# *Tacc2* Cas9-KO Strategy

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**Reviewer: Huan wang**

**Design Date: 2021-12-23**

# Project Overview

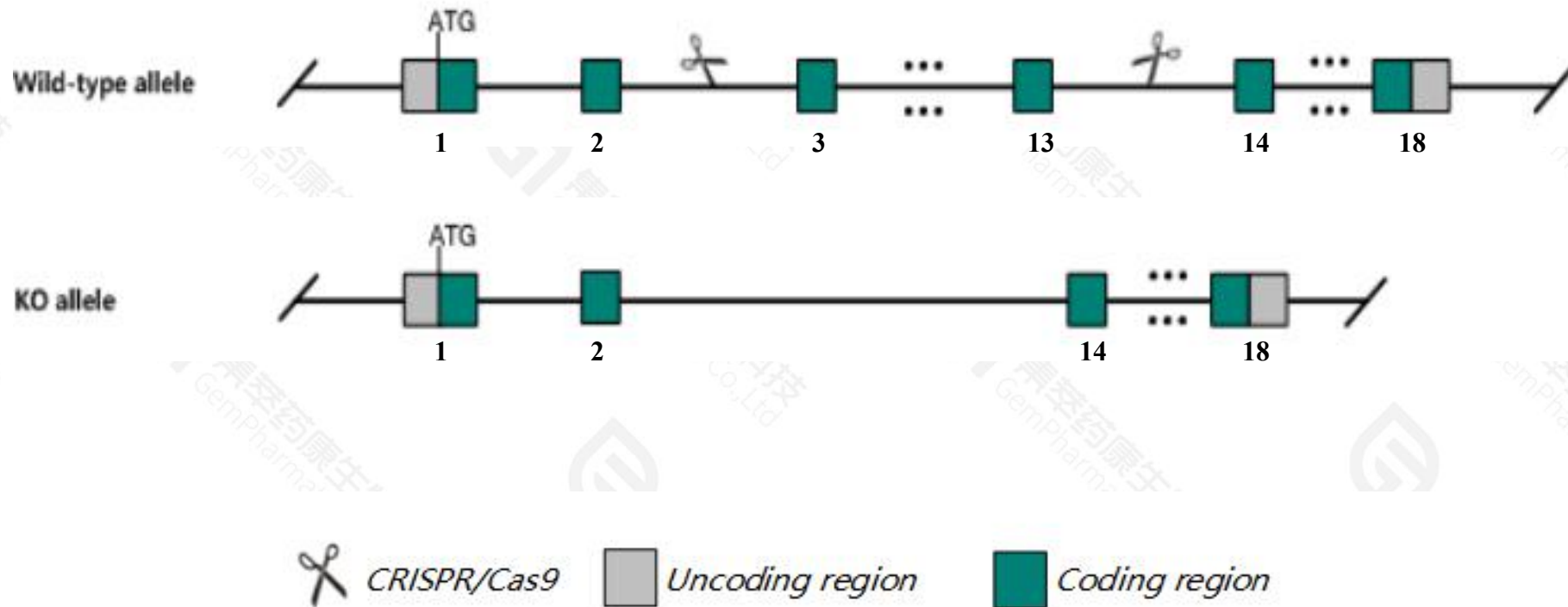| | |
|---|---|
| **Project Name** | *Tacc2* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tacc2* gene. The schematic diagram is as follows:

➢ The *Tacc2* gene has 19 transcripts. According to the structure of *Tacc2* gene, exon3-exon13 of *Tacc2-201*(ENSMUST00000033141.7) transcript is recommended as the knockout region.The region contains 2407bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tacc2* 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,homozygous null mice are healthy and fertile and do not display any increase in tumorigenesis.

➢ Transcript *Tacc2-210&218* &202&203 may not be affected.

➢ The partial intron of Fgfr2 gene will be deleted together in this strategy,The effect on transcript Fgfr2 is unknown.

➢ The *Tacc2* gene is located on the Chr7. 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）

## Tacc2 transforming, acidic coiled-coil containing protein 2 [Mus musculus (house mouse)]

Gene ID: 57752, updated on 17-Feb-2021

### ▲ Summary

| | |
|---|---|
| **Official Symbol** | Tacc2 provided by MGI |
| **Official Full Name** | transforming, acidic coiled-coil containing protein 2 provided by MGI |
| **Primary source** | MGI:MGI:1928899 |
| **See related** | Ensembl:ENSMUSG00000030852 |
| **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** | mKIAA4180 |
| **Summary** | This gene encodes a member of the transforming, acidic coiled-coil (TACC) family of proteins. Members of this family are centrosomal proteins that interact with microtubules and tubulin. TACC proteins are thought to be involved in centrosome/mitotic spindle dynamics and gene regulation. Alternative splicing of this gene results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2008] |
| **Expression** | Ubiquitous expression in heart adult (RPKM 13.1), bladder adult (RPKM 5.9) and 22 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

The gene has 19 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------|---------------|-----|---------|---------|------|---------|-------|
| Tacc2-203 | ENSMUST00000084513.12 | 9029 | 2879aa | Protein coding | CCDS21903 | | TSL:5 , GENCODE basic , APPRIS P4 , |
| Tacc2-201 | ENSMUST00000033141.7 | 3940 | 1036aa | Protein coding | CCDS21905 | | TSL:5 , GENCODE basic , APPRIS ALT2 , |
| Tacc2-202 | ENSMUST00000059145.14 | 3906 | 1146aa | Protein coding | CCDS21904 | | TSL:5 , GENCODE basic , APPRIS ALT2 , |
| Tacc2-205 | ENSMUST00000207282.2 | 3464 | 947aa | Protein coding | CCDS85432 | | TSL:1 , GENCODE basic , APPRIS ALT2 , |
| Tacc2-210 | ENSMUST00000207918.2 | 5804 | 1919aa | Protein coding | - | | CDS 3' incomplete , TSL:5 , |
| Tacc2-218 | ENSMUST00000215492.2 | 5312 | 1770aa | Protein coding | - | | CDS 3' incomplete , TSL:5 , |
| Tacc2-208 | ENSMUST00000207549.2 | 3492 | 568aa | Protein coding | - | | TSL:1 , GENCODE basic , APPRIS ALT2 , |
| Tacc2-217 | ENSMUST00000209108.2 | 3310 | 555aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Tacc2-207 | ENSMUST00000207395.2 | 2934 | 829aa | Protein coding | - | | CDS 5' incomplete , TSL:1 , |
| Tacc2-206 | ENSMUST00000207376.2 | 2557 | 696aa | Protein coding | - | | CDS 5' incomplete , TSL:5 , |
| Tacc2-219 | ENSMUST00000239258.2 | 2268 | 669aa | Protein coding | - | | CDS 3' incomplete , |
| Tacc2-214 | ENSMUST00000208722.2 | 3883 | 1020aa | Nonsense mediated decay | - | | TSL:5 , |
| Tacc2-215 | ENSMUST00000208743.2 | 3878 | 910aa | Nonsense mediated decay | - | | TSL:1 , |
| Tacc2-209 | ENSMUST00000207789.2 | 3146 | 255aa | Nonsense mediated decay | - | | TSL:5 , |
| Tacc2-212 | ENSMUST00000208106.2 | 766 | No protein | Processed transcript | - | | TSL:1 , |
| Tacc2-211 | ENSMUST00000207999.2 | 604 | No protein | Processed transcript | - | | TSL:5 , |
| Tacc2-216 | ENSMUST00000208882.2 | 419 | No protein | Processed transcript | - | | TSL:3 , |
| Tacc2-204 | ENSMUST00000207230.2 | 3668 | No protein | Retained intron | - | | TSL:1 , |
| Tacc2-213 | ENSMUST00000208661.2 | 2248 | No protein | Retained intron | - | | TSL:NA , |

The strategy is based on the design of *Tacc2-201* transcript,the transcription is shown below:



72.23 kb — Forward strand

Tacc2-201 >
protein coding
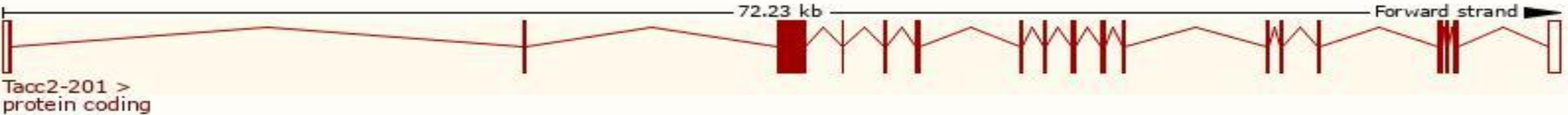
# Genomic location distribution
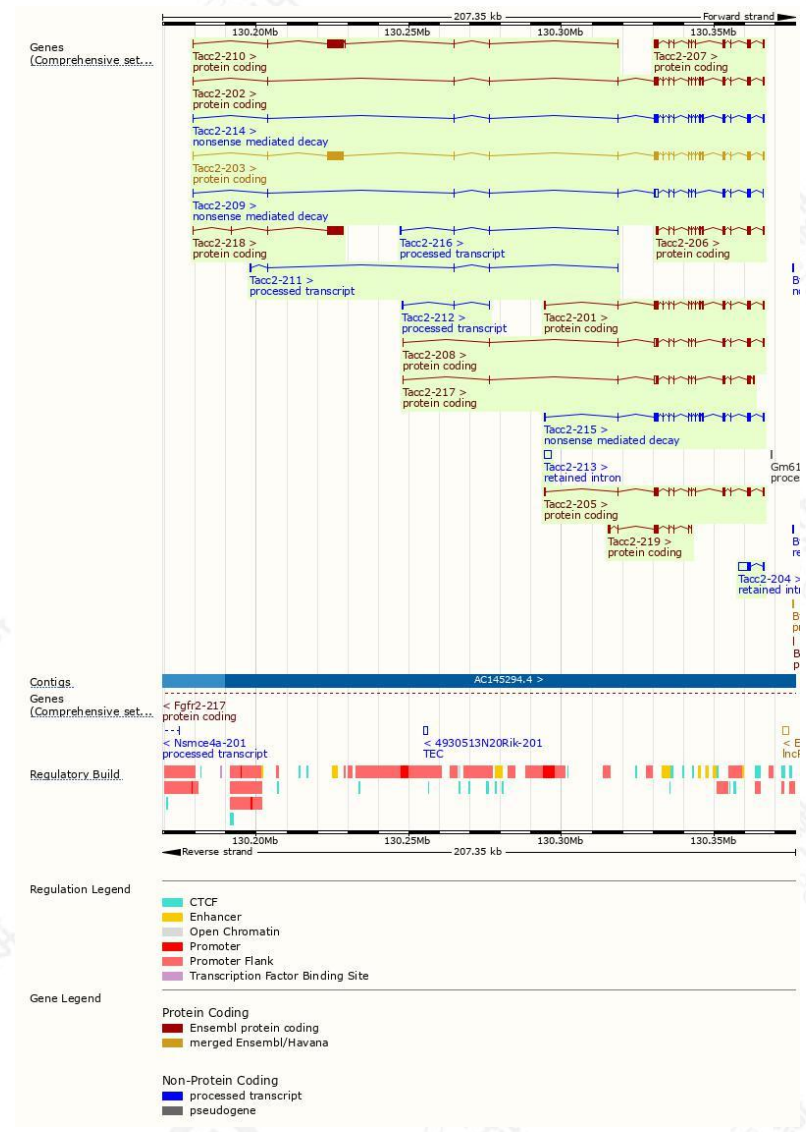
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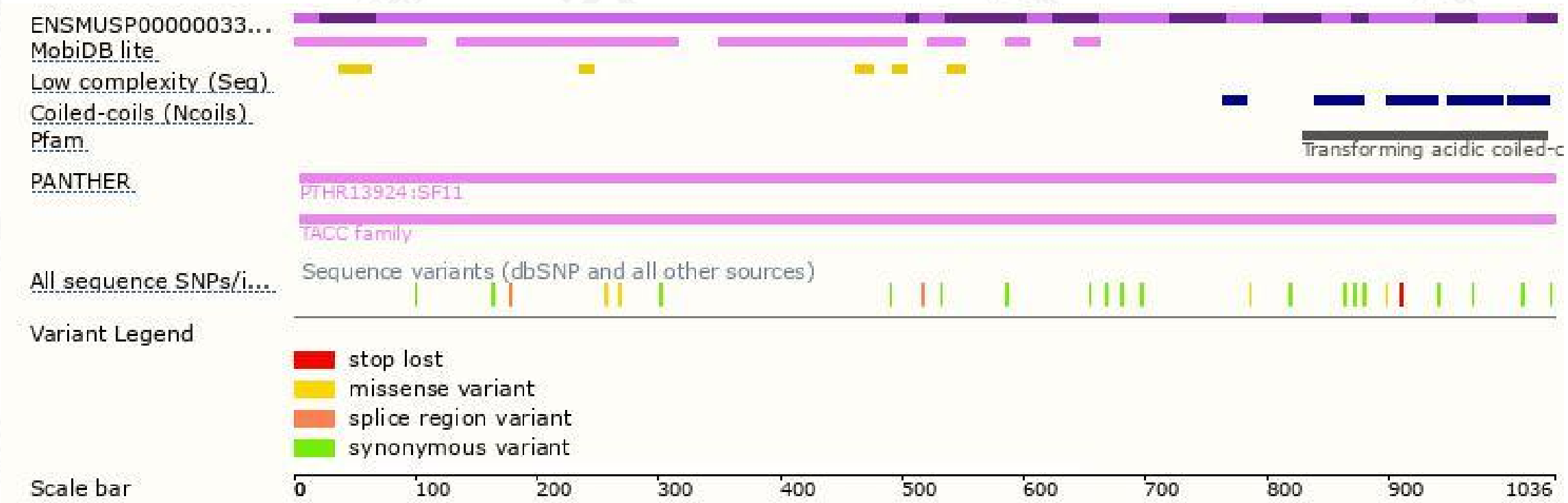
If you have any questions, you are welcome to inquire.
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