

# ***Blnk* Cas9-KO Strategy**

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**Reviewer:**

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# Project Overview

**Project Name**

*Blnk*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Blnk* gene has 3 transcripts. According to the structure of *Blnk* gene, exon2-exon3 of *Blnk-201* (ENSMUST00000054769.6) transcript is recommended as the knockout region. The region contains 116bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Blnk* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit a partial block in pre-B cell development, a lack of B1 B cells, reduced numbers of mature B cells, lower IgM and IgG3 serum levels, poor IgM immune responses, and a high incidence of pre-B cell lymphoma.
- The *Blnk* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Blnk B cell linker [ *Mus musculus* (house mouse) ]

Gene ID: 17060, updated on 10-Oct-2019

### Summary

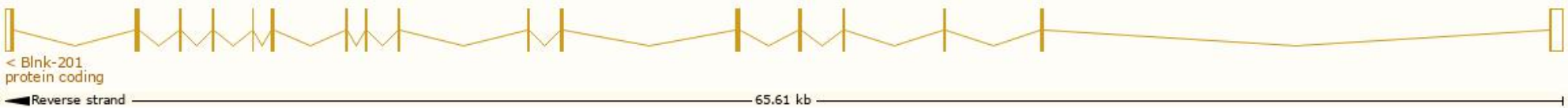
<b>Official Symbol</b>	Blnk provided by <a href="#">MGI</a>
<b>Official Full Name</b>	B cell linker provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:96878</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000061132</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Bca; BASH; Ly57; Ly-57; Lyw-57; SLP-65
<b>Expression</b>	Biased expression in spleen adult (RPKM 24.5), colon adult (RPKM 14.5) and 14 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

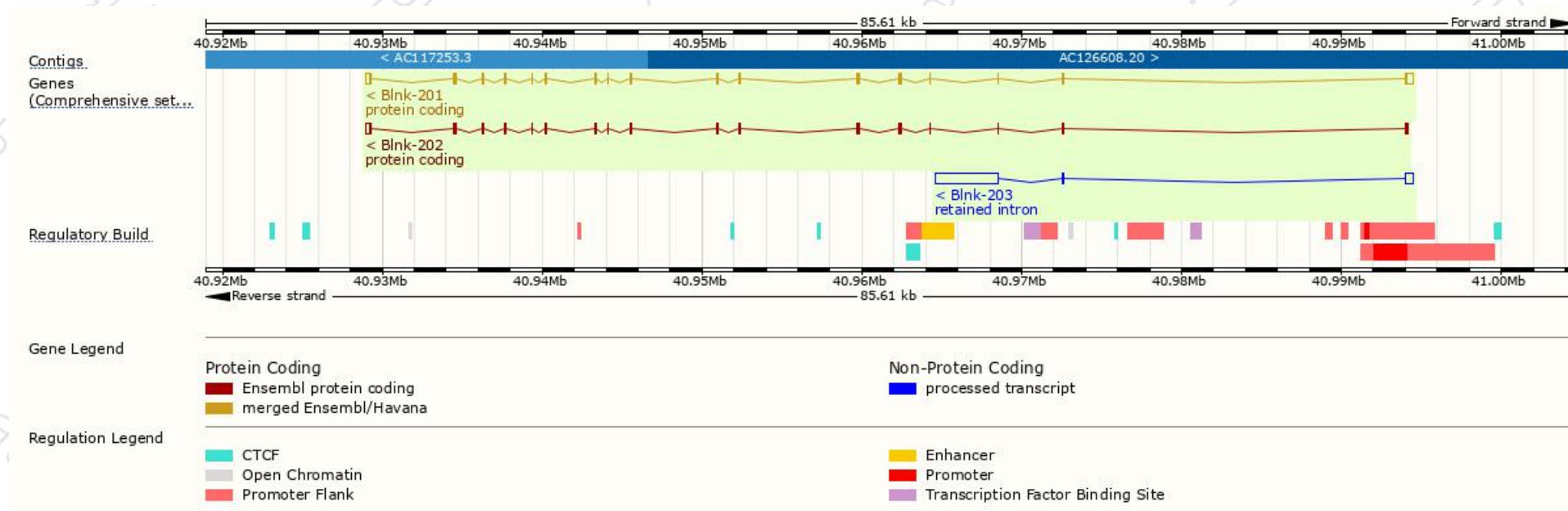
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Blnk-201	<a href="#">ENSMUST00000054769.6</a>	2097	<a href="#">457aa</a>	Protein coding	<a href="#">CCDS37983</a>	<a href="#">Q9QUN3</a>	TSL:1 GENCODE basic APPRIS P1
Blnk-202	<a href="#">ENSMUST00000117695.7</a>	1701	<a href="#">454aa</a>	Protein coding	-	<a href="#">D3YWR2</a>	TSL:1 GENCODE basic
Blnk-203	<a href="#">ENSMUST00000134568.1</a>	4534	No protein	Retained intron	-	-	TSL:1

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

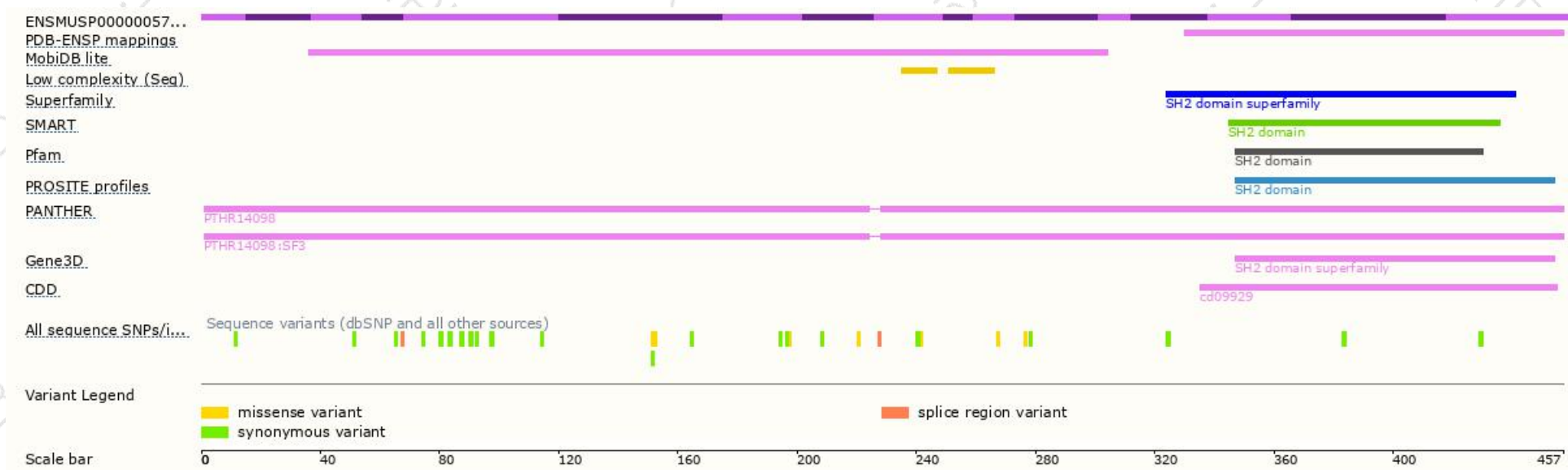


# Genomic location distribution

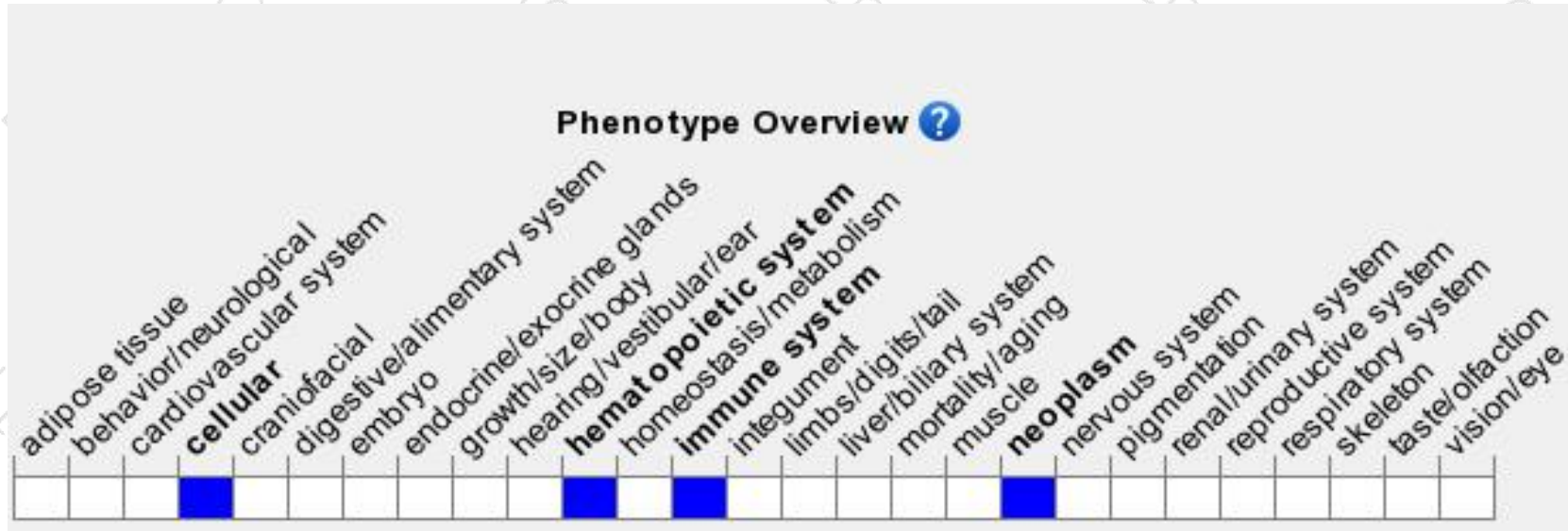




# Protein domain



# 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, Homozygotes for targeted null mutations exhibit a partial block in pre-B cell development, a lack of B1 B cells, reduced numbers of mature B cells, lower IgM and IgG3 serum levels, poor IgM immune responses, and a high incidence of pre-B cell lymphoma.

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

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