

# *Nsmce1* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Nsmce1*

**Project type**

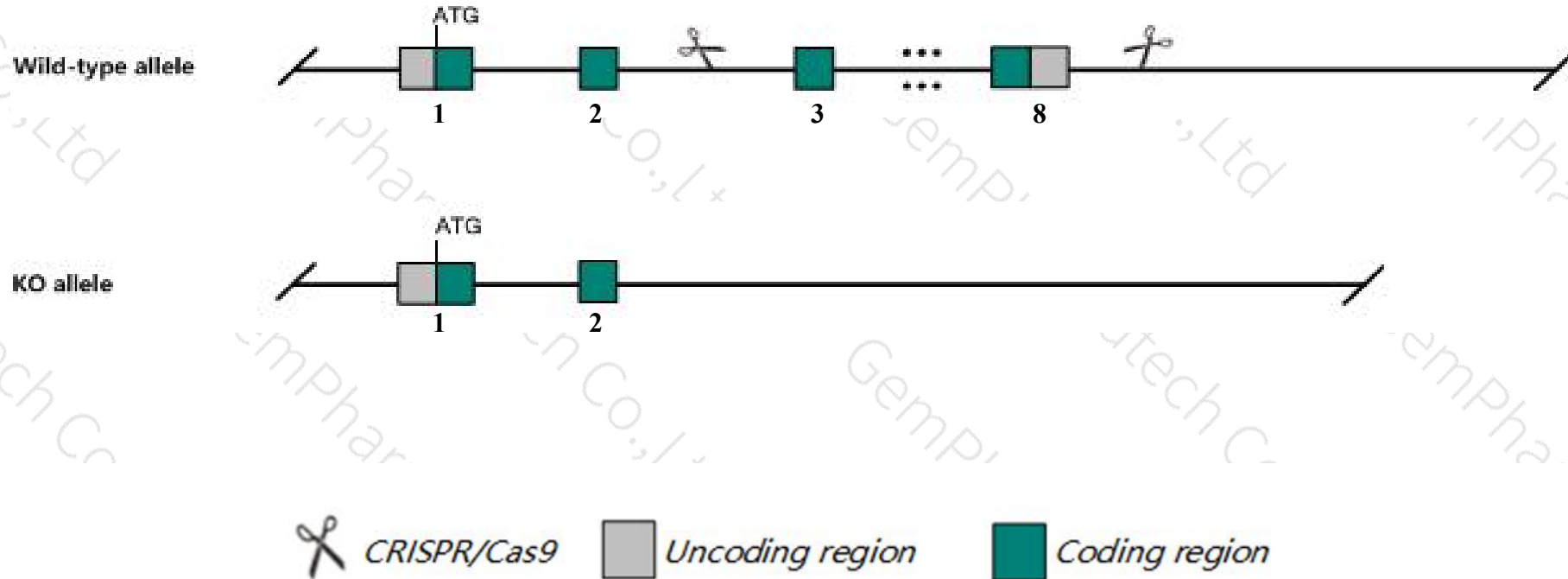
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nsmce1* gene. The schematic diagram is as follows:



- The *Nsmce1* gene has 3 transcripts. According to the structure of *Nsmce1* gene, exon3-exon8 of *Nsmce1-201* (ENSMUST00000033006.13) transcript is recommended as the knockout region. The region contains 665bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nsmce1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Nsmce1* gene is located on the Chr7. 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)

## Nsmce1 NSE1 homolog, SMC5-SMC6 complex component [Mus musculus (house mouse)]

Gene ID: 67711, updated on 6-Apr-2019

### Summary



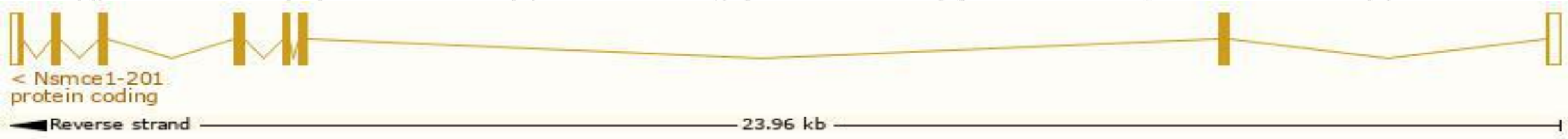
<b>Official Symbol</b>	Nsmce1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	NSE1 homolog, SMC5-SMC6 complex component provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914961</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030750</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2510027N19Rik
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 62.5), placenta adult (RPKM 30.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

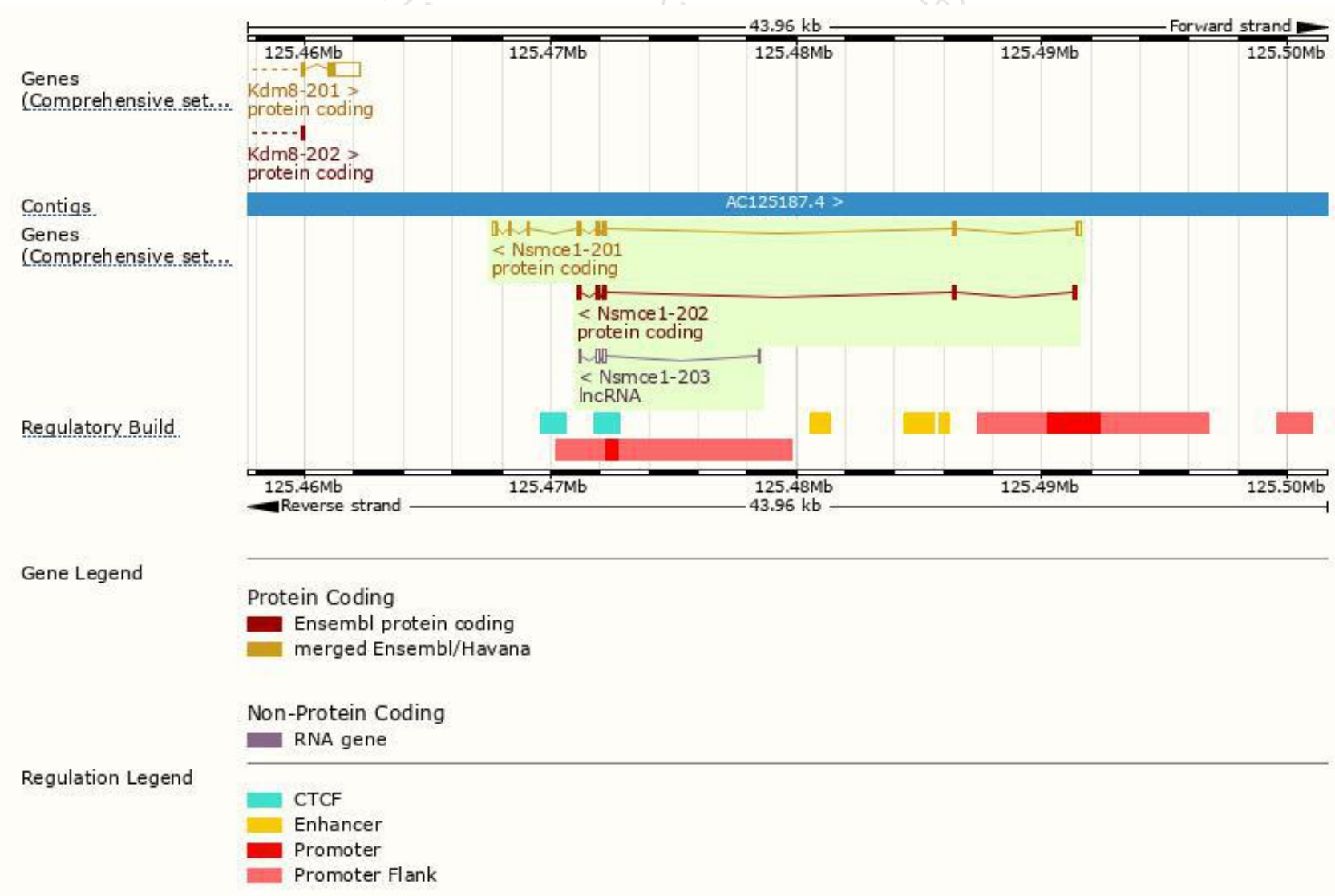
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nsmce1-201	<a href="#">ENSMUST00000033006.13</a>	1120	<a href="#">280aa</a>	Protein coding	<a href="#">CCDS21822</a>	<a href="#">A0A0R4J0C0</a>	TSL:1 GENCODE basic APPRIS P1
Nsmce1-202	<a href="#">ENSMUST00000138616.2</a>	598	<a href="#">200aa</a>	Protein coding	-	<a href="#">F6VZ99</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Nsmce1-203	<a href="#">ENSMUST00000149289.1</a>	398	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Nsmce1-201* transcript,The transcription is shown below

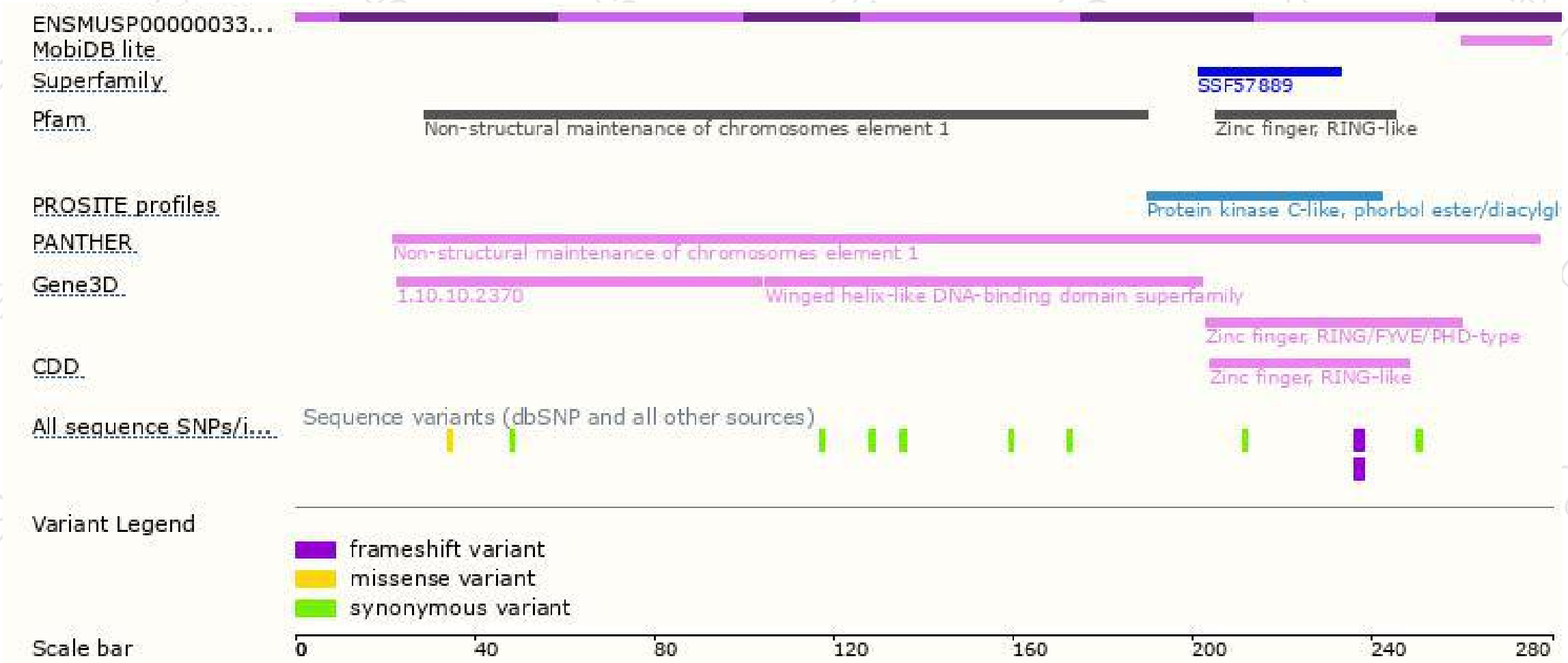


# Genomic location distribution





# Protein domain



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

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