

***Katna1* Cas9-KO Strategy**

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Project Overview

Project Name

Katna1

Project type

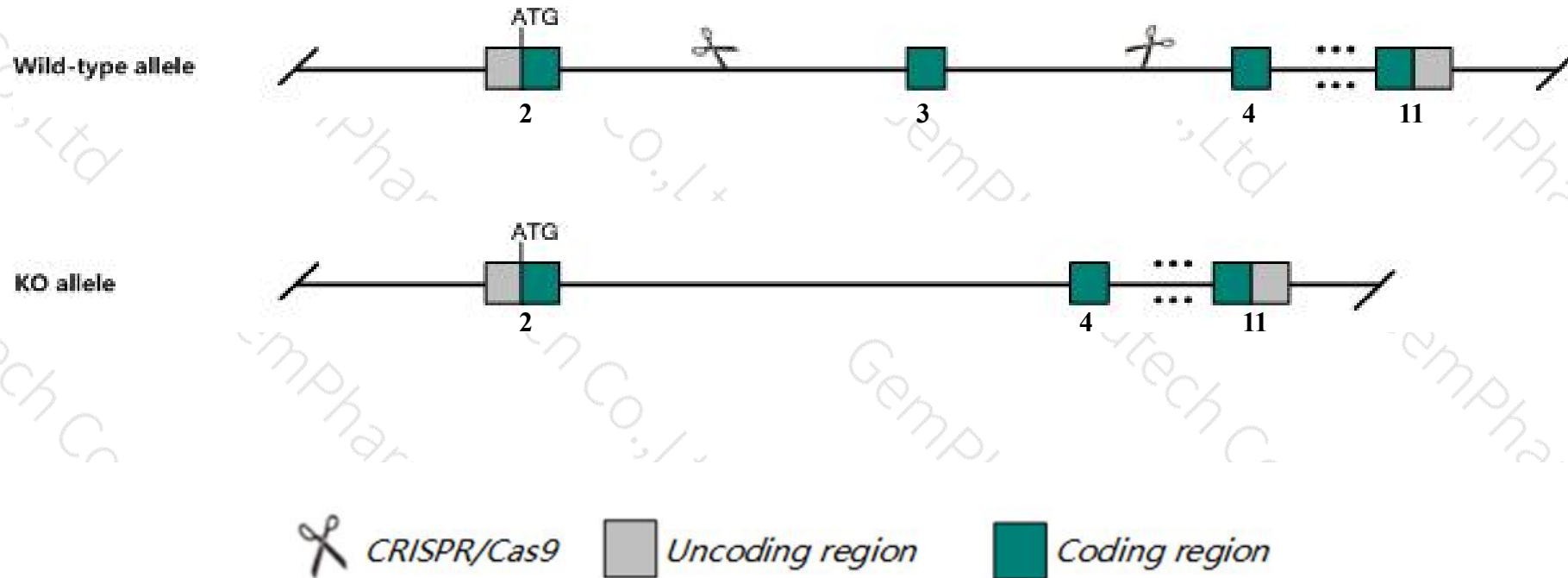
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Katnal* gene has 6 transcripts. According to the structure of *Katnal* gene, exon3 of *Katnal*-202 (ENSMUST00000165806.7) transcript is recommended as the knockout region. The region contains 158bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Katnal* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Katnal* gene is located on the Chr10. 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)

Katna1 katanin p60 (ATPase-containing) subunit A1 [*Mus musculus* (house mouse)]

Gene ID: 23924, updated on 12-Aug-2019

Summary

Official Symbol Katna1 provided by [MGI](#)

Official Full Name katanin p60 (ATPase-containing) subunit A1 provided by [MGI](#)

Primary source [MGI:MGI:1344353](#)

See related [Ensembl:ENSMUSG00000019794](#)

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

Expression Ubiquitous expression in CNS E11.5 (RPKM 6.5), placenta adult (RPKM 5.6) and 27 other tissues [See more](#)

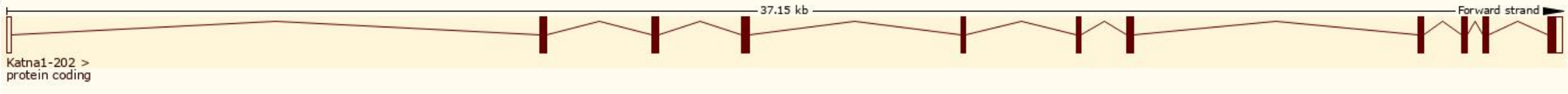
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

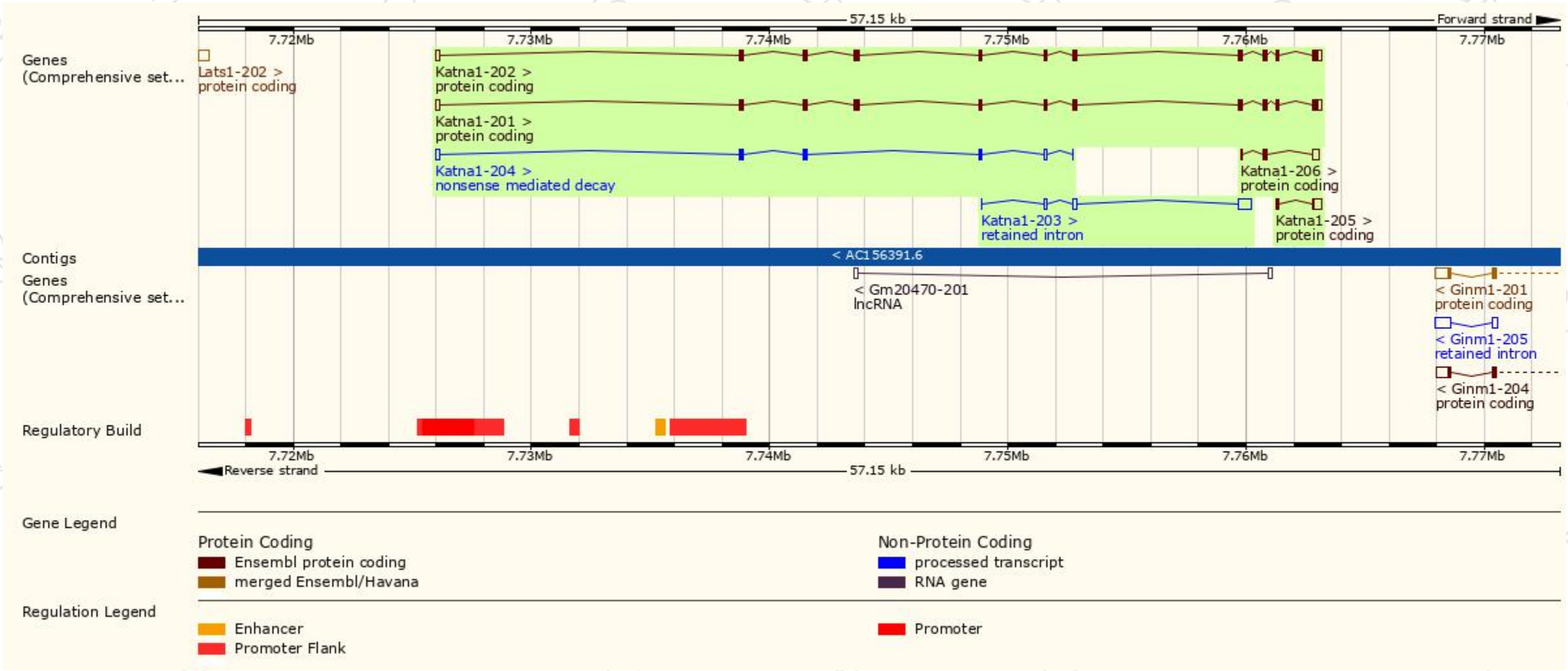
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Katna1-203	ENSMUST00000172400.1	825	No protein	Retained intron	-	-	TSL:2
Katna1-202	ENSMUST00000165806.7	1775	493aa	Protein coding	CCDS23689	E9PZI6	TSL:1 GENCODE basic APPRIS P2
Katna1-201	ENSMUST00000019929.12	1774	491aa	Protein coding	-	E9QKG2	TSL:1 GENCODE basic APPRIS ALT1
Katna1-205	ENSMUST00000173511.1	488	54aa	Protein coding	-	G3UYX0	CDS 5' incomplete TSL:5
Katna1-206	ENSMUST00000174007.1	462	66aa	Protein coding	-	G3UWK1	CDS 5' incomplete TSL:5
Katna1-204	ENSMUST00000173400.7	683	130aa	Nonsense mediated decay	-	G3UX83	TSL:5

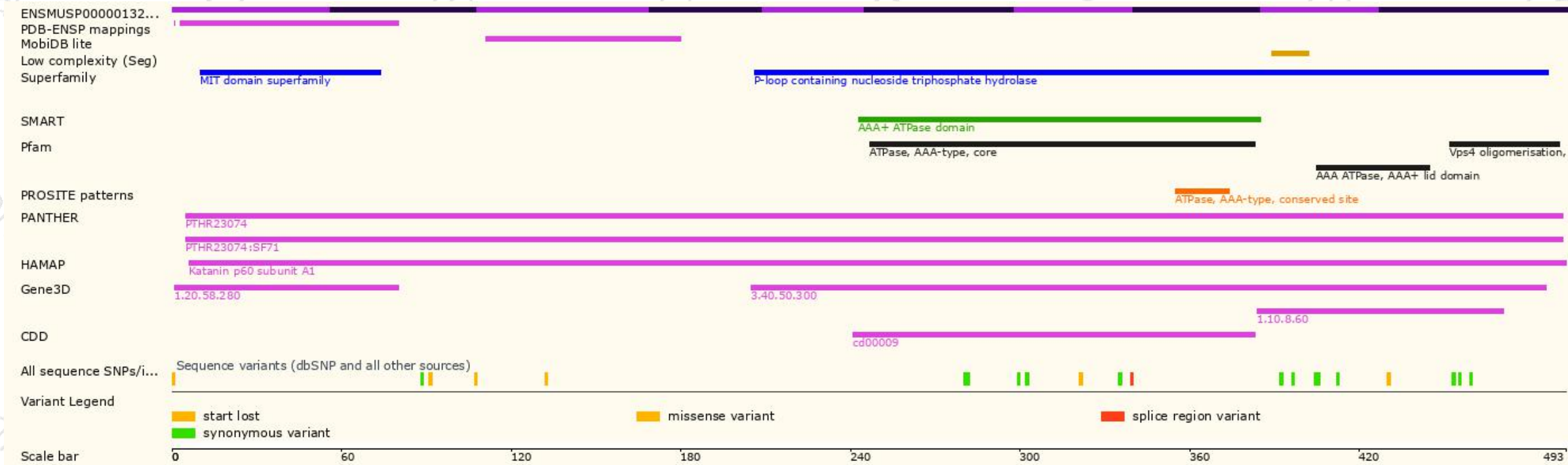
The strategy is based on the design of *Katna1-202* transcript, the transcription is shown below:



Genomic location distribution



Protein domain



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

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