

Tlr1 Cas9-KO Strategy

Designer:

Huan Wang

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Project Overview

Project Name

Tlr1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tlr1* gene. The schematic diagram is as follows:



- The *Tlr1* gene has 3 transcripts. According to the structure of *Tlr1* gene, exon4 of *Tlr1-202* (ENSMUST00000197315.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tlr1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mice display decreased macrophage peptoglycan-stimulated IL-6 production.
- The *Tlr1* gene is located on the Chr5. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Tlr1 toll-like receptor 1 [Mus musculus (house mouse)]

Gene ID: 21897, updated on 31-Jan-2019

Summary

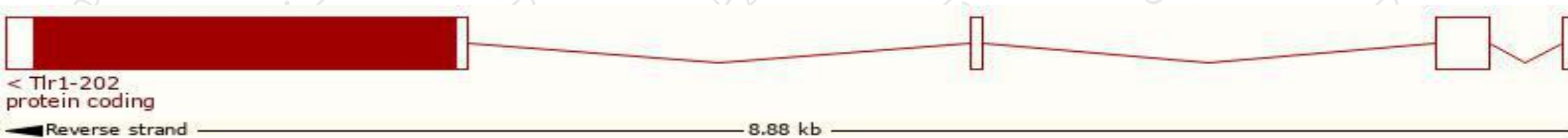
| | |
|---------------------------|---|
| Official Symbol | Tlr1 provided by MGI |
| Official Full Name | toll-like receptor 1 provided by MGI |
| Primary source | MGI:MGI:1341295 |
| See related | Ensembl:ENSMUSG00000044827 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Expression | Biased expression in spleen adult (RPKM 12.1), colon adult (RPKM 6.6) and 11 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

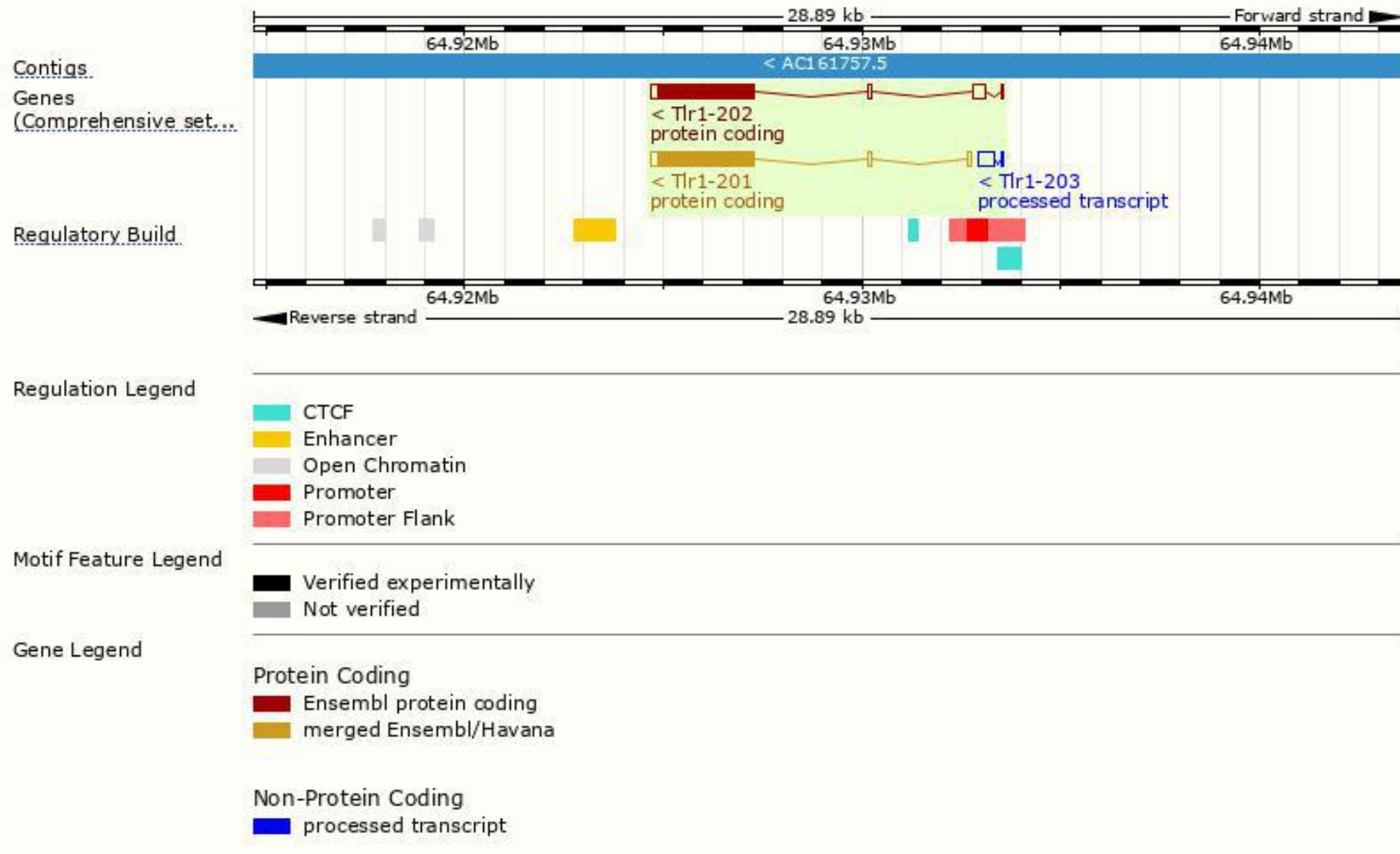
The gene has 3 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|-----------------------|----------------------|---------------------------|-------------------------------|-------------------------------|
| Tlr1-202 | ENSMUST00000197315.4 | 3025 | 795aa | Protein coding | CCDS19302 | B9EJ46 Q9EPQ1 | TSL:1 GENCODE basic APPRIS P1 |
| Tlr1-201 | ENSMUST00000059349.5 | 2783 | 795aa | Protein coding | CCDS19302 | B9EJ46 Q9EPQ1 | TSL:1 GENCODE basic APPRIS P1 |
| Tlr1-203 | ENSMUST00000197886.1 | 419 | No protein | Processed transcript | - | - | TSL:2 |

The strategy is based on the design of *Tlr1-202* transcript, The transcription is shown below



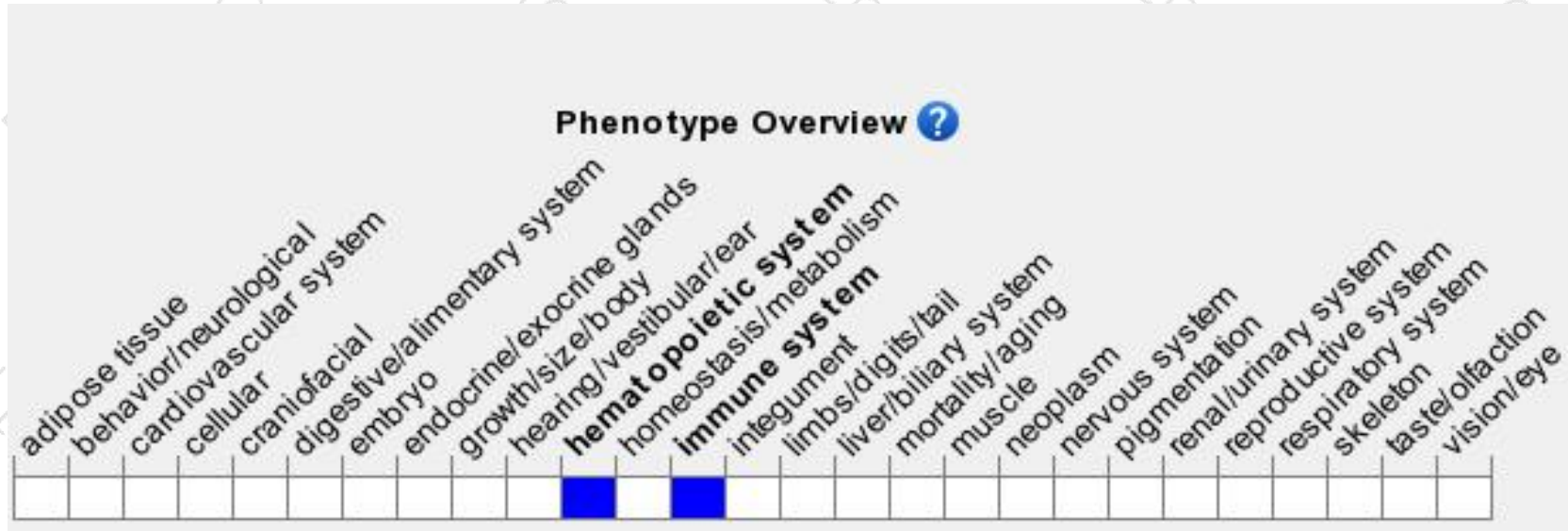
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



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

According to the existing MGI data, Homozygous null mice display decreased macrophage peptoglycan-stimulated IL-6 production.