Jam2 Cas9-KO Strategy

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Project Name	*Jam2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Jam2* gene. The schematic diagram is as follows:

Technical routes

➢ The *Jam2* gene has 4 transcripts. According to the structure of *Jam2* gene, exon2-exon5 of *Jam2-202* (ENSMUST00000114195.7) transcript is recommended as the knockout region.The region contains 530bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Jam2* gene. The brief process is as follows: CRISPR/Cas9 system

➢ According to the existing MGI data,Mice homozygous for a knock-out allele are viable, fertile and overtly normal with no detectable spermatogenesis abnormalities or defects in embryonic, neural and hematopoietic stem cell properties.

➢ The knockout region is near to the N-terminal of *Gm25908* gene,this strategy may influence the regulatory function of the N-terminal of *Gm25908* gene.

➢ The *Jam2* gene is located on the Chr16. 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）

Jam2 junction adhesion molecule 2 [*Mus musculus* (house mouse)]

Gene ID: 67374, updated on 24-Dec-2019

▲ Summary

Official Symbol	Jam2 provided by MGI
Official Full Name	junction adhesion molecule 2 provided by MGI
Primary source	MGI:MGI:1933820
See related	Ensembl:ENSMUSG00000053062
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	JAM-2; JAM-B; Jcam2; VE-JAM; 1110002N23Rik; 2410030G21Rik; 2410167M24Rik
Expression	Broad expression in heart adult (RPKM 20.4), frontal lobe adult (RPKM 12.0) and 21 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 16; 16 C3.3

See Jam2 in Genome Data Viewer

Exon count: 11

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (84774123..84826380)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (84774368..84823129)

Transcript information（Ensembl）

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

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jam2-202	ENSMUST00000114195.7	4370	298aa	Protein coding	CCDS37381	Q9JI59	TSL:1 GENCODE basic APPRIS P2
Jam2-201	ENSMUST00000098407.2	1998	181aa	Protein coding	-	Q9CWD9	TSL:1 GENCODE basic
Jam2-204	ENSMUST00000231910.1	1214	322aa	Protein coding	-	A0A338P721	GENCODE basic APPRIS ALT2
Jam2-203	ENSMUST00000138054.1	659	No protein	lncRNA	-	-	TSL:5

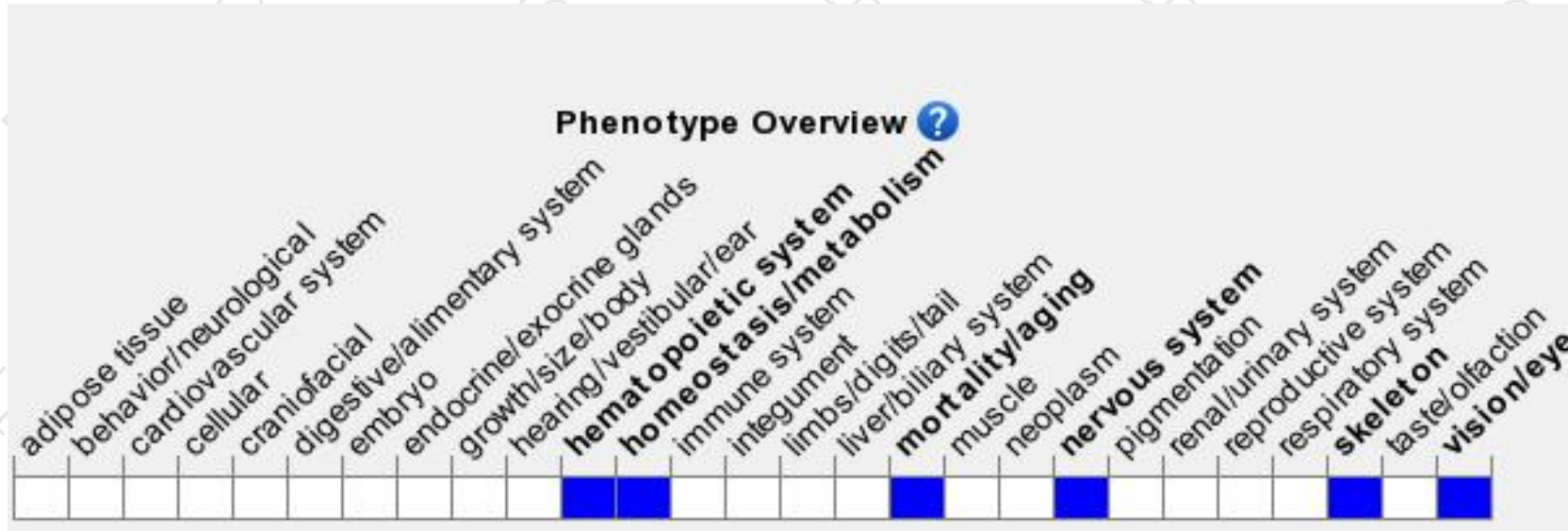The strategy is based on the design of *Jam2-202* transcript,The transcription is shown below
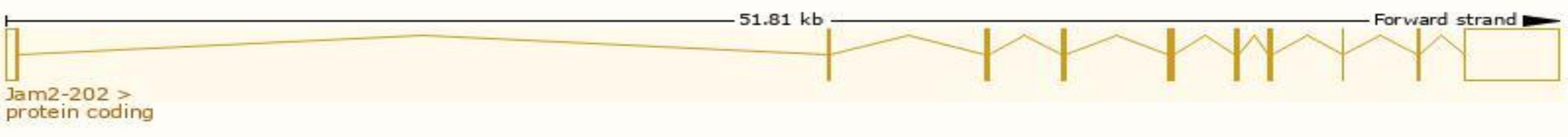
Genomic location distribution
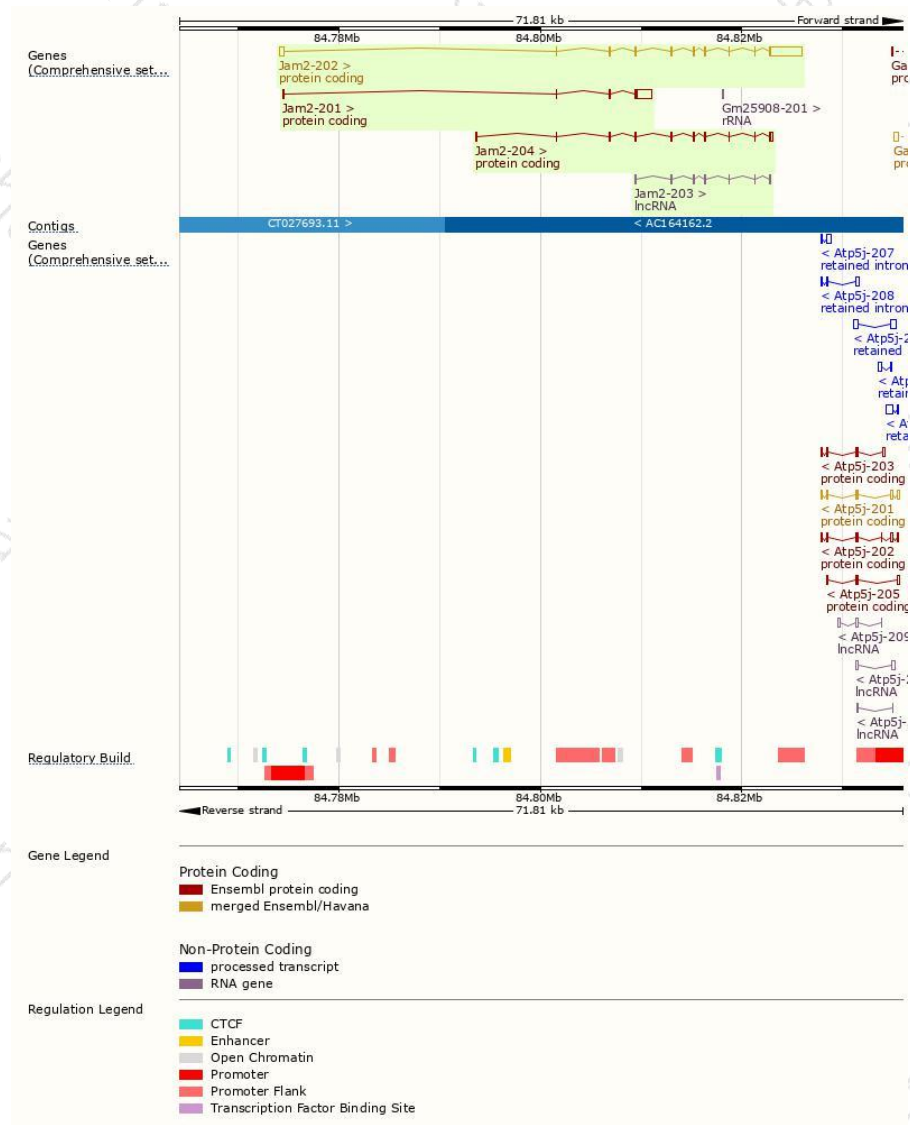
Protein domain
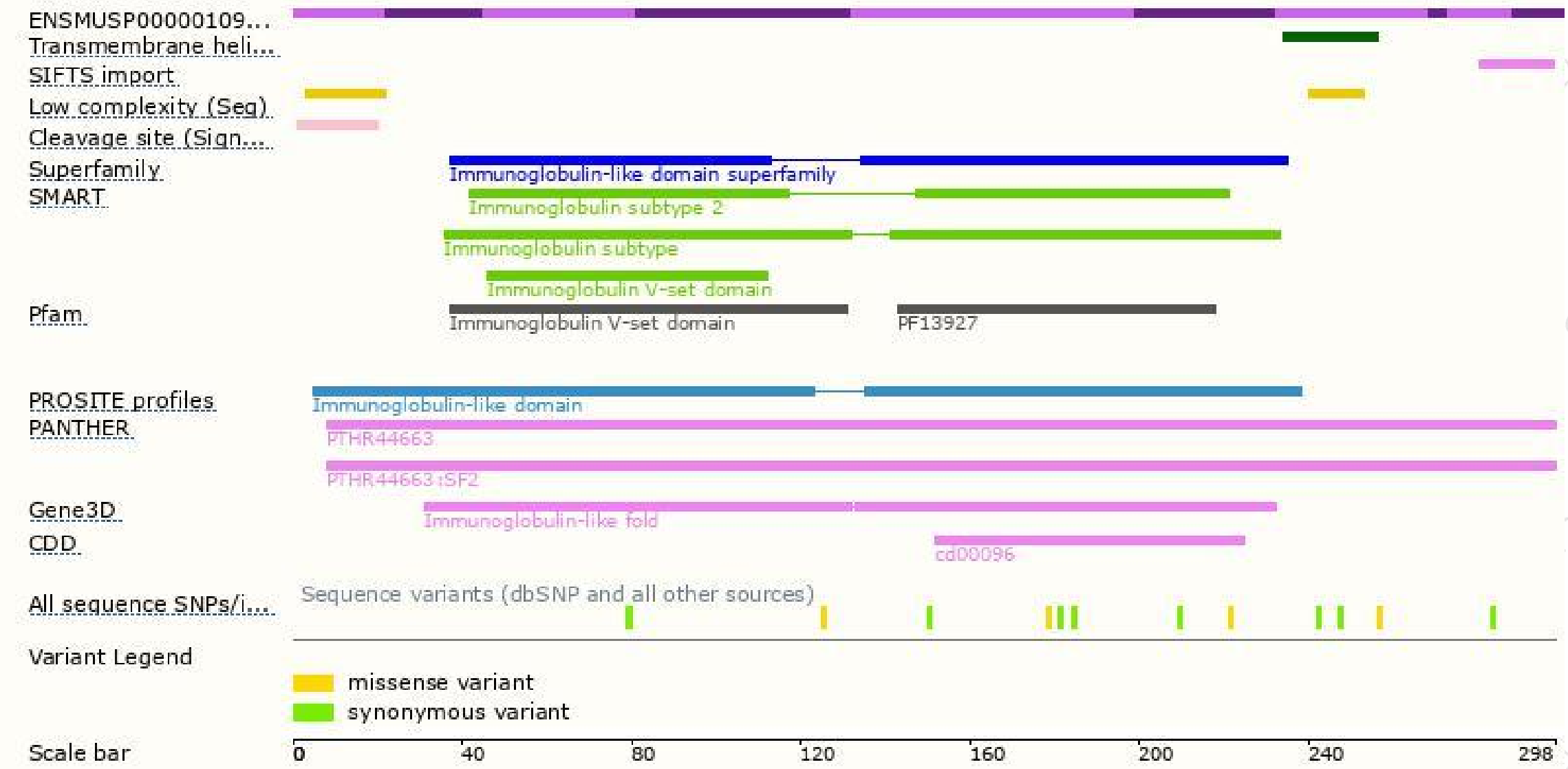
Mouse phenotype description(MGI)

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,Mice homozygous for a knock-out allele are viable, fertile and overtly normal with no detectable spermatogenesis abnormalities or defects in embryonic, neural and hematopoietic stem cell properties.

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