

Vim Cas9-KO Strategy

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Project Overview

Project Name

Vim

Project type

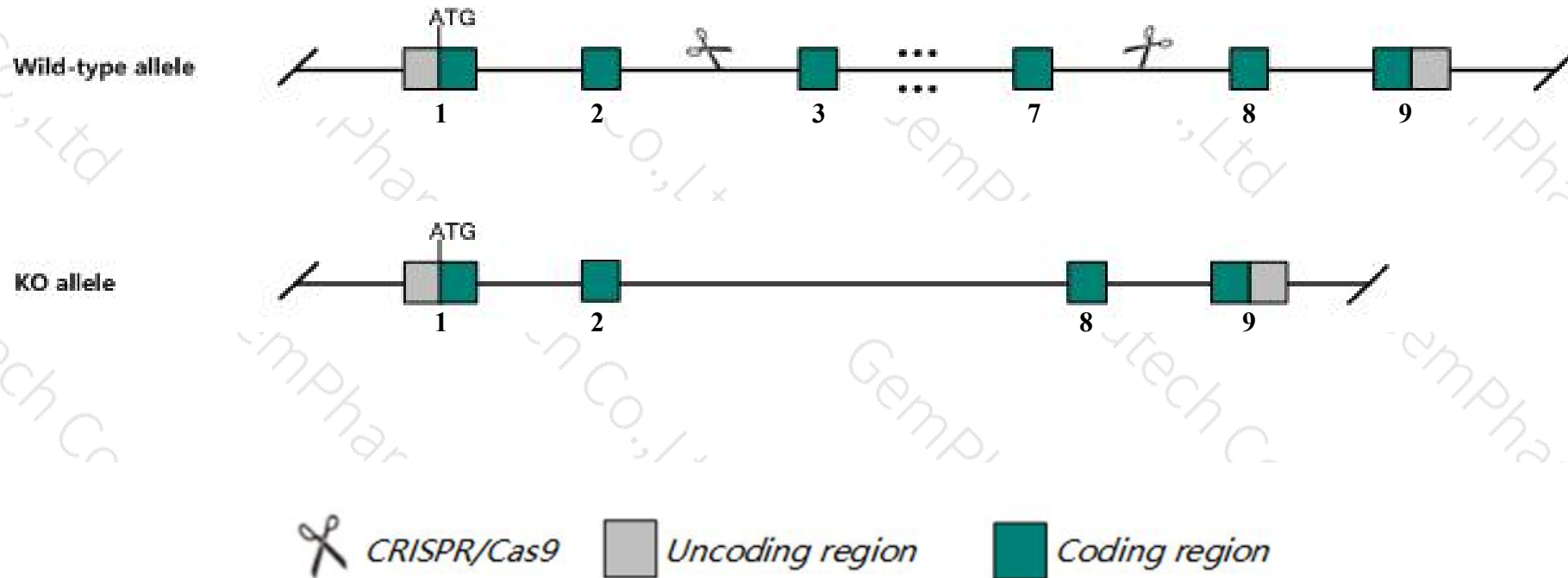
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Vim* gene has 6 transcripts. According to the structure of *Vim* gene, exon3-exon7 of *Vim-201* (ENSMUST00000028062.7) transcript is recommended as the knockout region. The region contains 649bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vim* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mutants exhibit impaired performance in motor coordination tests; cerebellum shows underdeveloped/abnormal Bergman glia and stunted, poorly branched Purkinje cells. Mutants are unable to survive experimental 75% reduction of kidney mass.
- The *Vim* gene is located on the Chr2. 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)

Vim vimentin [Mus musculus (house mouse)]

Gene ID: 22352, updated on 9-Apr-2019

Summary



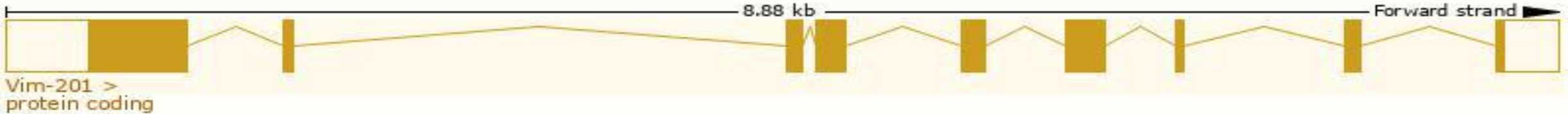
Official Symbol	Vim provided by MGI
Official Full Name	vimentin provided by MGI
Primary source	MGI:MGI:98932
See related	Ensembl:ENSMUSG000000026728
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Broad expression in subcutaneous fat pad adult (RPKM 622.6), mammary gland adult (RPKM 524.7) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

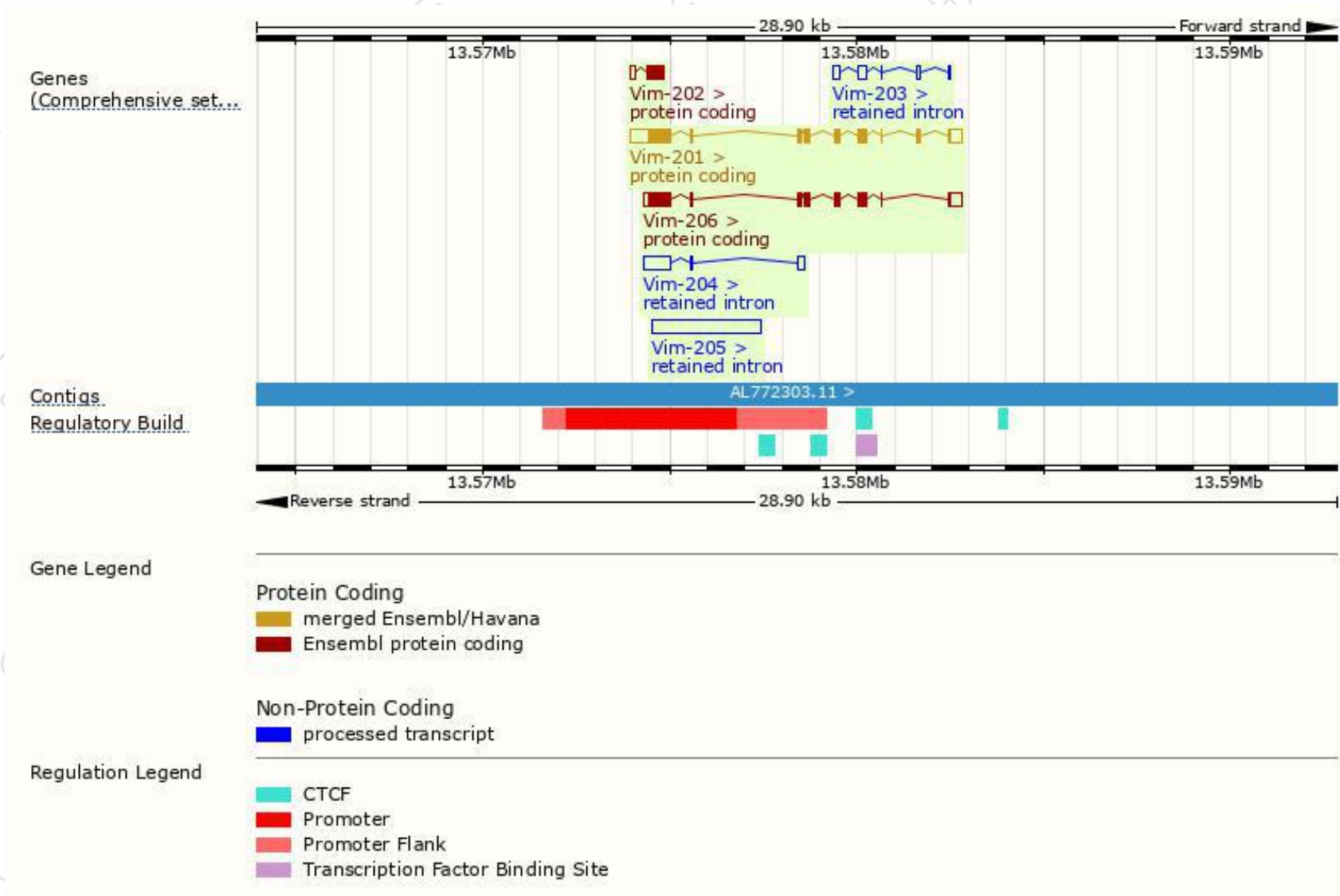
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vim-201	ENSMUST00000028062.7	2193	466aa	Protein coding	CCDS15696	P20152 Q5FWJ3	TSL:1 GENCODE basic APPRIS P2
Vim-206	ENSMUST00000193675.1	1777	427aa	Protein coding	-	A0A0A6YWC8	TSL:5 GENCODE basic APPRIS ALT2
Vim-202	ENSMUST00000141365.2	574	134aa	Protein coding	-	A2AKJ2	CDS 3' incomplete TSL:2
Vim-205	ENSMUST00000191615.1	2926	No protein	Retained intron	-	-	TSL:NA
Vim-204	ENSMUST00000155605.1	926	No protein	Retained intron	-	-	TSL:1
Vim-203	ENSMUST00000148248.2	535	No protein	Retained intron	-	-	TSL:2

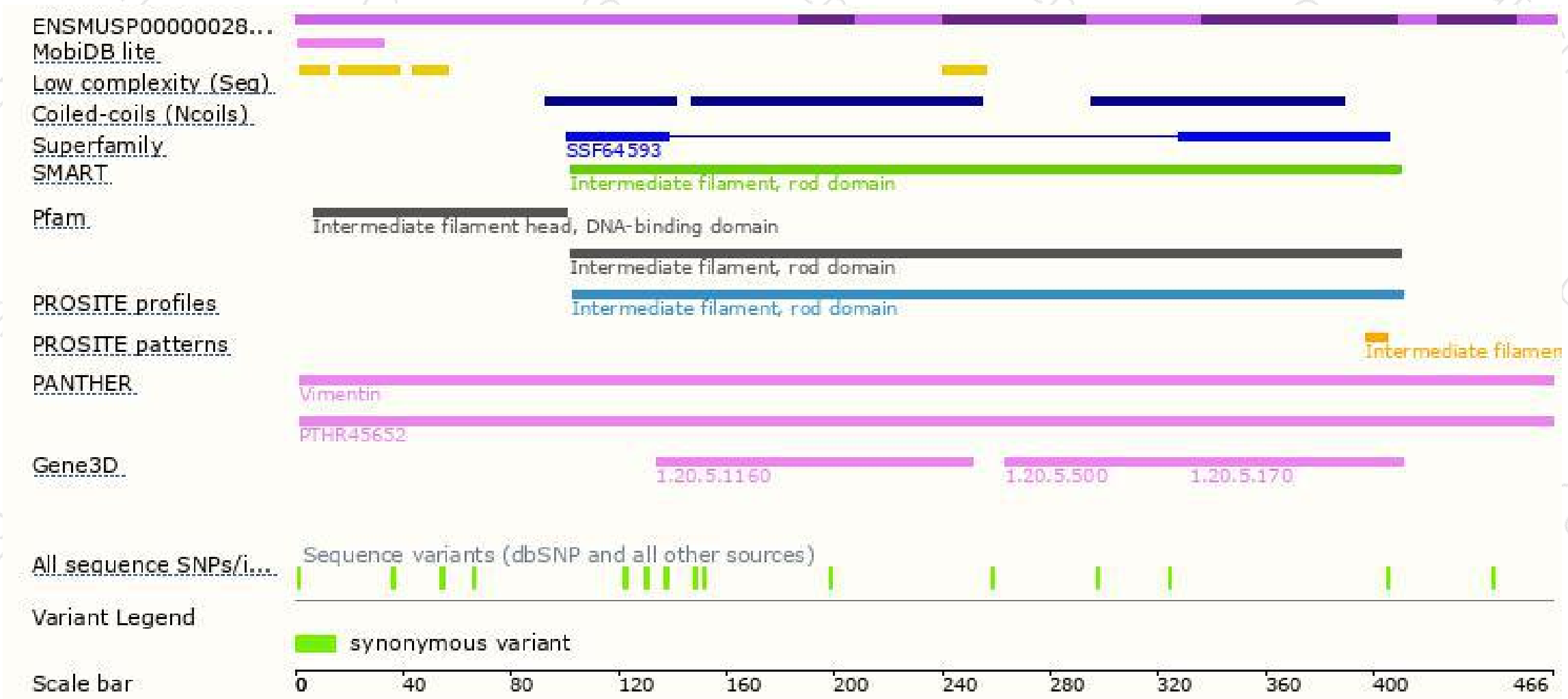
The strategy is based on the design of *Vim-201* transcript,The transcription is shown below



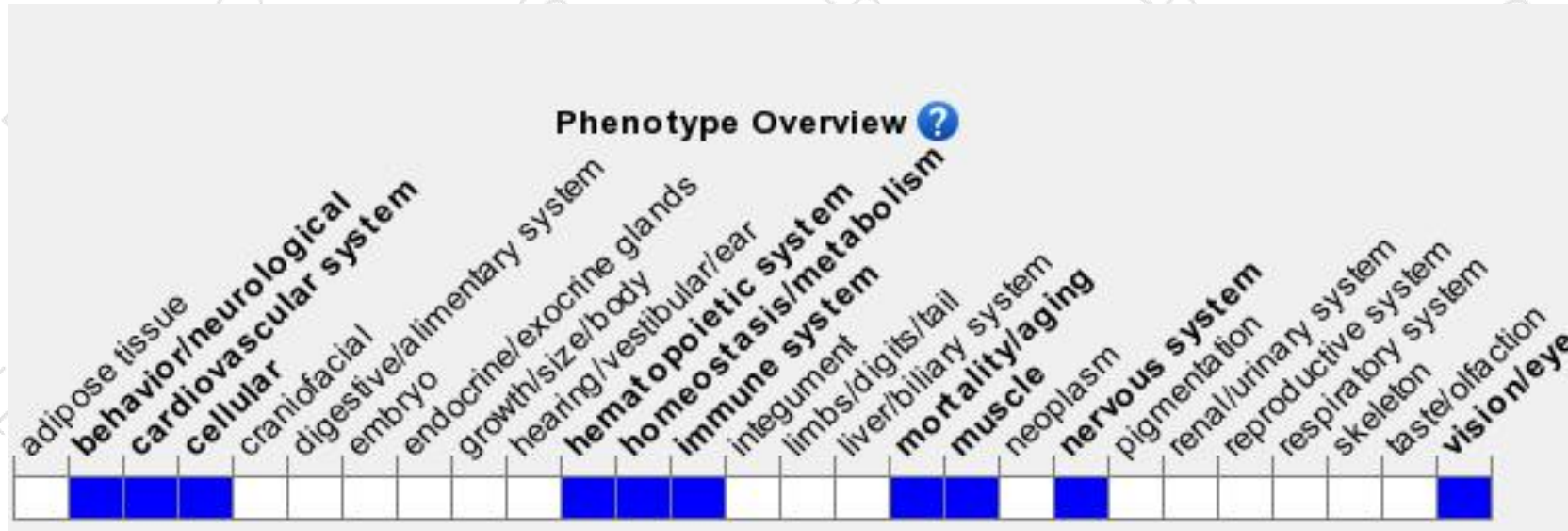
Genomic location distribution



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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