

# ***Tcf15* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Tcf15***

**Project type**

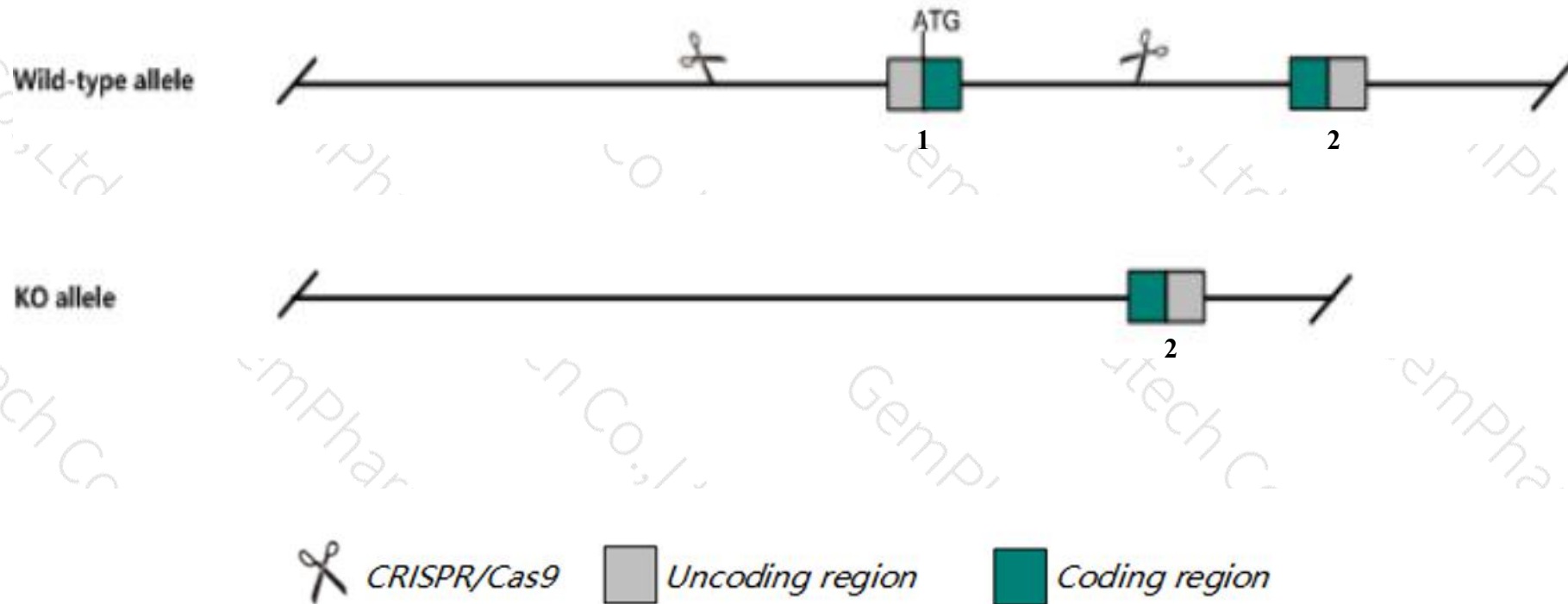
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tcf15* gene. The schematic diagram is as follows:



- The *Tcf15* gene has 1 transcript. According to the structure of *Tcf15* gene, exon1 of *Tcf15-201*(ENSMUST00000089112.5) 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 *Tcf15* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, in homozygotes for a targeted null mutation, cells of the paraxial mesoderm fail to form epithelia resulting in disrupted somites, patterning defects of the axial skeleton, peripheral nerves, and skeletal muscles, and perinatal lethality.
- The *Tcf15* 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)

## Tcf15 transcription factor 15 [ *Mus musculus* (house mouse) ]

Gene ID: 21407, updated on 26-Jun-2020

### Summary

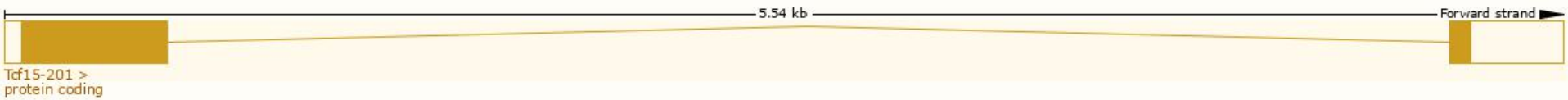
Official Symbol	Tcf15 provided by <a href="#">MGI</a>
Official Full Name	transcription factor 15 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:104664</a>
See related	<a href="#">Ensembl:ENSMUSG00000068079</a>
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Meso1; bHLH-EC2
Expression	Broad expression in adrenal adult (RPKM 9.0), mammary gland adult (RPKM 8.9) and 18 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

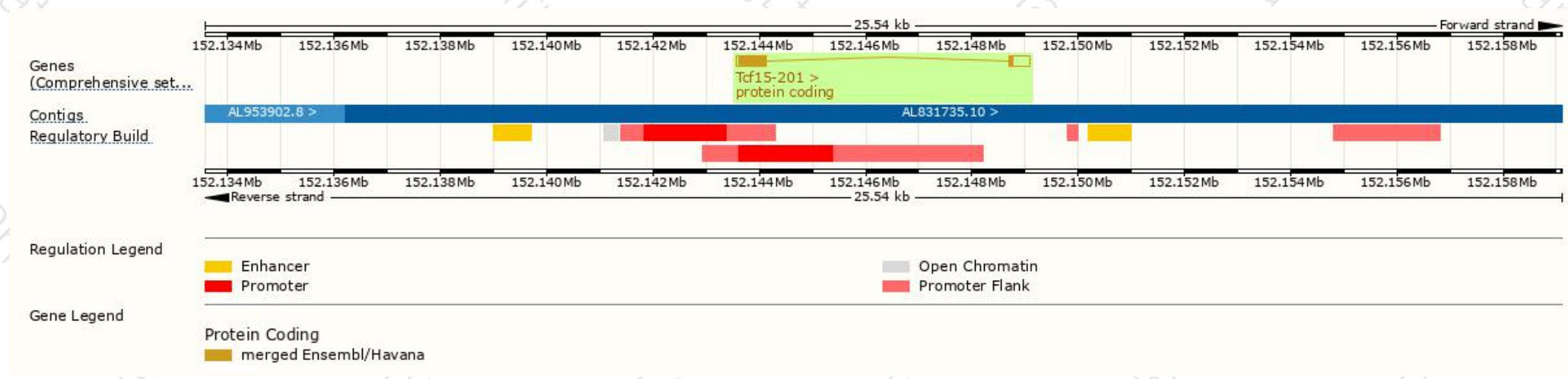
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tcf15-201	<a href="#">ENSMUST00000089112.5</a>	980	<a href="#">195aa</a>	Protein coding	<a href="#">CCDS16878</a>	<a href="#">Q60756</a>	TSL:1 Gencode basic APPRIS P1

The strategy is based on the design of *Tcf15-201* transcript, the transcription is shown below:

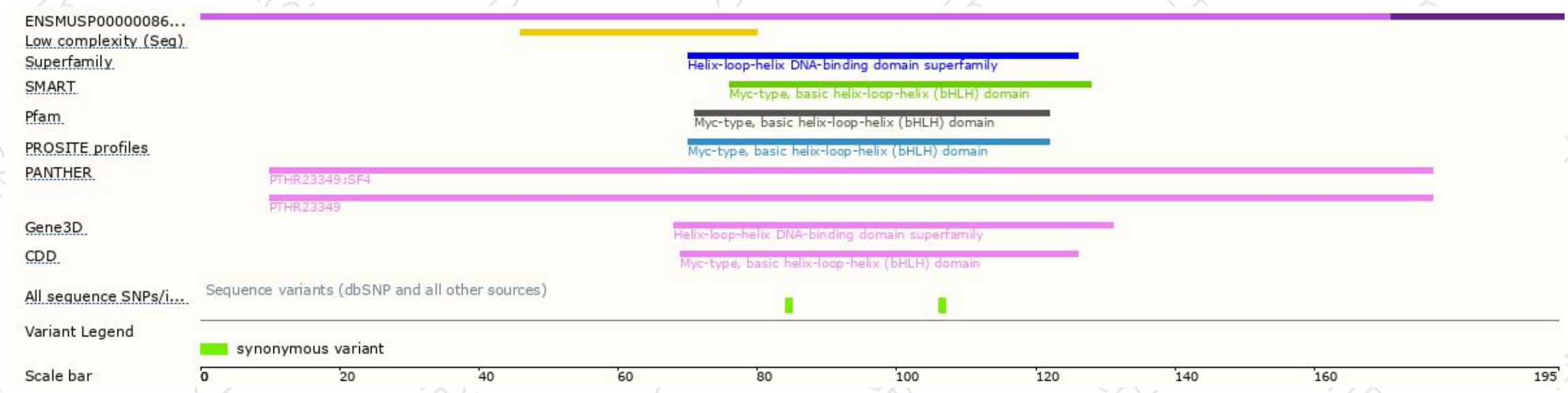


# Genomic location distribution

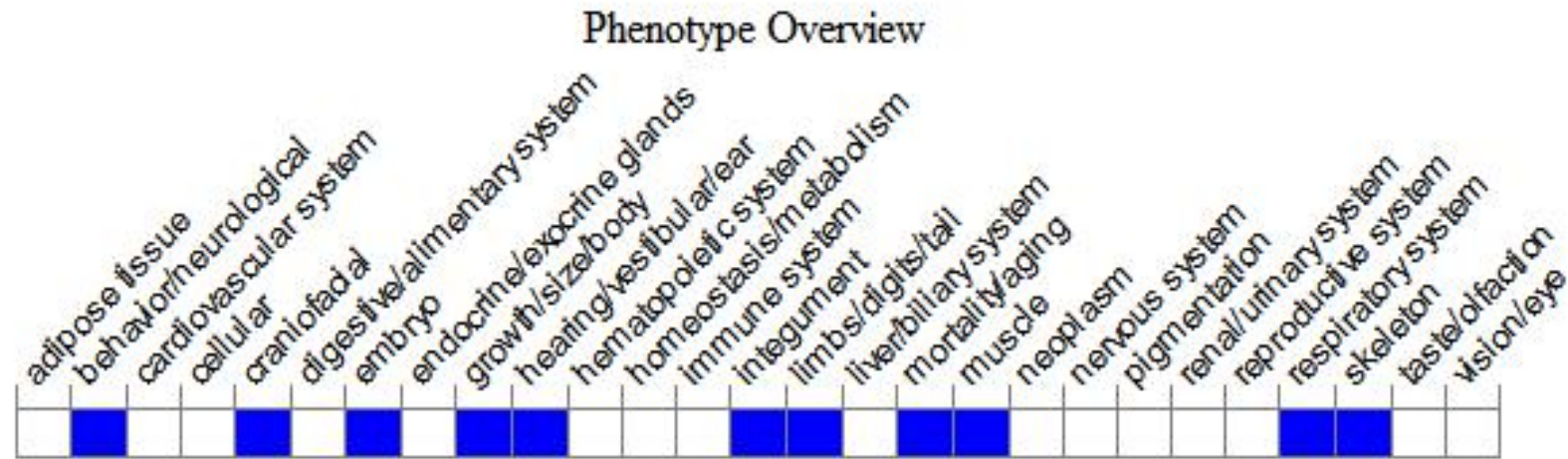




# Protein domain



# 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, in homozygotes for a targeted null mutation, cells of the paraxial mesoderm fail to form epithelia resulting in disrupted somites, patterning defects of the axial skeleton, peripheral nerves, and skeletal muscles, and perinatal lethality.

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

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