集萃药康
GemPharmatech

Hamp2 Cas9-KO Strategy

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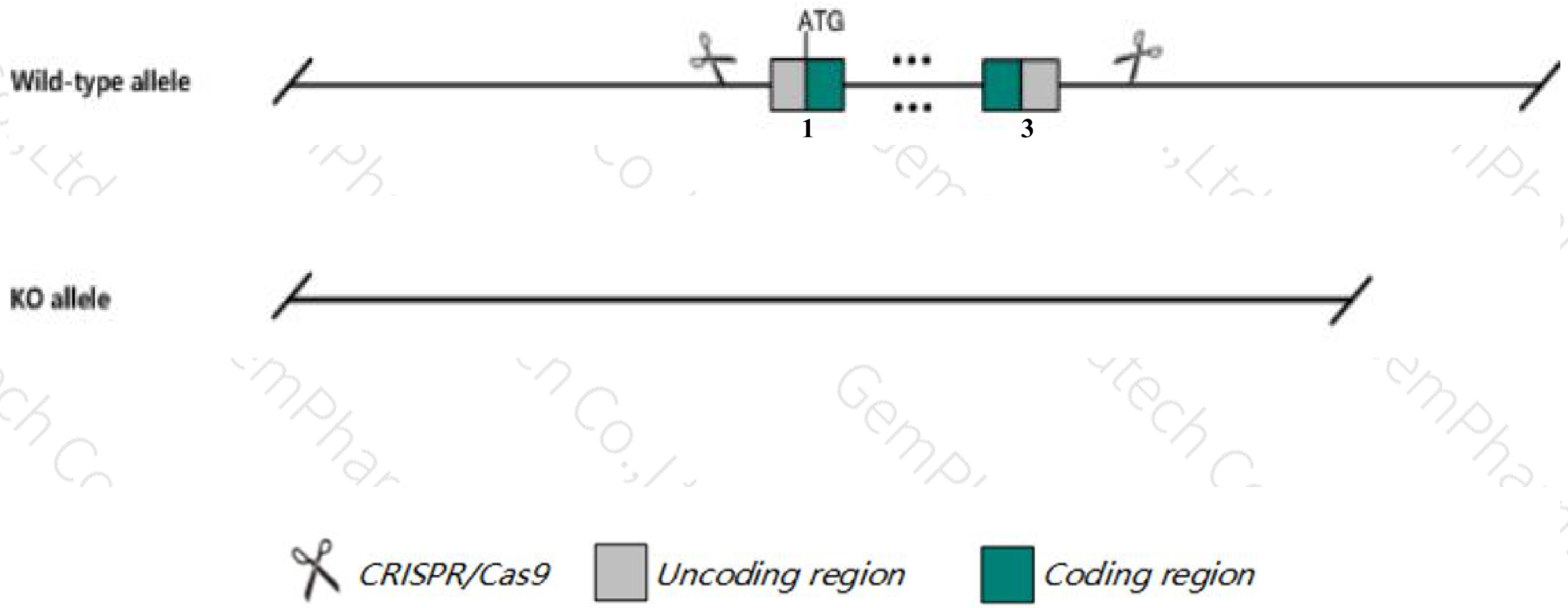
Reviewer：	**Xueting Zhang**
Design Date:	**2020-4-18**

Project Overview

Project Name	***Hamp2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hamp2* gene. The schematic diagram is as follows:



Technical routes

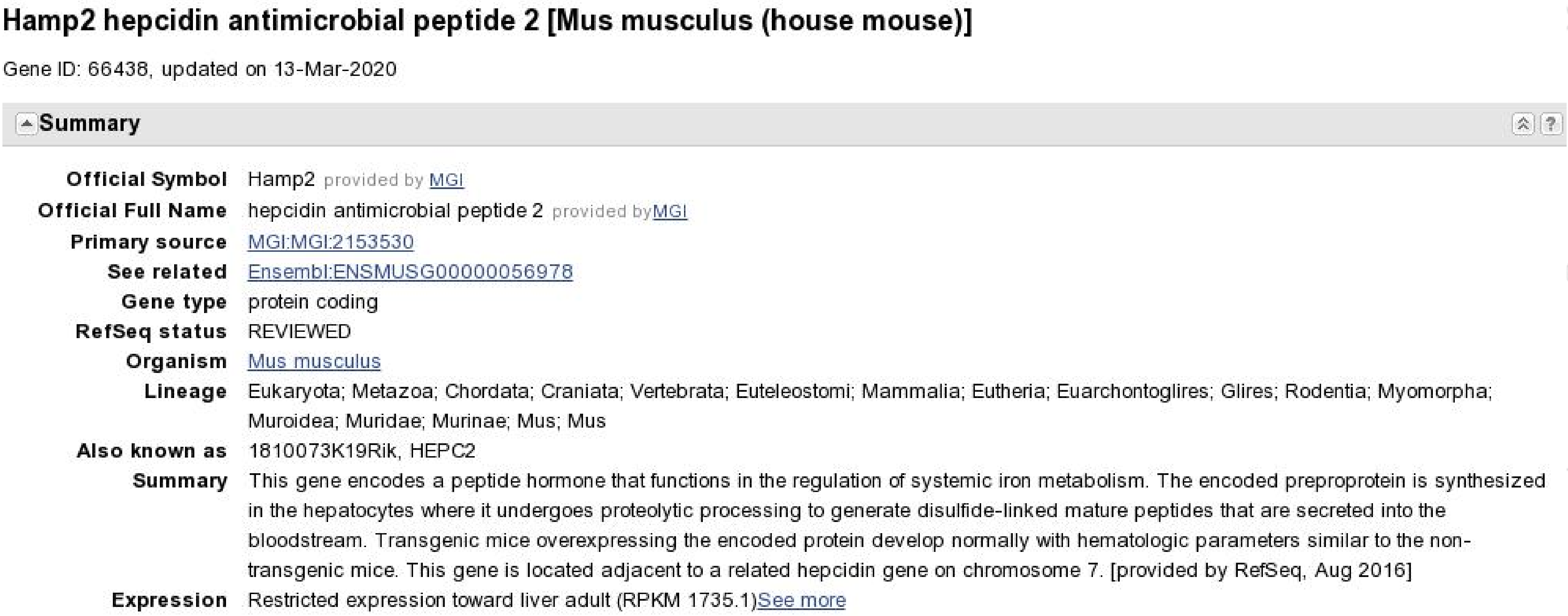
- The *Hamp2* gene has 3 transcripts. According to the structure of *Hamp2* gene, exon1-exon3 of *Hamp2-203* (ENSMUST00000217812.1) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hamp2* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

- *Gm44662*-201 and *Usf2-ps1*-201 gene may be destroyed.
- The *Hamp2* gene is located on the Chr7. 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）



Hamp2 hepcidin antimicrobial peptide 2 [Mus musculus (house mouse)]

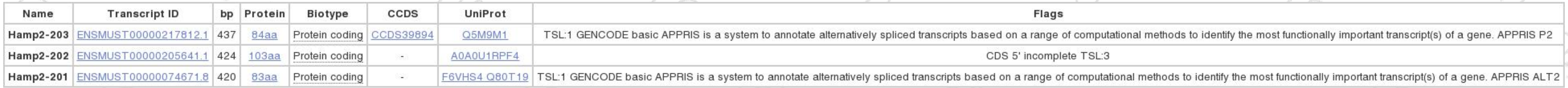
Gene ID: 66438, updated on 13-Mar-2020

Summary

Official Symbol	Hamp2 provided by MGI
Official Full Name	hepcidin antimicrobial peptide 2 provided by MGI
Primary source	MGI:MGI:2153530
See related	Ensembl:ENSMUSG00000056978
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	1810073K19Rik, HEPC2
Summary	This gene encodes a peptide hormone that functions in the regulation of systemic iron metabolism. The encoded preproprotein is synthesized in the hepatocytes where it undergoes proteolytic processing to generate disulfide-linked mature peptides that are secreted into the bloodstream. Transgenic mice overexpressing the encoded protein develop normally with hematologic parameters similar to the non-transgenic mice. This gene is located adjacent to a related hepcidin gene on chromosome 7. [provided by RefSeq, Aug 2016]
Expression	Restricted expression toward liver adult (RPKM 1735.1)See more

Transcript information（Ensembl）

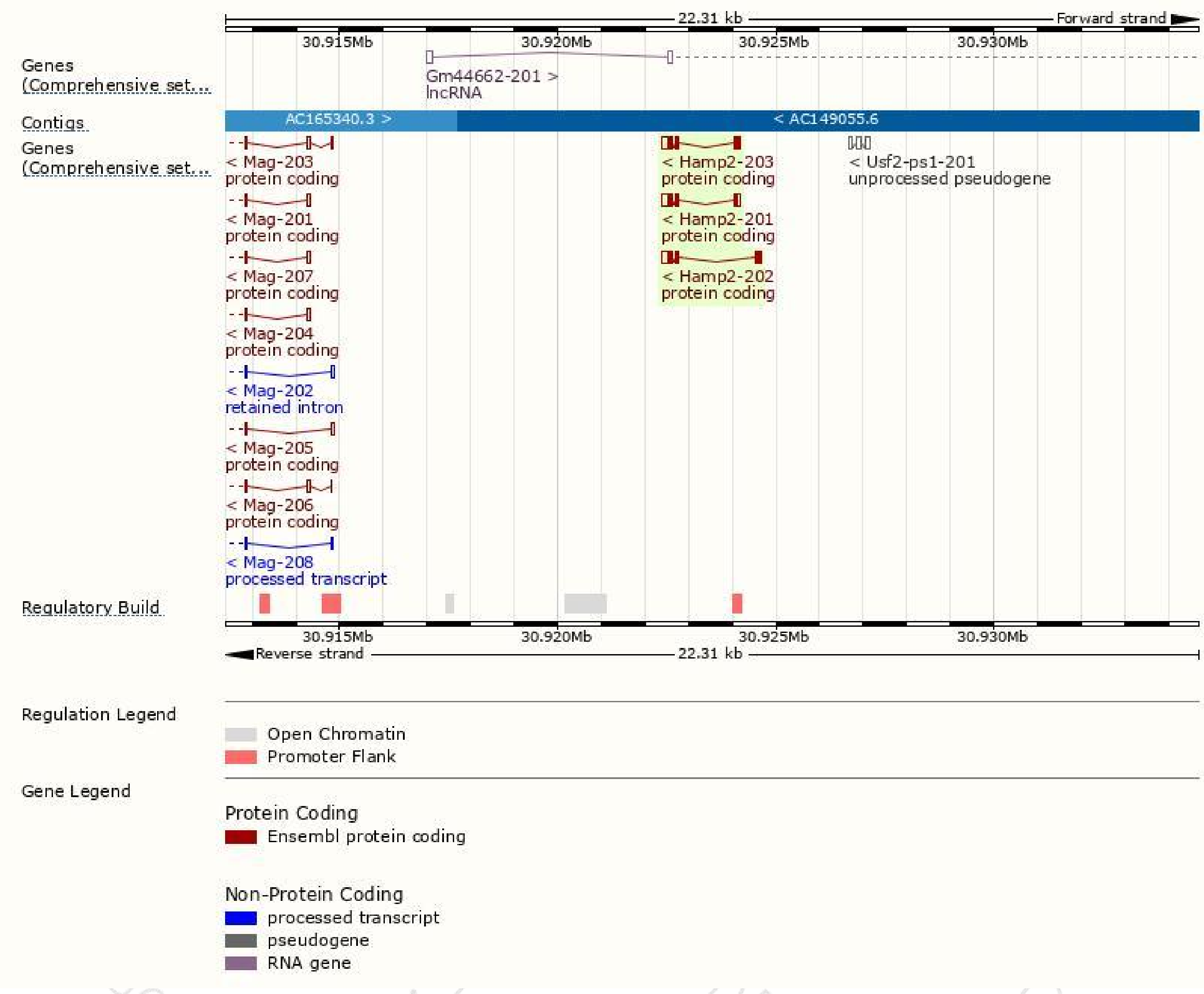
The gene has 3 transcripts,all transcripts are shown below:



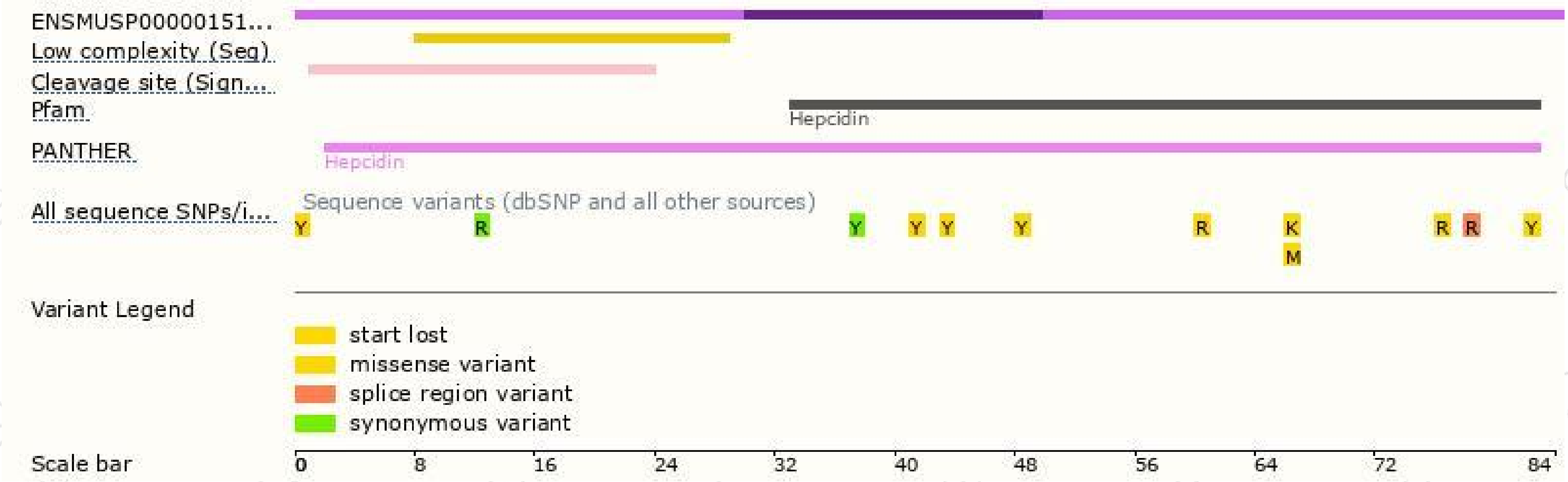
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hamp2-203	ENSMUST00000217812.1	437	84aa	Protein coding	CCDS39894	Q5M9M1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Hamp2-202	ENSMUST00000205641.1	424	103aa	Protein coding	-	A0A0U1RPF4	CDS 5' incomplete TSL:3
Hamp2-201	ENSMUST00000074671.8	420	83aa	Protein coding	-	F6VHS4 Q80T19	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2

The strategy is based on the design of *Hamp2-203* transcript,The transcription is shown below

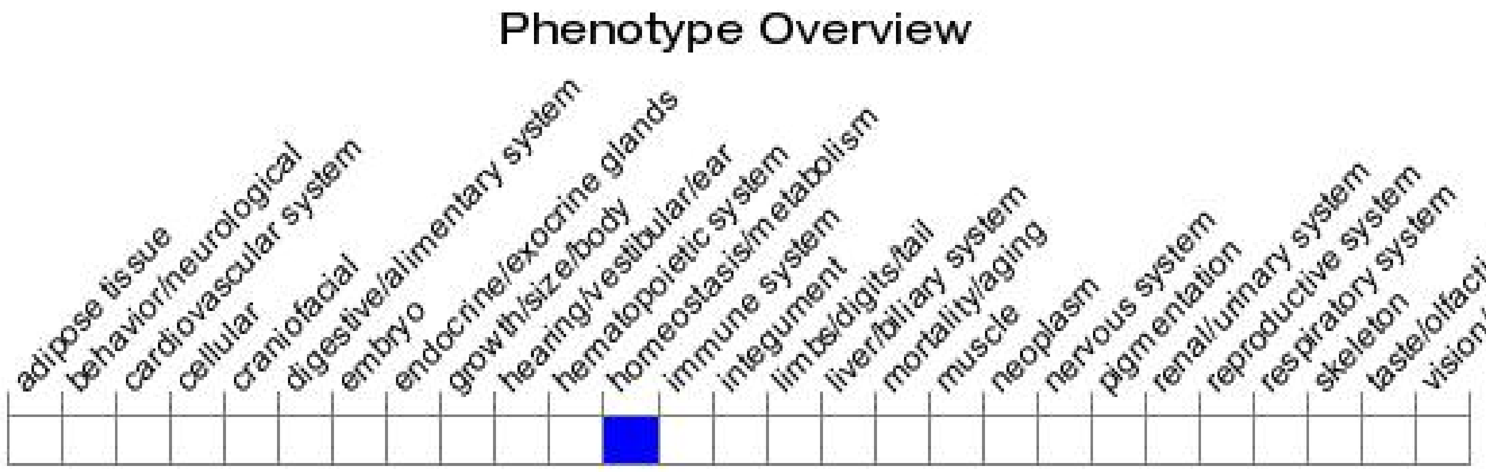
Genomic location distribution



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/).

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