Mep1a Cas9-KO Strategy

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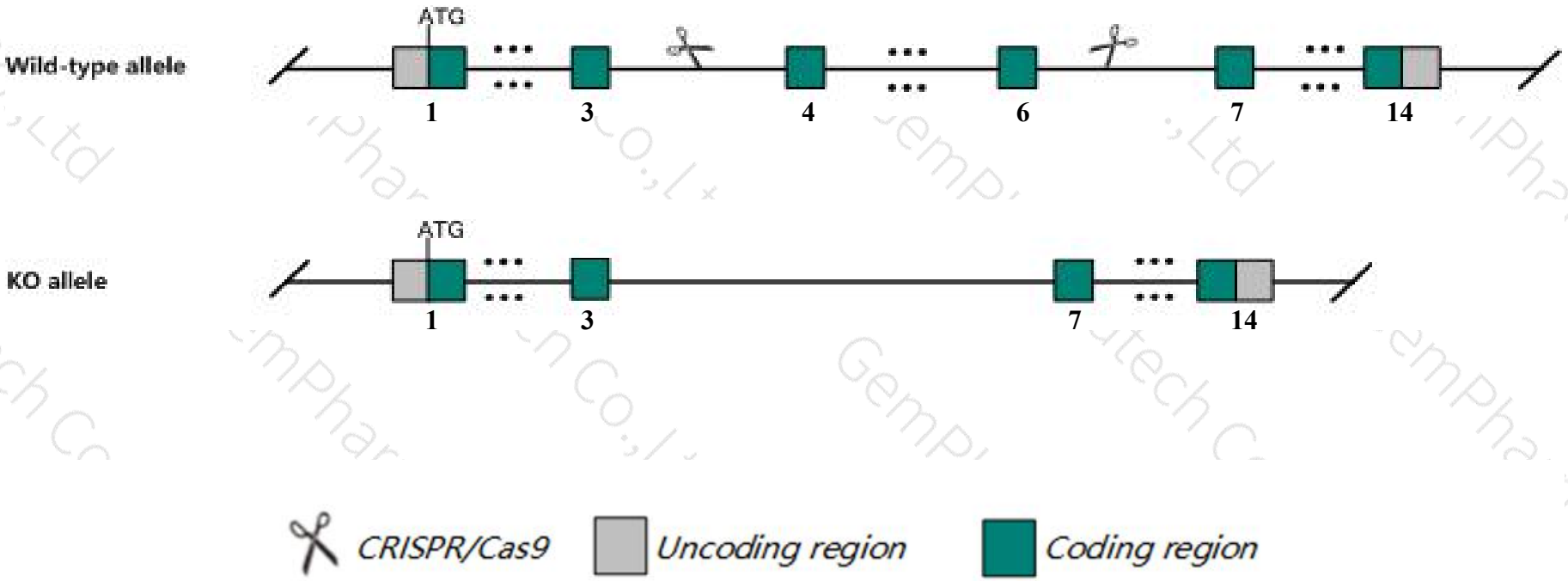
Project Overview

Project Name	***Mep1a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mep1a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mep1a* gene has 4 transcripts. According to the structure of *Mep1a* gene, exon4-exon6 of *Mep1a-201* (ENSMUST00000024707.8) transcript is recommended as the knockout region.The region contains 235bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mep1a* 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 decreased litter size, reduced LPS-induced renal injury and bladder inflammation, and increased susceptibility to sodium dextran sulfate-induced colitis.

- The *Mep1a* gene is located on the Chr17. 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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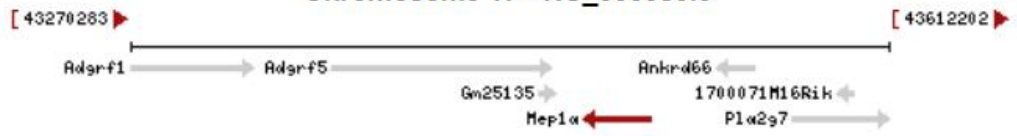
Mep1a meprin 1 alpha [*Mus musculus* (house mouse)]

Gene ID: 17287, updated on 10-Oct-2019

Summary

Official Symbol	Mep1a provided by MGI
Official Full Name	meprin 1 alpha provided by MGI
Primary source	MGI:MGI:96963
See related	Ensembl:ENSMUSG00000023914
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	Mep1; Mep-1; Mep-1a; AI098089; AW107200
Expression	Biased expression in kidney adult (RPKM 196.4), large intestine adult (RPKM 119.7) and 2 other tissues See more
Orthologs	human all

Chromosome 17 - NC_000083.6

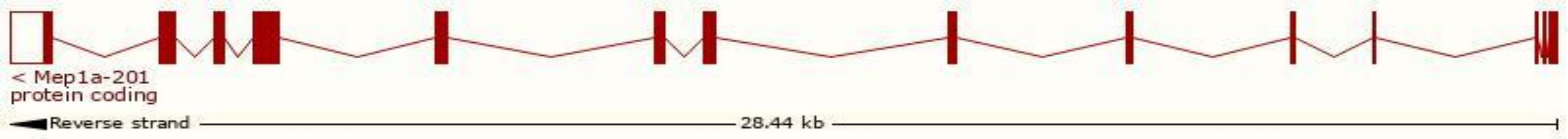


Transcript information（Ensembl）

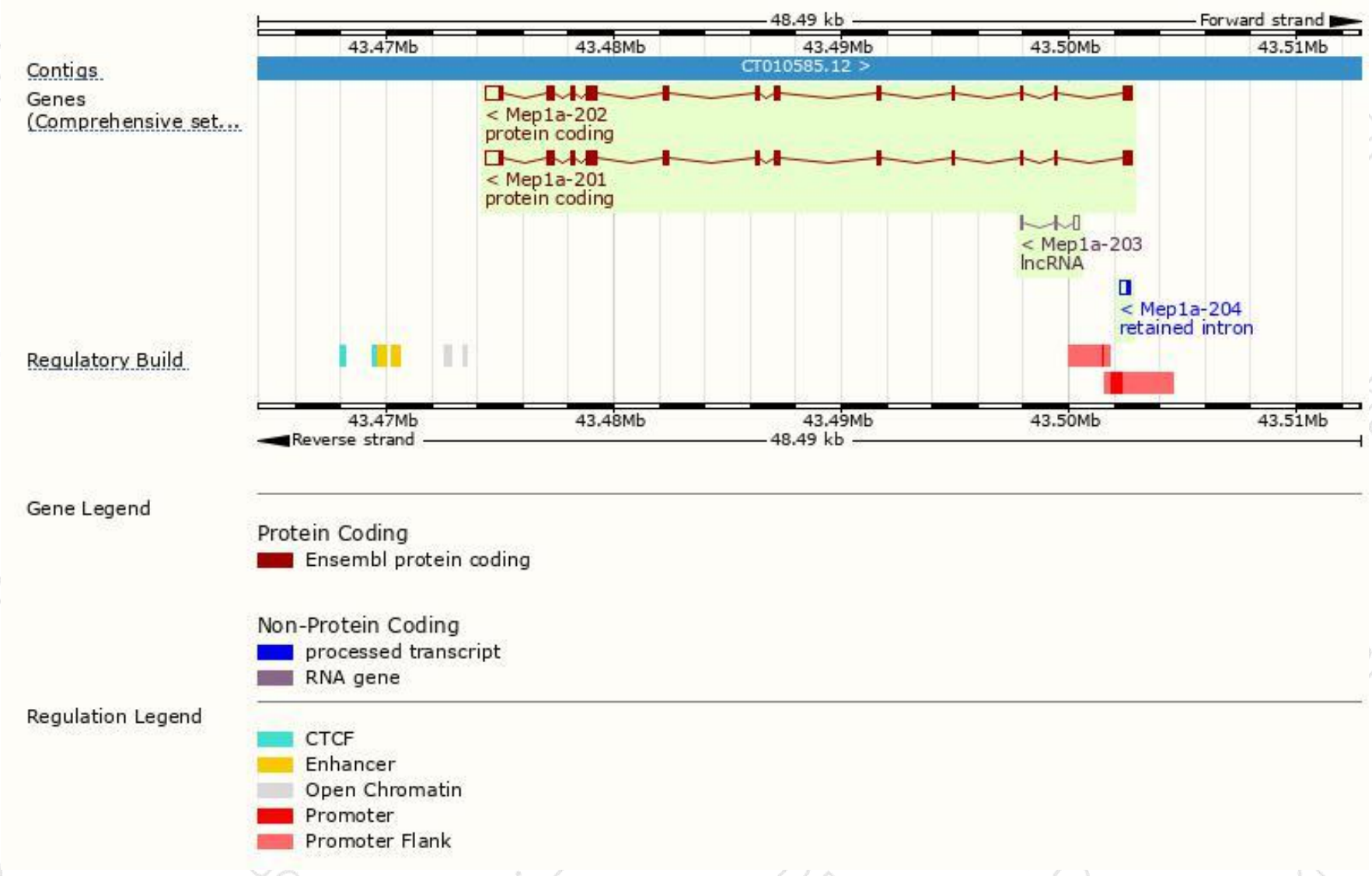
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Mep1a-201	ENSMUST00000024707.8	2921	760aa	ENSMUSP00000024707.8	Protein coding	CCDS37623	A0A0R4J043	TSL:1 GENCODE basic APPRIS P2
Mep1a-202	ENSMUST00000117137.7	2967	747aa	ENSMUSP00000113838.1	Protein coding	-	P28825	TSL:1 GENCODE basic APPRIS ALT2
Mep1a-204	ENSMUST00000152155.1	403	No protein	-	Retained intron	-	-	TSL:3
Mep1a-203	ENSMUST00000130964.1	356	No protein	-	lncRNA	-	-	TSL:3

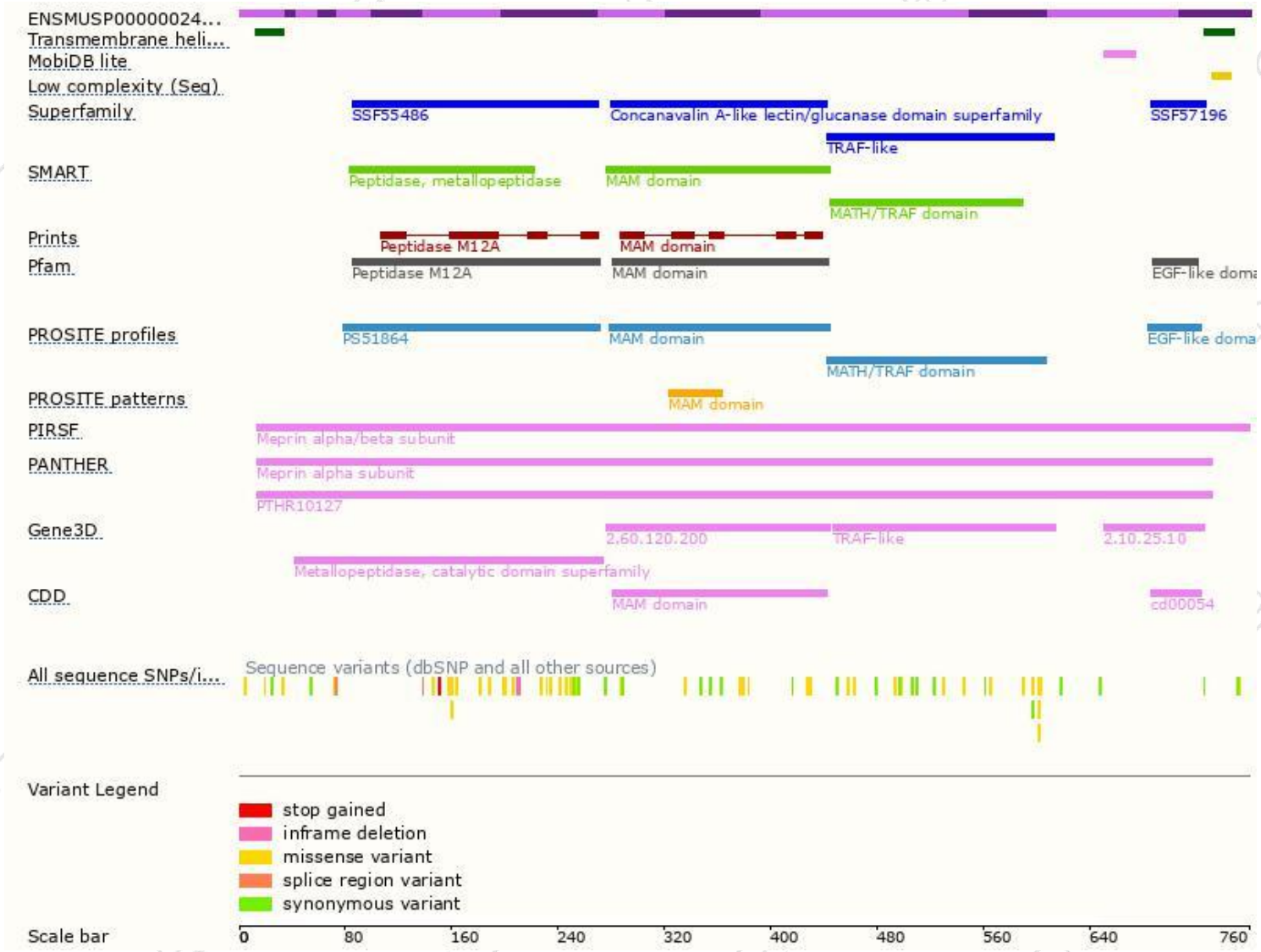
The strategy is based on the design of *Mep1a-201* transcript,The transcription is shown below



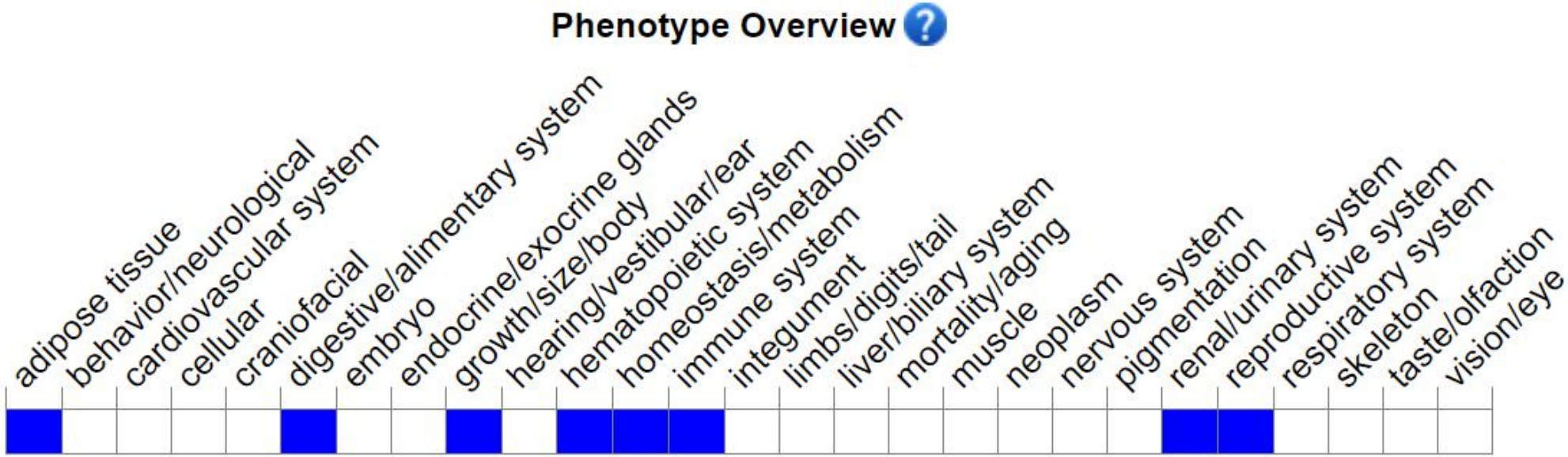
Genomic location distribution



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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