

Mxd1 Cas9-KO Strategy

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Project Overview

Project Name

Mxd1

Project type

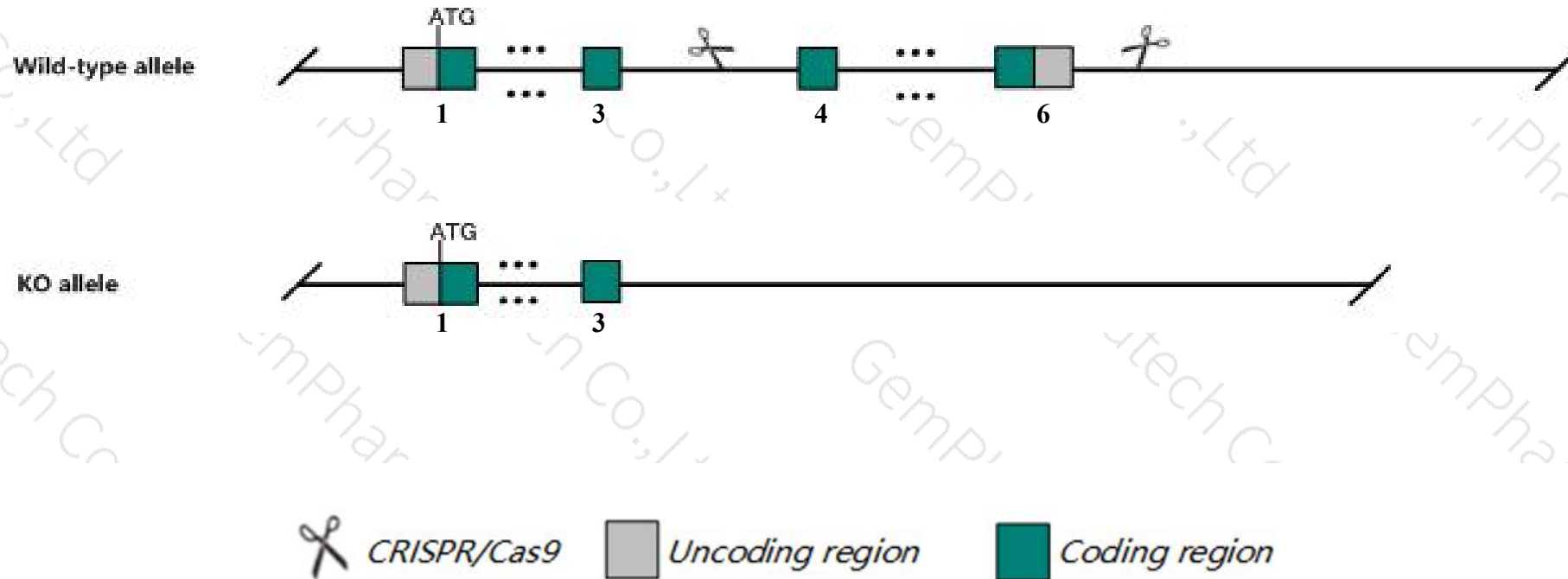
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mxd1* gene. The schematic diagram is as follows:



- The *Mxd1* gene has 4 transcripts. According to the structure of *Mxd1* gene, exon4-exon6 of *Mxd1-201* (ENSMUST00000001184.9) transcript is recommended as the knockout region. The region contains 484bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mxd1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit altered myelopoiesis, increased proliferative potential of bone marrow granulocytic precursors, increased sensitivity of myeloid cells to apoptosis-inducing stimuli, and inhibited cell cycle withdrawal during a late stage of granulocyte differentiation.
- The *Mxd1* gene is located on the Chr6. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Mxd1 MAX dimerization protein 1 [Mus musculus (house mouse)]

Gene ID: 17119, updated on 5-Mar-2019

Summary



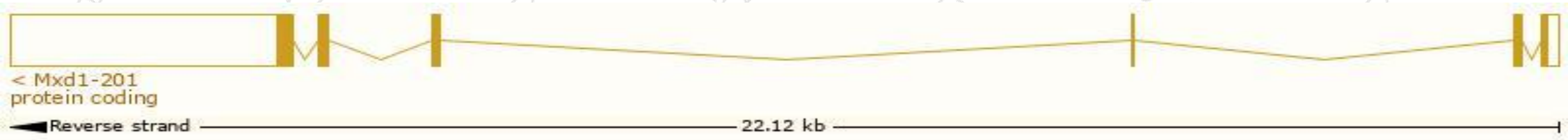
Official Symbol	Mxd1 provided by MGI
Official Full Name	MAX dimerization protein 1 provided by MGI
Primary source	MGI:MGI:96908
See related	Ensembl:ENSMUSG00000001156
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW122478, Mad, Mad1
Expression	Broad expression in small intestine adult (RPKM 105.0), colon adult (RPKM 95.6) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

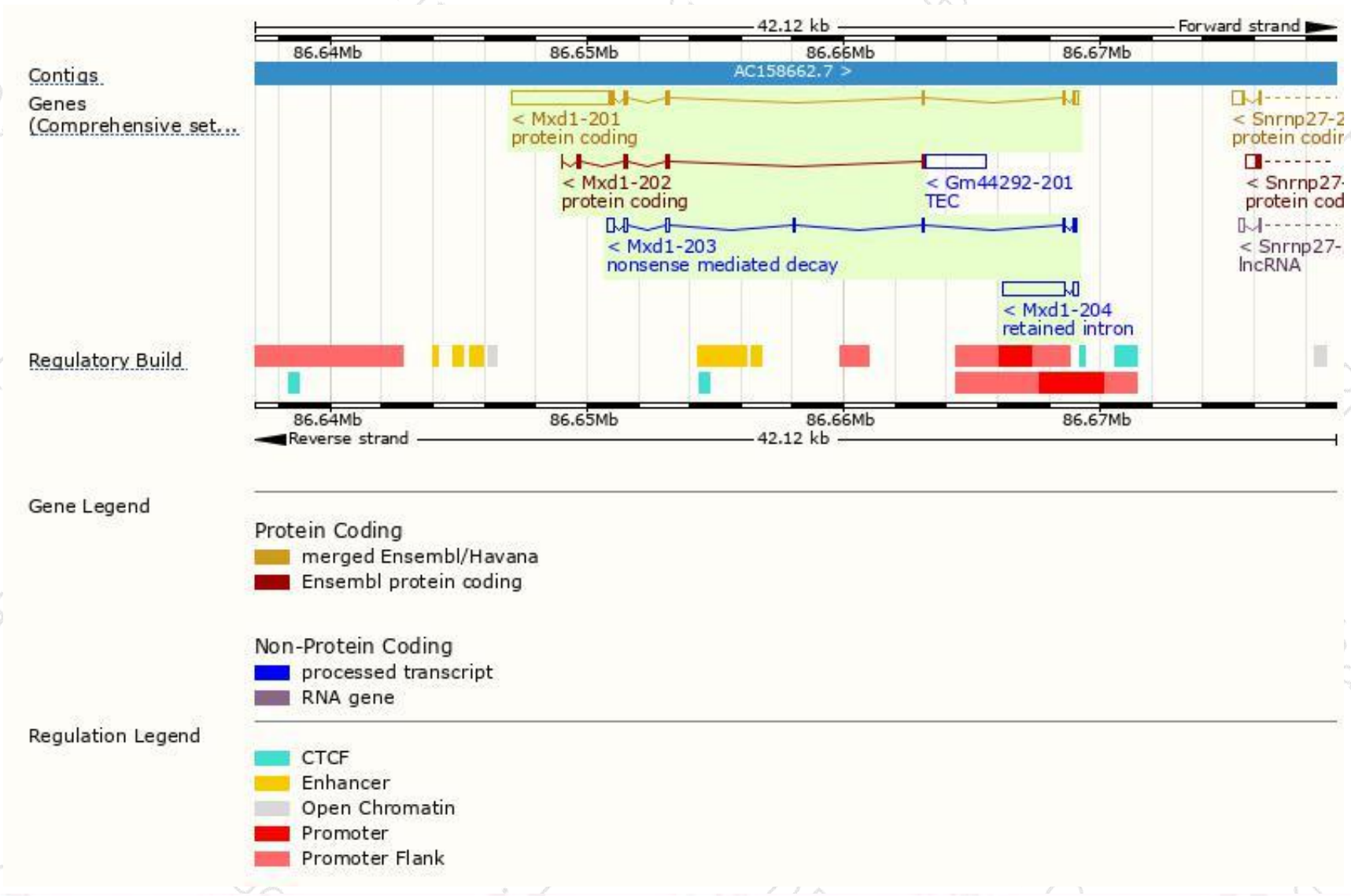
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mxd1-201	ENSMUST00000001184.9	4666	227aa	Protein coding	CCDS51835	Q8K1Z8	TSL:1 GENCODE basic APPRIS P1
Mxd1-202	ENSMUST00000203946.1	418	121aa	Protein coding	-	A0A0N4SVF6	CDS 5' incomplete TSL:5
Mxd1-203	ENSMUST00000204437.1	912	75aa	Nonsense mediated decay	-	A0A0N4SW68	TSL:3
Mxd1-204	ENSMUST00000205076.1	2615	No protein	Retained intron	-	-	TSL:1

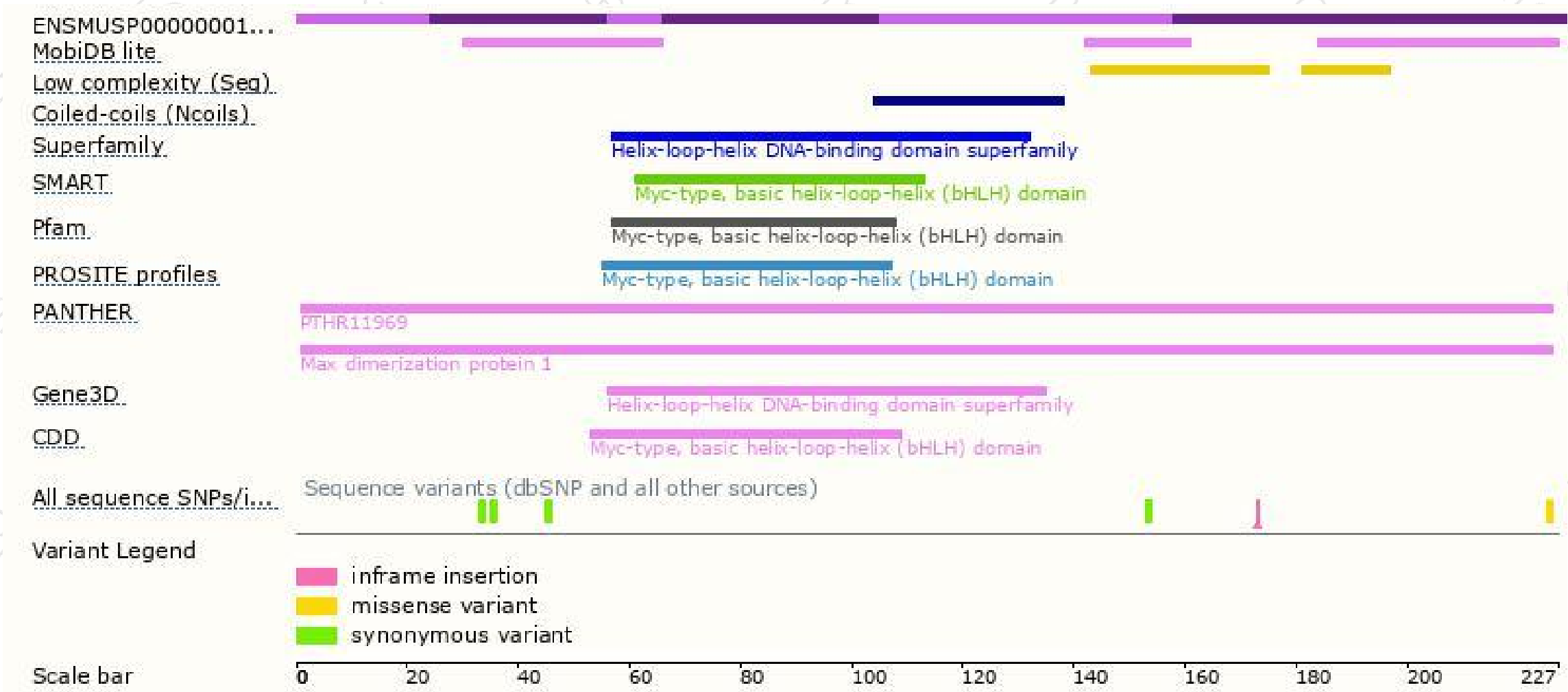
The strategy is based on the design of *Mxd1-201* transcript,The transcription is shown below



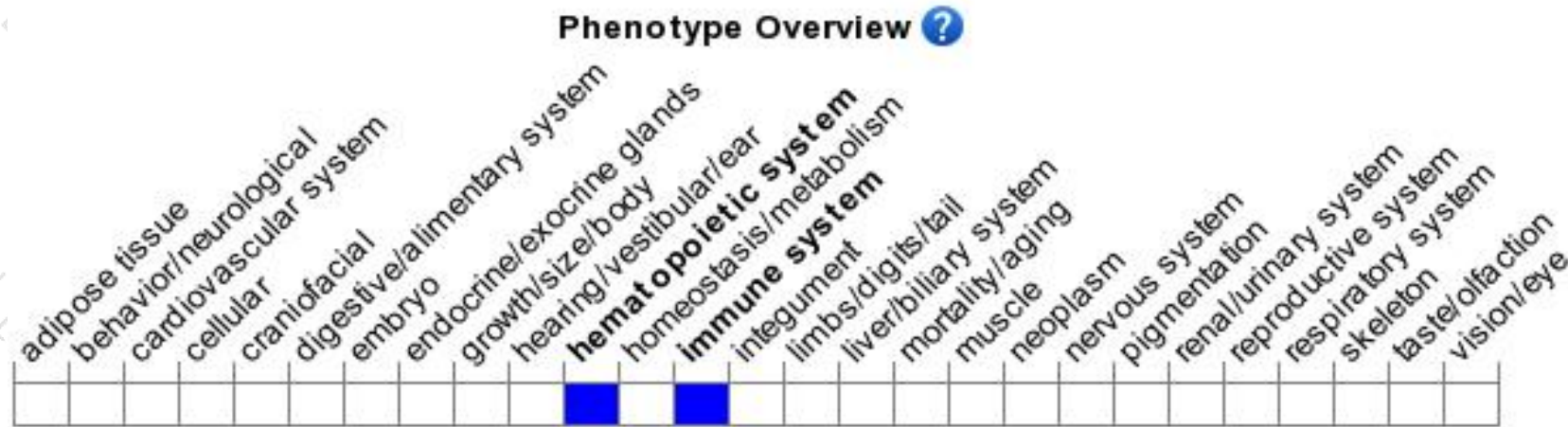
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit altered myelopoiesis, increased proliferative potential of bone marrow granulocytic precursors, increased sensitivity of myeloid cells to apoptosis-inducing stimuli, and inhibited cell cycle withdrawal during a late stage of granulocyte differentiation.

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

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