

Gys2 Cas9-CKO Strategy

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Project Overview

Project Name

Gys2

Project type

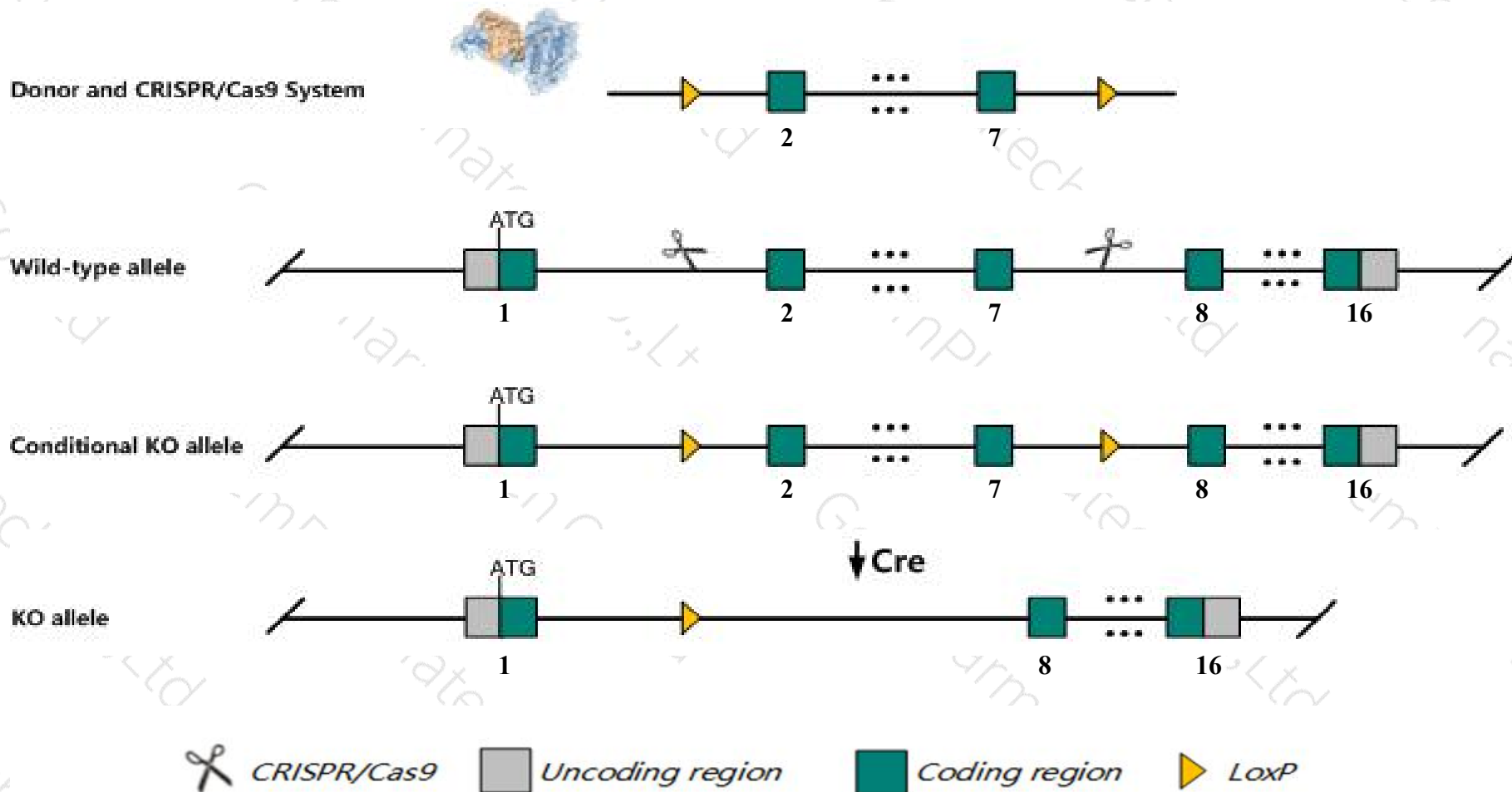
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gys2* gene. The schematic diagram is as follows:



Technical routes

- The *Gys2* gene has 2 transcripts. According to the structure of *Gys2* gene, exon2-exon7 of *Gys2-201* (ENSMUST00000032371.7) transcript is recommended as the knockout region. The region contains 941bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gys2* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a conditional allele knocked out in the liver results in abnormal glycogen homeostasis, altered glucose homeostasis, decreased exercise endurance, and a phenotype similar to patients with glycogen storage disease 0.
- The effect on transcript *Gys2*-202 is unknown.
- The *Gys2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Gys2 glycogen synthase 2 [*Mus musculus* (house mouse)]

Gene ID: 232493, updated on 12-Aug-2019

Summary

- Official Symbol** Gys2 provided by [MGI](#)
- Official Full Name** glycogen synthase 2 provided by [MGI](#)
- Primary source** [MGI:MGI:2385254](#)
- See related** [Ensembl:ENSMUSG00000030244](#)
- 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** LGS; BC021322
- Expression** Biased expression in liver E18 (RPKM 32.0), liver adult (RPKM 14.5) and 7 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 6; 6 G2 See Gys2 in [Genome Data Viewer](#)

Exon count: 18

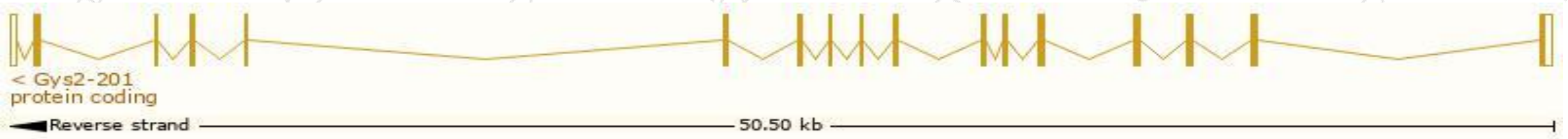
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (142422612..142473130, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (142371133..142421629, complement)

Transcript information (Ensembl)

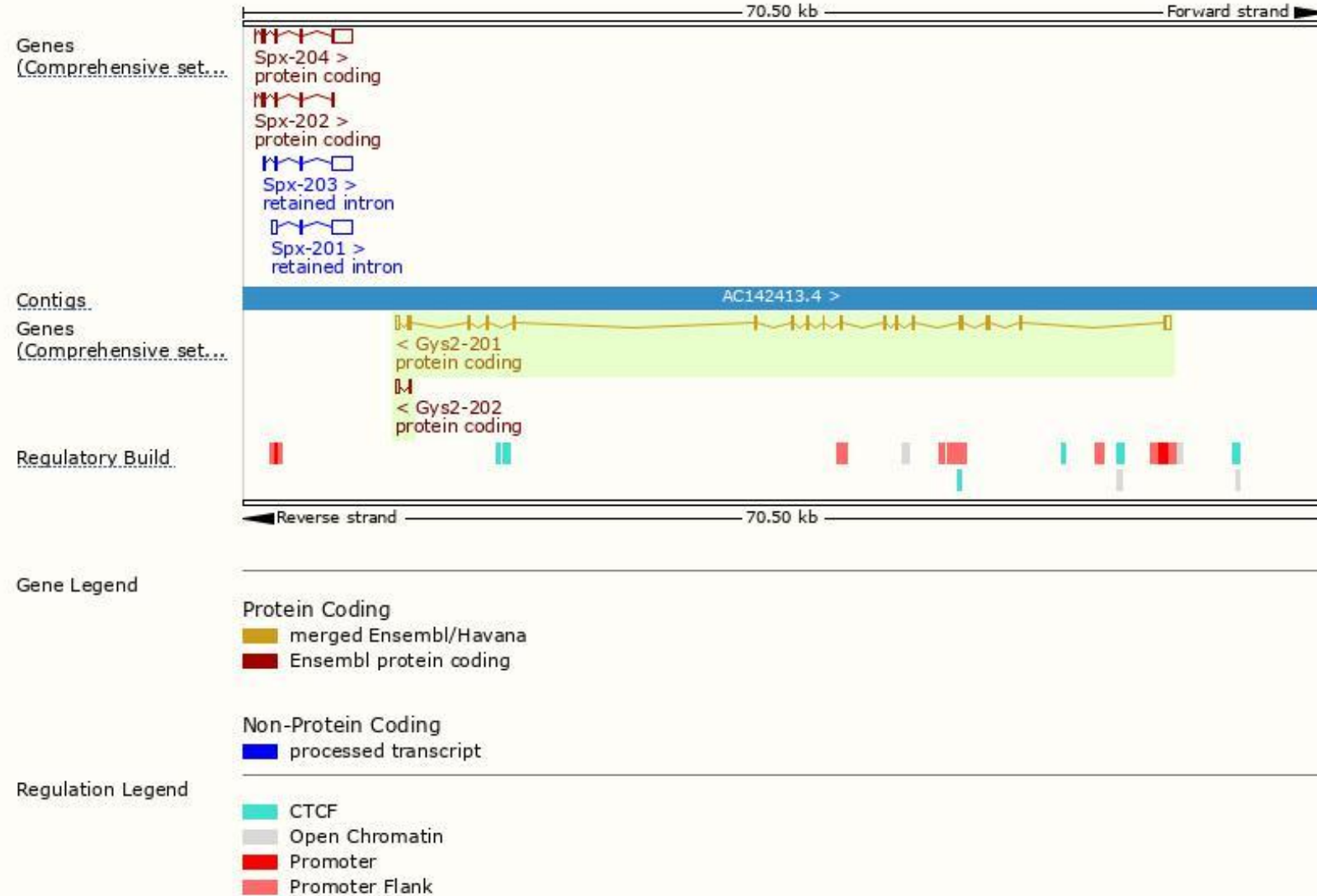
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gys2-201	ENSMUST00000032371.7	2657	704aa	Protein coding	CCDS20683	Q8VCB3	TSL:1 GENCODE basic APPRIS P1
Gys2-202	ENSMUST00000126939.1	314	34aa	Protein coding	-	A0A0N4SVR4	CDS 5' incomplete TSL:2

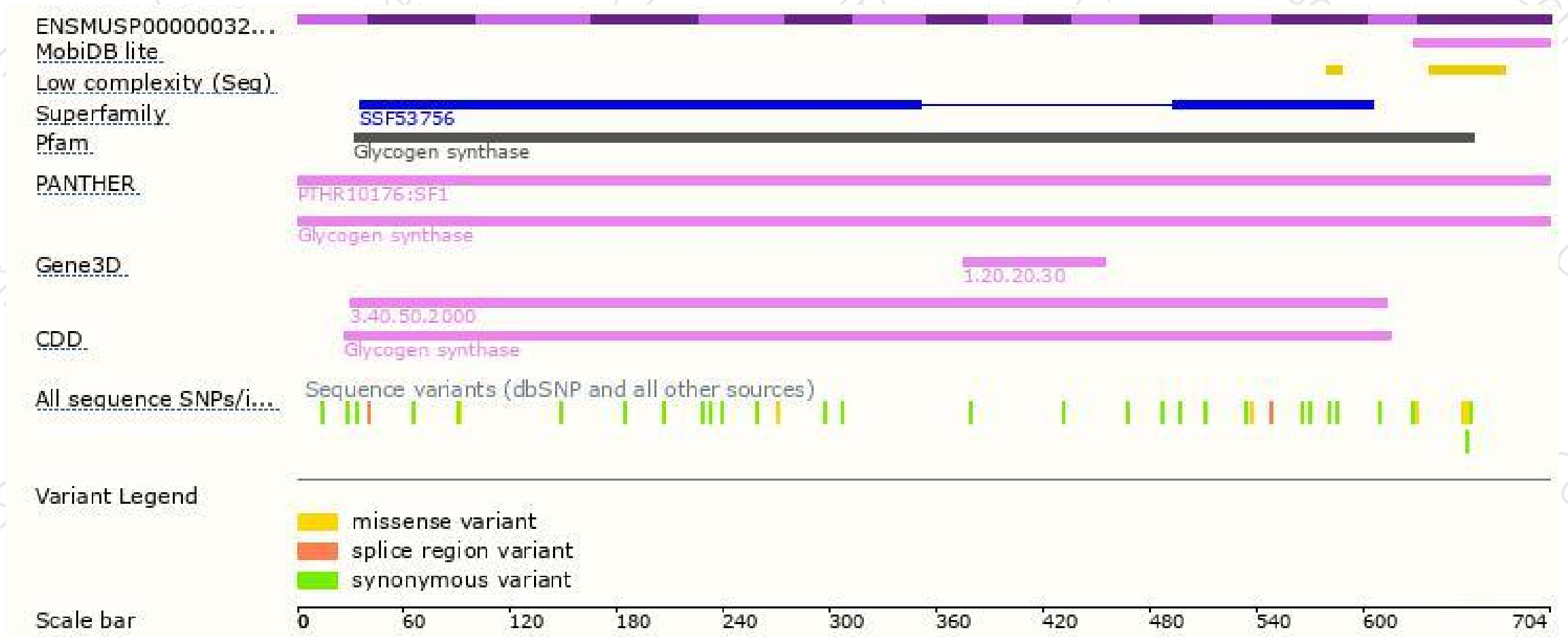
The strategy is based on the design of *Gys2-201* transcript,The transcription is shown below



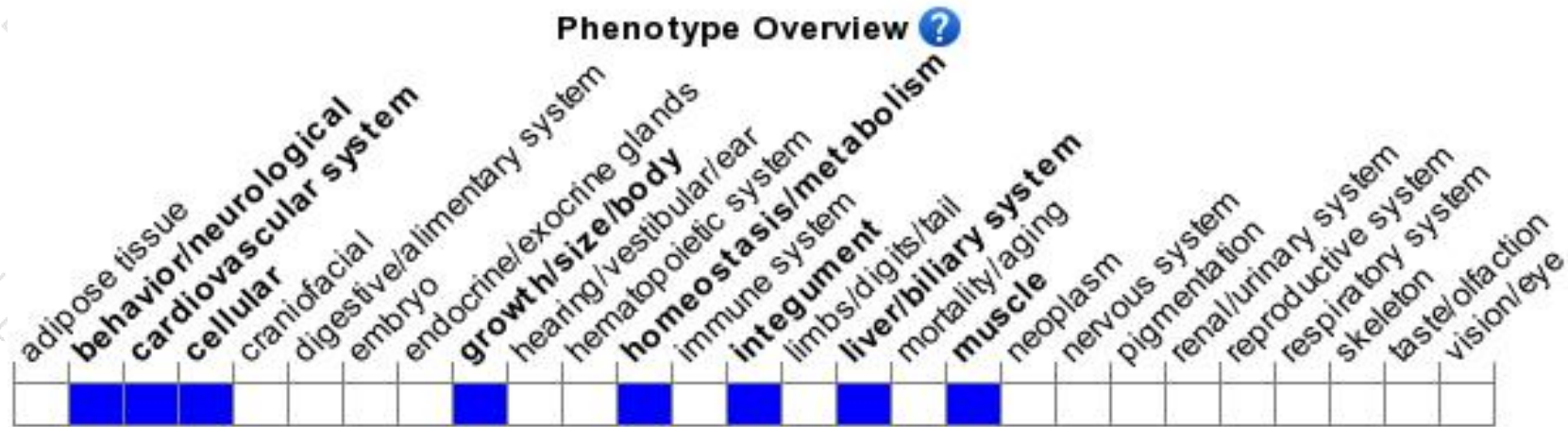
Genomic location distribution



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 conditional allele knocked out in the liver results in abnormal glycogen homeostasis, altered glucose homeostasis, decreased exercise endurance, and a phenotype similar to patients with glycogen storage disease 0.

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

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