

Ttl Cas9-KO Strategy

Designer:

Daohua Xu

Project Overview

Project Name

Ttl

Project type

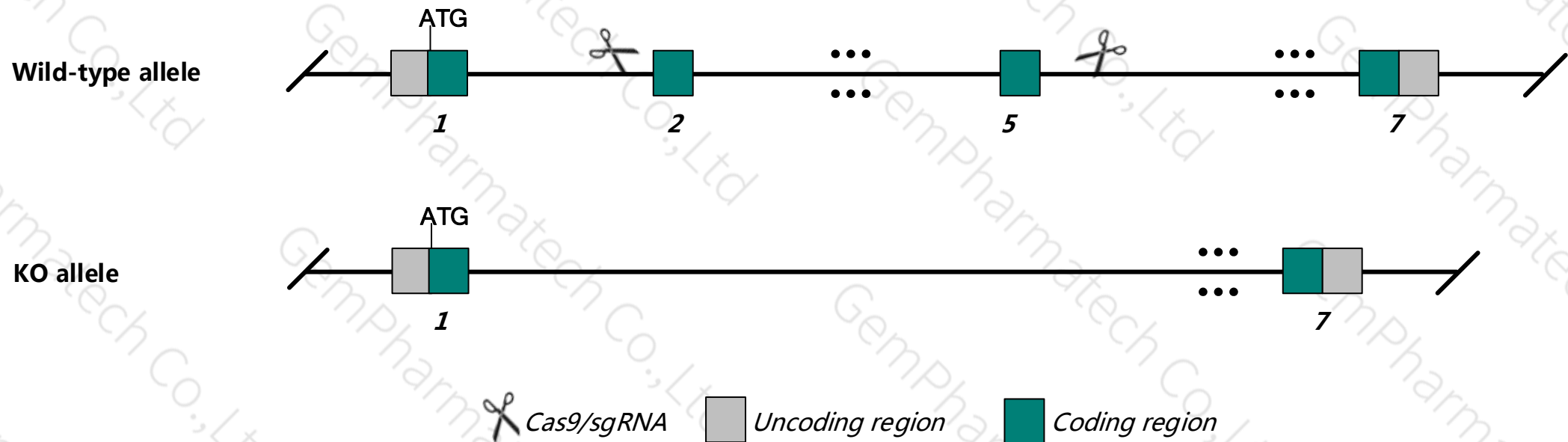
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



Technical routes

- The *Ttl* gene has 3 transcripts. According to the structure of *Ttl* gene, exon2-exon5 of *Ttl*-201 (ENSMUST00000035812.13) transcript is recommended as the knockout region. The region contains 718bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ttl* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data , Homozygous null mice display neonatal lethality, impaired breathing, and fail to form the internal capsule in the brain.
- The KO region contains the functional region of the *Gm14022* gene. Knockout the region may affect its function of *Gm14022* gene.
- The *Ttl* gene is located on the Chr2. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Ttl tubulin tyrosine ligase [*Mus musculus* (house mouse)]

Gene ID: 69737, updated on 28-Aug-2018

Summary

Official Symbol Ttl provided by [MGI](#)

Official Full Name tubulin tyrosine ligase provided by [MGI](#)

Primary source [MGI:MGI:1916987](#)

See related [Ensembl:ENSMUSG00000027394](#); [Vega:OTTMUSG00000015410](#)

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 AI848570; 2410003M22Rik; 2700049H19Rik

Expression Ubiquitous expression in CNS E18 (RPKM 12.5), cortex adult (RPKM 10.7) and 27 other tissues [See more](#)

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

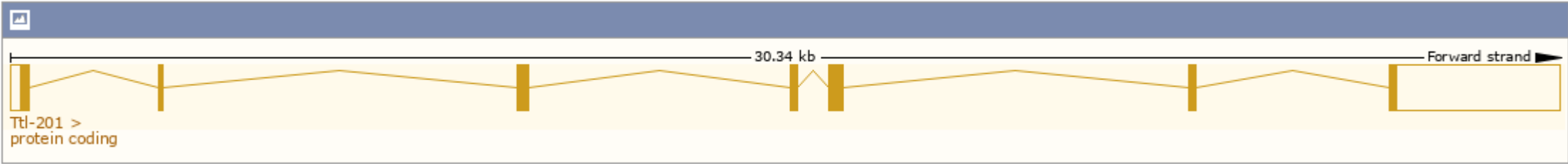
Transcript information (Ensembl)

The gene has 3 transcripts, and all transcripts are shown below :

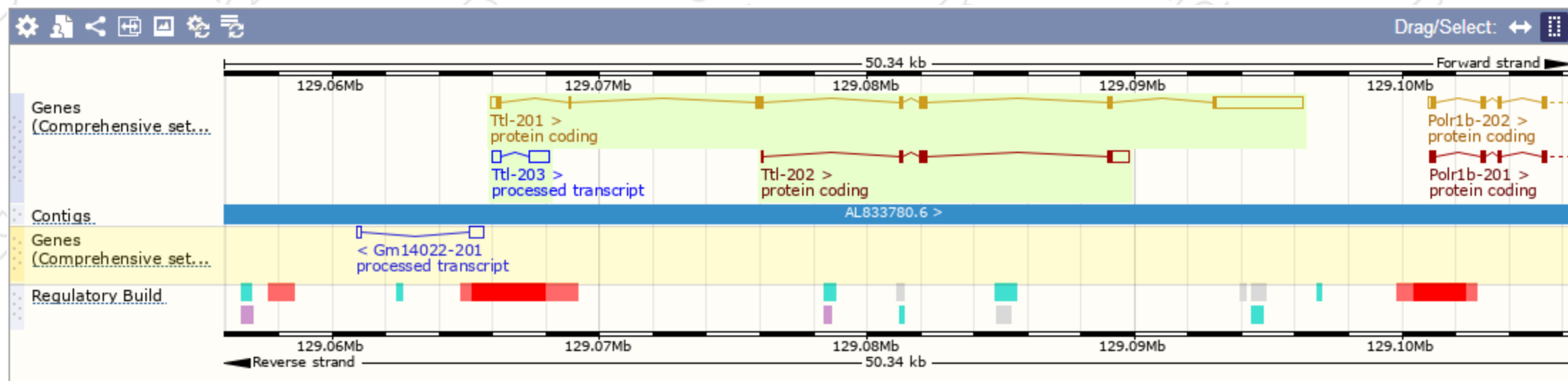
Show/hide columns (1 hidden)

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Ttl-201	ENSMUST00000035812.13	4567	377aa	Protein coding	CCDS16719	P38585	NM_027192 NP_081468	TSL:1 GENCODE basic APPRIS P1
Ttl-202	ENSMUST00000144120.1	1238	199aa	Protein coding	-	F6ZXS5	-	CDS 5' incomplete TSL:1
Ttl-203	ENSMUST00000144730.1	1053	No protein	Processed transcript	-	-	-	TSL:1

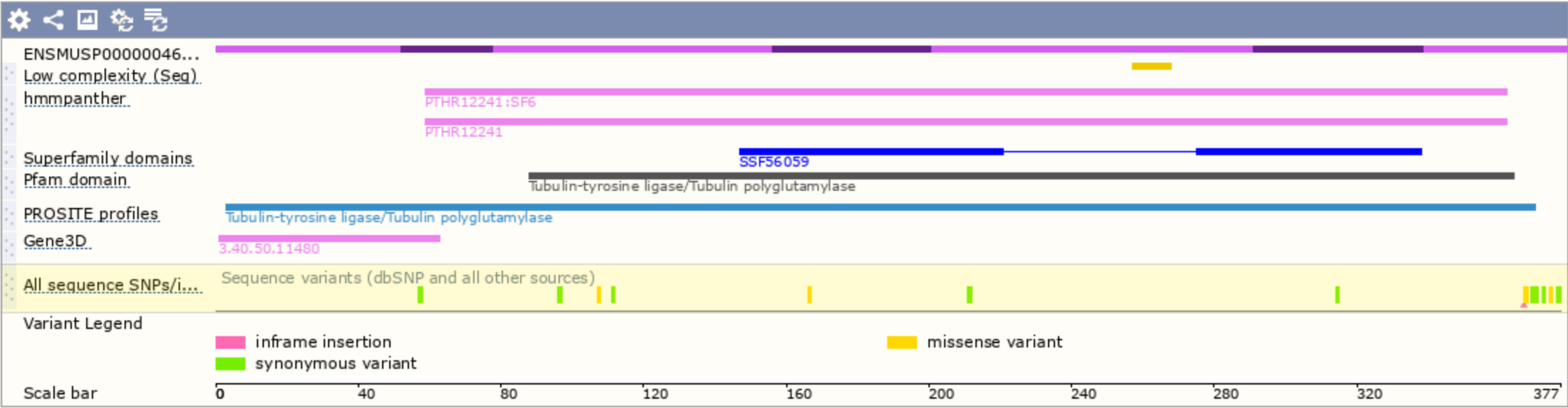
The strategy is based on the design of *Ttl-201* transcript, The transcription is shown below



Genomic location distribution

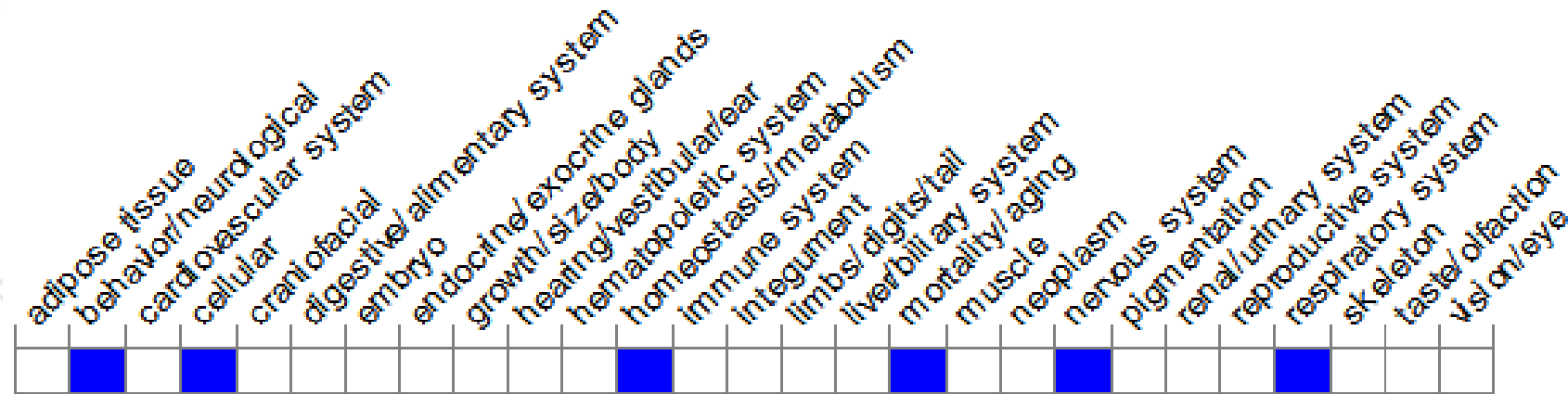


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Click cells to view annotations.

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.
Tel: 025-5864 1534

