Adam10 Cas9-CKO Strategy

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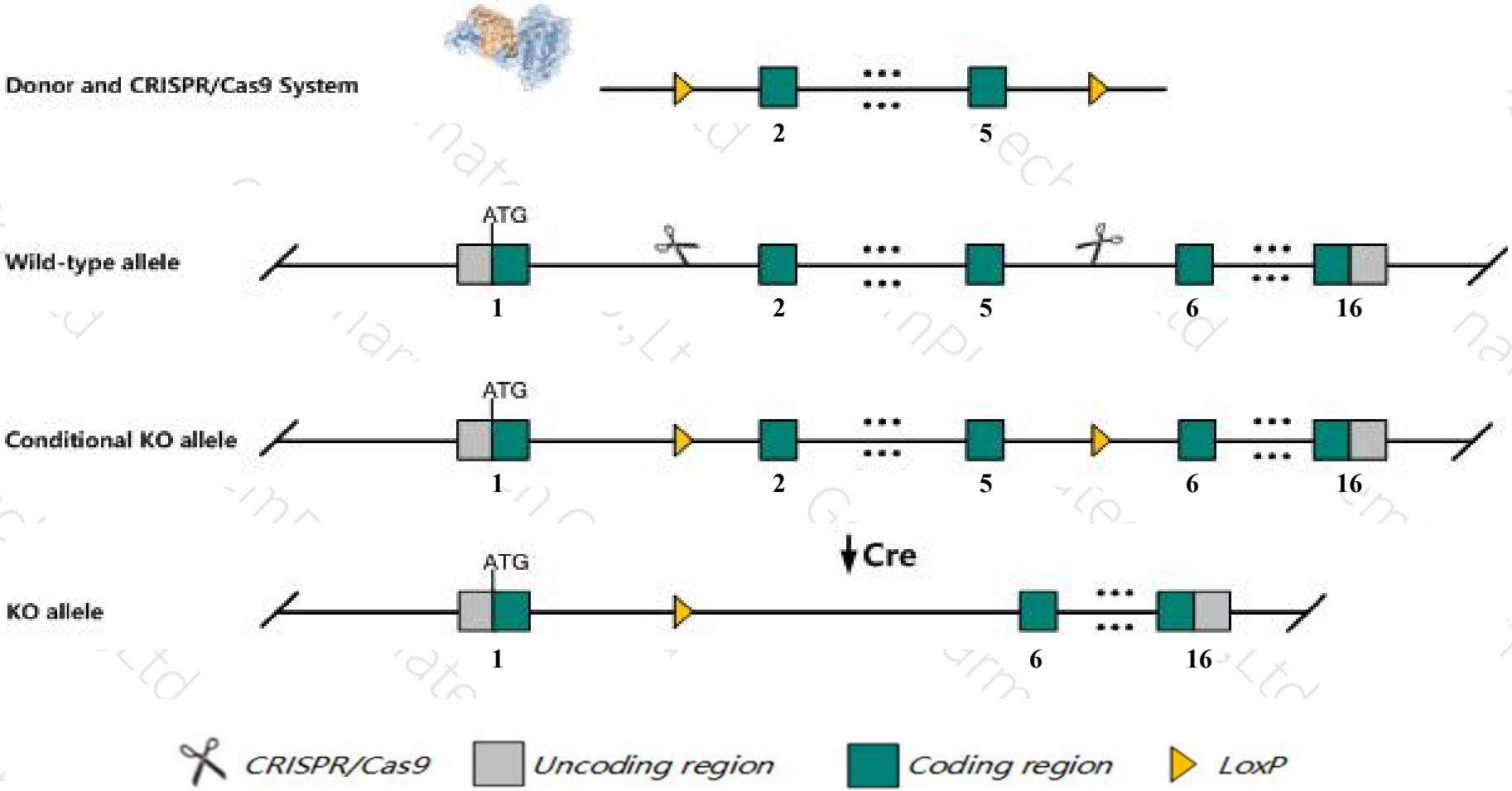
Project Overview

Project Name	***Adam10***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam10* gene. The schematic diagram is as follows:



Technical routes

- The *Adam10* gene has 4 transcripts. According to the structure of *Adam10* gene, exon2-exon5 of *Adam10-201* (ENSMUST00000067880.12) transcript is recommended as the knockout region.The region contains 530bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Adam10* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ According to the existing MGI data,Targeted inactivation of this gene leads to embryonic lethality at E9.5. Embryos homozygous for a knock-out allele display decreased size and multiple abnormalities related to Notch signaling, including defects of the developing central nervous system, somites, and cardiovascular system.

➢ The *Adam10* gene is located on the Chr9. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Adam10 a disintegrin and metallopeptidase domain 10 [Mus musculus (house mouse)]

Gene ID: 11487, updated on 9-Apr-2019

Summary

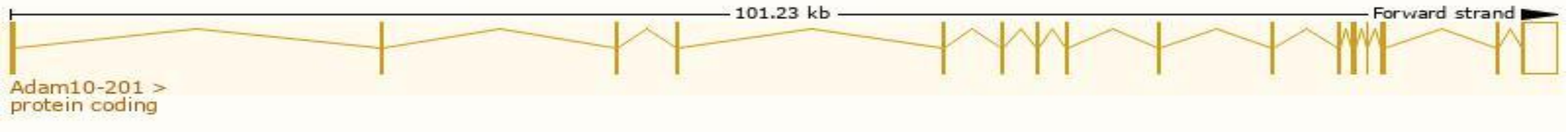
Official Symbol	Adam10 provided by MGI
Official Full Name	a disintegrin and metallopeptidase domain 10 provided by MGI
Primary source	MGI:MGI:109548
See related	Ensembl:ENSMUSG00000054693
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700031C13Rik, MADM, kuz, kuzbanian
Summary	This gene encodes a member of a disintegrin and metalloprotease (ADAM) family of endoproteases that play important roles in various biological processes including cell signaling, adhesion and migration. The encoded preproprotein undergoes proteolytic processing to generate a mature enzyme that is involved in the proteolytic release of membrane-bound proteins in a process called ectodomain shedding. Mice lacking the encoded protein die in utero with multiple defects of the developing central nervous system, somites, and cardiovascular system. [provided by RefSeq, May 2016]
Expression	Ubiquitous expression in liver E14 (RPKM 28.0), liver E14.5 (RPKM 23.2) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

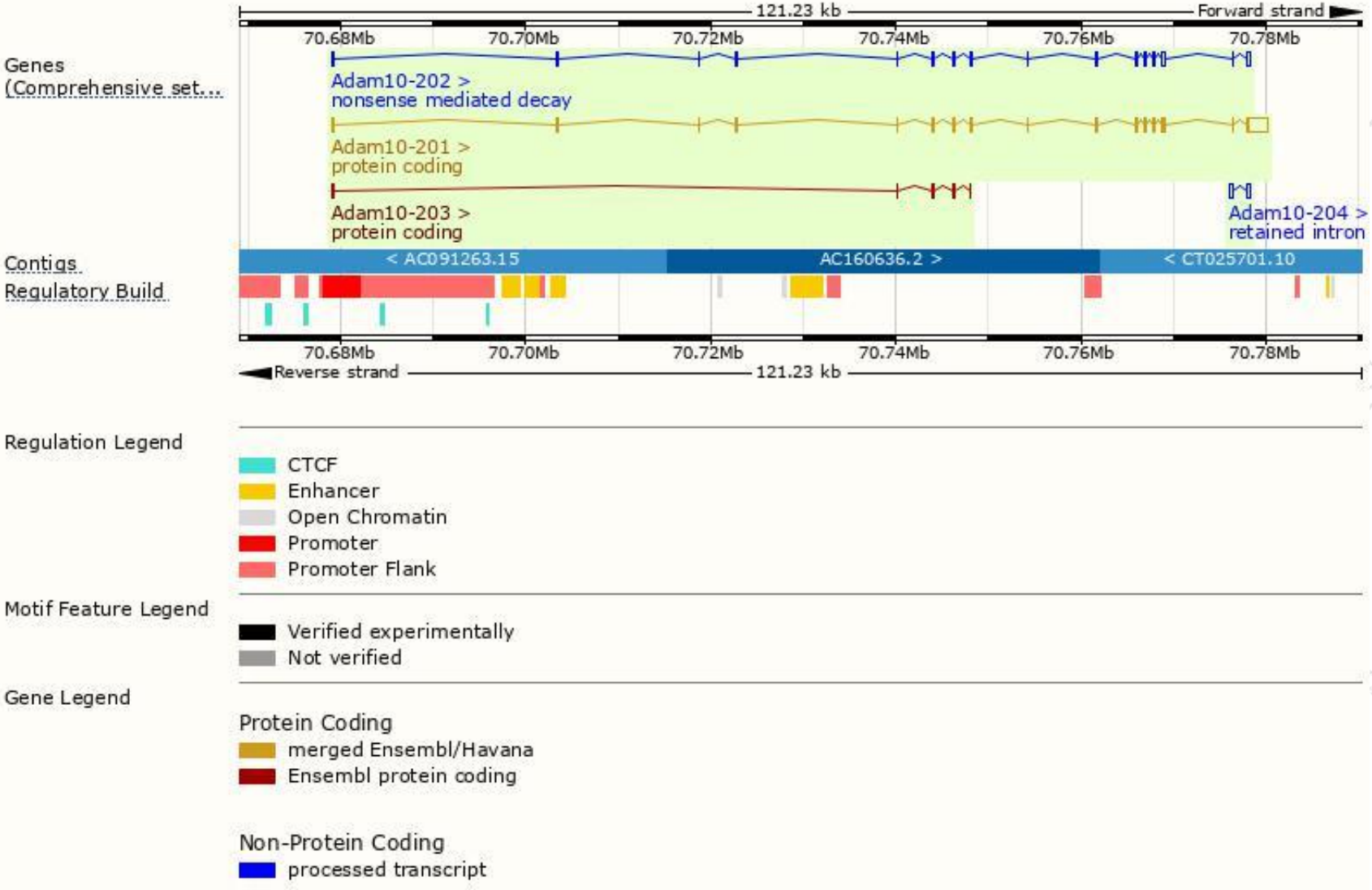
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam10-201	ENSMUST00000067880.12	4593	749aa	Protein coding	CCDS23323	O35598	TSL:1 GENCODE basic APPRIS P1
Adam10-203	ENSMUST00000144537.1	623	144aa	Protein coding	-	D3Z1E6	CDS 3' incomplete TSL:5
Adam10-202	ENSMUST00000140205.7	2720	513aa	Nonsense mediated decay	-	E9PYF2	TSL:5
Adam10-204	ENSMUST00000145377.1	826	No protein	Retained intron	-	-	TSL:2

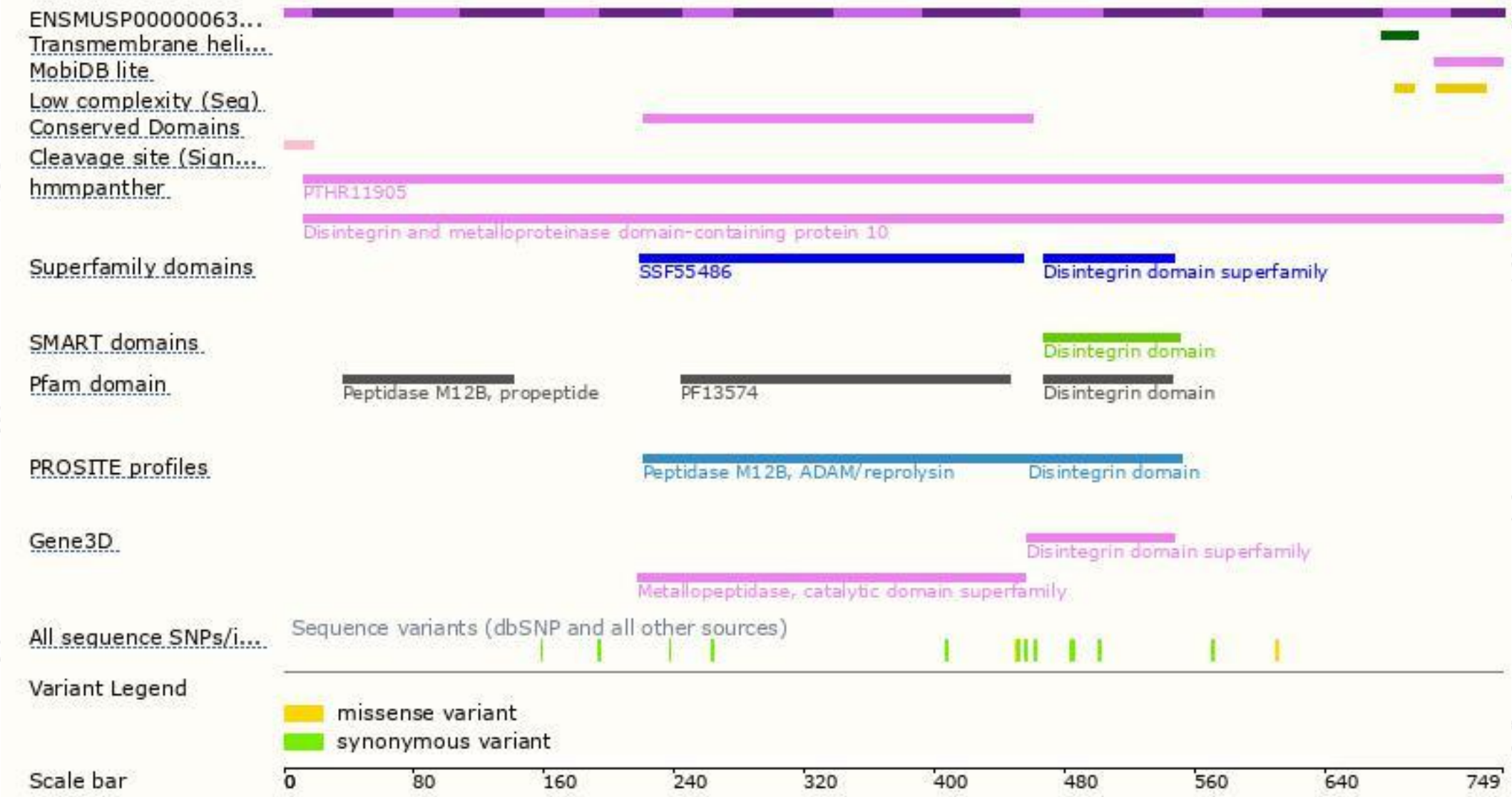
The strategy is based on the design of *Adam10-201* transcript,The transcription is shown below



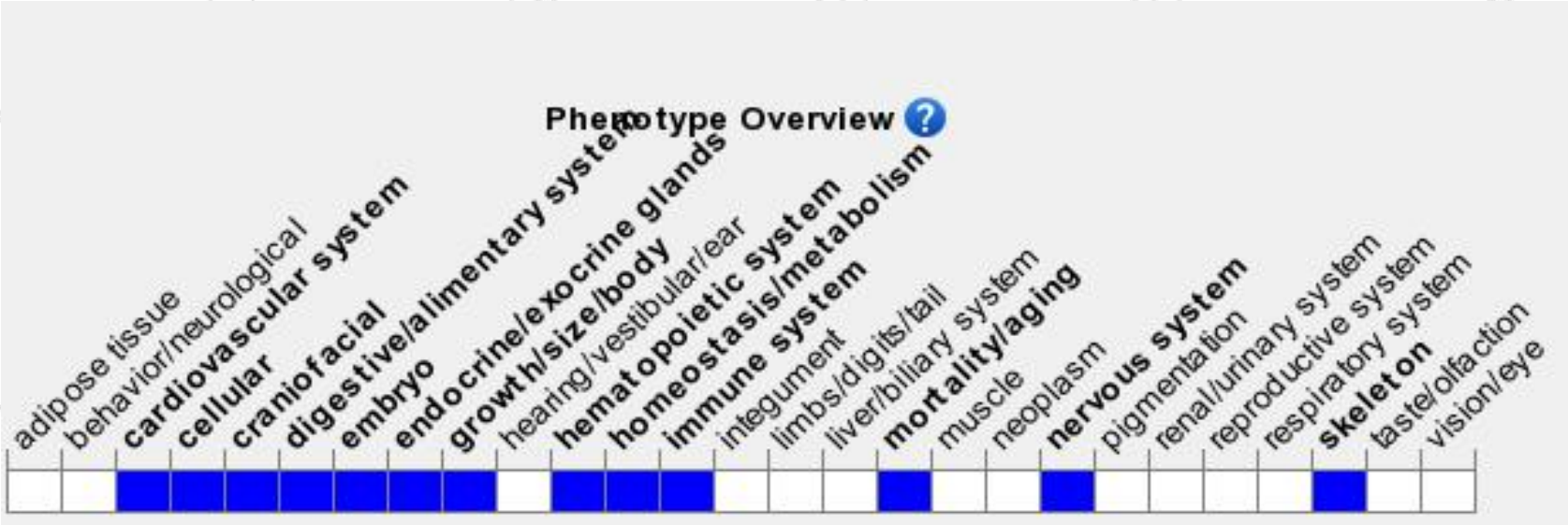
Genomic location distribution



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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