

Hjv Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

Date: 2023-5-19

Project Overview

Project Name

Hjv

Project type

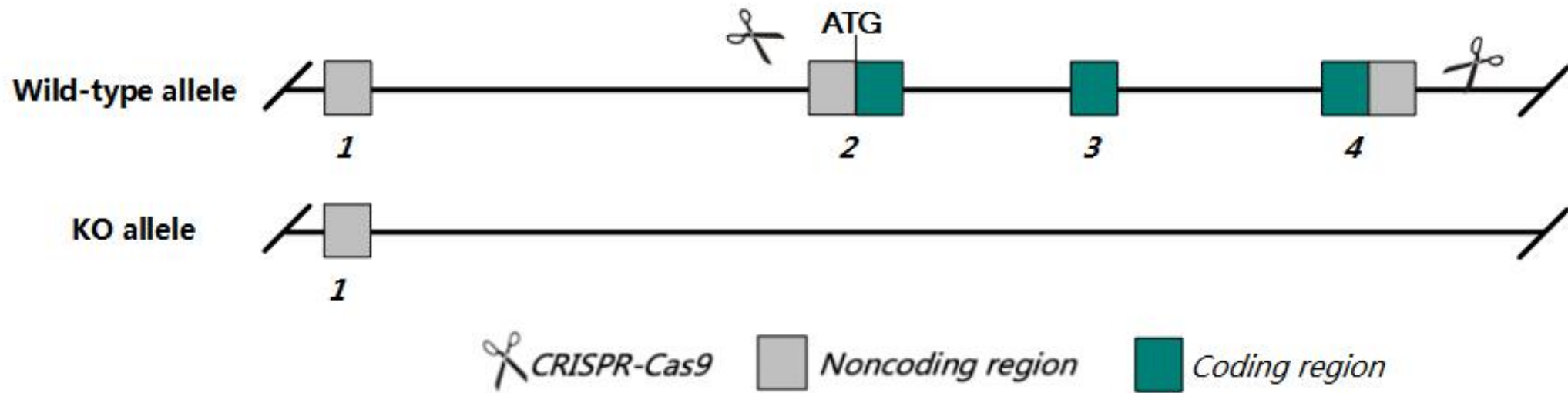
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hjv* gene has 1 transcript. According to the structure of *Hjv* gene, exon2-exon4 of *Hfe2-201* (ENSMUST00000049208.11) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Hjv* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit lack of hepcidin expression, severe iron overload and male sterility. Mice homozygous for a different knock-out allele display systemic iron overload, a severe deficit in hepcidin production, overexpression of ferroportin but normal male fertility.
- The *Hjv* gene is located on the Chr3. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Hjv hemojuvelin BMP co-receptor [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 69585, updated on 12-Apr-2023

Summary

Official Symbol

Hjv provided by MGI

Official Full Name

hemojuvelin BMP co-receptor provided by MGI

Primary source

MGI:MGI:1916835

See related

Ensembl:ENSMUSG00000038403AllianceGenome MGI:1916835

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

DL-M; Hfe2; Rgmc; hemojuvelin; 2310035L15Rik; 5230400G09Rik

Summary

Enables BMP binding activity and coreceptor activity. Involved in cellular iron ion homeostasis and negative regulation of transcription by RNA polymerase II. Acts upstream of or within several processes, including BMP signaling pathway; iron ion homeostasis; and negative regulation of BMP signaling pathway. Located in cell surface and extracellular space. Is expressed in several structures, including gonad; musculature; submandibular gland; trunk mesenchyme; and yolk sac. Used to study hemochromatosis type 2A. Human ortholog(s) of this gene implicated in hemochromatosis and hemochromatosis type 2A. Orthologous to human HJV (hemojuvelin BMP co-receptor). [provided by Alliance of Genome Resources, Apr 2022]

Expression

Biased expression in heart adult (RPKM 77.5), liver adult (RPKM 38.7) and 4 other tissues [See more](#)

Orthologs

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

NEW

Try the new [Gene table](#)

Try the new [Transcript table](#)

Genomic context

Location: 3; 3 F2.1 See Hjv in [Genome Data Viewer](#)

Exon count: 4

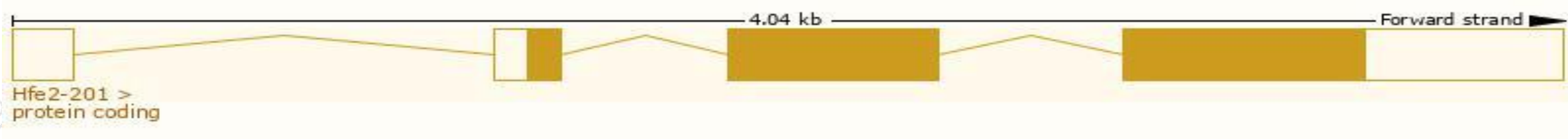
Annotation release	Status	Assembly	Chr	Location
RS_2023_04	current	GRCm39 (GCF_000001635.27)	3	NC_000069.7 (96432479..96436532)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	3	NC_000069.6 (96525163..96529216)

Transcript information (Ensembl)

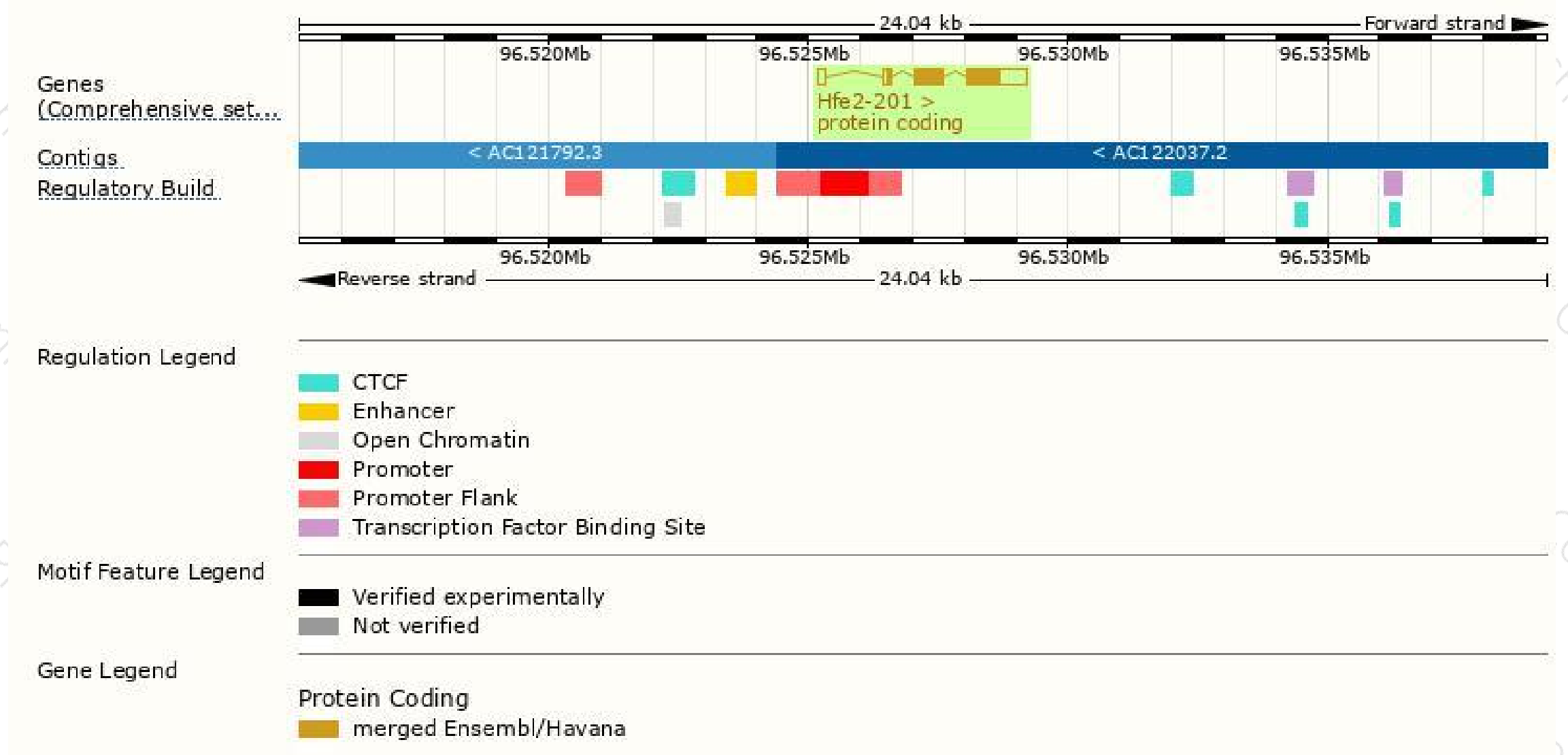
The gene has 1 transcript, and the transcript is shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000049208.11	Hjv-201	2028	420aa	Protein coding	CCDS51003	Q7TQ32-1	Ensembl Canonical Gencode basic APPRIS P1 TSL:1

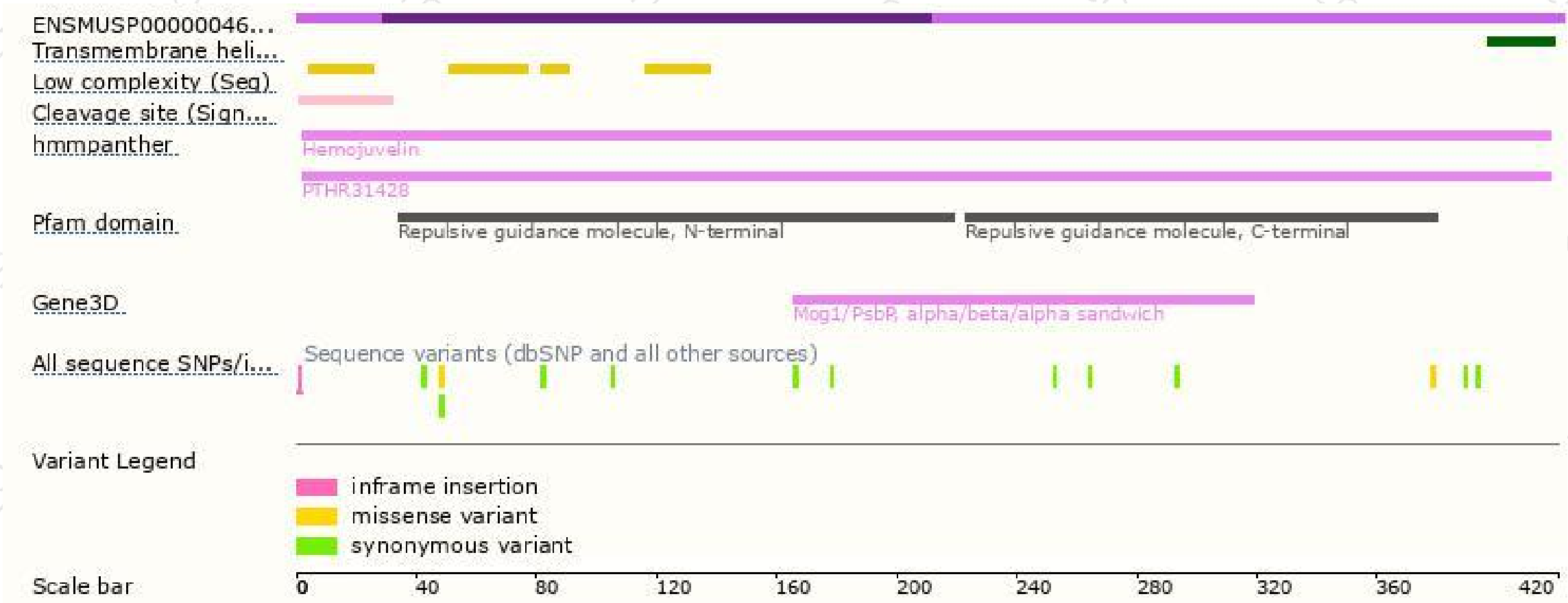
The strategy is based on the design of *Hfe2-201* transcript, The transcription is shown below



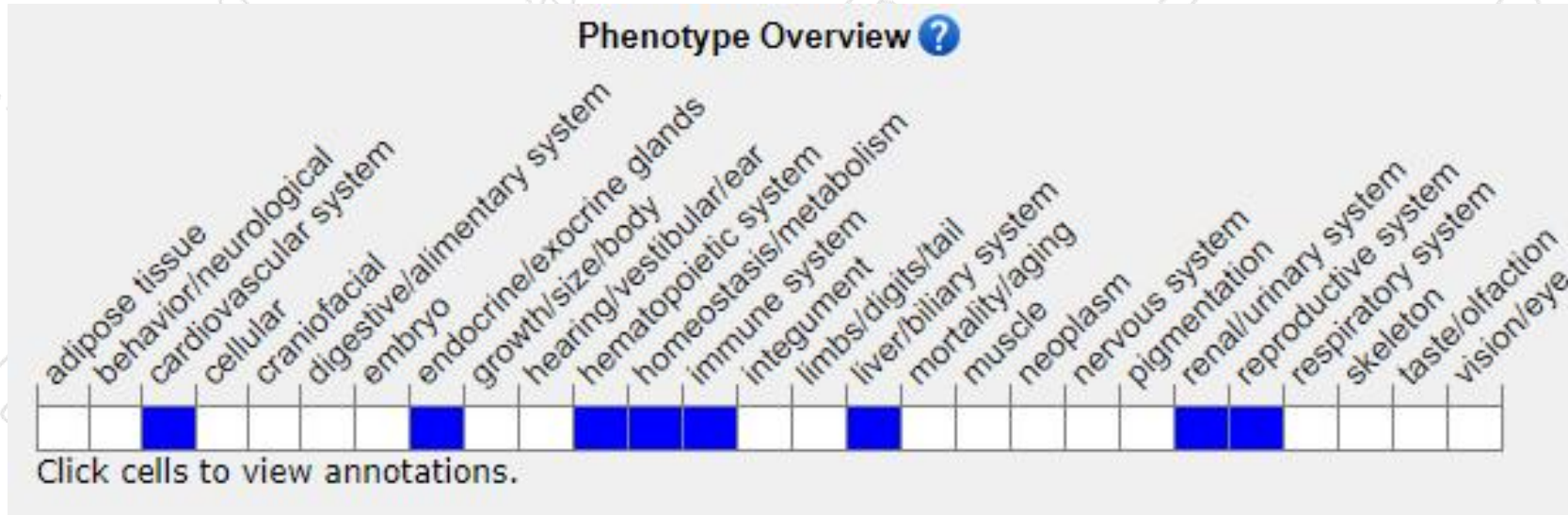
Genomic location distribution



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 lack of hepcidin expression, severe iron overload and male sterility. Mice homozygous for a different knock-out allele display systemic iron overload, a severe deficit in hepcidin production, overexpression of ferroportin but normal male fertility.

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

Tel: 025-5864 1534

