

Gpx3 Cas9-KO Strategy

Designer:	Yupeng Yang
Reviewer:	Shilei Zhu
Date:	2019/11/11

Project Overview

Project Name

Gpx3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gpx3* gene. The schematic diagram is as follows:



- The *Gpx3* gene has 3 transcripts. According to the structure of *Gpx3* gene, exon2 of *Gpx3-201* (ENSMUST00000082430.9) transcript is recommended as the knockout region. The region contains 154bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gpx3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit reduced glutathione peroxidase activity, increase plasma selenium levels when mice are fed a selenium supplemented diet, and reduced kidney selenium levels regardless of selenium supplementation.
- The *Gpx3* gene is located on the Chr11. 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)

Gpx3 glutathione peroxidase 3 [Mus musculus (house mouse)]

Gene ID: 14778, updated on 19-Mar-2019

Summary

Official Symbol Gpx3 provided by MGI

Official Full Name glutathione peroxidase 3 provided by MGI

Primary source MGI:MGI:105102

See related Ensembl:ENSMUSG00000018339

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AA960521, EGPx, GPx, GSHPx-3, GSHPx-P

Summary The protein encoded by this gene belongs to the glutathione peroxidase family, members of which catalyze the reduction of organic hydroperoxides and hydrogen peroxide (H₂O₂) by glutathione, and thereby protect cells against oxidative damage. Several isozymes of this gene family exist in vertebrates, which vary in cellular location and substrate specificity. This isozyme is secreted and is highly expressed in mouse kidney, which appears to be the major source of the enzyme in plasma. It has a role in mouse organogenesis, and dysregulation of this isozyme has been associated with obesity-related metabolic complications, platelet-dependent thrombosis, colitis-associated carcinoma, and thermosensitive phenotype. This isozyme is also a selenoprotein, containing the rare amino acid selenocysteine (Sec) at its active site. Sec is encoded by the UGA codon, which normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, designated the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon, rather than as a stop signal. Alternatively spliced transcript variants have been found for this gene. [provided by RefSeq, Aug 2016]

Expression Biased expression in kidney adult (RPKM 11946.2) and genital fat pad adult (RPKM 610.3)[See more](#)

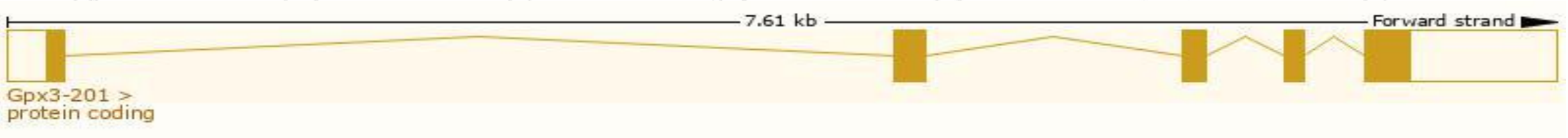
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gpx3-201	ENSMUST00000082430.9	1594	226aa	Protein coding	CCDS24703	P46412	TSL:1 GENCODE basic APPRIS P1
Gpx3-202	ENSMUST00000125094.7	829	199aa	Protein coding	-	A0A1C7ZMZ5	CDS 3' incomplete TSL:3
Gpx3-203	ENSMUST00000149324.1	693	217aa	Protein coding	-	A0A1C7ZMZ7	CDS 3' incomplete TSL:3

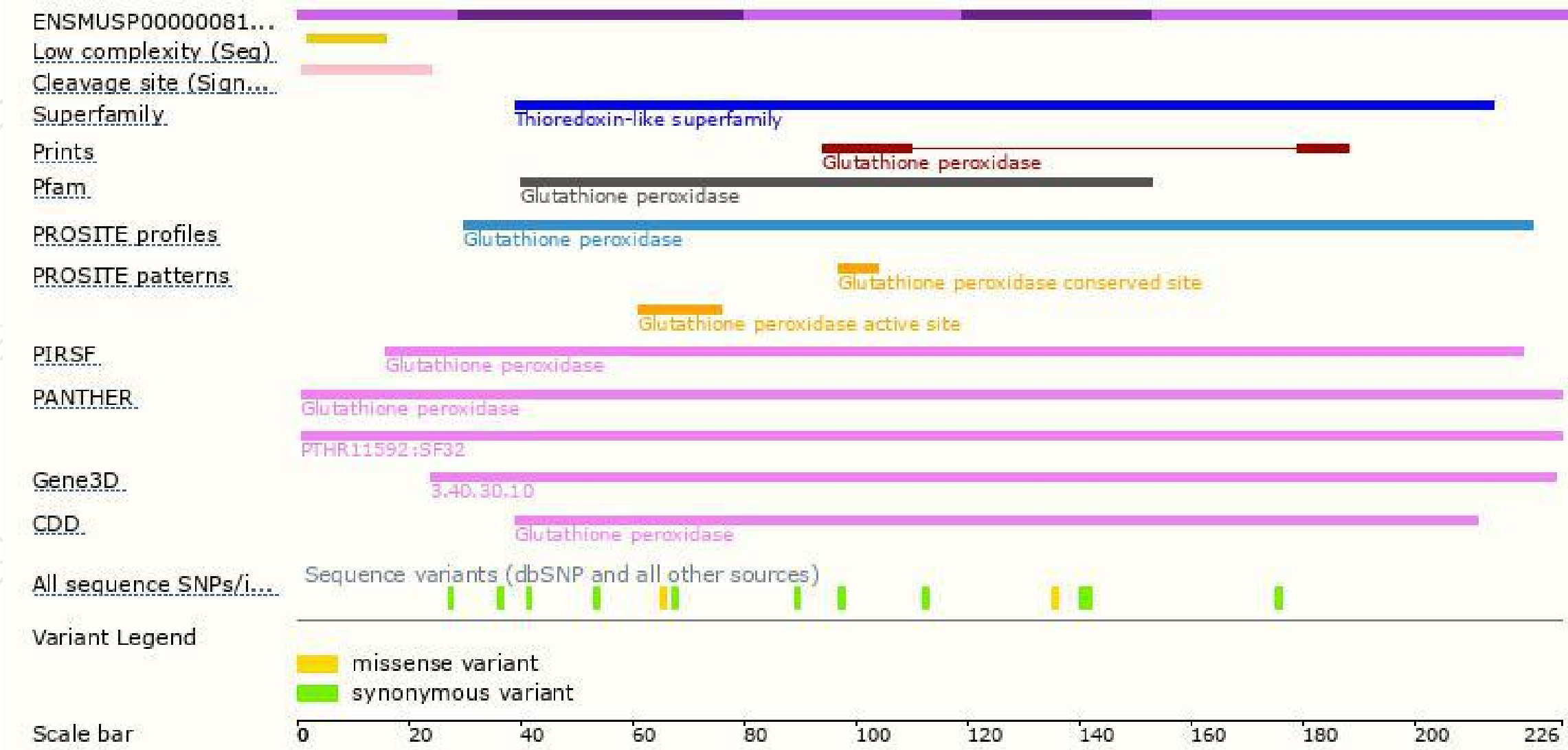
The strategy is based on the design of *Gpx3-201* transcript,The transcription is shown below



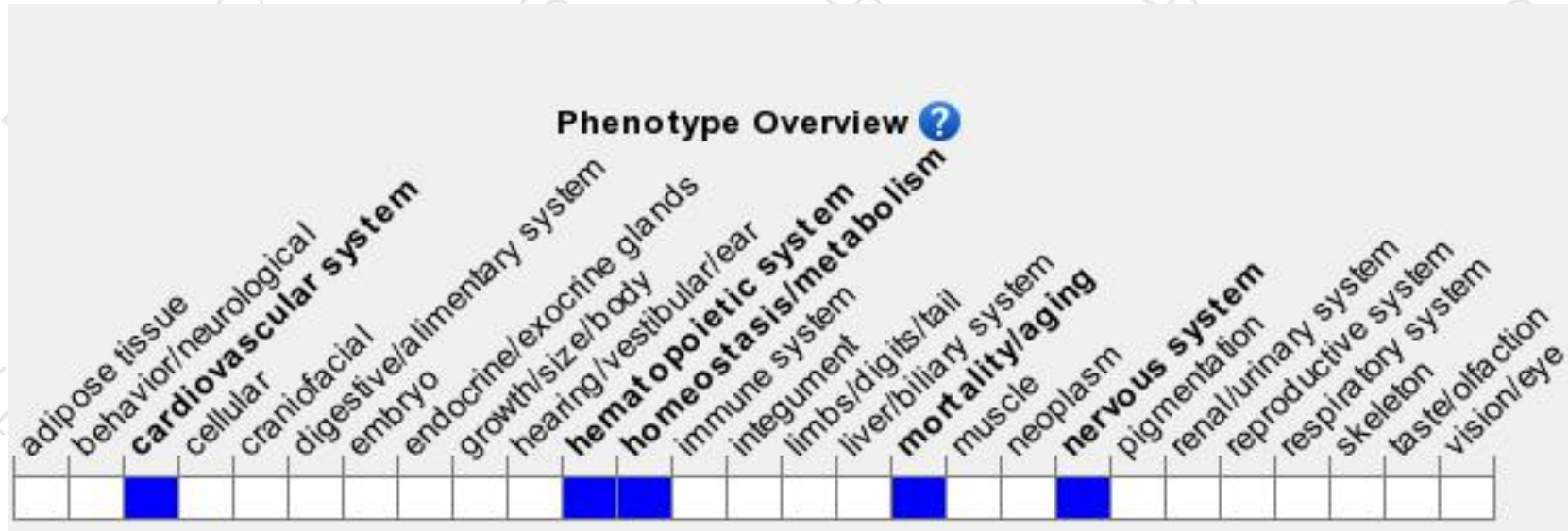
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit reduced glutathione peroxidase activity, increase plasma selenium levels when mice are fed a selenium supplemented diet, and reduced kidney selenium levels regardless of selenium supplementation.

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

Tel: 400-9660890

