Ttll6 Cas9-CKO Strategy

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Reviewer: Yumeng Wang

Design Date: 2023-02-06

Overview

Target Gene Name

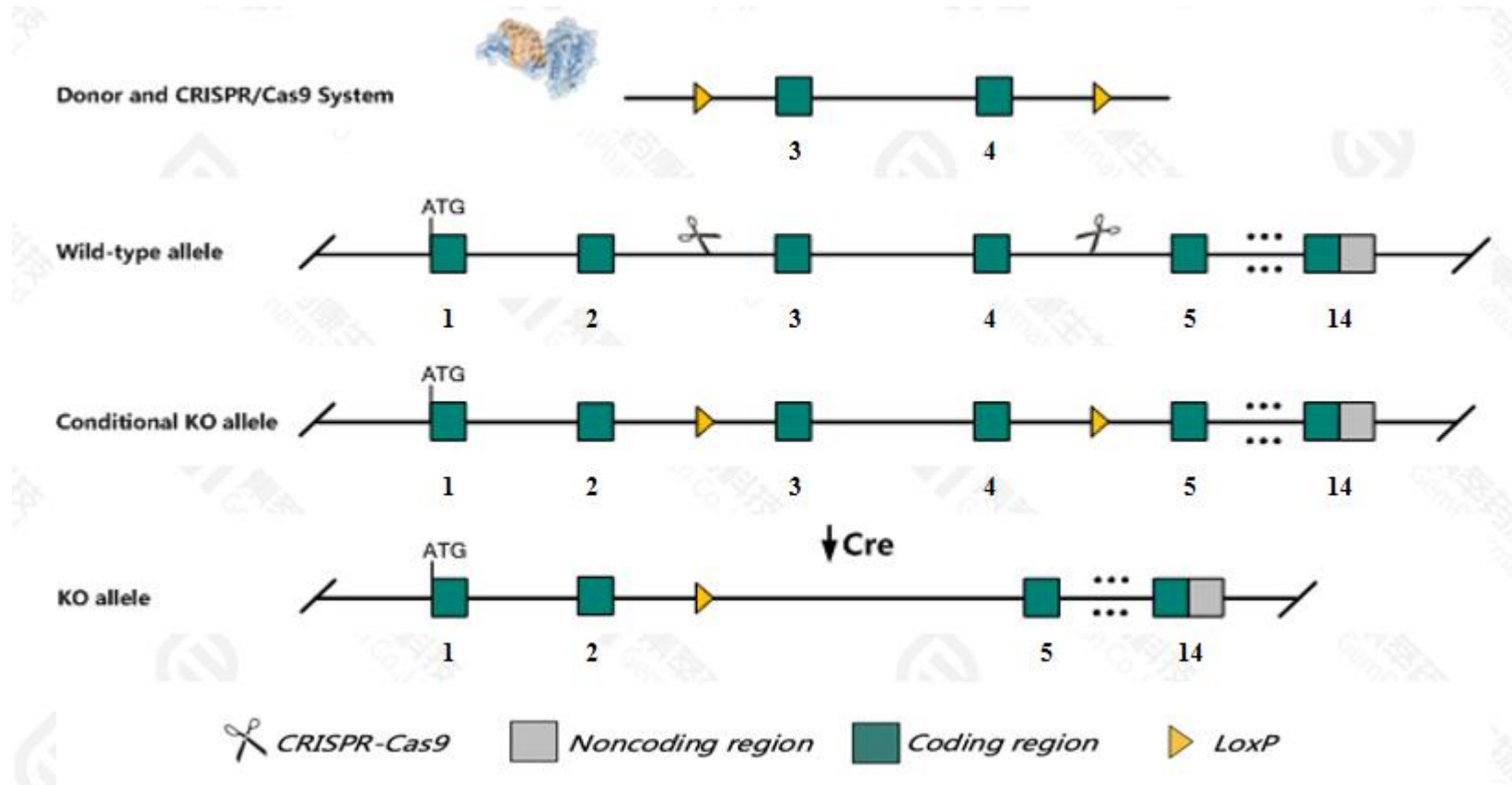- Ttll6

Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

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Strain Strategy

Schematic representation of CRISPR-Cas9 engineering used to edit the *Ttll6* gene.

Technical Information

- The *Ttll6* gene has 2 transcripts. According to the structure of *Ttll6* gene, exon3-exon4 of *Ttll6-202*(ENSMUST00000167258.8) transcript is recommended as the knockout region. The region contains 250bp of coding sequences. Knocking out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Ttll6* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

- 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.

Gene Information

Ttll6 tubulin tyrosine ligase-like family, member 6 [*Mus musculus* (house mouse)]

Gene ID: 237930, updated on 26-Sep-2022

Summary

Official Symbol	Ttll6 provided by MGI
Official Full Name	tubulin tyrosine ligase-like family, member 6 provided by MGI
Primary source	MGI:MGI:2683461
See related	Ensembl:ENSMUSG00000038756 AllianceGenome:MGI:2683461
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	t8130b59; D11Moh43e; D11Moh44e; 4932418K24Rik
Summary	Enables protein-glutamic acid ligase activity and tubulin binding activity. Involved in protein polyglutamylation. Acts upstream of or within microtubule bundle formation; microtubule severing; and positive regulation of cilium movement. Located in 9+0 non-motile cilium and ciliary basal body. Is expressed in several structures, including alimentary system; branchial arch; genitourinary system; inner ear; and primitive streak. Orthologous to human TTLL6 (tubulin tyrosine ligase like 6). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in testis adult (RPKM 23.0), colon adult (RPKM 7.5) and 1 other tissue See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

|	
Location:	11 D; 11 59.48 cM
Exon count:	15

See Ttll6 in Genome Data Viewer

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Transcript Information

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

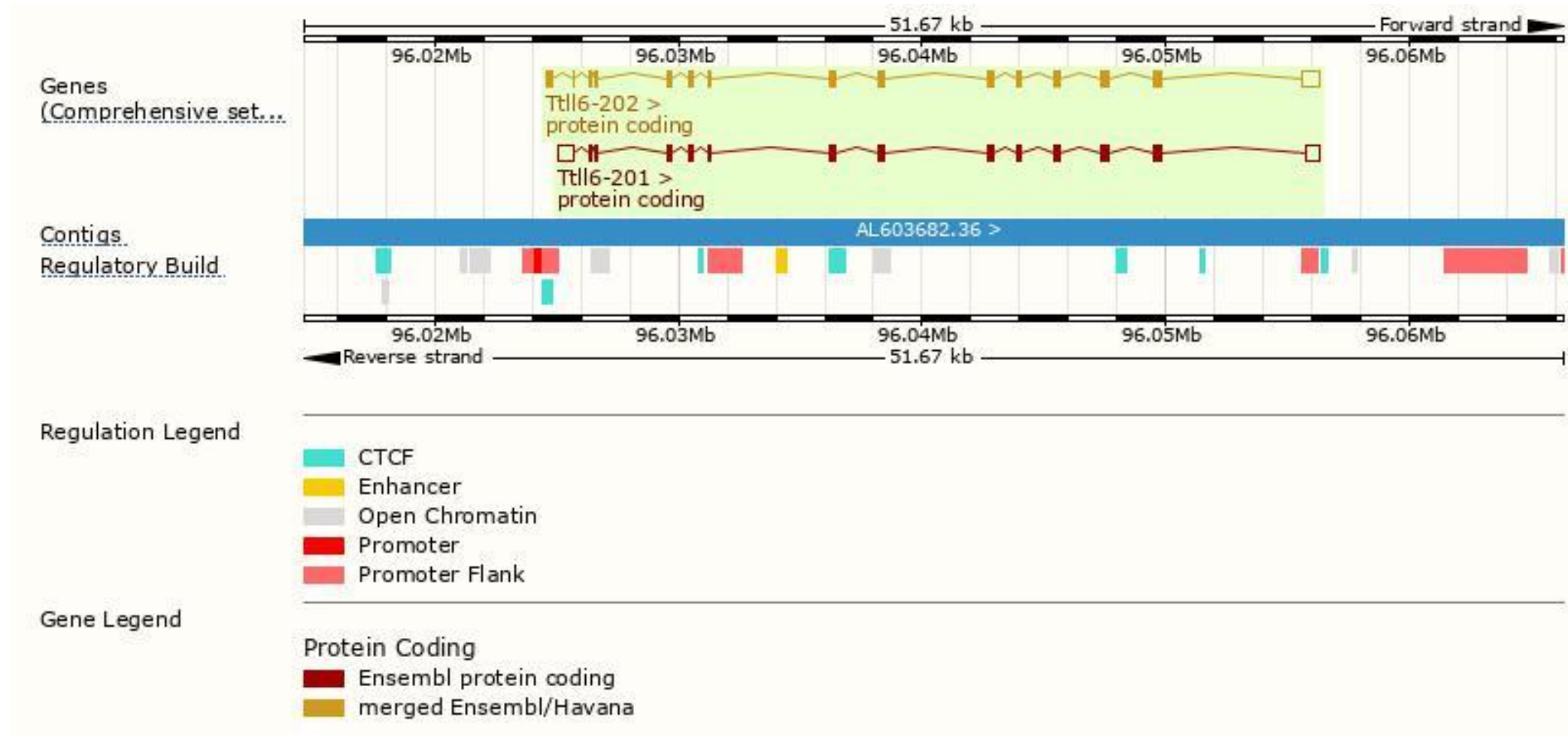| Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000167258.8	Ttll6-202	3205	822aa	Protein coding	CCDS25290	A4Q9E8-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000107680.2	Ttll6-201	3485	718aa	Protein coding		A4Q9E8-2	GENCODE basic TSL:5

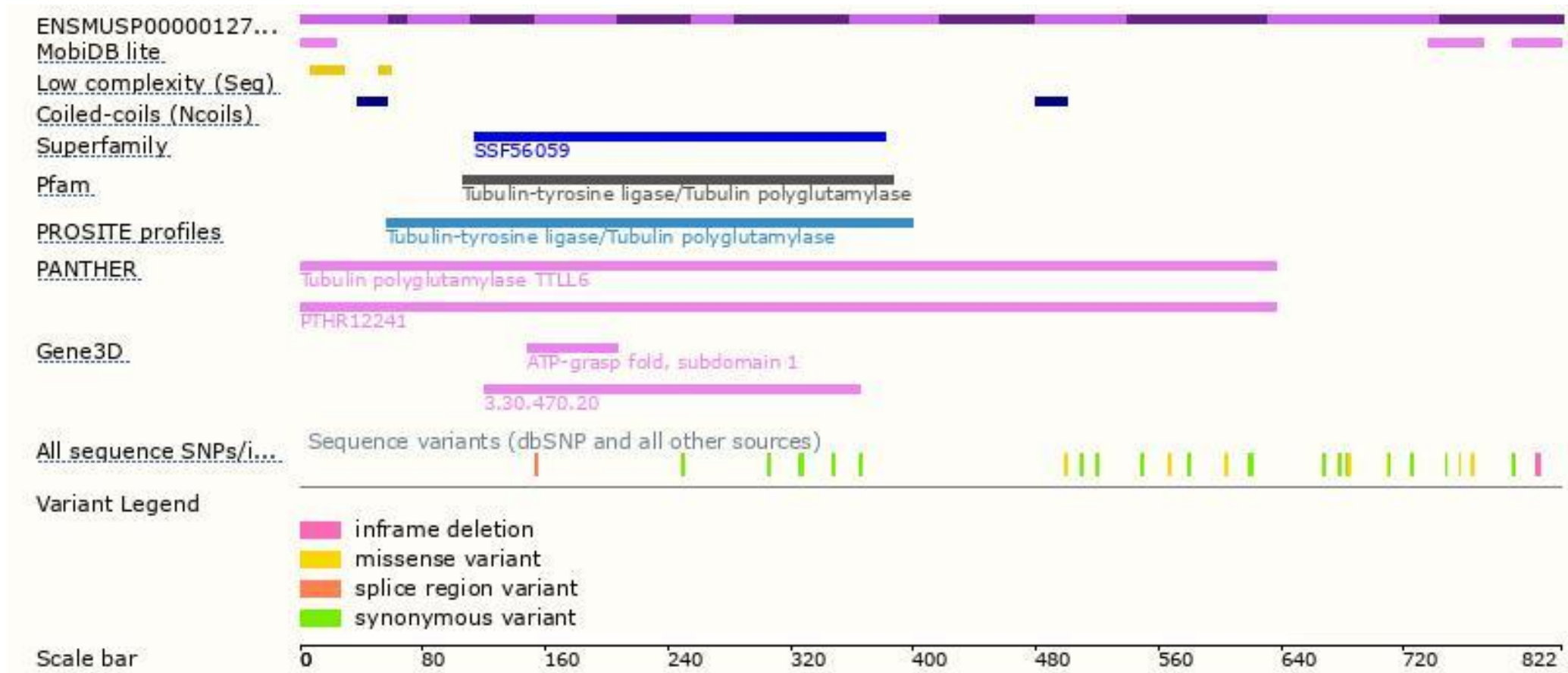The strategy is based on the design of *Ttll6*-202 transcript, the transcription is shown below:

Ttll6-202 >
protein coding

Source: https://www.ensembl.org

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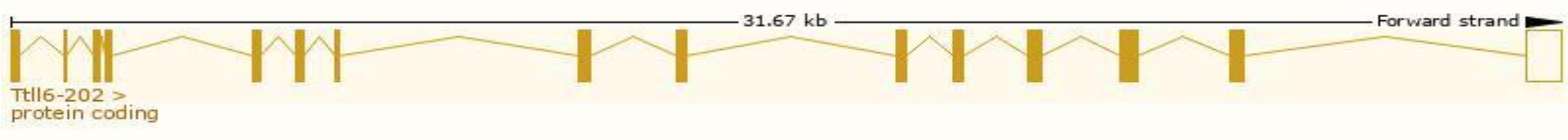
Genomic Information
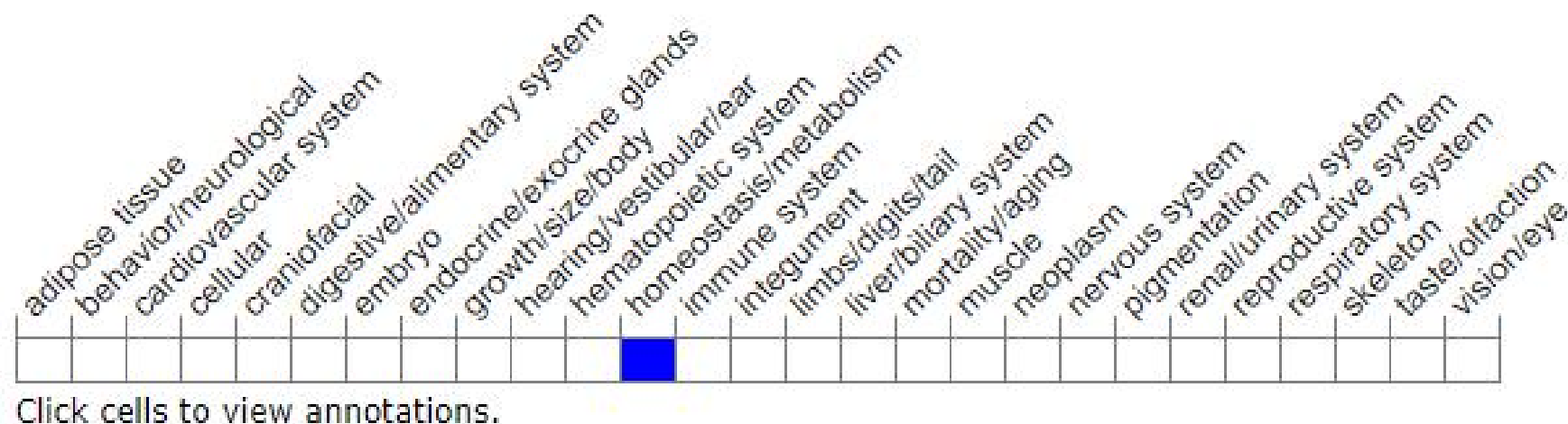
Protein Information

Source: : https://www.ensembl.org

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Mouse Phenotype Information (MGI)

- Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

Source: https://www.informatics.jax.org

Important Information

- The Intron2 is only 576bp ,loxp insertion may affect mRNA splicing.

- The *Ttll6* gene is located on the Chr11. 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.

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