Sipa1 Cas9-CKO Strategy

Designer: Daohua Xu
Reviewer：   Huimin Su
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Project Overview
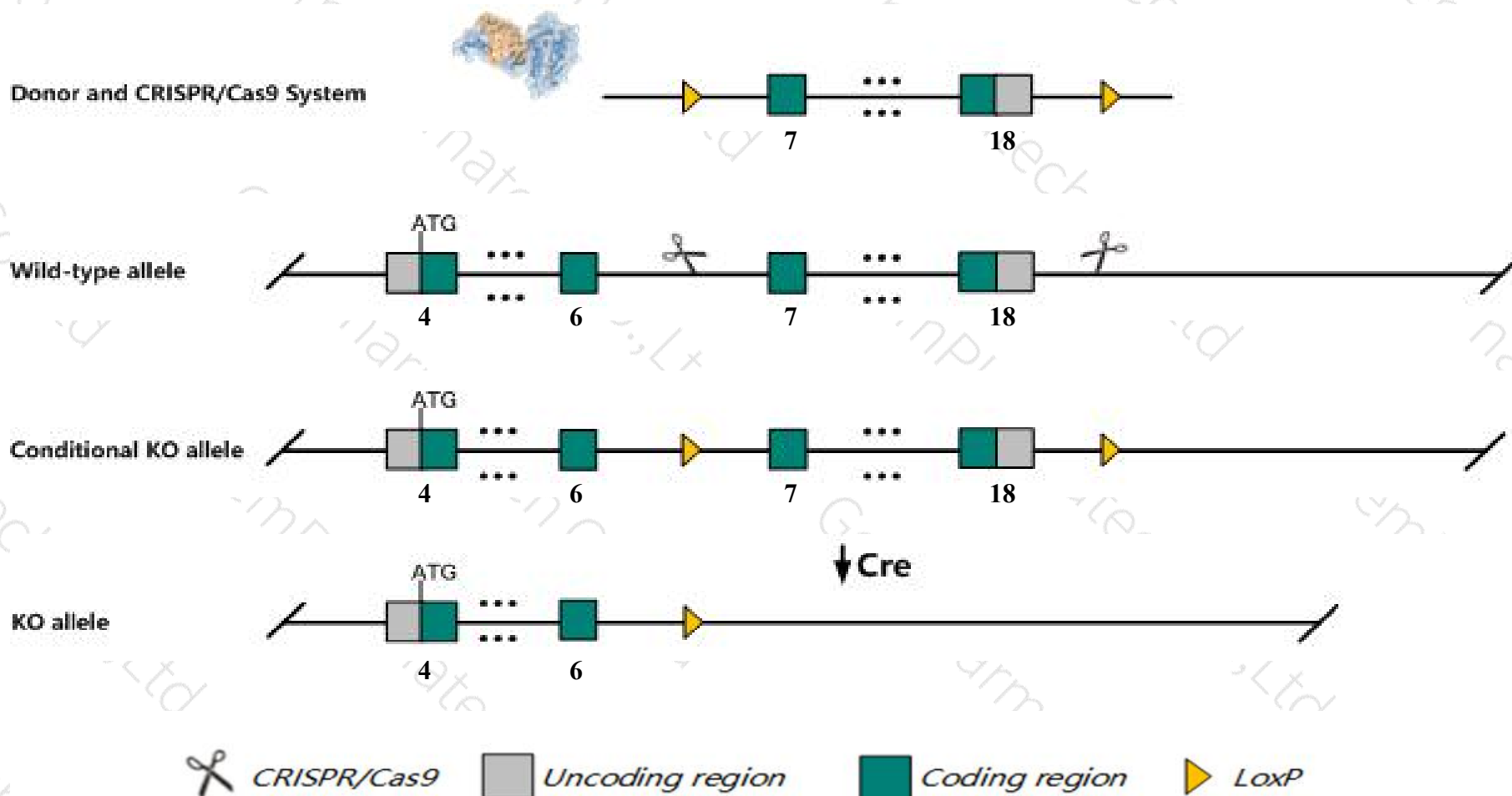
Project Name	*Sipa1*
Project type	Cas9-CKO
Strain background	C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sipa1* gene. The schematic diagram is as follows:

Technical routes

➤ The *Sipa1* gene has 13 transcripts. According to the structure of *Sipa1* gene, exon7-exon18 of *Sipa1-201* (ENSMUST00000071857.12) transcript is recommended as the knockout region.The region contains most 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 *Sipa1* 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.

Notice

➢ According to the existing MGI data,Homozygous null mice display chronic myelocytic leukemia in either the chronic phase or blast crisis.

➢ Transcript *Sipa1-210* may not be affected.

➢ The *Sipa1* gene is located on the Chr19. 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）

Sipa1 signal-induced proliferation associated gene 1 [Mus musculus (house mouse)]

Gene ID: 20469, updated on 3-Feb-2019

Summary

Official Symbol	Sipa1 provided by MGI
Official Full Name	signal-induced proliferation associated gene 1 provided by MGI
Primary source	MGI:MGI:107576
See related	Ensembl:ENSMUSG00000056917
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	Spa1
Expression	Broad expression in spleen adult (RPKM 156.5), thymus adult (RPKM 70.0) and 18 other tissuesSee more
Orthologs	human all

The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sipa1-201	ENSMUST00000071857.12	3812	1038aa	Protein coding	CCDS29474	E9Q0Y4	TSL:1 GENCODE basic APPRIS P1
Sipa1-202	ENSMUST00000080824.12	3741	1038aa	Protein coding	CCDS29474	E9Q0Y4	TSL:1 GENCODE basic APPRIS P1
Sipa1-203	ENSMUST00000164304.8	3584	1038aa	Protein coding	CCDS29474	E9Q0Y4	TSL:1 GENCODE basic APPRIS P1
Sipa1-204	ENSMUST00000169854.1	3583	1038aa	Protein coding	CCDS29474	E9Q0Y4	TSL:5 GENCODE basic APPRIS P1
Sipa1-205	ENSMUST00000236006.1	3513	1038aa	Protein coding	CCDS29474	-	GENCODE basic APPRIS P1
Sipa1-211	ENSMUST00000237874.1	3456	1038aa	Protein coding	CCDS29474	-	GENCODE basic APPRIS P1
Sipa1-207	ENSMUST00000236464.1	2801	693aa	Protein coding	-	Q3V403	GENCODE basic
Sipa1-210	ENSMUST00000237544.1	388	34aa	Protein coding	-	-	CDS 3' incomplete
Sipa1-208	ENSMUST00000236486.1	2893	No protein	Retained intron	-	-	
Sipa1-206	ENSMUST00000236332.1	245	No protein	Retained intron	-	-	
Sipa1-213	ENSMUST00000238092.1	679	No protein	lncRNA	-	-	
Sipa1-212	ENSMUST00000238020.1	470	No protein	lncRNA	-	-	
Sipa1-209	ENSMUST00000236827.1	143	No protein	lncRNA	-	-	

The strategy is based on the design of *Sipa1-201* transcript,The transcription is shown below

< Sipa1-201
protein coding

◄ Reverse strand   12.47 kb
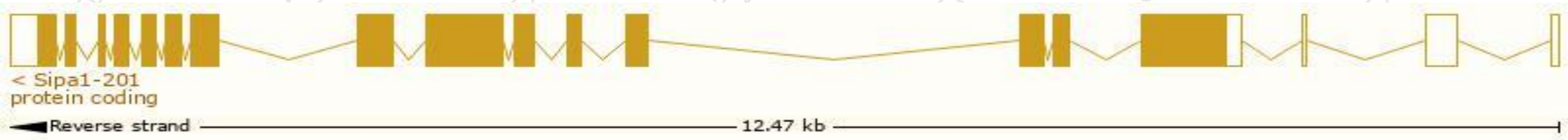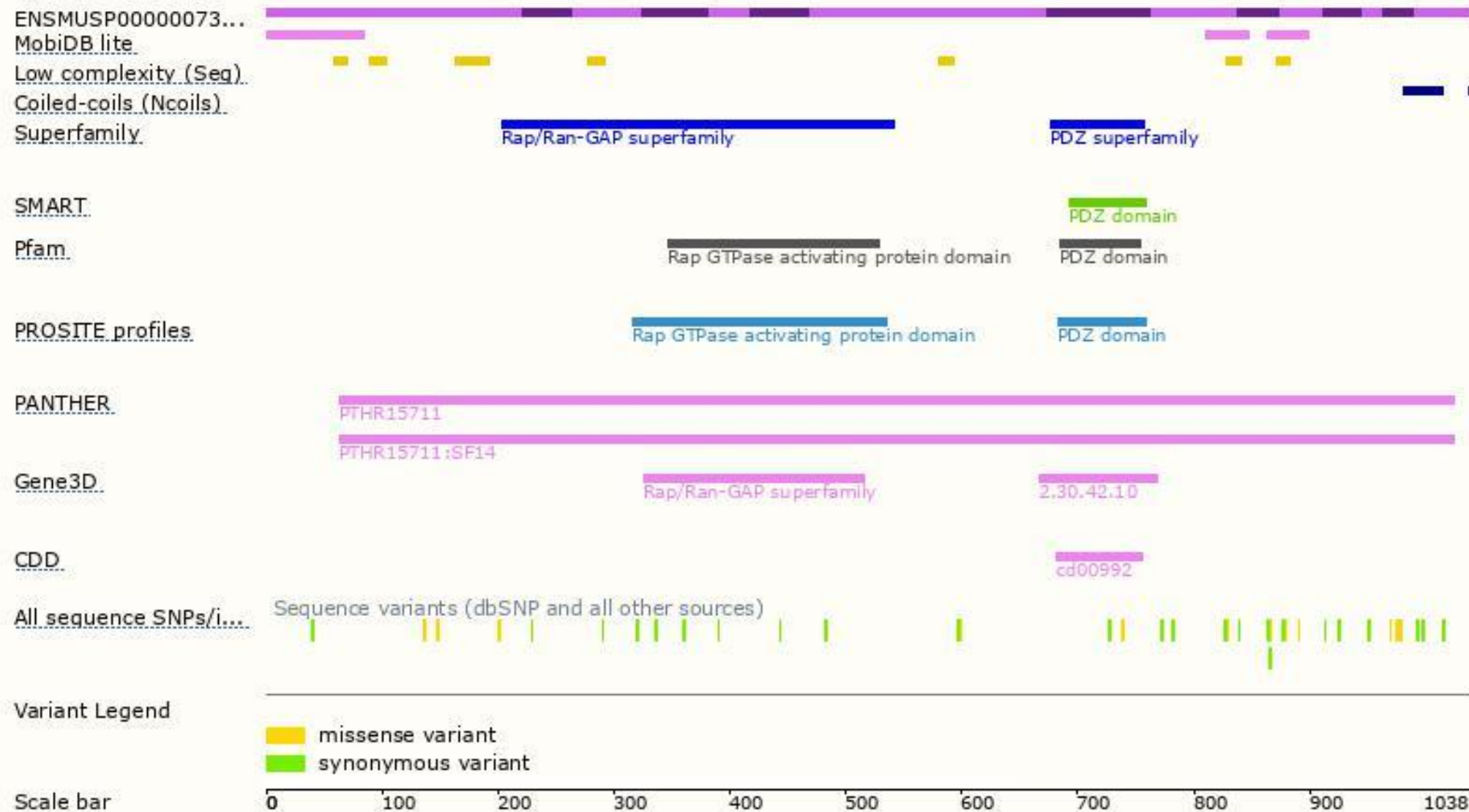
Genomic location distribution
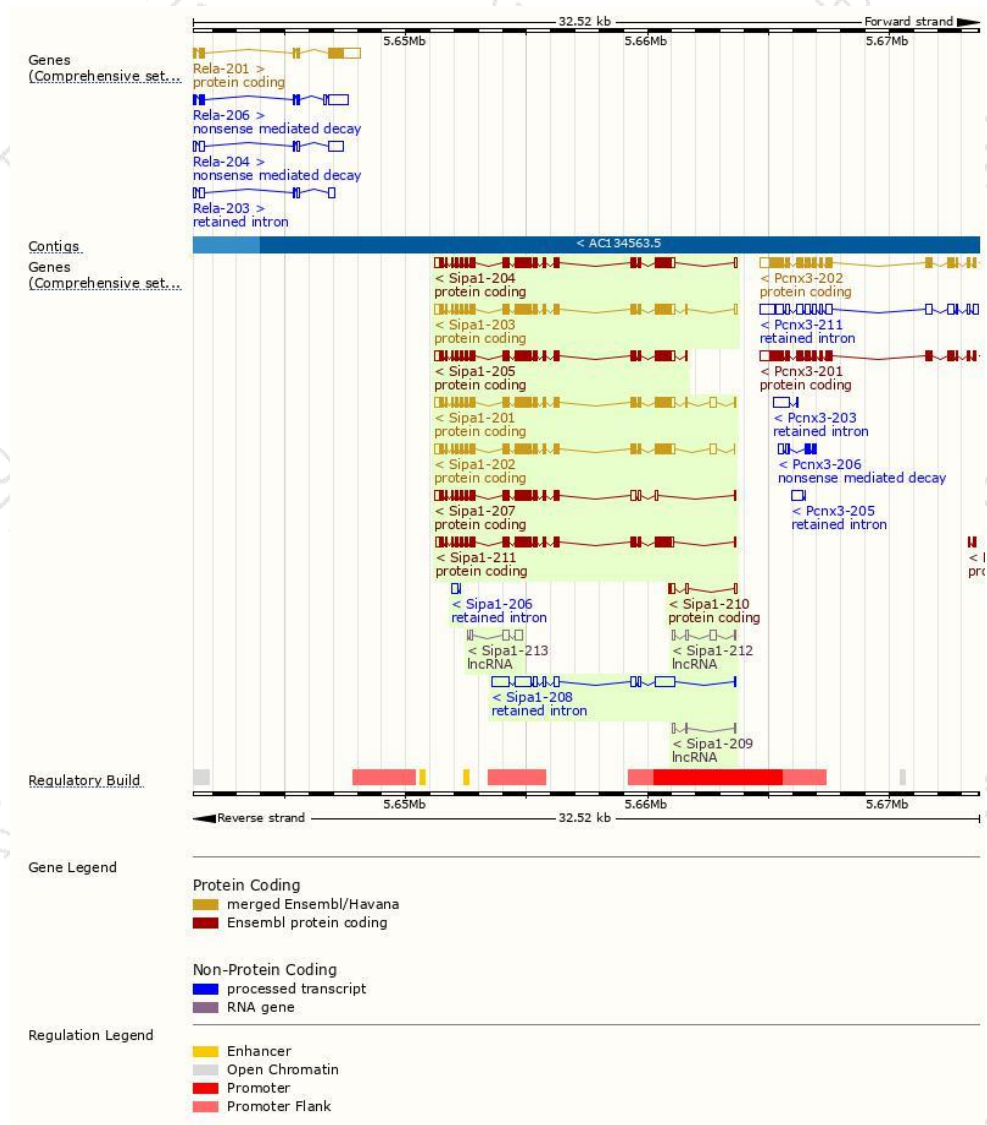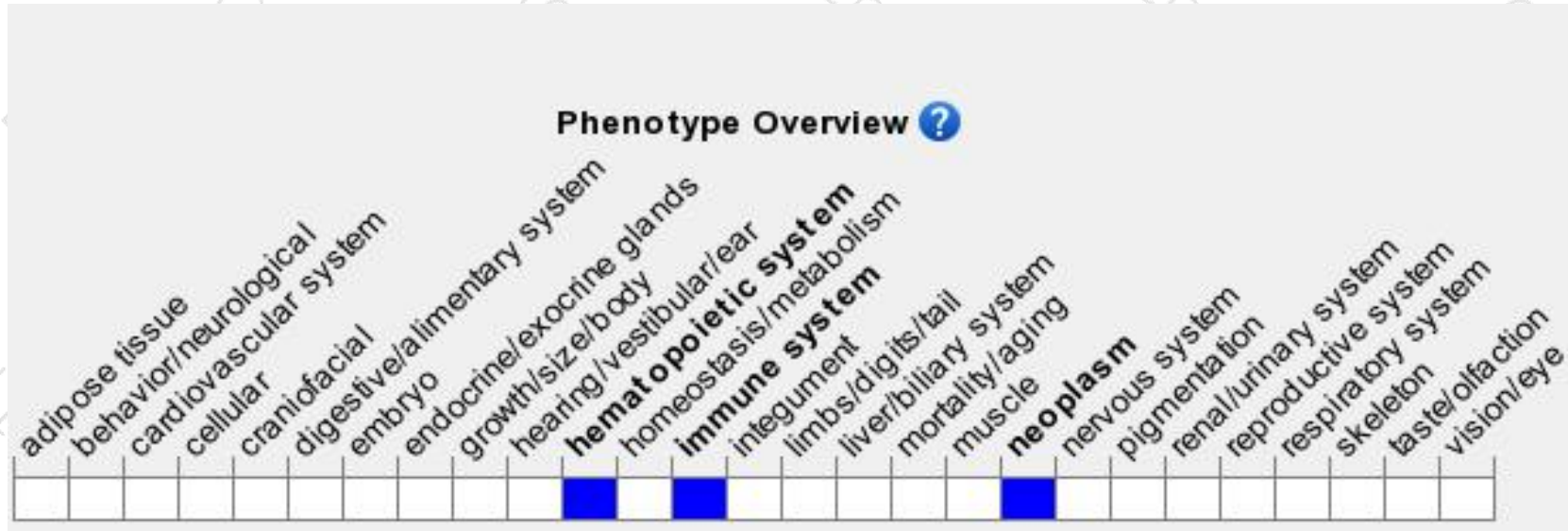
Protein domain

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 null mice display chronic myelocytic leukemia in either the chronic phase or blast crisis.

If you have any questions, you are welcome to inquire.
Tel: 400-9660890