

Kpna2 Cas9-KO Strategy

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Design Date:

2019-11-14

Project Overview

Project Name

Kpna2

Project type

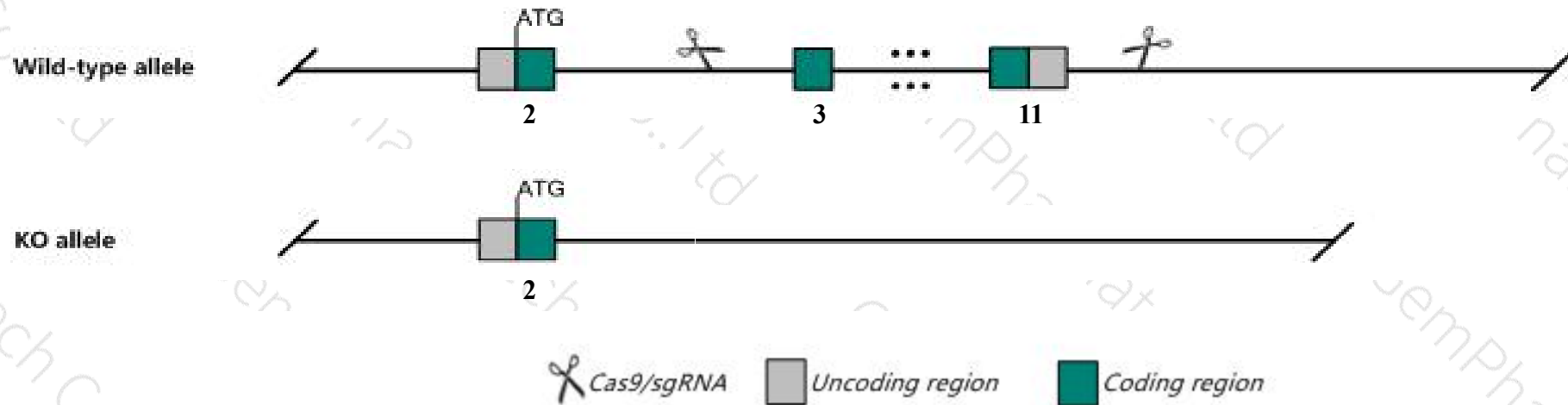
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kpna2* gene. The schematic diagram is as follows:



Technical routes

- The *Kpna2* gene has 7 transcripts. According to the structure of *Kpna2* gene, exon3-exon11 of *Kpna2-201* (ENSMUST00000018506.12) 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 *Kpna2* gene. The brief process is as follows: CRISPR/Cas9 system 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

- The *Kpna2* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Kpna2 karyopherin (importin) alpha 2 [Mus musculus (house mouse)]

Gene ID: 16647, updated on 3-Feb-2019

Summary



Official Symbol	Kpna2 provided by MGI
Official Full Name	karyopherin (importin) alpha 2 provided by MGI
Primary source	MGI:MGI:103561
See related	Ensembl:ENSMUSG00000018362
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	2410044B12Rik, IPOA1, PTAC58, Rch1
Expression	Broad expression in CNS E11.5 (RPKM 144.8), liver E14 (RPKM 99.0) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

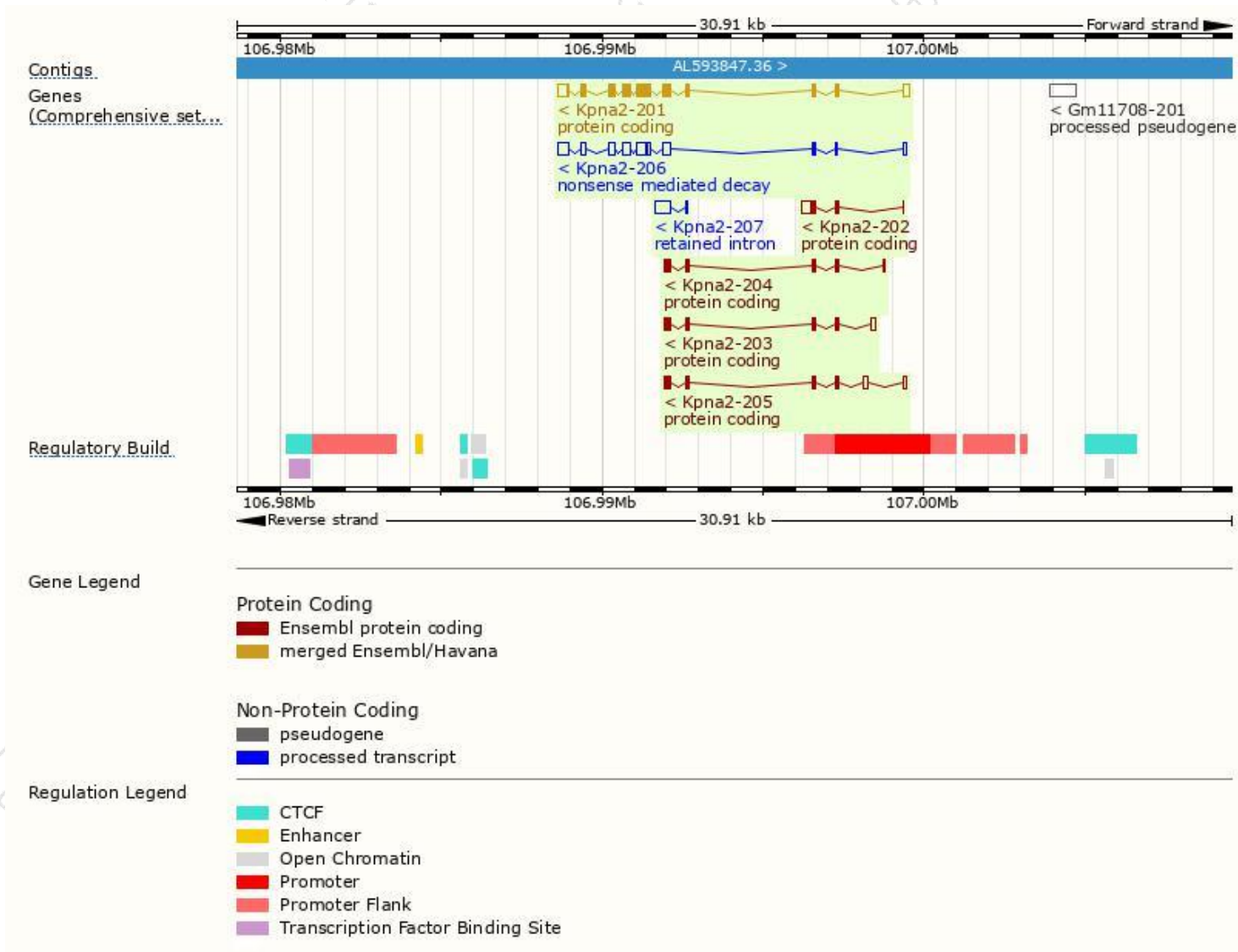
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kpna2-201	ENSMUST00000018506.12	2054	529aa	Protein coding	CCDS25565	P52293 Q52L97	TSL:1 GENCODE basic APPRIS P1
Kpna2-205	ENSMUST00000144834.7	732	163aa	Protein coding	-	A2A600	CDS 3' incomplete TSL:3
Kpna2-203	ENSMUST00000124541.7	659	170aa	Protein coding	-	A2A601	CDS 3' incomplete TSL:2
Kpna2-204	ENSMUST00000140362.7	568	189aa	Protein coding	-	A6PW68	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
Kpna2-202	ENSMUST00000106768.1	541	80aa	Protein coding	-	A2A602	TSL:2 GENCODE basic
Kpna2-206	ENSMUST00000145331.7	1843	75aa	Nonsense mediated decay	-	F2Z431	TSL:1
Kpna2-207	ENSMUST00000156495.1	534	No protein	Retained intron	-	-	TSL:2

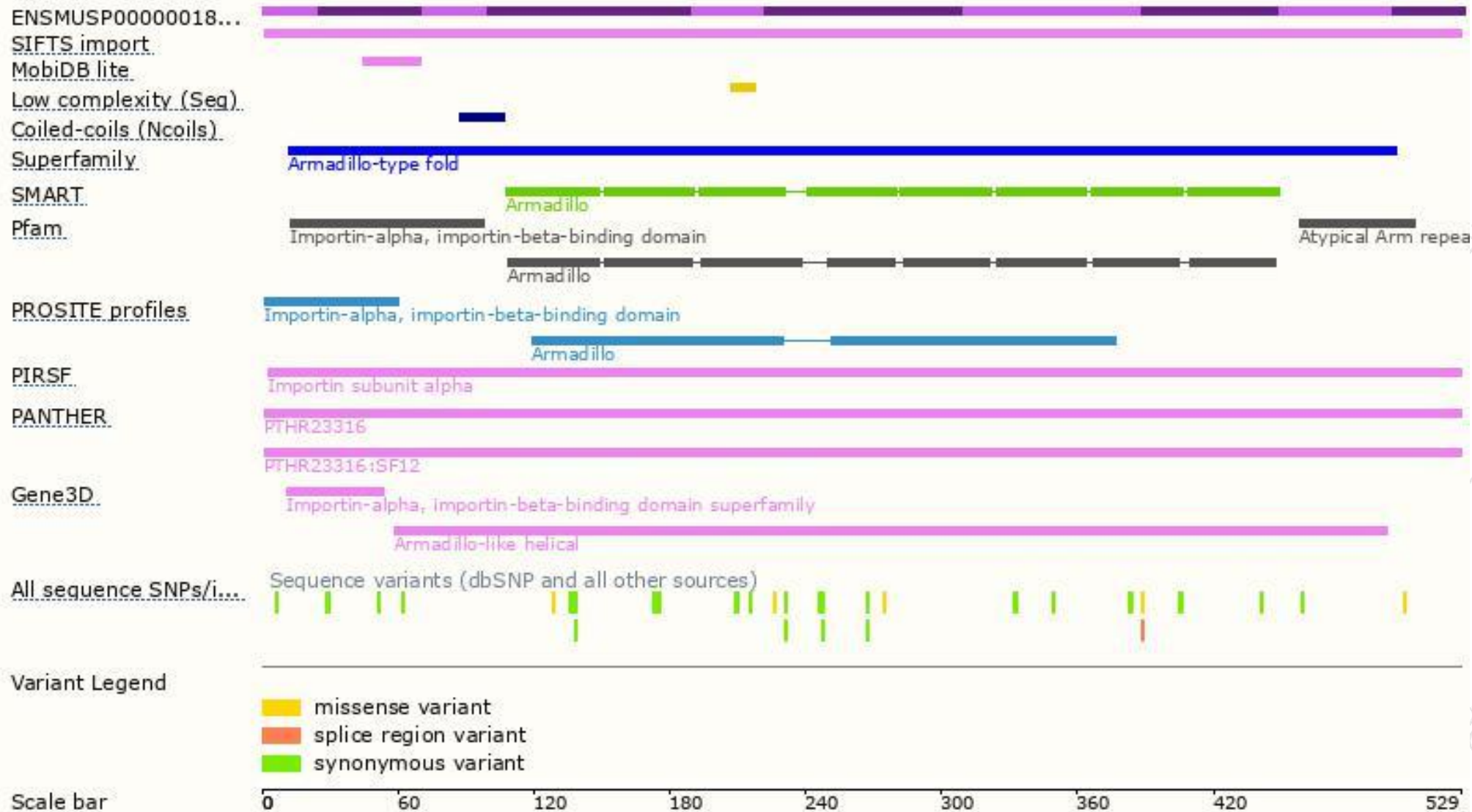
The strategy is based on the design of *Kpna2-201* transcript, The transcription is shown below



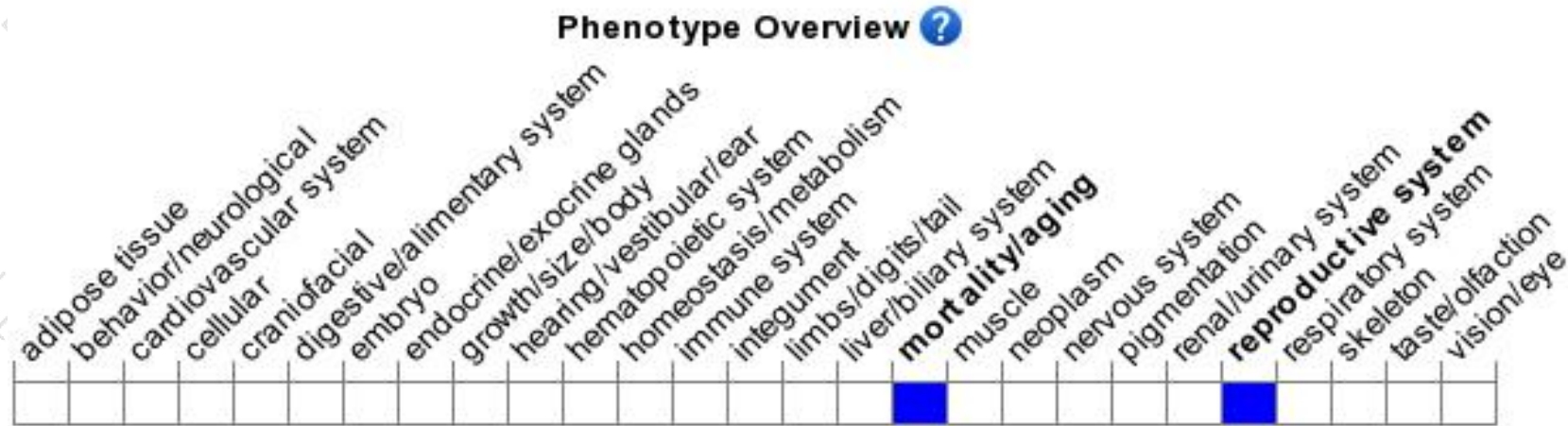
Genomic location distribution



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/>).

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

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