Hp Cas9-KO Strategy

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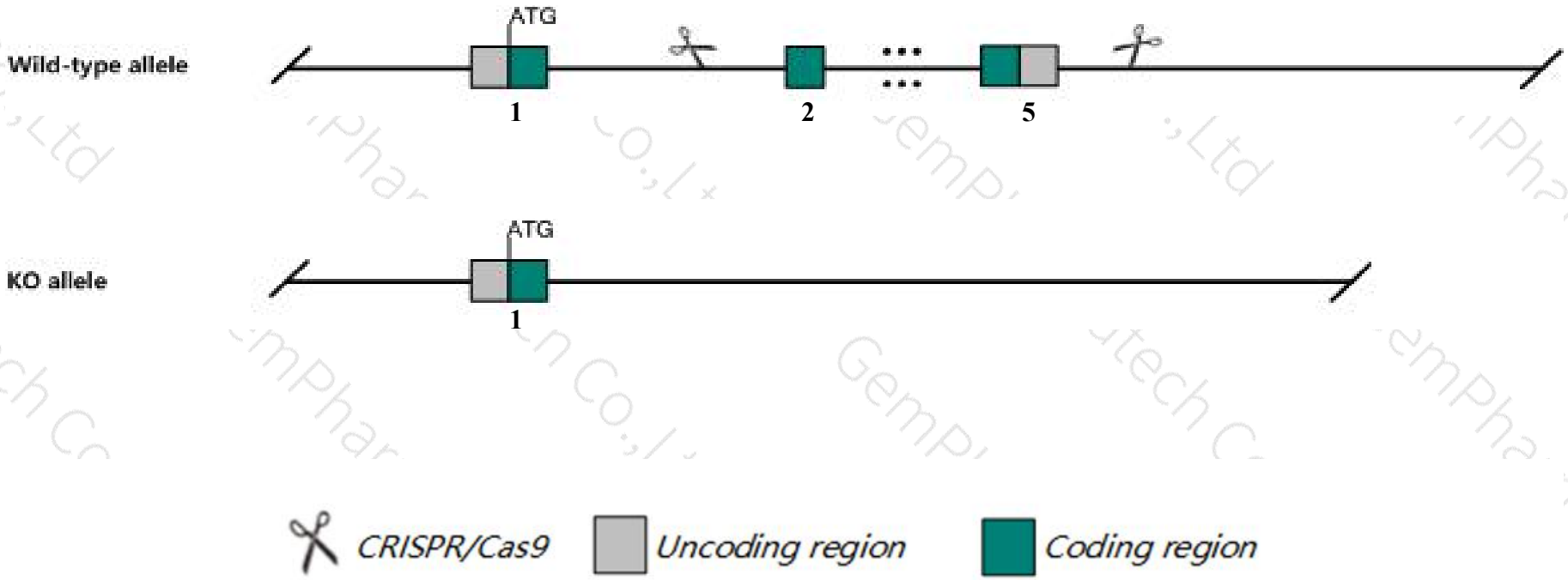
Design Date:2019-11-14

Project Overview

Project Name	***Hp***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Hp* gene has 3 transcripts. According to the structure of *Hp* gene, exon2-exon5 of *Hp-201* (ENSMUST00000074898.7) transcript is recommended as the knockout region.The region contains 1039bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hp* gene. The brief process is as follows: CRISPR/Cas9 system we

Notice

- According to the existing MGI data,Homozygotes for a null allele exhibit partial postnatal lethality, susceptibility to induced acute hemolysis, and altered renal iron loading during aging and after ischemic injury. Homozygotes for a knock-in allele show reduced cholesterol efflux and enhanced nephropathy in STZ-induced diabetes.

- The *Hp* gene is located on the Chr8. 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）

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Hp haptoglobin [Mus musculus (house mouse)]

Gene ID: 15439, updated on 19-Mar-2019

Summary

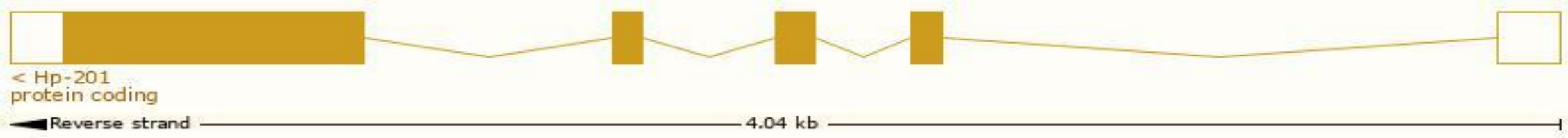
Official Symbol	Hp provided by MGI
Official Full Name	haptoglobin provided by MGI
Primary source	MGI:MGI:96211
See related	Ensembl:ENSMUSG00000031722
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	HP-1, preHP2
Summary	This gene encodes a plasma glycoprotein called haptoglobin that binds free hemoglobin. The encoded preproprotein undergoes proteolytic processing to generate alpha and beta subunits that form a disulfide-linked tetrameric protein that plays an important role in the sequestration and clearance of extracorpuscular hemoglobin. Mice lacking the encoded protein exhibit stunted development of lymphoid organs associated with lower counts of mature T and B cells in the blood and secondary lymphoid compartments. [provided by RefSeq, Aug 2016]
Expression	Biased expression in liver adult (RPKM 929.2), liver E18 (RPKM 861.9) and 6 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

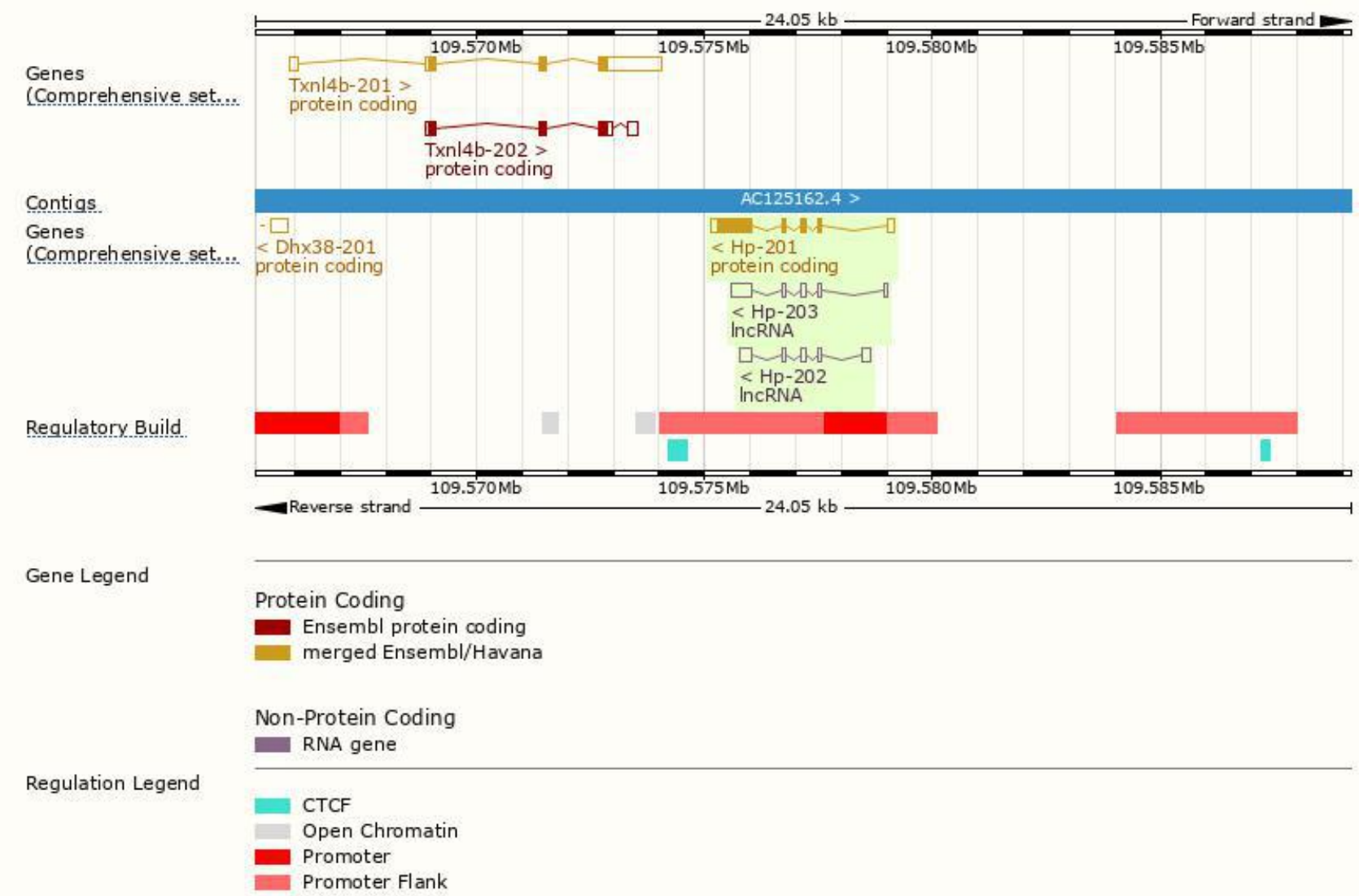
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hp-201	ENSMUST00000074898.7	1345	347aa	Protein coding	CCDS40470	Q3UBS3 Q61646	TSL:1 GENCODE basic APPRIS P1
Hp-203	ENSMUST00000212918.1	801	No protein	lncRNA	-	-	TSL:3
Hp-202	ENSMUST00000212018.1	749	No protein	lncRNA	-	-	TSL:3

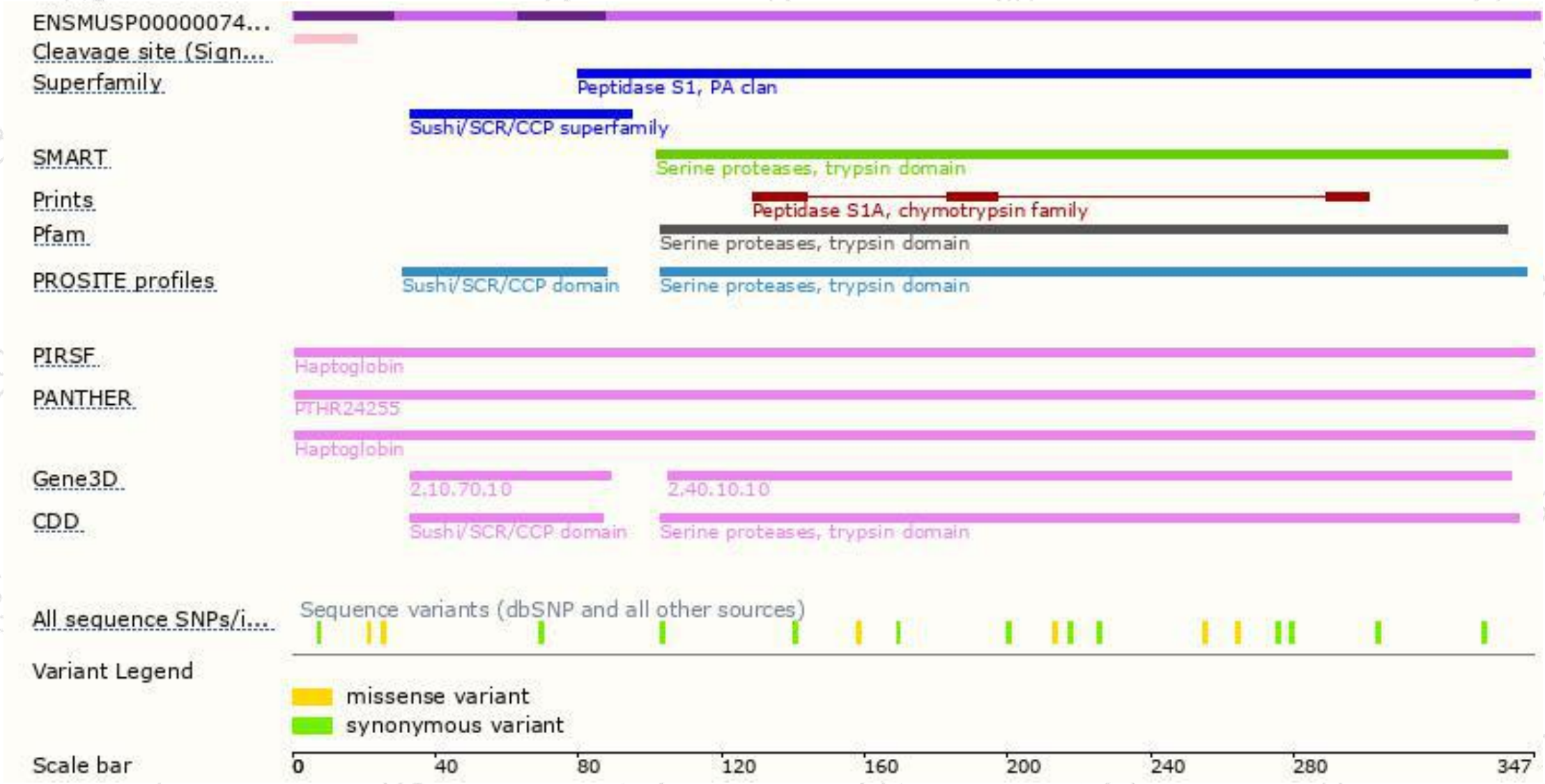
The strategy is based on the design of *Hp-201* transcript,The transcription is shown below



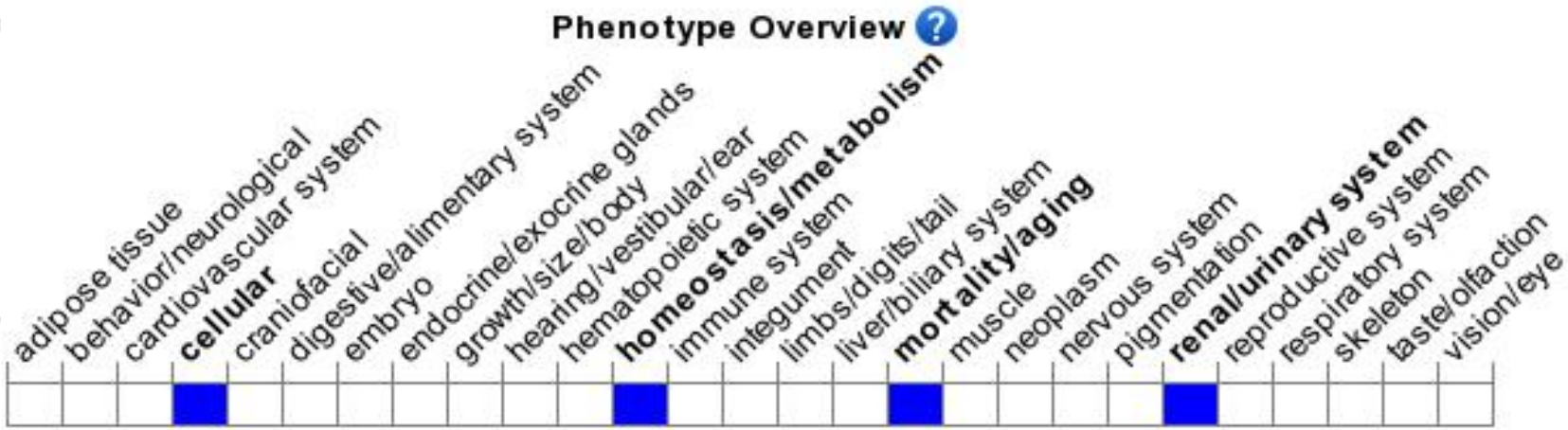
Genomic location distribution



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,Homozygotes for a null allele exhibit partial postnatal lethality, susceptibility to induced acute hemolysis, and altered renal iron loading during aging and after ischemic injury. Homozygotes for a knock-in allele show reduced cholesterol efflux and enhanced nephropathy in STZ-induced diabetes.

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

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