

Kdm6a CKO Strategy

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Overview

Target Gene Name

- *Kdm6a*

Project Type

- CKO

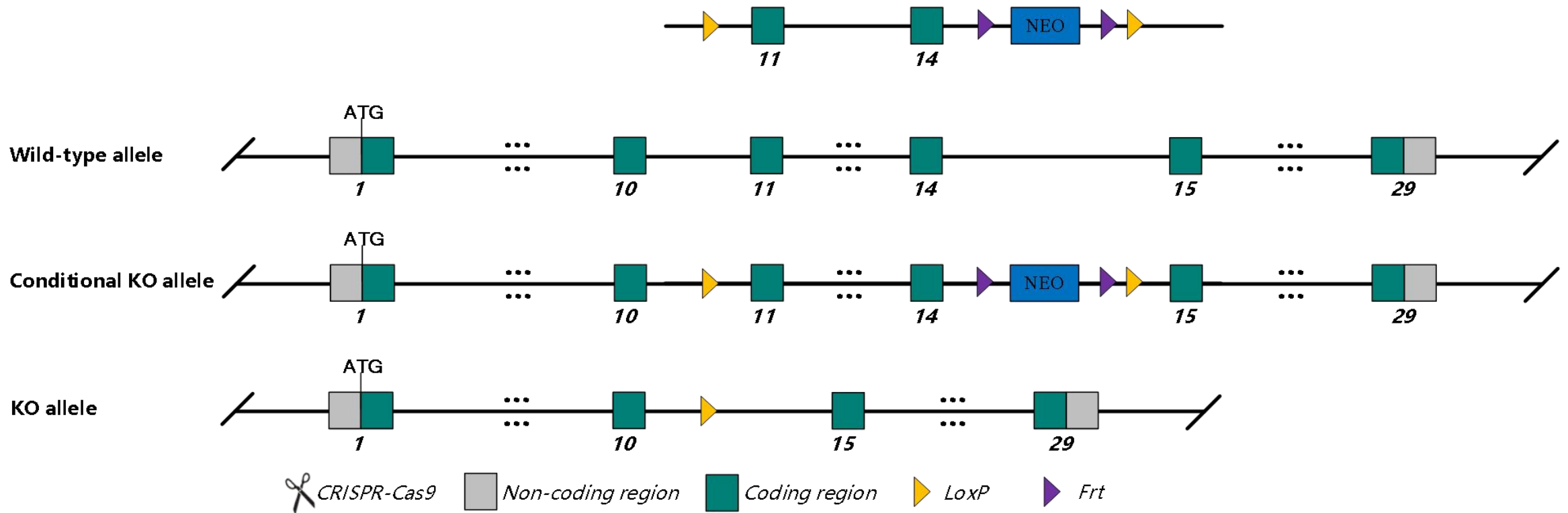
Genetic Background

- C57BL/6NGpt

Strain Strategy

This model will use ES cell mediated homologous recombination technology to edit the *Kdm6a* gene.

The schematic diagram is as follows:



Technical Information

- The *Kdm6a* gene has 10 transcripts. According to the structure of *Kdm6a* gene, exon11-14 of *Kdm6a-202* (ENSMUST00000052368.8) transcript is recommended as the knockout region. The region contains 544bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use ES cell targeting and homologous recombination technology to modify *Kdm6a* gene. The brief process is as follows: the targeting vector is constructed in vitro and the ES cells are electroporated. The ES clones screened by PCR and southern are injected into the donor blastocysts and transplanted into the pseudo-pregnant mother to further develop chimeric mice. A stable F1 generation mouse model was obtained by mating chimeric mice with C57BL/6N mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Gene Information

Kdm6a lysine (K)-specific demethylase 6A [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 22289, updated on 5-Mar-2024

Summary

Official Symbol Kdm6a provided by [MGI](#)
Official Full Name lysine (K)-specific demethylase 6A provided by [MGI](#)
Primary source [MGI:MGI:1095419](#)
See related [Ensembl:ENSMUSG000000037369](#) [AllianceGenome:MGI:1095419](#)
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 Utx
Summary Enables DNA binding activity; histone H3-tri/di-methyl-lysine-27 demethylase activity; and identical protein binding activity. Involved in chromatin remodeling. Acts upstream of or within several processes, including chordate embryonic development; embryonic morphogenesis; and histone H3-K27 demethylation. Located in nucleus. Part of histone methyltransferase complex. Is expressed in several structures, including early conceptus; gonad; liver; lung; and spleen. Used to study chronic myelomonocytic leukemia. Human ortholog(s) of this gene implicated in several diseases, including Kabuki syndrome; bladder urothelial carcinoma; gastrointestinal system cancer (multiple); lung carcinoma (multiple); and triple-receptor negative breast cancer. Orthologous to human KDM6A (lysine demethylase 6A). [provided by Alliance of Genome Resources, Apr 2022]
Expression Ubiquitous expression in limb E14.5 (RPKM 6.2), thymus adult (RPKM 6.1) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: X A1.2- A1.3; X 13.45 cM

See Kdm6a in [Genome Data Viewer](#)

Exon count: 31

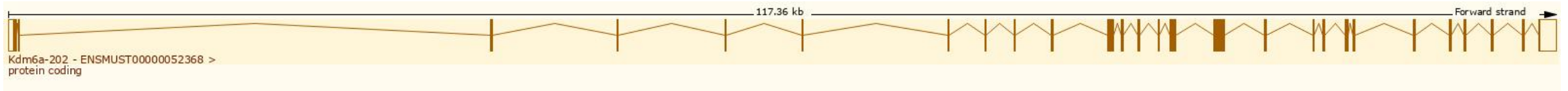
<https://www.ncbi.nlm.nih.gov/gene/22289>

Transcript Information

The gene has 10 transcripts, all transcripts are shown below:

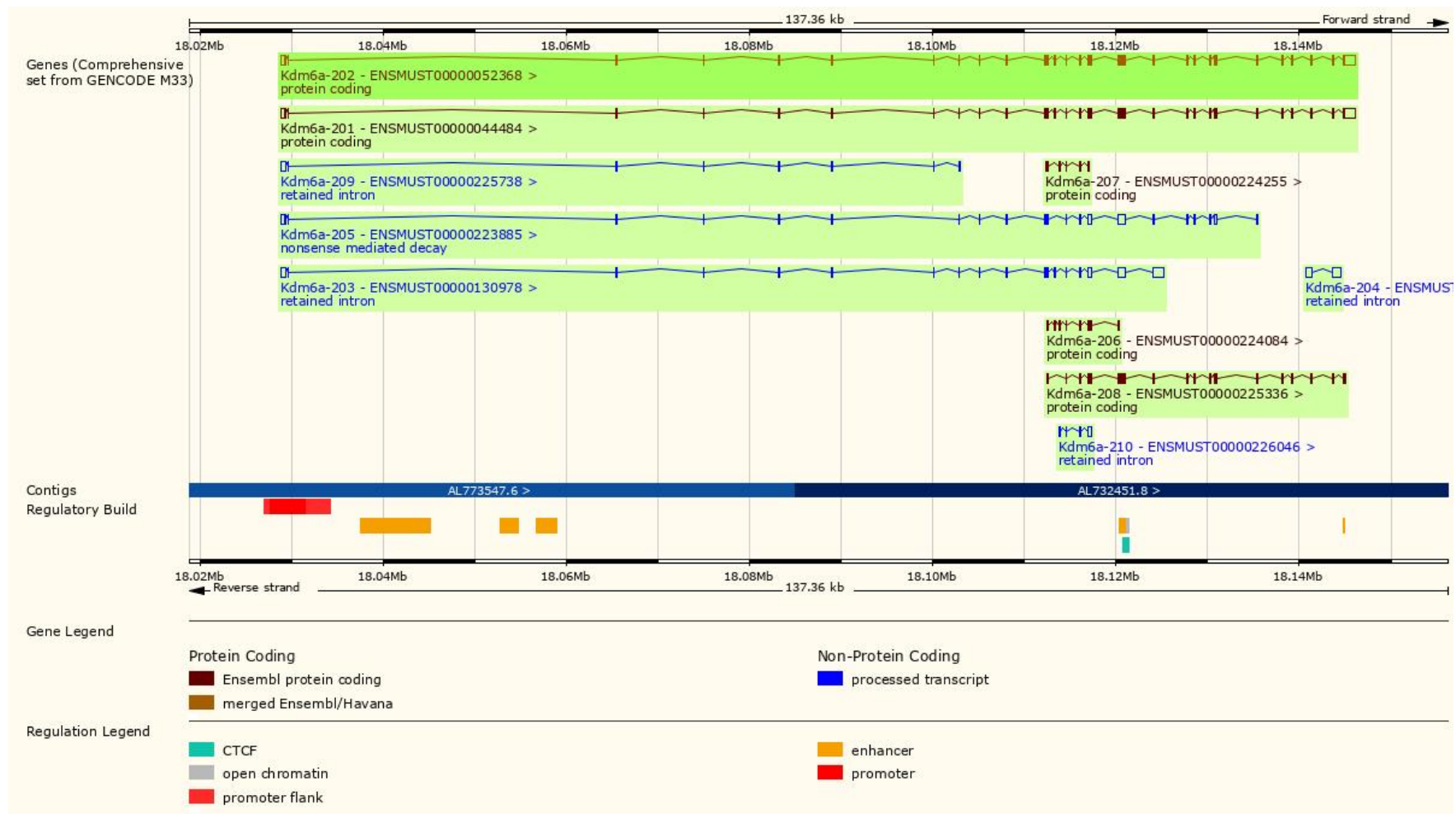
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|---------------------------------------|-----------|------|------------------------|-------------------------|---------------------------|----------------------------|---------------------------------------|
| ENSMUST00000052368.9 | Kdm6a-202 | 5935 | 1424aa | Protein coding | CCDS30037 | O70546-2 | Ensembl Canonical GENCODE basic TSL:1 |
| ENSMUST00000044484.13 | Kdm6a-201 | 5918 | 1401aa | Protein coding | CCDS81102 | O70546 | GENCODE basic APPRIS P1 TSL:5 |
| ENSMUST000000225336.2 | Kdm6a-208 | 3219 | 997aa | Protein coding | | A0A286YD05 | CDS 5' incomplete |
| ENSMUST000000224084.2 | Kdm6a-206 | 1107 | 369aa | Protein coding | | A0A286YD51 | CDS 5' and 3' incomplete |
| ENSMUST000000224255.2 | Kdm6a-207 | 710 | 236aa | Protein coding | | A0A286YCW2 | CDS 5' and 3' incomplete |
| ENSMUST000000223885.2 | Kdm6a-205 | 3717 | 224aa | Nonsense mediated decay | | A0A286YDX1 | - |
| ENSMUST000000130978.2 | Kdm6a-203 | 4193 | No protein | Retained intron | | - | TSL:1 |
| ENSMUST000000155161.2 | Kdm6a-204 | 1535 | No protein | Retained intron | | - | TSL:1 |
| ENSMUST000000225738.2 | Kdm6a-209 | 1049 | No protein | Retained intron | | - | - |
| ENSMUST000000226046.2 | Kdm6a-210 | 791 | No protein | Retained intron | | - | - |

The strategy is based on the design of *Kdm6a-202* transcript, the transcription is shown below:

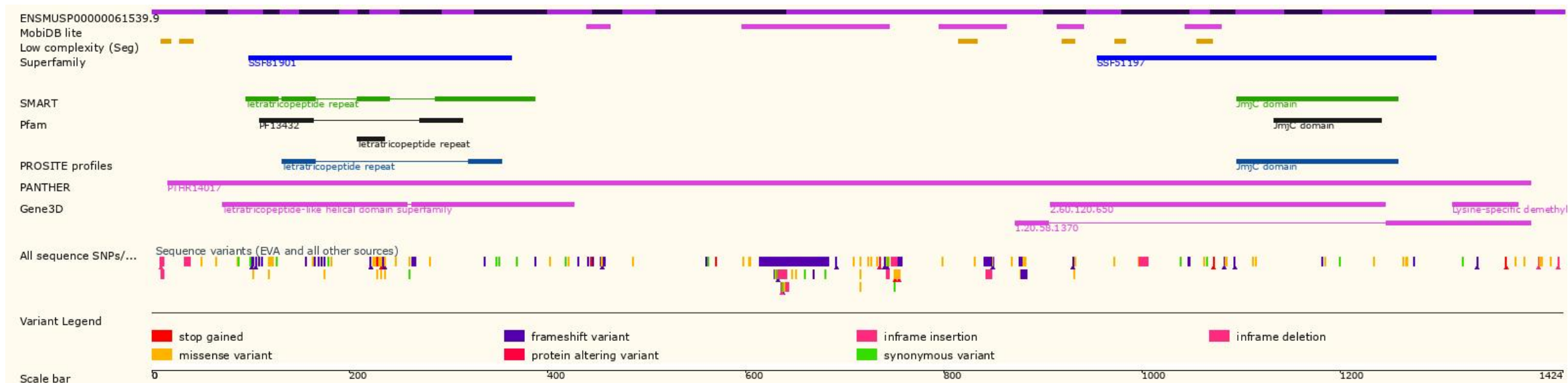


Source: <http://asia.ensembl.org/>

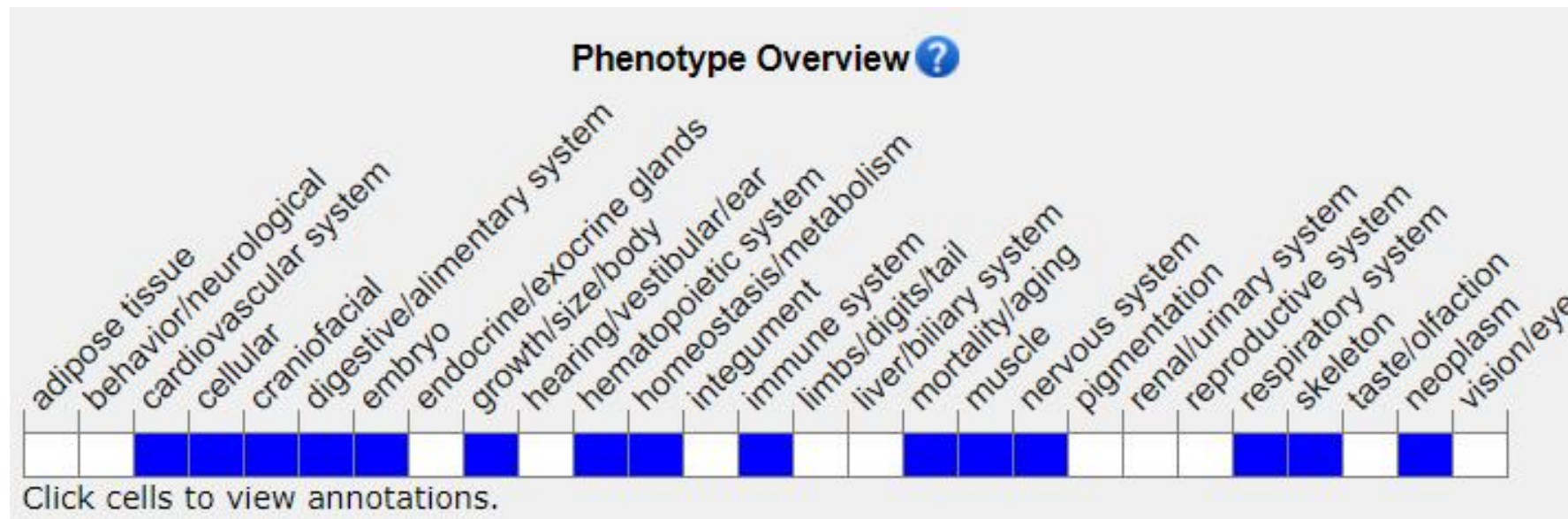
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



Mice homozygous for a knock-out allele exhibit embryonic lethality, caudal body truncation, abnormal neural tube closure and abnormal heart development. Mice hemizygous for this allele exhibit perinatal lethality, abnormal neural tube closure, inability to breath, exencephaly and atelectasis.

Important Information

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit embryonic lethality, caudal body truncation, abnormal neural tube closure and abnormal heart development. Mice hemizygous for this allele exhibit perinatal lethality, abnormal neural tube closure, inability to breath, exencephaly and atelectasis.
- The *Kdm6a* gene is located on the ChrX. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.