

Ube2e2 Cas9-CKO Strategy

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Project Overview

Project Name

Ube2e2

Project type

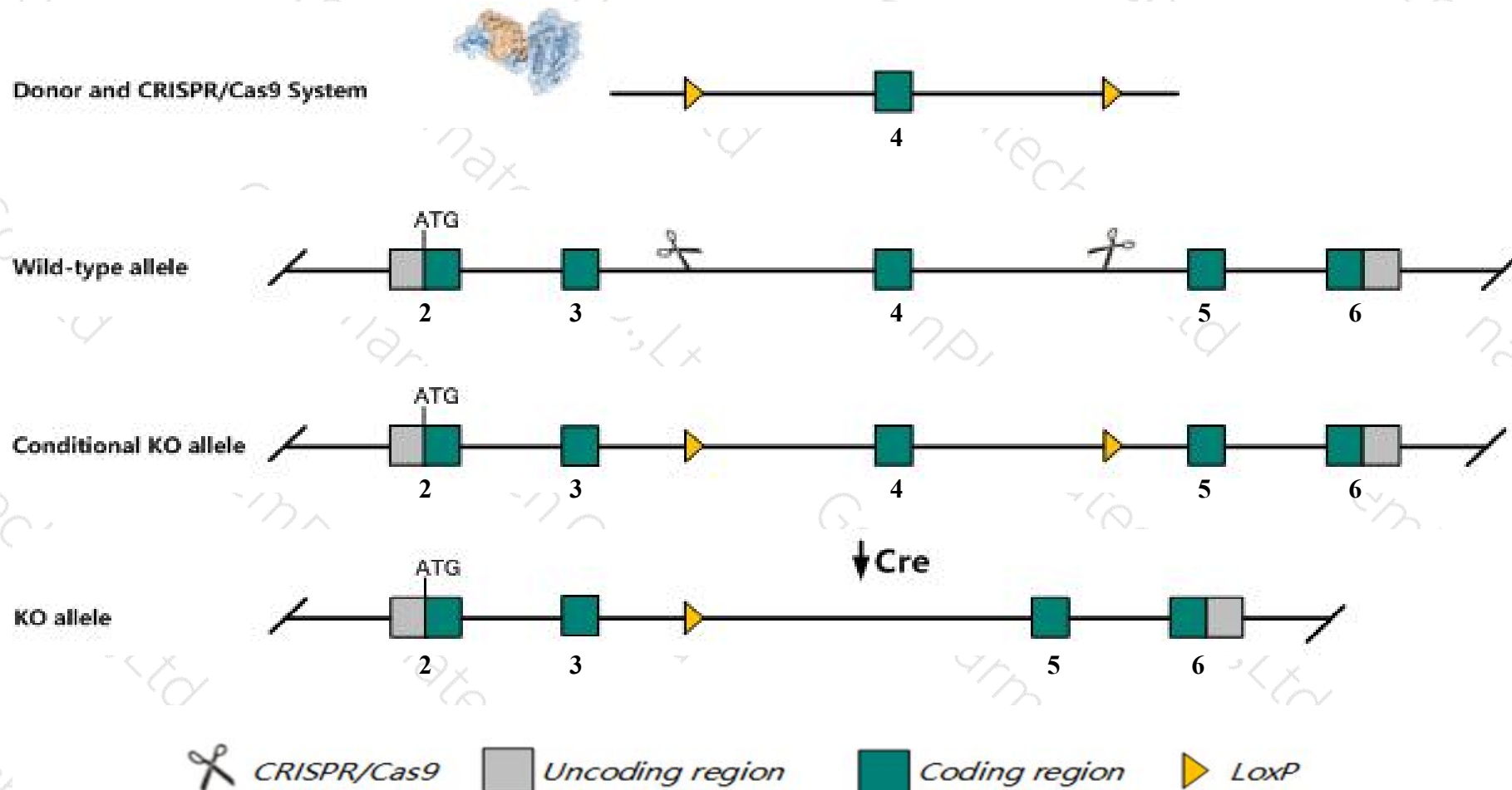
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ube2e2* gene. The schematic diagram is as follows:



Technical routes

- The *Ube2e2* gene has 14 transcripts. According to the structure of *Ube2e2* gene, exon4 of *Ube2e2-205* (ENSMUST00000150727.7) transcript is recommended as the knockout region. The region contains 133bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ube2e2* 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

- The *Ube2e2* gene is located on the Chr14. 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)

Ube2e2 ubiquitin-conjugating enzyme E2E 2 [Mus musculus (house mouse)]

Gene ID: 218793, updated on 31-Jan-2019

Summary



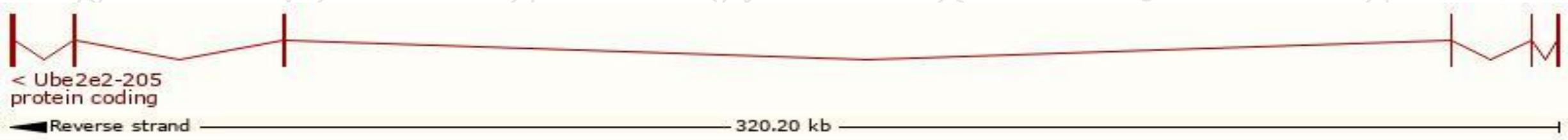
Official Symbol	Ube2e2 provided by MGI
Official Full Name	ubiquitin-conjugating enzyme E2E 2 provided by MGI
Primary source	MGI:MGI:2384997
See related	Ensembl:ENSMUSG00000058317
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC016265
Expression	Ubiquitous expression in CNS E18 (RPKM 15.9), cortex adult (RPKM 15.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

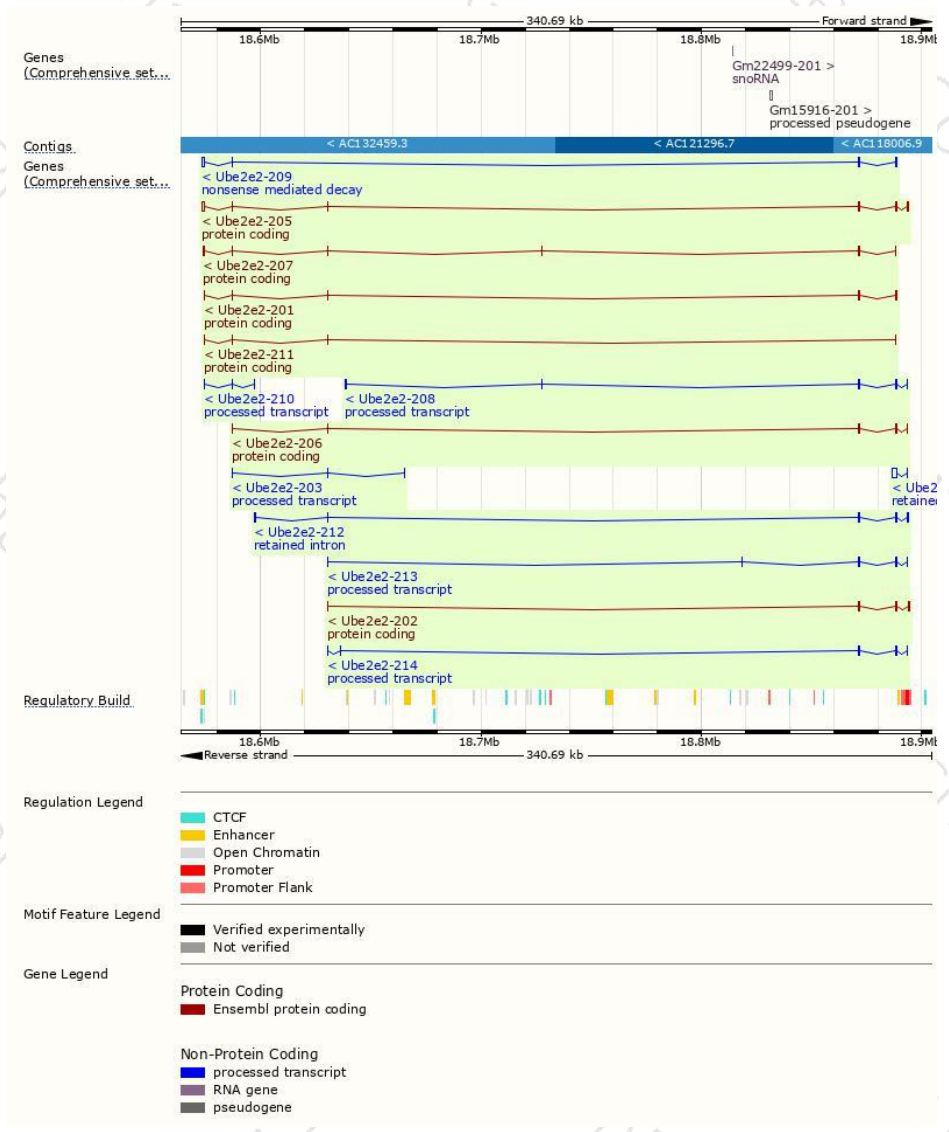
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ube2e2-205	ENSMUST00000150727.7	1523	201aa	Protein coding	CCDS26838	Q91W82	TSL:1 GENCODE basic APPRIS P1
Ube2e2-201	ENSMUST00000076133.9	606	201aa	Protein coding	CCDS26838	Q91W82	TSL:3 GENCODE basic APPRIS P1
Ube2e2-207	ENSMUST00000175643.7	757	167aa	Protein coding	-	H3BL69	CDS 5' incomplete TSL:3
Ube2e2-206	ENSMUST00000151926.7	666	181aa	Protein coding	-	D3YXD1	CDS 3' incomplete TSL:3
Ube2e2-202	ENSMUST00000124353.1	445	108aa	Protein coding	-	D3YW10	CDS 3' incomplete TSL:3
Ube2e2-211	ENSMUST00000176843.7	438	146aa	Protein coding	-	H3BL23	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ube2e2-209	ENSMUST00000176555.7	1200	92aa	Nonsense mediated decay	-	H3BJB5	TSL:5
Ube2e2-208	ENSMUST00000176062.2	647	No protein	Processed transcript	-	-	TSL:3
Ube2e2-214	ENSMUST00000177398.7	514	No protein	Processed transcript	-	-	TSL:3
Ube2e2-213	ENSMUST00000177259.7	423	No protein	Processed transcript	-	-	TSL:3
Ube2e2-203	ENSMUST00000135381.7	335	No protein	Processed transcript	-	-	TSL:3
Ube2e2-210	ENSMUST00000176672.1	328	No protein	Processed transcript	-	-	TSL:5
Ube2e2-204	ENSMUST00000144873.1	2135	No protein	Retained intron	-	-	TSL:1
Ube2e2-212	ENSMUST00000176931.7	772	No protein	Retained intron	-	-	TSL:3

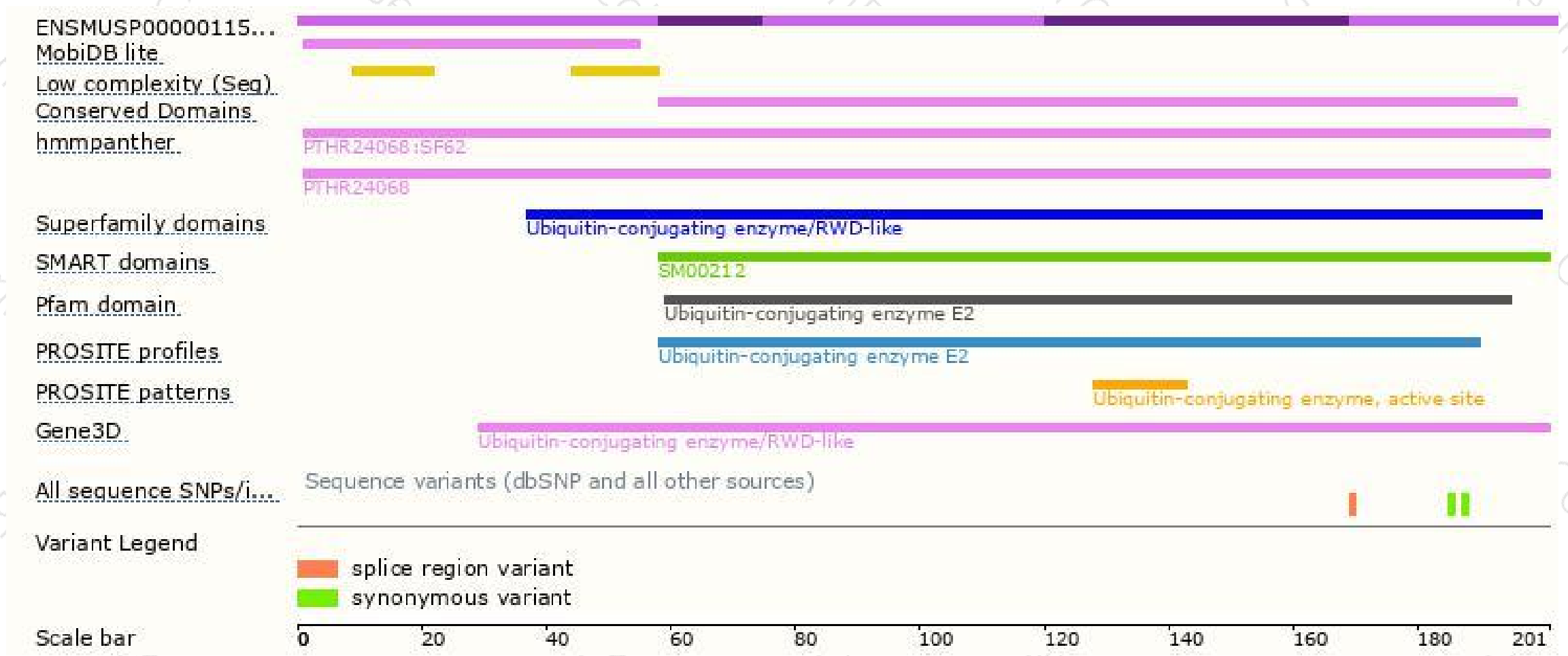
The strategy is based on the design of *Ube2e2-205* transcript,The transcription is shown below



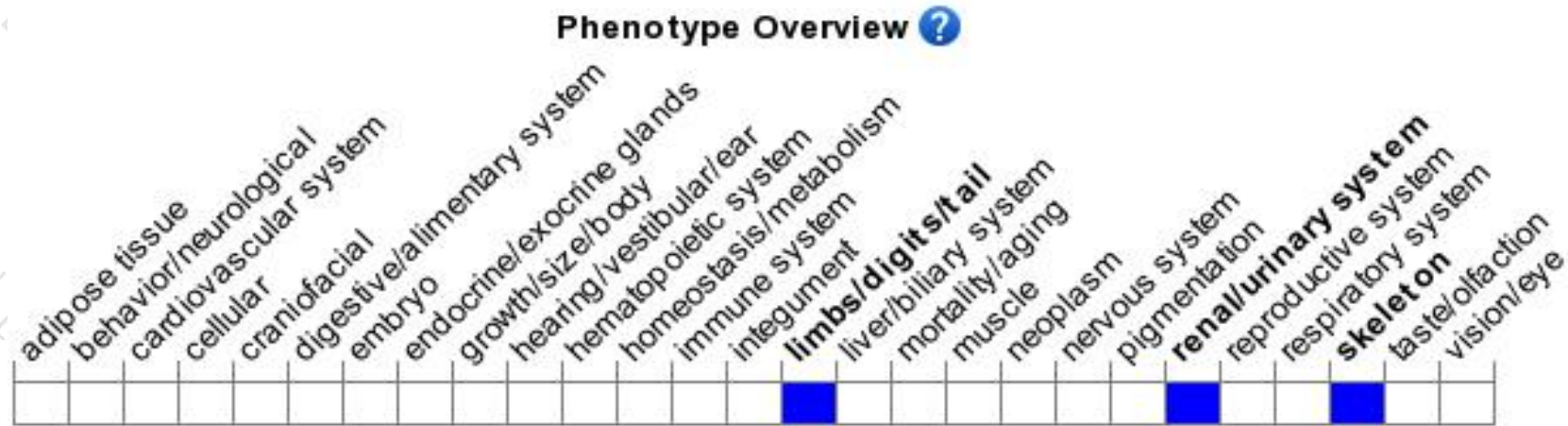
Genomic location distribution



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/>).

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

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