

Helz2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Helz2

Project type

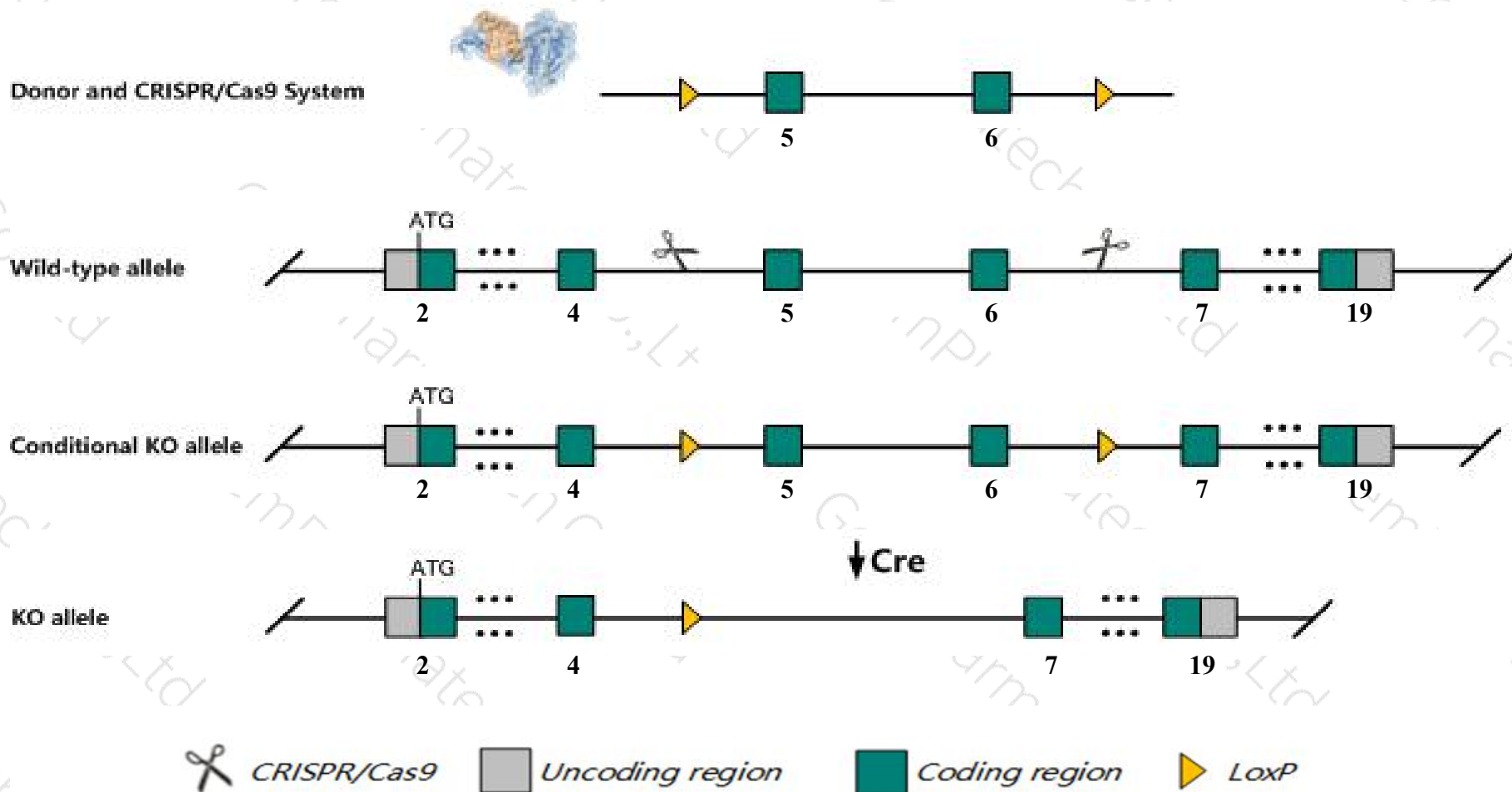
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Helz2* gene. The schematic diagram is as follows:



Technical routes

- The *Helz2* gene has 5 transcripts. According to the structure of *Helz2* gene, exon5-exon6 of *Helz2*-202 (ENSMUST00000108831.7) transcript is recommended as the knockout region. The region contains 1160bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Helz2* 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 knock-out allele exhibit slower weight gain, hyperleptinemia, increased oxygen consumption, decreased respiratory quotient, decreased liver triglyceride level and ameliorated hyperlipidemia and hepatosteatosis when fed a high-fat diet.
- The *Helz2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Helz2 helicase with zinc finger 2, transcriptional coactivator [*Mus musculus* (house mouse)]

Gene ID: 229003, updated on 12-Aug-2019

Summary

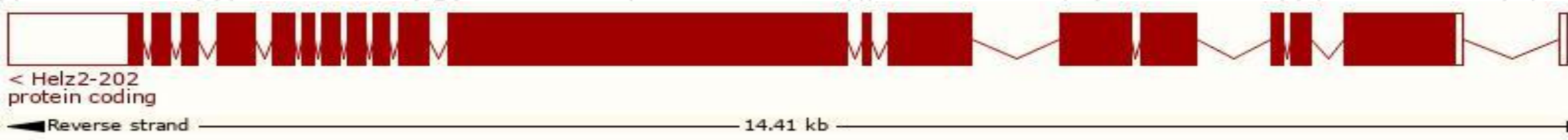
Official Symbol	Helz2 provided by MGI
Official Full Name	helicase with zinc finger 2, transcriptional coactivator provided by MGI
Primary source	MGI:MGI:2385169
See related	Ensembl:ENSMUSG00000027580
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PDIP1; mPDIP1; Pric285; mKIAA1769
Expression	Broad expression in spleen adult (RPKM 53.3), thymus adult (RPKM 35.0) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

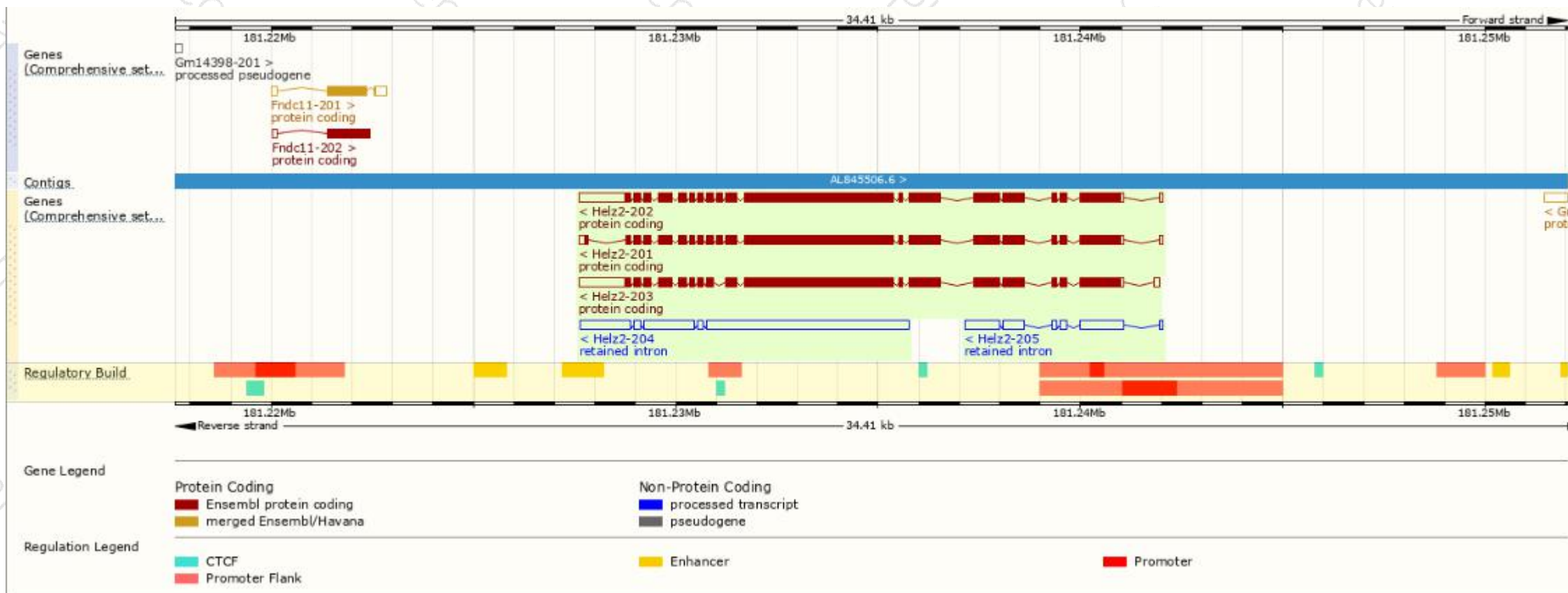
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Helz2-202	ENSMUST00000108831.7	10109	2947aa	Protein coding	CCDS38380	E9QAM5	TSL:5 GENCODE basic APPRIS P2
Helz2-203	ENSMUST00000121484.1	10063	2903aa	Protein coding	-	A2AS05	TSL:5 GENCODE basic
Helz2-201	ENSMUST00000094203.10	9162	2970aa	Protein coding	-	A2AS03	TSL:5 GENCODE basic APPRIS ALT2
Helz2-204	ENSMUST00000149417.1	7787	No protein	Retained intron	-	-	TSL:1
Helz2-205	ENSMUST00000155049.1	2800	No protein	Retained intron	-	-	TSL:1

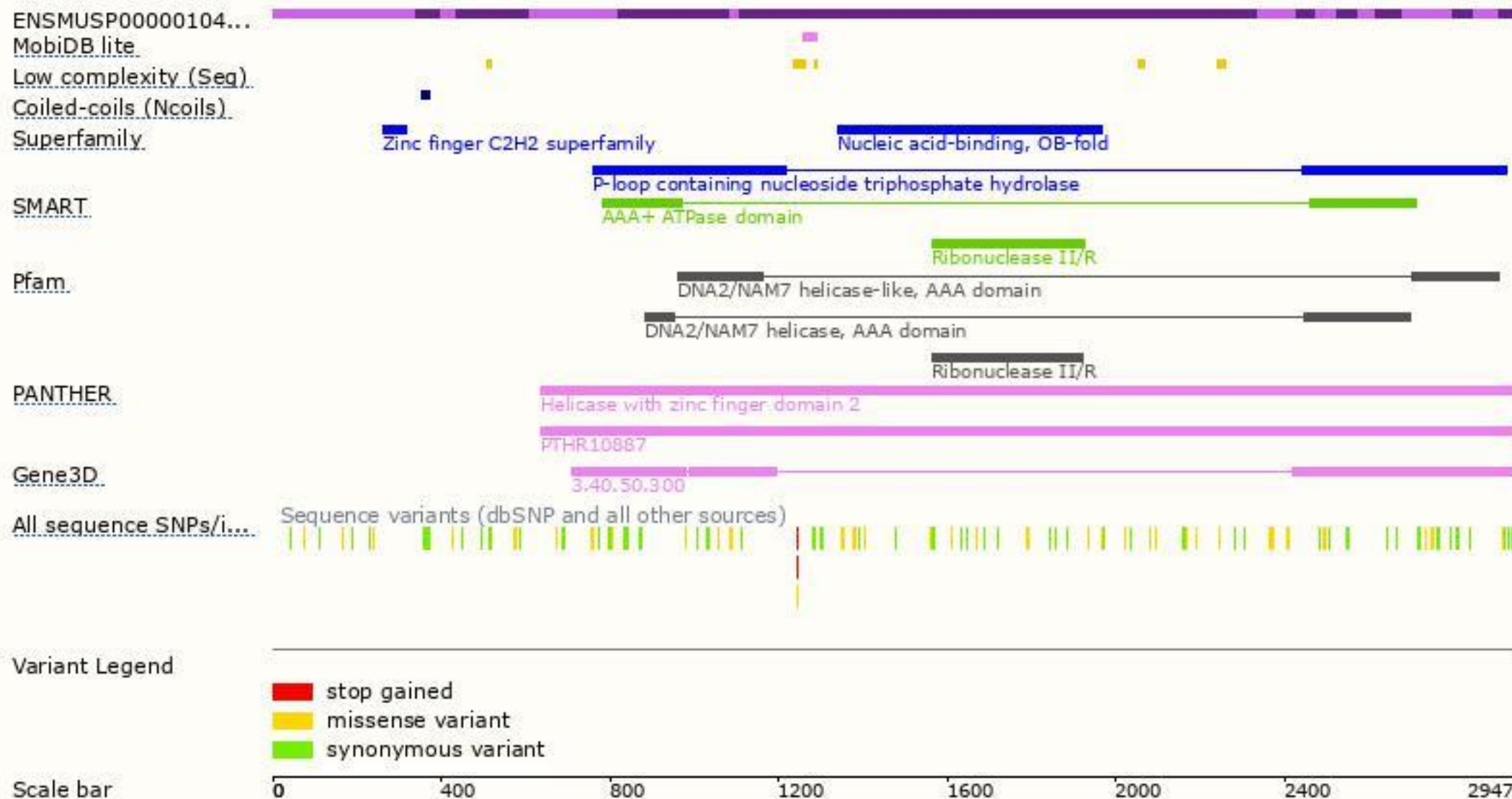
The strategy is based on the design of *Helz2-202* transcript,The transcription is shown below



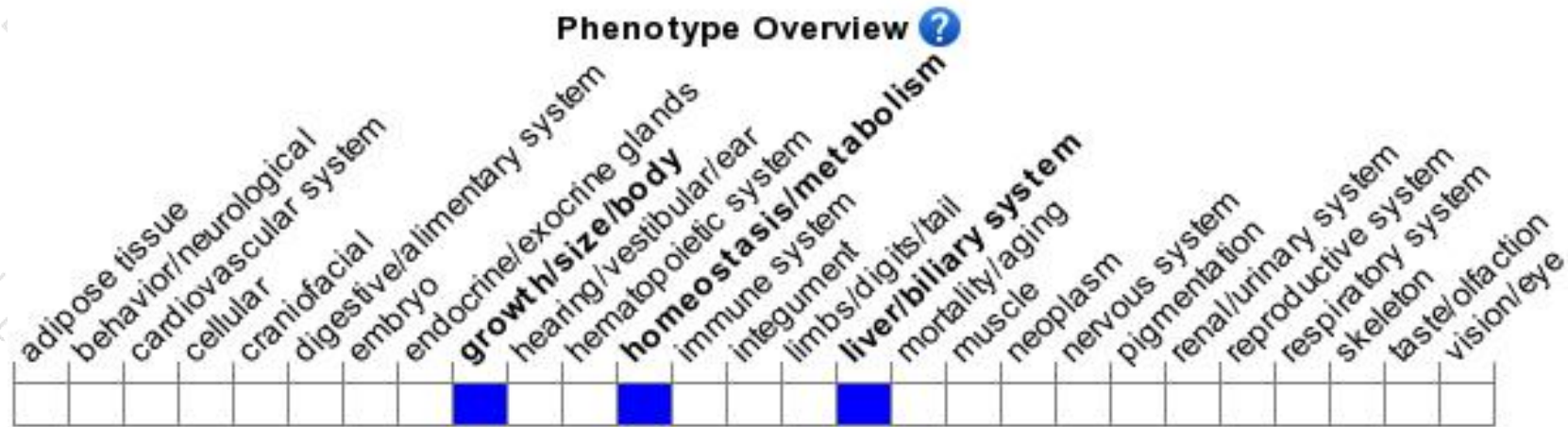
Genomic location distribution



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 slower weight gain, hyperleptinemia, increased oxygen consumption, decreased respiratory quotient, decreased liver triglyceride level and ameliorated hyperlipidemia and hepatosteatosis when fed a high-fat diet.

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

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