

LipC Cas9-CKO Strategy

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Project Overview

Project Name

Lipc

Project type

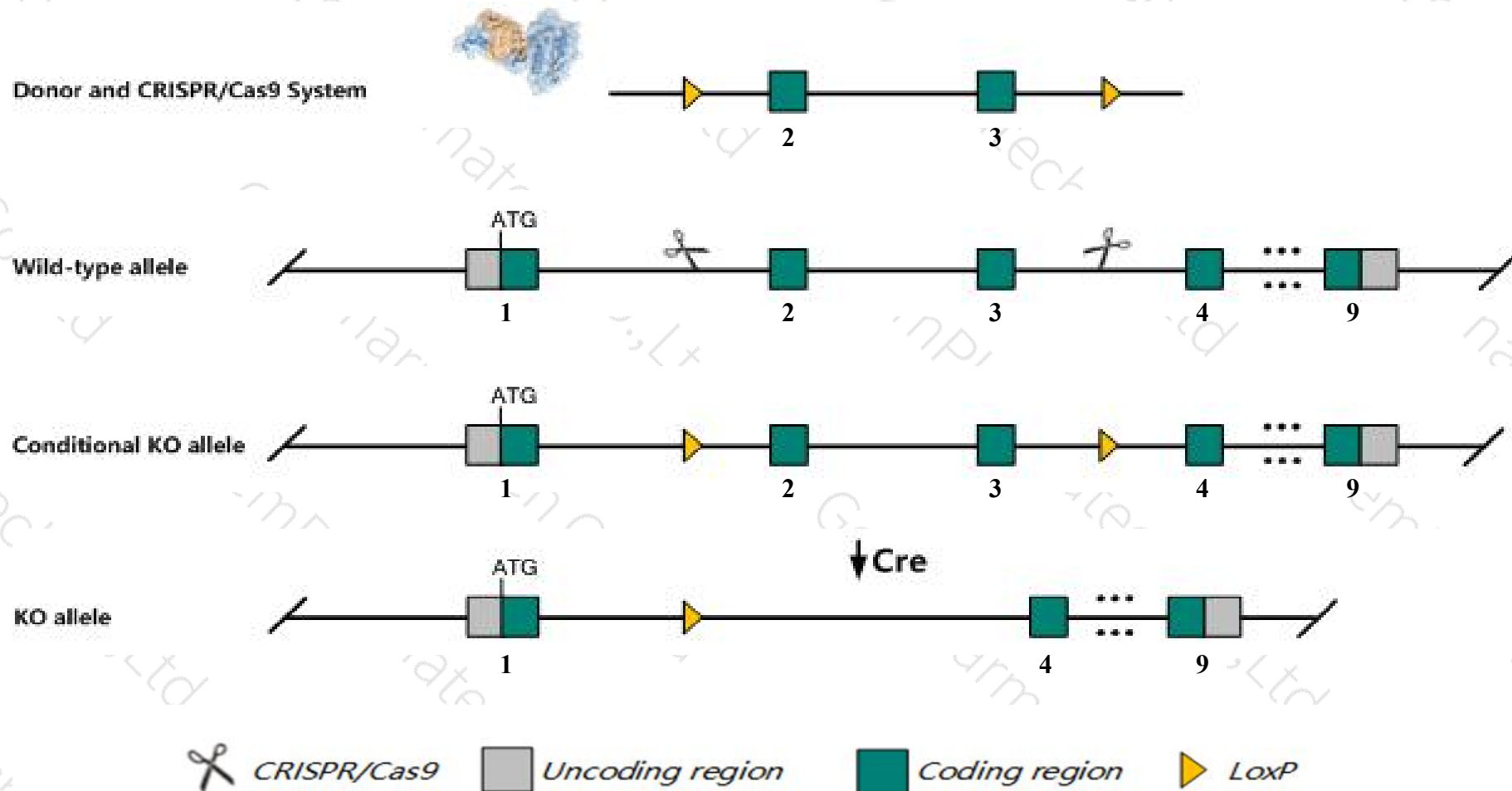
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Lipc* gene has 4 transcripts. According to the structure of *Lipc* gene, exon2-exon3 of *Lipc-201* (ENSMUST00000034731.9) transcript is recommended as the knockout region. The region contains 374bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lipc* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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, Homozygotes for a targeted null mutation exhibit elevated plasma total cholesterol, phospholipids, and high density lipoprotein cholesterol.
- The *Lipc* 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)

Lipc lipase, hepatic [*Mus musculus* (house mouse)]

Gene ID: 15450, updated on 24-Oct-2019

Summary

Official Symbol	Lipc provided by MGI
Official Full Name	lipase, hepatic provided by MGI
Primary source	MGI:MGI:96216
See related	Ensembl:ENSMUSG00000032207
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	HL; Hpl; AI256194
Expression	Biased expression in liver adult (RPKM 48.1), liver E18 (RPKM 35.8) and 3 other tissues See more
Orthologs	human all

Genomic context

Location: 9 D; 9 39.57 cM

See Lipc in [Genome Data Viewer](#)

Exon count: 14

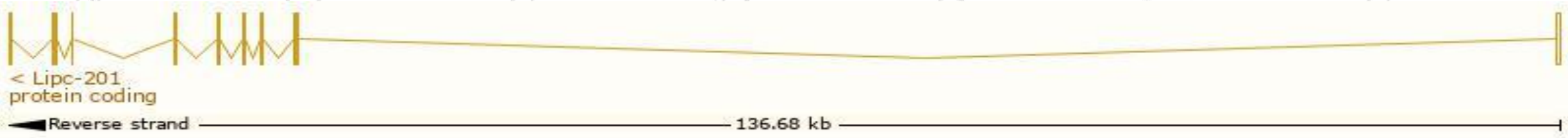
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (70798128..70952221, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (70645935..70782615, complement)

Transcript information (Ensembl)

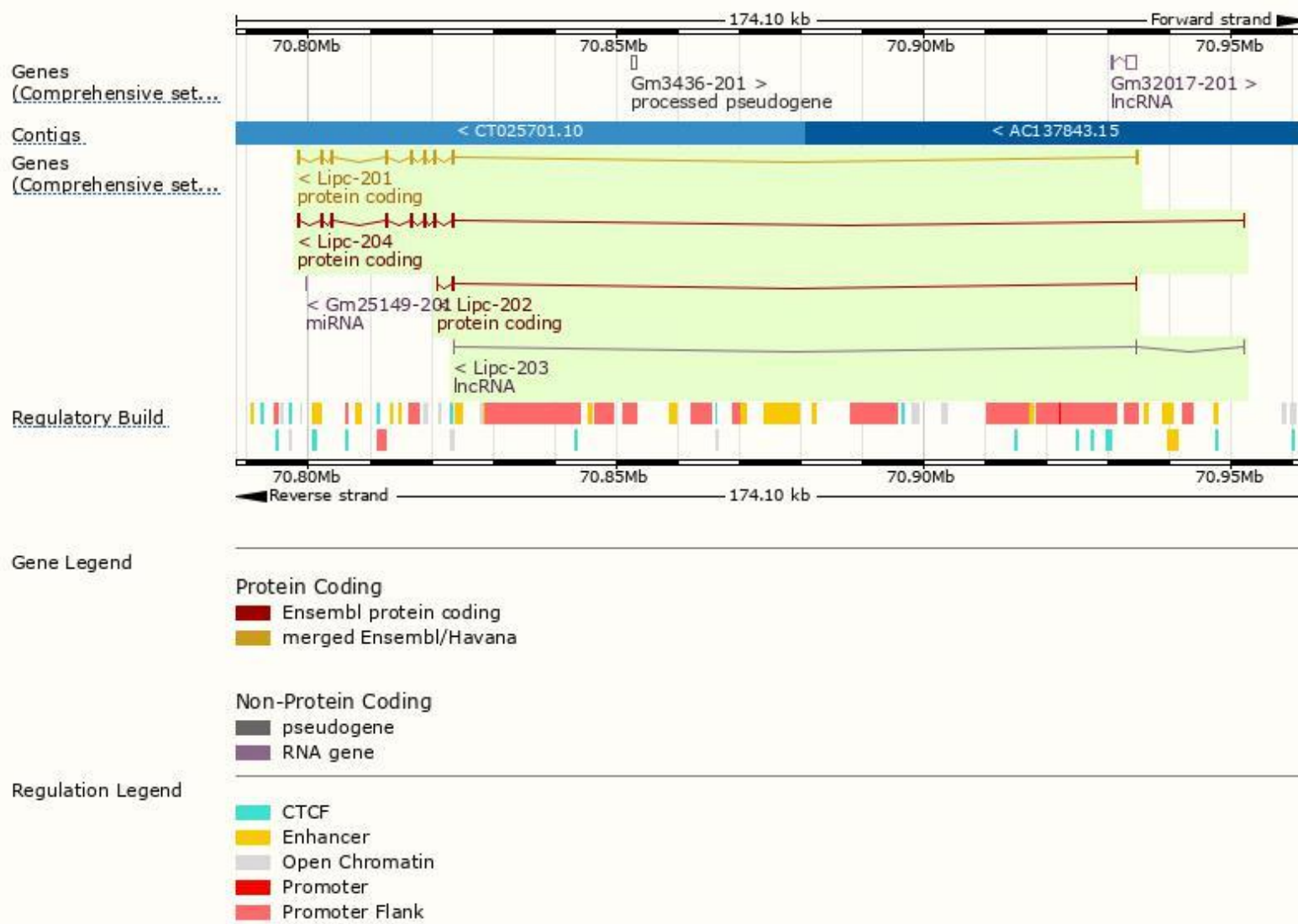
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lipc-201	ENSMUST00000034731.9	1920	510aa	Protein coding	CCDS23324	P27656	TSL:1 GENCODE basic APPRIS P2
Lipc-204	ENSMUST00000216798.1	1726	425aa	Protein coding	-	Q3TYU0	TSL:1 GENCODE basic APPRIS ALT2
Lipc-202	ENSMUST00000214995.1	376	107aa	Protein coding	-	A0A1L1SRU8	CDS 3' incomplete TSL:3
Lipc-203	ENSMUST00000215814.1	351	No protein	lncRNA	-	-	TSL:2

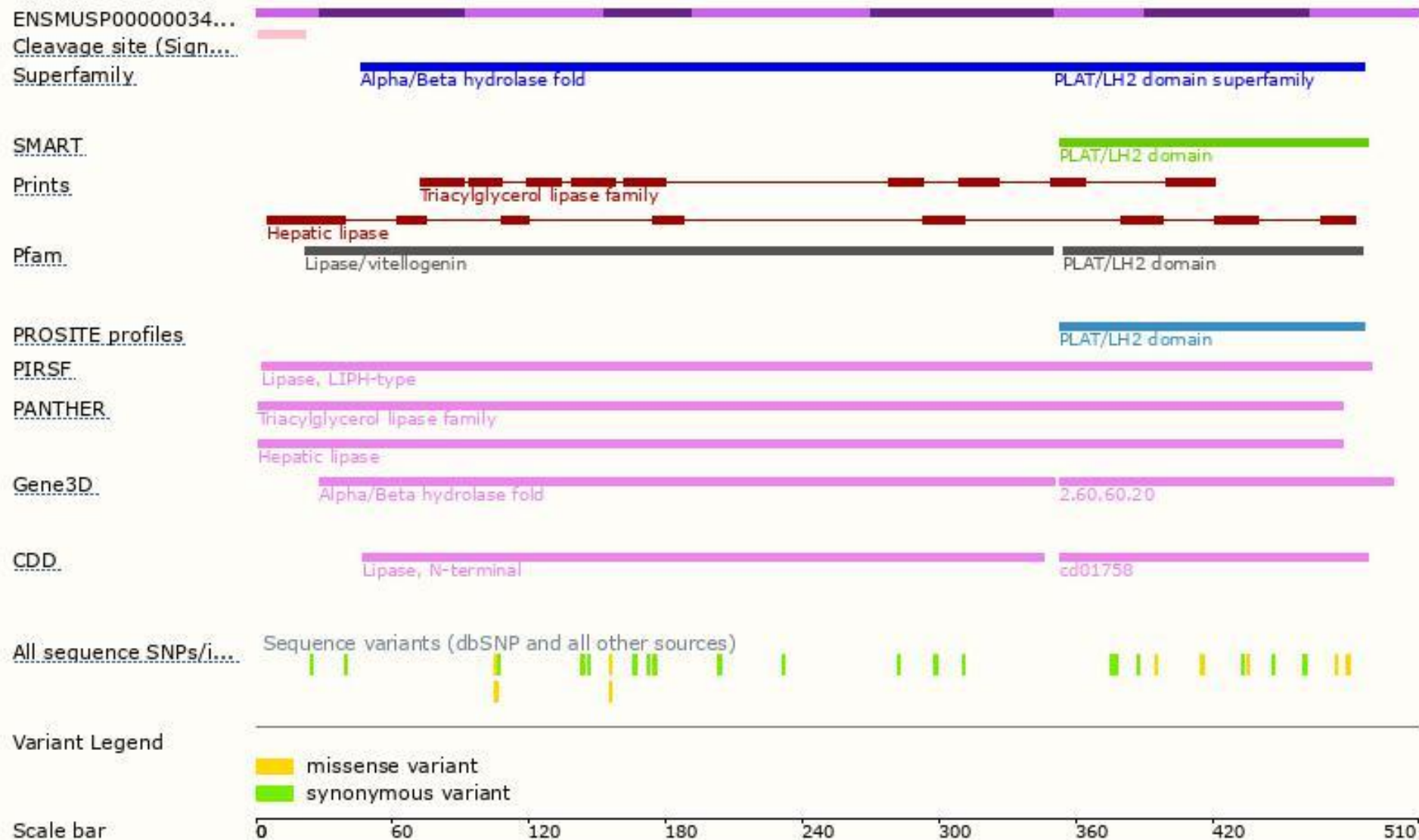
The strategy is based on the design of *Lipc-201* transcript,The transcription is shown below



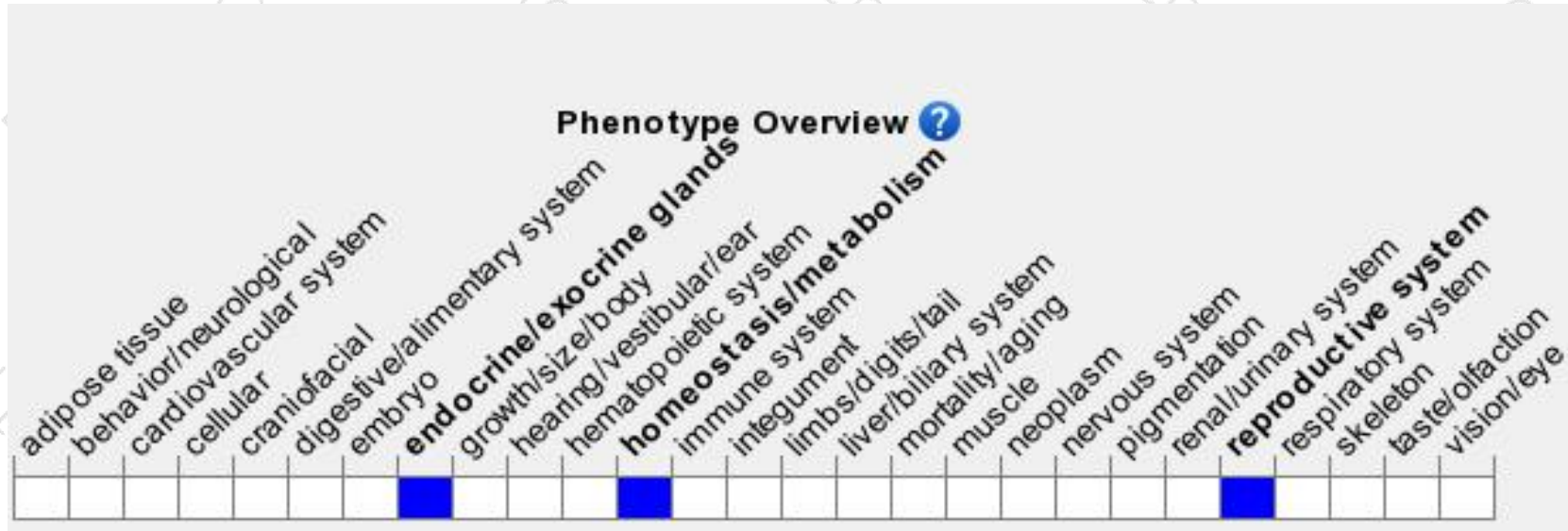
Genomic location distribution



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/>).

According to the existing MGI data, Homozygotes for a targeted null mutation exhibit elevated plasma total cholesterol, phospholipids, and high density lipoprotein cholesterol.

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

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