

Kpna7 Cas9-KO Strategy

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Project Overview

Project Name

Kpna7

Project type

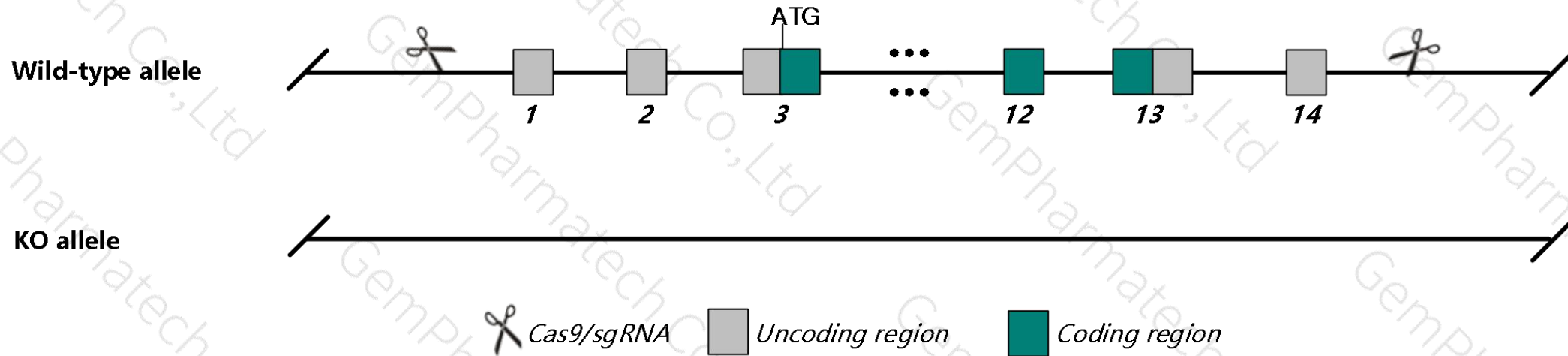
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kpna7* gene. The schematic diagram is as follows:



- The *Kpna7* gene has 6 transcripts. According to the structure of *Kpna7* gene, exon1-exon14 of *Kpna7-202* (ENSMUST00000110673.7) 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 *Kpna7* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous or heterozygous for a null mutation display smaller litter sizes with preferential loss of females and accelerated cell cycles post fertilization resulting in loss of embryos.
- The effect of transcripts 204,206 is unknown.
- The *Kpna7* gene is located on the Chr5. 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)

Kpna7 karyopherin alpha 7 (importin alpha 8) [*Mus musculus* (house mouse)]

Gene ID: 381686, updated on 10-Oct-2019

Summary

Official Symbol	Kpna7 provided by MGI
Official Full Name	karyopherin alpha 7 (importin alpha 8) provided by MGI
Primary source	MGI:MGI:2141165
See related	Ensembl:ENSMUSG00000038770
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	Gm1055; AW146299
Expression	Biased expression in ovary adult (RPKM 5.4) and testis adult (RPKM 2.0) See more
Orthologs	human all

Genomic context

Location: 5; 5 G2

Exon count: 14

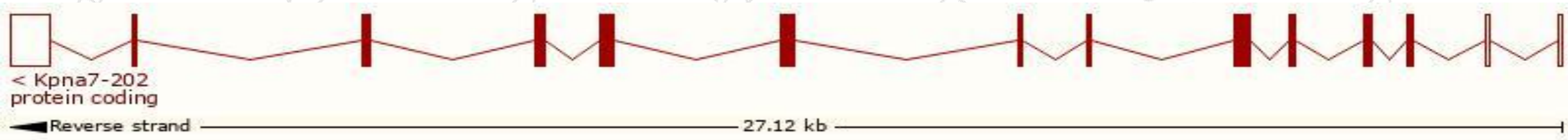
See Kpna7 in [Genome Data Viewer](#)

Transcript information (Ensembl)

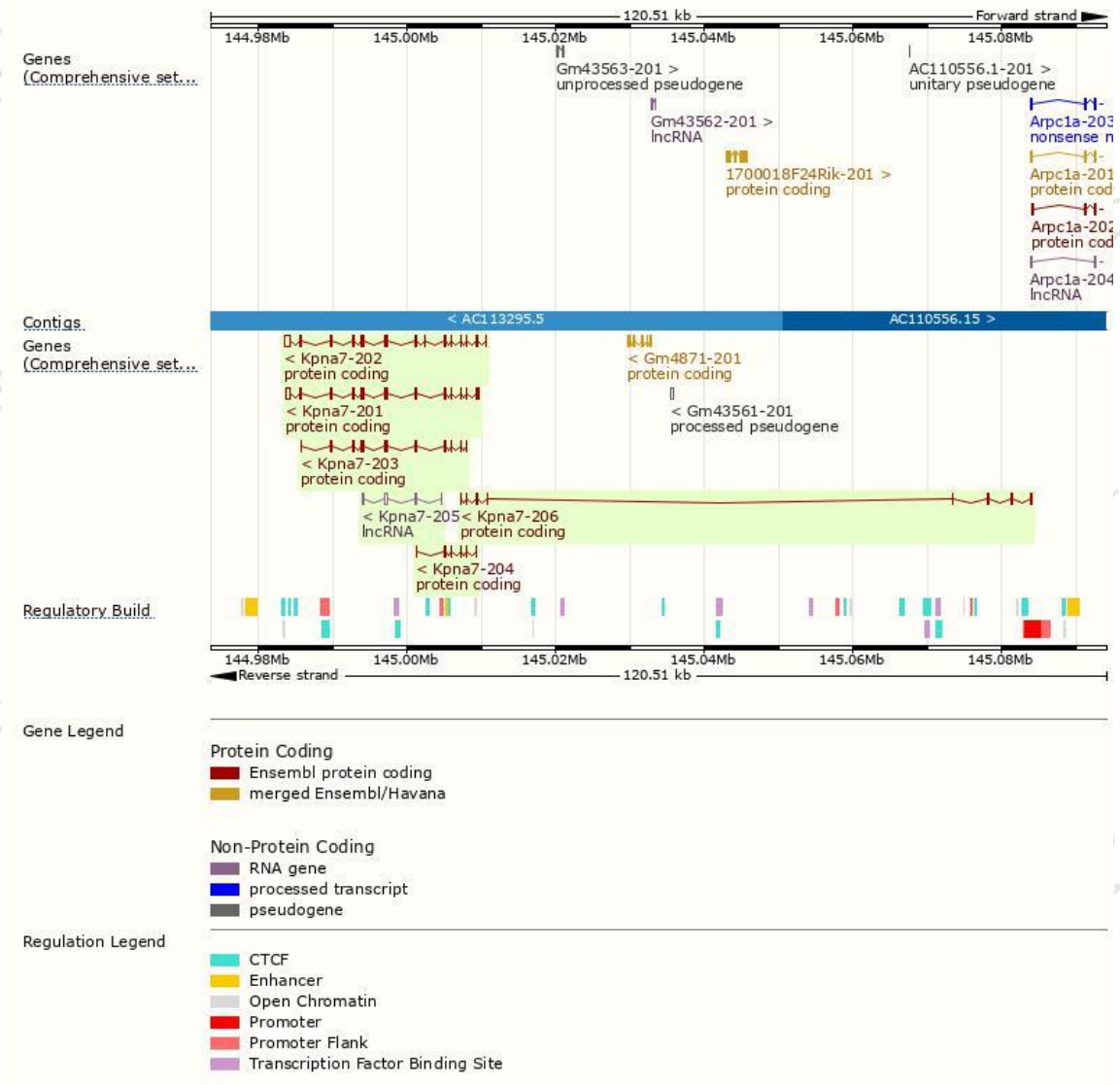
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kpna7-202	ENSMUST00000110673.7	2453	520aa	Protein coding	CCDS84996	C0LLJ0	TSL:5 GENCODE basic APPRIS ALT2
Kpna7-201	ENSMUST00000110672.7	2262	499aa	Protein coding	CCDS19852	C0LLJ0	TSL:1 GENCODE basic APPRIS P3
Kpna7-203	ENSMUST00000116454.9	1500	499aa	Protein coding	CCDS19852	C0LLJ0	TSL:1 GENCODE basic APPRIS P3
Kpna7-206	ENSMUST00000151196.1	676	38aa	Protein coding	-	D3Z0I2	CDS 3' incomplete TSL:5
Kpna7-204	ENSMUST00000139024.7	598	166aa	Protein coding	-	D3Z2P7	CDS 3' incomplete TSL:5
Kpna7-205	ENSMUST00000142866.1	538	No protein	lncRNA	-	-	TSL:2

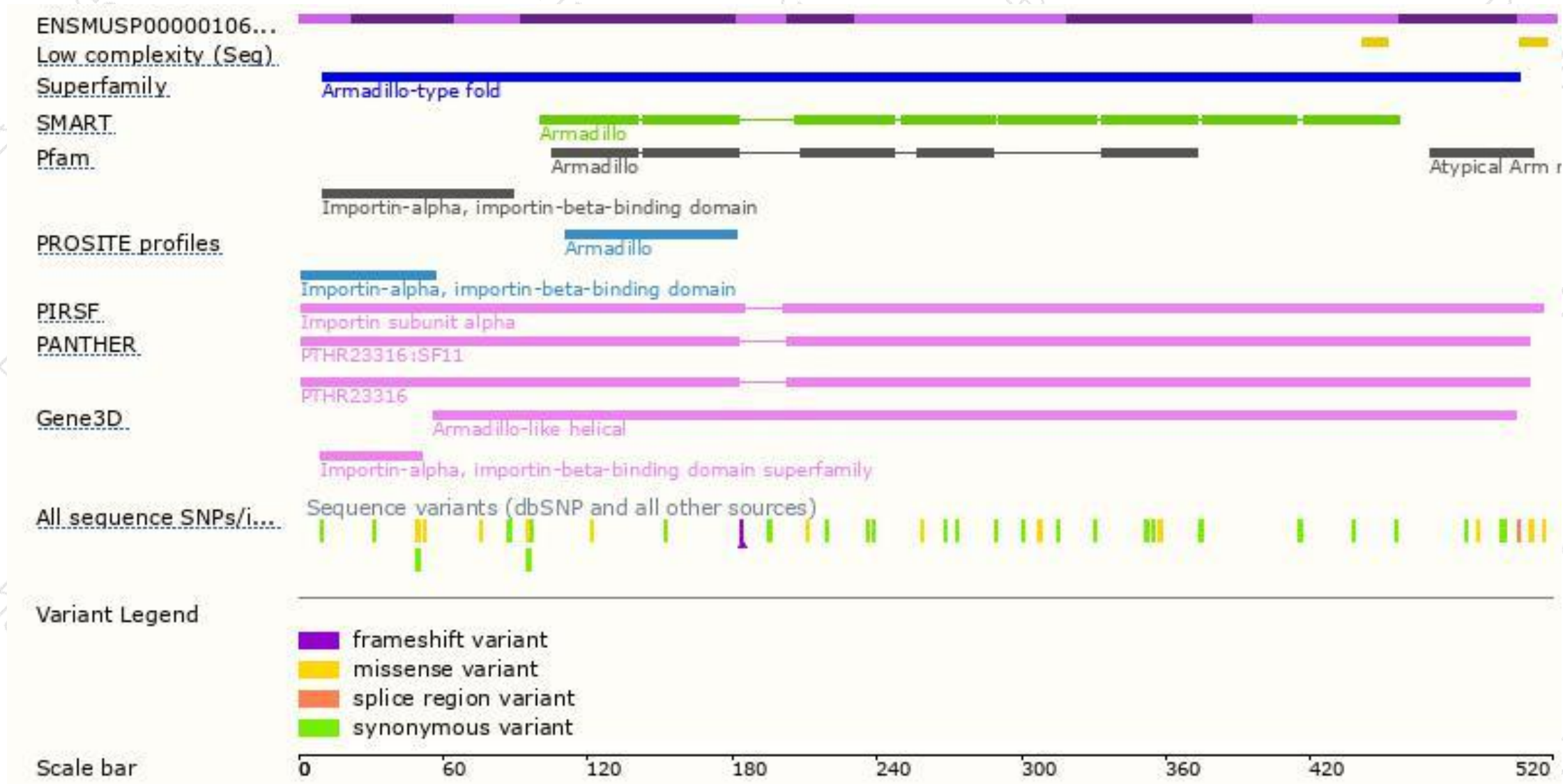
The strategy is based on the design of *Kpna7-202* transcript,The transcription is shown below



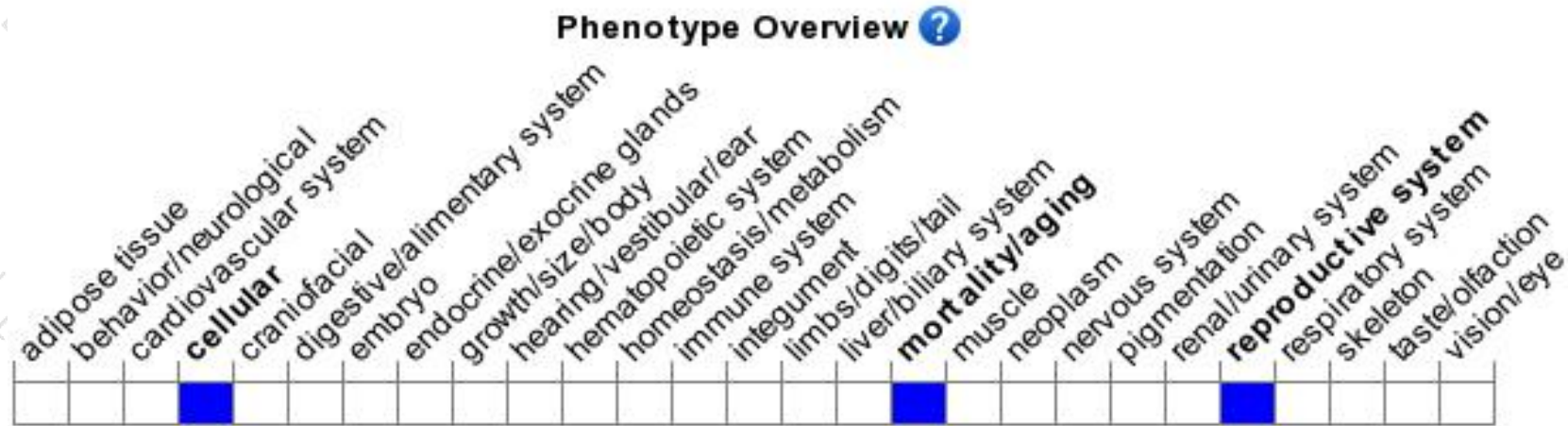
Genomic location distribution



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 or heterozygous for a null mutation display smaller litter sizes with preferential loss of females and accelerated cell cycles post fertilization resulting in loss of embryos.

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

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