Krt16 Cas9-KO Strategy

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Reviewer: Xueting Zhang

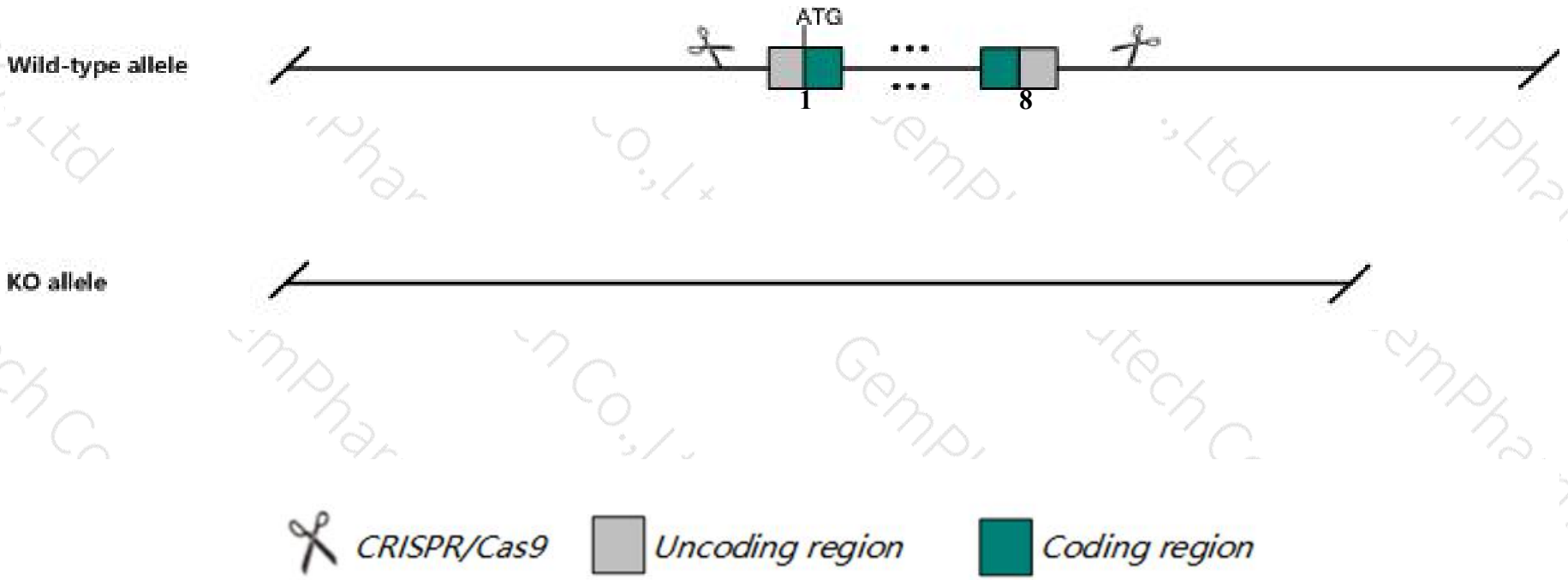
Design Date: 2020-01-31

Project Overview

Project Name	***Krt16***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Krt16* gene. The schematic diagram is as follows:



Technical routes

➢ The *Krt16* gene has 1 transcript. According to the structure of *Krt16* gene, exon1-exon8 of *Krt16-201* (ENSMUST00000007280.8) 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 *Krt16* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit partial neonatal and postnatal lethality, decreased body weight, abnormal tongue epithelium and hyperkertotic calluses in areas of physical pressure.

- The *Krt16* gene is located on the Chr11. 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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Krt16 keratin 16 [*Mus musculus* (house mouse)]

Gene ID: 16666, updated on 5-Jan-2020

Summary

Official Symbol	Krt16 provided by MGI
Official Full Name	keratin 16 provided by MGI
Primary source	MGI:MGI:96690
See related	Ensembl:ENSMUSG00000053797
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	K16; CK-16; Krt1-16; AI324768
Summary	The protein encoded by this gene is a member of the keratin gene family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. The encoded protein is a cytokeratin and acts as an innate immune system effector, promoting the inflammatory response upon breach of the skin barrier. Defects in this gene are a cause of pachyonychia congenita. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Biased expression in stomach adult (RPKM 8.3), limb E14.5 (RPKM 3.4) and 5 other tissues See more
Orthologs	human all

Genomic context

Location: 11; 11 D

See Krt16 in Genome Data Viewer

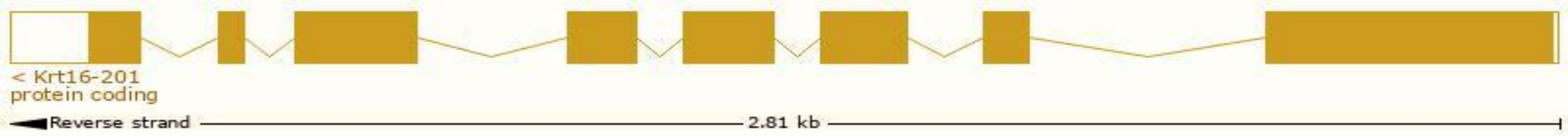
Exon count: 8

Transcript information（Ensembl）

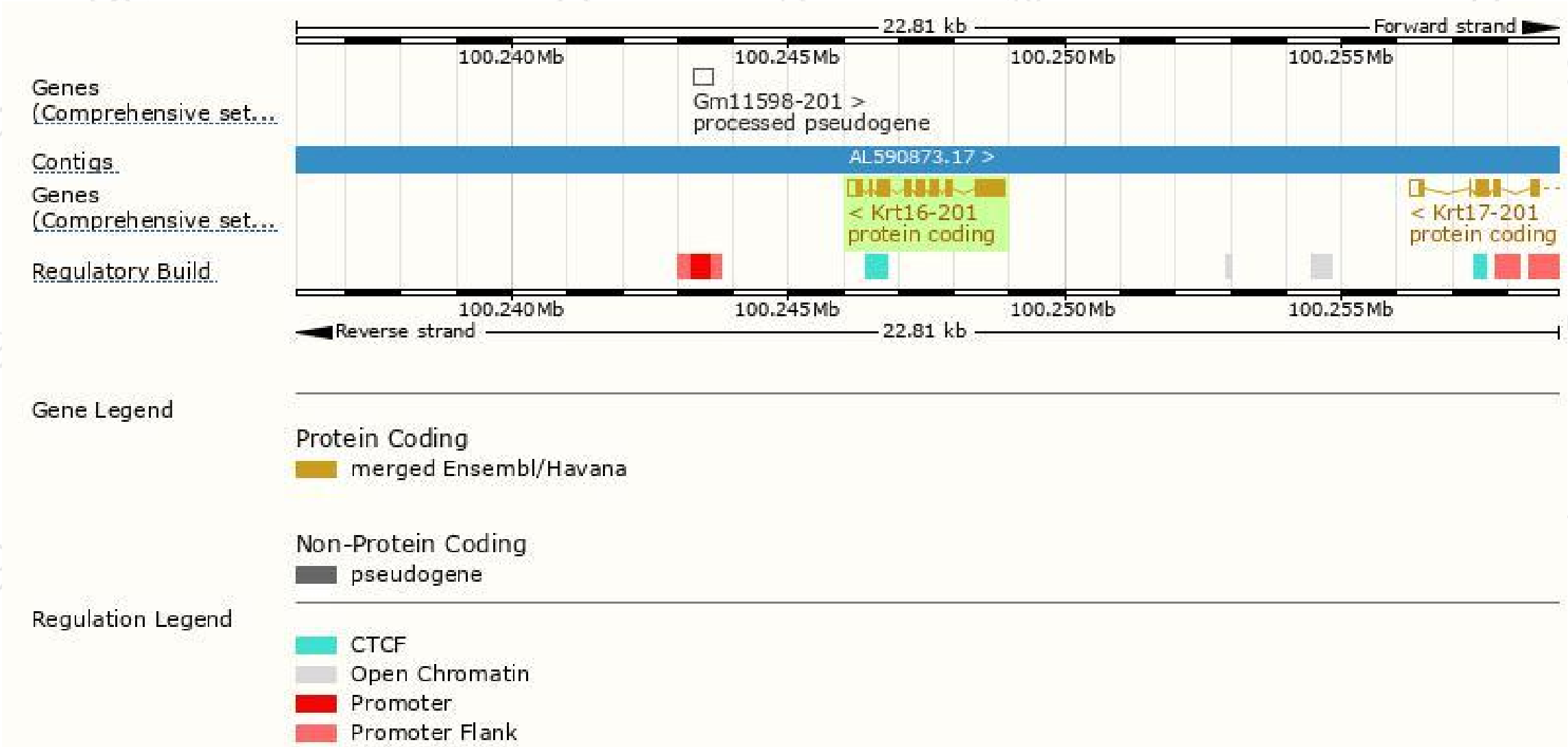
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Krt16-201	ENSMUST00000007280.8	1565	469aa	Protein coding	CCDS25414	Q3SYP5 Q9Z2K1	TSL:1 GENCODE basic APPRIS P1

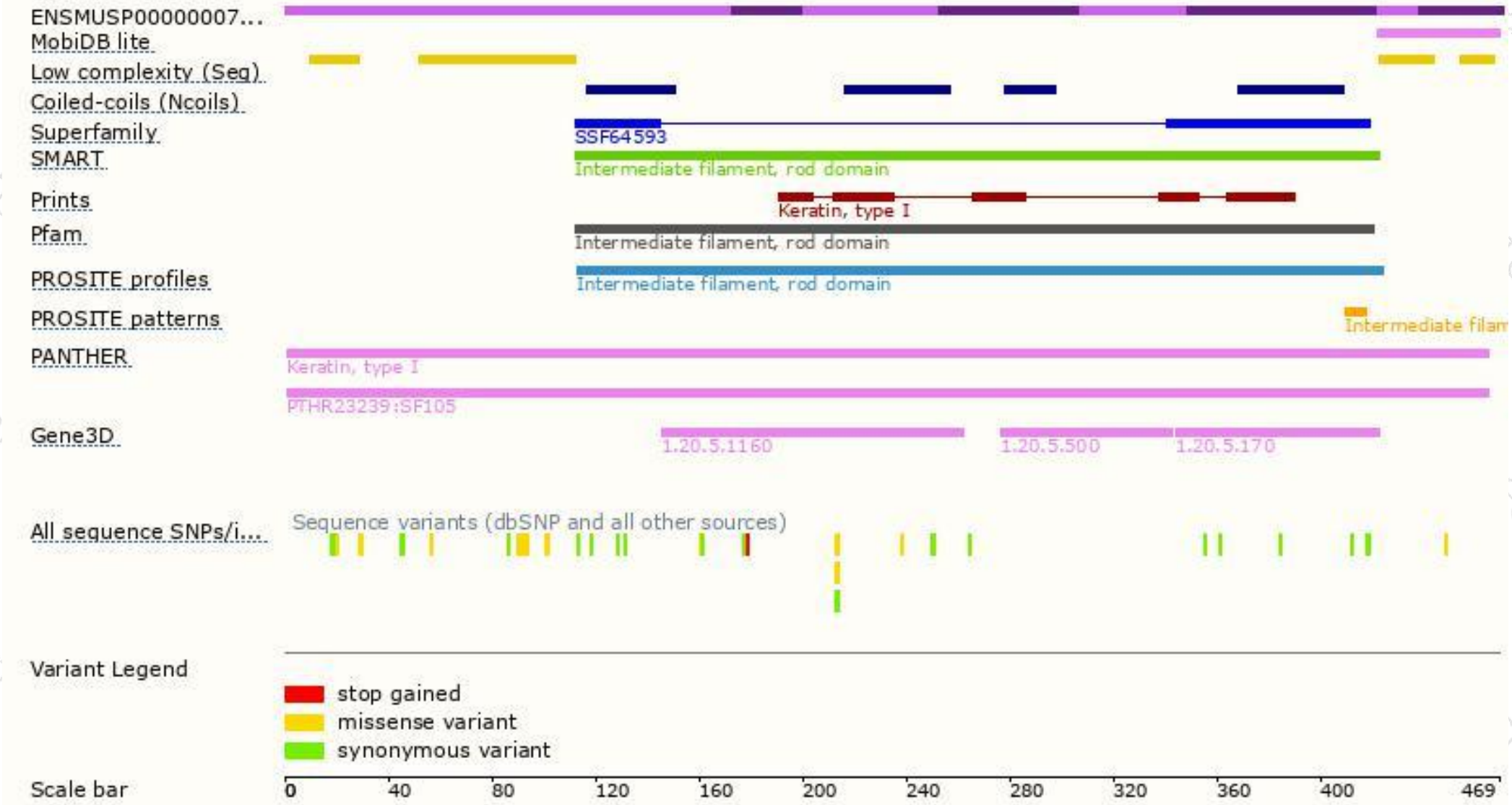
The strategy is based on the design of *Krt16-201* transcript,The transcription is shown below



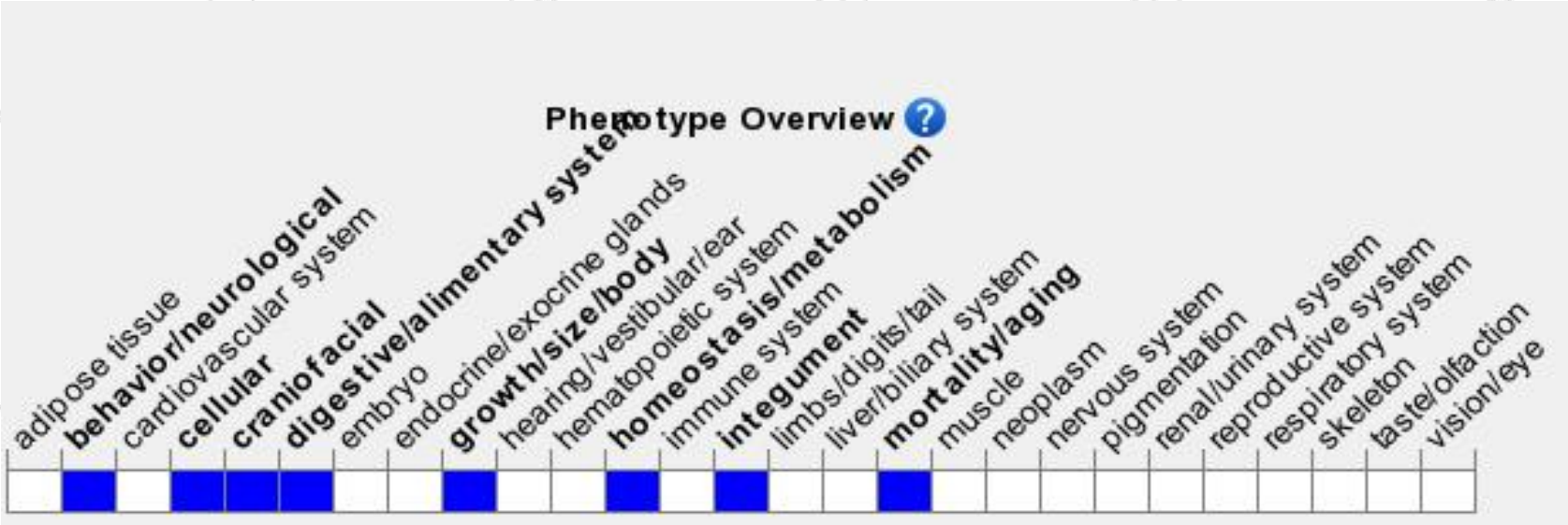
Genomic location distribution



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/).

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

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