Fcmr Cas9-CKO Strategy

Designer:Xiaojing Li
Reviewer:JiaYu
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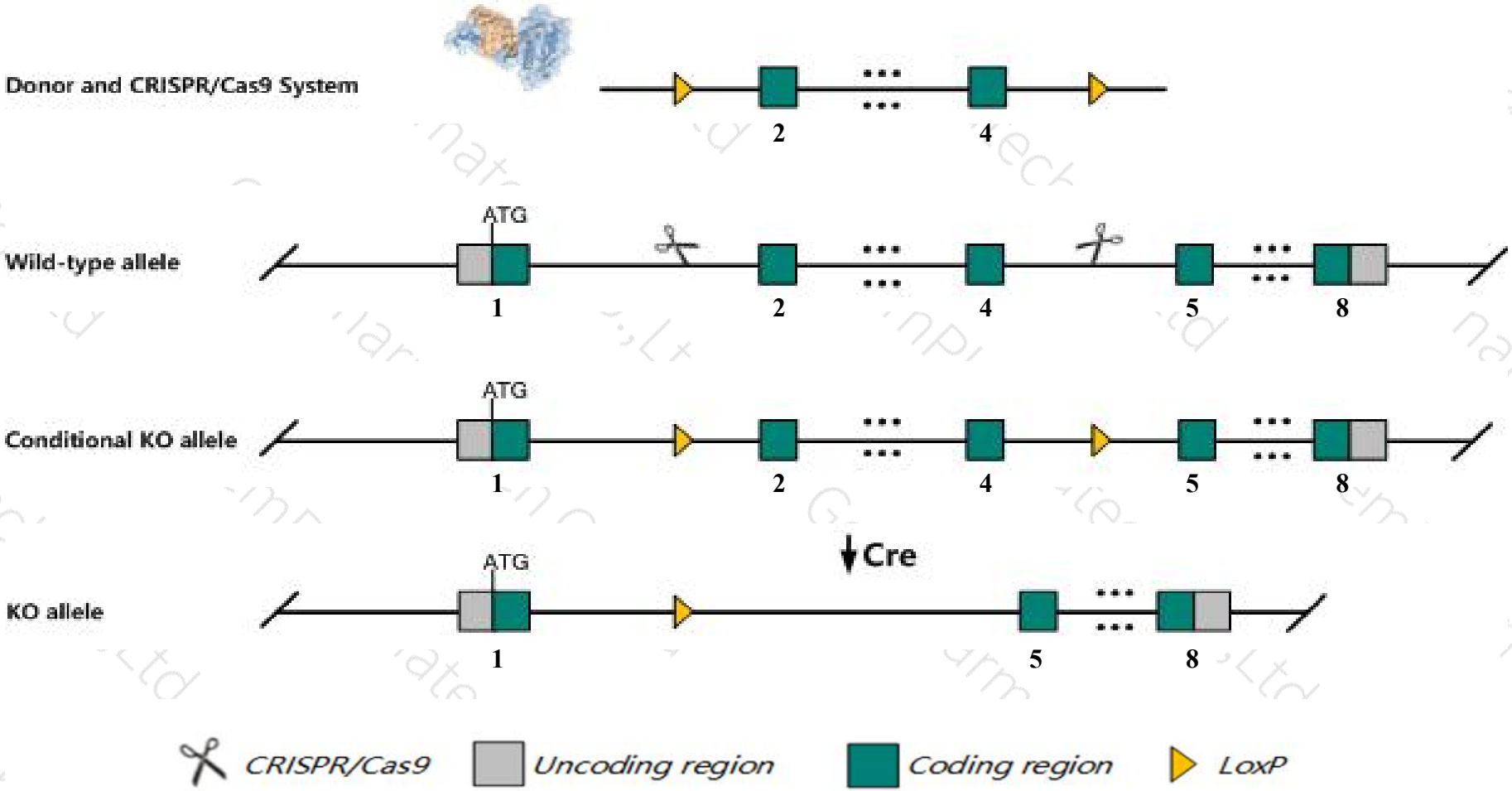
Project Overview

Project Name	***Fcmr***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- The *Fcmr* gene has 4 transcripts. According to the structure of *Fcmr* gene, exon2-exon4 of *Fcmr-201* (ENSMUST00000038829.6) transcript is recommended as the knockout region.The region contains 685bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fcmr* 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,Mice homozygous for knock-out alleles exhibit a slight decrease in B cell numbers reduced sensitivity to Gal-induced liver damage, increased granulocyte production of ROS and increased sensitivity to infection by Listeria monocytogenes.

➢ The *Fcmr* gene is located on the Chr1. 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）

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Fcmr Fc fragment of IgM receptor [*Mus musculus* (house mouse)]

Gene ID: 69169, updated on 14-Jan-2020

Summary

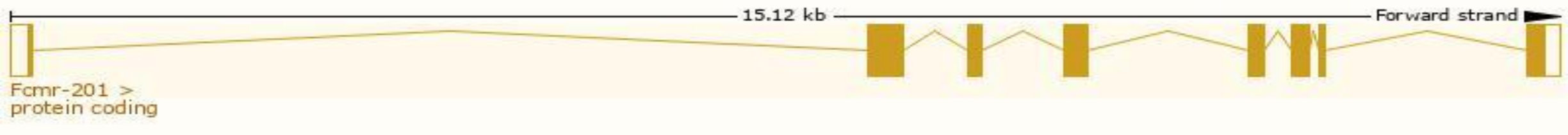
Official Symbol	Fcmr provided by MGI
Official Full Name	Fc fragment of IgM receptor provided by MGI
Primary source	MGI:MGI:1916419
See related	Ensembl:ENSMUSG00000042474
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Toso; Faim3; FcmuR; 1810037B05Rik
Expression	Biased expression in spleen adult (RPKM 125.7) and mammary gland adult (RPKM 37.6) See more
Orthologs	human all

Transcript information（Ensembl）

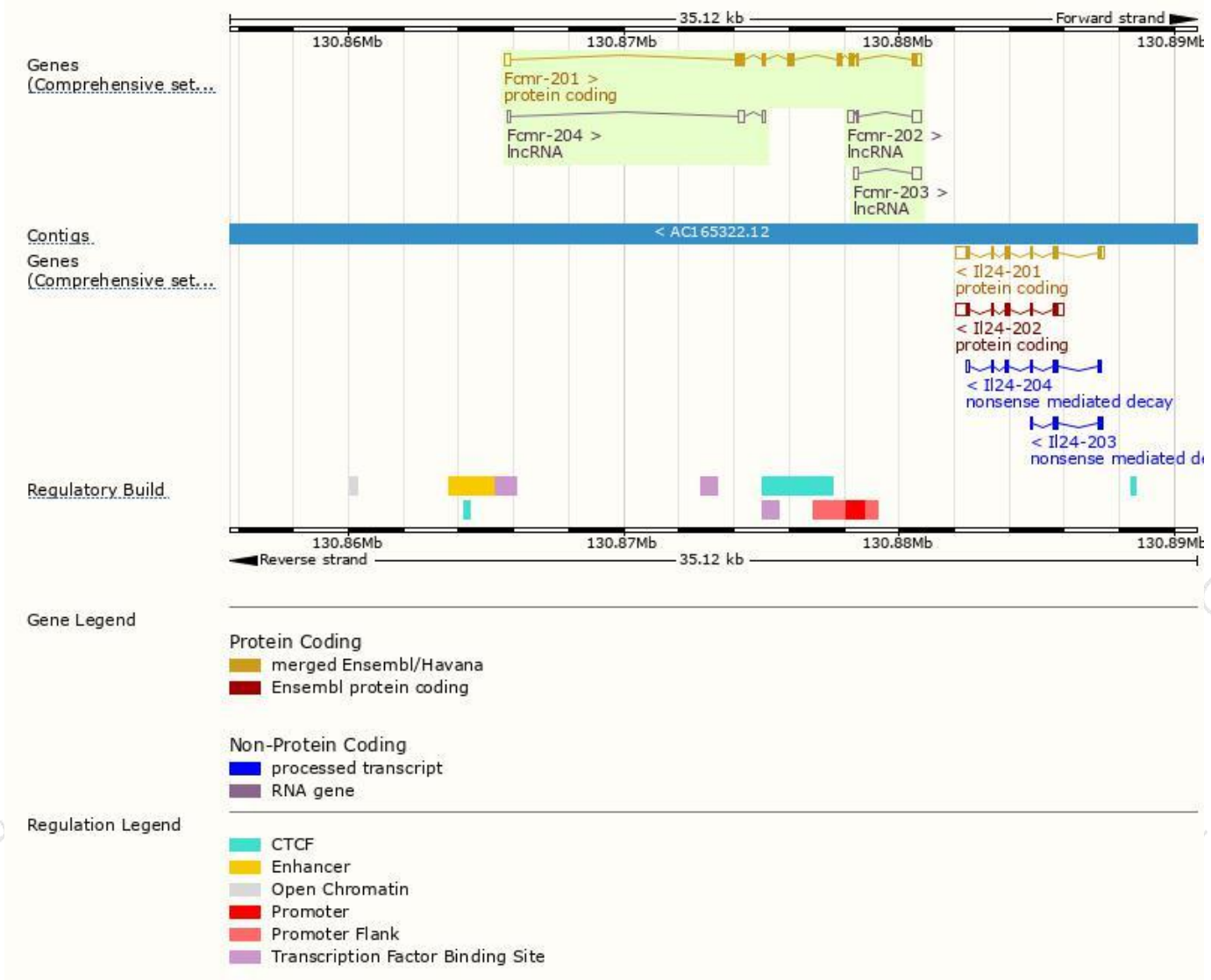
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fcmr-201	ENSMUST00000038829.6	1600	422aa	Protein coding	CCDS15261	A0A0G2LB91	TSL:1 GENCODE basic APPRIS P1
Fcmr-202	ENSMUST00000126821.1	548	No protein	lncRNA	-	-	TSL:2
Fcmr-203	ENSMUST00000145446.1	497	No protein	lncRNA	-	-	TSL:3
Fcmr-204	ENSMUST00000149355.1	433	No protein	lncRNA	-	-	TSL:3

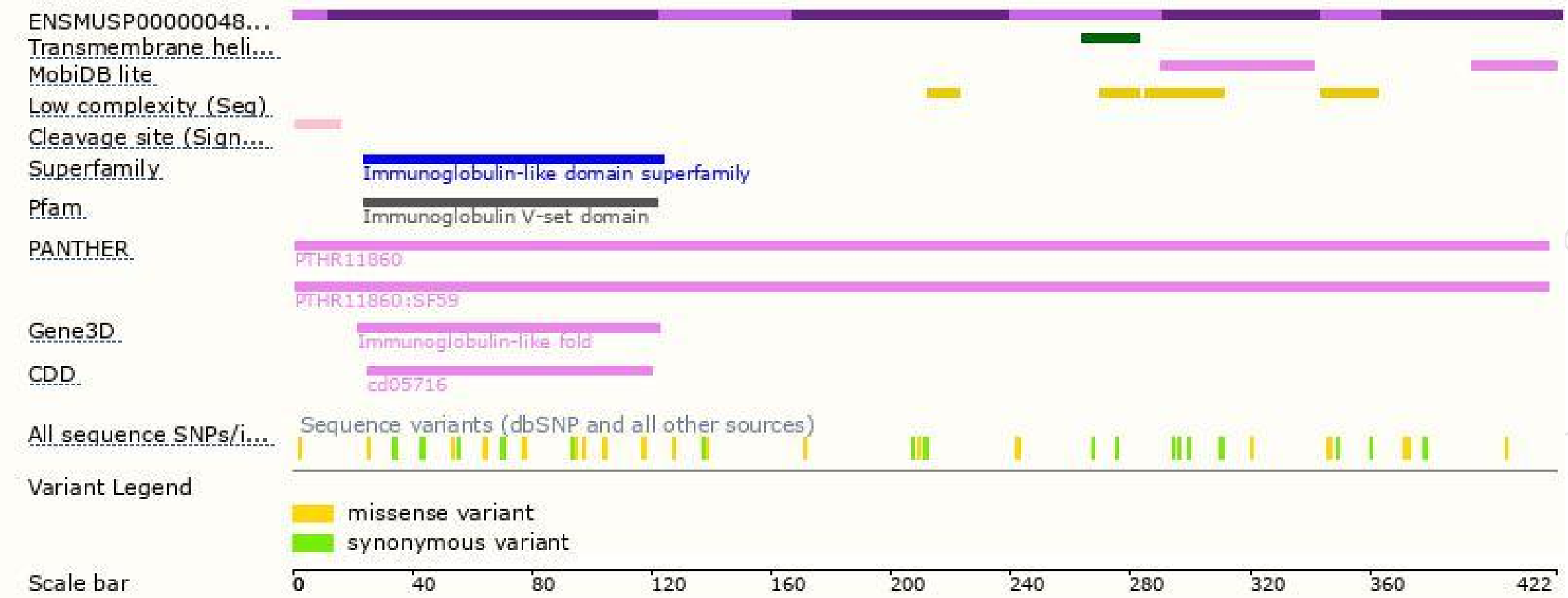
The strategy is based on the design of *Fcmr-201* transcript,The transcription is shown below



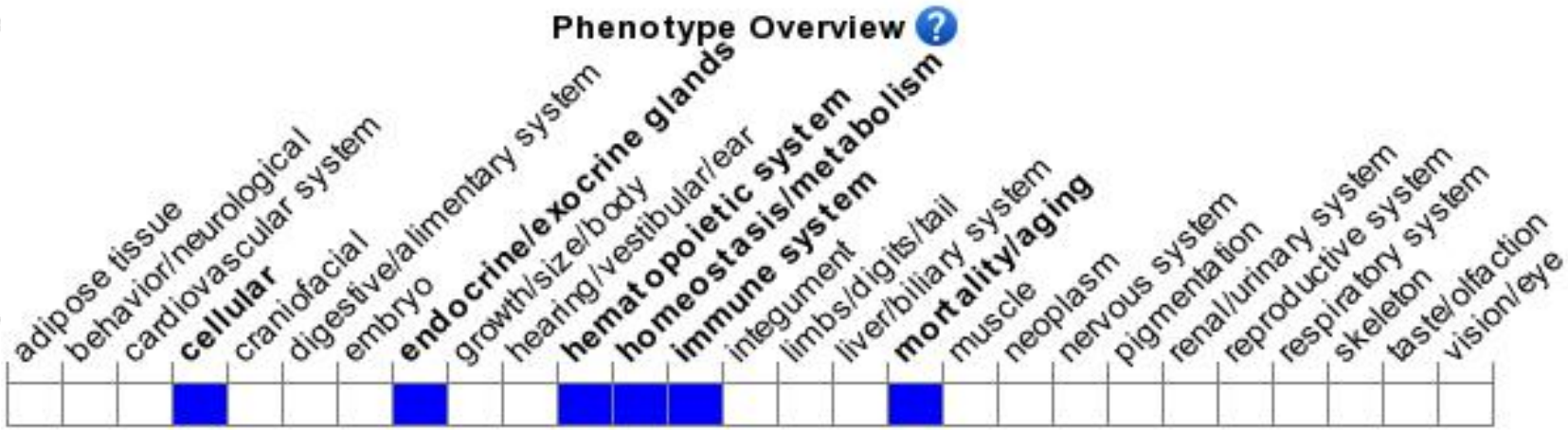
Genomic location distribution



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/).

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

Tel: 400-9660890

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