

Klf10 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Klf10

Project type

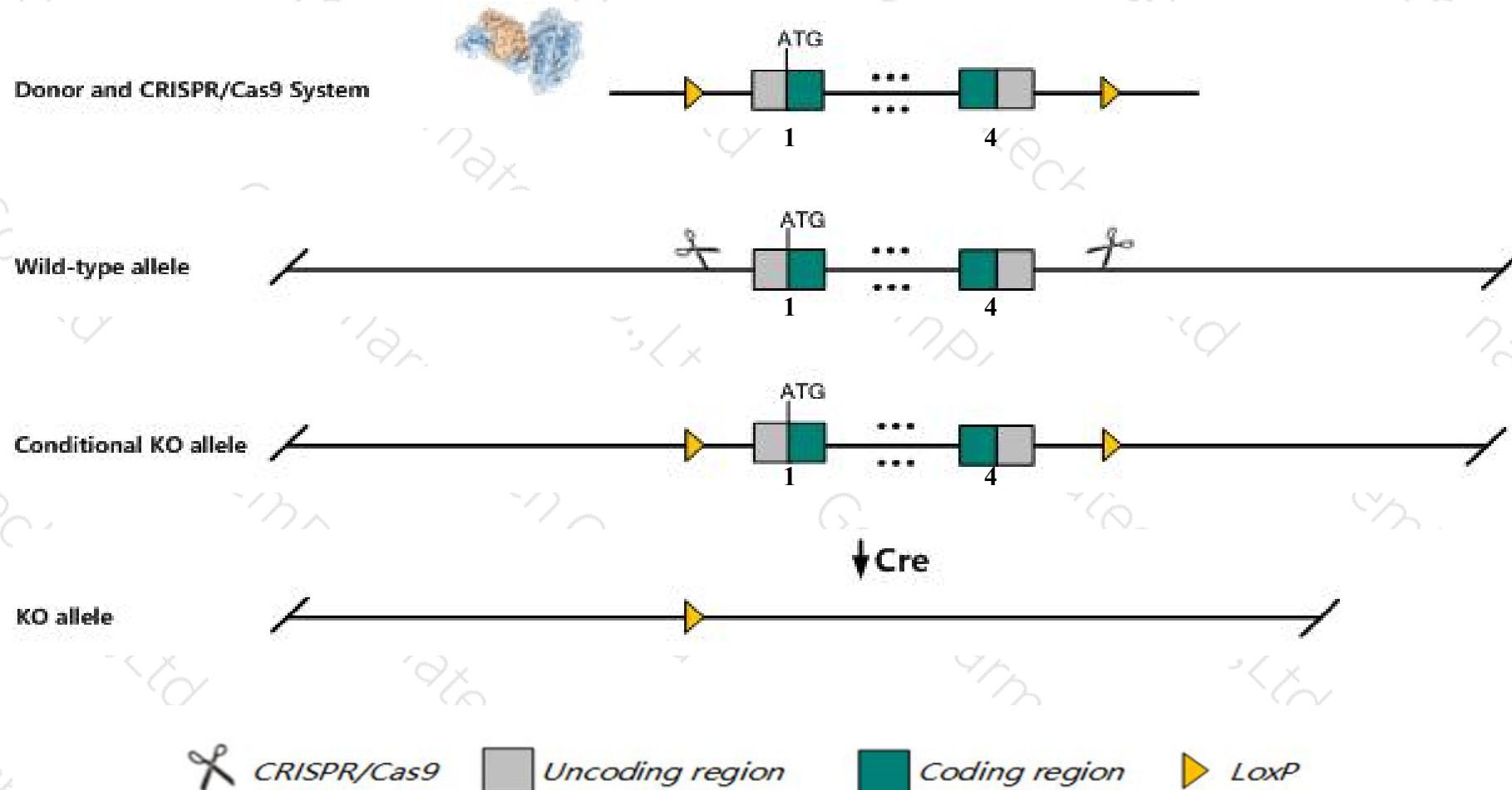
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klf10* gene. The schematic diagram is as follows:



Technical routes

- The *Klf10* gene has 6 transcripts. According to the structure of *Klf10* gene, exon1-exon4 of *Klf10-201* (ENSMUST00000074043.6) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Klf10* 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, Homozygous mutants display increased osteoblast formation and impaired osteoblast function.
- The *Klf10* gene is located on the Chr15. 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)

Klf10 Kruppel-like factor 10 [Mus musculus (house mouse)]

Gene ID: 21847, updated on 5-Mar-2019

Summary



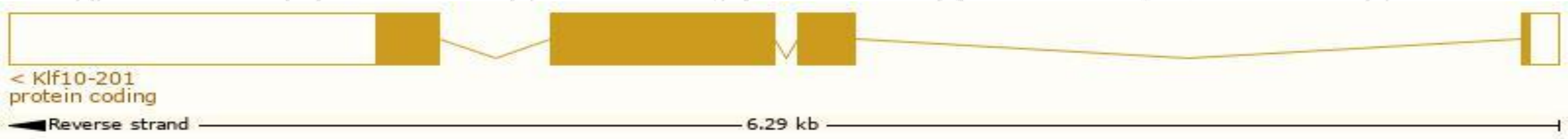
Official Symbol	Klf10 provided by MGI
Official Full Name	Kruppel-like factor 10 provided by MGI
Primary source	MGI:MGI:1101353
See related	Ensembl:ENSMUSG000000037465
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Al115143, EGR[a], Egral, Gdnfif, TIEG-1, Tieg, Tieg1, mGIF
Expression	Ubiquitous expression in bladder adult (RPKM 10.6), mammary gland adult (RPKM 9.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

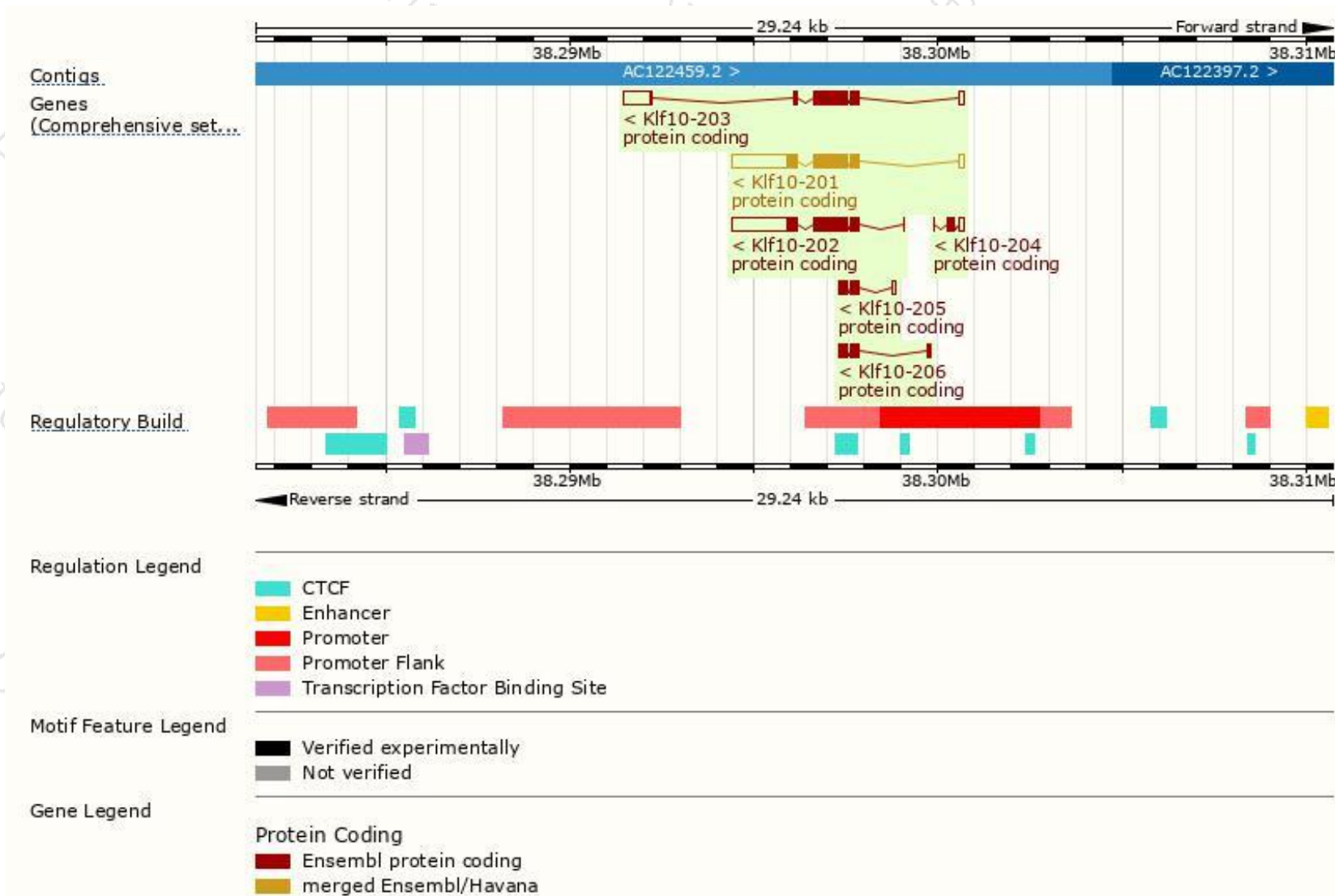
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Klf10-201	ENSMUST00000074043.6	3044	479aa	Protein coding	CCDS27438	O89091	TSL:1 GENCODE basic APPRIS P1
Klf10-202	ENSMUST00000226363.1	2917	464aa	Protein coding	-	A0A2I3BRS7	GENCODE basic
Klf10-203	ENSMUST00000227920.1	2144	434aa	Protein coding	-	Q8C900	GENCODE basic
Klf10-205	ENSMUST00000228732.1	536	151aa	Protein coding	-	A0A2I3BPZ3	CDS 3' incomplete
Klf10-206	ENSMUST00000228772.1	530	176aa	Protein coding	-	A0A2I3BQ59	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Klf10-204	ENSMUST00000228416.1	326	71aa	Protein coding	-	A0A2I3BRQ2	CDS 3' incomplete

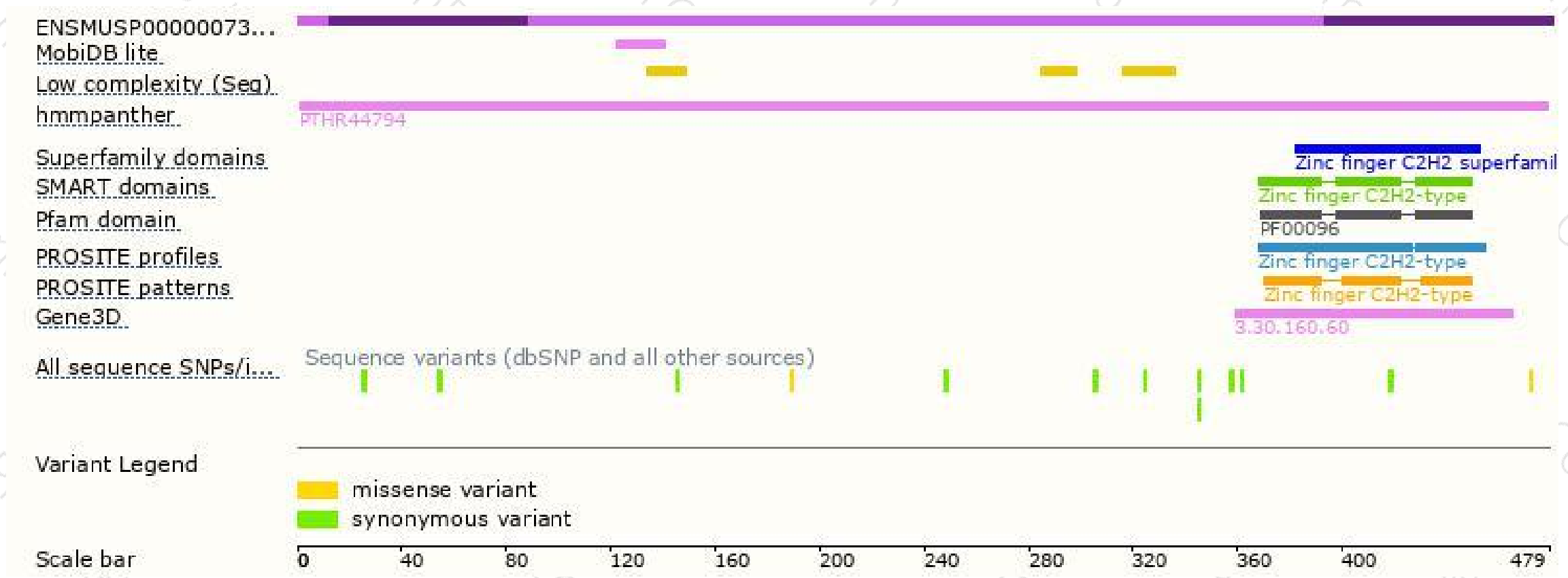
The strategy is based on the design of *Klf10-201* transcript,The transcription is shown below



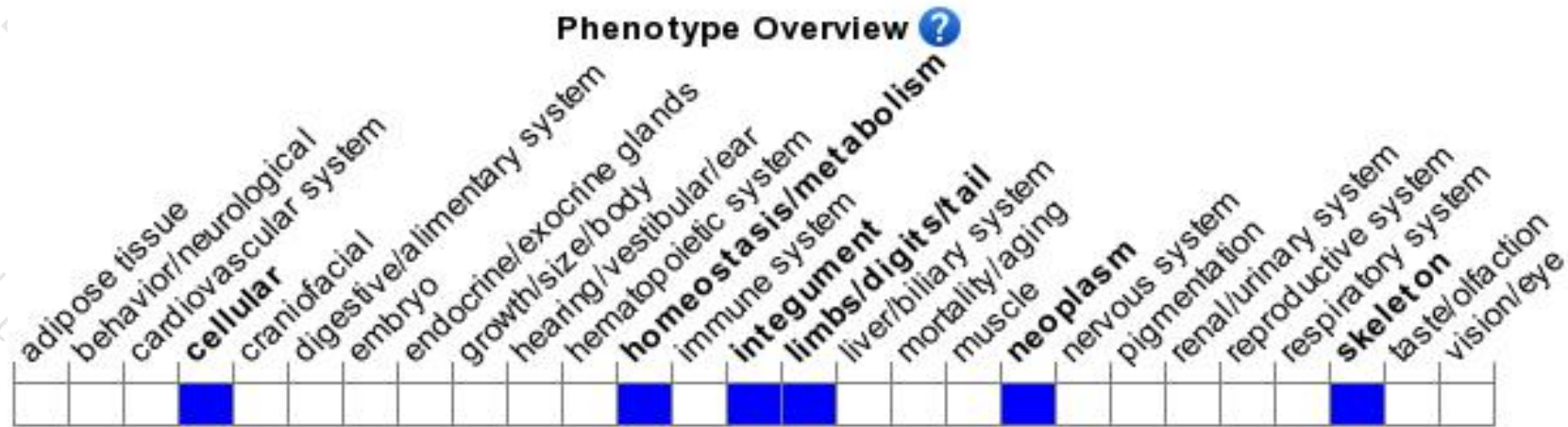
Genomic location distribution



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, Homozygous mutants display increased osteoblast formation and impaired osteoblast function.

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

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