

Acp5 Cas9-CKO Strategy

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Design Date:	2020-5-6

Project Overview

Project Name

Acp5

Project type

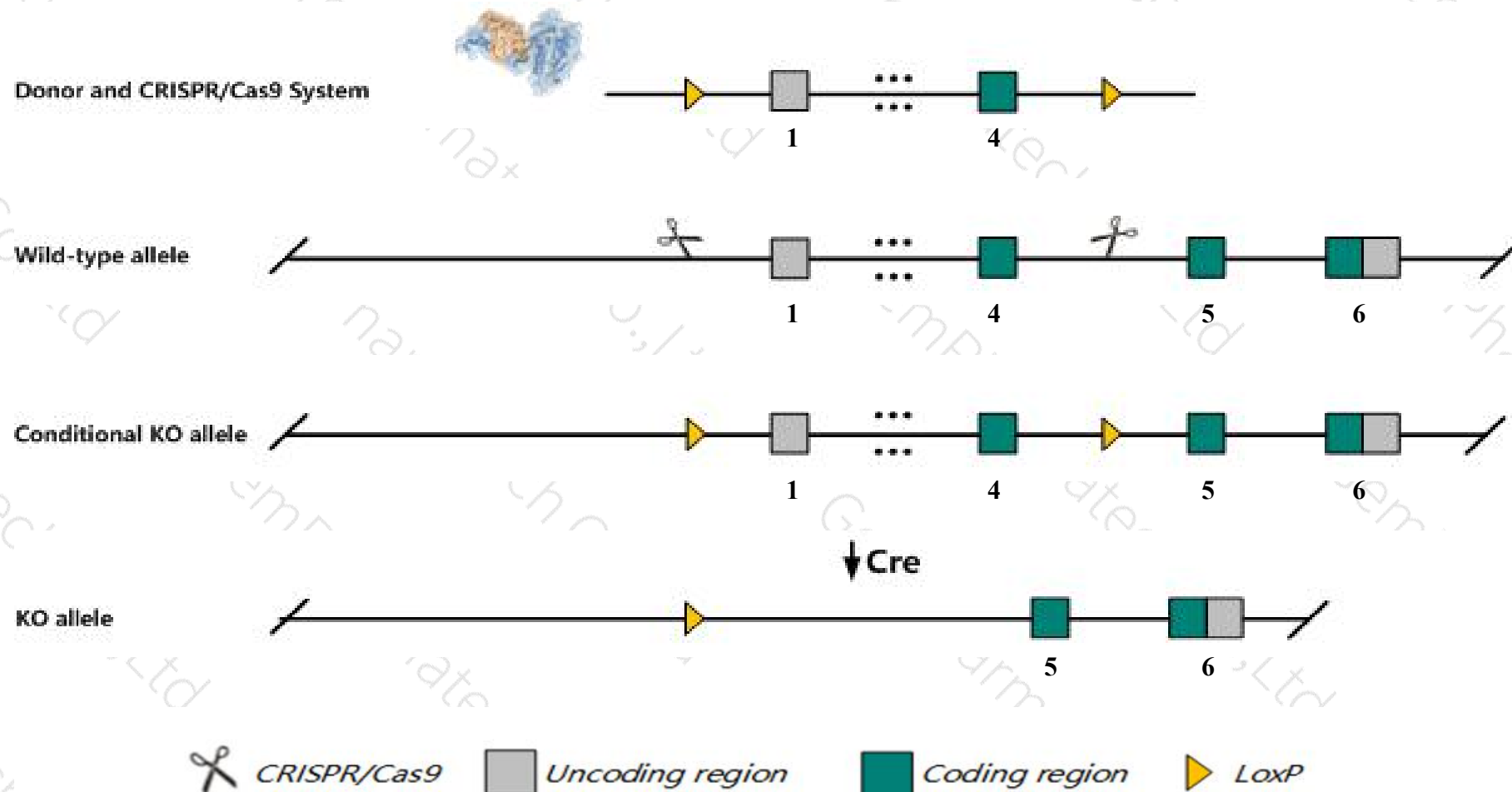
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acp5* gene. The schematic diagram is as follows:



- The *Acp5* gene has 6 transcripts. According to the structure of *Acp5* gene, exon1-exon4 of *Acp5*-206 (ENSMUST00000217643.1) transcript is recommended as the knockout region. The region contains start coding ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Acp5* 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, homozygous mutation of this gene results in skeletal defects such as osteopetrosis, and shortening and widening of the bones. heterozygous mutants display the same phenotype with lesser severity.
- The KO region contains the *6530413G14Rik* gene. Knockout the region may affect the function of *6530413G14Rik* gene.
- The *Acp5* 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)

Acp5 acid phosphatase 5, tartrate resistant [Mus musculus (house mouse)]

Gene ID: 11433, updated on 13-Mar-2020

Summary



Official Symbol Acp5 provided by [MGI](#)

Official Full Name acid phosphatase 5, tartrate resistant provided by [MGI](#)

Primary source [MGI:MGI:87883](#)

See related [Ensembl:ENSMUSG00000001348](#)

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 TRACP, TRAP

Expression Broad expression in subcutaneous fat pad adult (RPKM 123.7), colon adult (RPKM 116.7) and 17 other tissues [See more](#)

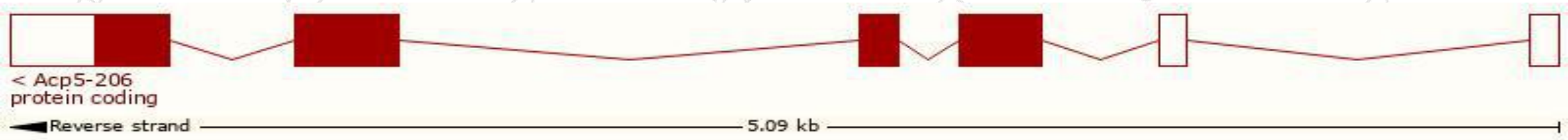
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

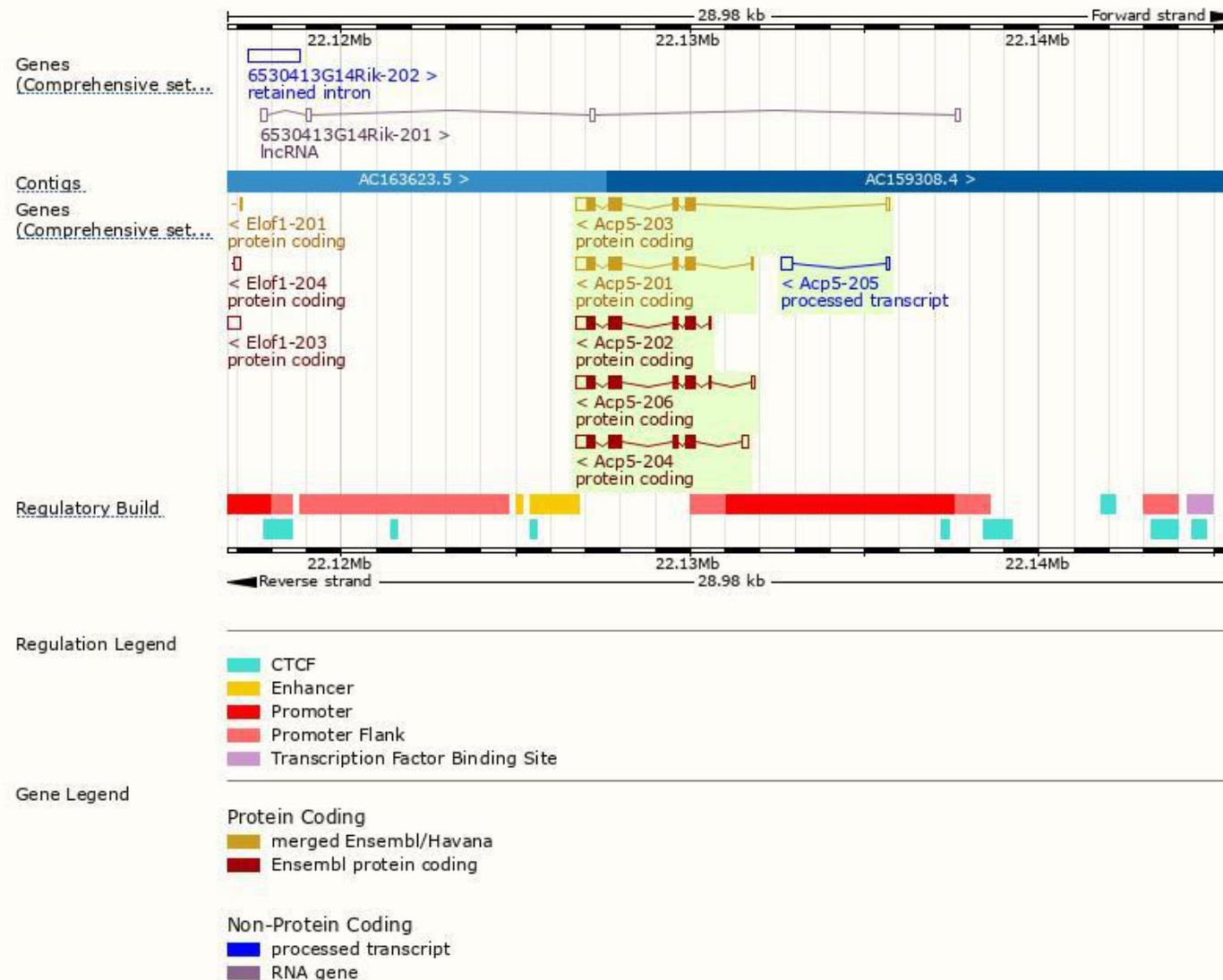
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acp5-206	ENSMUST00000217643.1	1447	327aa	Protein coding	CCDS22923	Q05117	TSL:5 GENCODE basic APPRIS P1
Acp5-204	ENSMUST00000213815.1	1419	327aa	Protein coding	CCDS22923	Q05117	TSL:5 GENCODE basic APPRIS P1
Acp5-203	ENSMUST00000165735.8	1376	327aa	Protein coding	CCDS22923	Q05117	TSL:1 GENCODE basic APPRIS P1
Acp5-201	ENSMUST00000069330.13	1356	327aa	Protein coding	CCDS22923	Q05117	TSL:1 GENCODE basic APPRIS P1
Acp5-202	ENSMUST00000115315.2	1349	327aa	Protein coding	CCDS22923	Q05117	TSL:2 GENCODE basic APPRIS P1
Acp5-205	ENSMUST00000216684.1	399	No protein	Processed transcript	-	-	TSL:2

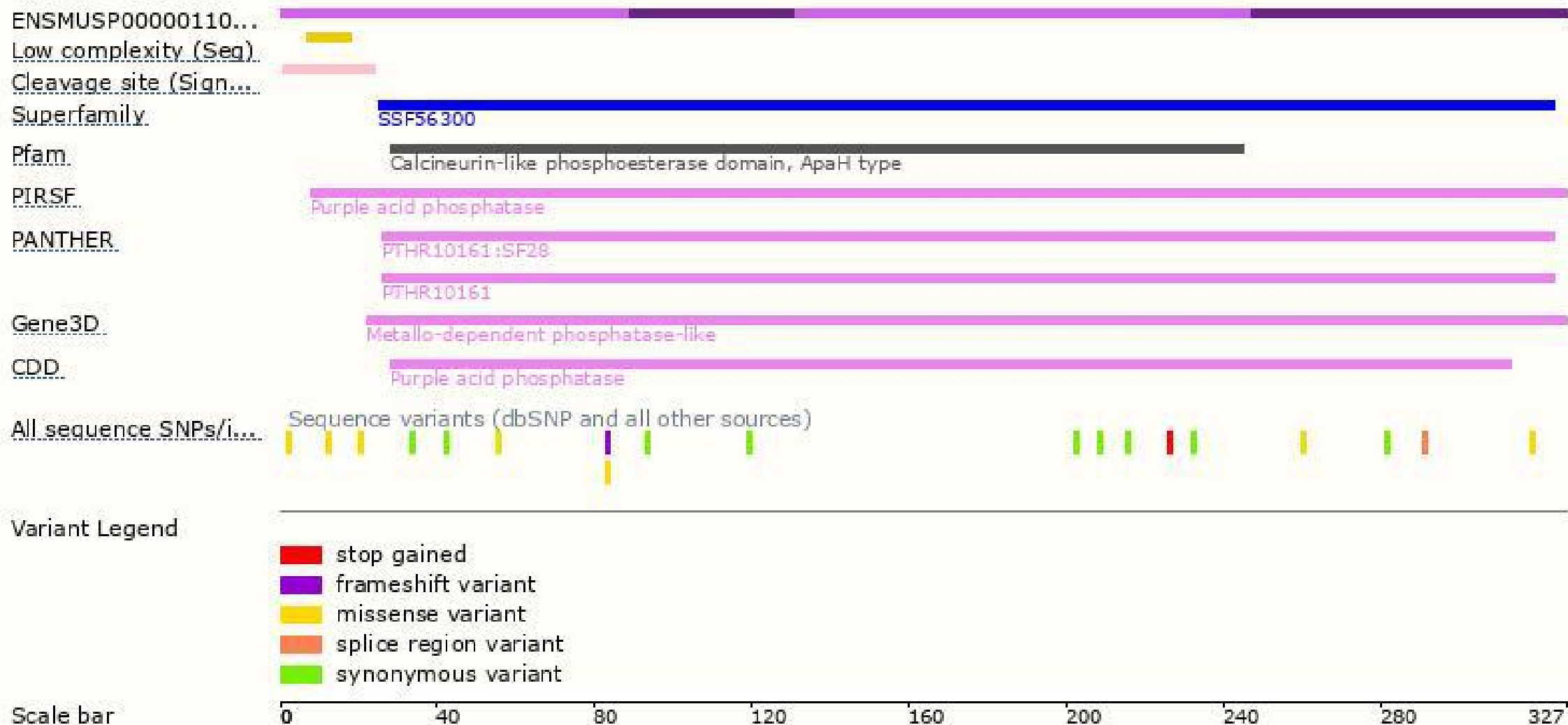
The strategy is based on the design of *Acp5-206* transcript,the transcription is shown below:



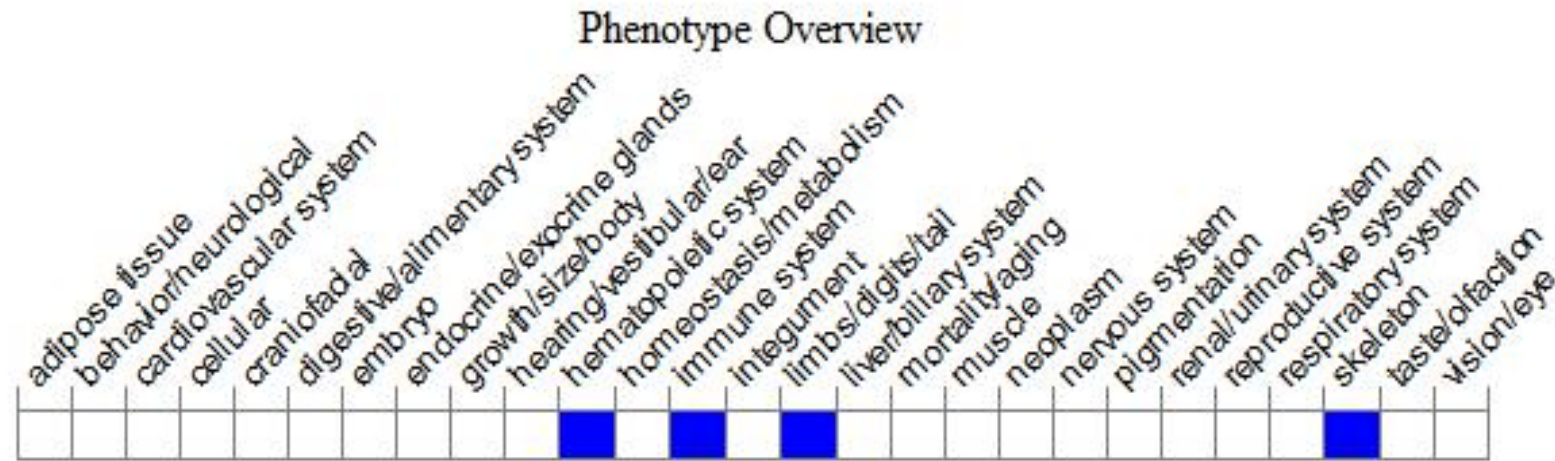
Genomic location distribution



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 mutation of this gene results in skeletal defects such as osteopetrosis, and shortening and widening of the bones. Heterozygous mutants display the same phenotype with lesser severity.

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

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