

Tlr7 Cas9-KO Strategy

Designer: Jinling Wang
Reviewer: Shilei Zhu
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Project Overview

Project Name

Tlr7

Project type

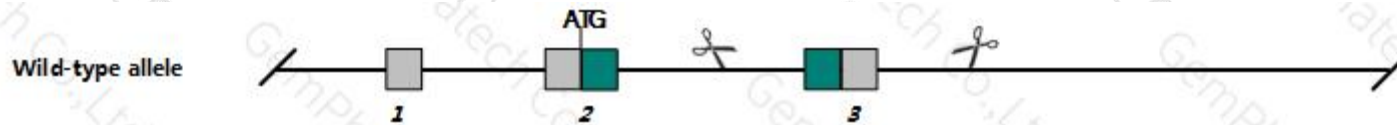
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tlr7* gene. The schematic diagram is as follows:



Technical routes

- The *Tlr7* gene has 6 transcripts. According to the structure of *Tlr7* gene, exon3 of *Tlr7*-201 (ENSMUST00000060719.11) transcript is recommended as the knockout region. The region contains most 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 *Tlr7* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 , The innate immune response to viral infection is affected in homozygous null mice. Mice homozygous or hemizygous for a point mutation produce little or no tumor necrosis factor (TNF) alpha in response to stimulation by a single stranded RNA analog.
- The KO region deletes most of the coding sequence, but does not result in frameshift.
- The *Tlr7* gene is located on the ChrX. 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)

Summary

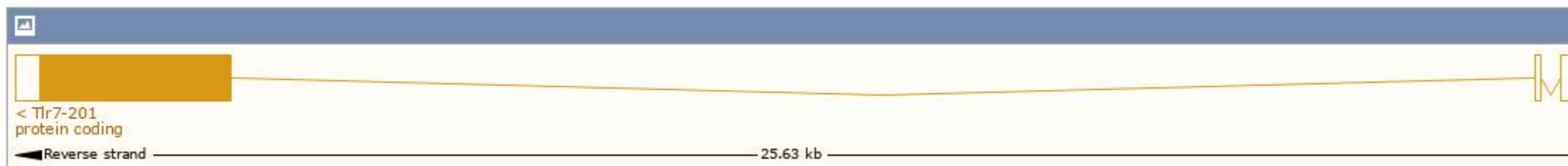
Official Symbol	Tlr7 provided by MGI
Official Full Name	toll-like receptor 7 provided by MGI
Primary source	MGI:MGI:2176882
See related	Ensembl:ENSMUSG00000044583
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information (Ensembl)

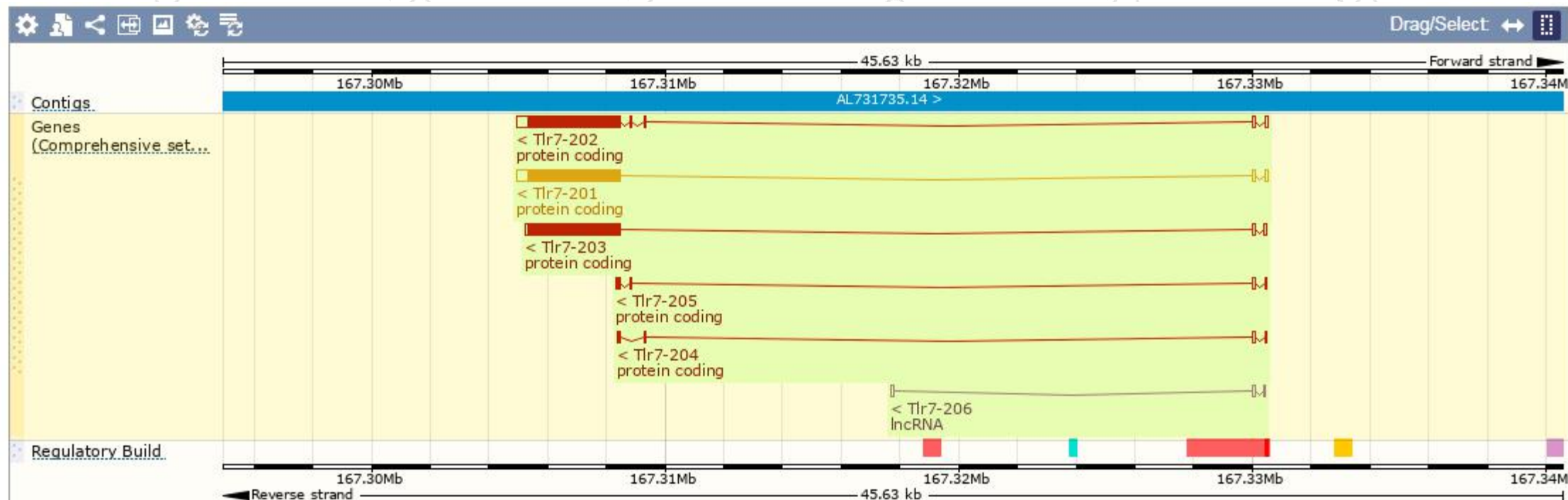
The gene has 6 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tlr7-202	ENSMUST00000112161.7	3897	1050aa	Protein coding	CCDS72469	P58681 Q548J0	TSL:1 GENCODE basic APPRIS P1
Tlr7-201	ENSMUST00000060719.11	3776	1050aa	Protein coding	CCDS30531	P58681 Q548J0	TSL:1 GENCODE basic APPRIS P1
Tlr7-203	ENSMUST00000112164.1	3468	1050aa	Protein coding	CCDS30531	P58681 Q548J0	TSL:1 GENCODE basic APPRIS P1
Tlr7-204	ENSMUST00000137492.7	384	47aa	Protein coding	-	A2AHJ2	CDS 3' incomplete TSL:3
Tlr7-205	ENSMUST00000145284.7	366	49aa	Protein coding	-	A2AHJ1	CDS 3' incomplete TSL:2
Tlr7-206	ENSMUST00000149507.1	261	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Tlr7-201* transcript, The transcription is shown below



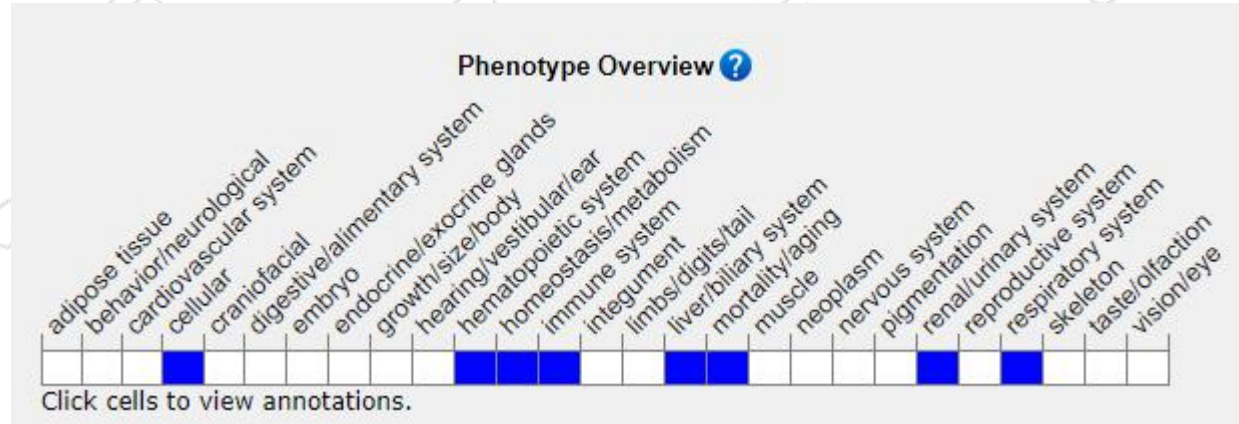
Genomic location distribution



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/>) .

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