

Bst1 Cas9-KO Strategy

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Project Overview

Project Name

Bst1

Project type

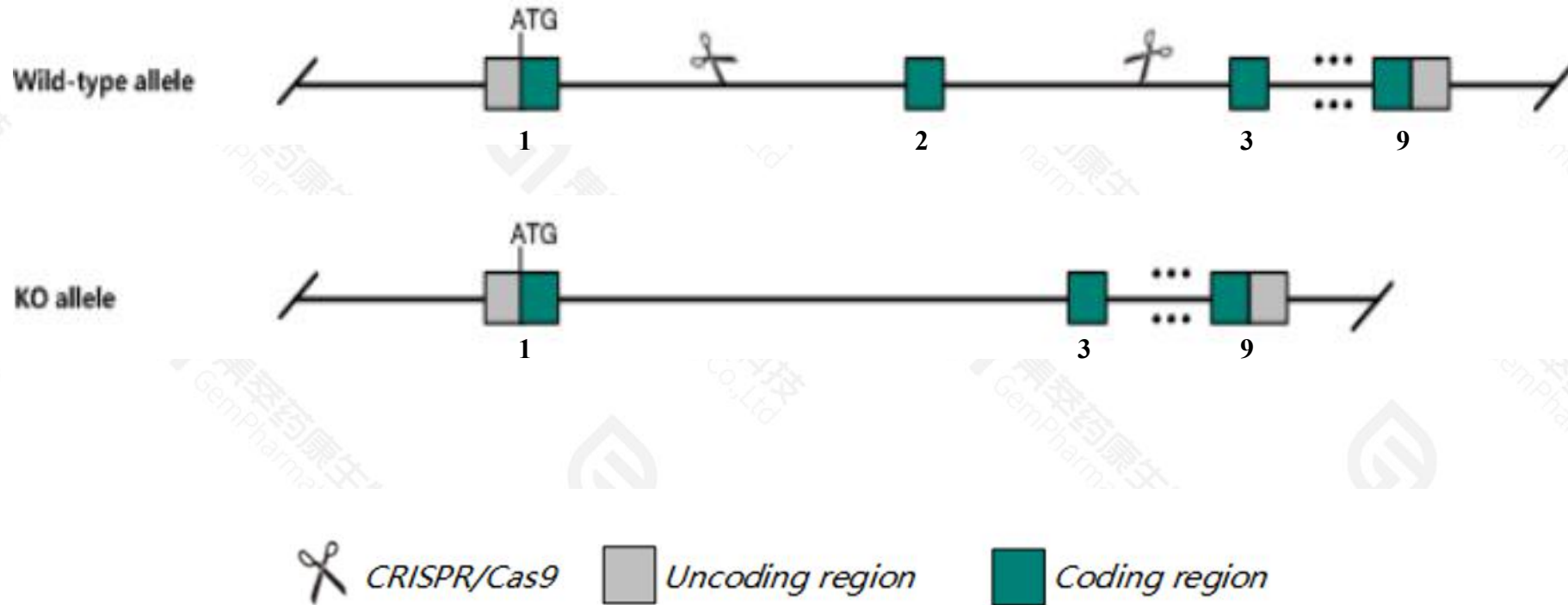
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bst1* gene. The schematic diagram is as follows:



- The *Bst1* gene has 4 transcripts. According to the structure of *Bst1* gene, exon2 of *Bst1-201*(ENSMUST00000101237.8) transcript is recommended as the knockout region. The region contains 127bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bst1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mice show delayed peritoneal B-1 cell development and a rise in CD38.
- The KO region contains partial intron of the *Fbxl5* gene. Knockout the region may affect the function of *Fbxl5* gene.
- The *Bst1* gene is located on the Chr5. 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)

Bst1 bone marrow stromal cell antigen 1 [Mus musculus (house mouse)]

Gene ID: 12182, updated on 13-Mar-2020

Summary



Official Symbol Bst1 provided by [MGI](#)

Official Full Name bone marrow stromal cell antigen 1 provided by [MGI](#)

Primary source [MGI:MGI:105370](#)

See related [Ensembl:ENSMUSG00000029082](#)

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 114/A10, A530073F09, BP-3, Bp3, Bsta1, CD157, Ly65

Expression Biased expression in small intestine adult (RPKM 27.4), duodenum adult (RPKM 25.5) and 7 other tissues [See more](#)

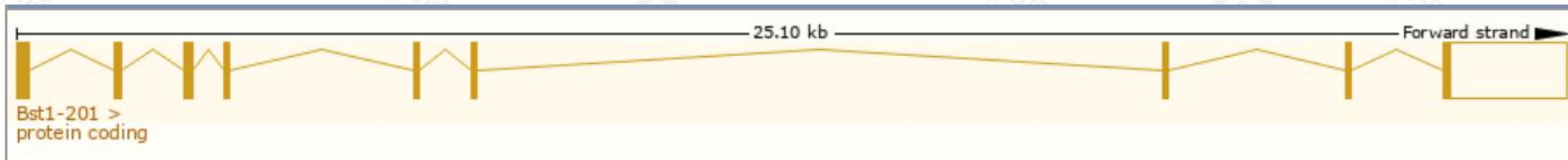
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

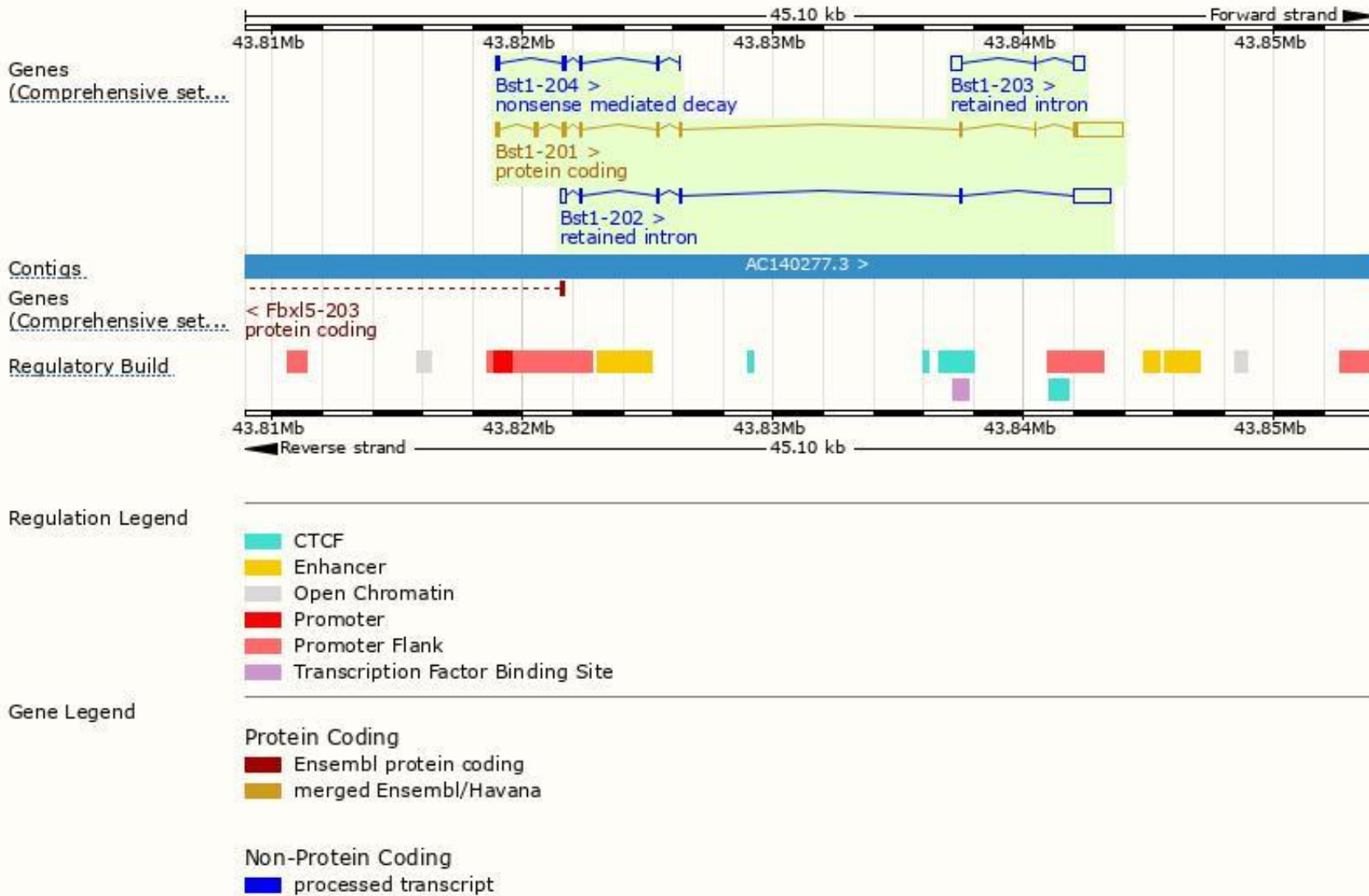
The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bst1-201	ENSMUST00000101237.7	2856	311aa	Protein coding	CCDS19264	A0A0R4J190	TSL:1 GENCODE basic APPRIS P1
Bst1-204	ENSMUST00000126976.5	512	67aa	Nonsense mediated decay	-	A0A0G2JG11	TSL:5
Bst1-202	ENSMUST00000118126.2	2054	No protein	Retained intron	-	-	TSL:1
Bst1-203	ENSMUST00000125838.2	908	No protein	Retained intron	-	-	TSL:3

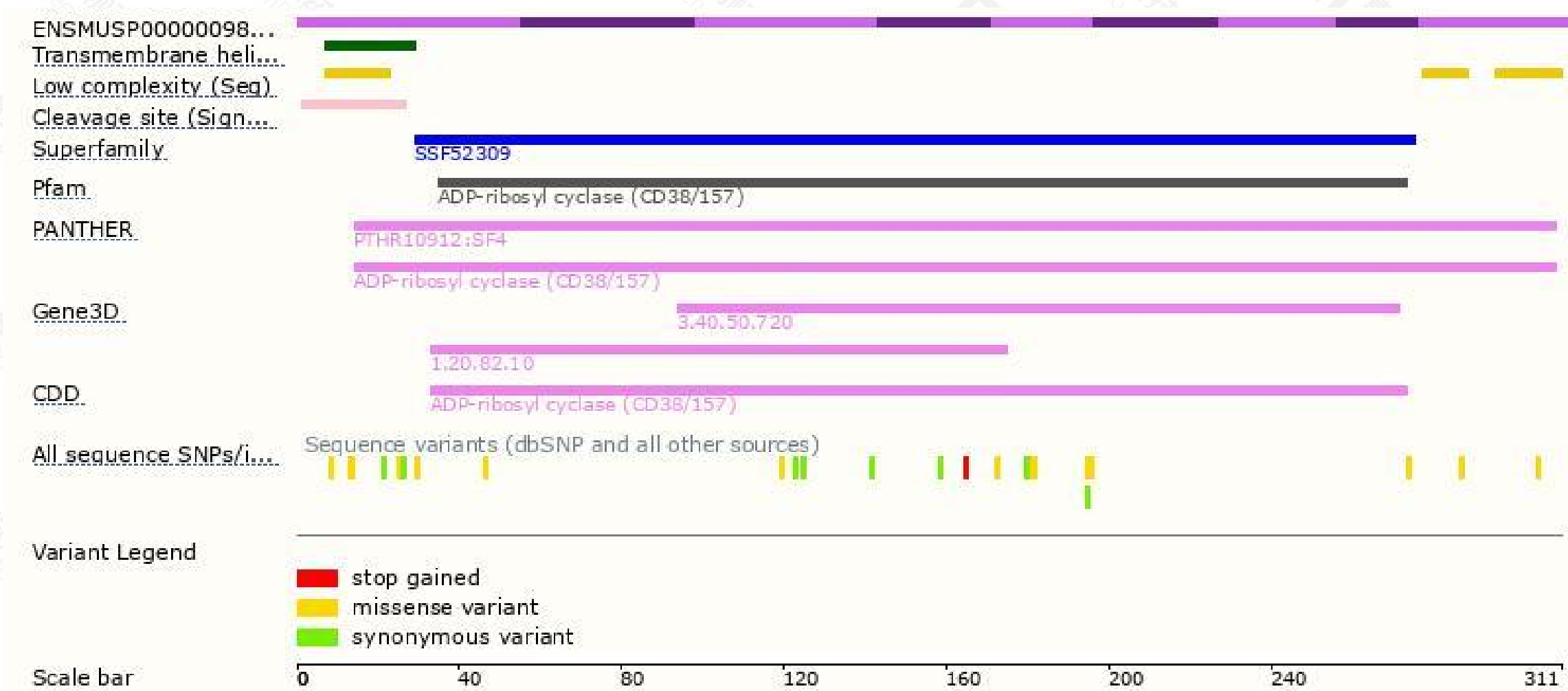
The strategy is based on the design of *Bst1-201* transcript, the transcription is shown below:



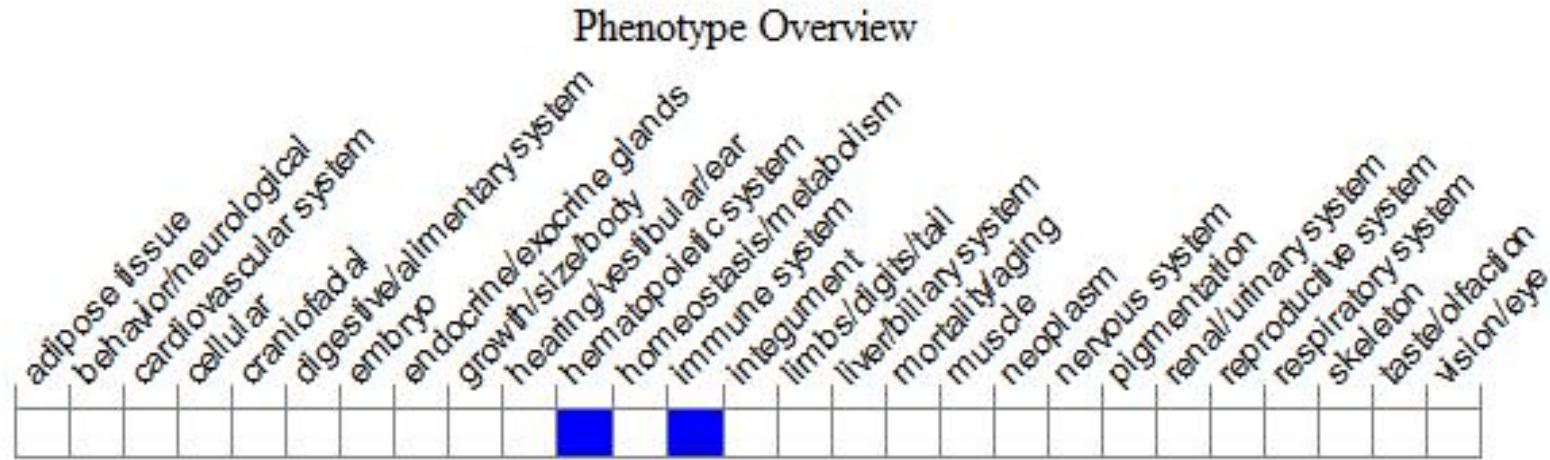
Genomic location distribution



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, homozygous null mice show delayed peritoneal B-1 cell development and a rise in CD38

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

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