

Kpna1 Cas9-KO Strategy

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Project Overview

Project Name

Kpna1

Project type

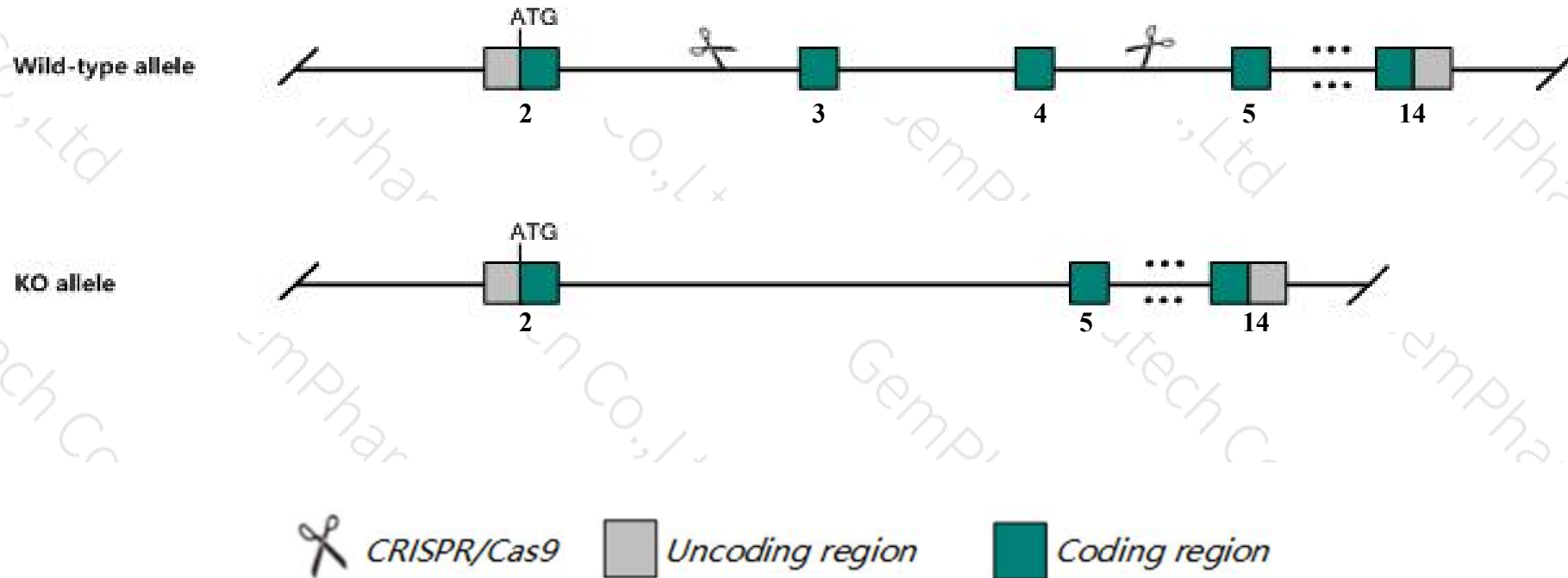
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kpna1* gene. The schematic diagram is as follows:



- The *Kpnal* gene has 10 transcripts. According to the structure of *Kpnal* gene, exon3-exon4 of *Kpnal-201* (ENSMUST00000004054.12) transcript is recommended as the knockout region. The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kpnal* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trap allele do not display any nervous system or behavioral abnormalities.
- Transcript *Kpna1*-202&204&206 may not be affected.
- The *Kpna1* gene is located on the Chr16. 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)

Kpna1 karyopherin (importin) alpha 1 [*Mus musculus* (house mouse)]

Gene ID: 16646, updated on 7-Dec-2019

Summary

- Official Symbol** Kpna1 provided by [MGI](#)
- Official Full Name** karyopherin (importin) alpha 1 provided by [MGI](#)
- Primary source** [MGI:MGI:103560](#)
- See related** [Ensembl:ENSMUSG00000022905](#)
- 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** NPI1; Rch2; IPOA5; mSRP1; AW494490
- Expression** Ubiquitous expression in CNS E18 (RPKM 11.6), cortex adult (RPKM 11.3) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 16; 16 B3 See Kpna1 in [Genome Data Viewer](#)

Exon count: 15

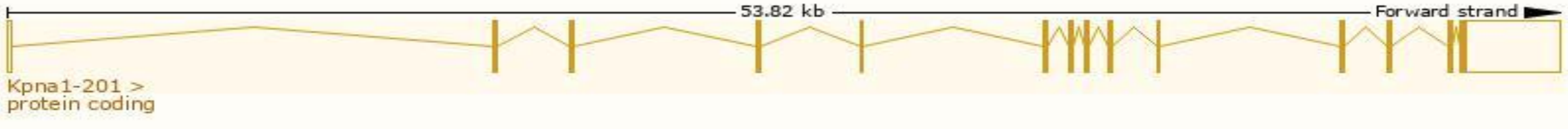
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (35983288..36037136)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (35983449..36036248)

Transcript information (Ensembl)

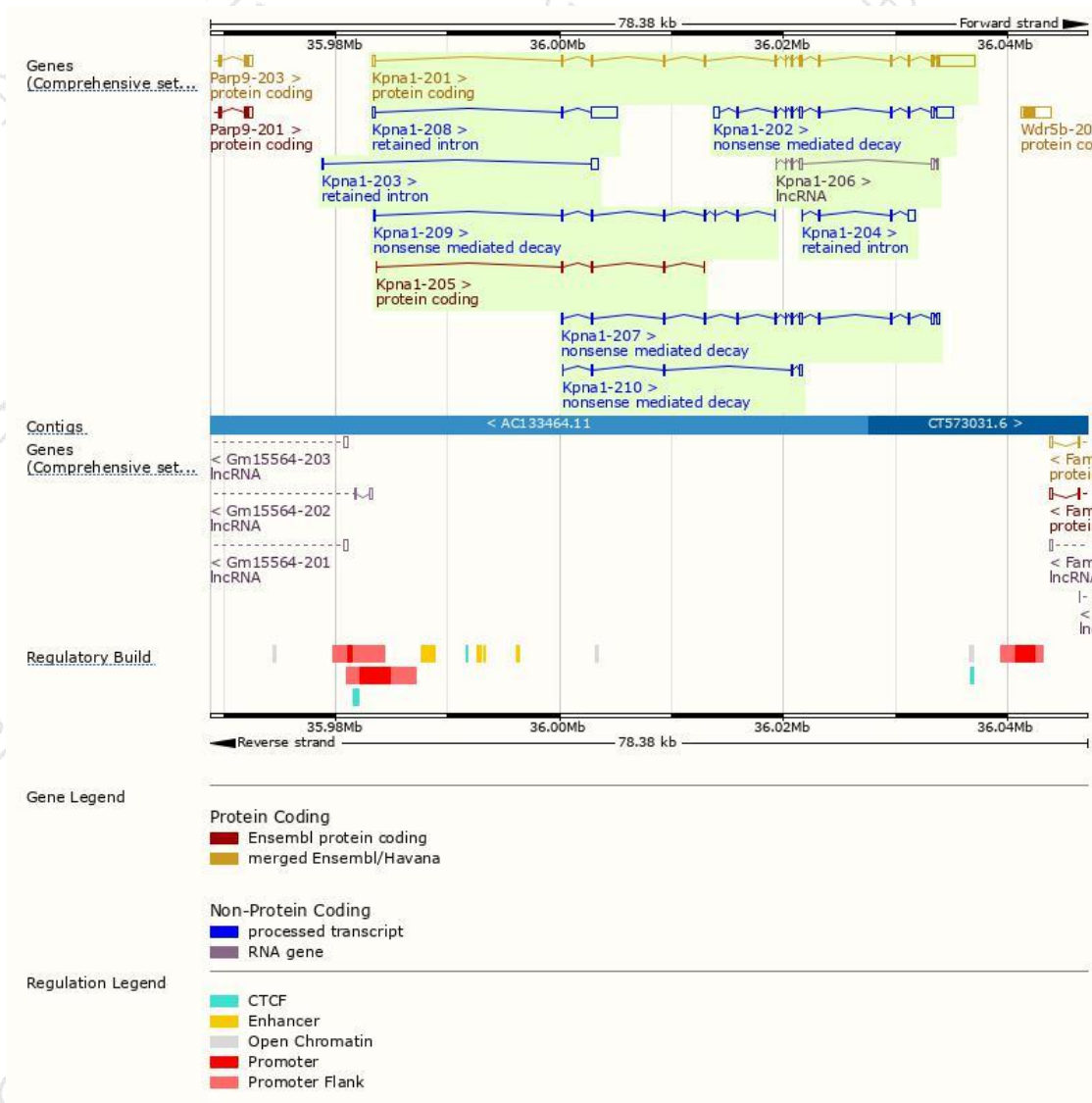
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kpna1-201	ENSMUST00000004054.12	5039	538aa	Protein coding	CCDS28144	Q60960	TSL:1 GENCODE basic APPRIS P1
Kpna1-205	ENSMUST00000173555.7	442	119aa	Protein coding	-	G3UWJ8	CDS 3' incomplete TSL:5
Kpna1-202	ENSMUST00000172534.7	2960	45aa	Nonsense mediated decay	-	G3UYD2	TSL:5
Kpna1-207	ENSMUST00000173696.7	1740	182aa	Nonsense mediated decay	-	G3UZK5	TSL:5
Kpna1-209	ENSMUST00000174500.7	780	145aa	Nonsense mediated decay	-	G3UXT6	TSL:5
Kpna1-210	ENSMUST00000174737.1	532	98aa	Nonsense mediated decay	-	G3UXW7	CDS 5' incomplete TSL:5
Kpna1-208	ENSMUST00000173715.1	2664	No protein	Retained intron	-	-	TSL:1
Kpna1-204	ENSMUST00000173469.1	815	No protein	Retained intron	-	-	TSL:2
Kpna1-203	ENSMUST00000172991.1	667	No protein	Retained intron	-	-	TSL:1
Kpna1-206	ENSMUST00000173641.1	690	No protein	lncRNA	-	-	TSL:5

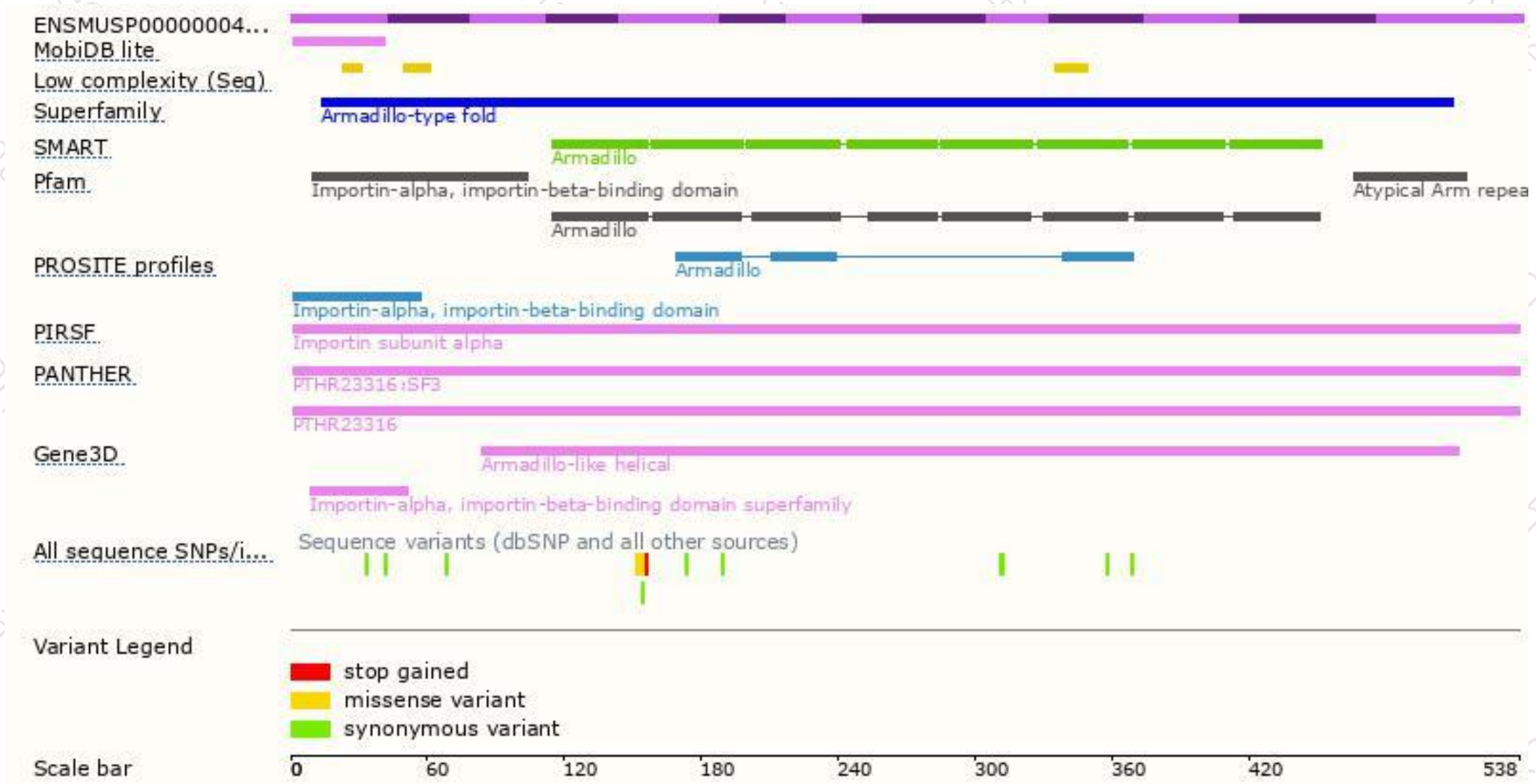
The strategy is based on the design of *Kpna1-201* transcript,The transcription is shown below



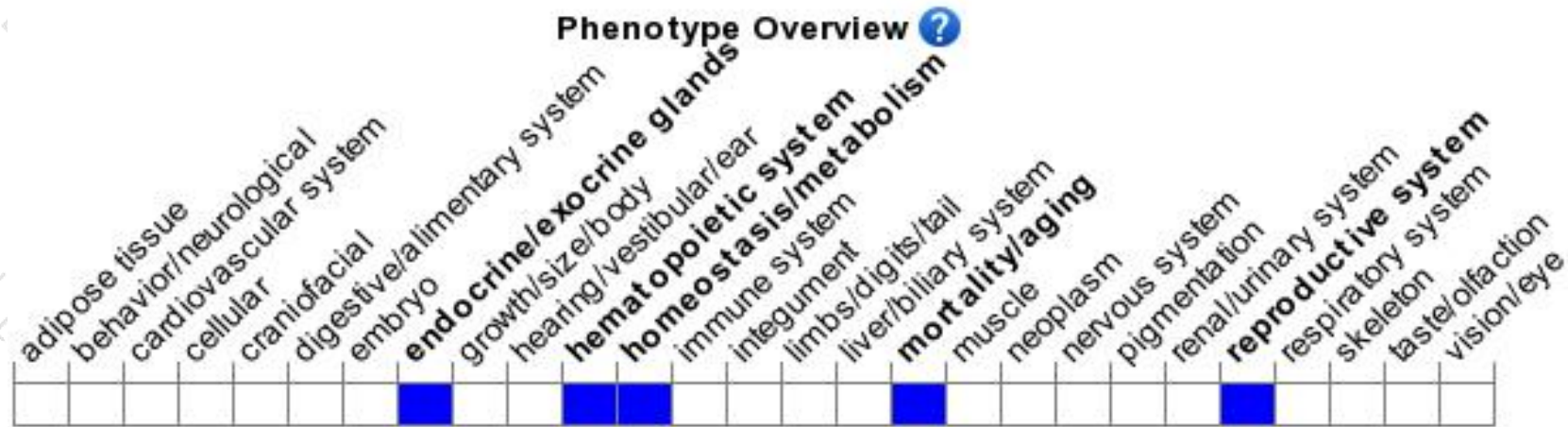
Genomic location distribution



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 do not display any nervous system or behavioral abnormalities.

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

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