

Mta1 Cas9-CKO Strategy

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Project Overview

Project Name

Mta1

Project type

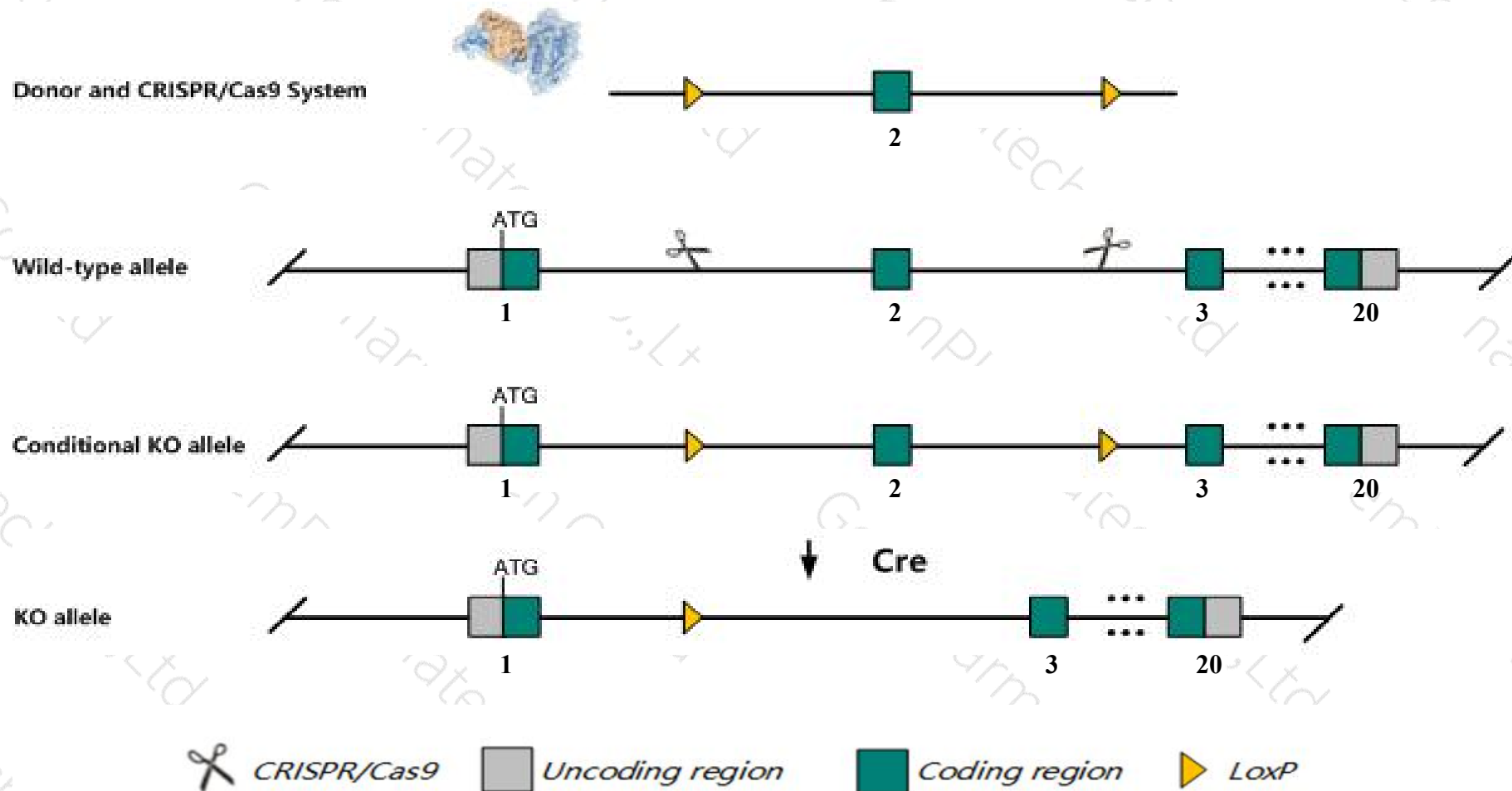
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Mtal* gene has 8 transcripts. According to the structure of *Mtal* gene, exon2 of *Mtal*-205 (ENSMUST00000109727.8) transcript is recommended as the knockout region. The region contains 68bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mtal* 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 increased cellular sensitivity to ionizing radiation and increased retinal cell proliferation at E14.5.
- The *Mtal* gene is located on the Chr12. 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)

Mta1 metastasis associated 1 [*Mus musculus* (house mouse)]

Gene ID: 116870, updated on 8-Dec-2019

Summary

Official Symbol	Mta1 provided by MGI
Official Full Name	metastasis associated 1 provided by MGI
Primary source	MGI:MGI:2150037
See related	Ensembl:ENSMUSG00000021144
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
Expression	Ubiquitous expression in ovary adult (RPKM 62.3), adrenal adult (RPKM 52.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

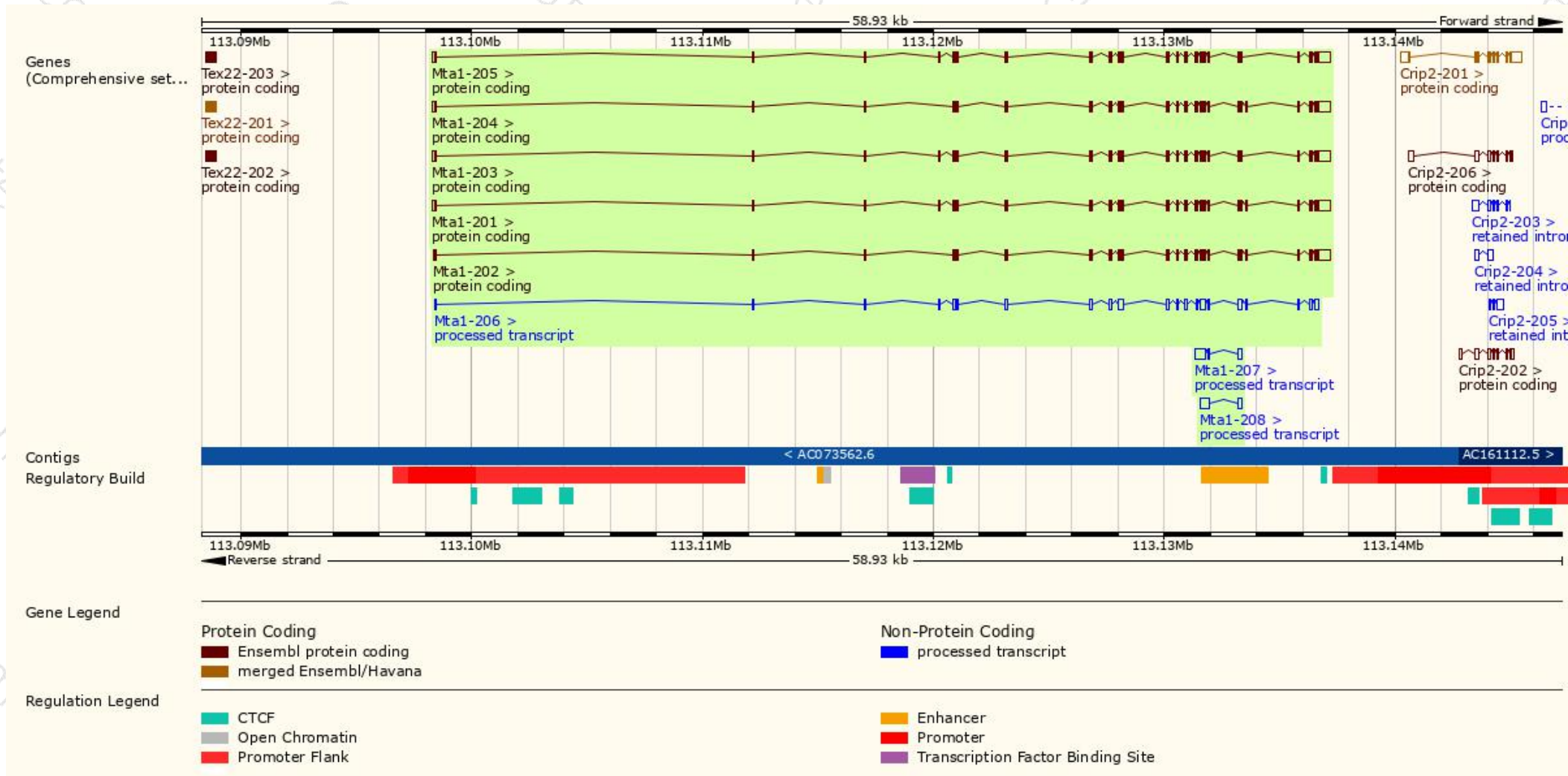
The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mta1-205	ENSMUST00000109727.8	2789	703aa	Protein coding	CCDS84004	E9PX23	TSL:1 GENCODE basic
Mta1-204	ENSMUST00000109726.7	2775	698aa	Protein coding	CCDS36574	F8WHY8	TSL:1 GENCODE basic APPRIS P2
Mta1-201	ENSMUST0000009099.12	2826	715aa	Protein coding	-	M1VHG1 Q8K4B0	TSL:5 GENCODE basic APPRIS ALT2
Mta1-203	ENSMUST00000109723.7	2790	703aa	Protein coding	-	E9PX23	TSL:5 GENCODE basic
Mta1-202	ENSMUST00000069690.4	2697	698aa	Protein coding	-	F8WHY8	TSL:5 GENCODE basic APPRIS ALT2
Mta1-206	ENSMUST00000130926.7	2119	No protein	Processed transcript	-	-	TSL:5
Mta1-207	ENSMUST00000134488.1	717	No protein	Processed transcript	-	-	TSL:3
Mta1-208	ENSMUST00000156030.1	584	No protein	Processed transcript	-	-	TSL:3

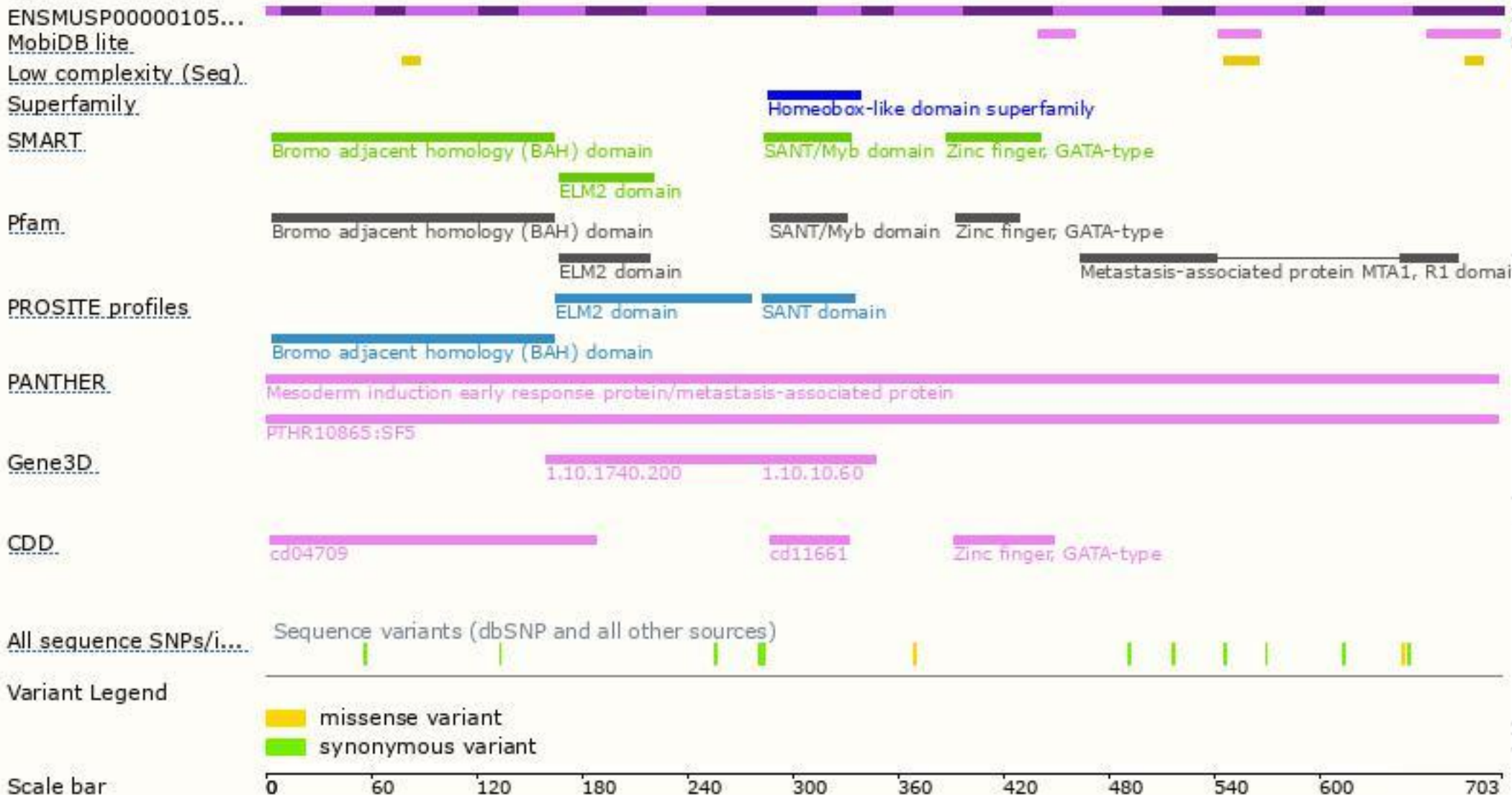
The strategy is based on the design of *Mta1-205* transcript, the transcription is shown below:



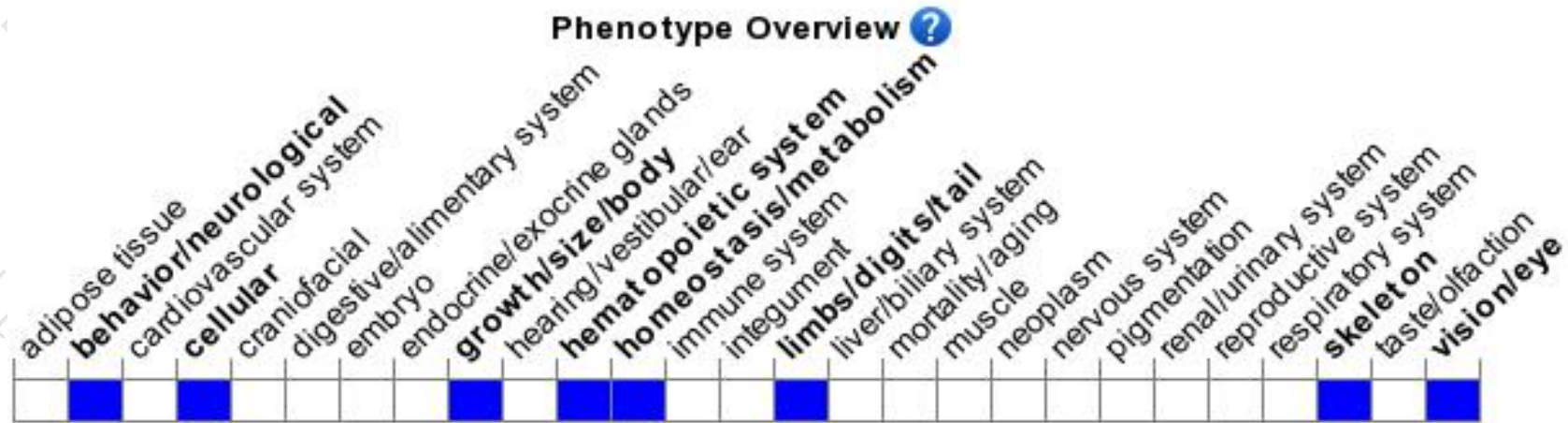
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit increased cellular sensitivity to ionizing radiation and increased retinal cell proliferation at E14.5.

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

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