

***Zbtb16* Cas9-CKO Strategy**

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Design Date: 2019-9-19
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Project Overview

Project Name

Zbtb16

Project type

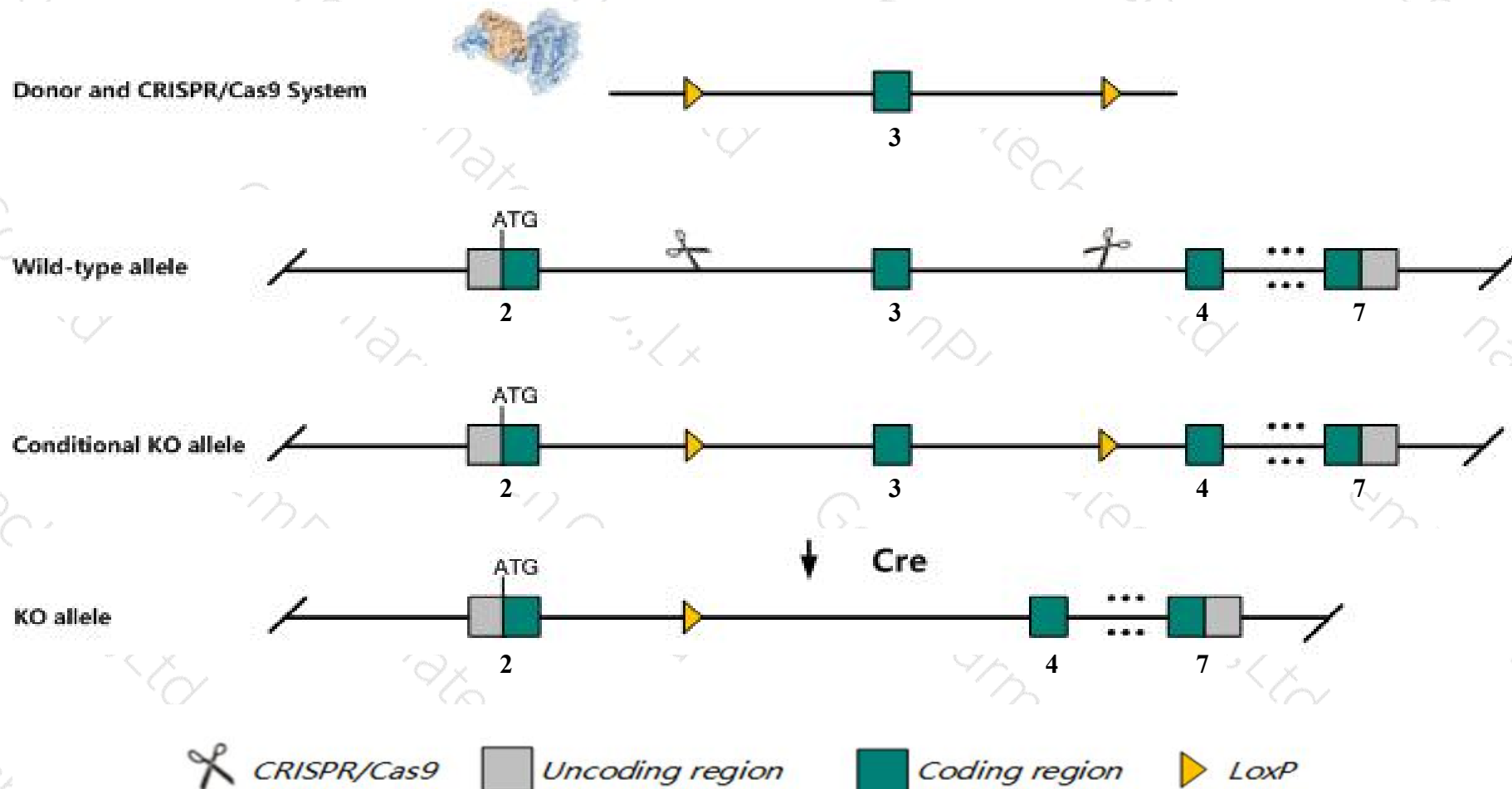
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb16* gene. The schematic diagram is as follows:



Technical routes

- The *Zbtb16* gene has 2 transcripts. According to the structure of *Zbtb16* gene, exon3 of *Zbtb16-201* (ENSMUST00000093852.4) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zbtb16* 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 exhibit abnormal anterior-posterior patterning, with skeletal abnormalities of the limb, especially the hindlimb, and homeotic transformations of anterior skeletal elements into posterior structures. Males develop infertility due to loss of germline cells with age.
- The *Zbtb16* 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)

Zbtb16 zinc finger and BTB domain containing 16 [Mus musculus (house mouse)]

Gene ID: 235320, updated on 19-Mar-2019

Summary



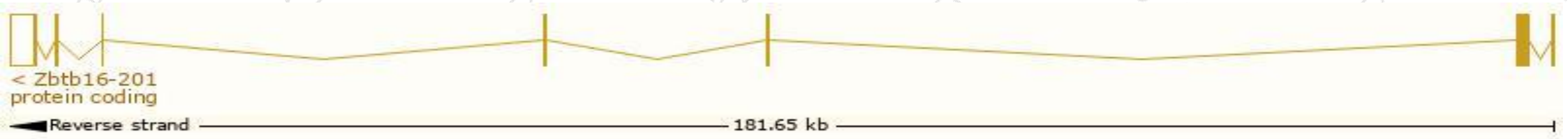
Official Symbol	Zbtb16 provided by MGI
Official Full Name	zinc finger and BTB domain containing 16 provided by MGI
Primary source	MGI:MGI:103222
See related	Ensembl:ENSMUSG00000066687
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI467657, PLZF, Zfp145, lu
Expression	Broad expression in lung adult (RPKM 8.1), subcutaneous fat pad adult (RPKM 7.3) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

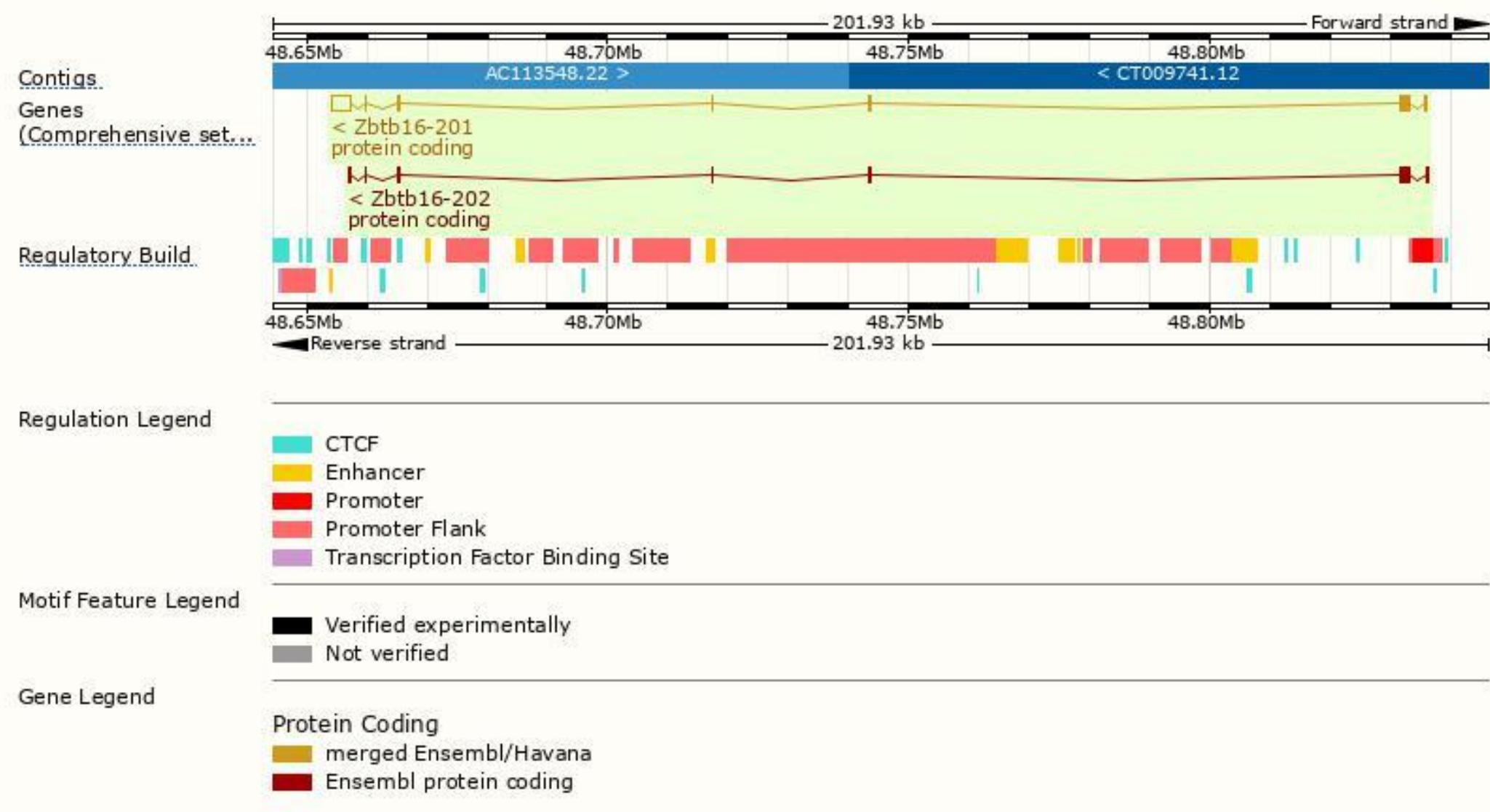
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb16-201	ENSMUST00000093852.4	5114	673aa	Protein coding	CCDS23158	Q3UQ17	TSL:1 GENCODE basic APPRIS P1
Zbtb16-202	ENSMUST00000216150.1	2505	673aa	Protein coding	CCDS23158	Q3UQ17	TSL:1 GENCODE basic APPRIS P1

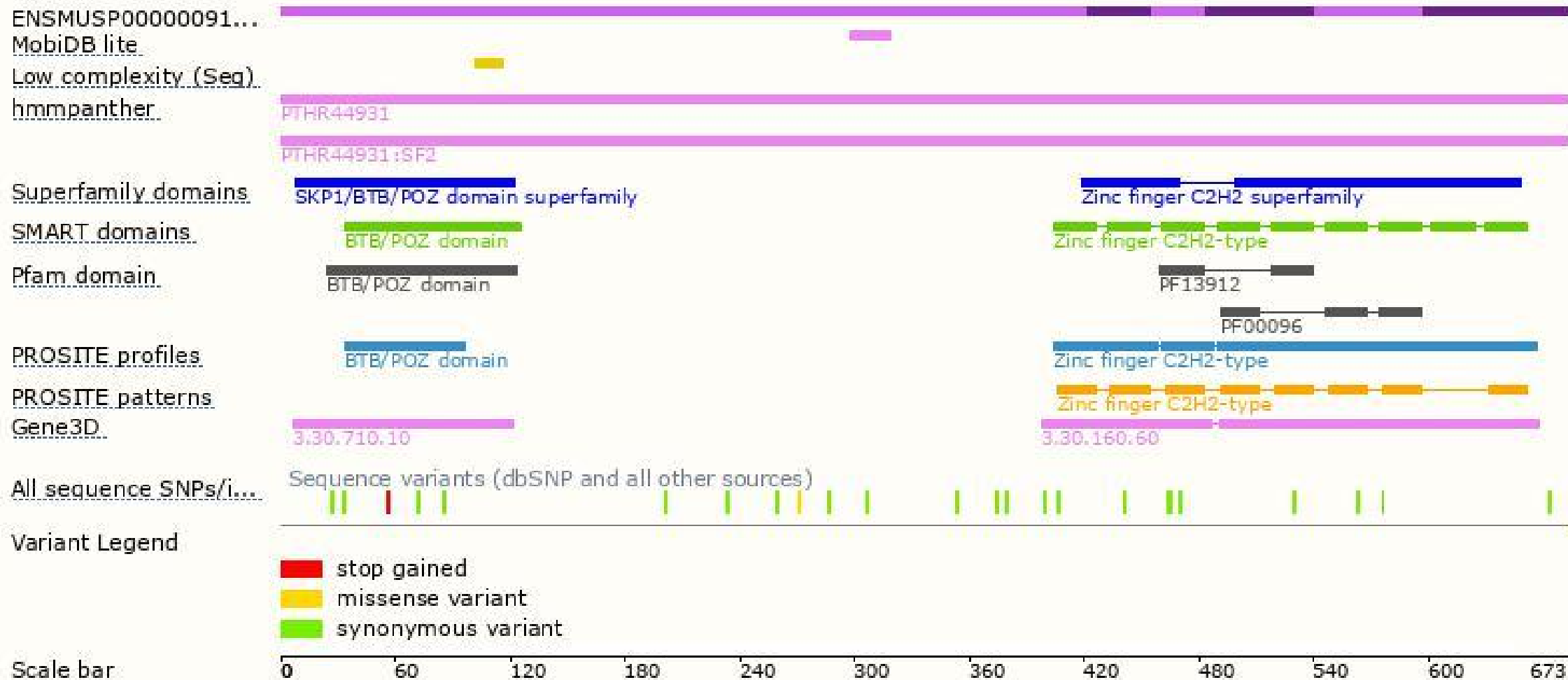
The strategy is based on the design of *Zbtb16-201* transcript,The transcription is shown below



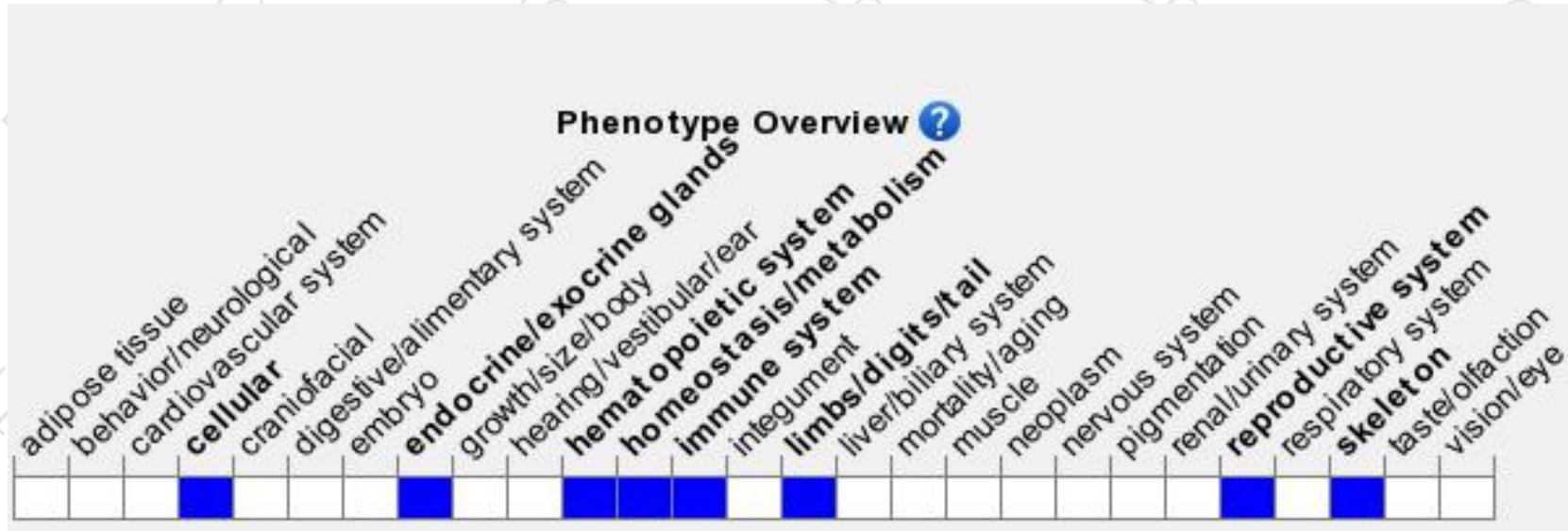
Genomic location distribution



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 exhibit abnormal anterior-posterior patterning, with skeletal abnormalities of the limb, especially the hindlimb, and homeotic transformations of anterior skeletal elements into posterior structures. Males develop infertility due to loss of germline cells with age.

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

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