

# ***Snu13* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Snu13***

**Project type**

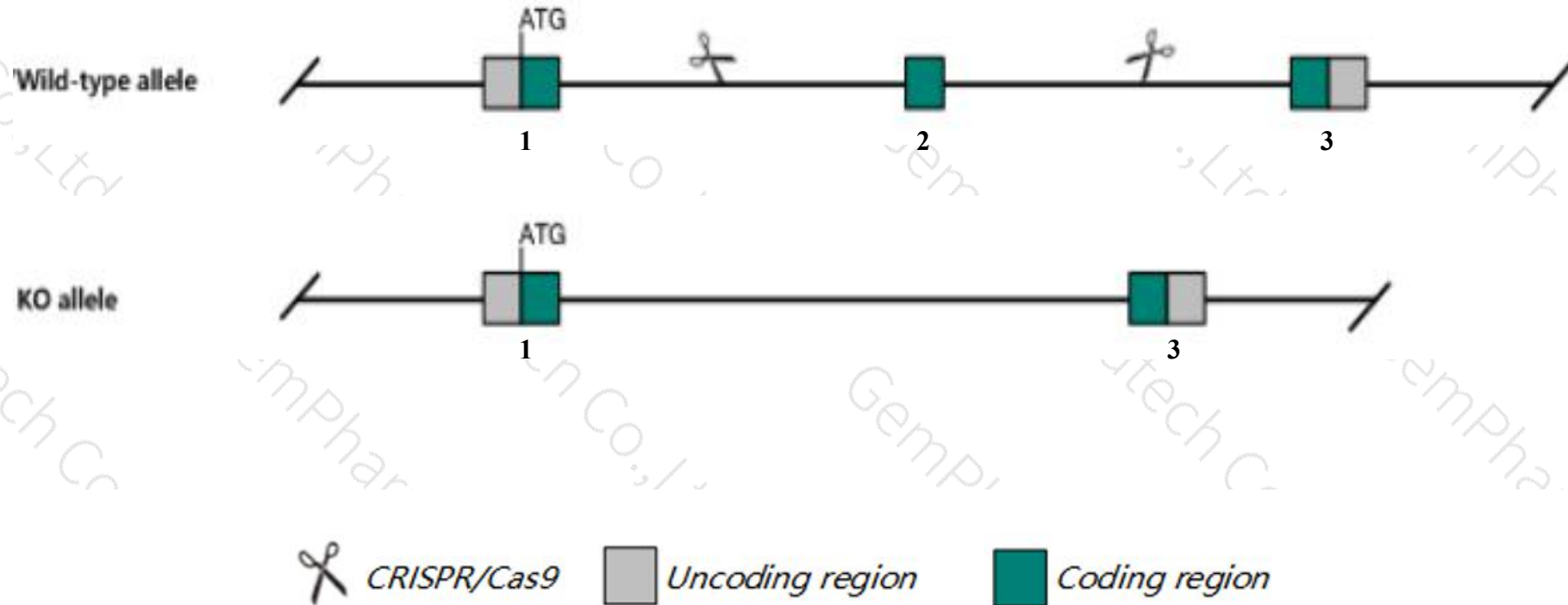
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snu13* gene. The schematic diagram is as follows:



- The *Snu13* gene has 4 transcripts. According to the structure of *Snu13* gene, exon2 of *Snu13-202* (ENSMUST00000080622.8) transcript is recommended as the knockout region. The region contains 121bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snu13* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Snu13* gene is located on the Chr15. 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.



## Snu13 SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5) [Mus musculus (house mouse)]

Gene ID: 20826, updated on 13-Mar-2020

### Summary



**Official Symbol** Snu13 provided by [MGI](#)

**Official Full Name** SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5) provided by [MGI](#)

**Primary source** [MGI:MGI:893586](#)

**See related** [Ensembl:ENSMUSG00000063480](#)

**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** FA-1, Fta1, Nhp211, Ssfa1

**Expression** Ubiquitous expression in liver E14.5 (RPKM 88.8), liver E14 (RPKM 82.9) and 28 other tissues [See more](#)

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

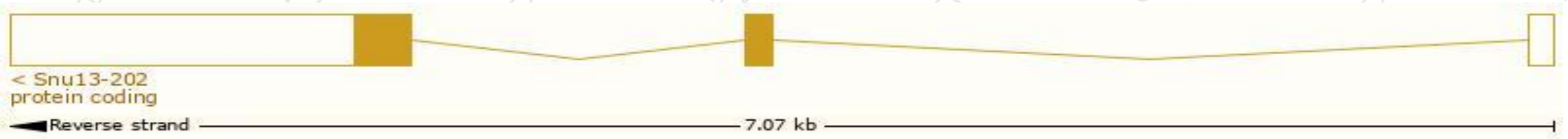
# Transcript information Ensembl



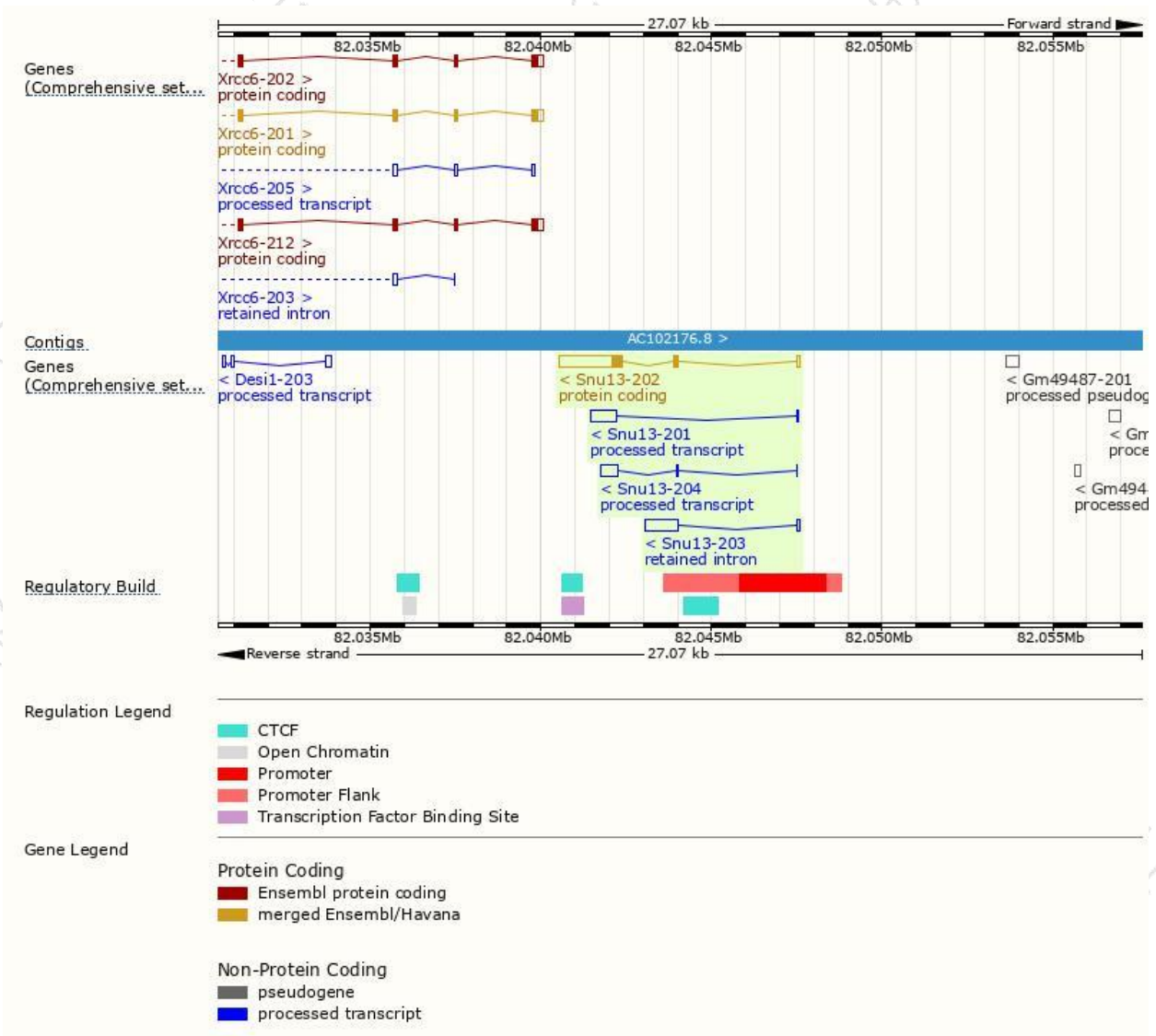
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snu13-202	<a href="#">ENSMUST00000080622.8</a>	2077	<a href="#">128aa</a>	Protein coding	<a href="#">CCDS37154</a>	<a href="#">Q9D0T1</a>	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
Snu13-201	<a href="#">ENSMUST00000072904.4</a>	769	No protein	Processed transcript	-	-	TSL:5
Snu13-204	<a href="#">ENSMUST00000230953.1</a>	593	No protein	Processed transcript	-	-	
Snu13-203	<a href="#">ENSMUST00000166578.1</a>	1061	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Snu13-202* transcript,the transcription is shown below:

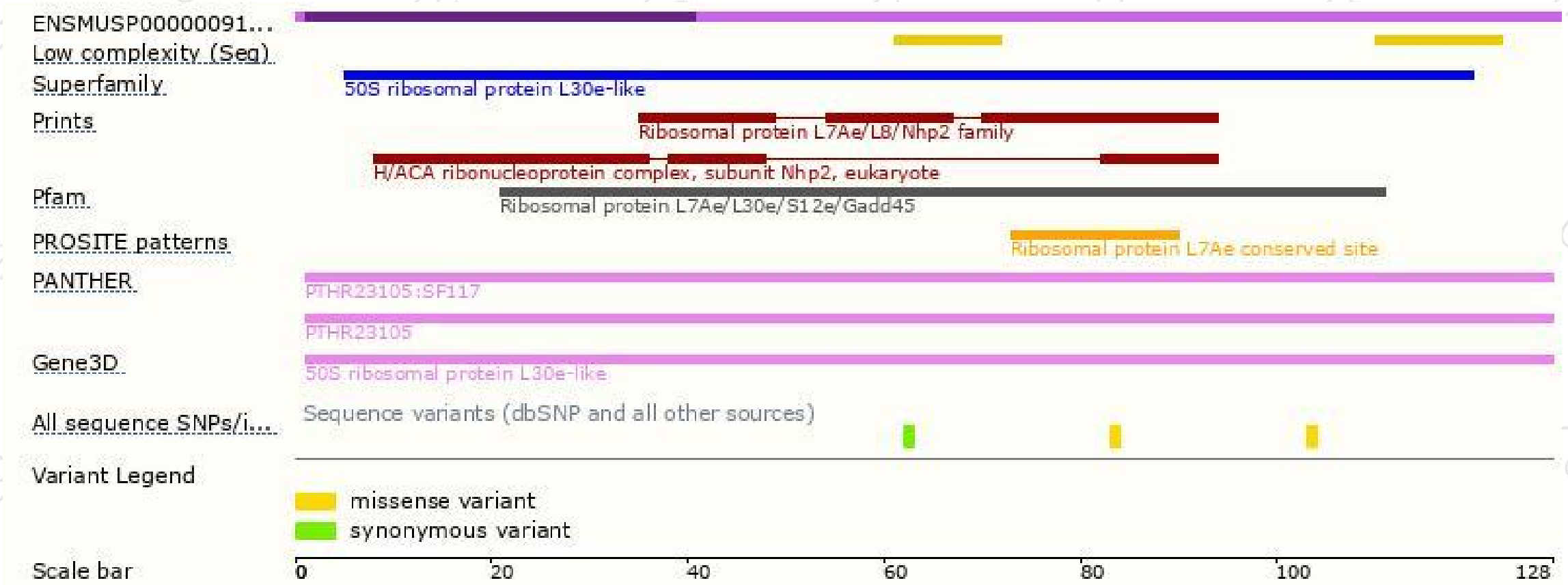


# Genomic location distribution





# Protein domain



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

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