Kcnk3 Cas9-KO Strategy

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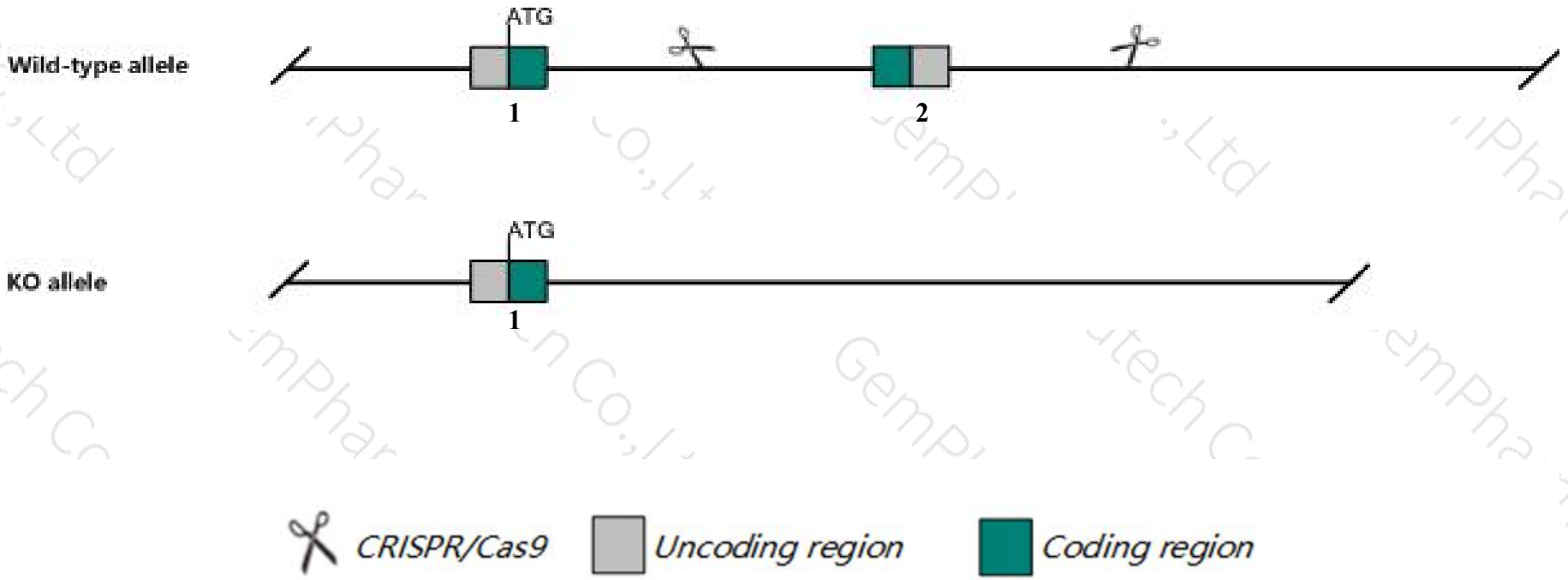
Project Overview

Project Name	***Kcnk3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnk3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnk3* gene has 2 transcripts. According to the structure of *Kcnk3* gene, exon2 of *Kcnk3-201* (ENSMUST00000066295.3) transcript is recommended as the knockout region.The region contains most 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 *Kcnk3* gene. The brief process is as follows: CRISPR/Cas9 system wer

Notice

- According to the existing MGI data,Mice homozygous for a null alleles exhibit decreased pH sensitivitive of action potential in serotonergic neurons.

- The *Kcnk3* 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）

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Kcnk3 potassium channel, subfamily K, member 3 [*Mus musculus* (house mouse)]

Gene ID: 16527, updated on 12-Aug-2019

Summary

Official Symbol	Kcnk3 provided by MGI
Official Full Name	potassium channel, subfamily K, member 3 provided by MGI
Primary source	MGI:MGI:1100509
See related	Ensembl:ENSMUSG00000049265
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	TASK; Task-1; cTBAK-1
Expression	Biased expression in adrenal adult (RPKM 1700.1) and heart adult (RPKM 66.4) See more
Orthologs	human all

Genomic context

Location: 5 B1; 5 16.68 cM

See Kcnk3 in Genome Data Viewer

Exon count: 2

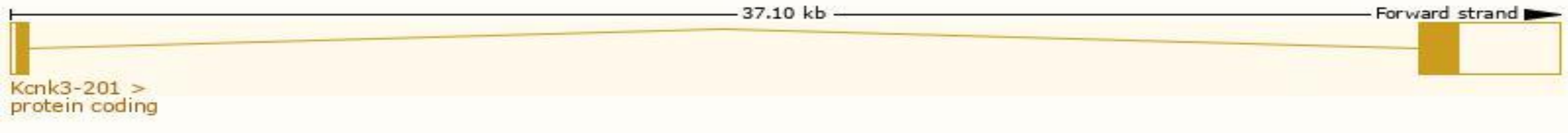
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (30588170..30625270)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (30890543..30927643)

Transcript information（Ensembl）

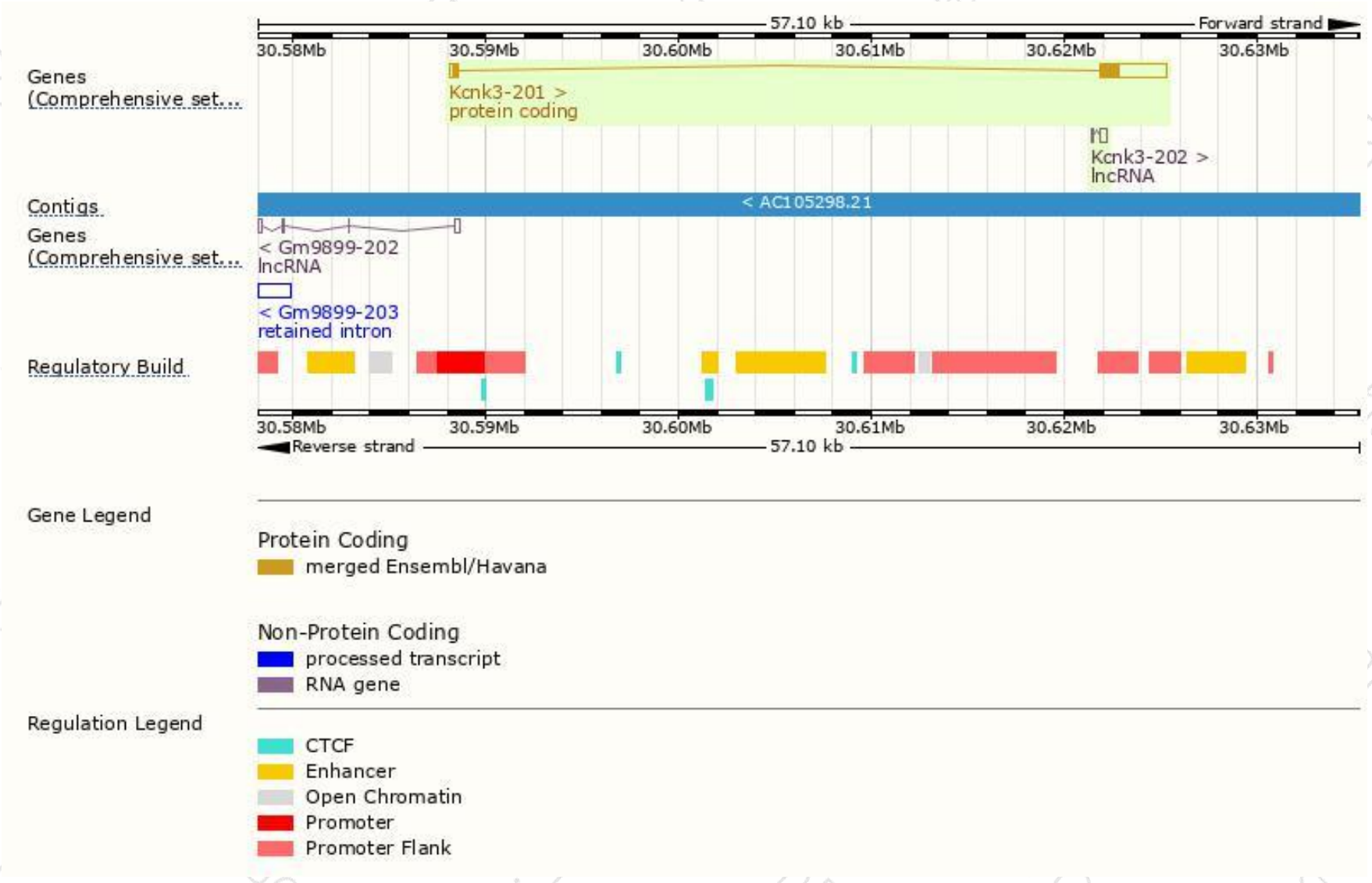
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnk3-201	ENSMUST00000066295.3	3811	409aa	Protein coding	CCDS19160	O35111	TSL:1 GENCODE basic APPRIS P1
Kcnk3-202	ENSMUST00000197428.1	507	No protein	lncRNA	-	-	TSL:2

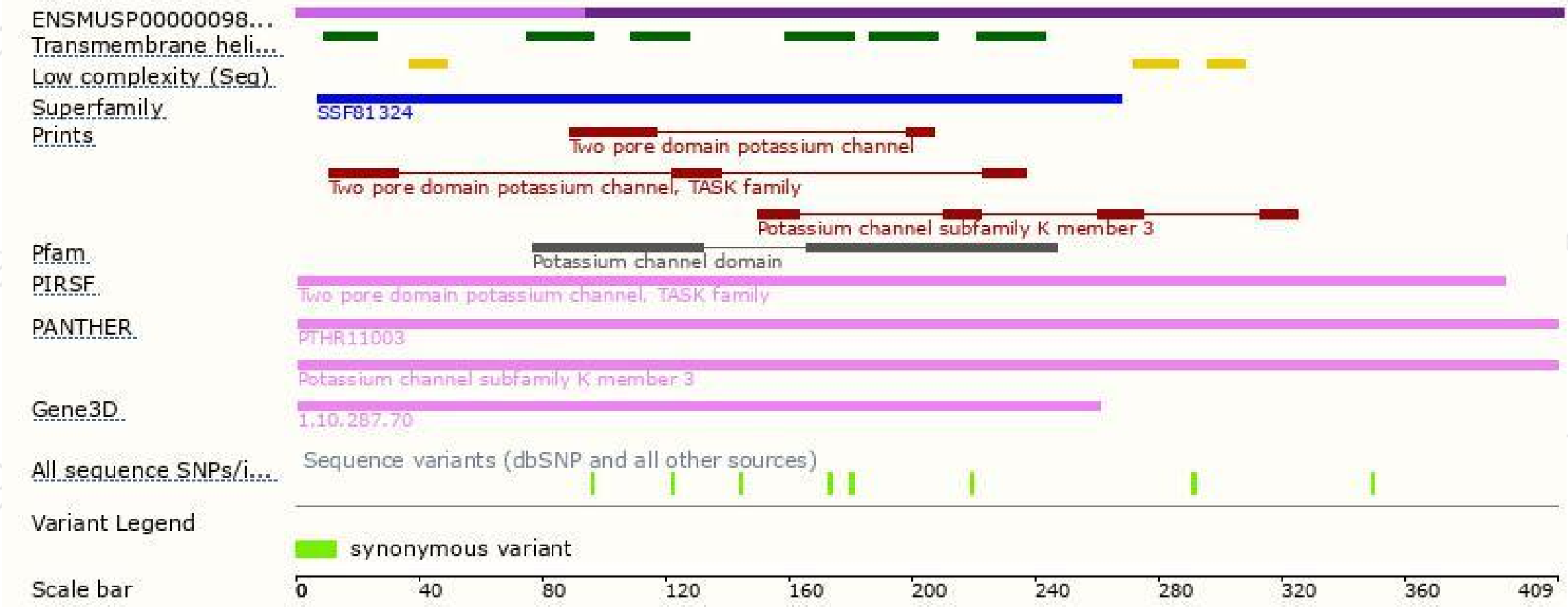
The strategy is based on the design of *Kcnk3-201* transcript,The transcription is shown below



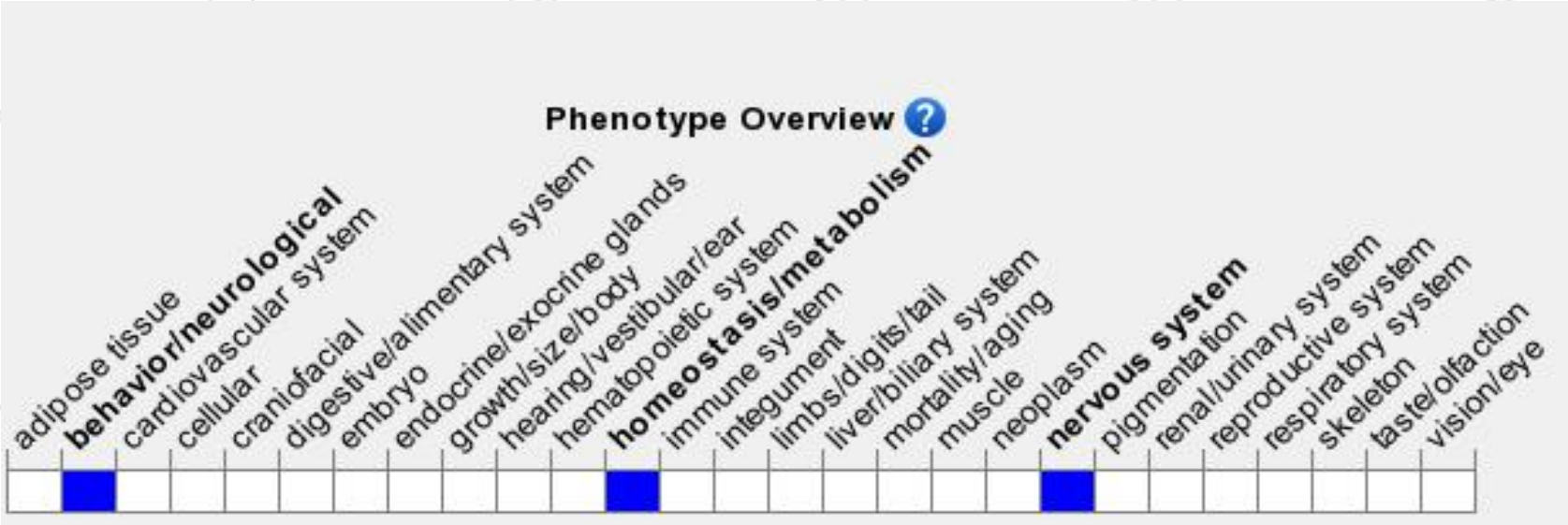
Genomic location distribution



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.

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