

Vsig4 Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Yumeng Wang

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Project Overview

Project Name

Vsig4

Project type

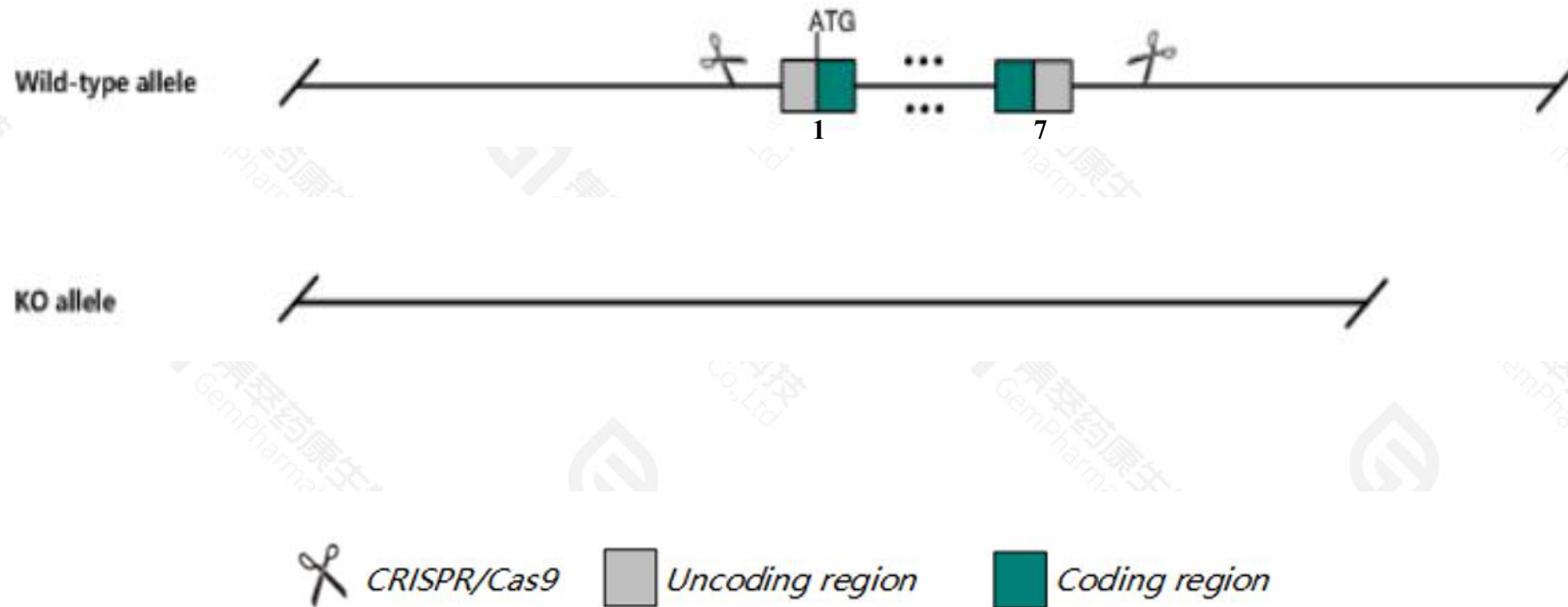
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vsig4* gene. The schematic diagram is as follows:



- The *Vsig4* gene has 2 transcripts. According to the structure of *Vsig4* gene, exon1-exon7 of *Vsig4-201*(ENSMUST00000050707.2) transcript is recommended as the knockout region. The region contains all 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 *Vsig4* 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, mice homozygous for a knock-out allele fail to exhibit complement-dependent clearance of *Staphylococcus aureus* from the circulation and are more susceptible to *Listeria monocytogenes* infection.
- The *Vsig4* gene is located on the ChrX. 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.

Vsig4 V-set and immunoglobulin domain containing 4 [Mus musculus (house mouse)]

Gene ID: 278180, updated on 13-Mar-2020

Summary



Official Symbol Vsig4 provided by [MGI](#)

Official Full Name V-set and immunoglobulin domain containing 4 provided by [MGI](#)

Primary source [MGI:MGI:2679720](#)

See related [Ensembl:ENSMUSG00000044206](#)

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 A530061A11, BC025105, CR, CRlg, Z39I, Z39IG

Expression Biased expression in liver E18 (RPKM 5.0), liver adult (RPKM 2.5) and 1 other tissue [See more](#)

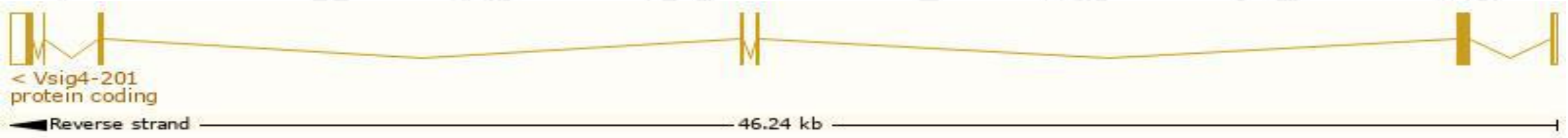
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

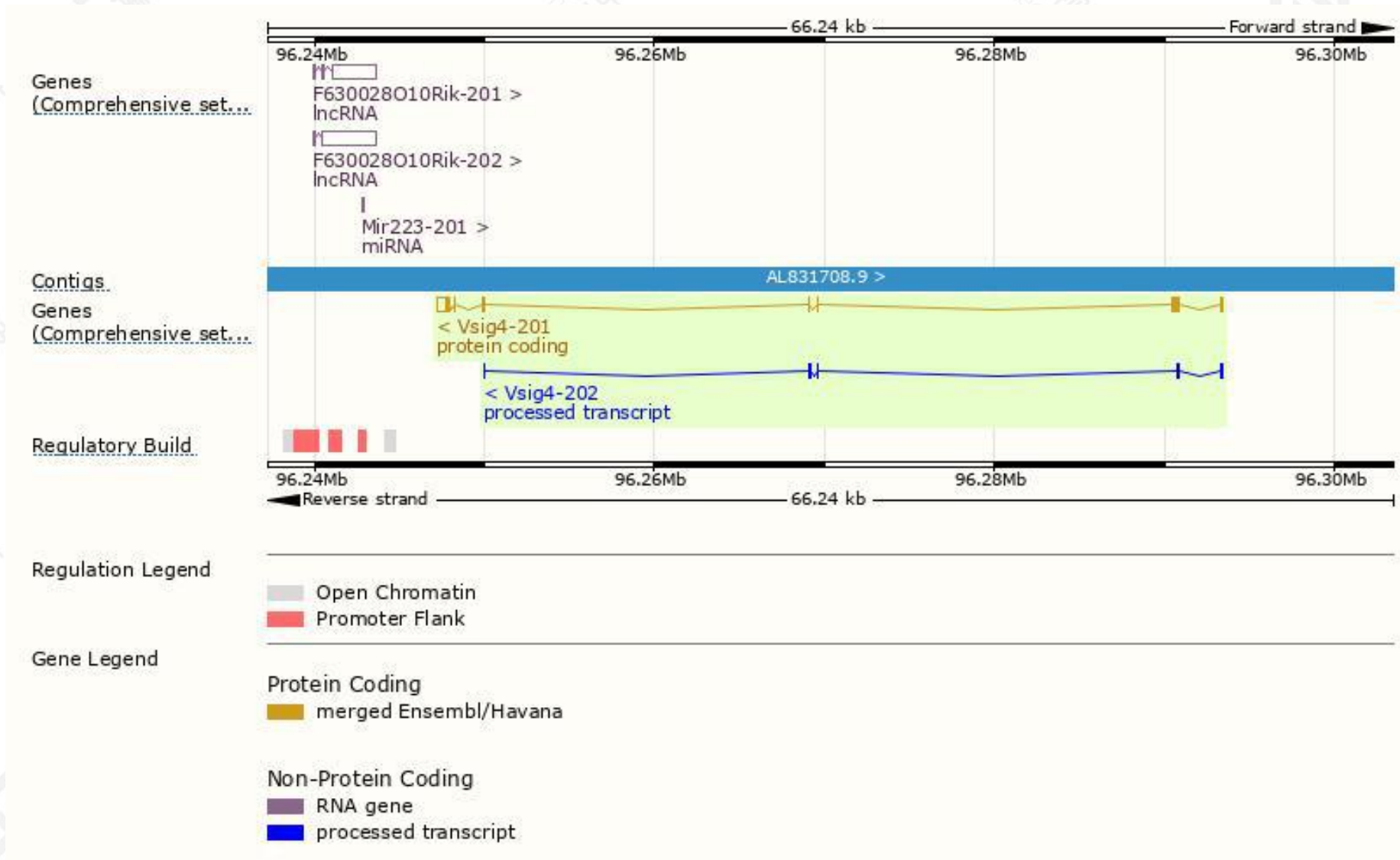
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vsig4-201	ENSMUST00000050707.2	1432	280aa	Protein coding	CCDS30288	F6TUL9	TSL:1 GENCODE basic APPRIS P1
Vsig4-202	ENSMUST00000146830.1	410	No protein	Processed transcript	-	-	TSL:3

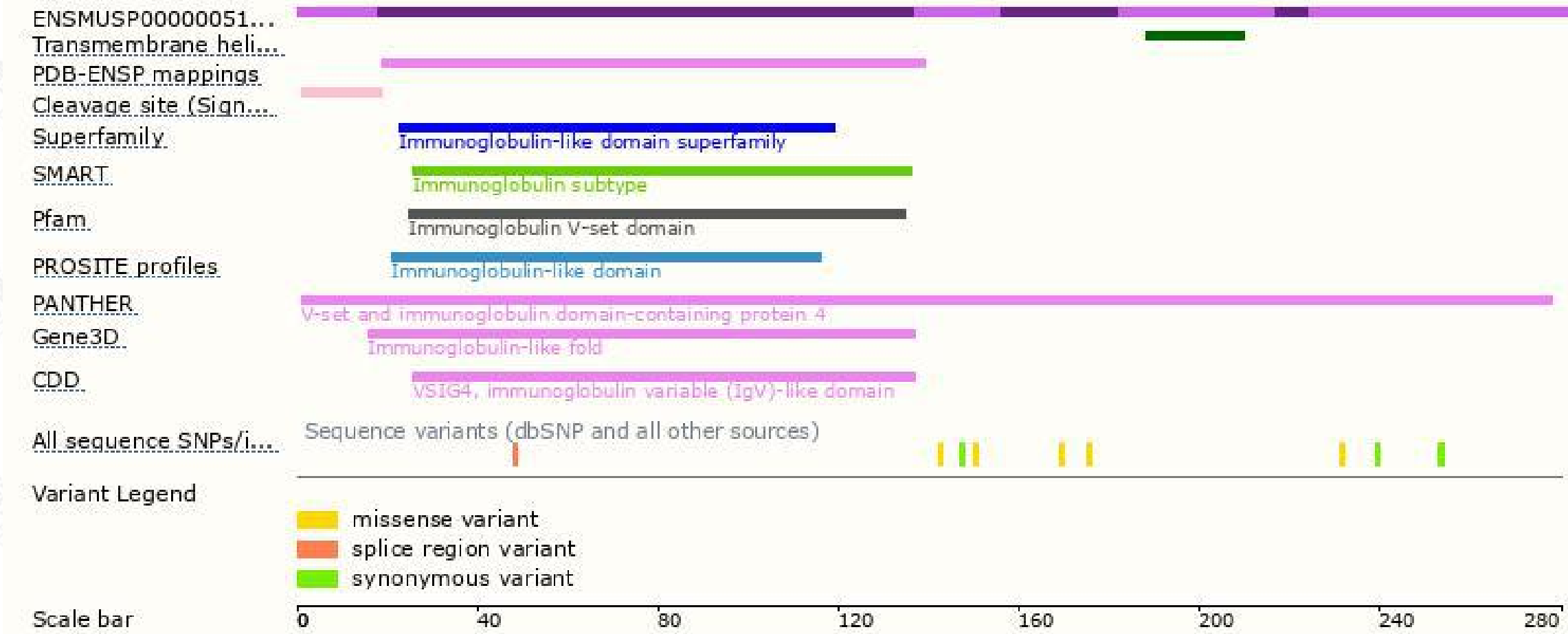
The strategy is based on the design of *Vsig4-201* transcript,the transcription is shown below:



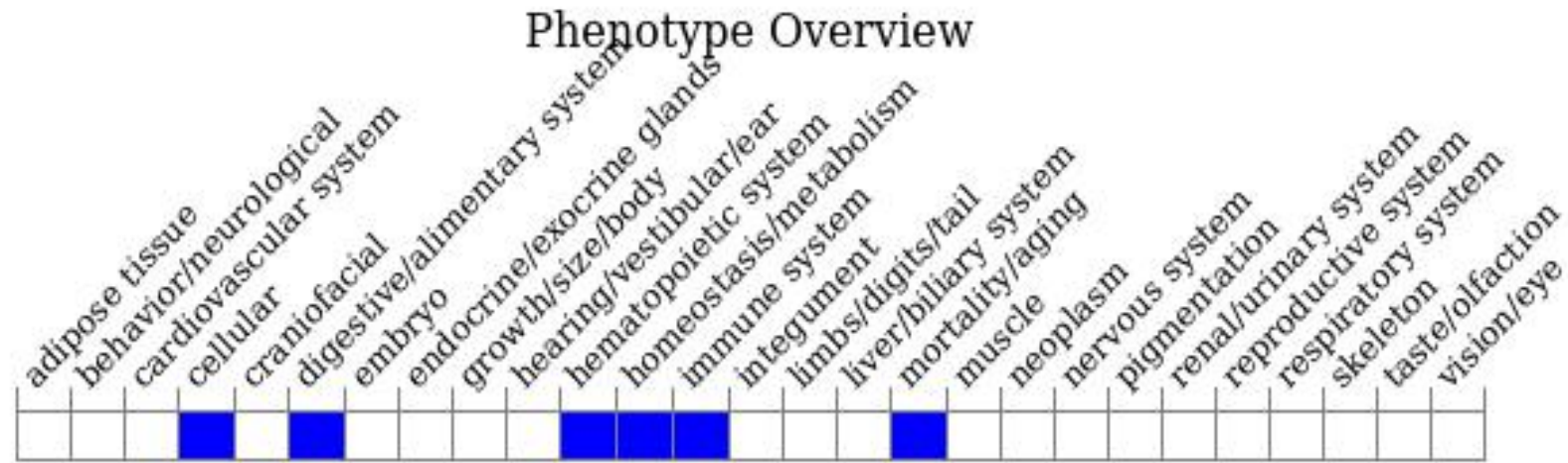
Genomic location distribution



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 fail to exhibit complement-dependent clearance of *Staphylococcus aureus* from the circulation and are more susceptible to *Listeria monocytogenes* infection.

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

