

Zfp110 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Zfp110

Project type

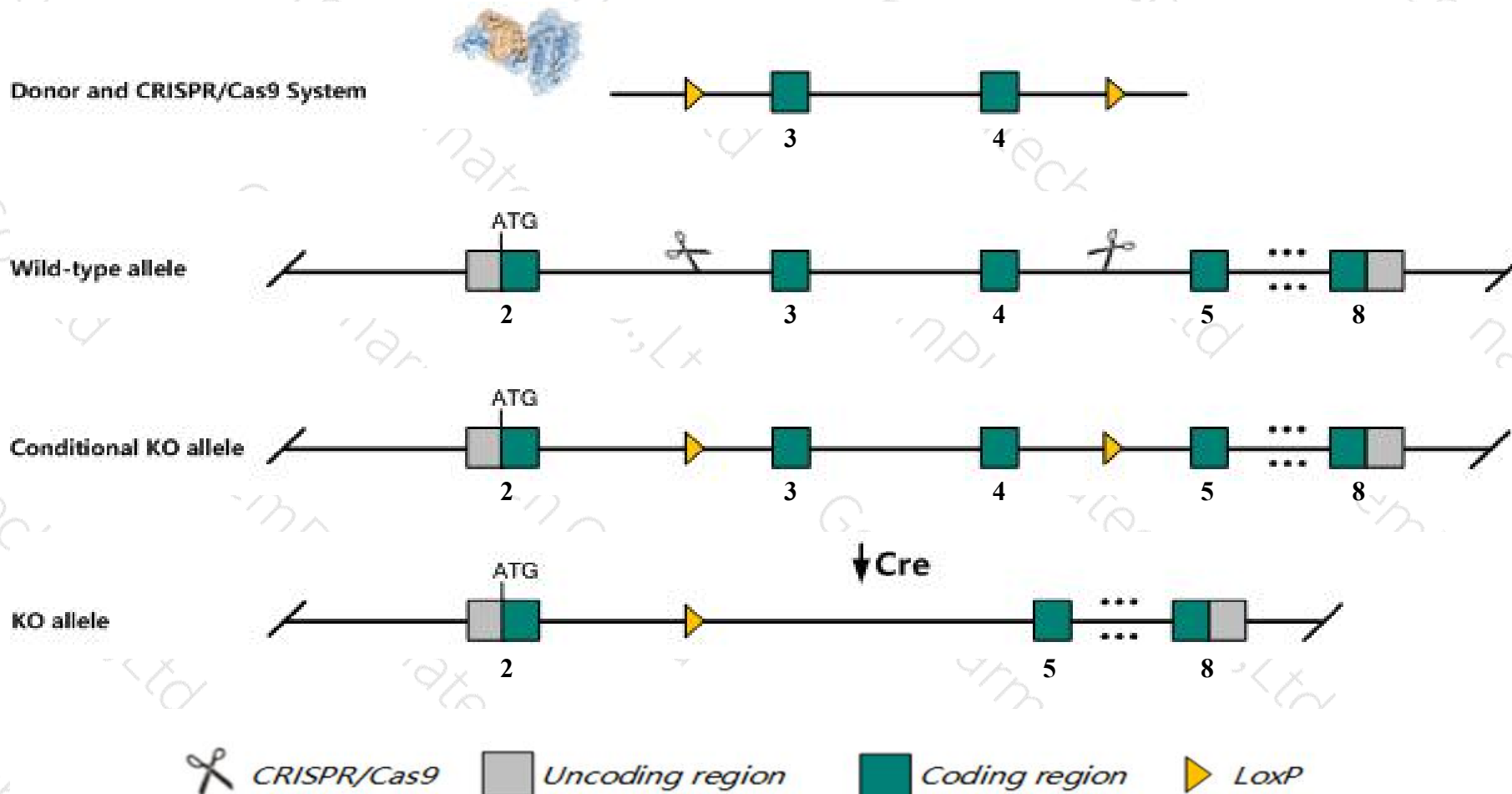
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp110* gene. The schematic diagram is as follows:



- The *Zfp110* gene has 5 transcripts. According to the structure of *Zfp110* gene, exon3-exon4 of *Zfp110-201* (ENSMUST00000004614.14) transcript is recommended as the knockout region. The region contains 223bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp110* 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 on a C57BL/6 background die at embryonic day 12. On a strain 129 background, mutants are viable and fertile, but males are more docile and testis weight is greatly reduced. On an F2 background, 20% of homozygous pups die neonatally.
- The effect on transcripts 204 is unknown.
- The *Zfp110* gene is located on the Chr7. 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)

Zfp110 zinc finger protein 110 [*Mus musculus* (house mouse)]

Gene ID: 65020, updated on 24-Oct-2019

Summary

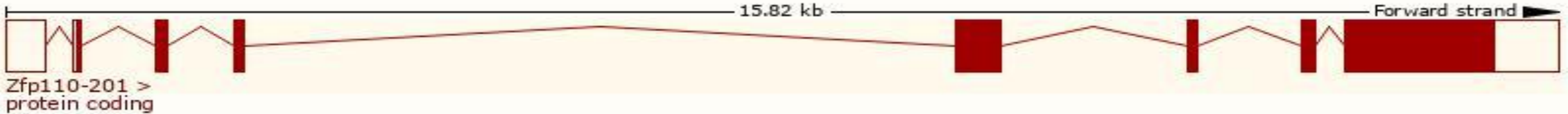
Official Symbol	Zfp110 provided by MGI
Official Full Name	zinc finger protein 110 provided by MGI
Primary source	MGI:MGI:1890378
See related	Ensembl:ENSMUSG00000058638
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	NRIF; Nrif1; N28112; 2900024E01Rik
Expression	Ubiquitous expression in testis adult (RPKM 14.6), bladder adult (RPKM 7.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

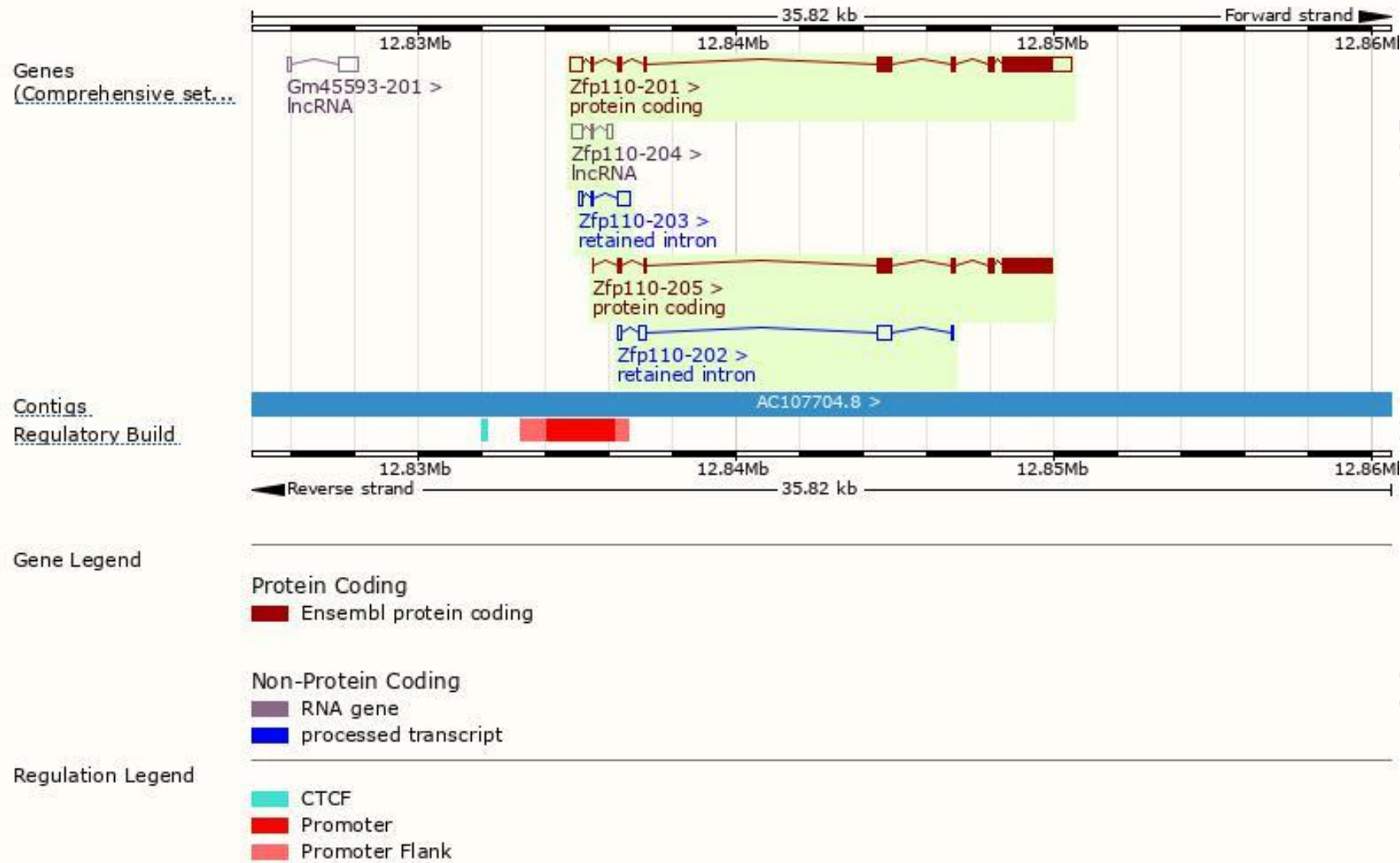
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp110-201	ENSMUST00000004614.14	3591	832aa	Protein coding	CCDS20814	A0A0R4J249	TSL:1 GENCODE basic APPRIS P1
Zfp110-205	ENSMUST00000168247.1	2499	832aa	Protein coding	CCDS20814	A0A0R4J249	TSL:5 GENCODE basic APPRIS P1
Zfp110-202	ENSMUST00000137718.2	828	No protein	Retained intron	-	-	TSL:5
Zfp110-203	ENSMUST00000148041.1	603	No protein	Retained intron	-	-	TSL:2
Zfp110-204	ENSMUST00000154011.7	570	No protein	lncRNA	-	-	TSL:3

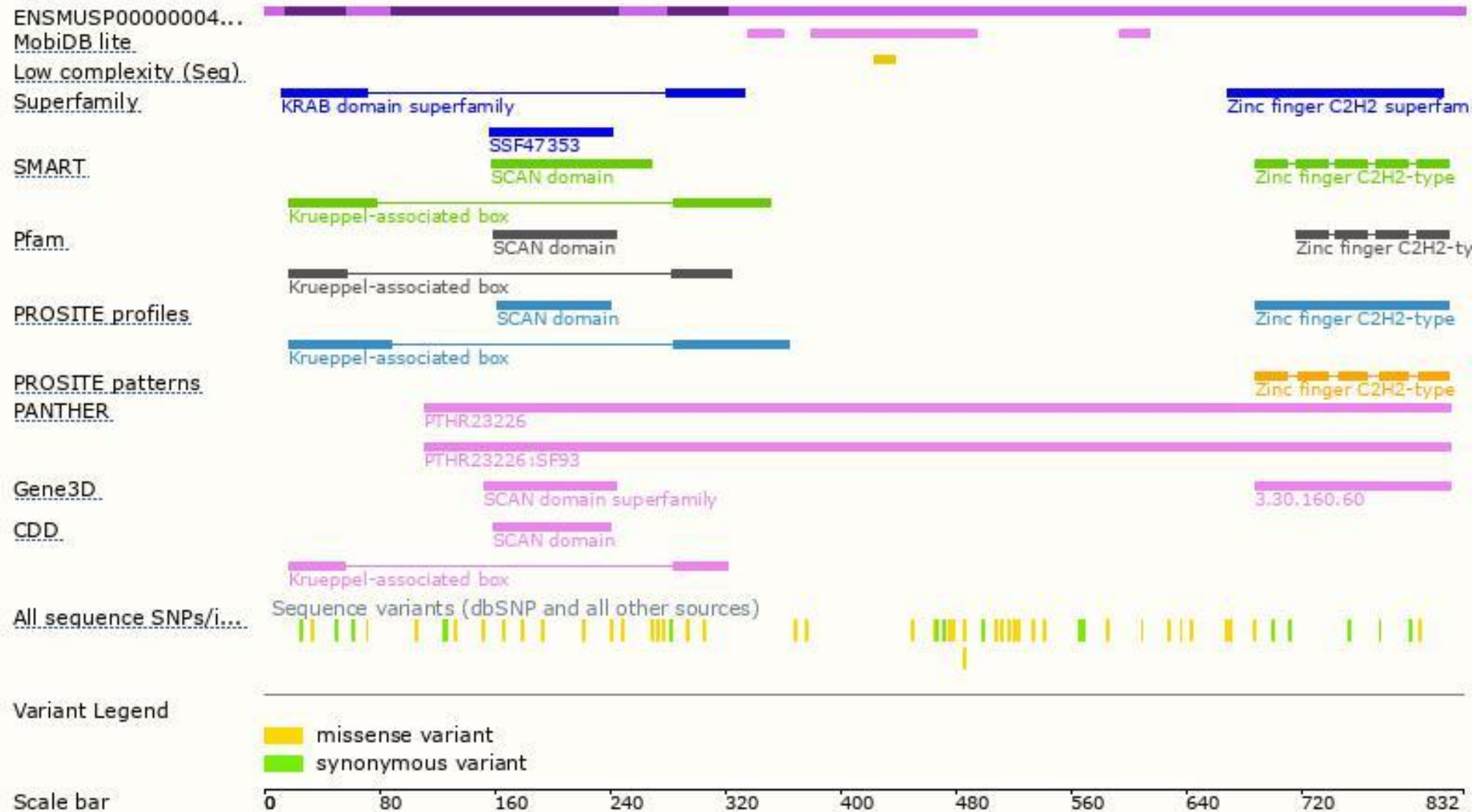
The strategy is based on the design of *Zfp110-201* transcript,The transcription is shown below



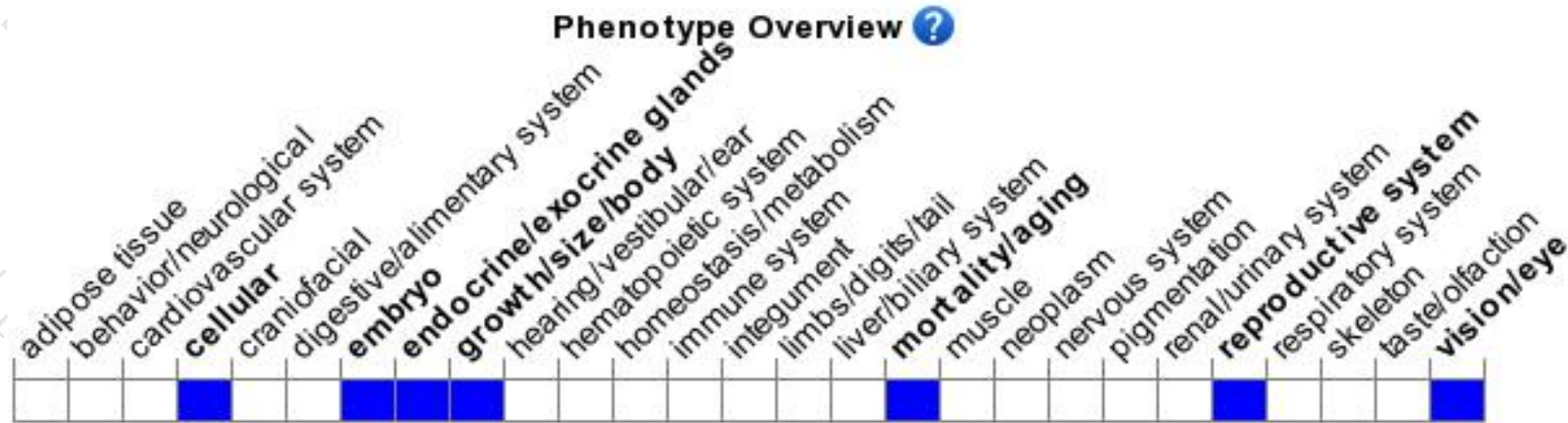
Genomic location distribution



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 on a C57BL/6 background die at embryonic day 12. On a strain 129 background, mutants are viable and fertile, but males are more docile and testis weight is greatly reduced. On an F2 background, 20% of homozygous pups die neonatally.

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

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