



Ube2f Cas9-CKO Strategy

Designer:

Qiong Zhou

Design Date:

2018/5/29

Project Overview

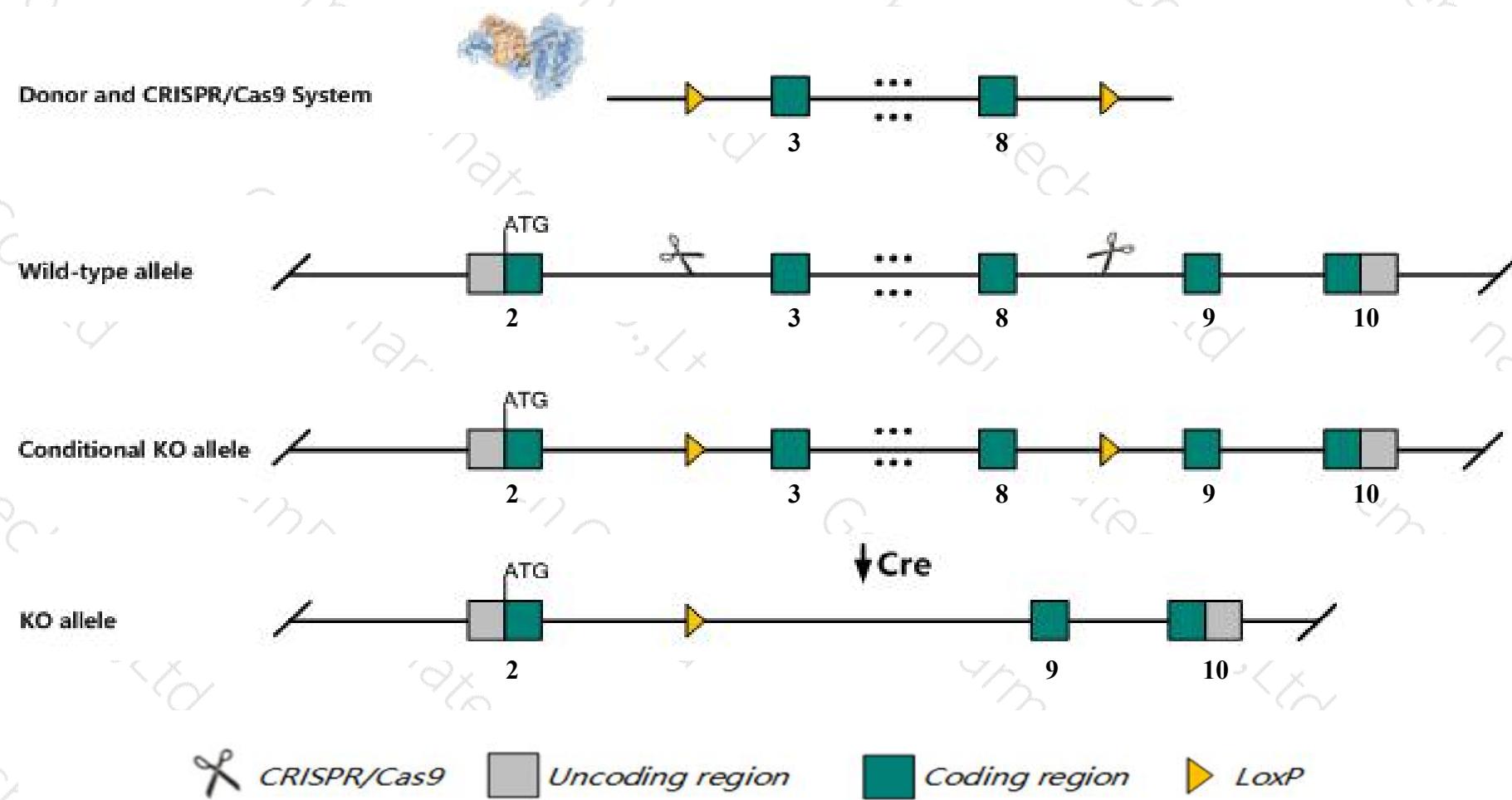
Project Name***Ube2f***

Project type**Cas9-CKO**

Strain background**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ube2f* gene. The schematic diagram is as follows:



Technical routes

- The *Ube2f* gene has 11 transcripts. According to the structure of *Ube2f* gene, exon3-exon8 of *Ube2f-203* (ENSMUST00000171165.7) transcript is recommended as the knockout region. The region contains 326bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ube2f* 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.



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Notice

- The *Ube2f* 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)

Ube2f ubiquitin-conjugating enzyme E2F (putative) [Mus musculus (house mouse)]

Gene ID: 67921, updated on 31-Jan-2019

Summary



Official Symbol Ube2f provided by [MGI](#)

Official Full Name ubiquitin-conjugating enzyme E2F (putative) provided by [MGI](#)

Primary source [MGI:MGI:1915171](#)

See related [Ensembl:ENSMUSG00000034343](#)

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 2510010F15Rik, AI851109

Expression Ubiquitous expression in testis adult (RPKM 22.6), placenta adult (RPKM 14.6) and 28 other tissues [See more](#)

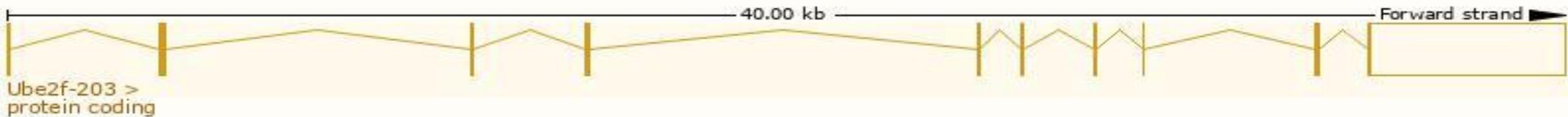
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

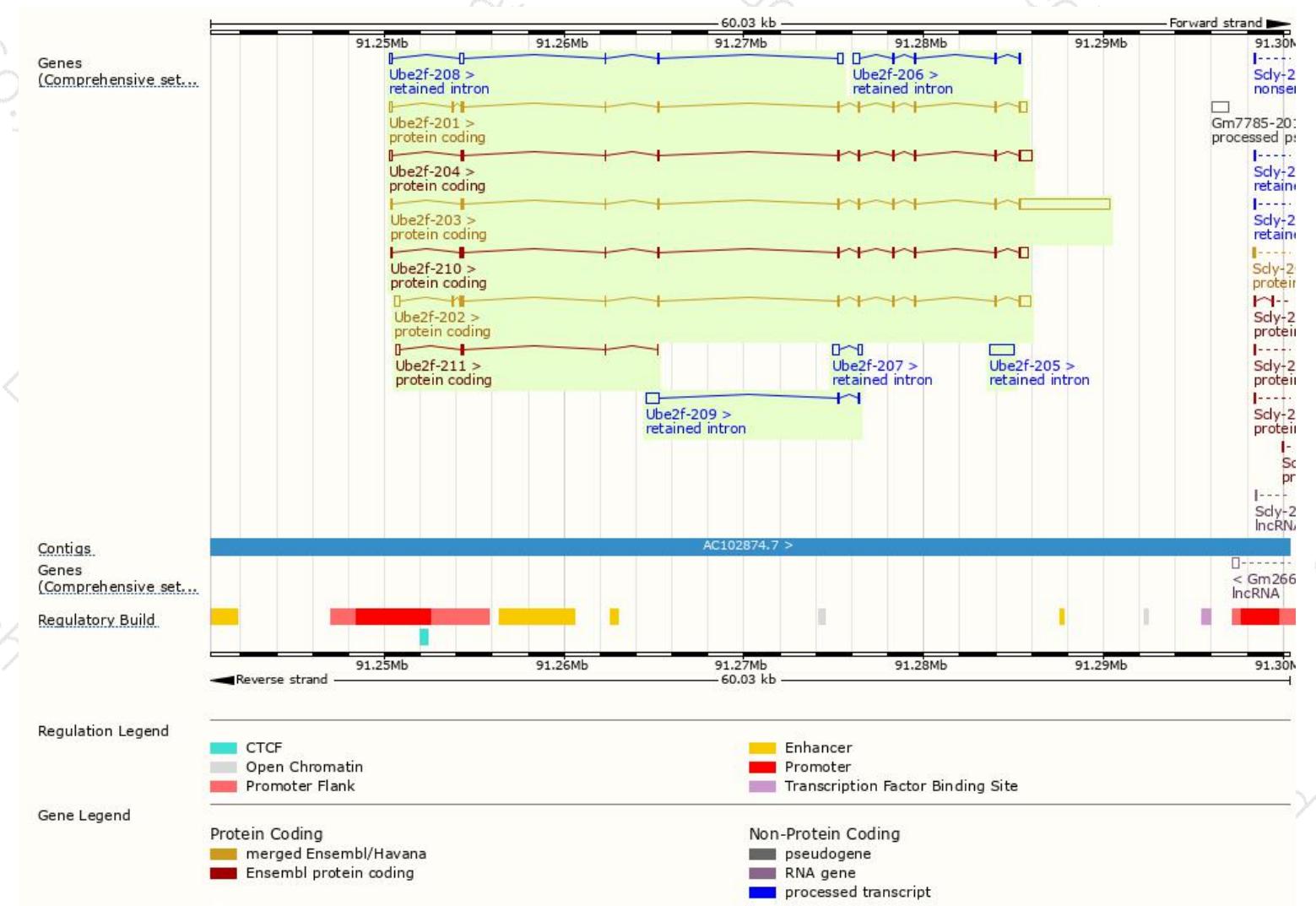
The gene has 11 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------------|---------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|-------------------------------|
| Ube2f-203 | ENSMUST00000171165.7 | 5654 | 185aa | Protein coding | CCDS48322 | Q9CY34 | TSL:1 GENCODE basic APPRIS P1 |
| Ube2f-202 | ENSMUST00000171112.7 | 1547 | 185aa | Protein coding | CCDS48322 | Q9CY34 | TSL:1 GENCODE basic APPRIS P1 |
| Ube2f-204 | ENSMUST00000178627.7 | 1363 | 185aa | Protein coding | CCDS48322 | Q9CY34 | TSL:1 GENCODE basic APPRIS P1 |
| Ube2f-201 | ENSMUST00000059743.11 | 1154 | 185aa | Protein coding | CCDS48322 | Q9CY34 | TSL:1 GENCODE basic APPRIS P1 |
| Ube2f-210 | ENSMUST00000191368.6 | 1110 | 185aa | Protein coding | CCDS48322 | Q9CY34 | TSL:1 GENCODE basic APPRIS P1 |
| Ube2f-211 | ENSMUST00000191533.1 | 382 | 56aa | Protein coding | - | AOA087WQR9 | CDS 3' incomplete TSL:5 |
| Ube2f-205 | ENSMUST00000185697.1 | 1365 | No protein | Retained intron | - | - | TSL:NA |
| Ube2f-209 | ENSMUST00000189589.1 | 823 | No protein | Retained intron | - | - | TSL:3 |
| Ube2f-208 | ENSMUST00000188576.1 | 639 | No protein | Retained intron | - | - | TSL:3 |
| Ube2f-206 | ENSMUST00000185950.1 | 587 | No protein | Retained intron | - | - | TSL:2 |
| Ube2f-207 | ENSMUST00000187494.1 | 520 | No protein | Retained intron | - | - | TSL:3 |

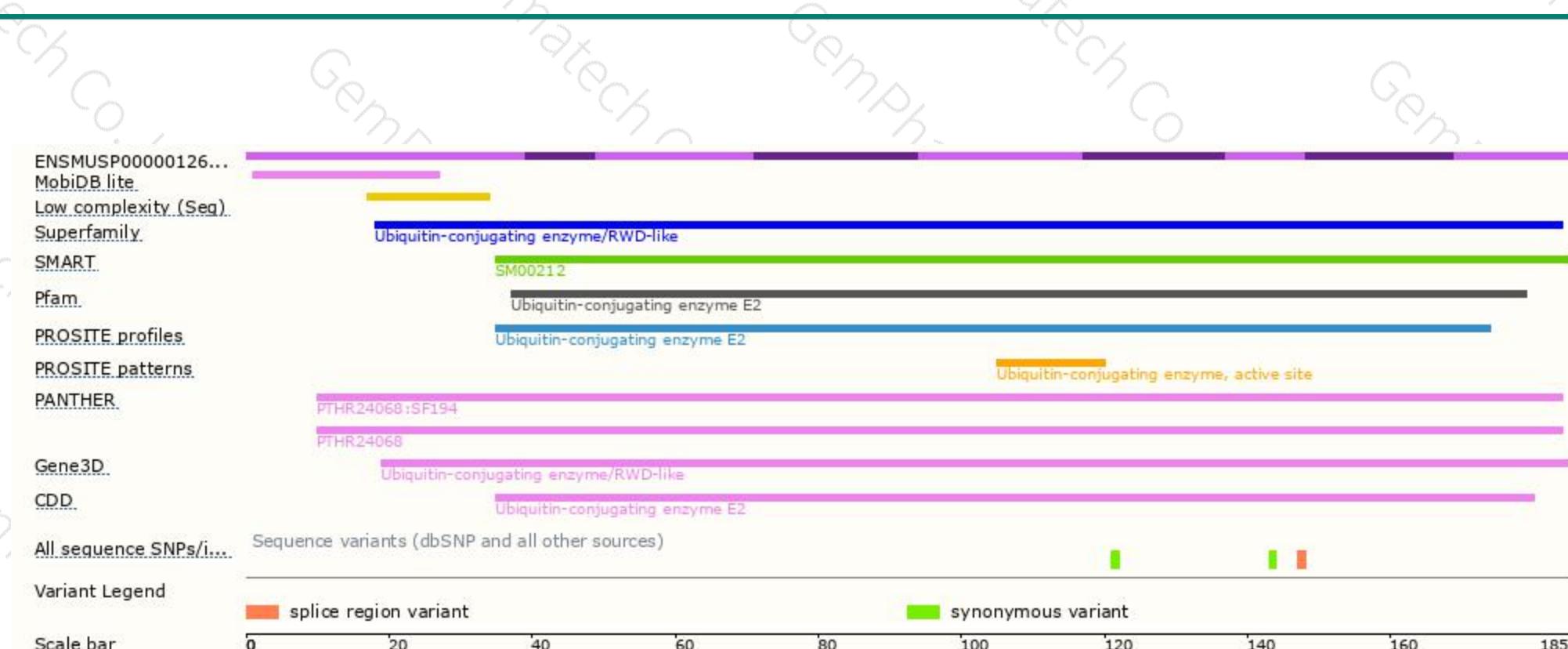
The strategy is based on the design of *Ube2f-203* transcript, The transcription is shown below



Genomic location distribution



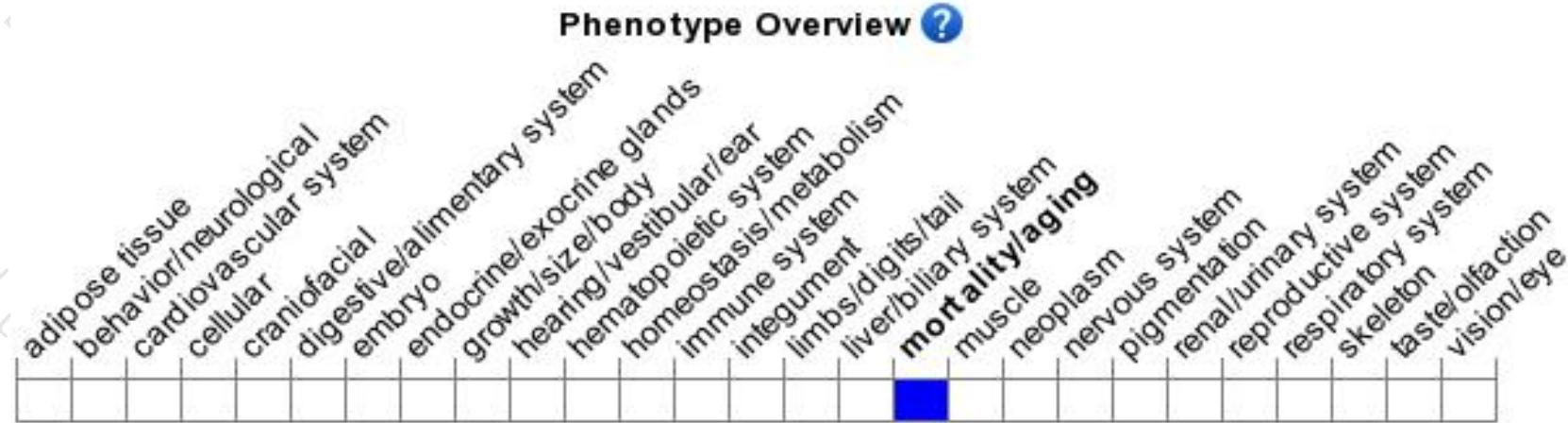
Protein domain





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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.

Tel: 400-9660890



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