

Cnksr3 Cas9-KO Strategy

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Project Overview

Project Name

Cnksr3

Project type

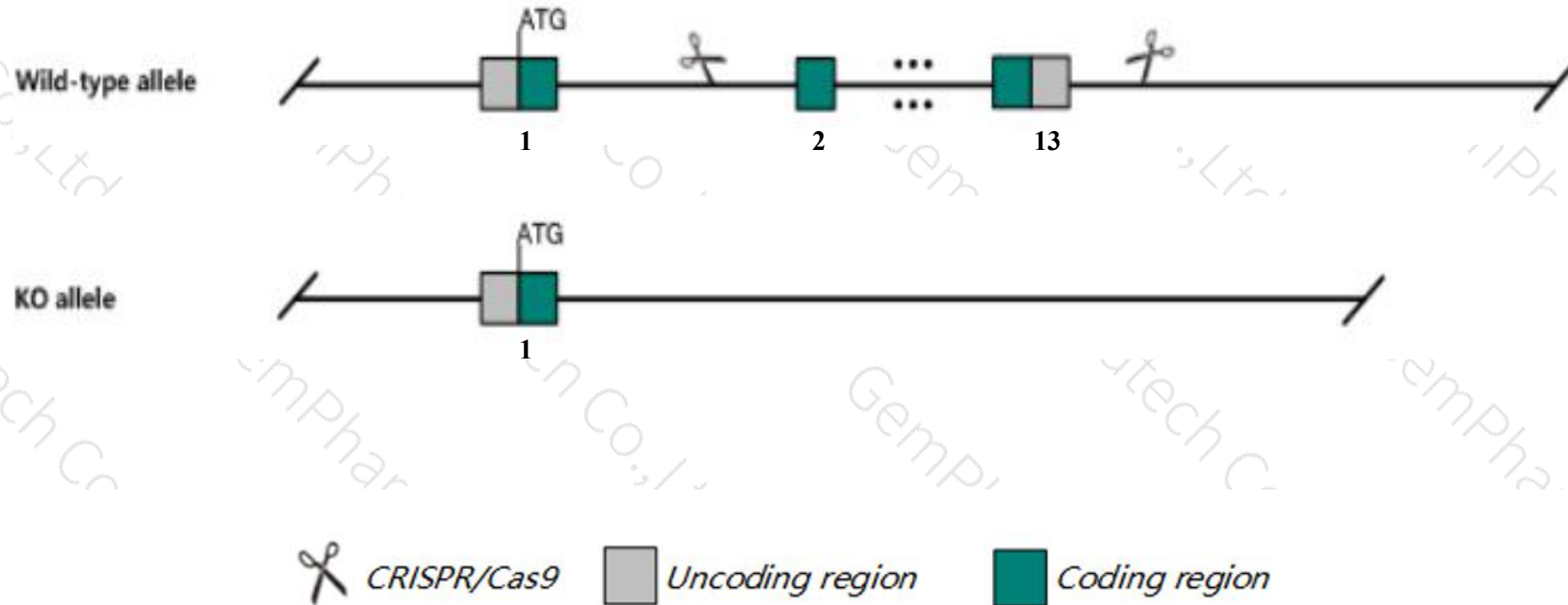
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cnksr3* gene. The schematic diagram is as follows:



- The *Cnksr3* gene has 2 transcripts. According to the structure of *Cnksr3* gene, exon2-exon13 of *Cnksr3-201* (ENSMUST00000015346.11) 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 *Cnksr3* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Cnksr3* 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)

Cnksr3 Cnksr family member 3 [Mus musculus (house mouse)]

Gene ID: 215748, updated on 13-Mar-2020

Summary



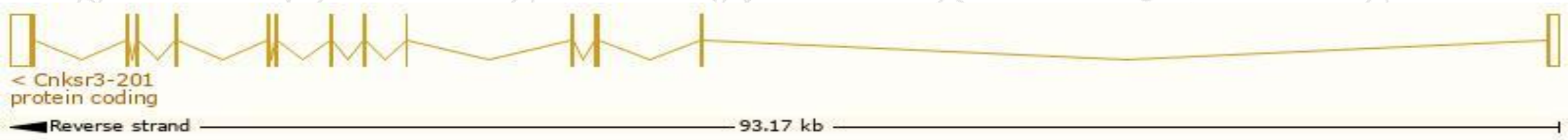
Official Symbol	Cnksr3 provided by MGI
Official Full Name	Cnksr family member 3 provided by MGI
Primary source	MGI:MGI:2674130
See related	Ensembl:ENSMUSG00000015202
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6820402C05, BC024086, Magi1
Expression	Ubiquitous expression in cerebellum adult (RPKM 8.5), bladder adult (RPKM 8.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

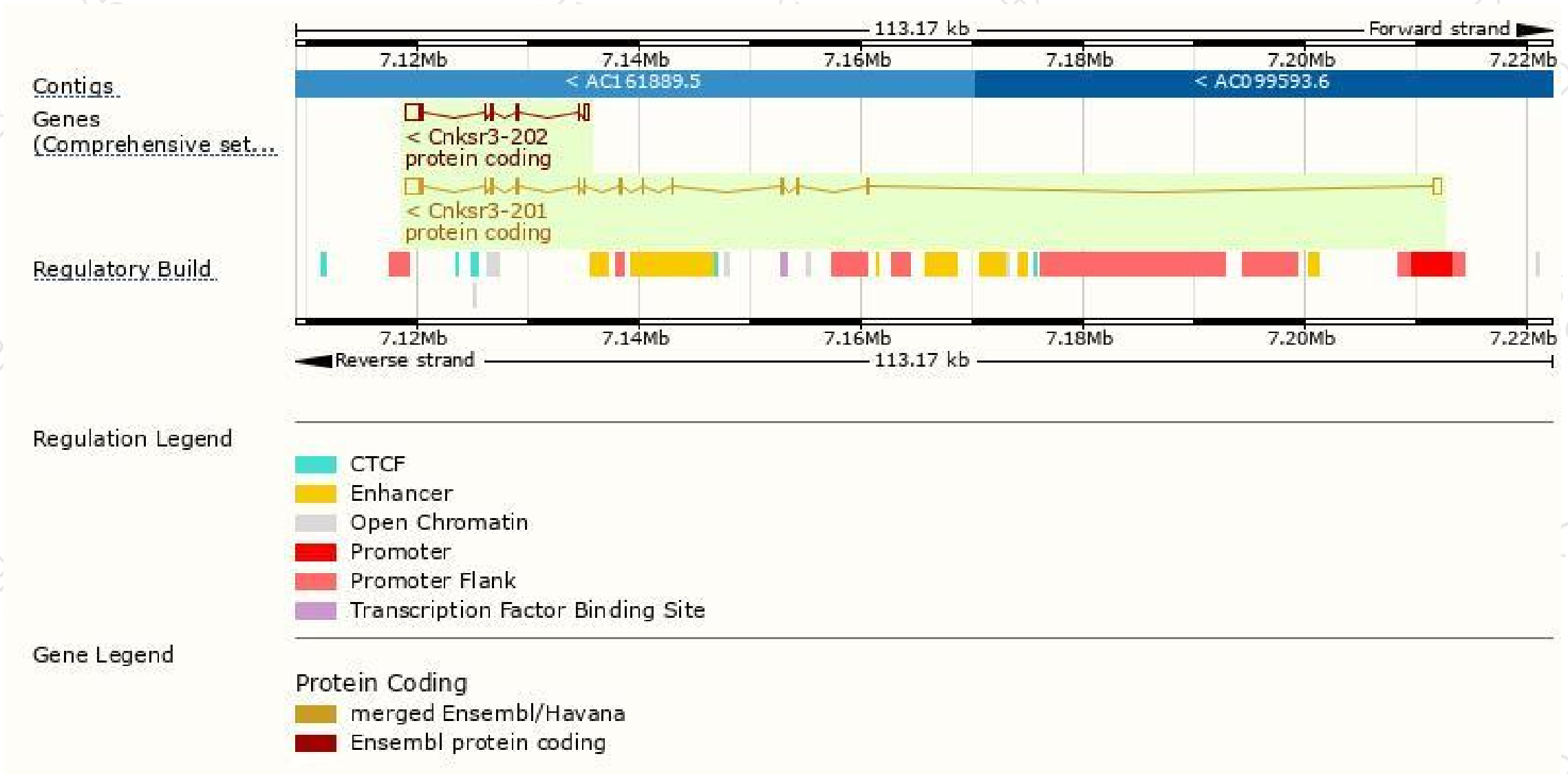
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnksr3-201	ENSMUST00000015346.11	3447	555aa	Protein coding	CCDS56690	Q8BMA3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Cnksr3-202	ENSMUST00000150282.1	2554	314aa	Protein coding	-	Q8BMA3	TSL:1 GENCODE basic

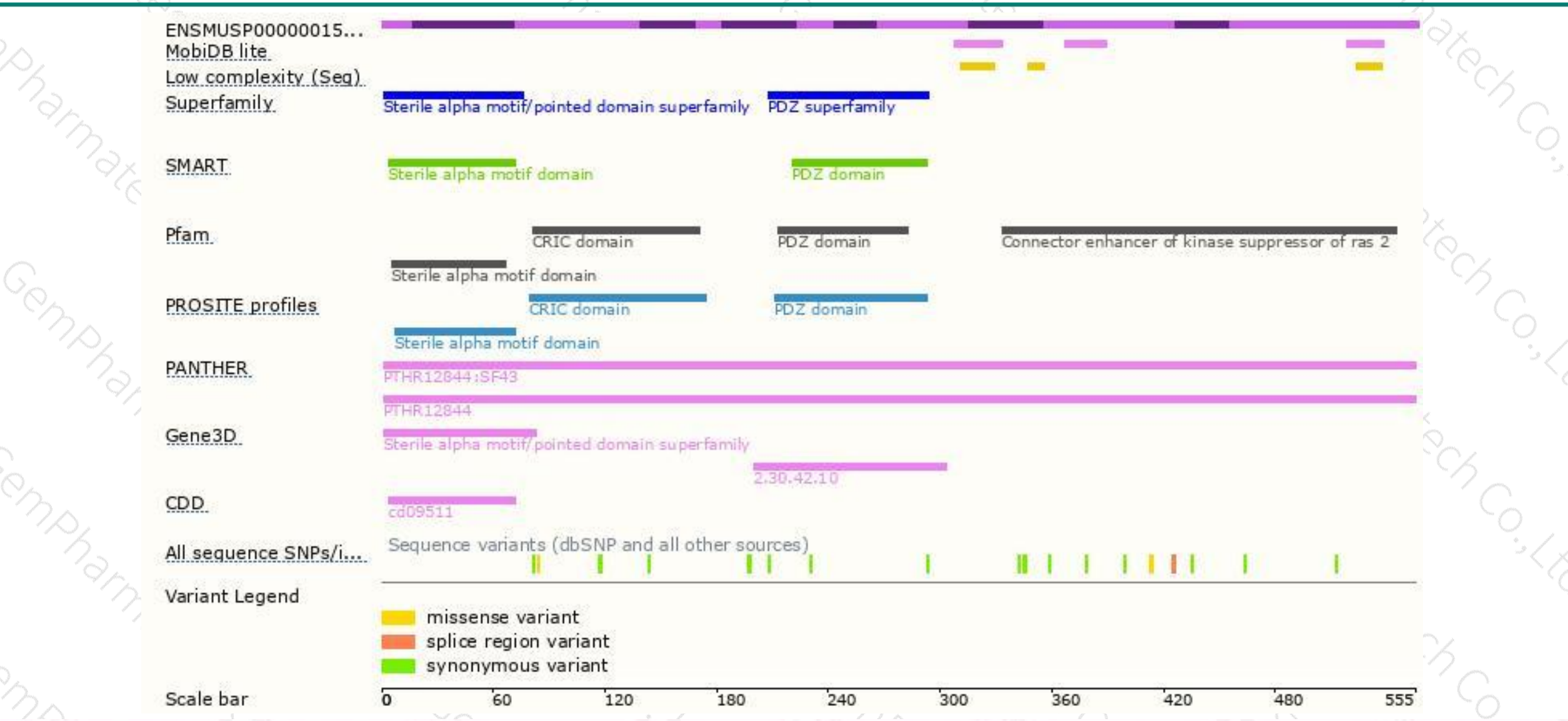
The strategy is based on the design of *Cnksr3-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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