

Epyc Cas9-KO Strategy

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Project Overview

Project Name

Epyc

Project type

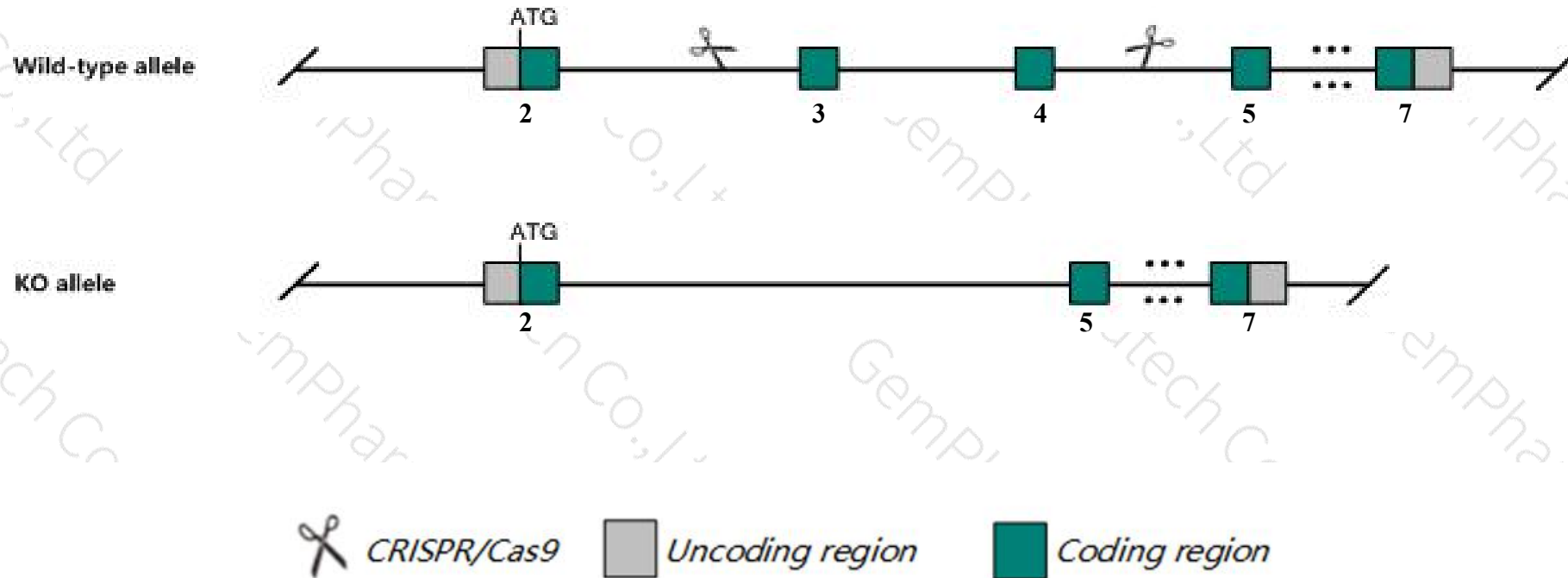
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Epyc* gene has 2 transcripts. According to the structure of *Epyc* gene, exon3-exon4 of *Epyc*-202 (ENSMUST00000105285.3) transcript is recommended as the knockout region. The region contains 334bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epyc* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, Mice homozygous for a knock-out exhibit short femurs and borderline osteoarthritis at 9 months of age.
- The *Epyc* gene is located on the Chr10. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Epyc epiphycan [*Mus musculus* (house mouse)]

Gene ID: 13516, updated on 12-Aug-2019

Summary

- Official Symbol [Epyc](#) provided by [MGI](#)
- Official Full Name [epiphycan](#) provided by [MGI](#)
- Primary source [MGI:MGI:107942](#)
- See related [Ensembl:ENSMUSG00000019936](#)
- Gene type protein coding
- RefSeq status PROVISIONAL
- Organism [Mus musculus](#)
- Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as [Dspg3](#); [PG-Lb](#); [SLRR3B](#)
- Expression Biased expression in [limb E14.5](#) (RPKM 25.0), [testis adult](#) (RPKM 5.6) and 1 other tissue [See more](#)
- Orthologs [human](#) [all](#)

Genomic context

Location: 10 C3; 10 50.35 cM See Epyc in [Genome Data Viewer](#)

Exon count: 8

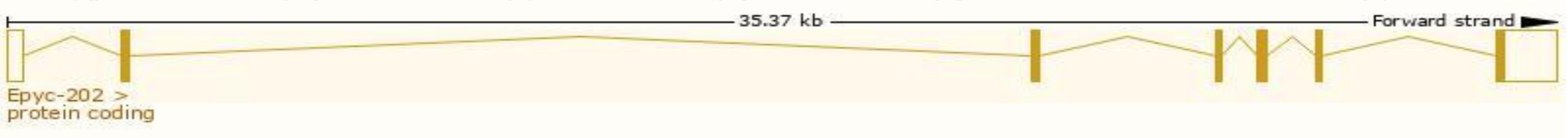
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (97644068..97681908)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (97106702..97144534)

Transcript information (Ensembl)

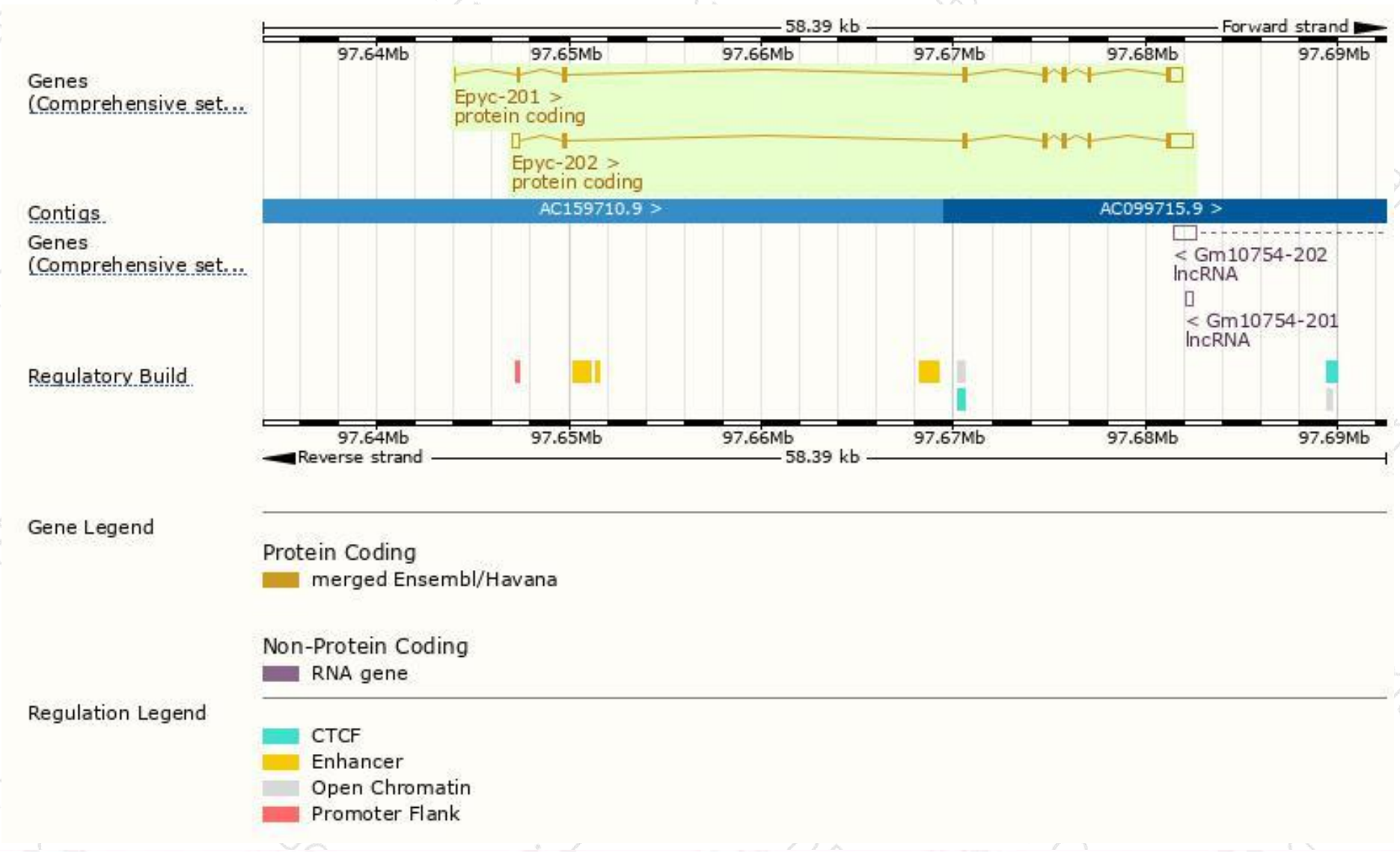
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epyc-202	ENSMUST00000105285.3	2539	322aa	Protein coding	CCDS24143	P70186	TSL:1 GENCODE basic APPRIS P1
Epyc-201	ENSMUST00000020094.7	1723	322aa	Protein coding	CCDS24143	P70186	TSL:1 GENCODE basic APPRIS P1

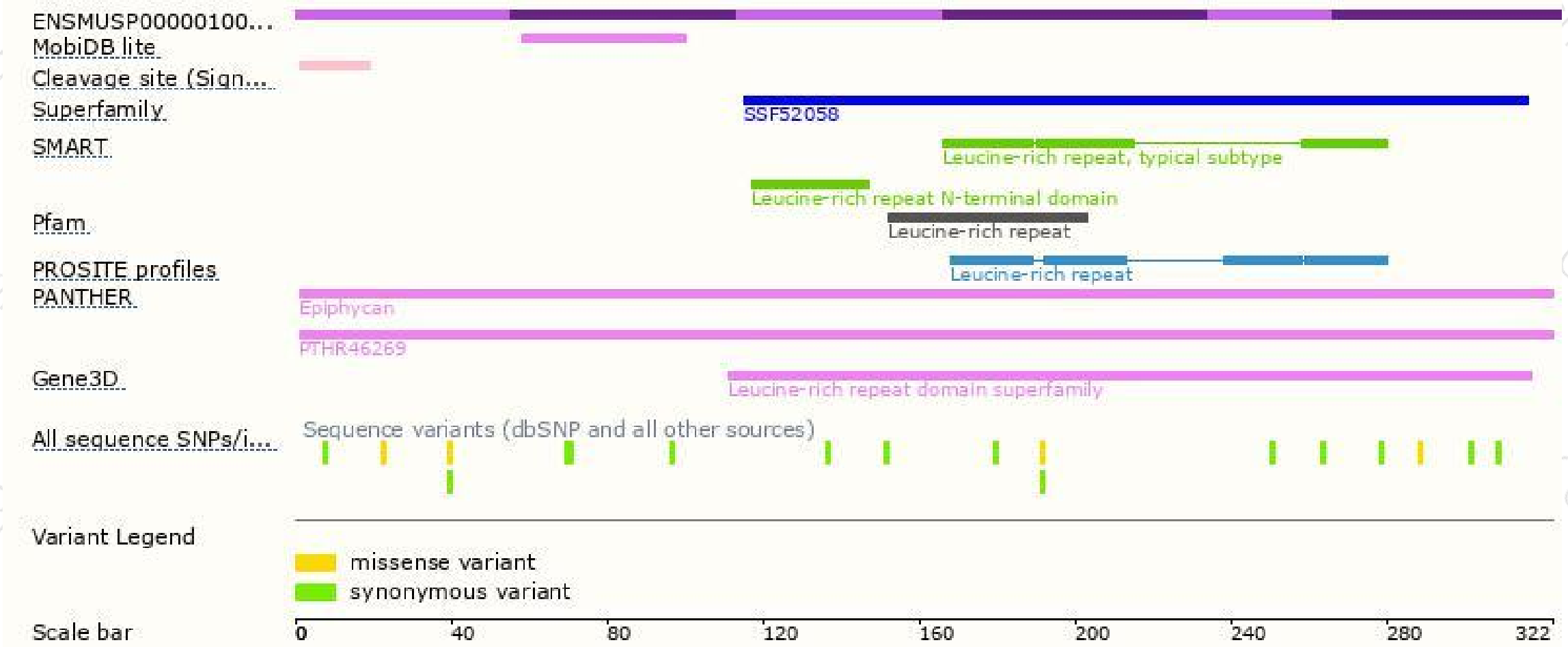
The strategy is based on the design of *Epyc-202* transcript,The transcription is shown below



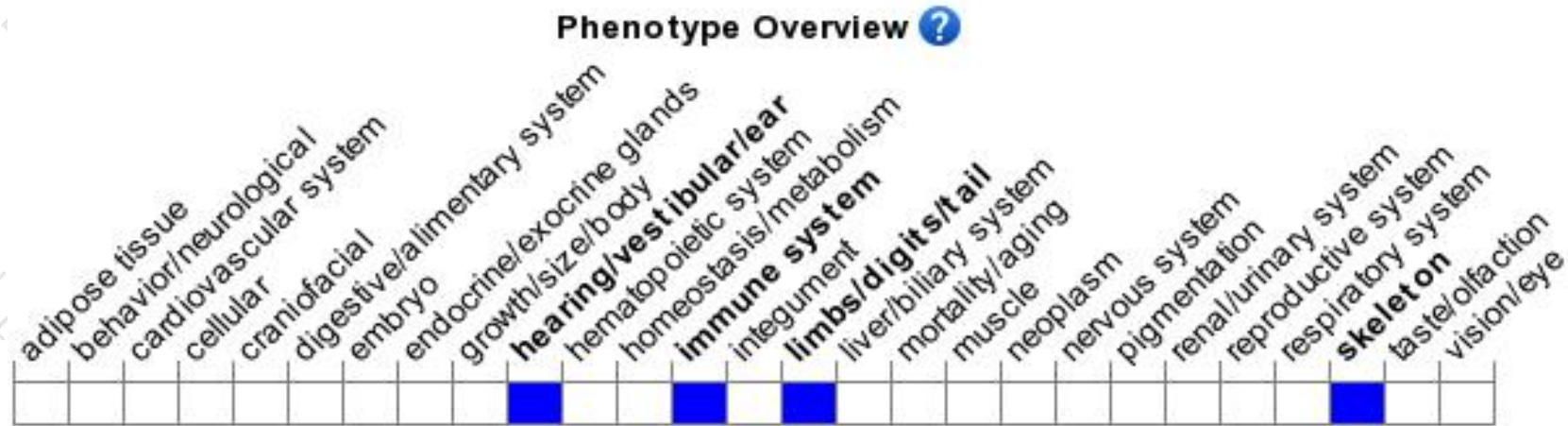
Genomic location distribution



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/>).

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

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