

Pygb Cas9-KO Strategy

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Project Overview

Project Name

Pygb

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Pygb* gene has 5 transcripts. According to the structure of *Pygb* gene, exon2-exon3 of *Pygb-201* (ENSMUST00000045441.7) transcript is recommended as the knockout region. The region contains 181bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pygb* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Pygb* gene is located on the Chr2. 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)

Pygb brain glycogen phosphorylase [Mus musculus (house mouse)]

Gene ID: 110078, updated on 7-Apr-2019

Summary



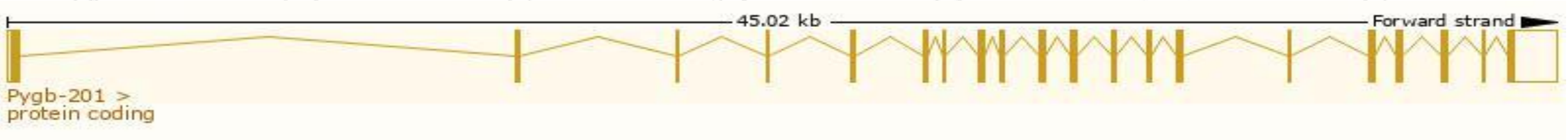
Official Symbol	Pygb provided by MGI
Official Full Name	brain glycogen phosphorylase provided by MGI
Primary source	MGI:MGI:97828
See related	Ensembl:ENSMUSG00000033059
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Broad expression in heart adult (RPKM 143.6), bladder adult (RPKM 120.3) and 26 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
Pygb-201	ENSMUST00000045441.7	3909	843aa	Protein coding	CCDS16862	Q8CI94	TSL:1 GENCODE basic APPRIS P1
Pygb-202	ENSMUST00000129610.1	808	No protein	Retained intron	-	-	TSL:2
Pygb-205	ENSMUST00000154366.1	659	No protein	Retained intron	-	-	TSL:3
Pygb-203	ENSMUST00000135717.1	531	No protein	Retained intron	-	-	TSL:1
Pygb-204	ENSMUST00000139938.1	789	No protein	lncRNA	-	-	TSL:3

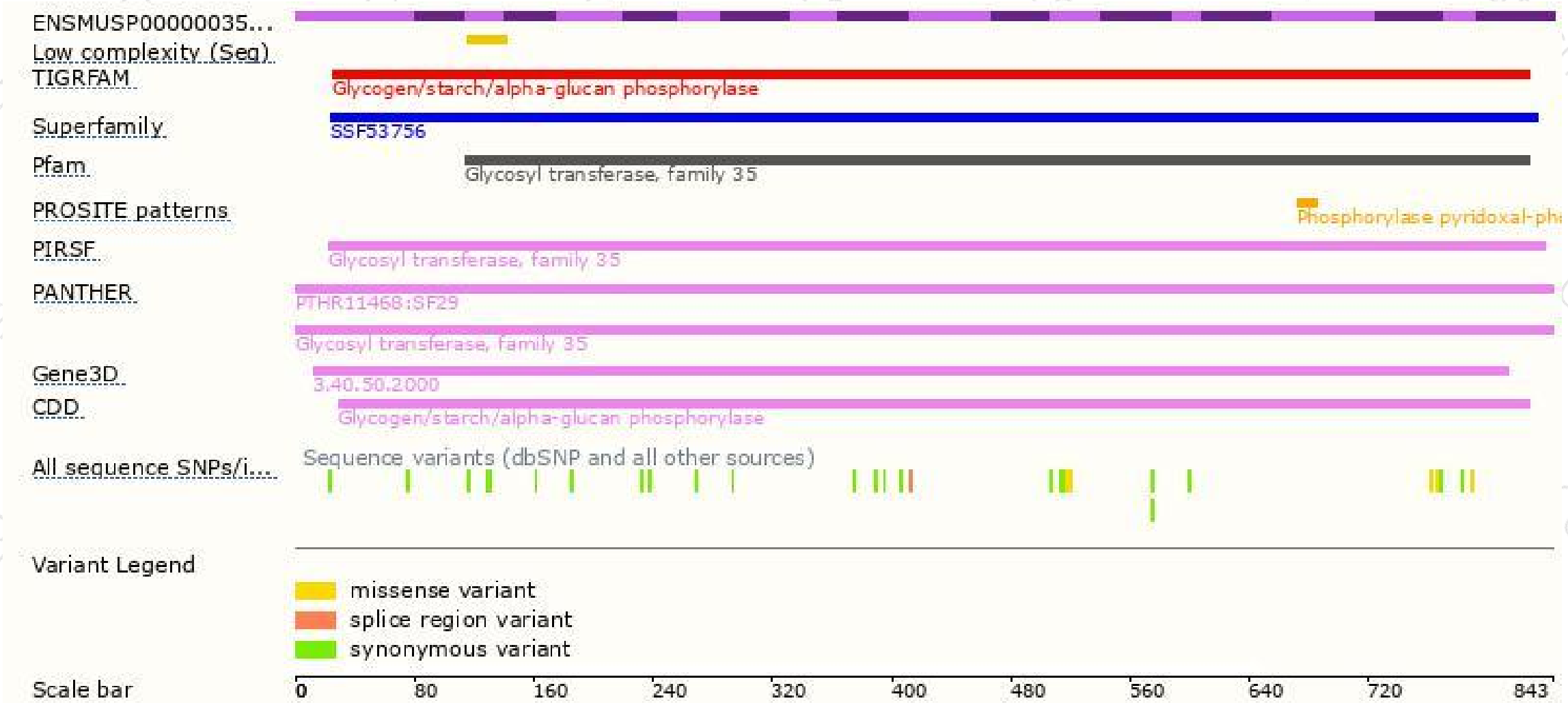
The strategy is based on the design of *Pygb-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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