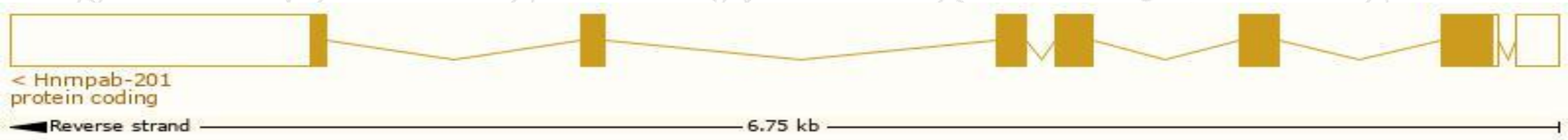
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

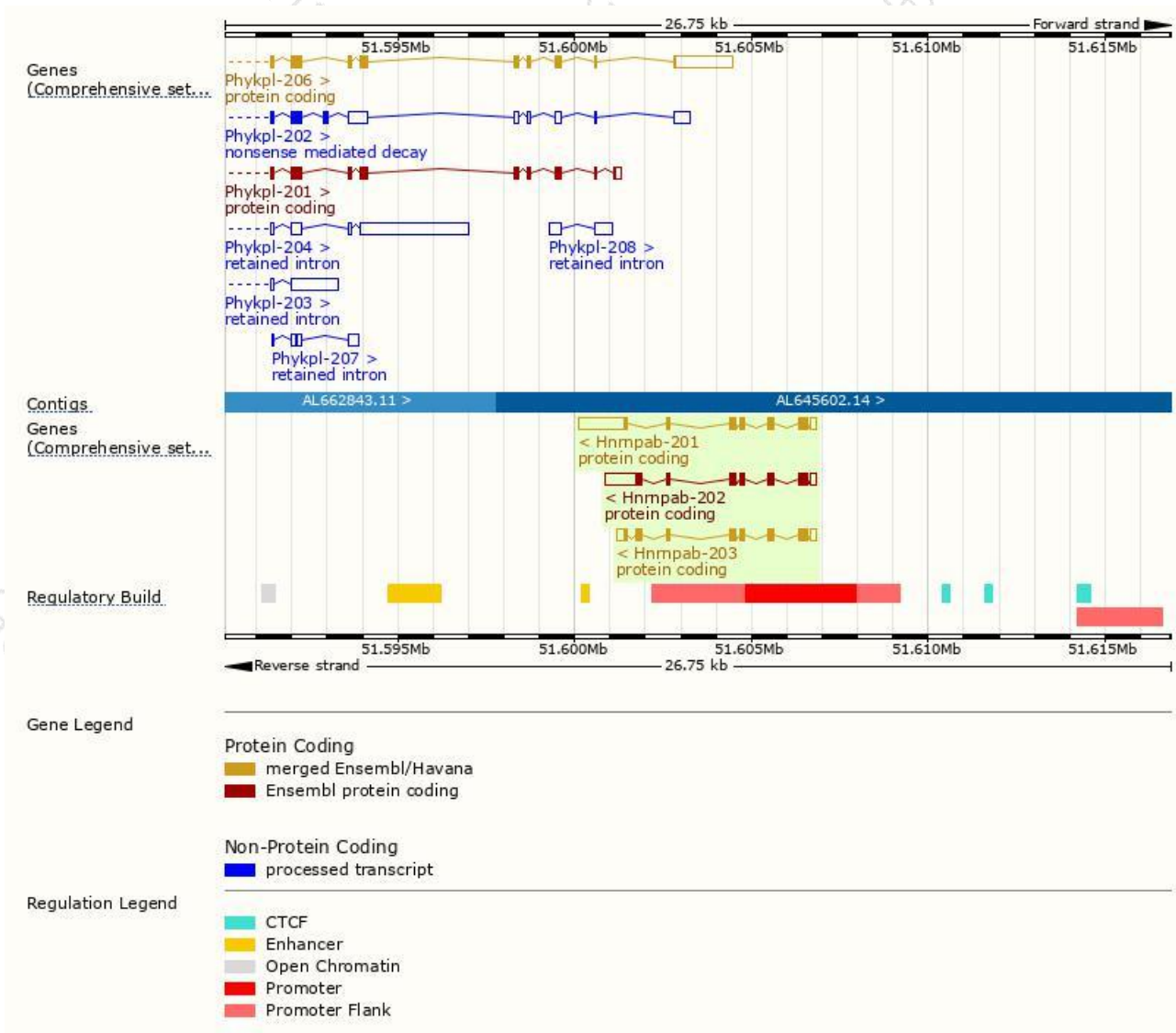
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpab-201	ENSMUST00000074669.9	2370	285aa	Protein coding	CCDS24654	Q544Z3 Q99020	TSL:1 GENCODE basic APPRIS P3
Hnrnpab-203	ENSMUST00000109103.3	1437	332aa	Protein coding	CCDS48787	Q20BD0	TSL:1 GENCODE basic APPRIS ALT2
Hnrnpab-202	ENSMUST00000101249.8	2013	311aa	Protein coding	-	Q80XR6	TSL:1 GENCODE basic APPRIS ALT2

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



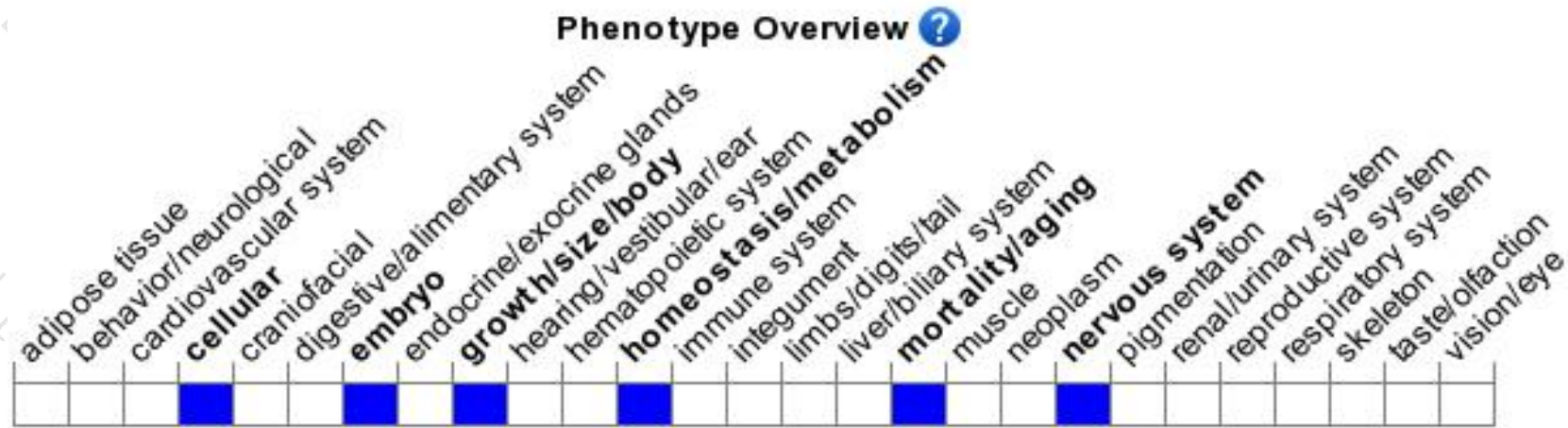
Genomic location distribution



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 knock-out allele exhibit abnormal neuron differentiation, increased susceptibility to neuronal excitotoxicity and long neurites.

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

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