# *Tor4a* Cas9-KO Strategy


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**Reviewer:** Yanhua Shen

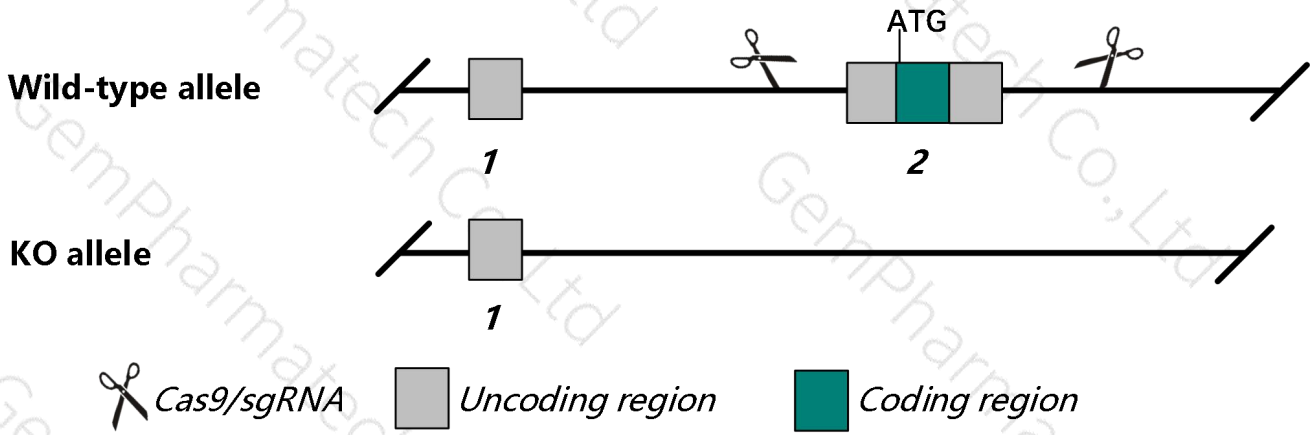

**Design Date:** 2020-4-29

# Project Overview

| | |
|---|---|
| **Project Name** | ***Tor4a*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tor4a* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Tor4a* gene has 3 transcripts. According to the structure of *Tor4a* gene, exon2 of *Tor4a-201* (ENSMUST00000081869.6) 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 *Tor4a* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- The effect on transcript *Tor4a*-202&203 is unknown.
- The *Tor4a* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Tor4a torsin family 4, member A [Mus musculus (house mouse)]

Gene ID: 227612, updated on 13-Mar-2020

### Summary

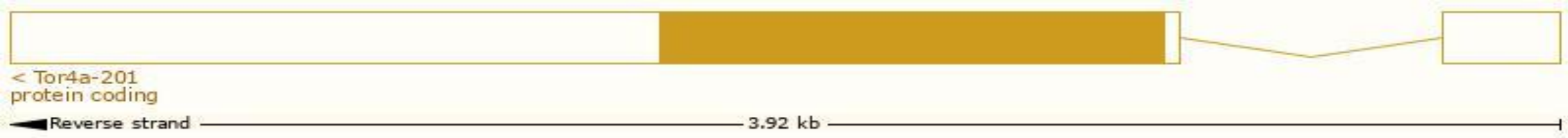
| | |
|---|---|
| **Official Symbol** | Tor4a provided by MGI |
| **Official Full Name** | torsin family 4, member A provided by MGI |
| **Primary source** | MGI:MGI:2442720 |
| **See related** | Ensembl:ENSMUSG00000059555 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | A830007P12Rik |
| **Expression** | Broad expression in spleen adult (RPKM 28.6), colon adult (RPKM 23.1) and 20 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

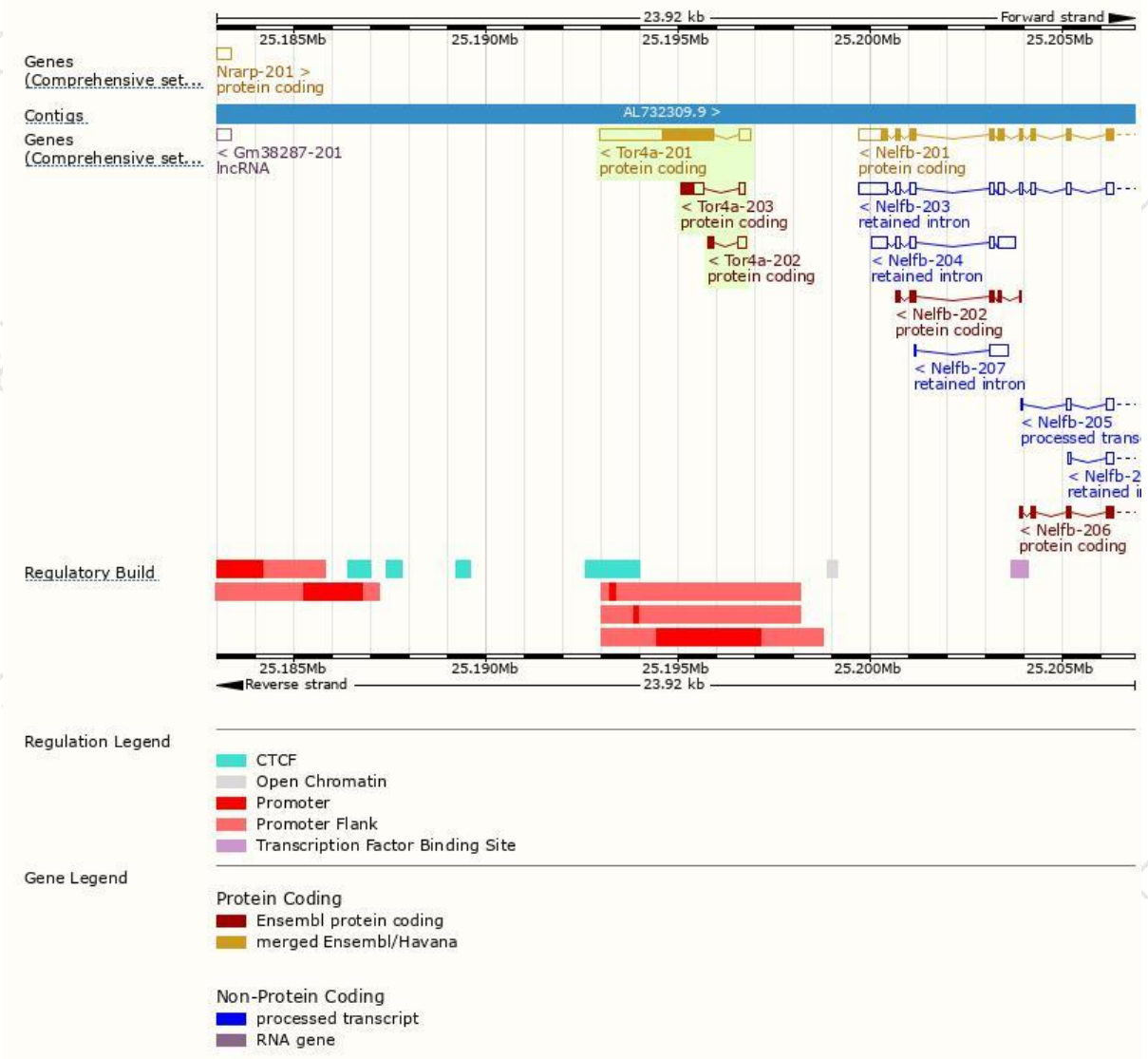
The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Tor4a-201 | ENSMUST00000081869.6 | 3255 | 426aa | Protein coding | CCDS15750 | Q8BH02 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Tor4a-203 | ENSMUST00000142857.1 | 774 | 111aa | Protein coding | - | A0A0A6YXM0 | CDS 3' incomplete TSL:3 |
| Tor4a-202 | ENSMUST00000137920.1 | 360 | 32aa | Protein coding | - | A0A0A6YWQ0 | CDS 3' incomplete TSL:5 |

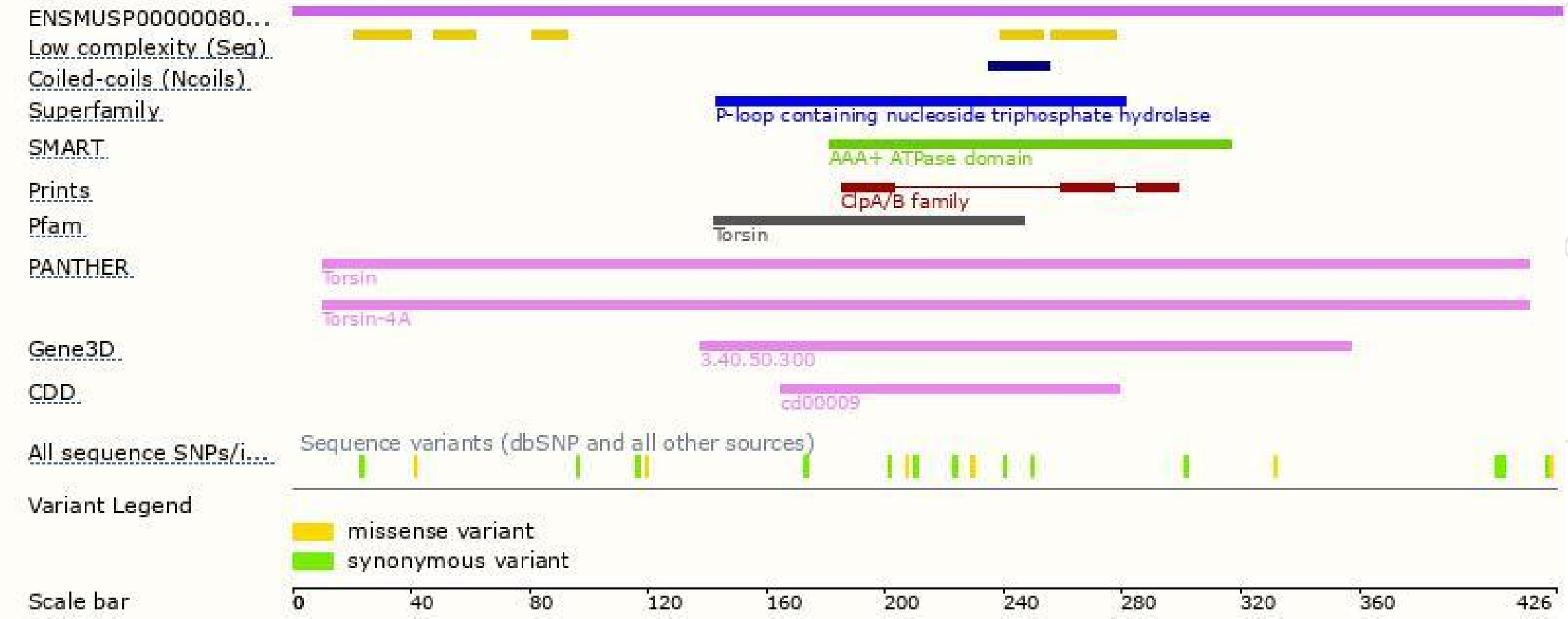
The strategy is based on the design of *Tor4a-201* transcript,the transcription is shown below:



# Genomic location distribution



# Protein domain



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

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