

# *Tdrd3* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Tdrd3***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tdrd3* gene. The schematic diagram is as follows:



- The *Tdrd3* gene has 6 transcripts. According to the structure of *Tdrd3* gene, exon4 of *Tdrd3-202* (ENSMUST00000168275.8) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tdrd3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mice for a hypomorphic allele show increased genomic instability, and increased c-Myc/Igh translocation and R loop formation in B cells.
- Transcript 206 is unaffected.
- The *Tdrd3* gene is located on the Chr14. 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)

## Tdrd3 tudor domain containing 3 [ *Mus musculus* (house mouse) ]

Gene ID: 219249, updated on 12-Aug-2019

### Summary

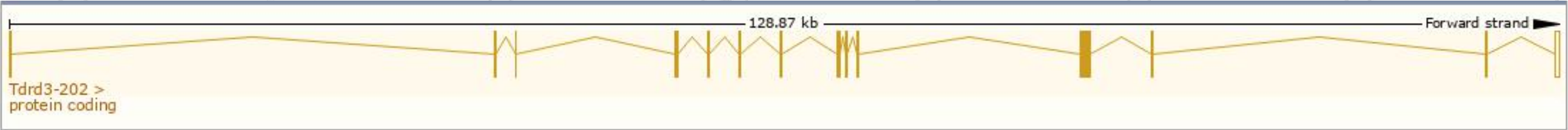
Official Symbol	Tdrd3 provided by <a href="#">MGI</a>
Official Full Name	tudor domain containing 3 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2444023</a>
See related	<a href="#">Ensembl:ENSMUSG00000022019</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6720468N18; 4732418C03Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 1.6), limb E14.5 (RPKM 1.5) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

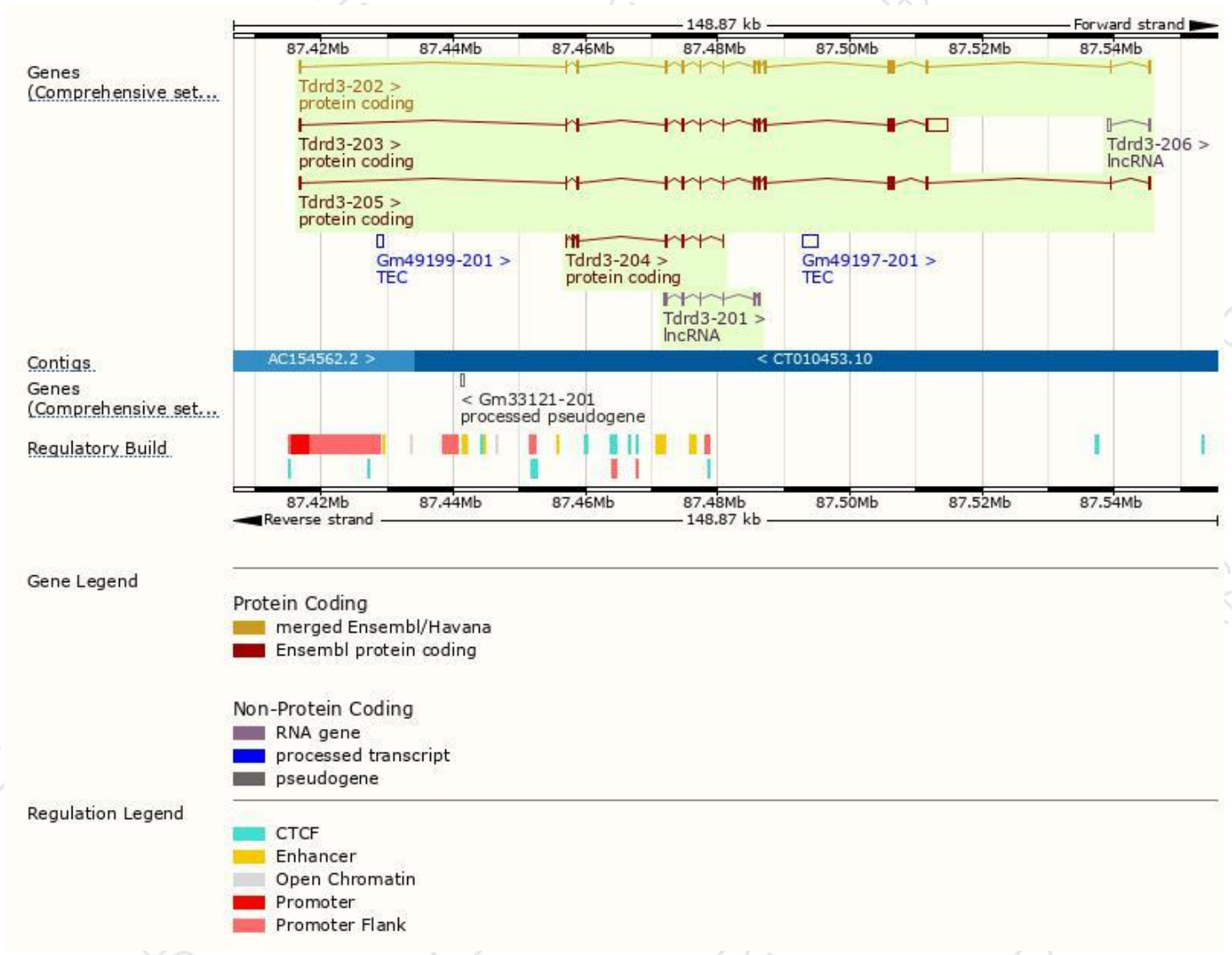
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tdrd3-203	<a href="#">ENSMUST00000169504.7</a>	5280	<a href="#">716aa</a>	Protein coding	<a href="#">CCDS56972</a>	<a href="#">Q91W18</a>	TSL:1 GENCODE basic
Tdrd3-202	<a href="#">ENSMUST00000168275.8</a>	2657	<a href="#">743aa</a>	Protein coding	<a href="#">CCDS27305</a>	<a href="#">Q91W18</a>	TSL:1 GENCODE basic APPRIS P1
Tdrd3-205	<a href="#">ENSMUST00000170865.7</a>	2530	<a href="#">737aa</a>	Protein coding	-	<a href="#">Q91W18</a>	TSL:1 GENCODE basic
Tdrd3-204	<a href="#">ENSMUST00000170712.7</a>	636	<a href="#">212aa</a>	Protein coding	-	<a href="#">F6ZI20</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Tdrd3-201	<a href="#">ENSMUST00000163714.1</a>	849	No protein	lncRNA	-	-	TSL:3
Tdrd3-206	<a href="#">ENSMUST00000227304.1</a>	669	No protein	lncRNA	-	-	

The strategy is based on the design of *Tdrd3-202* transcript,The transcription is shown below



# Genomic location distribution

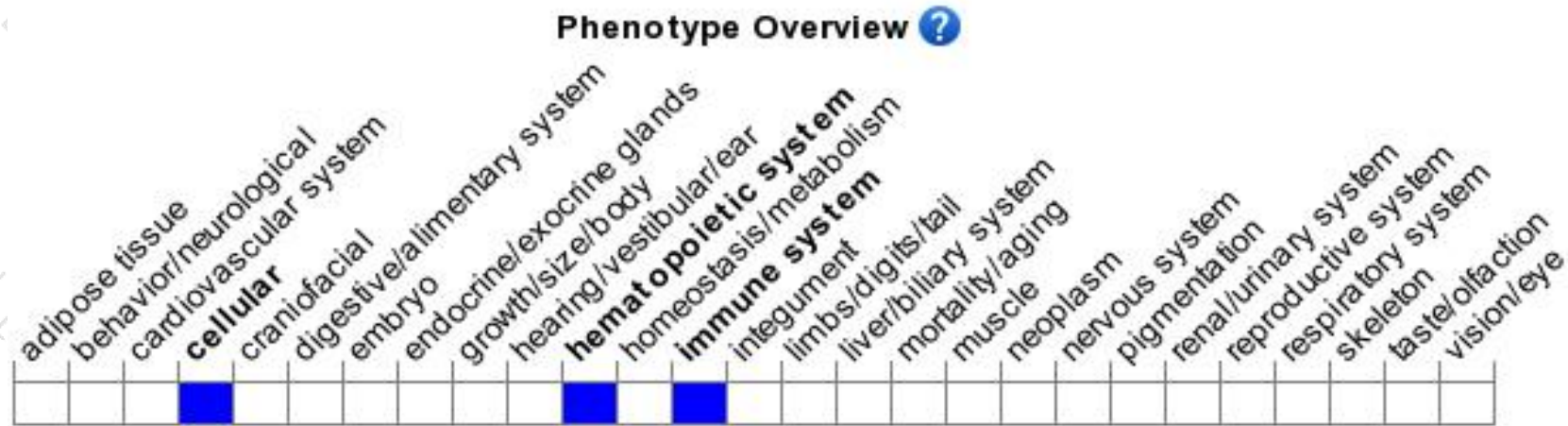




# Protein domain



# 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 mice for a hypomorphic allele show increased genomic instability, and increased c-Myc/Igh translocation and R loop formation in B cells.

If you have any questions, you are welcome to inquire.

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