

# ***Mettl17* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Mettl17***

**Project type**

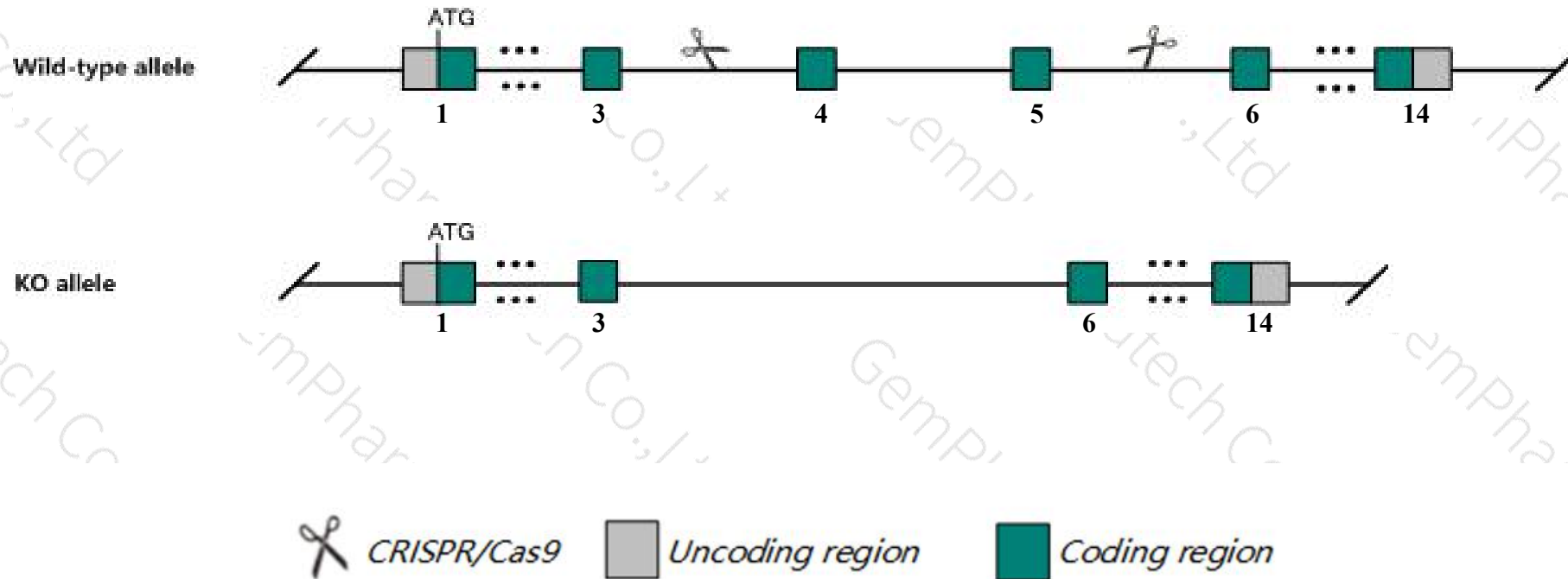
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mettl17* gene. The schematic diagram is as follows:



- The *Mettl17* gene has 16 transcripts. According to the structure of *Mettl17* gene, exon4-exon5 of *Mettl17-201* (ENSMUST00000047899.12) transcript is recommended as the knockout region. The region contains 164bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mettl17* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Mettl17*-211,213,216 may not be affected.
- The *Mettl17* gene is located on the Chr14. 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)

## Mettl17 methyltransferase like 17 [Mus musculus (house mouse)]

Gene ID: 52535, updated on 31-Jan-2019

### Summary



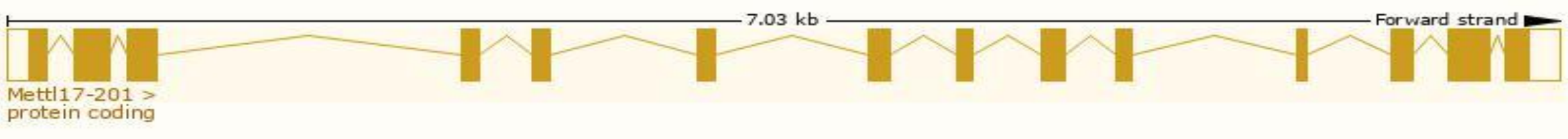
<b>Official Symbol</b>	Mettl17 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	methyltransferase like 17 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1098577</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000004561</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	2310032K15Rik, D14Ertd209e, Mett11d1
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 18.3), CNS E14 (RPKM 17.3) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

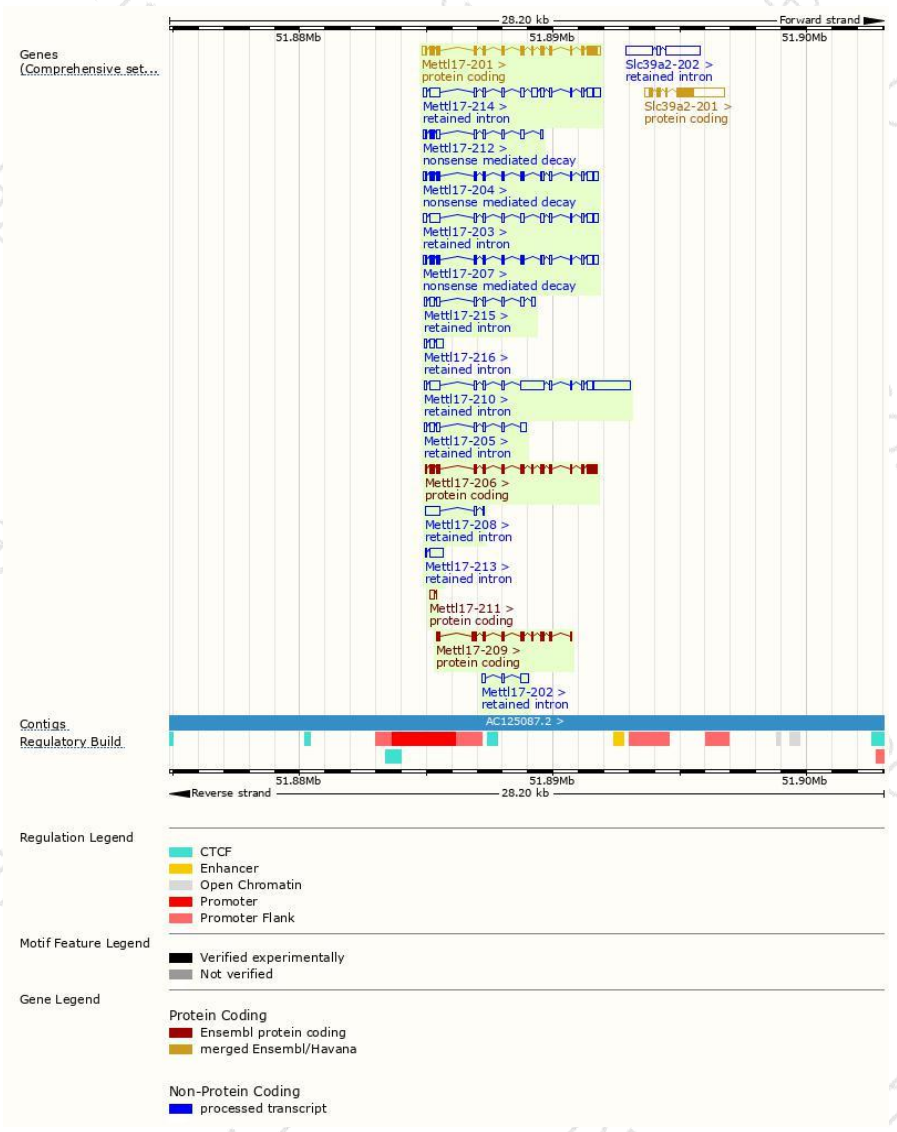
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mettl17-201	<a href="#">ENSMUST00000047899.12</a>	1623	<a href="#">461aa</a>	Protein coding	<a href="#">CCDS36913</a>	<a href="#">Q3U2U7</a>	TSL:1 GENCODE basic APPRIS P2
Mettl17-206	<a href="#">ENSMUST00000164902.7</a>	1461	<a href="#">486aa</a>	Protein coding	-	<a href="#">E9Q7K9</a>	TSL:5 GENCODE basic APPRIS ALT2
Mettl17-209	<a href="#">ENSMUST00000165568.2</a>	840	<a href="#">280aa</a>	Protein coding	-	<a href="#">F7AGB5</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:5
Mettl17-211	<a href="#">ENSMUST00000167984.1</a>	197	<a href="#">14aa</a>	Protein coding	-	<a href="#">E9PYZ3</a>	CDS 3' incomplete TSL:3
Mettl17-207	<a href="#">ENSMUST00000165100.7</a>	1430	<a href="#">236aa</a>	Nonsense mediated decay	-	<a href="#">E9Q0X9</a>	TSL:1
Mettl17-204	<a href="#">ENSMUST00000164252.7</a>	1426	<a href="#">236aa</a>	Nonsense mediated decay	-	<a href="#">E9Q0X9</a>	TSL:1
Mettl17-212	<a href="#">ENSMUST00000168217.7</a>	809	<a href="#">78aa</a>	Nonsense mediated decay	-	<a href="#">E9Q5R5</a>	TSL:5
Mettl17-210	<a href="#">ENSMUST00000166408.7</a>	3404	No protein	Retained intron	-	-	TSL:2
Mettl17-214	<a href="#">ENSMUST00000168413.7</a>	1844	No protein	Retained intron	-	-	TSL:2
Mettl17-203	<a href="#">ENSMUST00000163603.7</a>	1513	No protein	Retained intron	-	-	TSL:1
Mettl17-215	<a href="#">ENSMUST00000169019.7</a>	890	No protein	Retained intron	-	-	TSL:1
Mettl17-205	<a href="#">ENSMUST00000164801.7</a>	796	No protein	Retained intron	-	-	TSL:2
Mettl17-208	<a href="#">ENSMUST00000165150.1</a>	703	No protein	Retained intron	-	-	TSL:2
Mettl17-213	<a href="#">ENSMUST00000168409.1</a>	582	No protein	Retained intron	-	-	TSL:2
Mettl17-216	<a href="#">ENSMUST00000170887.7</a>	531	No protein	Retained intron	-	-	TSL:2
Mettl17-202	<a href="#">ENSMUST00000077846.6</a>	472	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Mettl17-201* transcript,The transcription is shown below

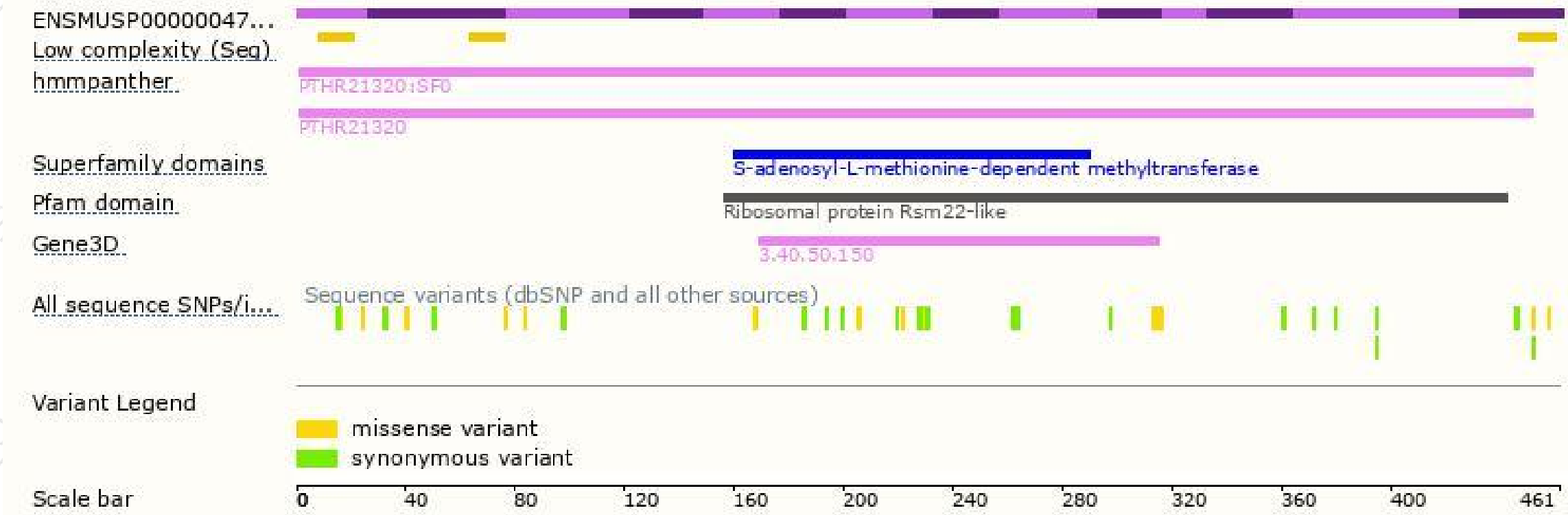


# Genomic location distribution





# Protein domain



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

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