

# *Prmt1* Cas9-KO Strategy

**Designer:**

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# Project Overview

**Project Name**

*Prmt1*

**Project type**

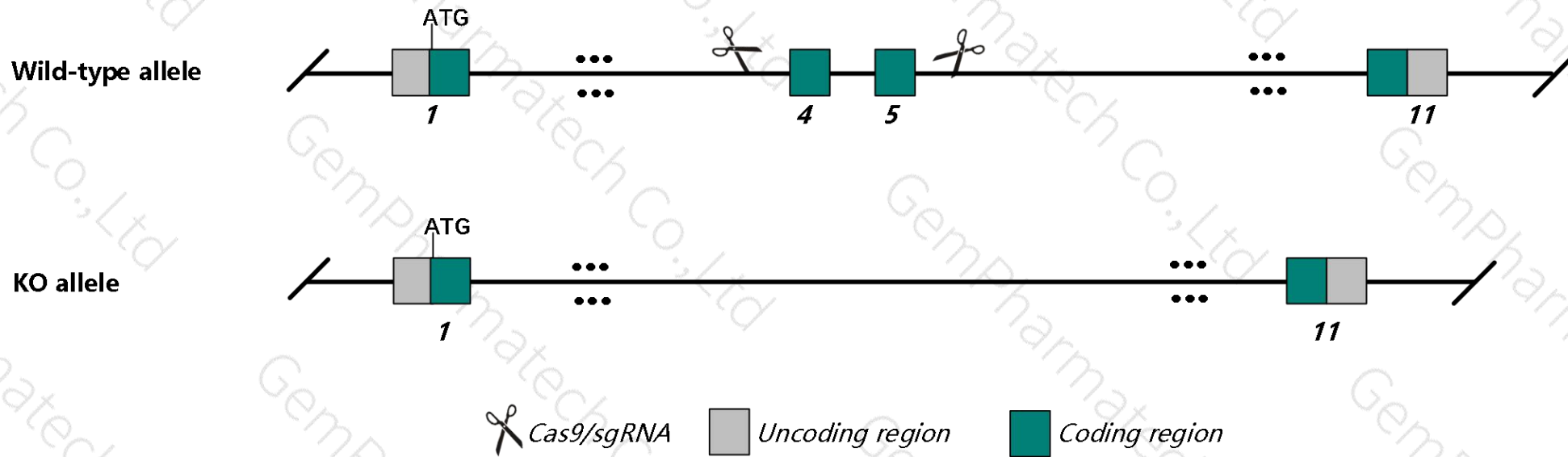
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt1* gene. The schematic diagram is as follows:



- The *Prmt1* gene has 14 transcripts. According to the structure of *Prmt1* gene, exon4-exon5 of *Prmt1*-202 (ENSMUST00000107843.10) transcript is recommended as the knockout region. The region contains 220bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prmt1* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, Embryos homozygous for a null mutation die before E6.5 and exhibit abnormal embryonic tissue morphology.
- The *Prmt1* 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)

## Prmt1 protein arginine N-methyltransferase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 15469, updated on 10-Aug-2019

### Summary

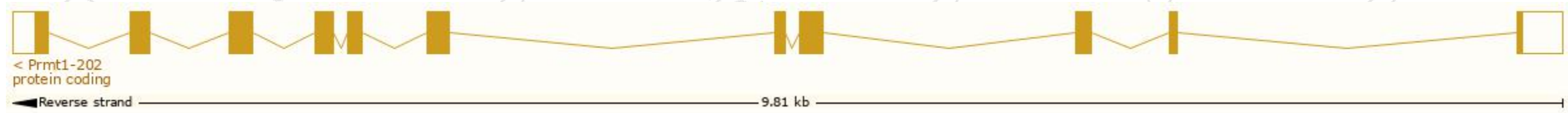
<b>Official Symbol</b>	Prmt1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	protein arginine N-methyltransferase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:107846</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000109324</a>
<b>Gene type</b>	protein coding
<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>	Mrmt1; Hrmt1l2; AW214366; 6720434D09Rik
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 124.9), CNS E18 (RPKM 124.2) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

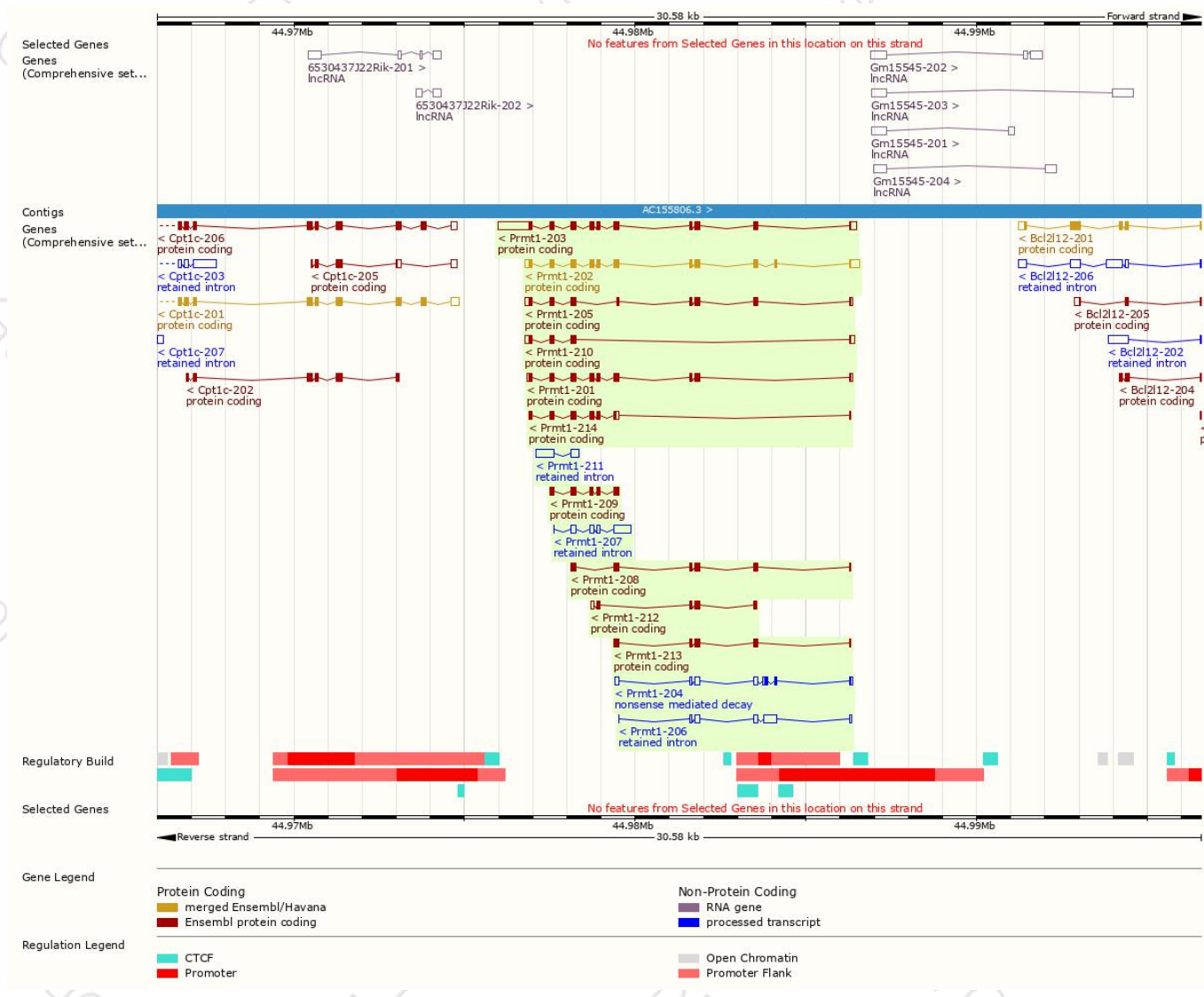
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prmt1-203	<a href="#">ENSMUST00000207370.1</a>	2147	<a href="#">353aa</a>	Protein coding	<a href="#">CCDS57547</a>	<a href="#">Q3UIG8</a> <a href="#">Q9JIF0</a>	TSL:1 GENCODE basic APPRIS ALT 1
Prmt1-202	<a href="#">ENSMUST00000107843.10</a>	1508	<a href="#">371aa</a>	Protein coding	<a href="#">CCDS21222</a>	<a href="#">Q9JIF0</a>	TSL:1 GENCODE basic APPRIS P3
Prmt1-205	<a href="#">ENSMUST00000207659.1</a>	945	<a href="#">254aa</a>	Protein coding	<a href="#">CCDS85293</a>	<a href="#">A0A140LJ70</a>	TSL:5 GENCODE basic
Prmt1-201	<a href="#">ENSMUST00000045325.13</a>	1071	<a href="#">318aa</a>	Protein coding	-	<a href="#">A0A171KXD3</a>	TSL:5 GENCODE basic
Prmt1-214	<a href="#">ENSMUST00000209124.1</a>	741	<a href="#">208aa</a>	Protein coding	-	<a href="#">A0A140LHF7</a>	TSL:5 GENCODE basic
Prmt1-208	<a href="#">ENSMUST00000208312.1</a>	659	<a href="#">217aa</a>	Protein coding	-	<a href="#">A0A140LHS4</a>	CDS 3' incomplete TSL:5
Prmt1-210	<a href="#">ENSMUST00000208829.1</a>	621	<a href="#">122aa</a>	Protein coding	-	<a href="#">A0A140LJ68</a>	TSL:5 GENCODE basic
Prmt1-209	<a href="#">ENSMUST00000208778.1</a>	578	<a href="#">193aa</a>	Protein coding	-	<a href="#">A0A140LJF4</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
Prmt1-213	<a href="#">ENSMUST00000209056.2</a>	490	<a href="#">164aa</a>	Protein coding	-	<a href="#">A0A140LI33</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
Prmt1-212	<a href="#">ENSMUST00000208938.1</a>	467	<a href="#">113aa</a>	Protein coding	-	<a href="#">A0A140LIF7</a>	CDS 5' incomplete TSL:3
Prmt1-204	<a href="#">ENSMUST00000207522.1</a>	724	<a href="#">55aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LJG1</a>	TSL:5
Prmt1-207	<a href="#">ENSMUST00000207735.1</a>	834	No protein	Retained intron	-	-	TSL:2
Prmt1-206	<a href="#">ENSMUST00000207702.1</a>	758	No protein	Retained intron	-	-	TSL:3
Prmt1-211	<a href="#">ENSMUST00000208897.1</a>	742	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Prmt1-202* transcript,The transcription is shown below:

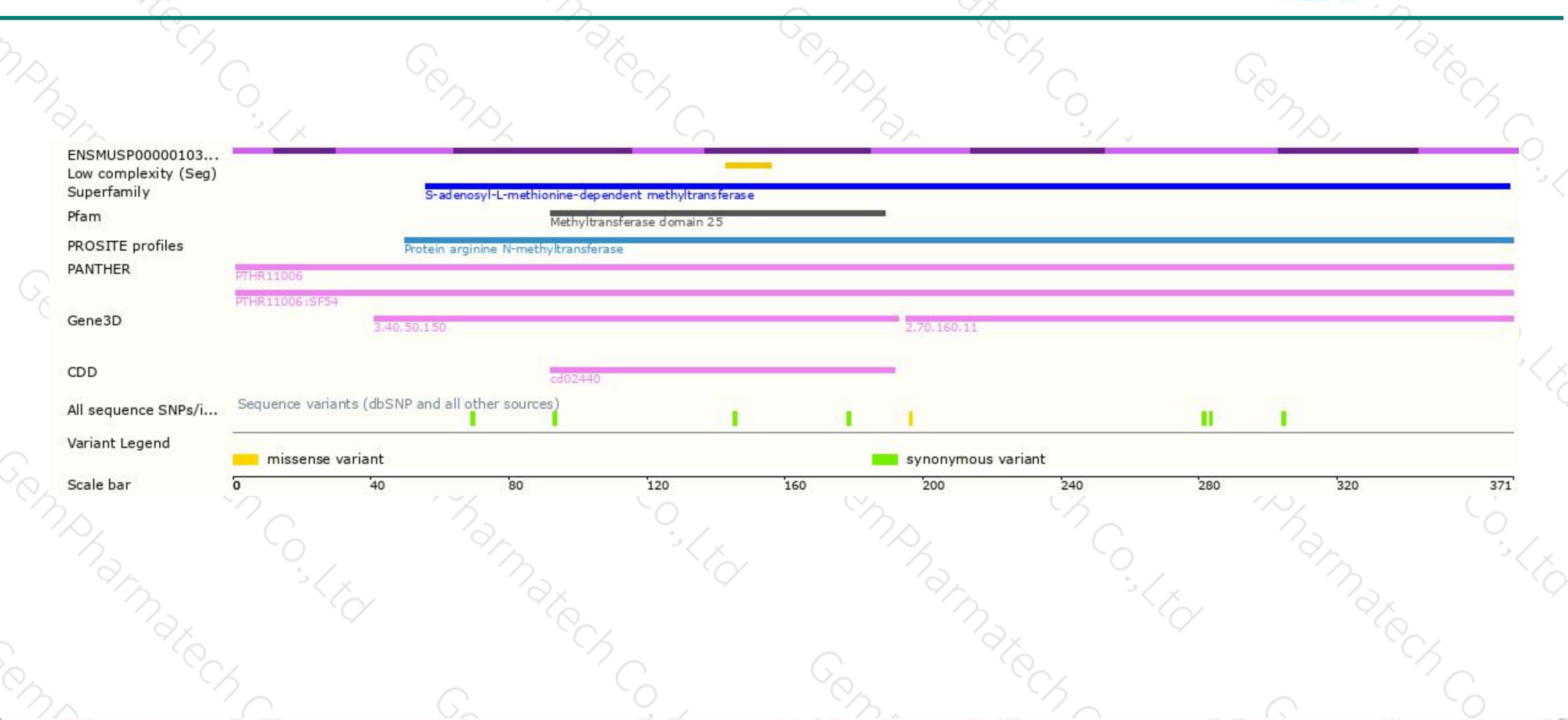


# Genomic location distribution

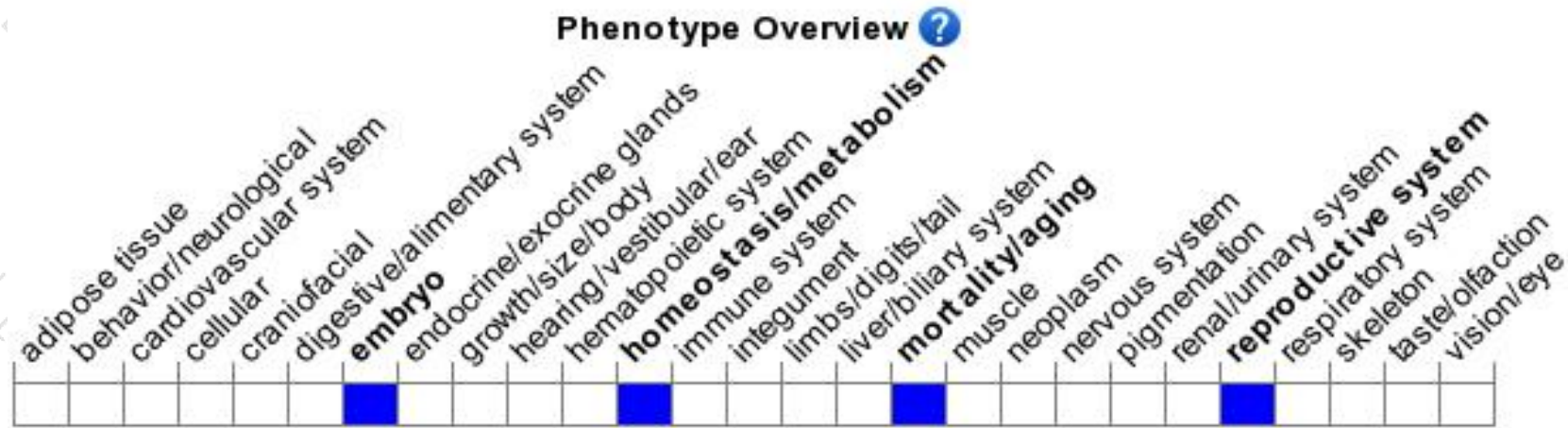




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Embryos homozygous for a null mutation die before E6.5 and exhibit abnormal embryonic tissue morphology.

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

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