

Ppp6c Cas9-CKO Strategy

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Design Date: 2022/7/12

Project Overview

Project Name

Ppp6c

Project type

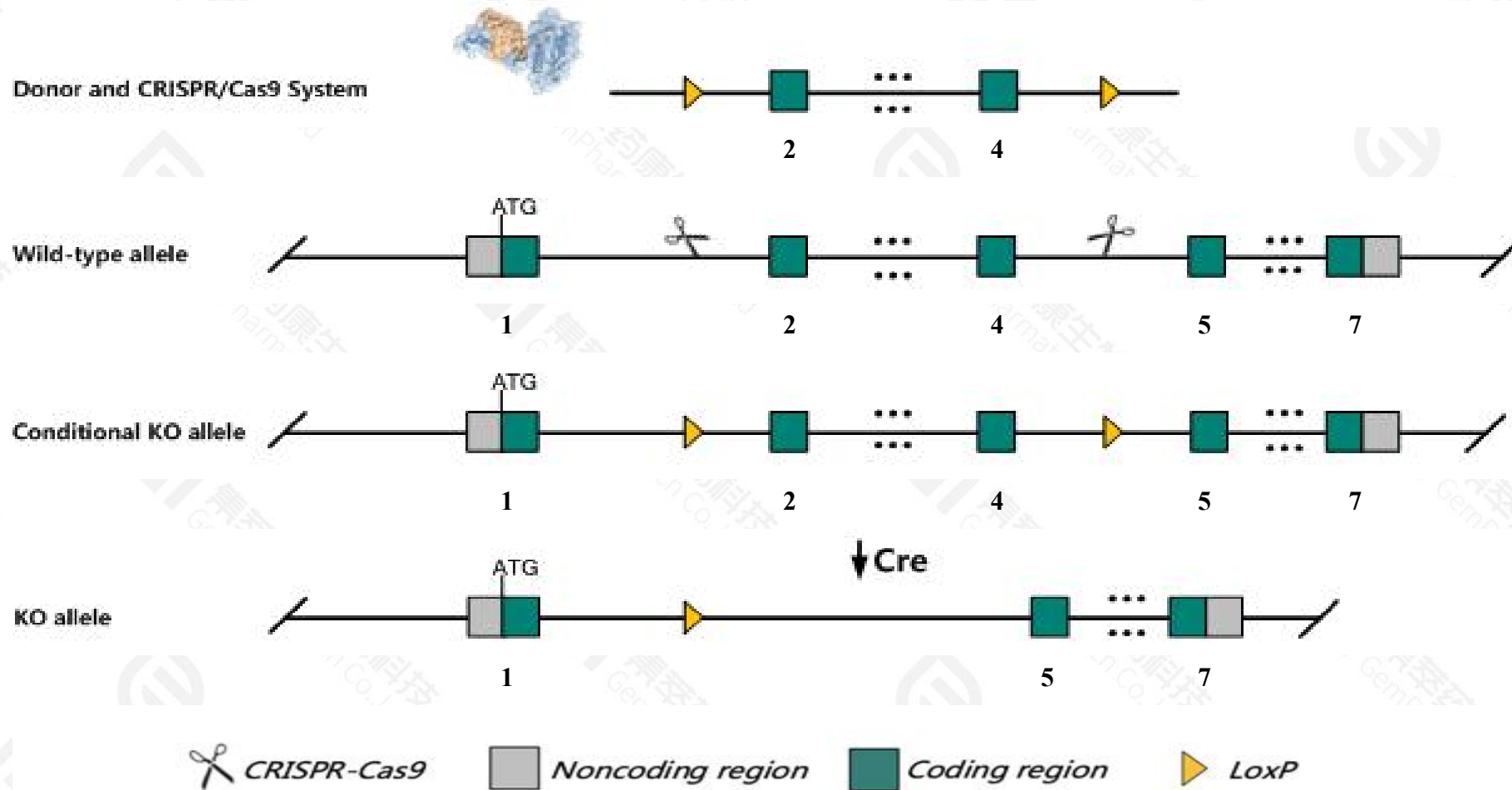
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Ppp6c* gene. The schematic diagram is as follows:



- The *Ppp6c* gene has 5 transcripts. According to the structure of *Ppp6c* gene, exon2-exon4 of *Ppp6c-201*(ENSMUST00000028087.6) transcript is recommended as the knockout region. The region contains 304bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ppp6c* 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 knock-out allele exhibit abnormal embryonic development and embryonic lethality. Mice homozygous for a conditional allele activated in skin cells exhibit increased susceptibility to chemically induced skin tumors with increased proliferative and inflammatory responses in the skin.
- The *Ppp6c* gene is located on the Chr 2. 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)

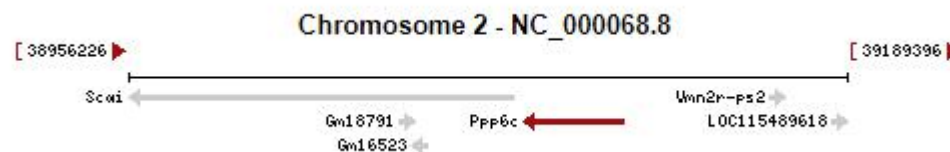
Ppp6c protein phosphatase 6, catalytic subunit [*Mus musculus* (house mouse)]

Gene ID: 67857, updated on 29-May-2022

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Summary

Official Symbol	Ppp6c provided by MGI
Official Full Name	protein phosphatase 6, catalytic subunit provided by MGI
Primary source	MGI:MGI:1915107
See related	Ensembl:ENSMUSG00000026753 AllianceGenome:MGI:1915107
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	Pp6C; 2310003C10Rik
Summary	Predicted to enable protein serine/threonine phosphatase activity. Predicted to act upstream of or within protein dephosphorylation. Predicted to be located in cytosol. Is expressed in central nervous system; pancreas epithelium; and retina. Orthologous to human PPP6C (protein phosphatase 6 catalytic subunit). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in placenta adult (RPKM 11.6), bladder adult (RPKM 11.3) and 28 other tissues See more
Orthologs	human all

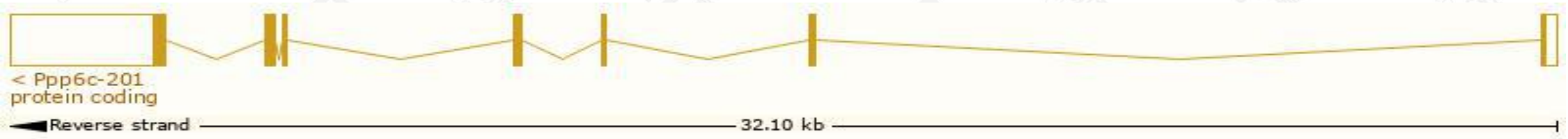


Transcript information (Ensembl)

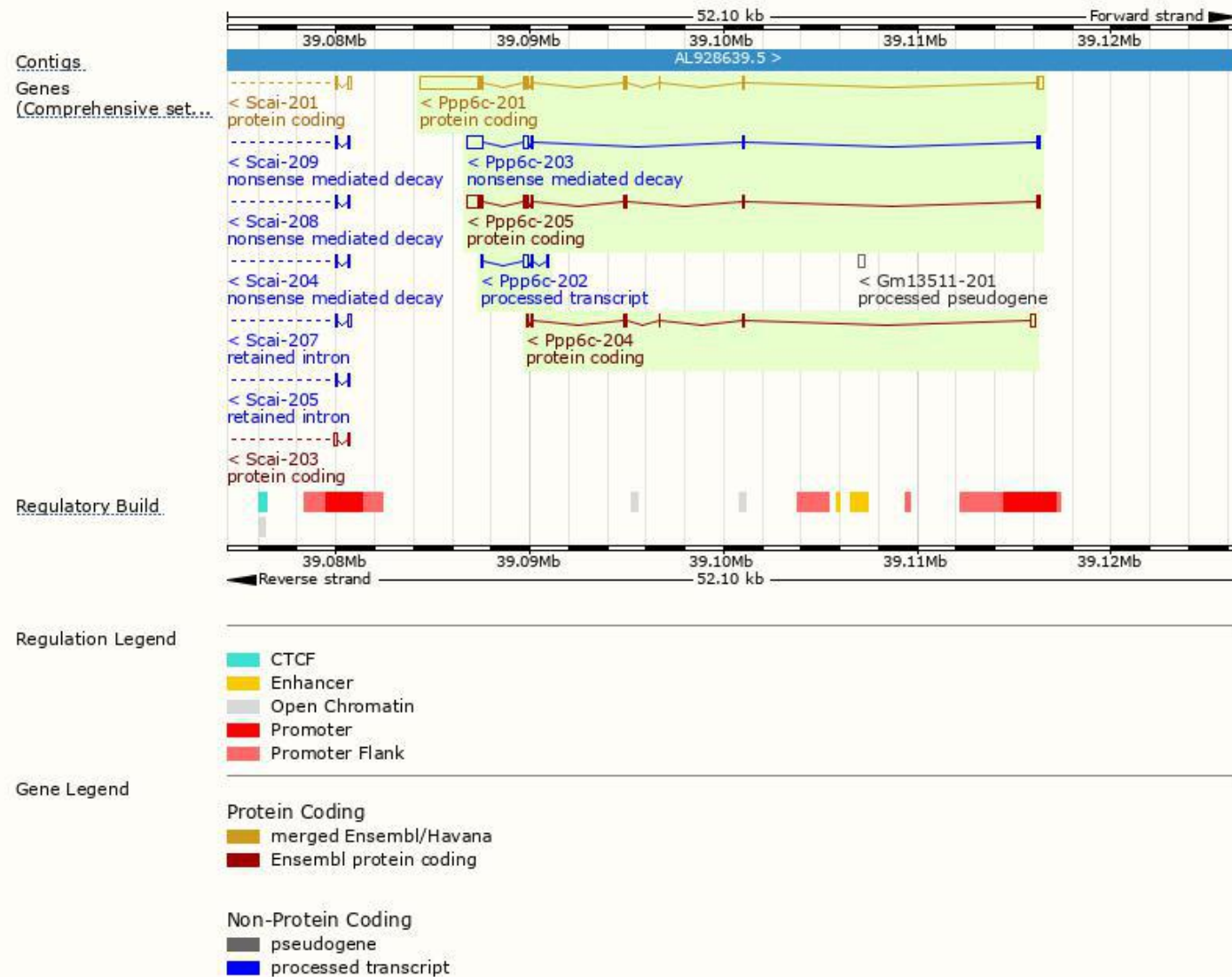
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp6c-201	ENSMUST00000028087.5	4115	305aa	Protein coding	CCDS16017	Q9CQR6	TSL:1 GENCODE basic APPRIS P1
Ppp6c-205	ENSMUST00000204701.2	1495	283aa	Protein coding	-	A0A0N4SVL9	TSL:5 GENCODE basic
Ppp6c-204	ENSMUST00000204368.1	635	83aa	Protein coding	-	A0A0N4SW66	CDS 3' incomplete TSL:5
Ppp6c-203	ENSMUST00000204257.2	1358	81aa	Nonsense mediated decay	-	A0A0N4SVE2	TSL:5
Ppp6c-202	ENSMUST00000143733.1	487	No protein	Processed transcript	-	-	TSL:3

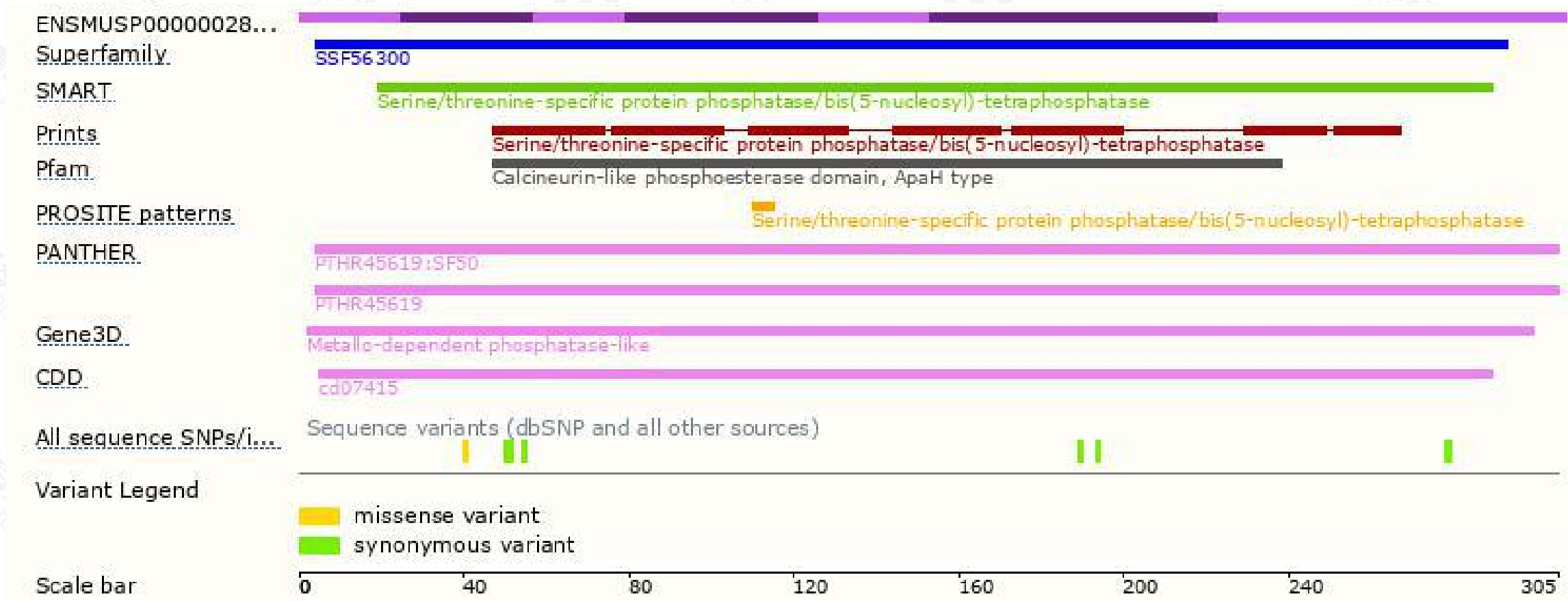
The strategy is based on the design of *Ppp6c-201* transcript,the transcription is shown below:



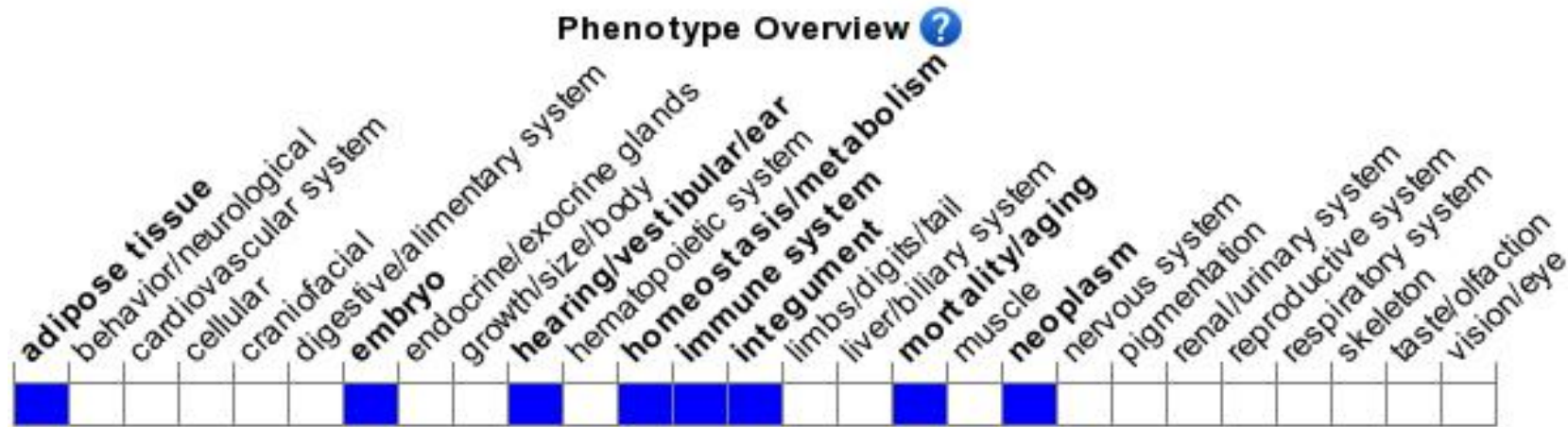
Genomic location distribution



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, mice homozygous for a knock-out allele exhibit abnormal embryonic development and embryonic lethality. Mice homozygous for a conditional allele activated in skin cells exhibit increased susceptibility to chemically induced skin tumors with increased proliferative and inflammatory responses in the skin.

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