

Tgfbr3 Cas9-KO Strategy

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Project Overview

Project Name

Tgfbr3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tgfbr3* gene. The schematic diagram is as follows:



- The *Tgfbr3* gene has 4 transcripts. According to the structure of *Tgfbr3* gene, exon3 of *Tgfbr3-201* (ENSMUST00000031224.14) transcript is recommended as the knockout region. The region contains 185bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tgfbr3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene usually die as embryos. The very few individuals that survive are poorly fertile with abnormalities of the spleen, liver, heart, and skeletal system.
- The *Tgfb³* 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)

Tgfb3 transforming growth factor, beta receptor III [*Mus musculus* (house mouse)]

Gene ID: 21814, updated on 12-Aug-2019

Summary

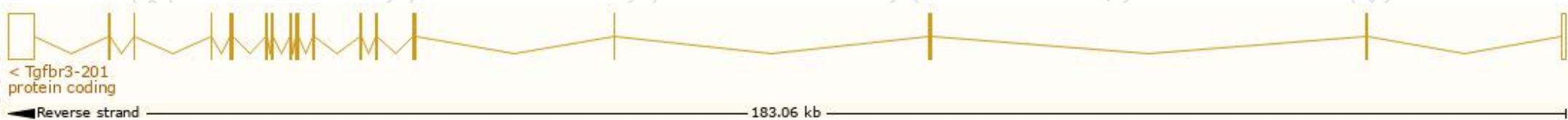
| | |
|---------------------------|---|
| Official Symbol | Tgfb3 provided by MGI |
| Official Full Name | transforming growth factor, beta receptor III provided by MGI |
| Primary source | MGI:MGI:104637 |
| See related | Ensembl:ENSMUSG00000029287 |
| Gene type | protein coding |
| RefSeq status | 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 | TBR3; AU015626; AW215636; 1110036H20Rik |
| Expression | Broad expression in adrenal adult (RPKM 38.6), bladder adult (RPKM 20.1) and 20 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

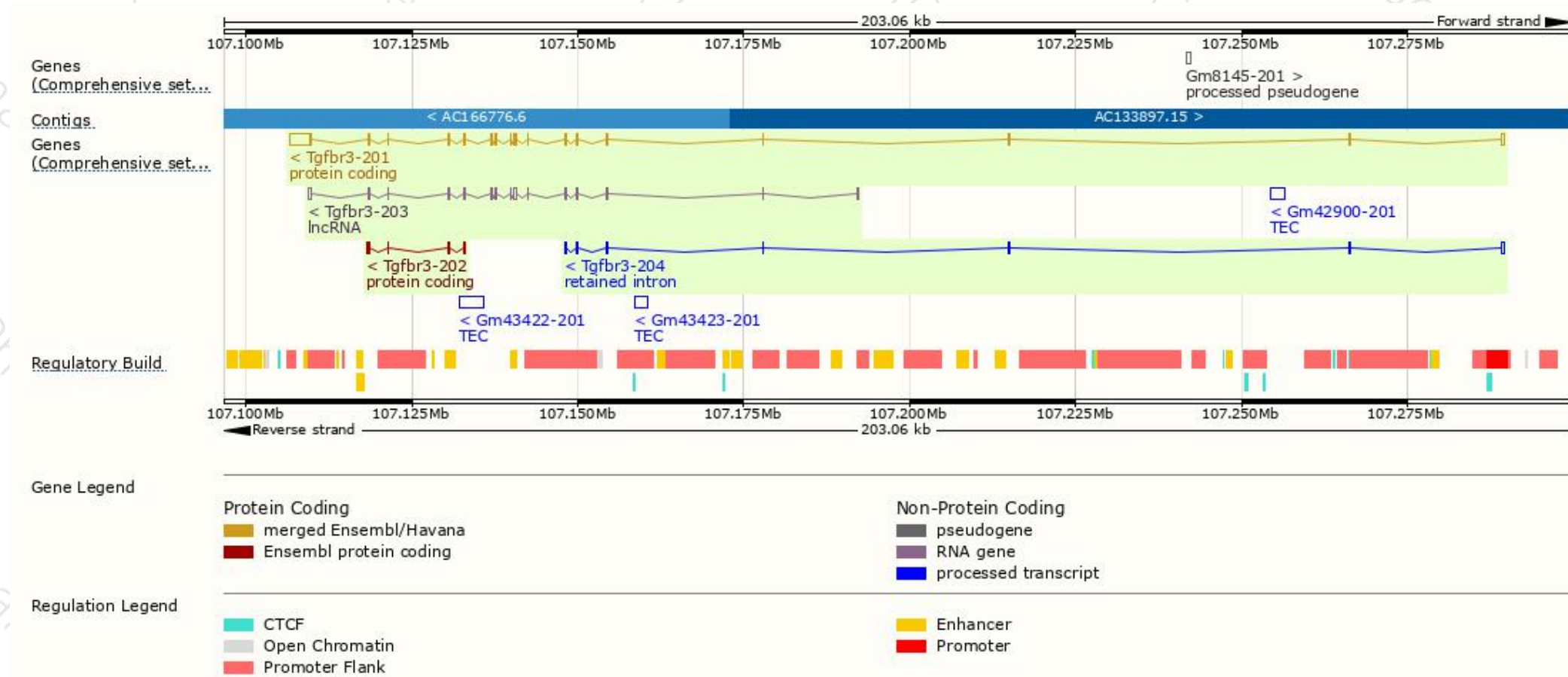
The gene has 4 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|-------------------------------|
| Tgfb3-201 | ENSMUST00000031224.14 | 6087 | 850aa | Protein coding | CCDS19499 | A0A0R4J097 | TSL:1 Gencode basic APPRIS P1 |
| Tgfb3-202 | ENSMUST00000136882.1 | 687 | 156aa | Protein coding | - | F6VPT9 | CDS 5' incomplete TSL:2 |
| Tgfb3-204 | ENSMUST00000146591.1 | 1368 | No protein | Retained intron | - | - | TSL:1 |
| Tgfb3-203 | ENSMUST00000138469.7 | 2849 | No protein | lncRNA | - | - | TSL:1 |

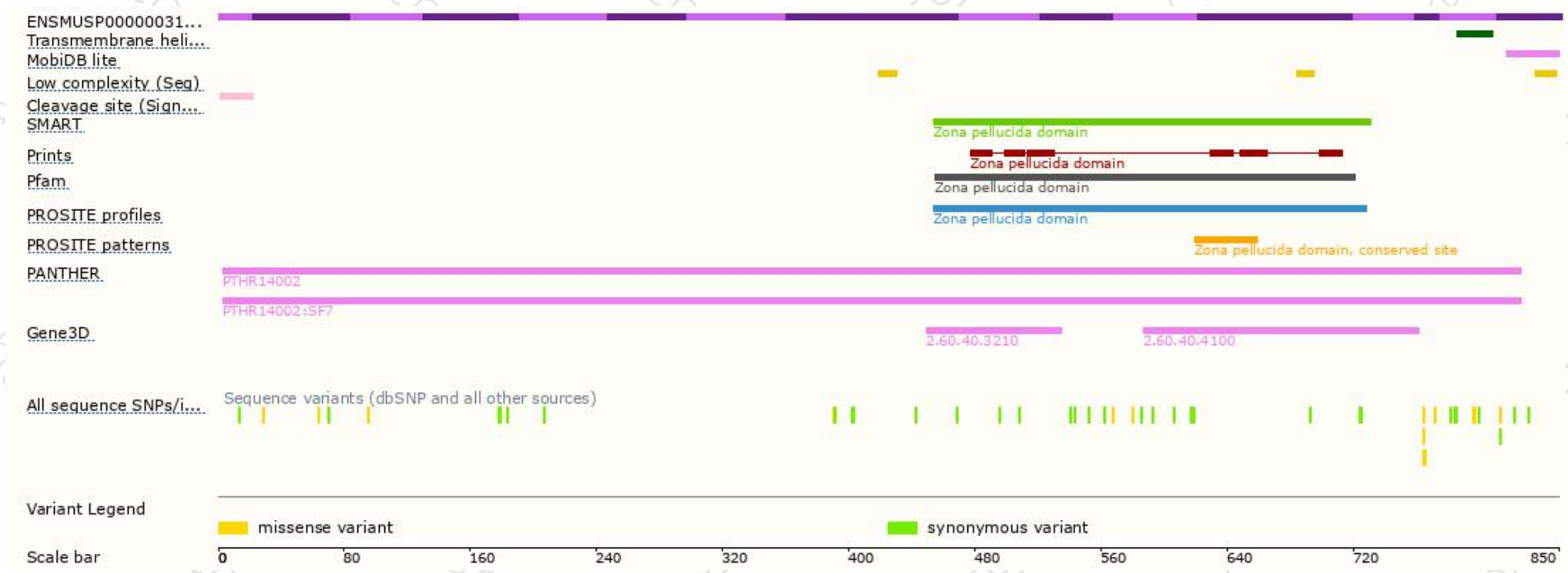
The strategy is based on the design of *Tgfb3-201* transcript,The transcription is shown below



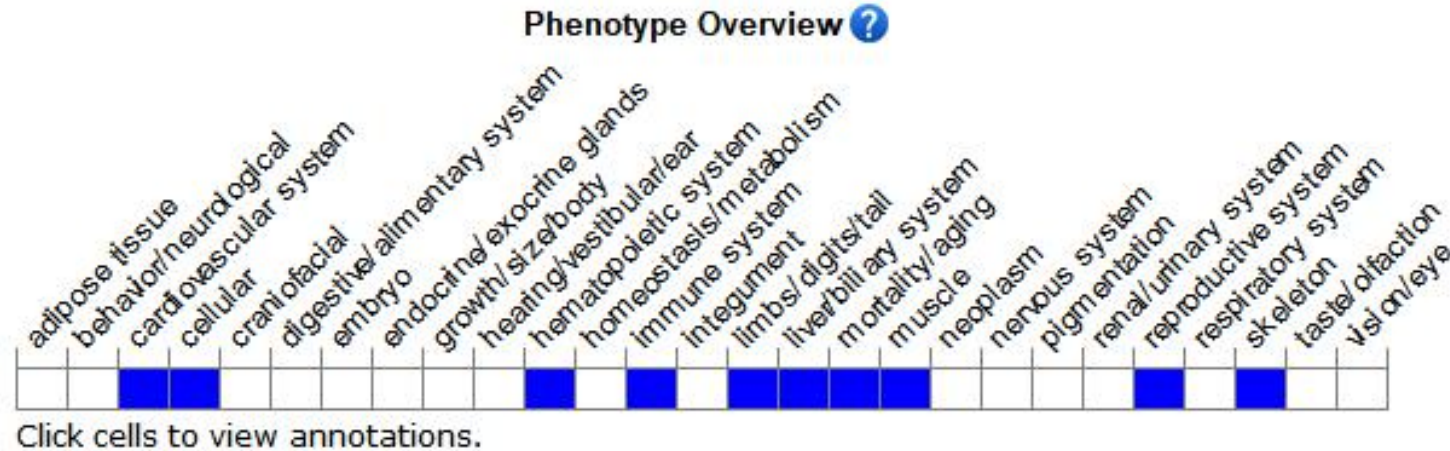
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for disruptions in this gene usually die as embryos. The very few individuals that survive are poorly fertile with abnormalities of the spleen, liver, heart, and skeletal system.

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

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