

Tigar Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Tigar

Project type

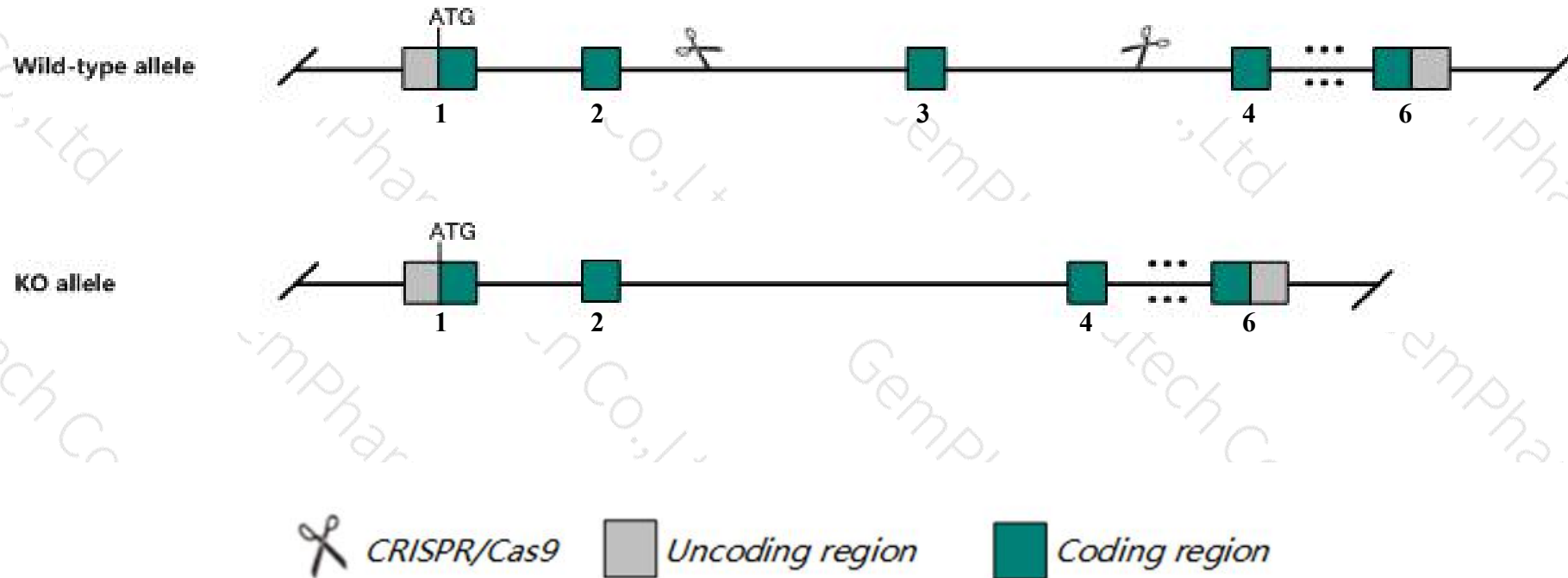
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Tigar* gene has 2 transcripts. According to the structure of *Tigar* gene, exon3 of *Tigar-201* (ENSMUST00000039913.8) transcript is recommended as the knockout region. The region contains 122bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tigar* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit improved response to myocardial infarction associated with increased autophagy, mitophagy, levels of reactive oxygen species production and decreased mitochondria DNA damage. Mice homozygous for a different allele exhibit impaired crypt regeneration.
- The *Tigar* gene is located on the Chr6. 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)

Tigar Trp53 induced glycolysis repulatory phosphatase [Mus musculus (house mouse)]

Gene ID: 319801, updated on 5-Feb-2019

Summary



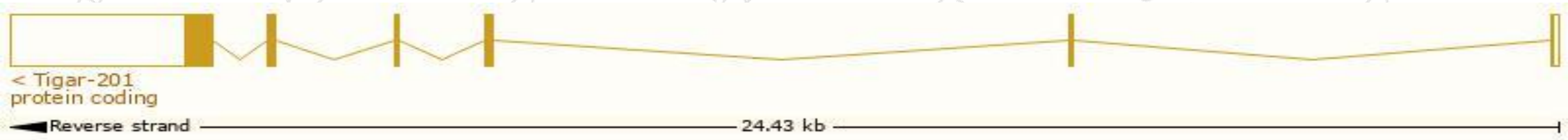
Official Symbol	Tigar provided by MGI
Official Full Name	Trp53 induced glycolysis repulatory phosphatase provided by MGI
Primary source	MGI:MGI:2442752
See related	Ensembl:ENSMUSG00000038028
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9630033F20Rik, AA793651, AI595337, C79710, C85509
Expression	Ubiquitous expression in heart adult (RPKM 8.1), cerebellum adult (RPKM 5.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

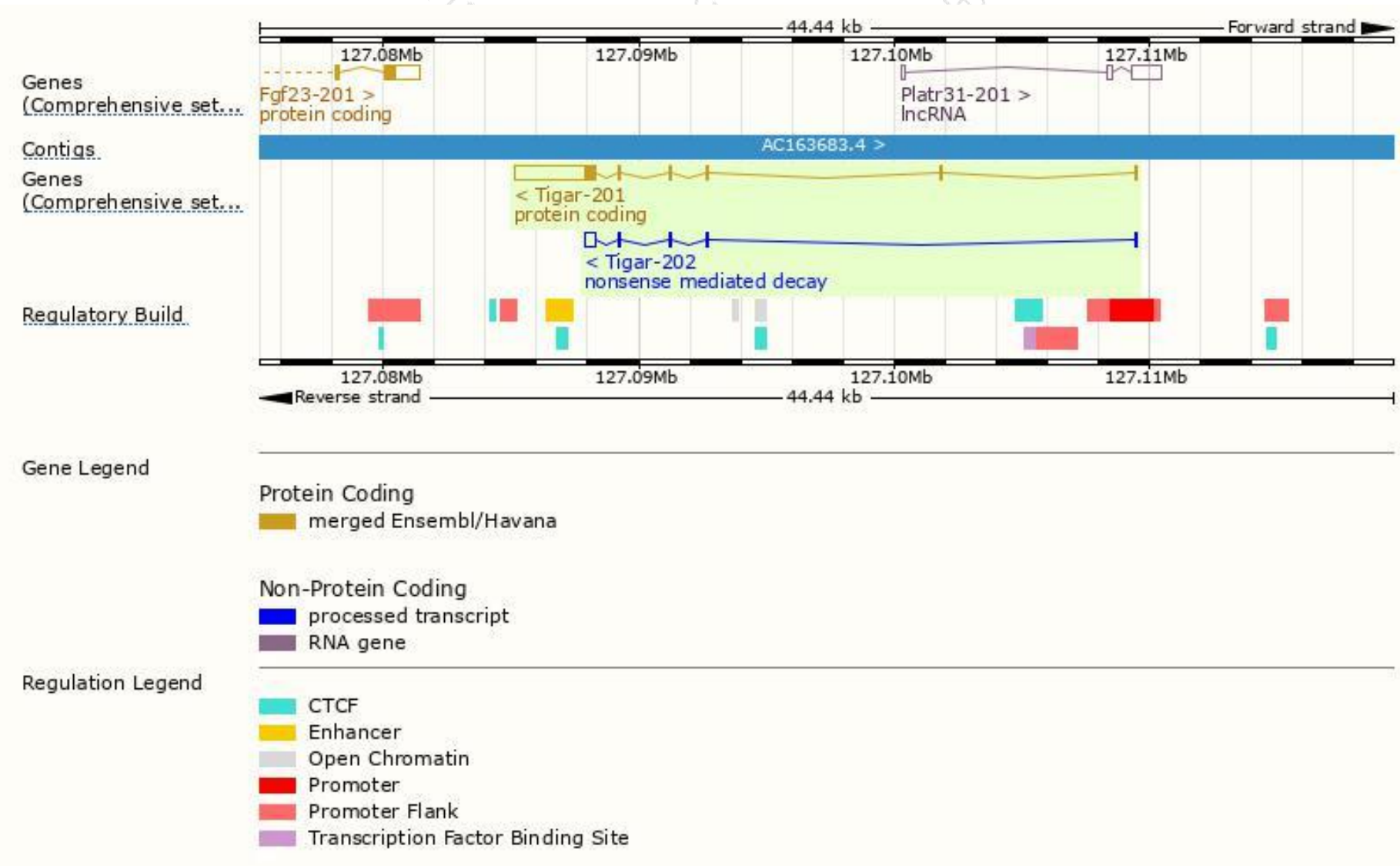
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tigar-201	ENSMUST00000039913.8	3651	269aa	Protein coding	CCDS20563	B2RWB7 Q8BZA9	TSL:1 GENCODE basic APPRIS P1
Tigar-202	ENSMUST00000200988.1	855	49aa	Nonsense mediated decay	-	A0A0J9YV11	TSL:5

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



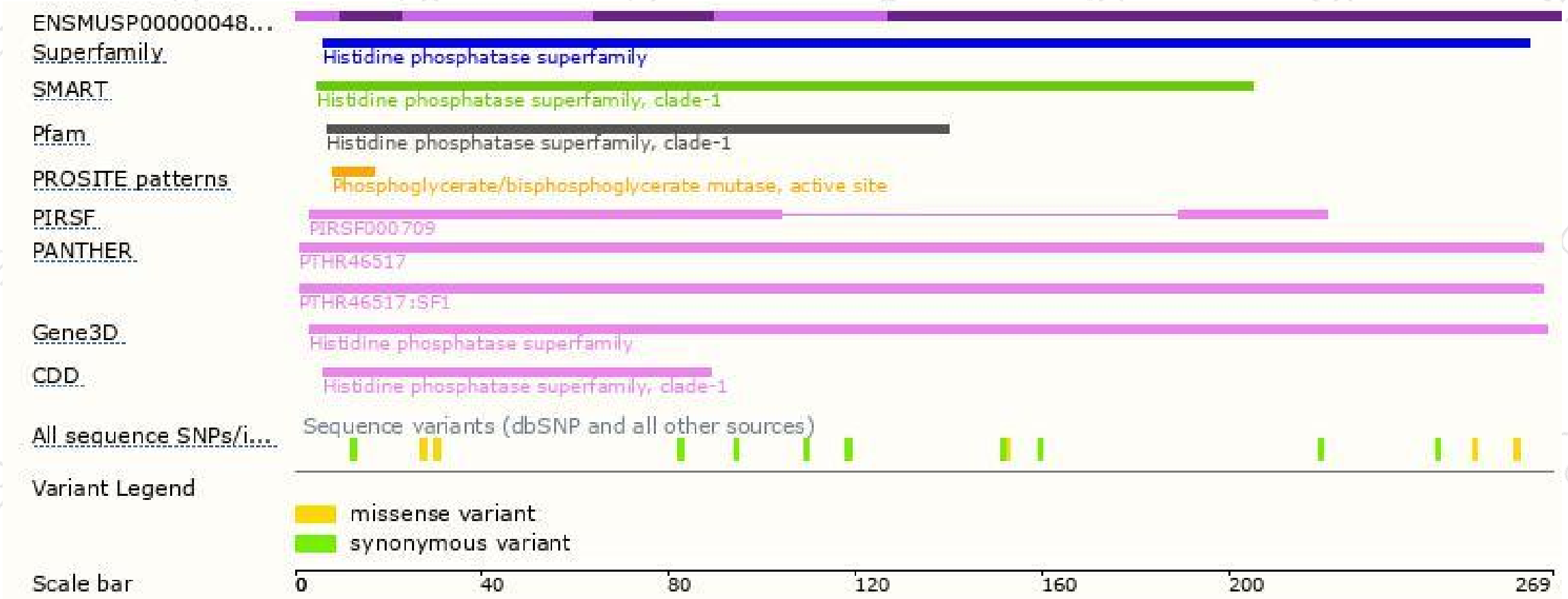
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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 exhibit improved response to myocardial infarction associated with increased autophagy, mitophagy, levels of reactive oxygen species production and decreased mitochondria DNA damage. Mice homozygous for a different allele exhibit impaired crypt regeneration.

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

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