

Apobec1 Cas9-CKO Strategy

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Date: 2019-11-13

Project Overview

Project Name

Apobec1

Project type

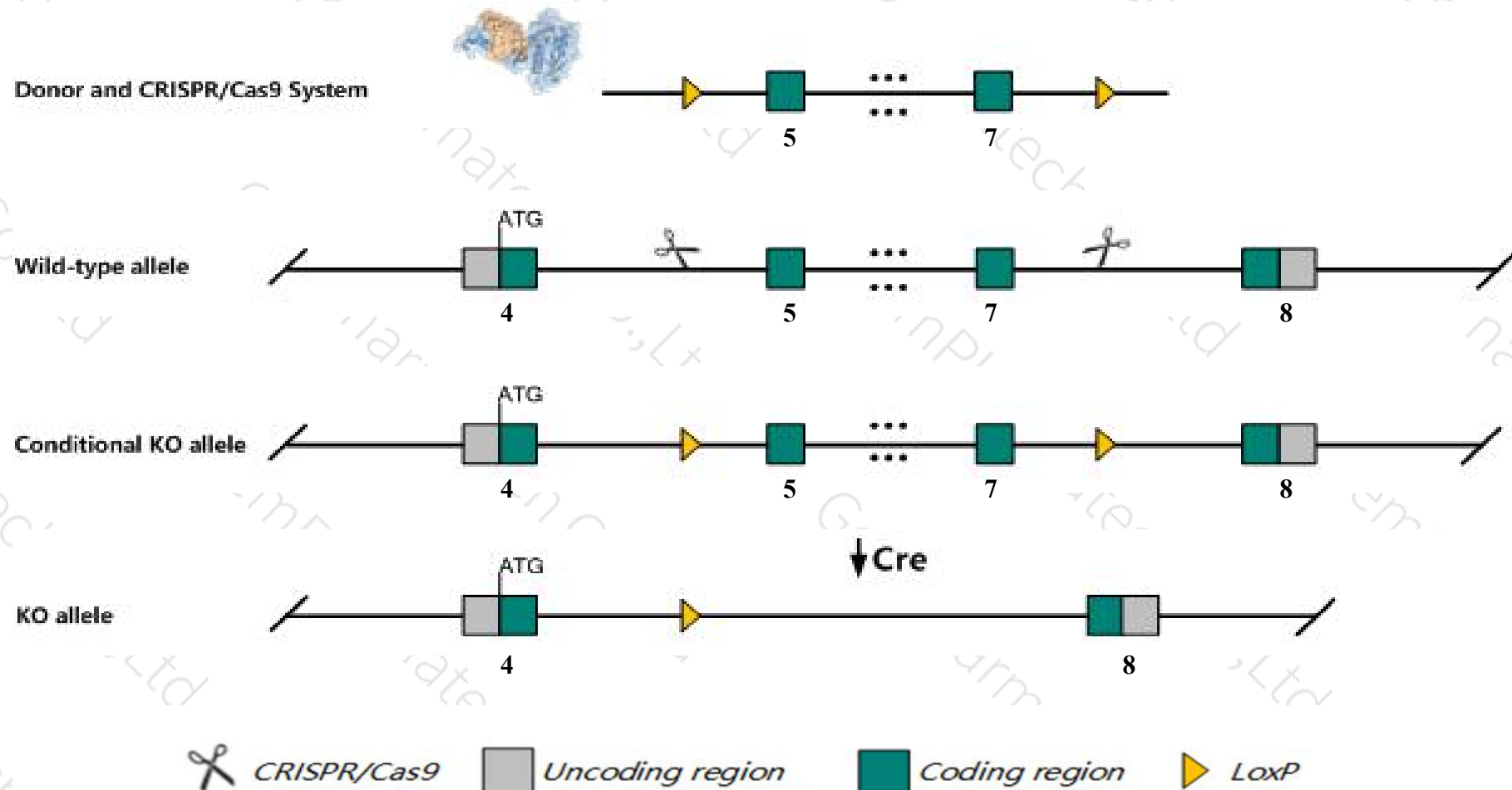
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Apobec1* gene. The schematic diagram is as follows:



Technical routes

- The *Apobec1* gene has 9 transcripts. According to the structure of *Apobec1* gene, exon5-exon7 of *Apobec1*-202 (ENSMUST00000112586.7) transcript is recommended as the knockout region. The region contains 545bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Apobec1* 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.

- According to the existing MGI data, Mice homozygous for a null allele exhibit abnormal lipid homeostasis.
- Transcript *Apobec1*-209 may not be affected.
- The *Apobec1* gene is located on the Chr6. 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)

Apobec1 apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 [*Mus musculus* (house mouse)]

Gene ID: 11810, updated on 5-Nov-2019

Summary

Official Symbol	Apobec1 provided by MGI
Official Full Name	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 provided by MGI
Primary source	MGI:MGI:103298
See related	Ensembl:ENSMUSG00000040613
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cdar1
Expression	Broad expression in mammary gland adult (RPKM 5.7), spleen adult (RPKM 5.4) and 25 other tissues See more
Orthologs	human all

Genomic context

Location: 6 F1; 6 57.68 cM

See Apobec1 in [Genome Data Viewer](#)

Exon count: 10

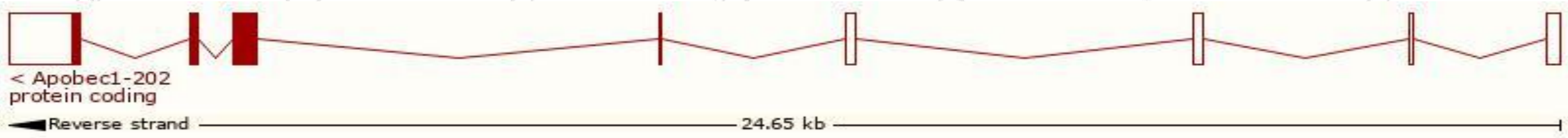
Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p6 (GCF_000001635.26)	6	NC_000072.6 (122577792..122603024, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (122527810..122552462, complement)

Transcript information (Ensembl)

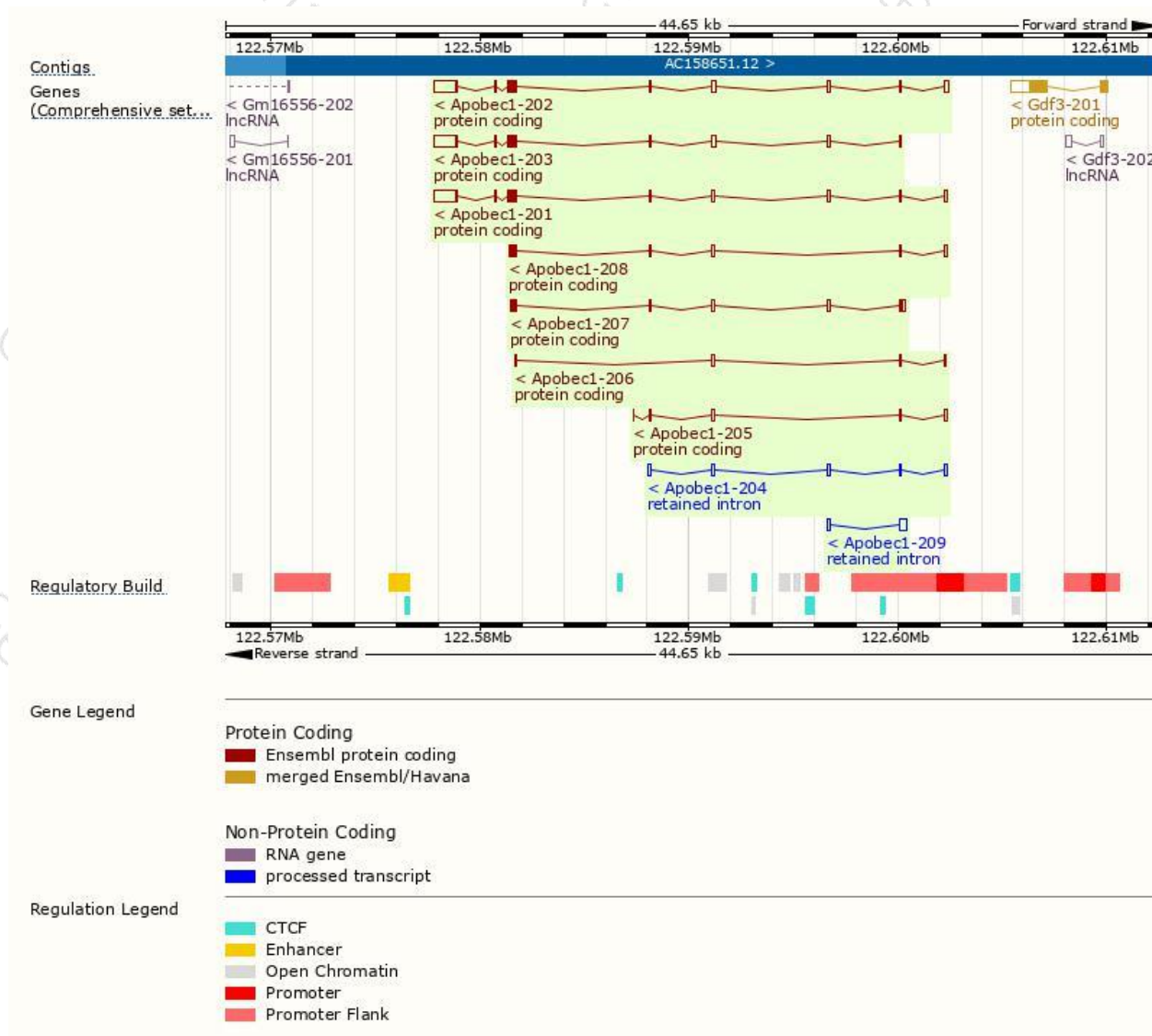
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Apobec1-202	ENSMUST00000112586.7	2265	229aa	Protein coding	CCDS20498	P51908 Q3U9G8	TSL:1 GENCODE basic APPRIS P1
Apobec1-201	ENSMUST00000112585.7	2127	229aa	Protein coding	CCDS20498	P51908 Q3U9G8	TSL:1 GENCODE basic APPRIS P1
Apobec1-203	ENSMUST00000112587.10	2072	229aa	Protein coding	CCDS20498	P51908 Q3U9G8	TSL:5 GENCODE basic APPRIS P1
Apobec1-207	ENSMUST00000203204.2	775	113aa	Protein coding	-	A0A0N4SVL6	CDS 3' incomplete TSL:2
Apobec1-208	ENSMUST00000203309.2	666	121aa	Protein coding	-	A0A0N4SW85	CDS 3' incomplete TSL:2
Apobec1-206	ENSMUST00000203197.2	372	43aa	Protein coding	-	A0A0N4SV86	CDS 3' incomplete TSL:3
Apobec1-205	ENSMUST00000147760.7	360	25aa	Protein coding	-	D3Z675	CDS 3' incomplete TSL:5
Apobec1-204	ENSMUST00000143356.1	560	No protein	Retained intron	-	-	TSL:3
Apobec1-209	ENSMUST00000204035.1	520	No protein	Retained intron	-	-	TSL:3

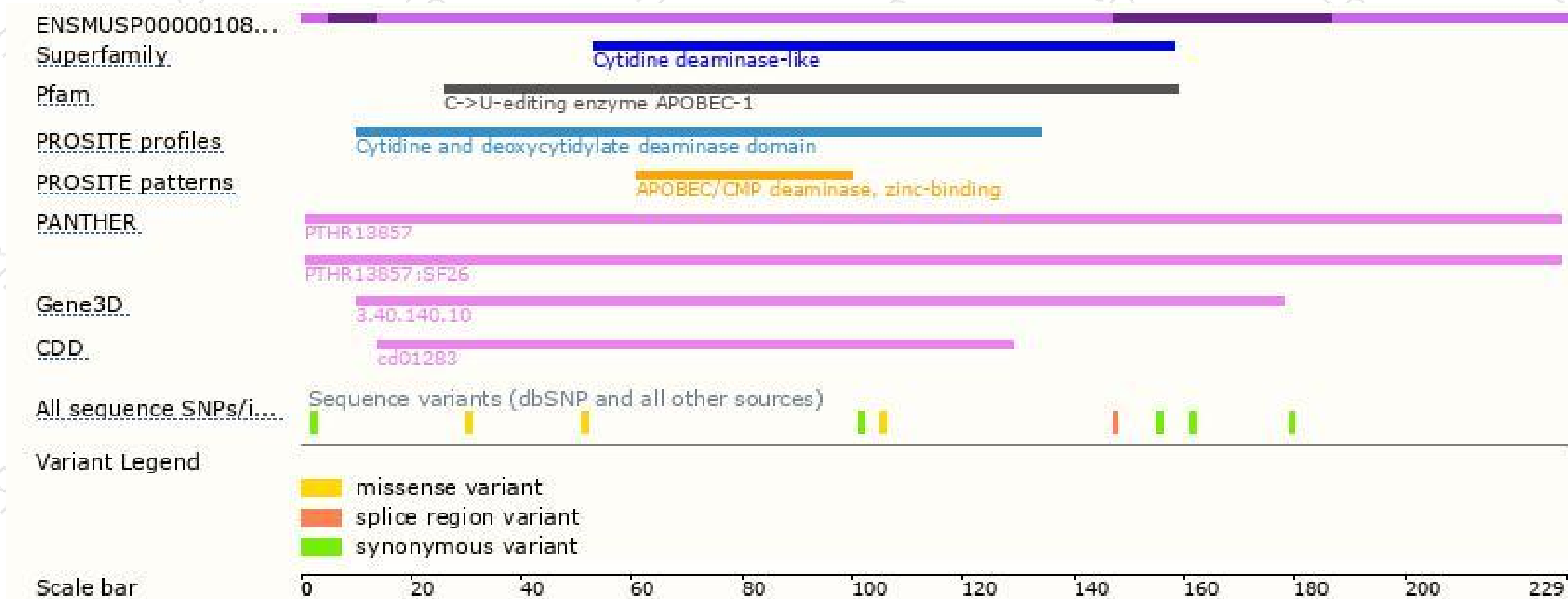
The strategy is based on the design of *Apobec1-202* transcript,The transcription is shown below



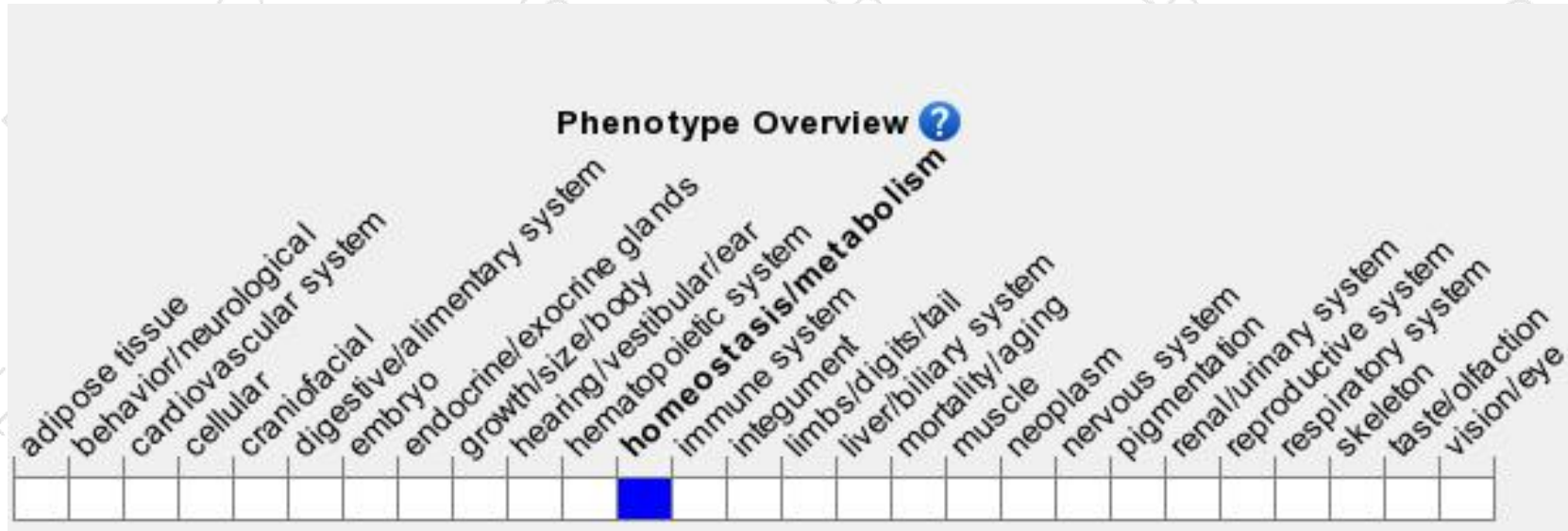
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a null allele exhibit abnormal lipid homeostasis.

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

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