

Pam16 Cas9-KO Strategy

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Project Overview

Project Name

Pam16

Project type

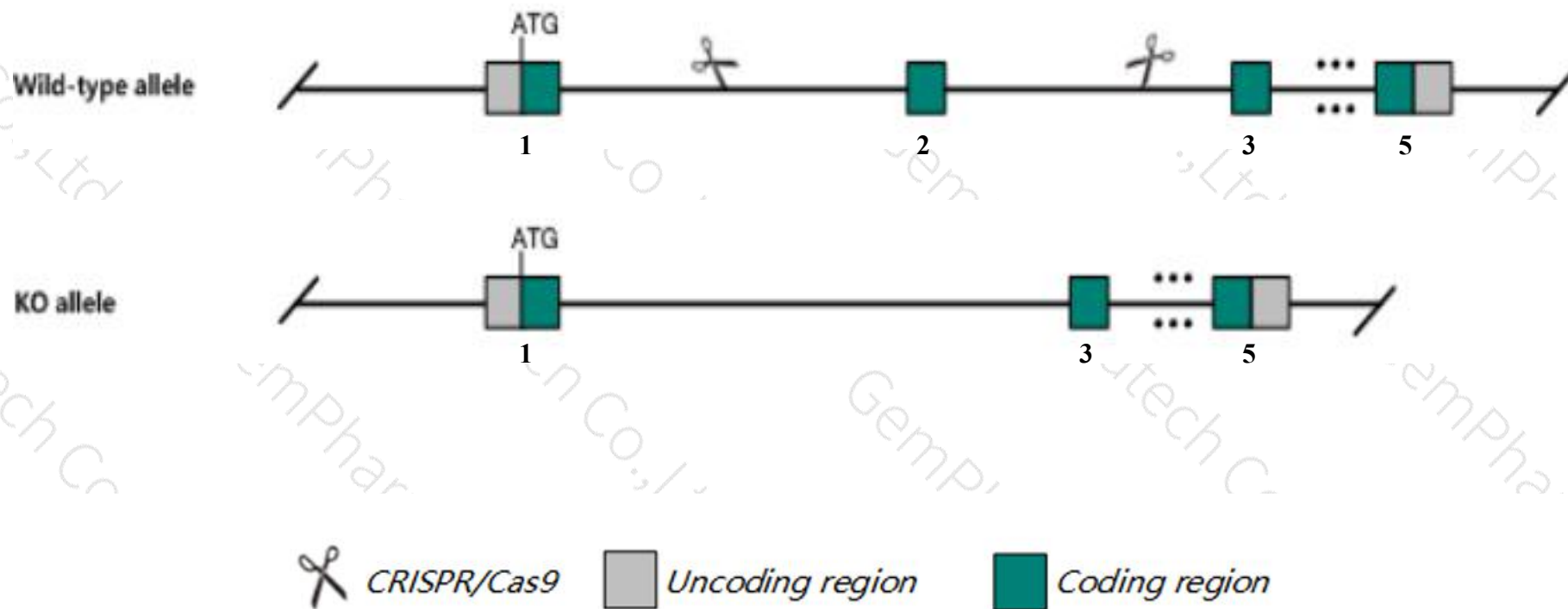
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pam16* gene. The schematic diagram is as follows:



- The *Pam16* gene has 5 transcripts. According to the structure of *Pam16* gene, exon2 of *Pam16-201* (ENSMUST00000014445.6) transcript is recommended as the knockout region. The region contains 85bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pam16* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Pam16* 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)

Pam16 presequence translocase-associated motor 16 homolog (S. cerevisiae) [Mus musculus (house mouse)]

Gene ID: 66449, updated on 13-Mar-2020

Summary



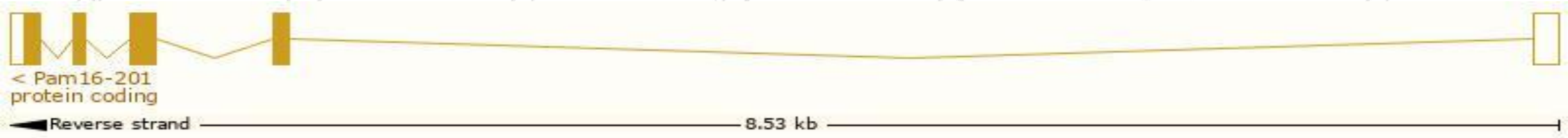
Official Symbol	Pam16 provided by MGI
Official Full Name	presequence translocase-associated motor 16 homolog (S. cerevisiae) provided by MGI
Primary source	MGI:MGI:1913699
See related	Ensembl:ENSMUSG00000014301
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2010110I09Rik, AV006767, CGI-136, Magmas, Tim16, Timm16
Expression	Ubiquitous expression in testis adult (RPKM 60.5), thymus adult (RPKM 48.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

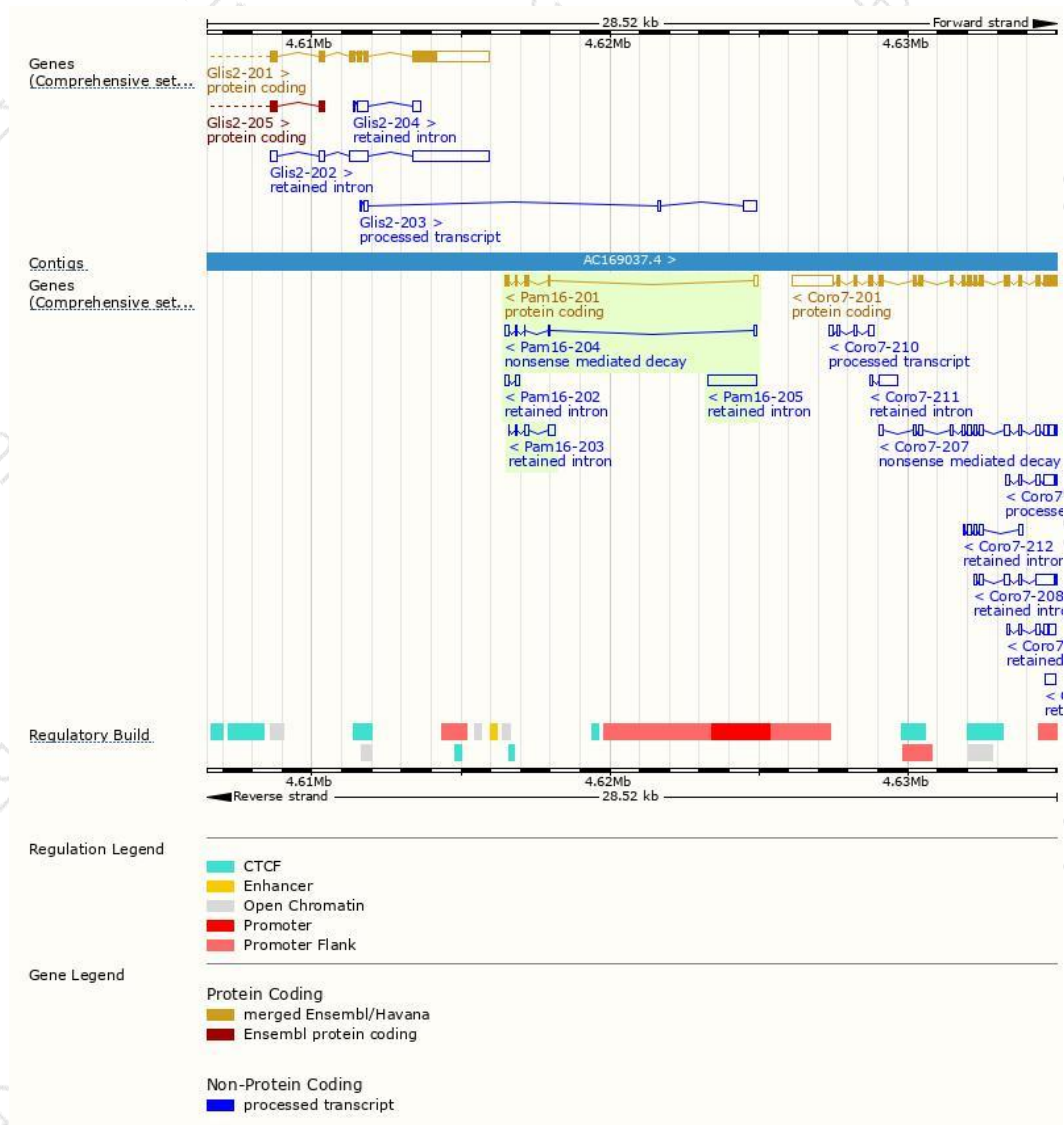
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pam16-201	ENSMUST00000014445.6	596	125aa	Protein coding	CCDS37241	Q9CQV1	TSL:1 GENCODE basic APPRIS P1
Pam16-204	ENSMUST00000156889.7	431	39aa	Nonsense mediated decay	-	D6RI93	TSL:3
Pam16-205	ENSMUST00000229767.1	1634	No protein	Retained intron	-	-	
Pam16-203	ENSMUST00000139534.1	471	No protein	Retained intron	-	-	TSL:2
Pam16-202	ENSMUST00000131250.7	346	No protein	Retained intron	-	-	TSL:2

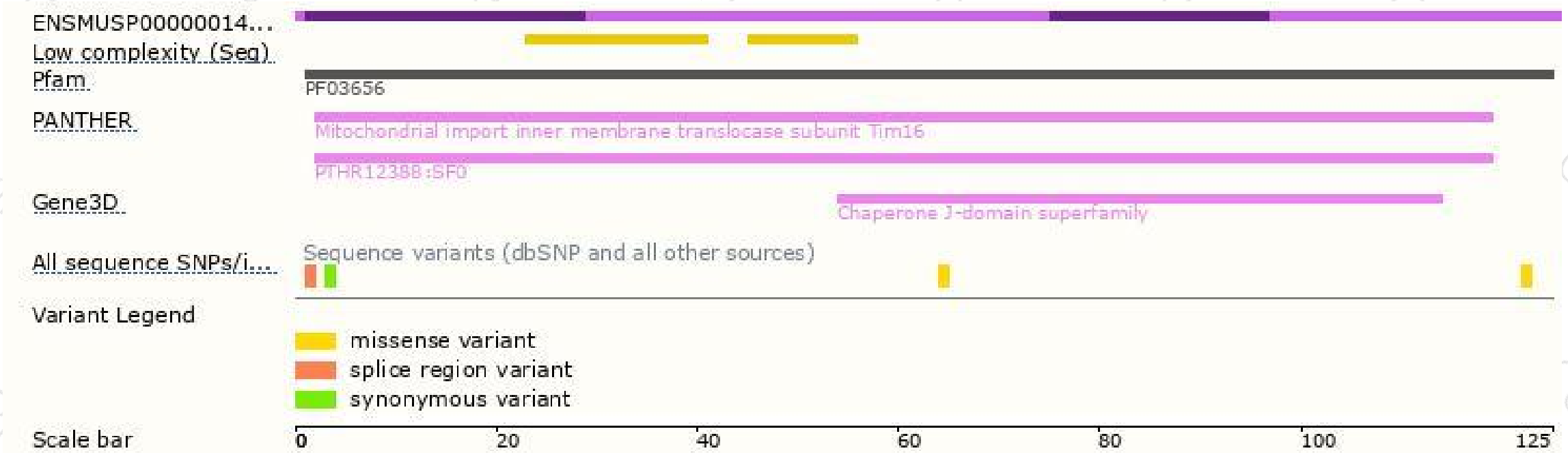
The strategy is based on the design of *Pam16-201* transcript,the transcription is shown below:



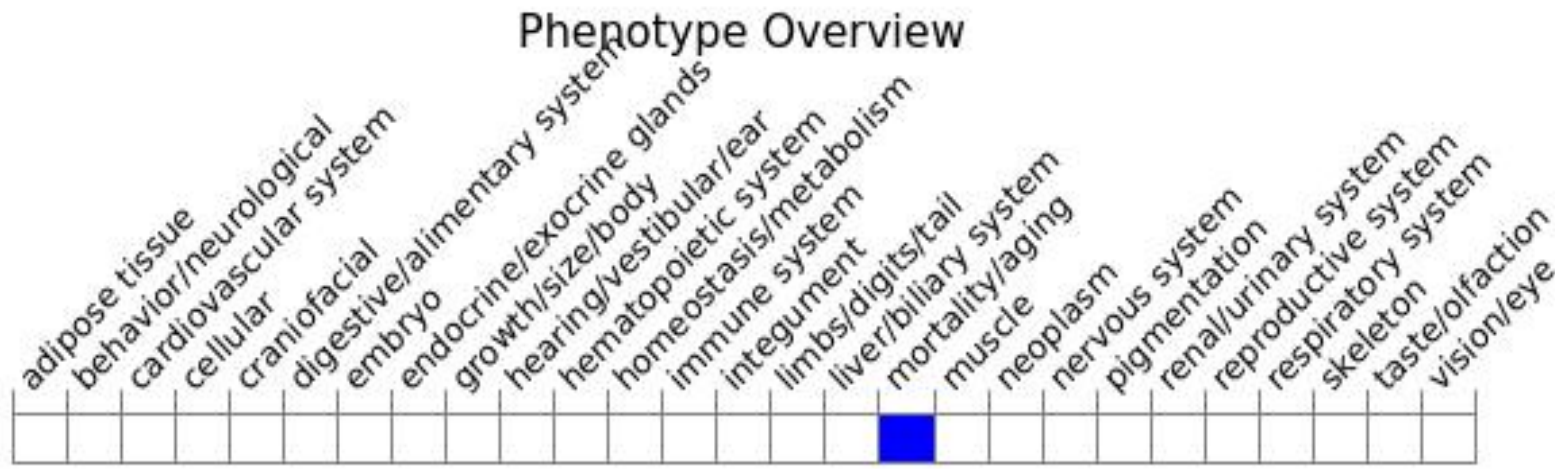
Genomic location distribution



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/>).

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

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