

Mzf1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Mzf1

Project type

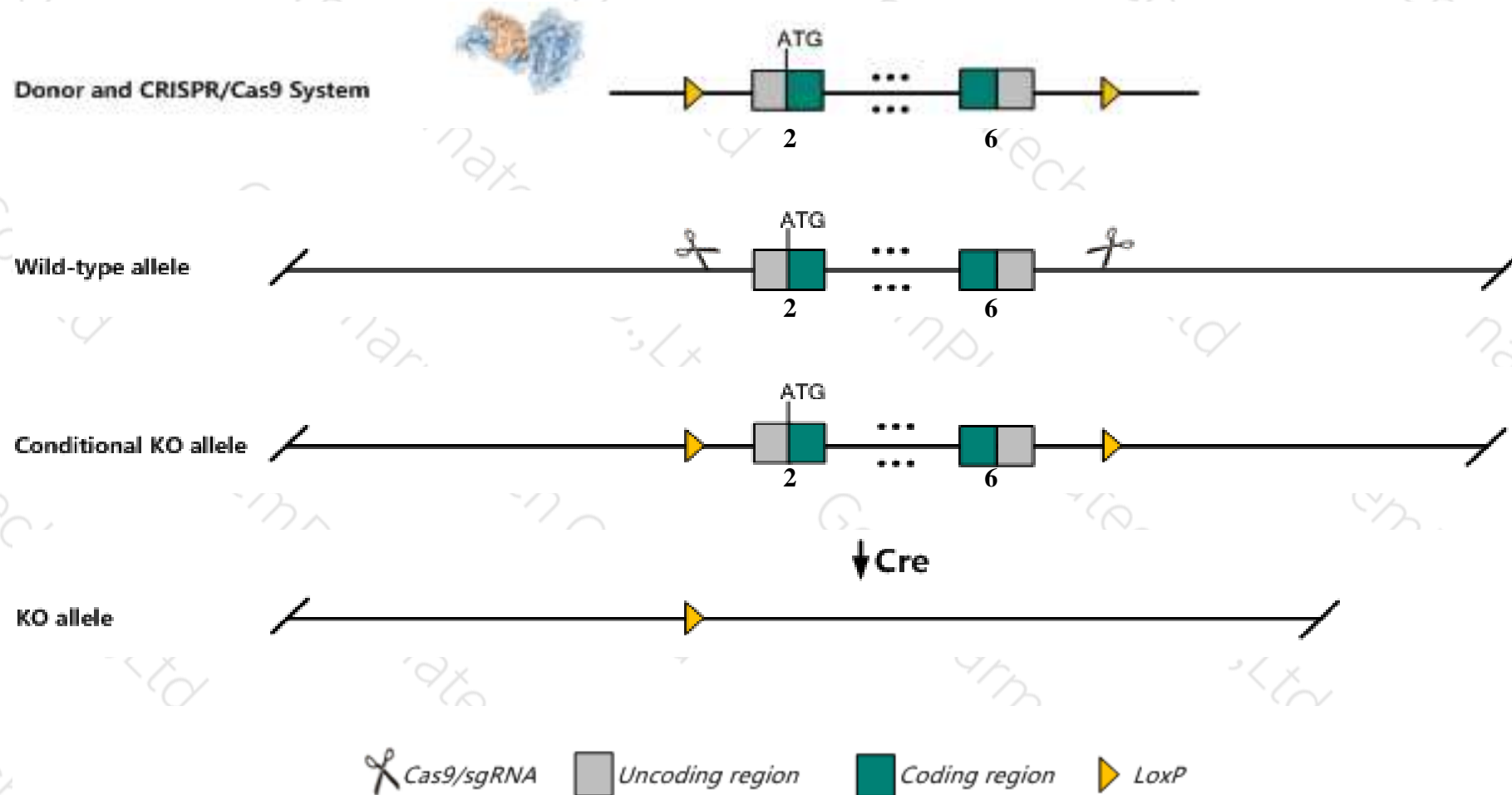
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mzf1* gene. The schematic diagram is as follows:



- The *Mzf1* gene has 7 transcripts. According to the structure of *Mzf1* gene, exon2-exon6 of *Mzf1*-205 (ENSMUST00000182515.7) 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 *Mzf1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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 are prone to late-onset (>2 yr) neoplasias characterized by infiltration, enlargement and disruption of the liver by monomorphic cells of myeloid origin; hemopoietic progenitors show increased ability to sustain long-term hemopoiesis.
- The *Mzf1* is close to 5'UTR region of *Chmp2a* and *Ube2m* gene. Knockout the region may affect the function of *Chmp2a* and *Ube2m* gene.
- The *Mzf1* 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)

Mzf1 myeloid zinc finger 1 [*Mus musculus* (house mouse)]

Gene ID: 109889, updated on 12-Aug-2019

Summary

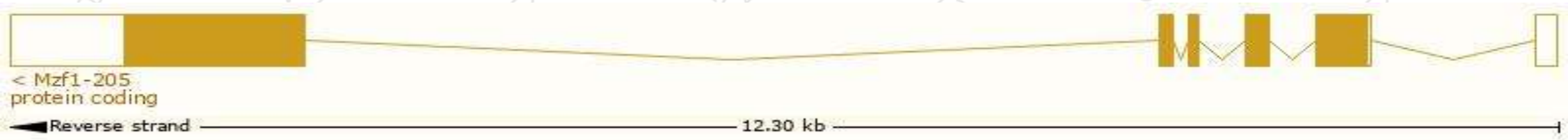
Official Symbol	Mzf1 provided by MGI
Official Full Name	myeloid zinc finger 1 provided by MGI
Primary source	MGI:MGI:107457
See related	Ensembl:ENSMUSG00000030380
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mzf2; Mzf-2; Zfp98; Znf42; Zfp121
Expression	Ubiquitous expression in adrenal adult (RPKM 1.8), frontal lobe adult (RPKM 1.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

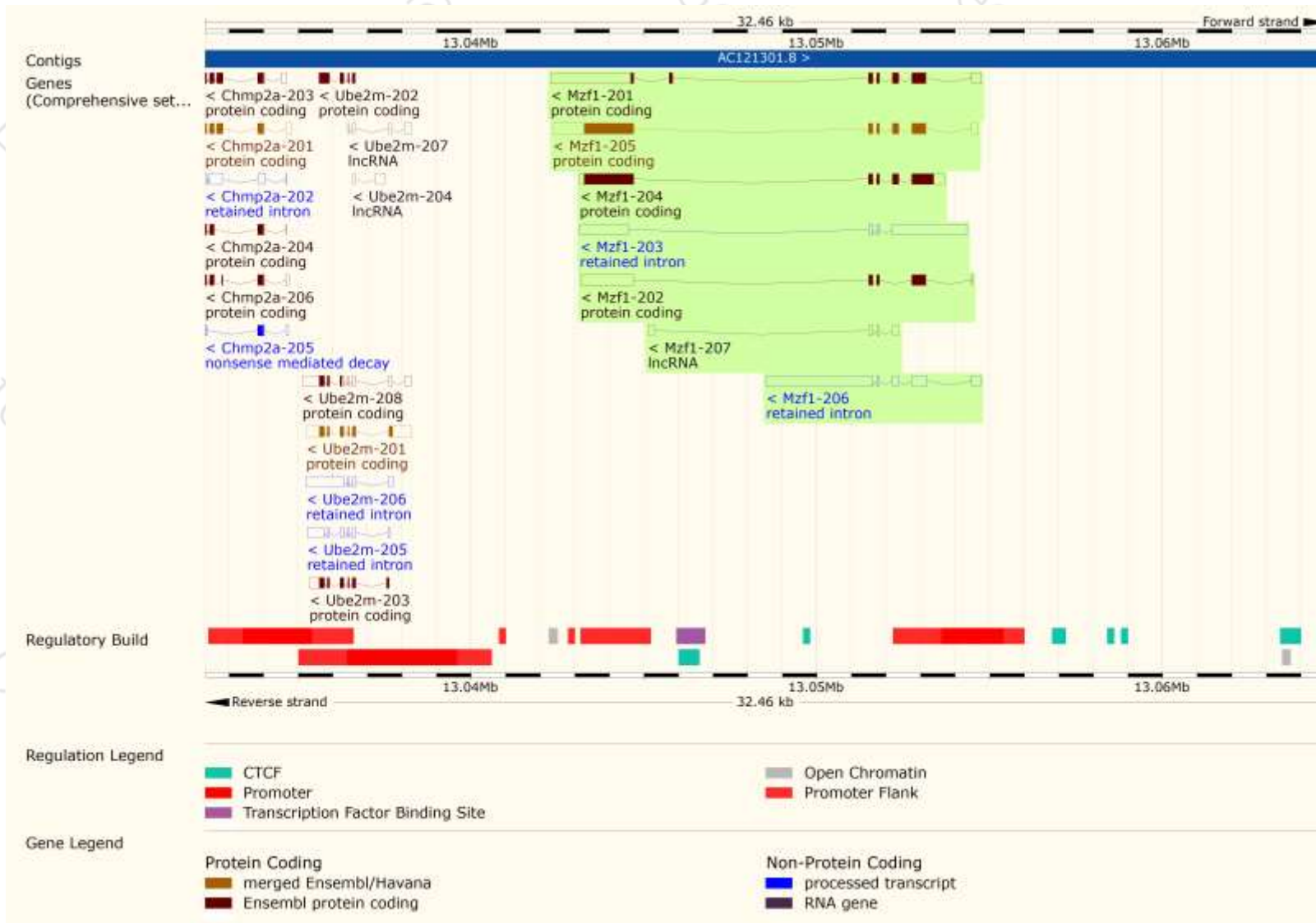
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mzf1-205	ENSMUST00000182515.7	3340	735aa	Protein coding	CCDS20826	A1L358	TSL:1 GENCODE basic APPRIS P2
Mzf1-201	ENSMUST00000069289.14	3597	320aa	Protein coding	-	F6VC78	TSL:1 GENCODE basic
Mzf1-204	ENSMUST00000182490.1	2872	814aa	Protein coding	-	S4R1L6	TSL:1 GENCODE basic APPRIS ALT2
Mzf1-202	ENSMUST00000182087.1	2197	190aa	Protein coding	-	S4R1C2	TSL:1 GENCODE basic
Mzf1-207	ENSMUST00000210727.1	578	No protein	Processed transcript	-	-	TSL:5
Mzf1-206	ENSMUST00000183176.1	4015	No protein	Retained intron	-	-	TSL:1
Mzf1-203	ENSMUST00000182293.7	3749	No protein	Retained intron	-	-	TSL:1

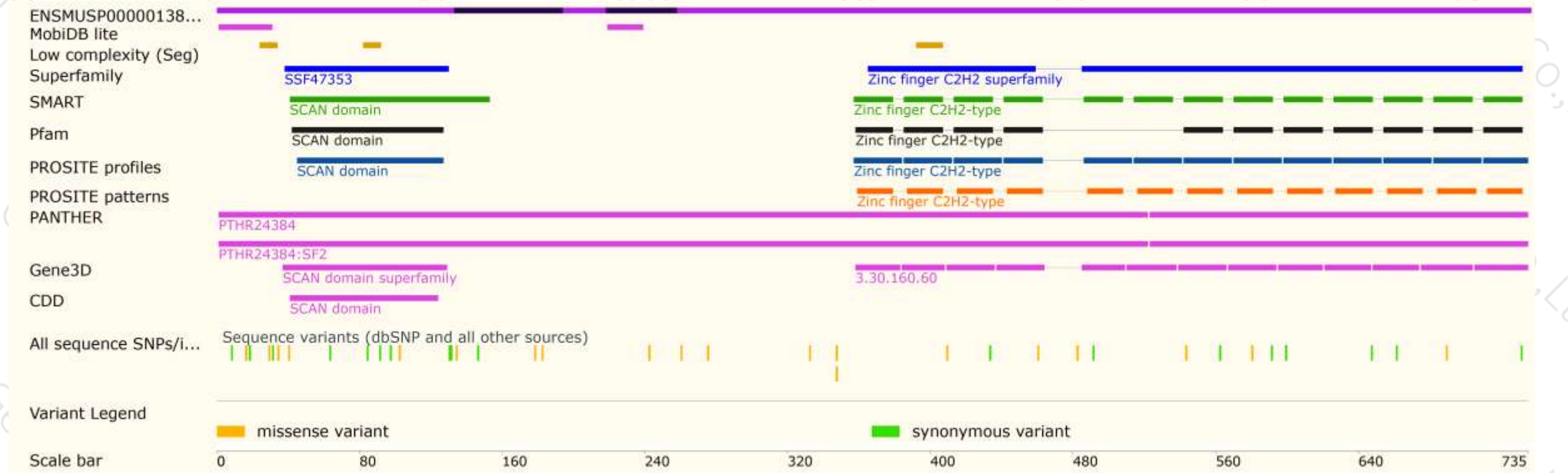
The strategy is based on the design of *Mzf1-205* transcript,The transcription is shown below



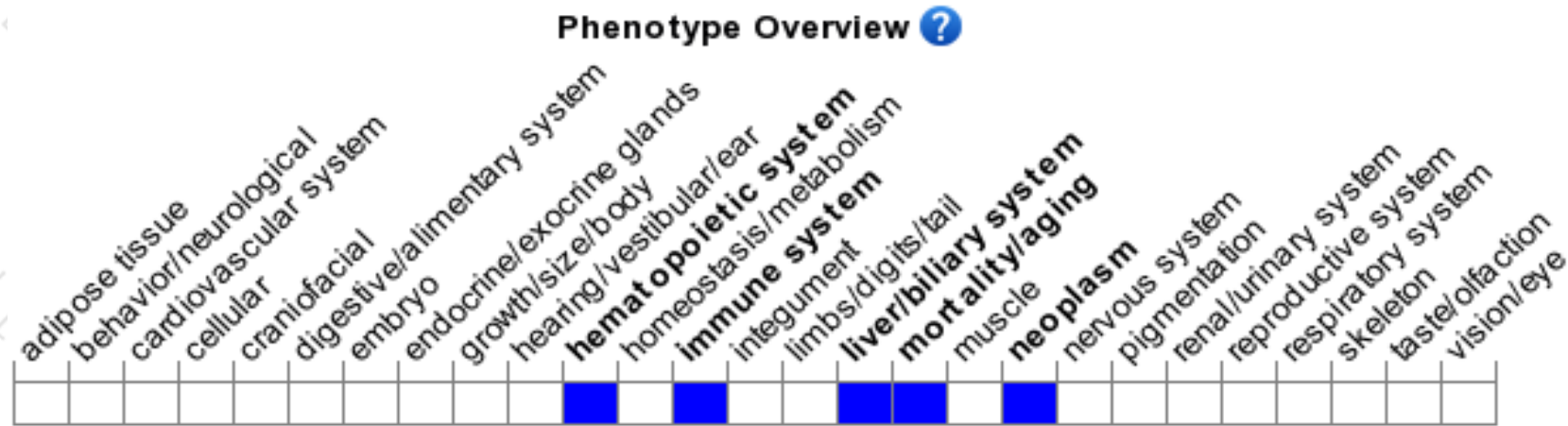
Genomic location distribution



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 are prone to late-onset (>2 yr) neoplasias characterized by infiltration, enlargement and disruption of the liver by monomorphic cells of myeloid origin; hemopoietic progenitors show increased ability to sustain long-term hemopoiesis.

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

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