

Ttll1 Cas9-CKO Strategy

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Design Date: 2023-02-06

Overview

Target Gene Name

- Ttl11

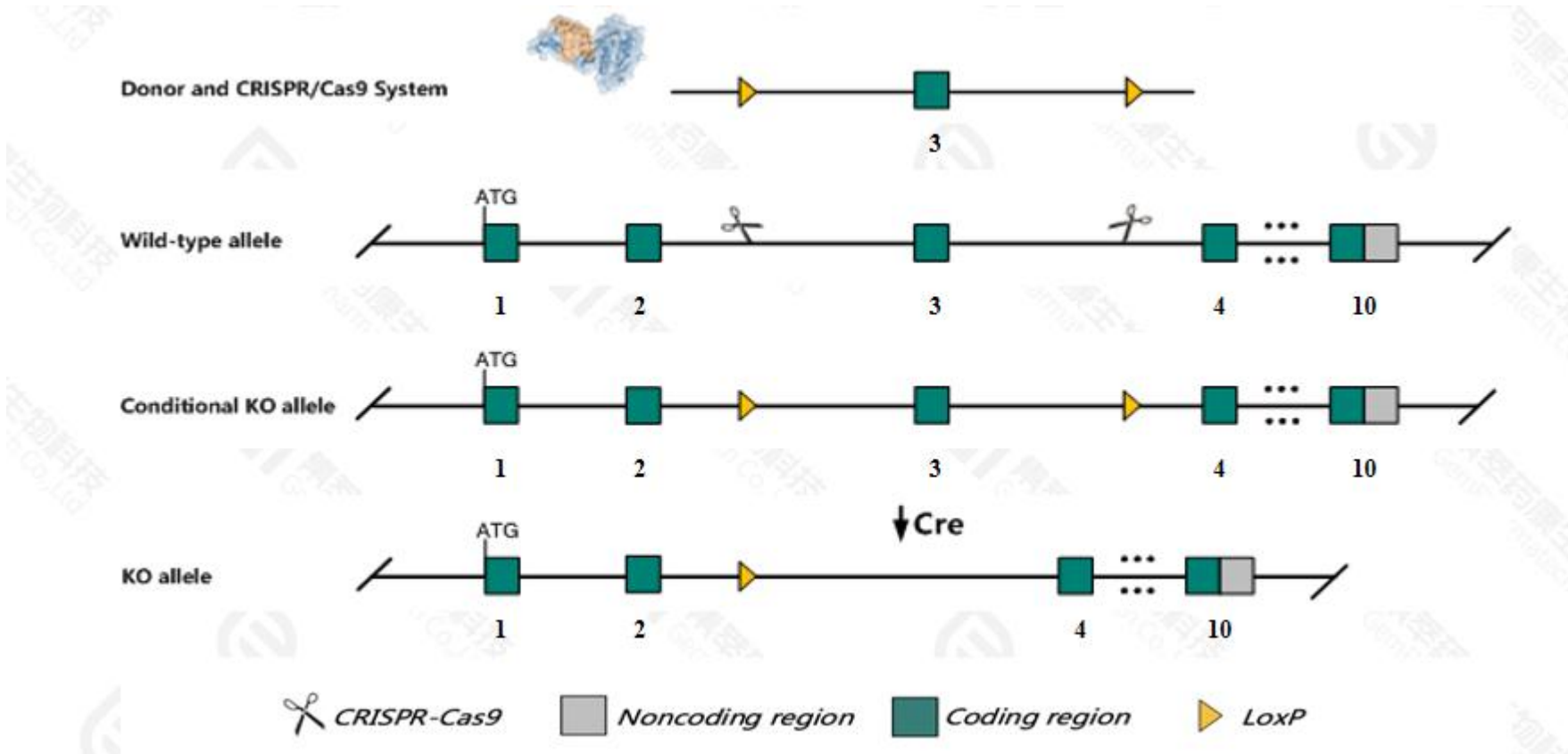
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ttll1* gene.

Technical Information

- The *Ttll1* gene has 9 transcripts. According to the structure of *Ttll1* gene, exon3 of *Ttll1*-201 (ENSMUST00000028248.11) transcript is recommended as the knockout region. The region contains 134bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ttll1* 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

Ttll11 tubulin tyrosine ligase-like family, member 11 [*Mus musculus* (house mouse)]

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Gene ID: 74410, updated on 24-Jan-2023

Summary

Official Symbol [Ttll11](#) provided by [MGI](#)
Official Full Name tubulin tyrosine ligase-like family, member 11 provided by [MGI](#)
Primary source [MGI:MGI:1921660](#)
See related [Ensembl:ENSMUSG00000026885](#) [AllianceGenome:MGI:1921660](#)
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 D2Ert624e; 4932702F08Rik; 4933424A20Rik
Summary Predicted to enable tubulin binding activity and tubulin-glutamic acid ligase activity. Acts upstream of or within microtubule severing and protein polyglutamylation. Located in ciliary basal body. Is expressed in retina. Orthologous to human TTLL11 (tubulin tyrosine ligase like 11). [provided by Alliance of Genome Resources, Apr 2022]
Expression Biased expression in testis adult (RPKM 19.6), cortex adult (RPKM 7.2) and 9 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: 2 B; 2 23.9 cM

Exon count: 10

See Ttll11 in [Genome Data Viewer](#)

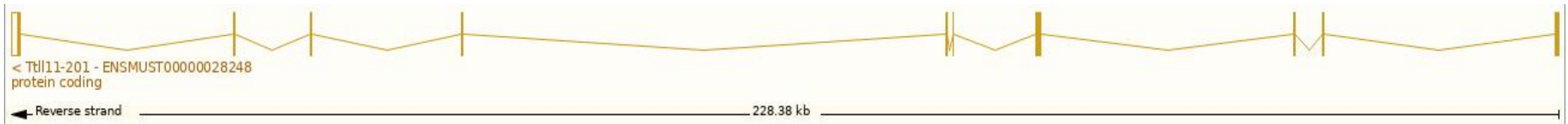
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

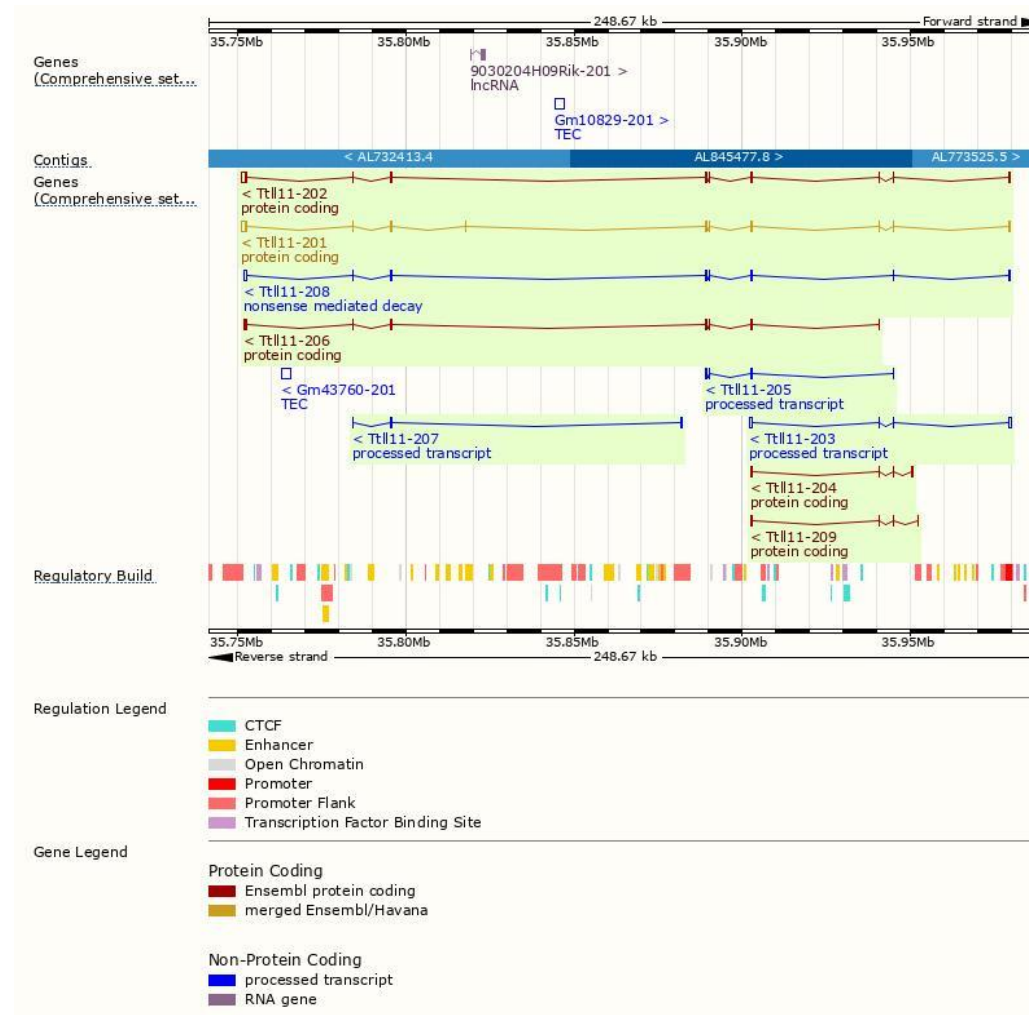
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000028248.11	Ttll11-201	3176	727aa	Protein coding	CCDS50579	A4Q9F4-1	Ensembl Canonical GENCODE basic APPRIS P2 TSL:1
ENSMUST00000112976.9	Ttll11-202	3077	694aa	Protein coding		A4Q9F4-2	GENCODE basic APPRIS ALT2 TSL:5
ENSMUST00000160906.2	Ttll11-206	1820	511aa	Protein coding		F7BQM5	TSL:1 CDS 5' incomplete
ENSMUST00000140201.8	Ttll11-204	839	210aa	Protein coding		E0CY35	TSL:3 CDS 3' incomplete
ENSMUST00000162172.2	Ttll11-209	838	204aa	Protein coding		E0CXL9	TSL:2 CDS 3' incomplete
ENSMUST00000161970.8	Ttll11-208	2654	190aa	Nonsense mediated decay		E0CZ80	TSL:5
ENSMUST00000127742.8	Ttll11-203	1768	No protein	Protein coding CDS not defined		-	TSL:5
ENSMUST00000160284.2	Ttll11-205	852	No protein	Protein coding CDS not defined		-	TSL:5
ENSMUST00000160939.2	Ttll11-207	458	No protein	Protein coding CDS not defined		-	TSL:3

The strategy is based on the design of *Ttll11-201* transcript, the transcription is shown below:

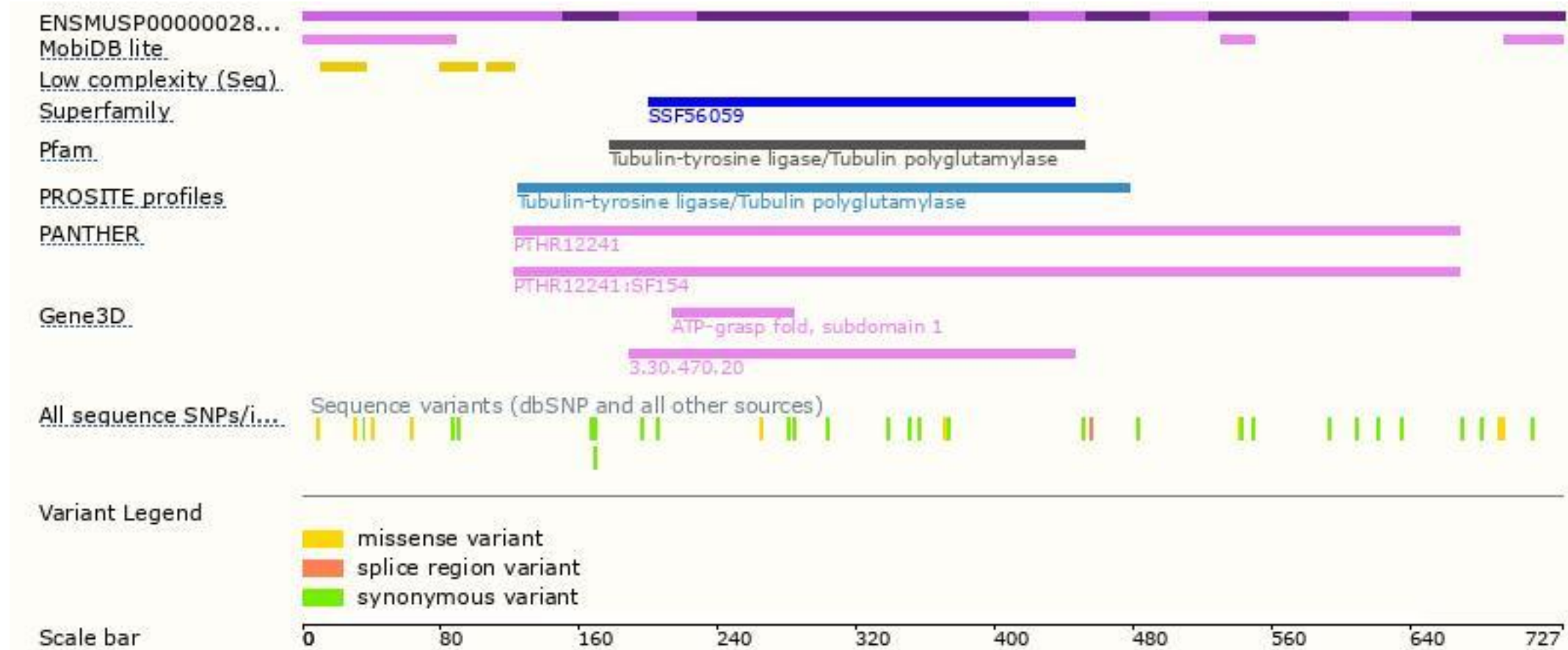


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- The *Ttll1* 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 biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.