

***Zbtb20* Cas9-CKO Strategy**

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Project Overview

Project Name

Zbtb20

Project type

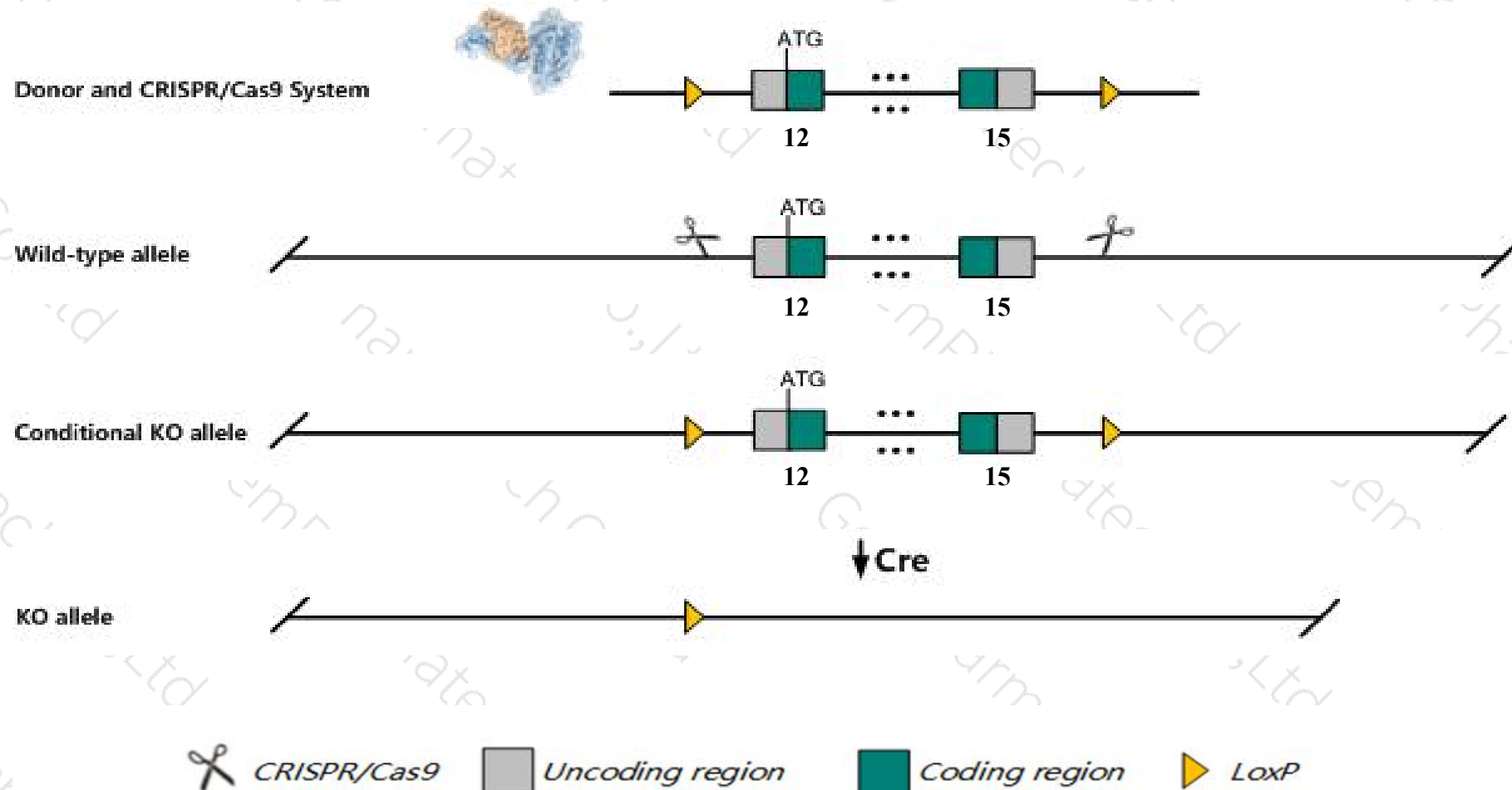
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb20* gene. The schematic diagram is as follows:



Technical routes

- The *Zbtb20* gene has 21 transcripts. According to the structure of *Zbtb20* gene, exon12-exon15 of *Zbtb20*-204(ENSMUST00000114694.8) 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 *Zbtb20* 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 a knock-out allele exhibit growth retardation, disrupted homeostasis, and premature death.
- The KO region contains functional region of the Mir568 gene. Knockout the region may affect the function of Mir568 gene.
- The *Zbtb20* gene is located on the Chr16. 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)

Zbtb20 zinc finger and BTB domain containing 20 [Mus musculus (house mouse)]

Gene ID: 56490, updated on 13-Mar-2020

Summary



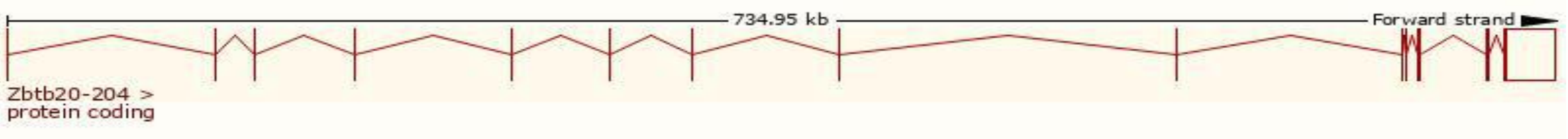
Official Symbol	Zbtb20 provided by MGI
Official Full Name	zinc finger and BTB domain containing 20 provided by MGI
Primary source	MGI:MGI:1929213
See related	Ensembl:ENSMUSG00000022708
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1300017A20Rik, 7330412A13Rik, A930017C21Rik, D16Wsu73e, DPZF, HOF, J20, ODA-8S, Oda8, Tg(PDGFB-APPSwInd)20Lms, Zfp288
Expression	Ubiquitous expression in genital fat pad adult (RPKM 5.3), heart adult (RPKM 4.7) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

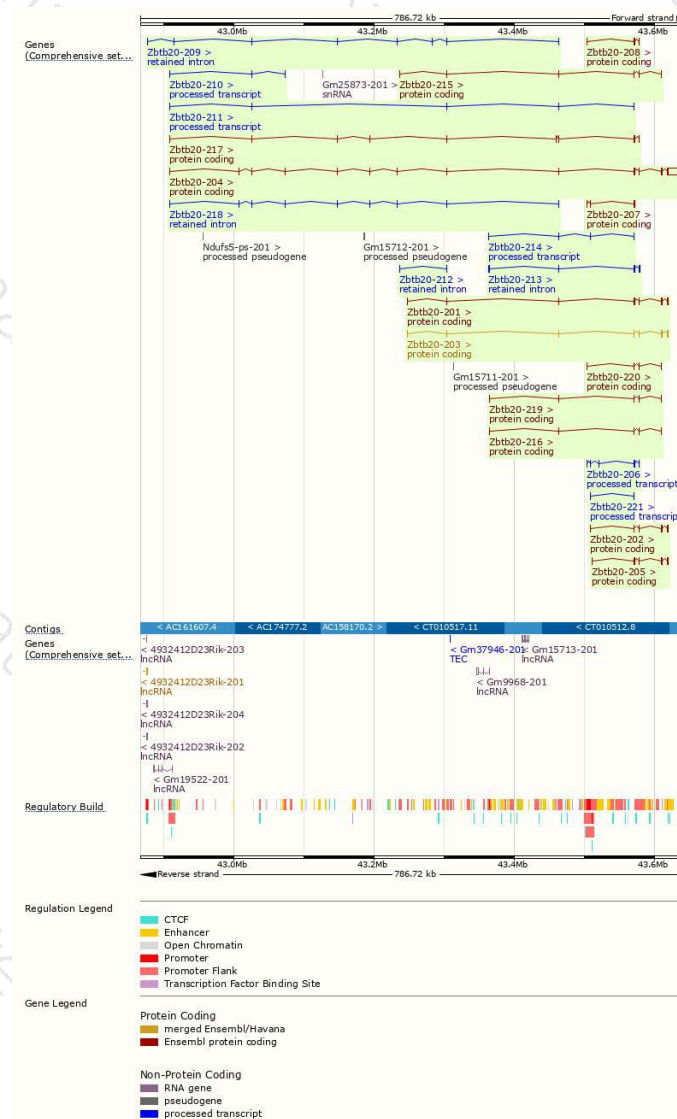
The gene has 21 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb20-204	ENSMUST00000114694.8	26901	741aa	Protein coding	CCDS28178	Q8K0L9	TSL:5 GENCODE basic APPRIS P3
Zbtb20-201	ENSMUST00000079441.12	3086	741aa	Protein coding	CCDS28178	Q8K0L9	TSL:5 GENCODE basic APPRIS P3
Zbtb20-205	ENSMUST00000114695.2	2977	741aa	Protein coding	CCDS28178	Q8K0L9	TSL:1 GENCODE basic APPRIS P3
Zbtb20-203	ENSMUST00000114691.7	2891	668aa	Protein coding	CCDS49851	Q8K0L9	TSL:1 GENCODE basic APPRIS ALT2
Zbtb20-202	ENSMUST00000114690.7	2759	668aa	Protein coding	CCDS49851	Q8K0L9	TSL:1 GENCODE basic APPRIS ALT2
Zbtb20-220	ENSMUST00000156981.7	837	138aa	Protein coding	-	E0CYH3	CDS 3' incomplete TSL:3
Zbtb20-215	ENSMUST00000146708.7	821	75aa	Protein coding	-	E0CXK1	CDS 3' incomplete TSL:3
Zbtb20-219	ENSMUST00000156367.7	787	131aa	Protein coding	-	E0CYJ9	CDS 3' incomplete TSL:3
Zbtb20-217	ENSMUST00000151244.7	754	63aa	Protein coding	-	E0CX28	CDS 3' incomplete TSL:3
Zbtb20-216	ENSMUST00000148775.7	590	60aa	Protein coding	-	E0CXT9	CDS 3' incomplete TSL:3
Zbtb20-208	ENSMUST00000126100.7	463	3aa	Protein coding	-	-	CDS 3' incomplete TSL:5
Zbtb20-207	ENSMUST00000123047.7	439	3aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Zbtb20-206	ENSMUST00000122875.7	736	No protein	Processed transcript	-	-	TSL:3
Zbtb20-210	ENSMUST00000131689.7	425	No protein	Processed transcript	-	-	TSL:2
Zbtb20-211	ENSMUST00000132881.7	418	No protein	Processed transcript	-	-	TSL:3
Zbtb20-214	ENSMUST00000141941.7	414	No protein	Processed transcript	-	-	TSL:3
Zbtb20-221	ENSMUST00000162745.7	267	No protein	Processed transcript	-	-	TSL:5
Zbtb20-213	ENSMUST00000139491.7	2063	No protein	Retained intron	-	-	TSL:1
Zbtb20-212	ENSMUST00000134537.2	645	No protein	Retained intron	-	-	TSL:3
Zbtb20-218	ENSMUST00000151290.7	593	No protein	Retained intron	-	-	TSL:3
Zbtb20-209	ENSMUST00000126354.7	563	No protein	Retained intron	-	-	TSL:3

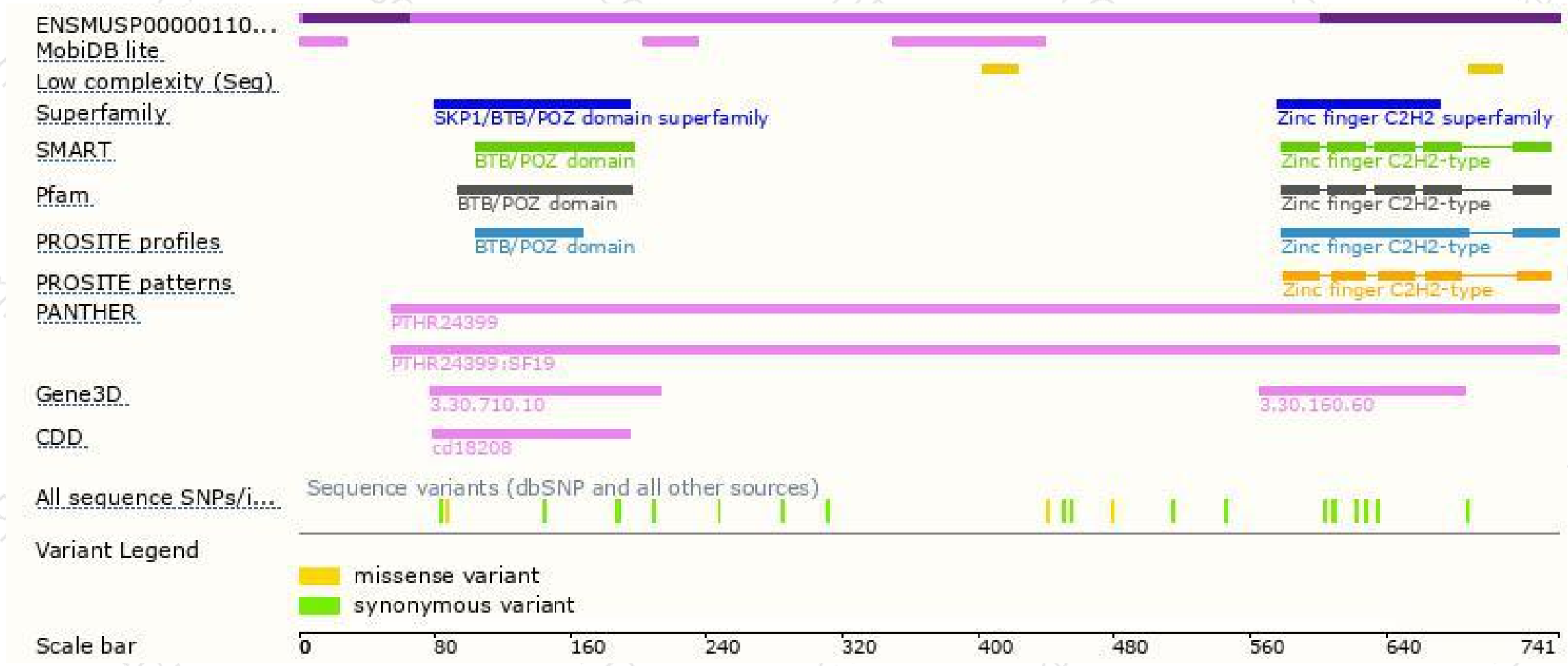
The strategy is based on the design of *Zbtb20-204* transcript,the transcription is shown below:



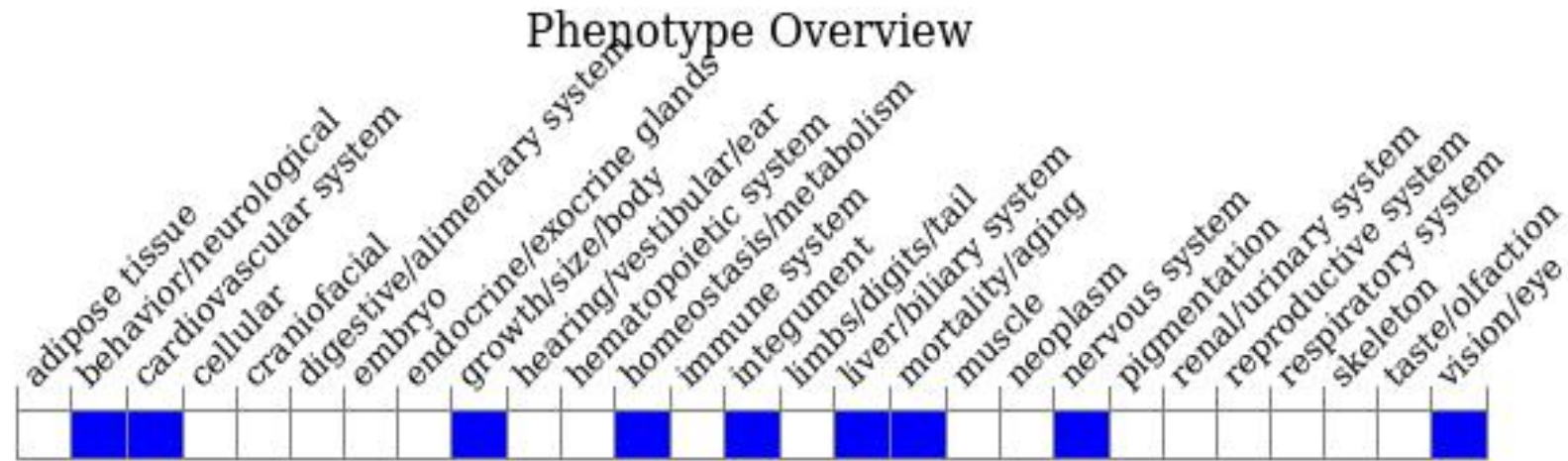
Genomic location distribution



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 a knock-out allele exhibit growth retardation, disrupted homeostasis, and premature death.

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

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