

# ***Tgif2 Cas9-KO Strategy***

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**Reviewer:**

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# Project Overview

**Project Name**

***Tgif2***

**Project type**

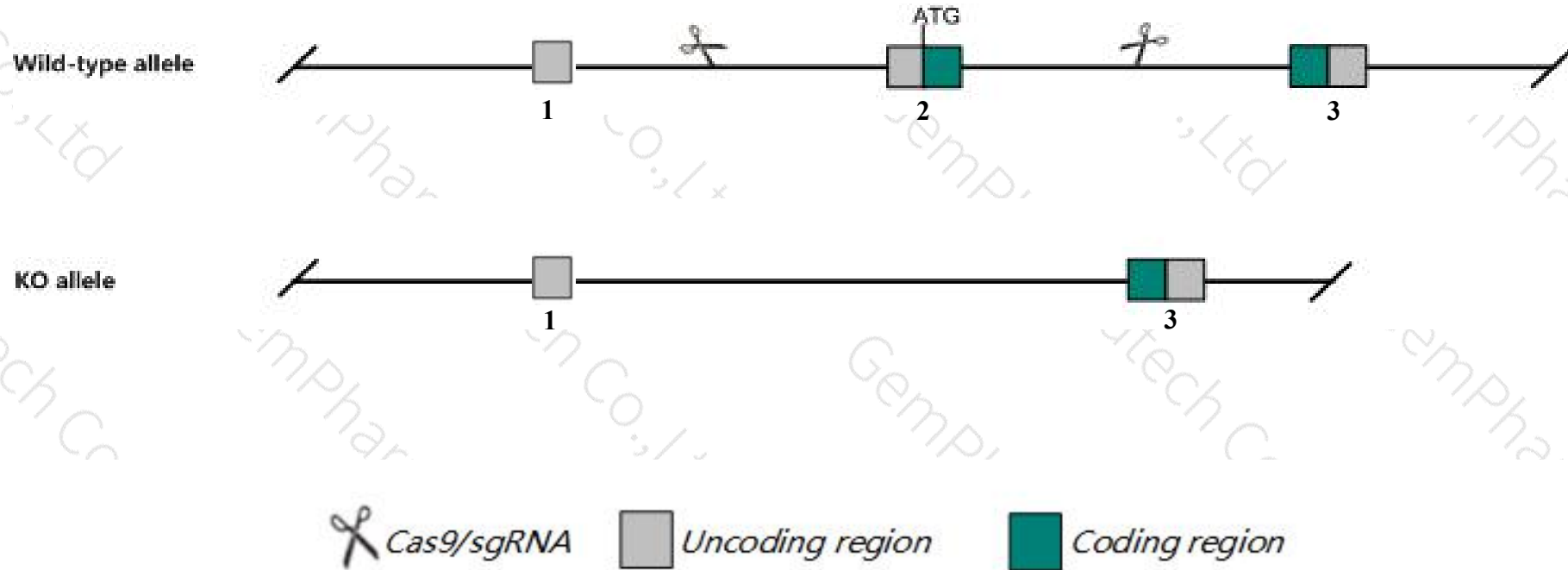
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tgif2* gene. The schematic diagram is as follows:



- The *Tgif2* gene has 5 transcripts. According to the structure of *Tgif2* gene, exon2 of *Tgif2-202* (ENSMUST00000081335.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tgif2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mice are viable and do not display any gross defects.
- The exon2 of *5430405H02Rik-203*(LncRNA) will be deleted.
- The 5-terminal regulation of *Gm14230* may be affected.
- The *Tgif2* 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.

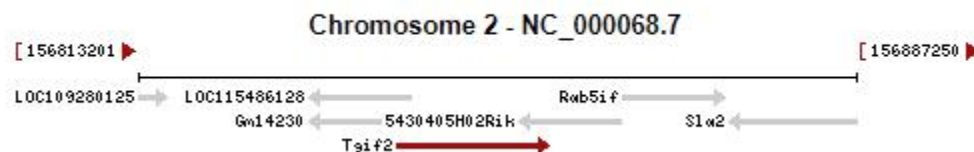
# Gene information (NCBI)

## Tgif2 TGFB-induced factor homeobox 2 [ *Mus musculus* (house mouse) ]

Gene ID: 228839, updated on 10-Oct-2019

### Summary

|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Tgif2 provided by MGI                                                                                                                                                     |
| Official Full Name | TGFB-induced factor homeobox 2 provided by MGI                                                                                                                            |
| Primary source     | MGI:MGI:1915299                                                                                                                                                           |
| See related        | Ensembl:ENSMUSG00000062175                                                                                                                                                |
| Gene type          | protein coding                                                                                                                                                            |
| RefSeq status      | VALIDATED                                                                                                                                                                 |
| Organism           | <i>Mus musculus</i>                                                                                                                                                       |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as      | C80753; C81206; 4921501K24; 5730599O09Rik                                                                                                                                 |
| Expression         | Broad expression in CNS E11.5 (RPKM 11.1), limb E14.5 (RPKM 10.5) and 25 other tissues <a href="#">See more</a>                                                           |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

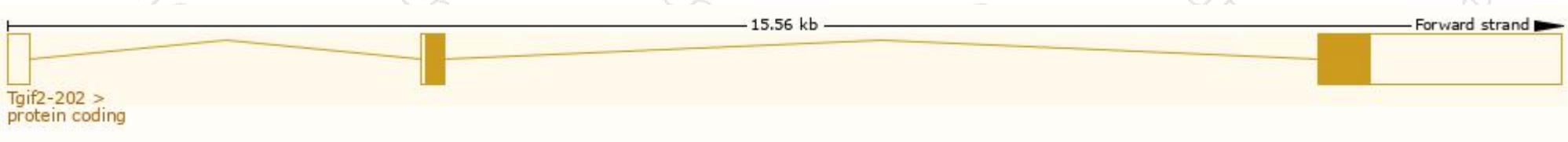


# Transcript information (Ensembl)

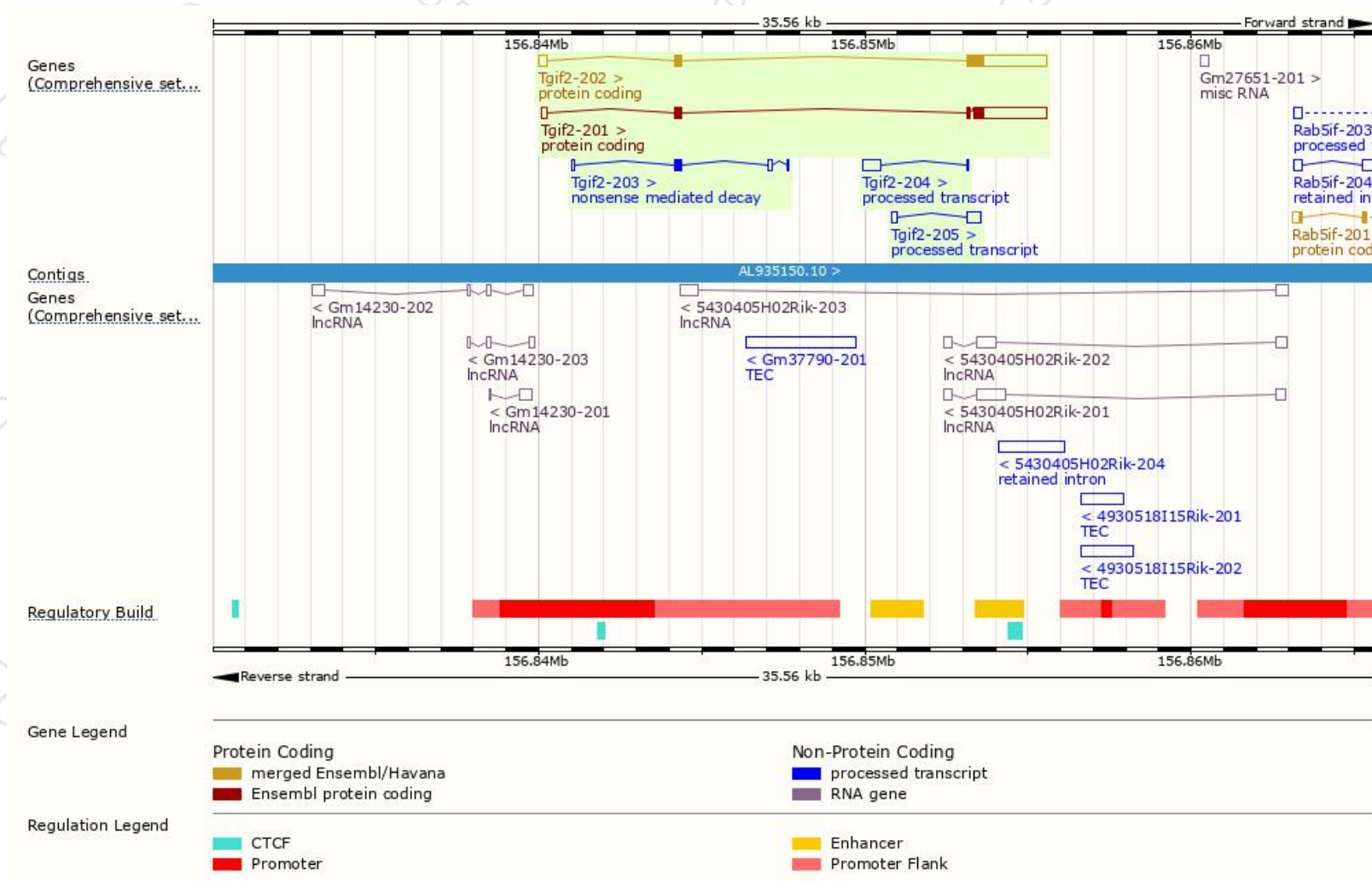
The gene has 5 transcripts,all transcripts are shown below:

| Name      | Transcript ID                         | bp   | Protein               | Biotype                 | CCDS                      | UniProt                                       | Flags                         |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|-----------------------------------------------|-------------------------------|
| Tgif2-202 | <a href="#">ENSMUST00000081335.12</a> | 2900 | <a href="#">237aa</a> | Protein coding          | <a href="#">CCDS16969</a> | <a href="#">A2AVY9</a> <a href="#">Q8C0Y1</a> | TSL:1 GENCODE basic APPRIS P1 |
| Tgif2-201 | <a href="#">ENSMUST00000073352.9</a>  | 2690 | <a href="#">198aa</a> | Protein coding          | <a href="#">CCDS71173</a> | <a href="#">Q3TZS1</a>                        | TSL:1 GENCODE basic           |
| Tgif2-203 | <a href="#">ENSMUST00000150078.1</a>  | 484  | <a href="#">68aa</a>  | Nonsense mediated decay | -                         | <a href="#">H3BJF0</a>                        | TSL:3                         |
| Tgif2-204 | <a href="#">ENSMUST00000175634.1</a>  | 594  | No protein            | Processed transcript    | -                         | -                                             | TSL:3                         |
| Tgif2-205 | <a href="#">ENSMUST00000176281.1</a>  | 564  | No protein            | Processed transcript    | -                         | -                                             | TSL:5                         |

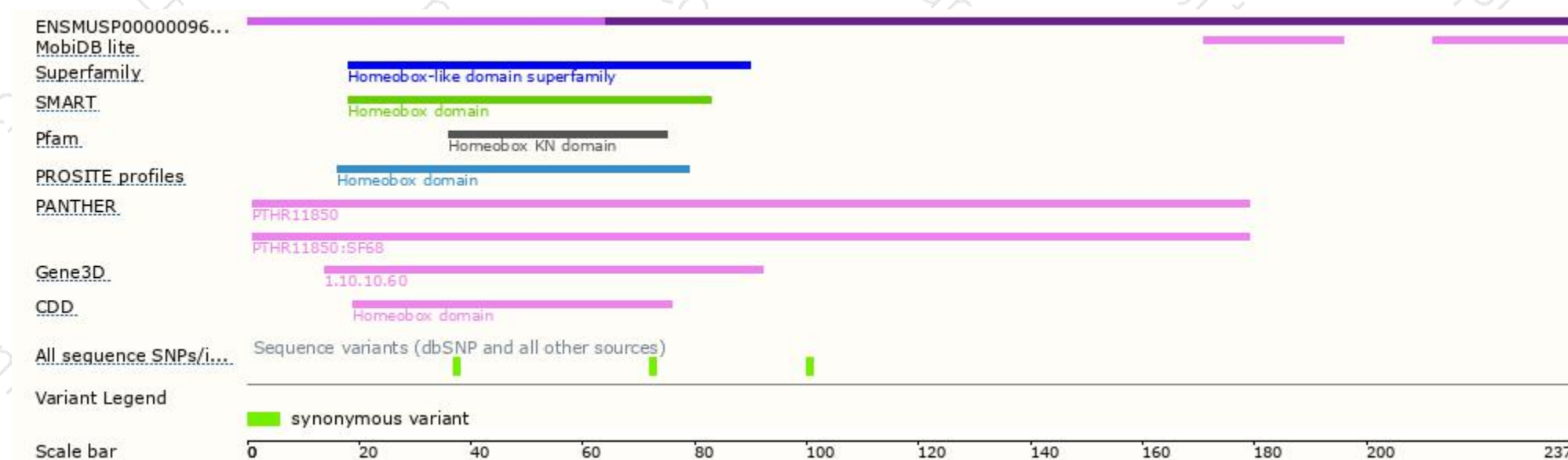
The strategy is based on the design of *Tgif2-202* transcript,The transcription is shown below



# 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 are viable and do not display any gross defects.

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

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