

# ***Jam3*** Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Jam3***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Jam3* gene. The schematic diagram is as follows:



- The *Jam3* gene has 5 transcripts. According to the structure of *Jam3* gene, exon2-exon5 of *Jam3-201* (ENSMUST00000034472.15) transcript is recommended as the knockout region. The region contains 536bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Jam3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Approximately 60% of mice homozygous for a targeted mutation exhibit postnatal lethality. Males are infertile and display small testes and arrested differentiation of round spermatids into spermatozoa, as shown by the absence of acrosomes, elongated nuclei, and morphological signs of polarization.
- The KO region contains functional region of the *Gm48796* gene. Knockout the region may affect the function of *Gm48796* gene.
- The *Jam3* gene is located on the Chr9. 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)

## Jam3 junction adhesion molecule 3 [Mus musculus (house mouse)]

Gene ID: 83964, updated on 31-Jan-2019

### Summary



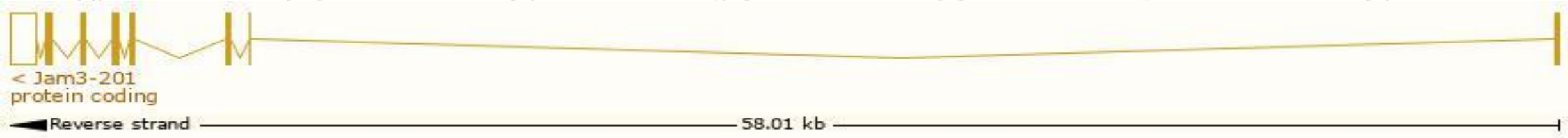
<b>Official Symbol</b>	Jam3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	junction adhesion molecule 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1933825</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000031990</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	1110002N23Rik, JAM-3, JAM-C, Jcam3
<b>Expression</b>	Broad expression in CNS E11.5 (RPKM 37.0), limb E14.5 (RPKM 30.4) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

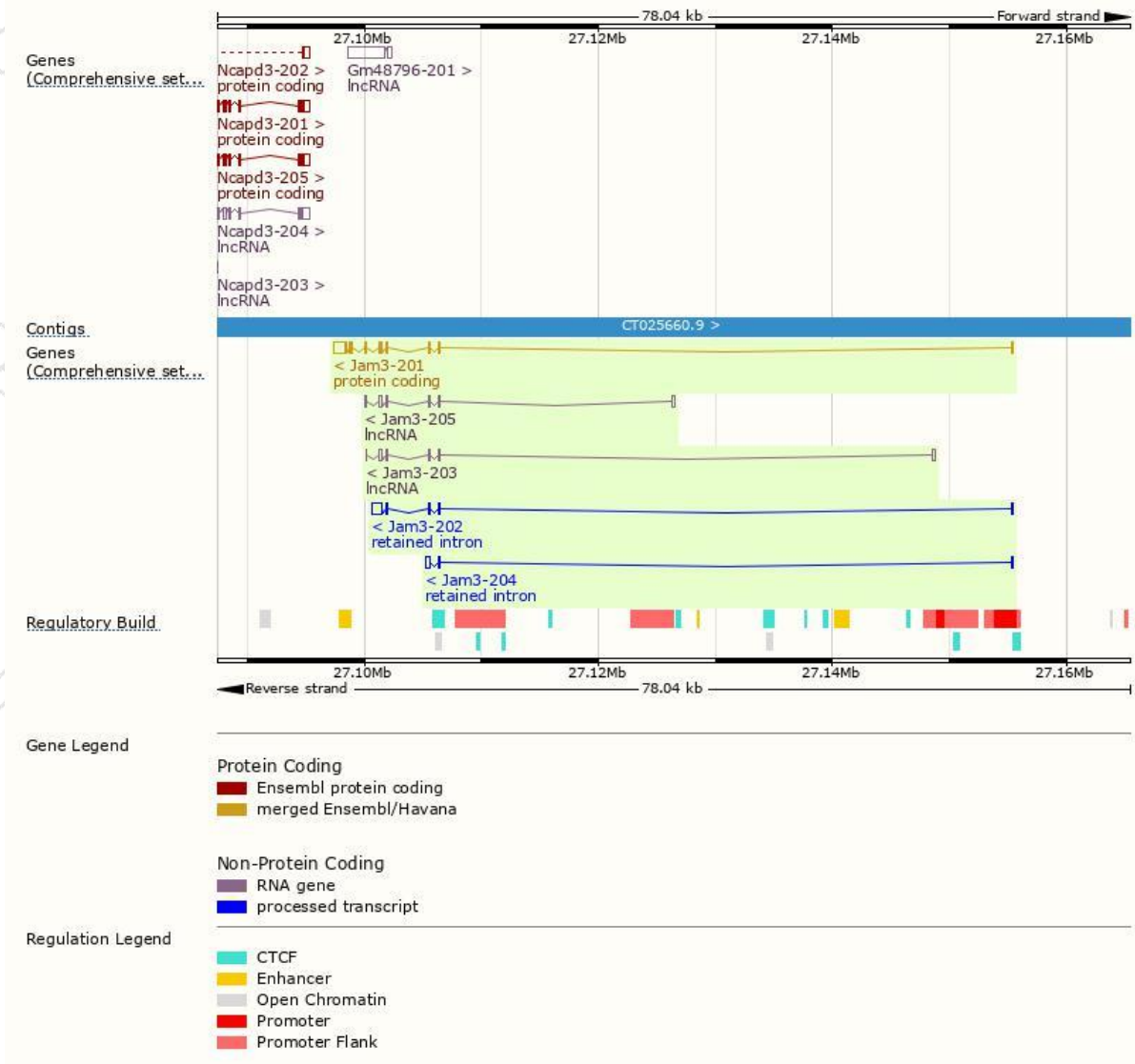
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jam3-201	<a href="#">ENSMUST00000034472.15</a>	1942	<a href="#">310aa</a>	Protein coding	<a href="#">CCDS22939</a>	<a href="#">Q9D8B7</a>	TSL:1 GENCODE basic APPRIS P1
Jam3-202	<a href="#">ENSMUST00000167074.1</a>	1234	No protein	Retained intron	-	-	TSL:1
Jam3-204	<a href="#">ENSMUST00000213682.1</a>	597	No protein	Retained intron	-	-	TSL:2
Jam3-205	<a href="#">ENSMUST00000215446.1</a>	863	No protein	lncRNA	-	-	TSL:3
Jam3-203	<a href="#">ENSMUST00000213170.1</a>	731	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Jam3-201* transcript,The transcription is shown below

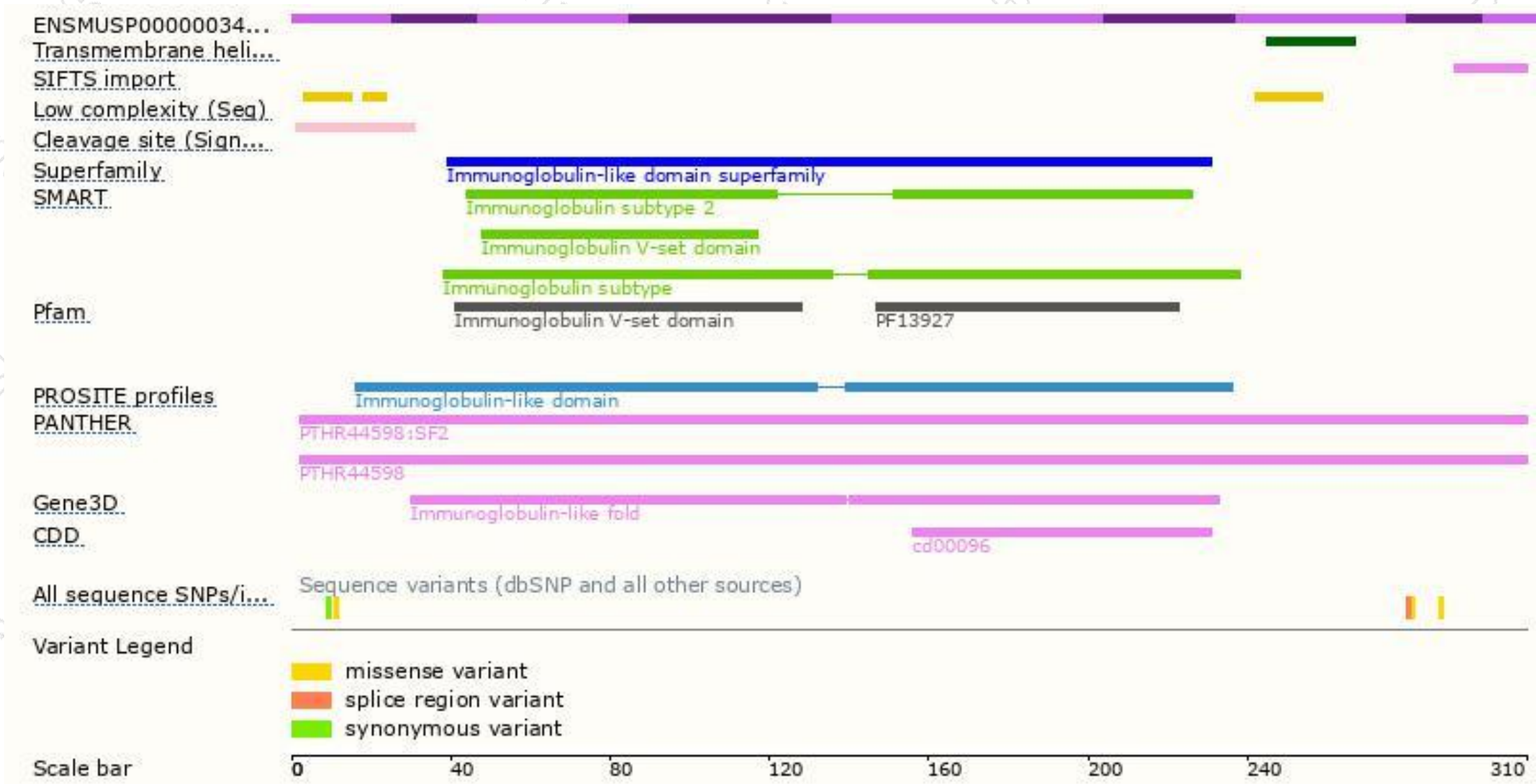


# Genomic location distribution

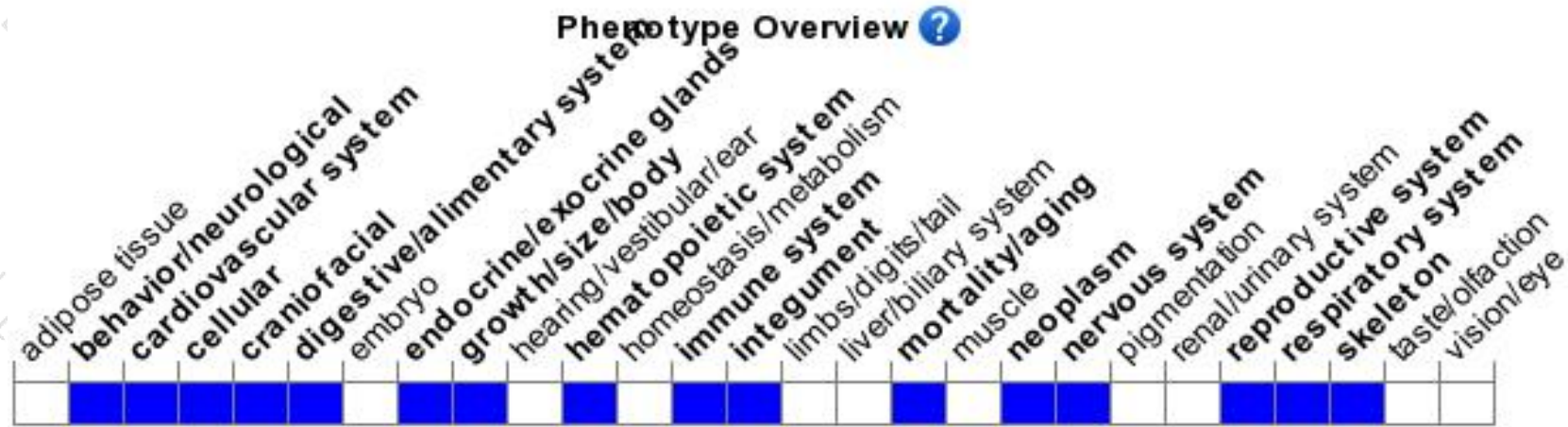




# Protein domain



# 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, Approximately 60% of mice homozygous for a targeted mutation exhibit postnatal lethality. Males are infertile and display small testes and arrested differentiation of round spermatids into spermatozoa, as shown by the absence of acrosomes, elongated nuclei, and morphological signs of polarization.

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

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