

Meis1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Meis1

Project type

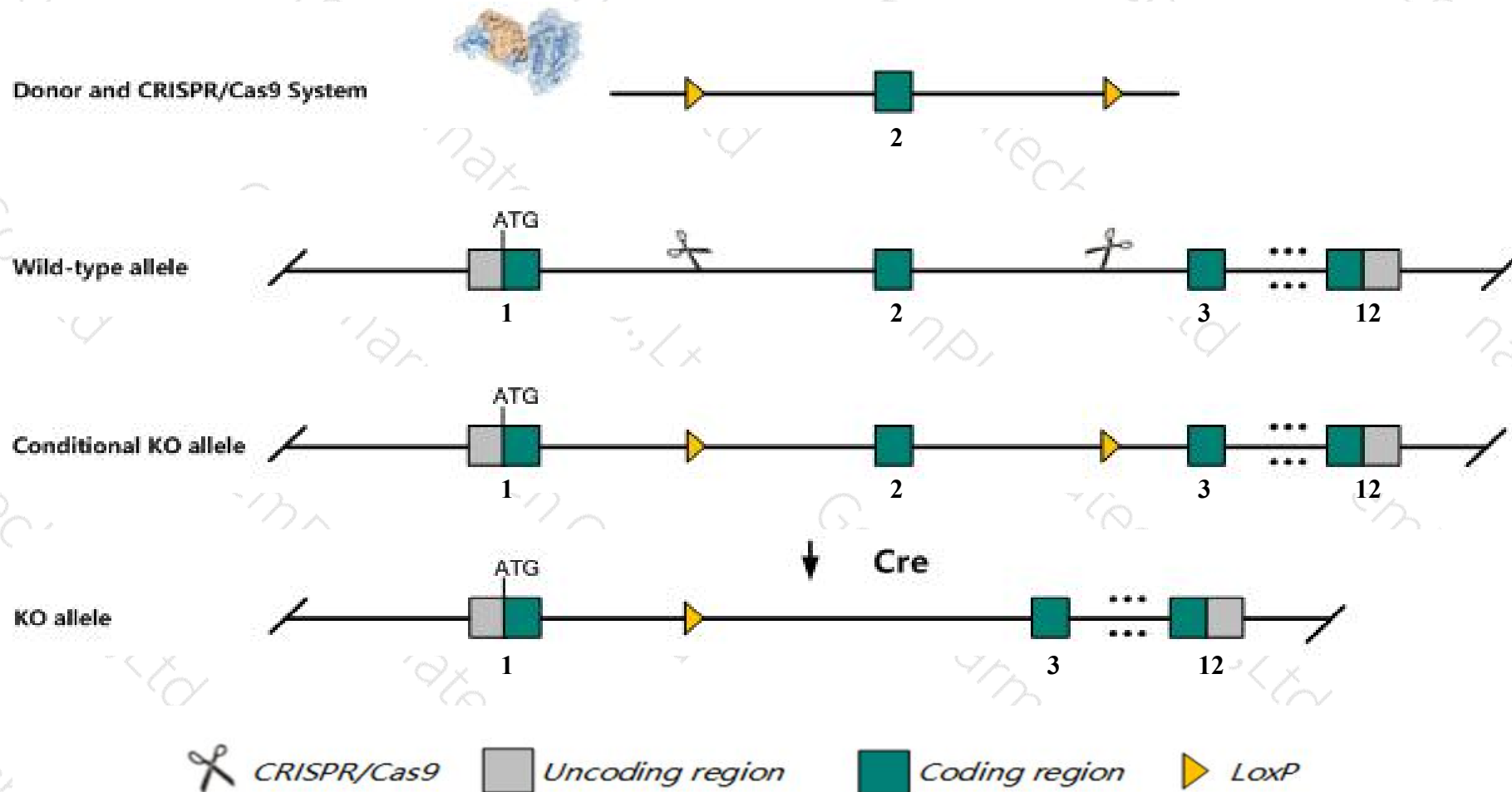
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Meis1* gene. The schematic diagram is as follows:



- The *Meis1* gene has 9 transcripts. According to the structure of *Meis1* gene, exon2 of *Meis1*-209 (ENSMUST00000185131.7) transcript is recommended as the knockout region. The region contains 227bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Meis1* 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 mutant mice die during gestation and exhibit eye, vasculature, and hematopoietic defects. Mice homozygous for a conditional allele activated in HSCs exhibit altered bone marrow cell development, altered HSC physiology and increased reactive oxygen species production.
- The *Meis1* gene is located on the Chr11. 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)

Meis1 Meis homeobox 1 [Mus musculus (house mouse)]

Gene ID: 17268, updated on 24-Feb-2019

Summary



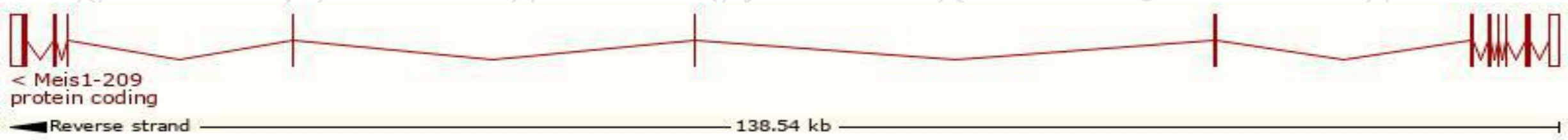
Official Symbol	Meis1 provided by MGI
Official Full Name	Meis homeobox 1 provided by MGI
Primary source	MGI:MGI:104717
See related	Ensembl:ENSMUSG00000020160
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C530044H18Rik, Evi8
Expression	Broad expression in bladder adult (RPKM 25.6), CNS E11.5 (RPKM 9.3) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

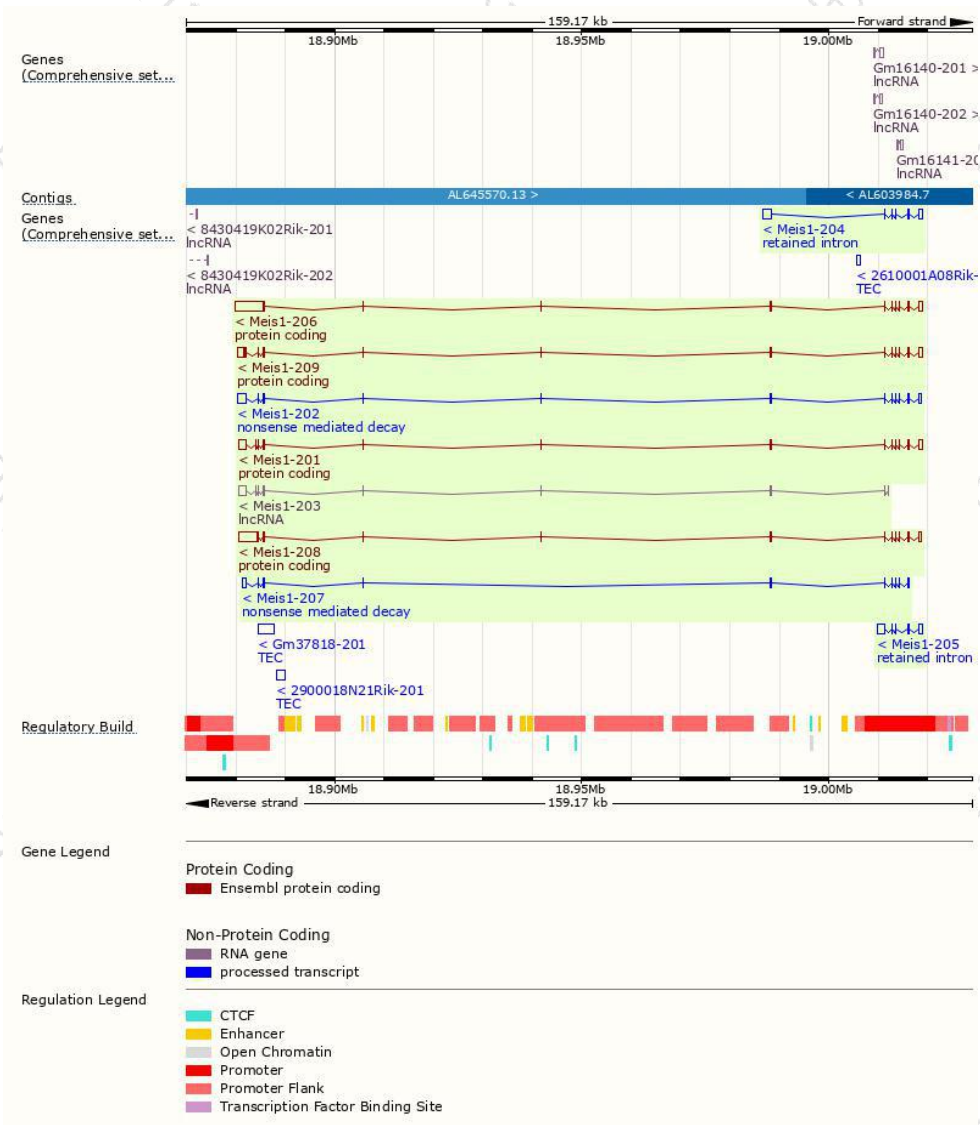
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Meis1-209	ENSMUST00000185131.7	3346	465aa	Protein coding	CCDS24453	Q60954	TSL:1 GENCODE basic APPRIS P3
Meis1-201	ENSMUST00000068264.13	3196	390aa	Protein coding	CCDS56760	Q60954	TSL:1 GENCODE basic APPRIS ALT1
Meis1-206	ENSMUST00000144988.7	7553	370aa	Protein coding	-	Q60954	TSL:2 GENCODE basic
Meis1-208	ENSMUST00000177417.7	5308	385aa	Protein coding	-	H3BLB6	TSL:5 GENCODE basic
Meis1-202	ENSMUST00000102878.10	3095	349aa	Nonsense mediated decay	-	A0A0A0MQB8	TSL:5
Meis1-207	ENSMUST00000177357.3	1530	225aa	Nonsense mediated decay	-	V9GXB5	CDS 5' incomplete TSL:5
Meis1-204	ENSMUST00000125722.7	2784	No protein	Retained intron	-	-	TSL:1
Meis1-205	ENSMUST00000137300.1	2636	No protein	Retained intron	-	-	TSL:1
Meis1-203	ENSMUST00000118661.7	2008	No protein	lncRNA	-	-	TSL:2

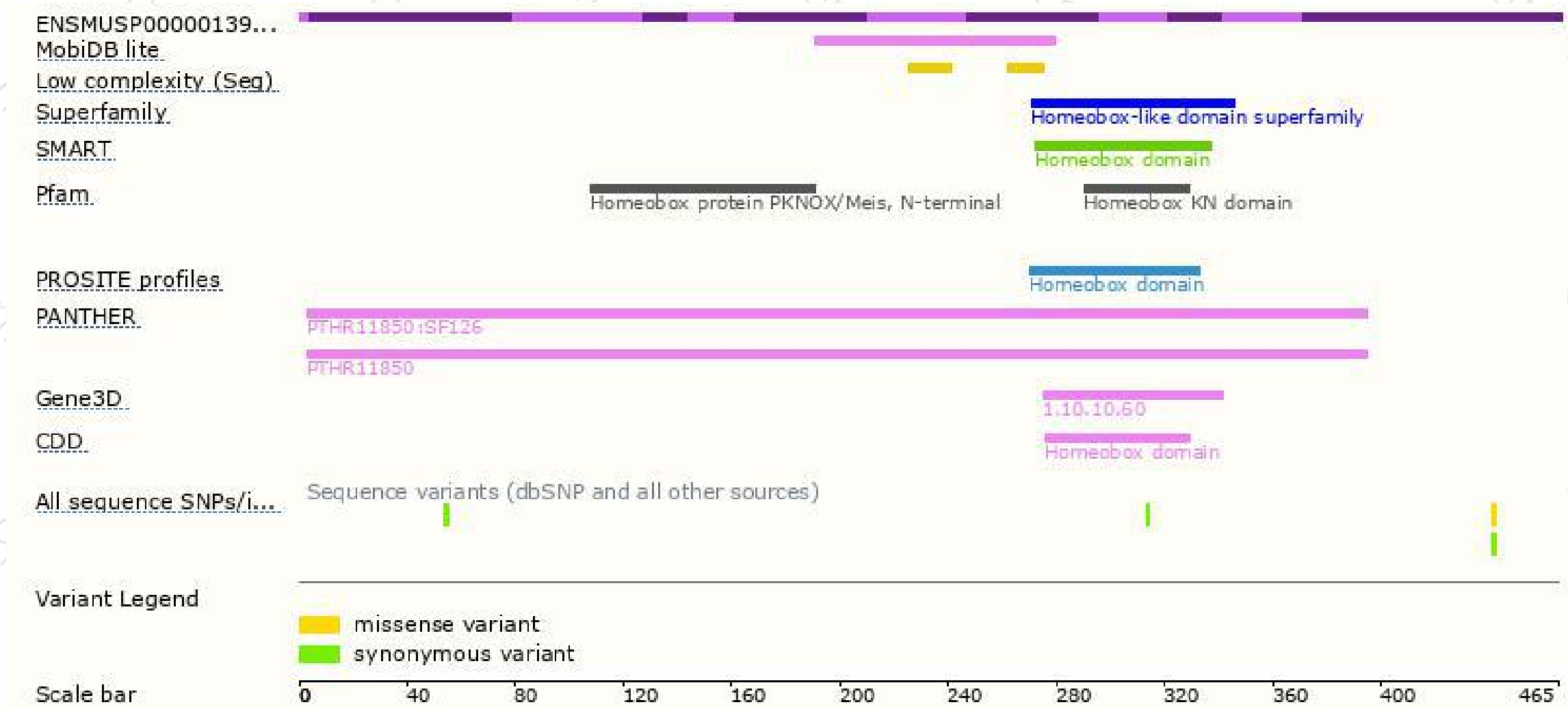
The strategy is based on the design of *Meis1-209* transcript,The transcription is shown below



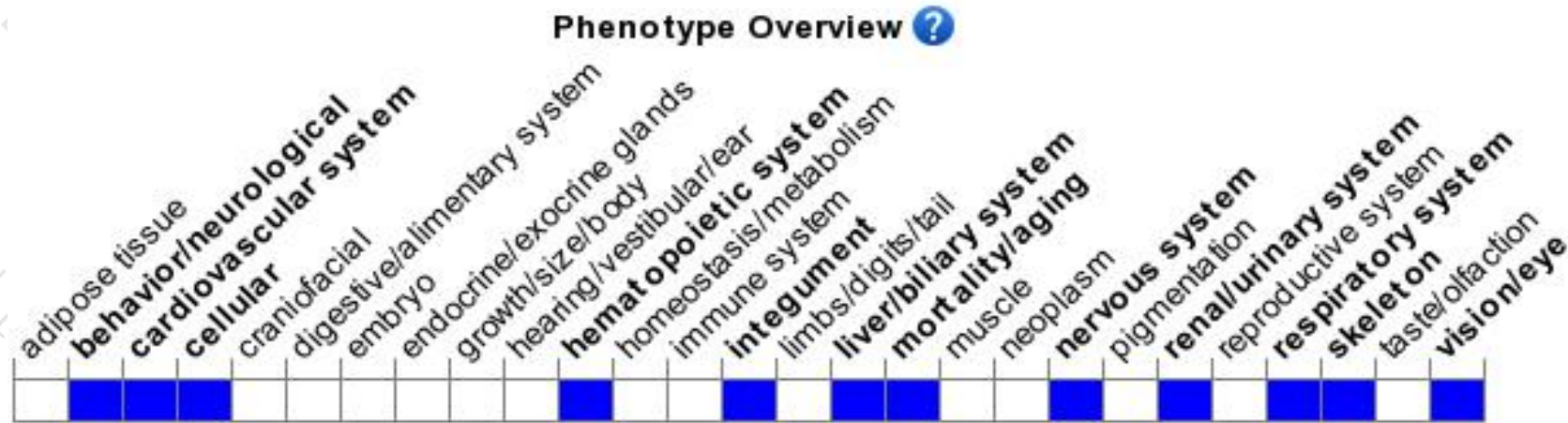
Genomic location distribution



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 mutant mice die during gestation and exhibit eye, vasculature, and hematopoietic defects. Mice homozygous for a conditional allele activated in HSCs exhibit altered bone marrow cell development, altered HSC physiology and increased reactive oxygen species production.

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

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