

Gk5 Cas9-CKO Strategy

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Project Overview

Project Name

Gk5

Project type

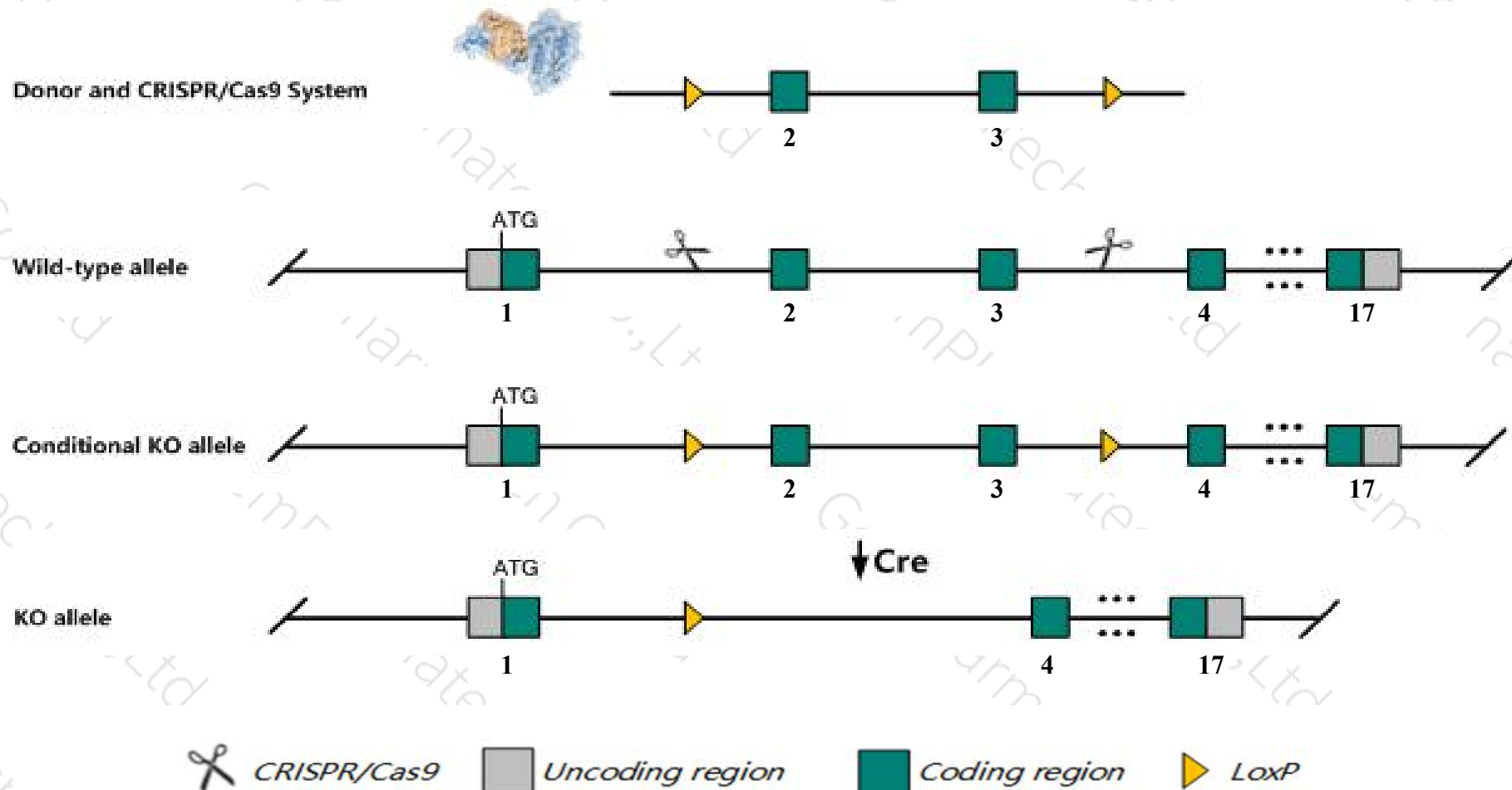
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gk5* gene. The schematic diagram is as follows:



- The *Gk5* gene has 5 transcripts. According to the structure of *Gk5* gene, exon2-exon3 of *Gk5-202* (ENSMUST00000122383.2) transcript is recommended as the knockout region. The region contains 170bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gk5* 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 ENU-induced alleles exhibit skin phenotype and alopecia.
- The *Gk5* 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)

Gk5 glycerol kinase 5 (putative) [*Mus musculus* (house mouse)]

Gene ID: 235533, updated on 24-Oct-2019

Summary

Official Symbol Gk5 provided by [MGI](#)

Official Full Name glycerol kinase 5 (putative) provided by [MGI](#)

Primary source [MGI:MGI:2443336](#)

See related [Ensembl:ENSMUSG000000041440](#)

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 AV095337; C330018K18Rik; G630067D24Rik

Expression Ubiquitous expression in genital fat pad adult (RPKM 2.4), limb E14.5 (RPKM 1.9) and 27 other tissues [See more](#)

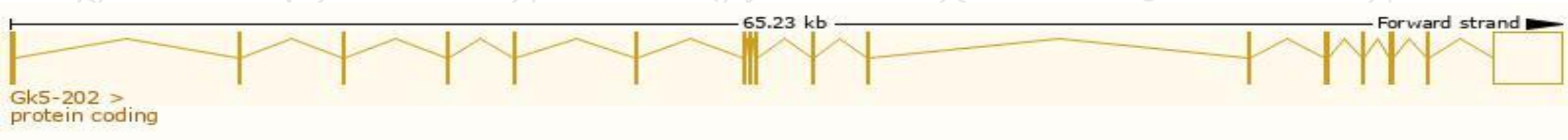
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

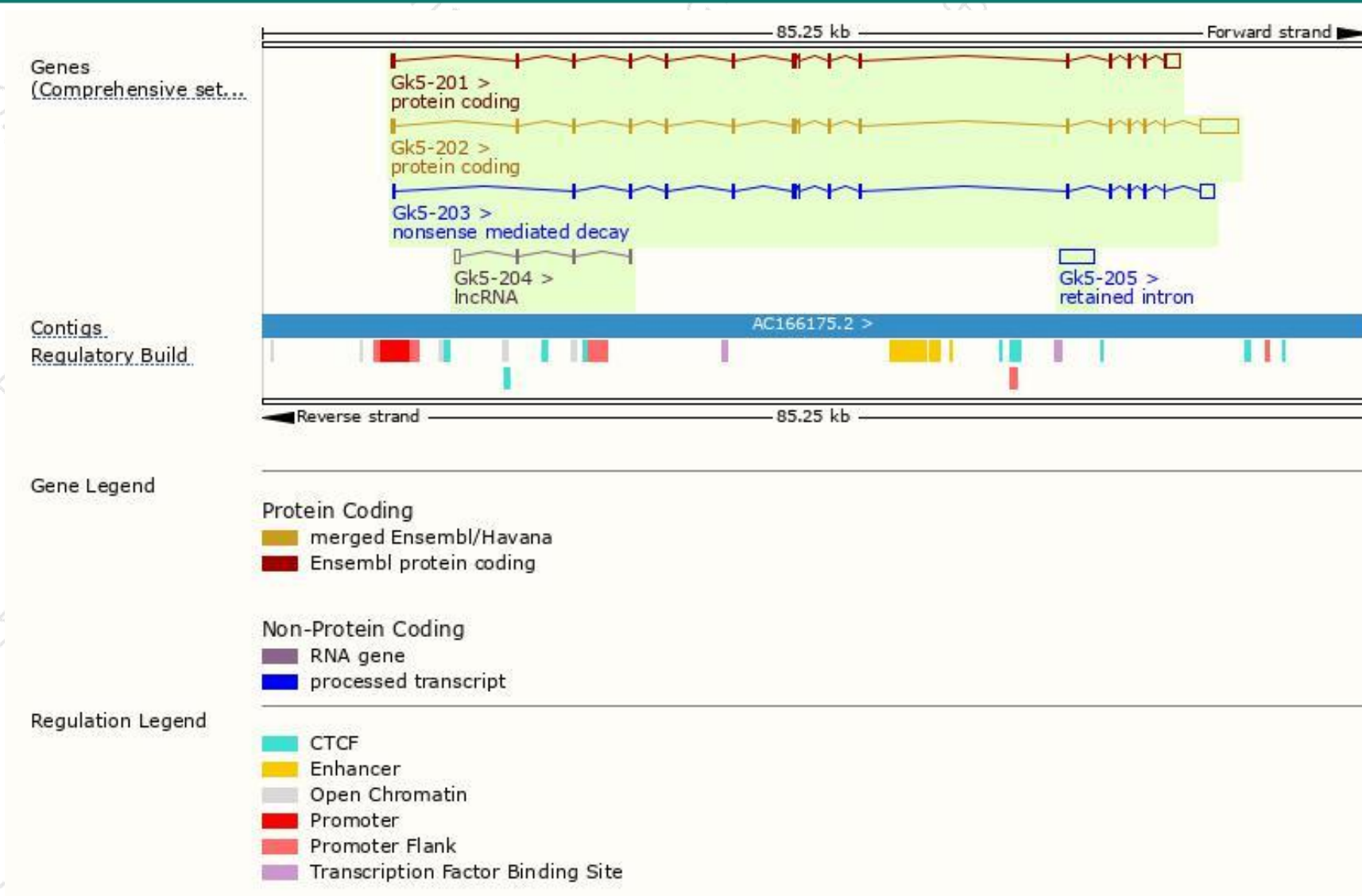
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gk5-202	ENSMUST00000122383.2	4455	516aa	Protein coding	CCDS52891	Q8BX05	TSL:1 GENCODE basic APPRIS P2
Gk5-201	ENSMUST00000085217.11	2815	534aa	Protein coding	-	Q8BX05	TSL:1 GENCODE basic APPRIS ALT2
Gk5-203	ENSMUST00000129774.1	2506	59aa	Nonsense mediated decay	-	D6RCU4	TSL:1
Gk5-205	ENSMUST00000189249.1	2550	No protein	Retained intron	-	-	TSL:NA
Gk5-204	ENSMUST00000136496.1	632	No protein	lncRNA	-	-	TSL:3

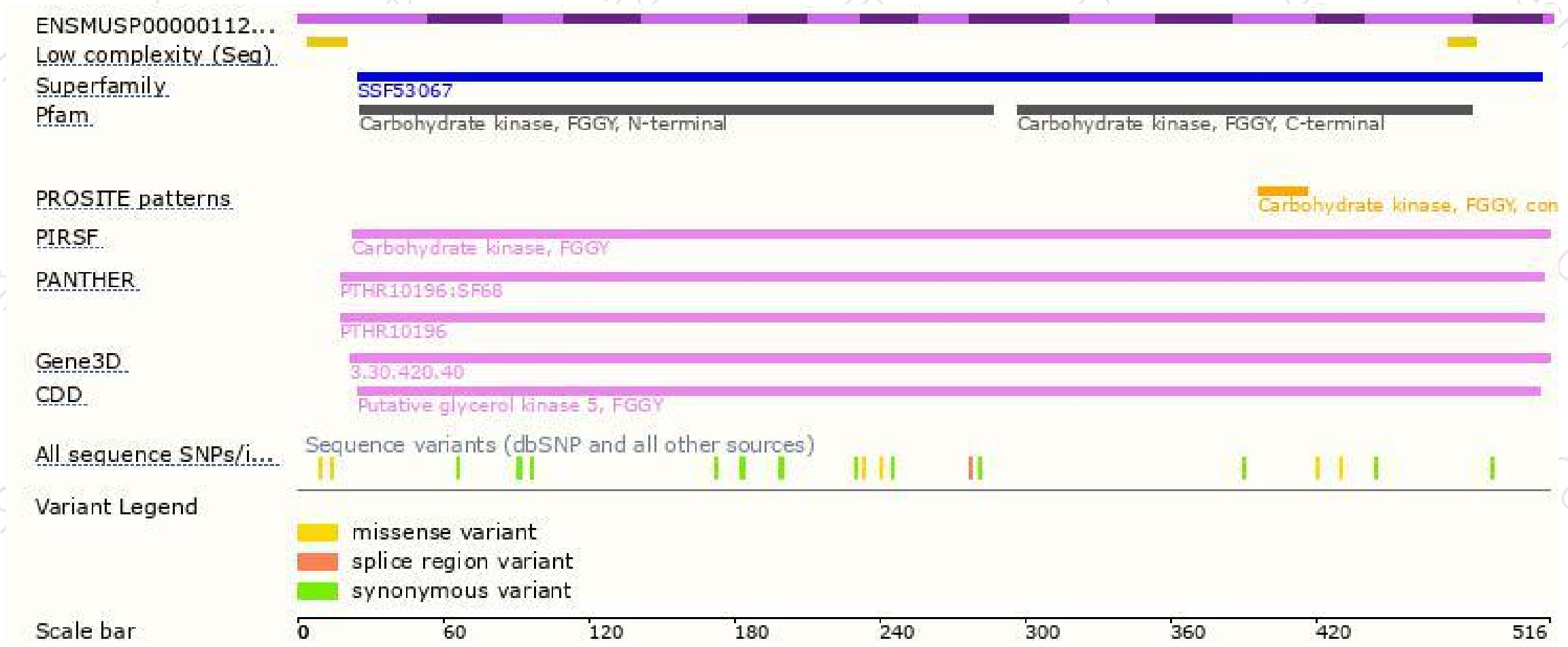
The strategy is based on the design of *Gk5-202* transcript,The transcription is shown below



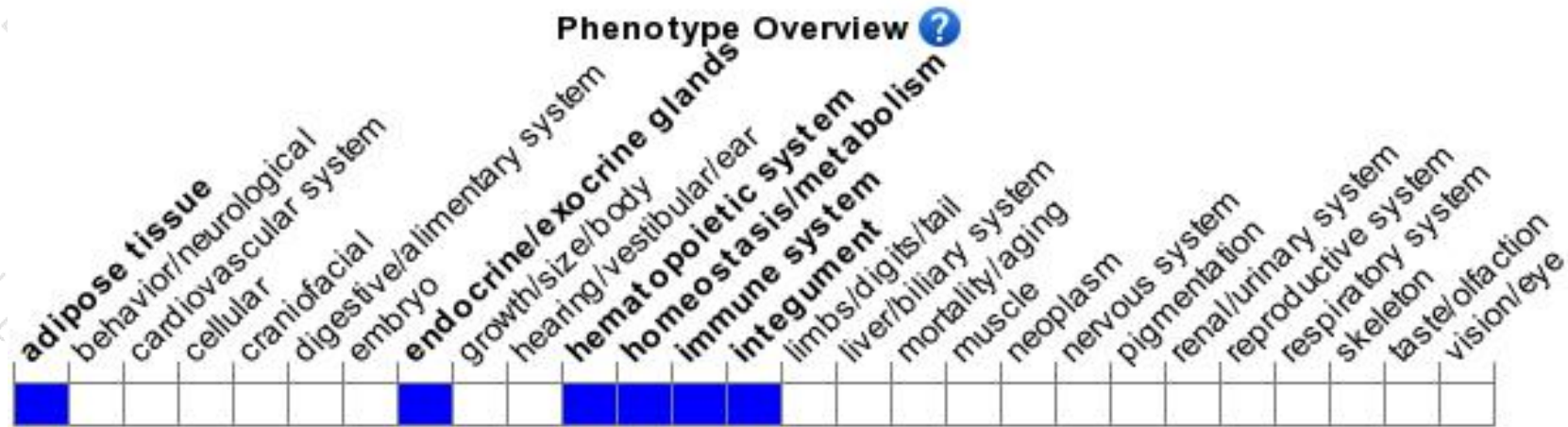
Genomic location distribution



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 ENU-induced alleles exhibit skin phenotype and alopecia.

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

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