# *Ctcf-c.1699 C>T* Mouse Model Strategy

## -CRISPR/Cas9 technology

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**Reviewer: Yanhua Shen**

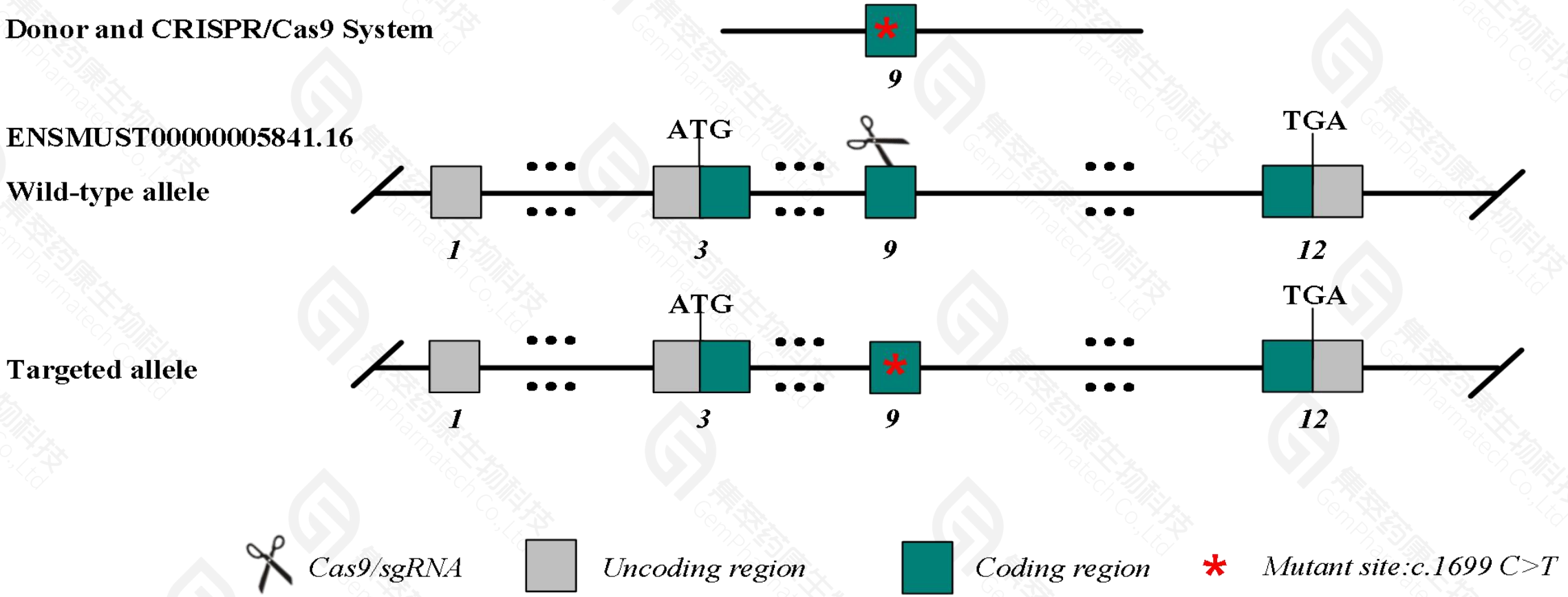
**Design Date: 2021-5-7**

# Project Overview

| | |
|---|---|
| **Project Name** | **Ctcf-c.1699 C>T** |
| **Project type** | **cas9-ki(PM)** |
| **Strain background** | **C57BL/6JGpt** |

# Strategy

This model uses CRISPR/Cas9 technology to edit the *Ctcf* gene and the schematic diagram is as follow:



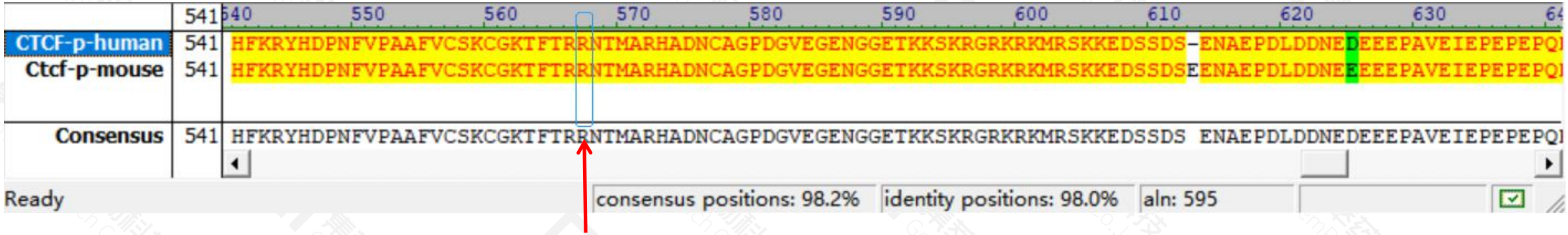
# Technical Description

- The mouse *Ctcf* gene has 6 transcripts.
- This project produced *Ctcf-c.1699 C>T* point mutation on exon9 of the transcript of *Ctcf*-201(ENSMUST00000005841.16). The 1699th nucleotide of *Ctcf* CDS is mutated from C to T, The 567th amino acid will be mutated from R(Arg) to W(Trp).
- The mouse *Ctcf*-201 transcript contains 12 exons. The translation initiation site ATG is located at exon3, and the translation termination site TGA is located at exon12, encoding 736aa.
- In this project, *Ctcf* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, sgRNA and donor vectors were constructed. Cas9, sgRNA and donor were injected into the fertilized eggs of C57BL/6JGpt mice for homologous recombination, and obtained positive F0 mice identified by PCR and sequencing analysis. The stable inheritable positive F1 mice model was obtained by mating F0 mice with C57BL/6JGpt mice.

# Notice

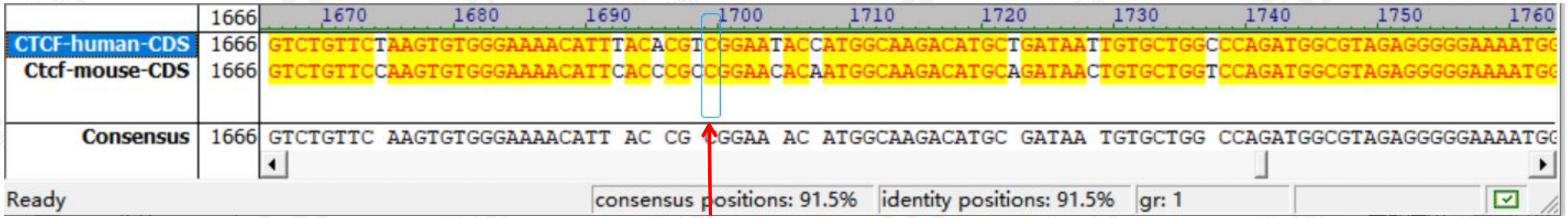
- According to the data of MGI, mice homozygous for a null allele die prior at implantation. Mice homozygous for a conditional allele activated in T cells exhibit a defect in the transition from immature single positive T cells to double positive T cells.
- One or two synonymous mutations of amino acids will be intronduced on exon9 of *Ctcf*.
- The strategy may affect the normal splicing of the target gene.
- Mouse *Ctcf* gene is located on Chr8. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr8, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

# Analysis of Homology




h*CTCF*-P-567R-m*Ctcf*-P-567R

Identity positions： 98.0%

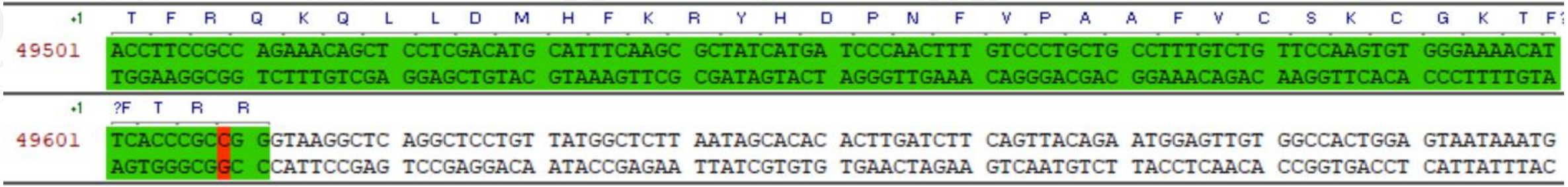



h*CTCF*-CCDS-1699C-m*Ctcf*-CCDS-1699C

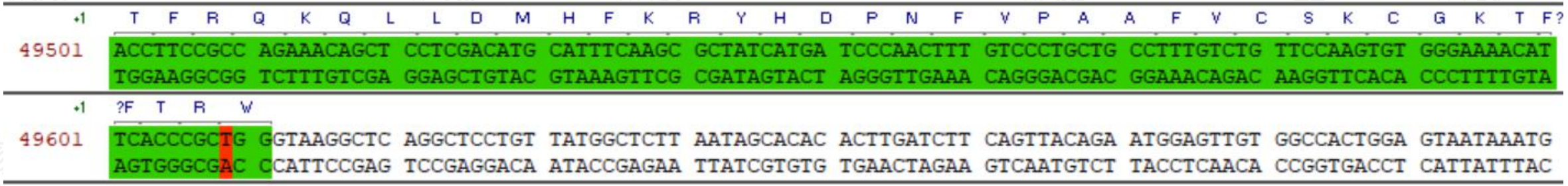
# Mutation Site

集萃药康 GemPharmatech

**Before mutation**




**After mutation**




The green region is exon9 of *Ctcf-201,* and the red region represents the c.1699C>T mutation site.

# Gene name and location (NCBI)

集萃药康 GemPharmatech

**Ctcf CCCTC-binding factor [ *Mus musculus* (house mouse) ]**

Download Datasets

Gene ID: 13018, updated on 24-Apr-2021

**Summary**

| | |
|---|---|
| **Official Symbol** | Ctcf provided by MGI |
| **Official Full Name** | CCCTC-binding factor provided by MGI |
| **Primary source** | MGI:MGI:109447 |
| **See related** | Ensembl:ENSMUSG00000005698 |
| **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** | AW108038 |
| **Expression** | Ubiquitous expression in CNS E11.5 (RPKM 18.2), thymus adult (RPKM 13.4) and 27 other tissues See more |
| **Orthologs** | human all |

NEW **Try the new Gene table**

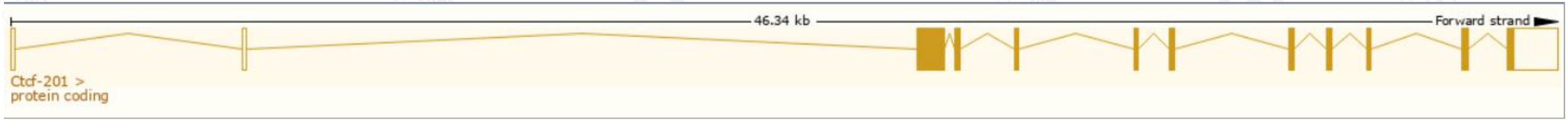
**Try the new Transcript table**

# Transcript information（Ensembl）

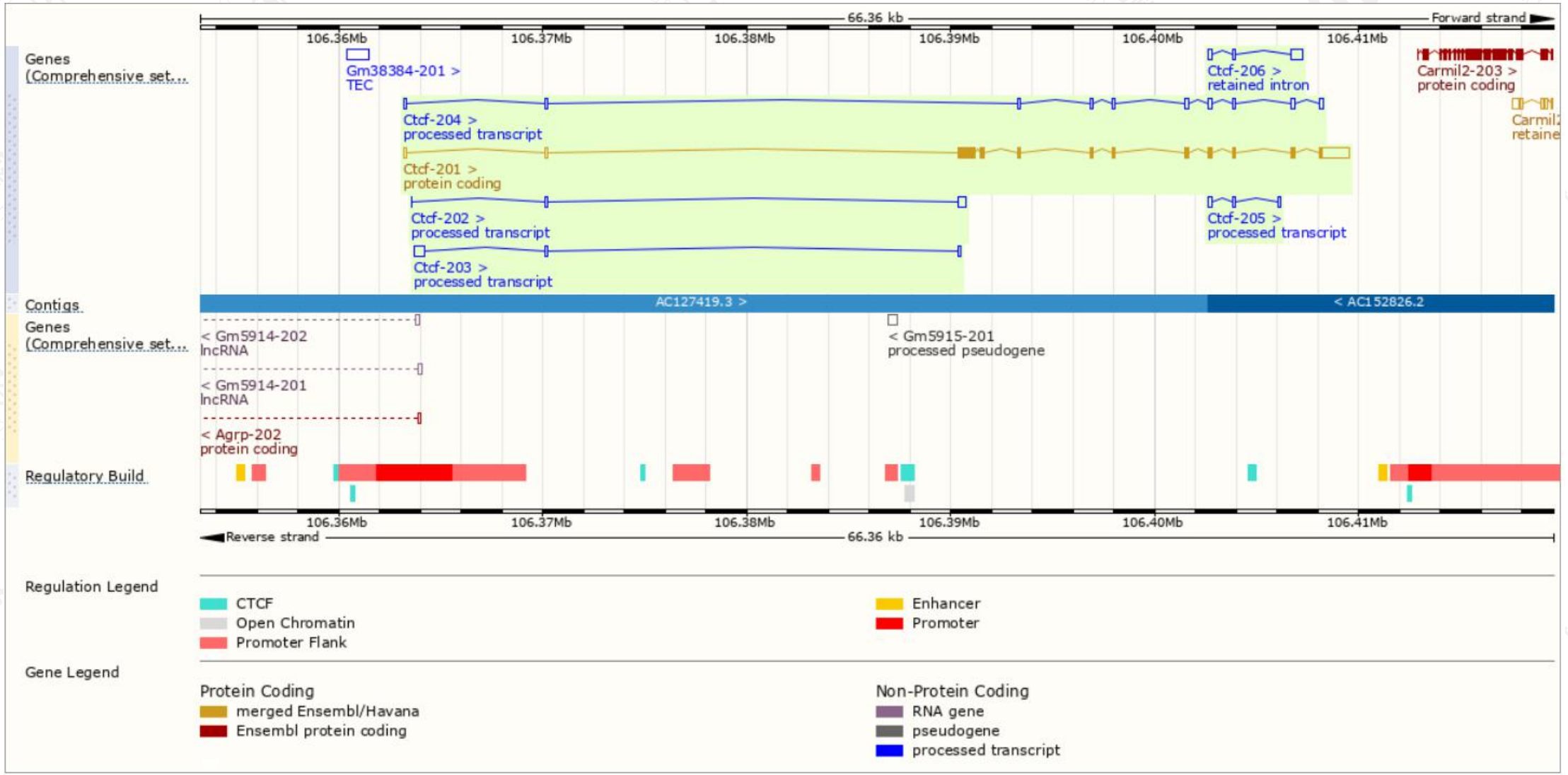
The gene has 6 transcripts, and all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|---|---|---|---|---|---|---|---|
| Ctcf-201 | ENSMUST00000005841.16 | 3782 | 736aa | Protein coding | CCDS22606 | Q61164 | GENCODE basic APPRIS P1 TSL:1 |
| Ctcf-204 | ENSMUST00000132679.8 | 1554 | No protein | Processed transcript | - | - | TSL:5 |
| Ctcf-203 | ENSMUST00000129388.2 | 729 | No protein | Processed transcript | - | - | TSL:3 |
| Ctcf-202 | ENSMUST00000128510.8 | 528 | No protein | Processed transcript | - | - | TSL:3 |
| Ctcf-205 | ENSMUST00000137735.8 | 469 | No protein | Processed transcript | - | - | TSL:3 |
| Ctcf-206 | ENSMUST00000156436.2 | 851 | No protein | Retained intron | - | - | TSL:3 |

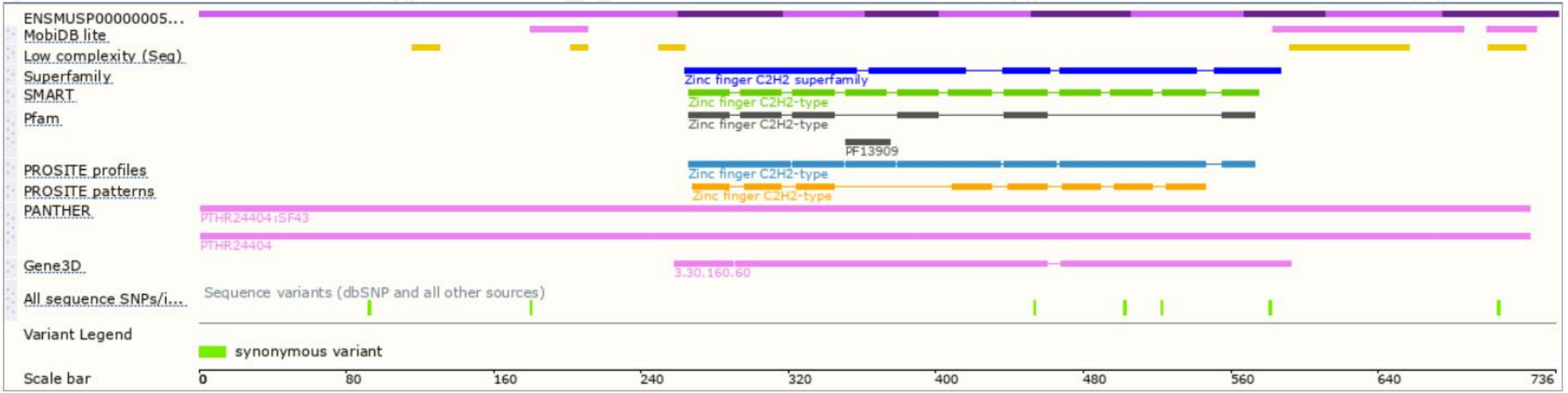
The strategy is based on the design of *Ctcf-201* transcript, the transcription is shown below:



# Genomic location distribution

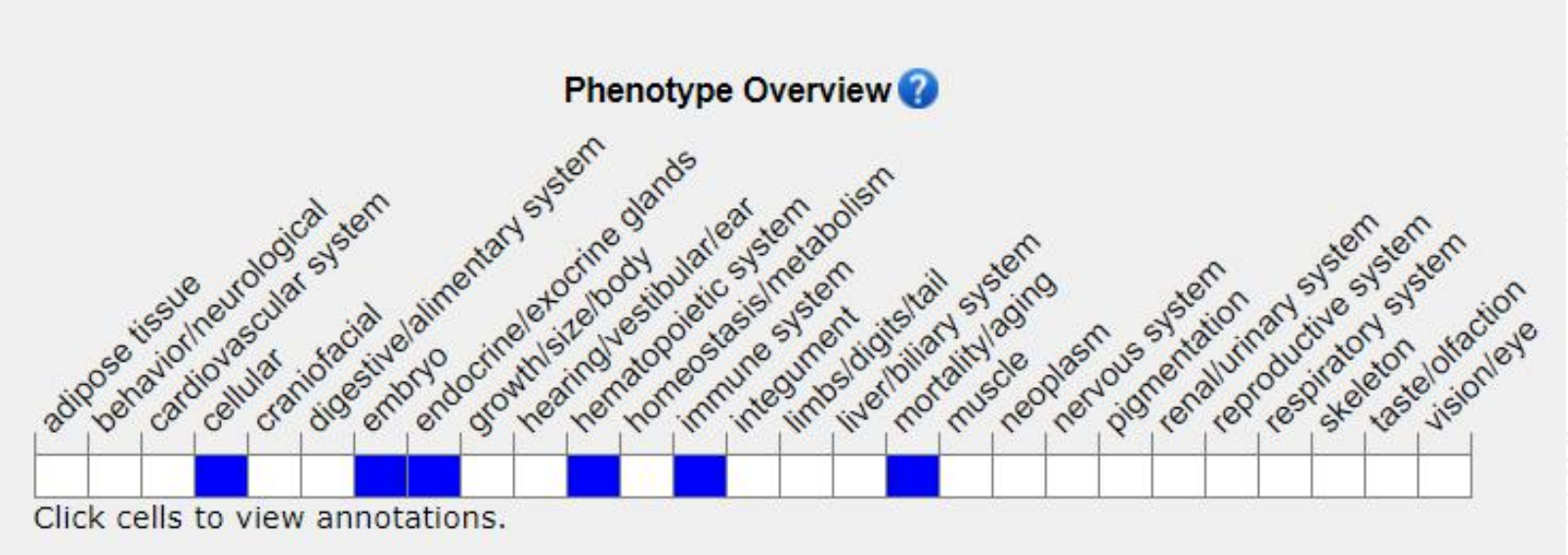


# Protein domain



# Mouse phenotype description(MGI )

URL link is as follows:
http://www.informatics.jax.org/marker/MGI:109447




Mice homozygous for a null allele die prior at implantation. Mice homozygous for a conditional allele activated in T cells exhibit a defect in the transition from immature single positive T cells to double positive T cells.

If you have any questions, please feel free to contact us.
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