

Pcdh18 Cas9-KO Strategy

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Project Overview

Project Name

Pcdh18

Project type

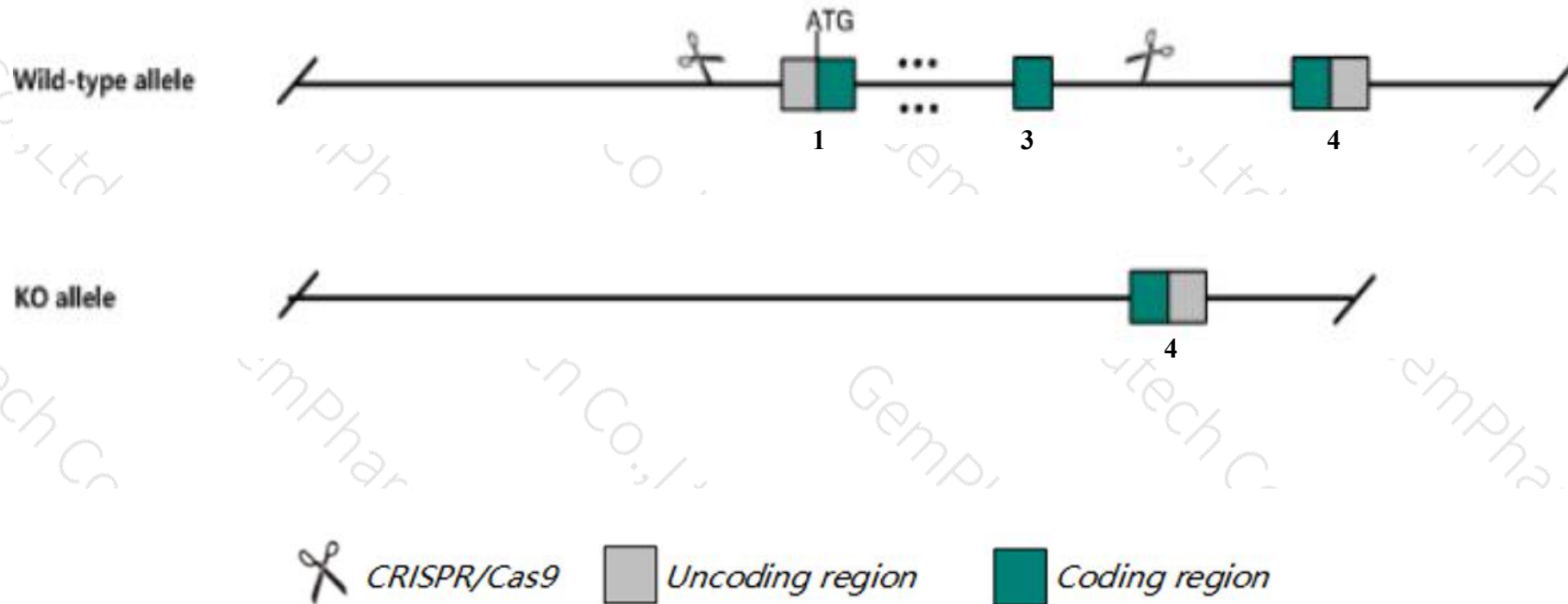
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pcdh18* gene. The schematic diagram is as follows:



- The *Pcdh18* gene has 5 transcripts. According to the structure of *Pcdh18* gene, exon1-exon3 of *Pcdh18-201* (ENSMUST00000035931.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pcdh18* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Pcdh18* gene is located on the Chr3. 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)

Pcdh18 protocadherin 18 [Mus musculus (house mouse)]

Gene ID: 73173, updated on 13-Mar-2020

Summary



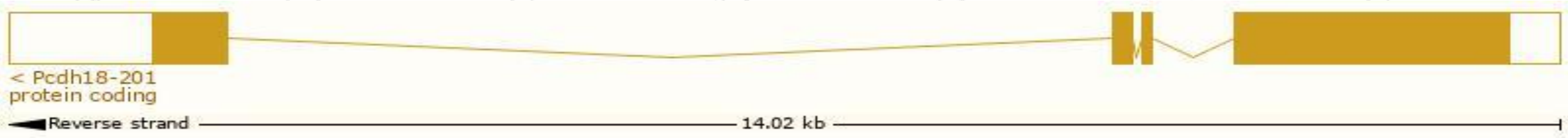
Official Symbol	Pcdh18 provided by MGI
Official Full Name	protocadherin 18 provided by MGI
Primary source	MGI:MGI:1920423
See related	Ensembl:ENSMUSG000000037892
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110038E07Rik, BB095589, PCDH68L
Expression	Biased expression in limb E14.5 (RPKM 26.7), CNS E11.5 (RPKM 14.7) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

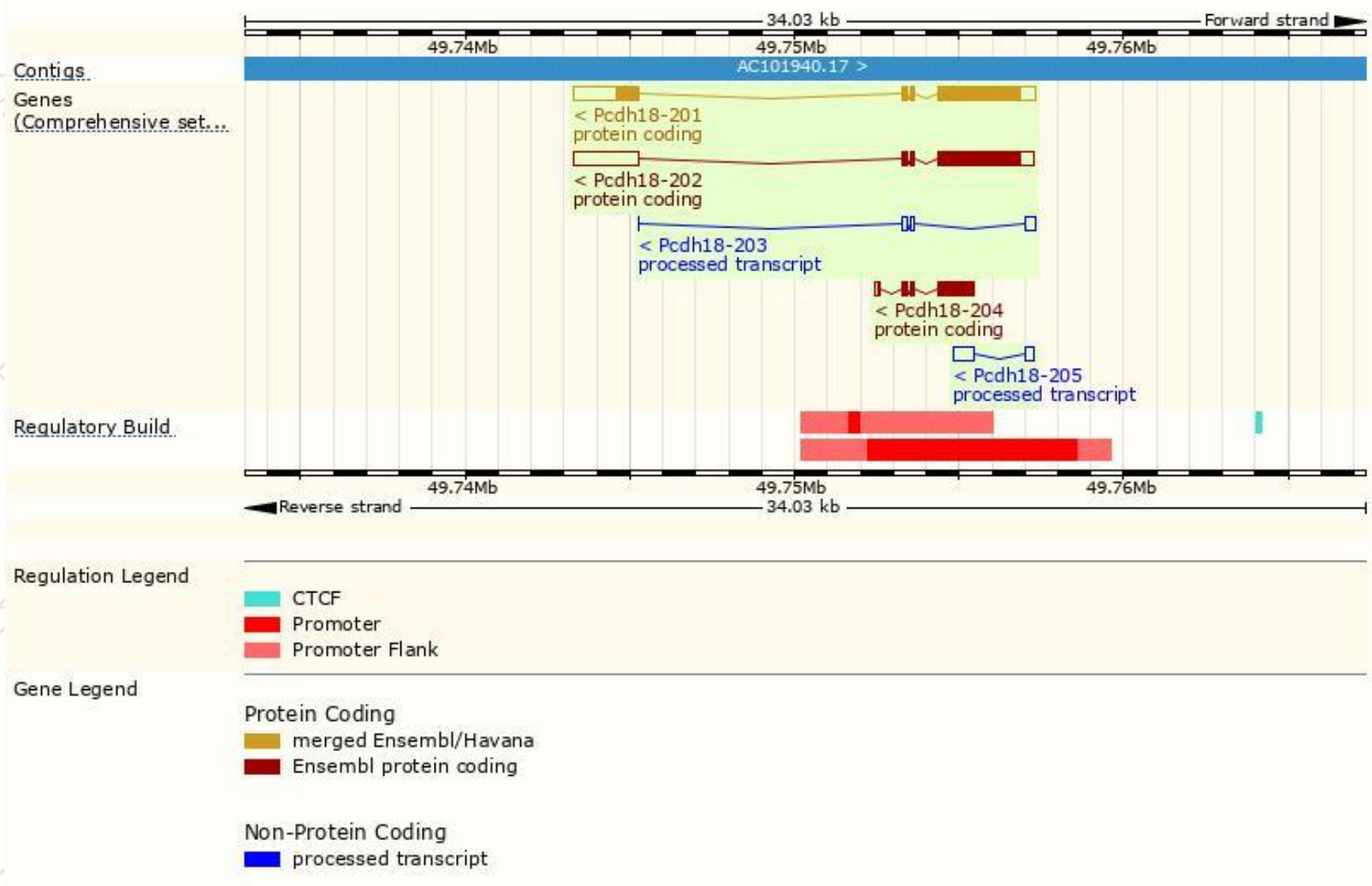
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pcdh18-201	ENSMUST00000035931.12	5168	1134aa	Protein coding	CCDS17334	Q8VHR0	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 P1
Pcdh18-202	ENSMUST00000191794.1	5146	917aa	Protein coding	-	A0A0A6YXH7	TSL:5 GENCODE basic
Pcdh18-204	ENSMUST00000194603.1	1515	455aa	Protein coding	-	A0A0A6YXT8	CDS 5' incomplete TSL:1
Pcdh18-205	ENSMUST00000195086.1	890	No protein	Processed transcript	-	-	TSL:2
Pcdh18-203	ENSMUST00000193600.1	545	No protein	Processed transcript	-	-	TSL:5

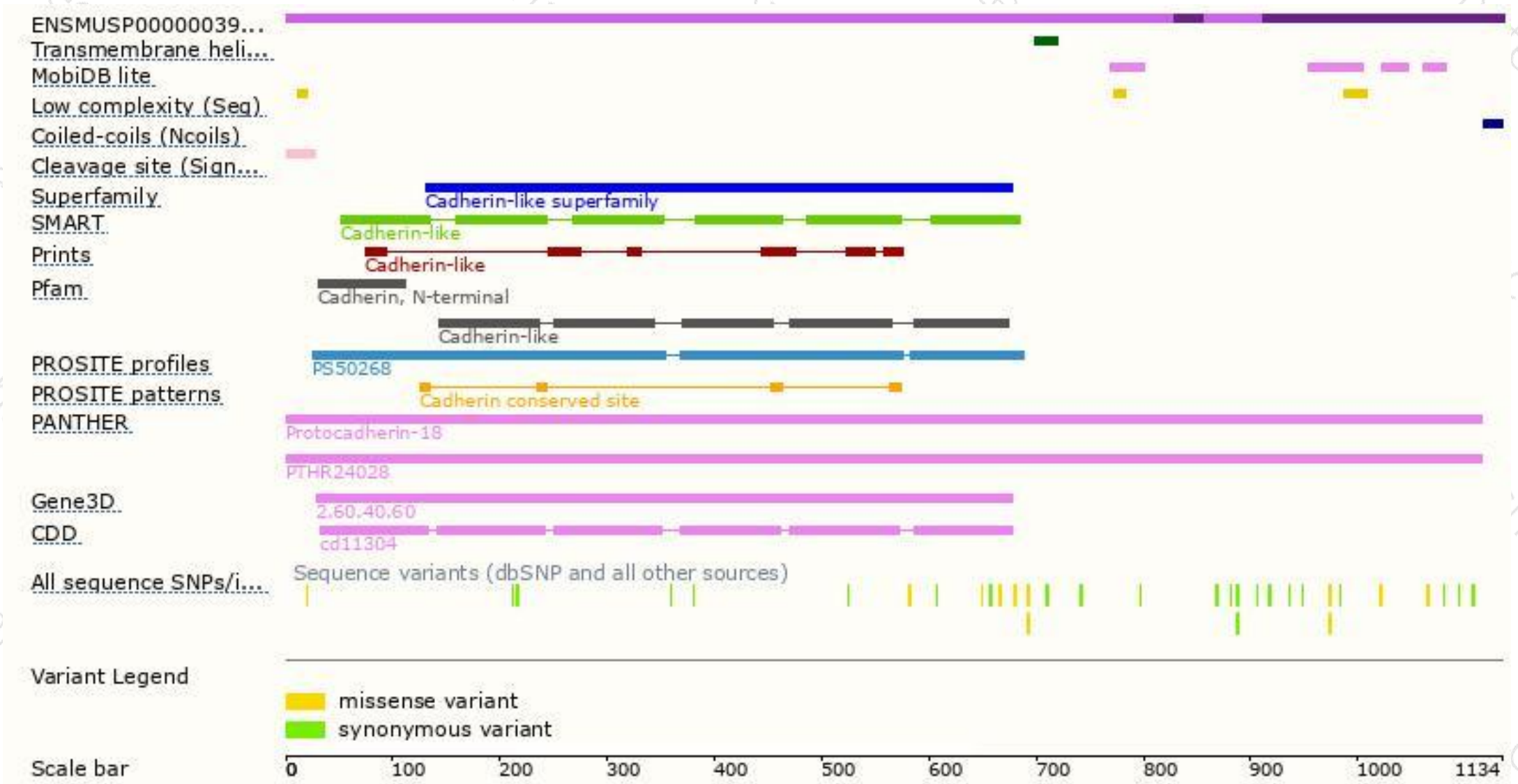
The strategy is based on the design of *Pcdh18-201* transcript,The transcription is shown below



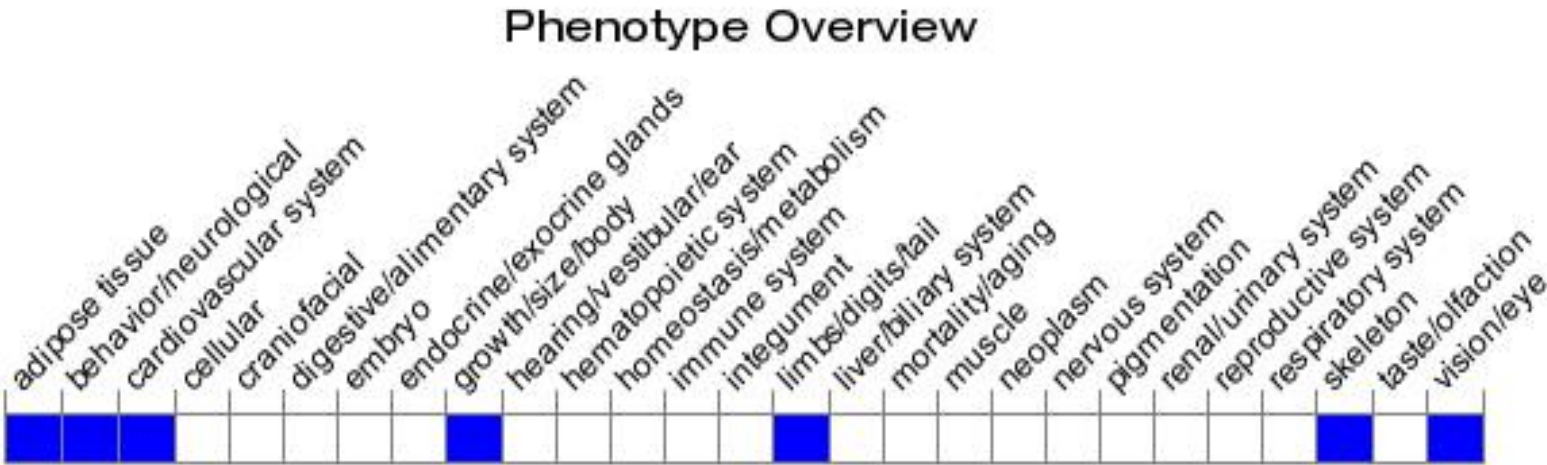
Genomic location distribution



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/>).

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

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