

# ***Tsks* Cas9-KO Strategy**

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**Reviewer: Daohua Xu**

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# Project Overview

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**Project Name**

***Tsk***

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**Project type**

**Cas9-KO**

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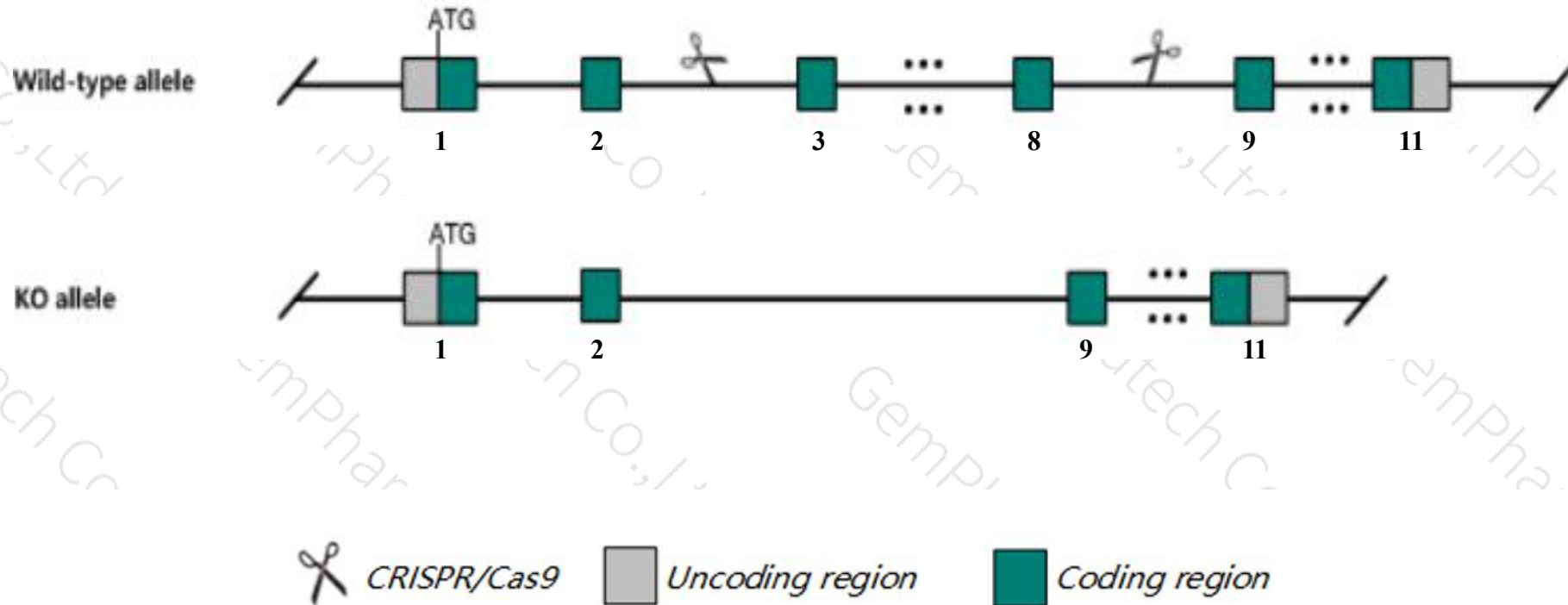
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Tsks* gene has 4 transcripts. According to the structure of *Tsks* gene, exon3-exon8 of *Tsks*-202(ENSMUST00000120929.8) transcript is recommended as the knockout region. The region contains 947bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tsks* 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.

- The *Tsks* 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)

## Tsks testis-specific serine kinase substrate [ *Mus musculus* (house mouse) ]

Gene ID: 22116, updated on 25-Sep-2020

### Summary

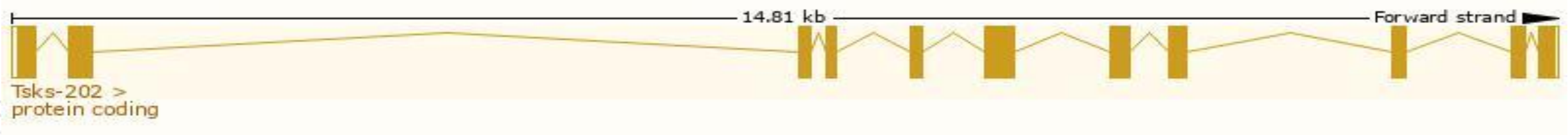
Official Symbol	Tsks provided by <a href="#">MGI</a>
Official Full Name	testis-specific serine kinase substrate provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1347560</a>
See related	<a href="#">Ensembl:ENSMUSG00000059891</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<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	Ts; Tss; Stk22; Tssks1; Stk22s1
Summary	This gene is a member of a small family of testis-specific serine/threonine kinases. This gene may play a role in testicular physiology or spermiogenesis. Its expression is restricted to the testis during the last stages of spermatid maturation. Alternative splicing results in multiple transcript variants encoding distinct proteins. [provided by RefSeq, Jul 2008]
Expression	Restricted expression toward testis adult (RPKM 199.6) <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

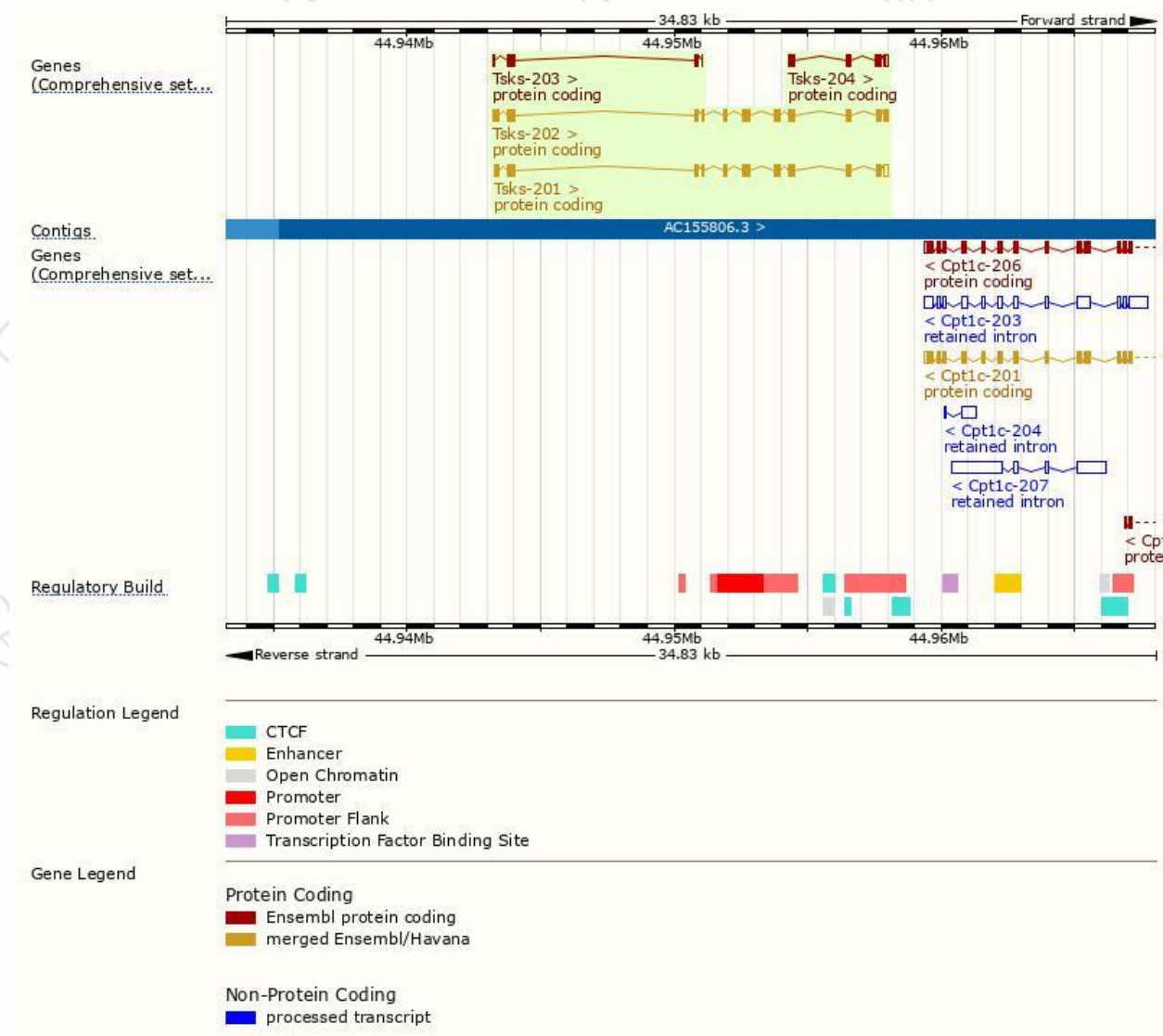
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tsks-202	<a href="#">ENSMUST00000120929.8</a>	1843	<a href="#">585aa</a>	Protein coding	<a href="#">CCDS52240</a>	<a href="#">Q54887</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Tsks-201	<a href="#">ENSMUST00000080233.8</a>	1806	<a href="#">525aa</a>	Protein coding	<a href="#">CCDS39946</a>	<a href="#">Q147V4</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Tsks-204	<a href="#">ENSMUST00000208475.1</a>	651	<a href="#">185aa</a>	Protein coding	-	<a href="#">A0A140LIA8</a>	CDS 5' incomplete TSL:5
Tsks-203	<a href="#">ENSMUST00000207719.1</a>	388	<a href="#">109aa</a>	Protein coding	-	<a href="#">A0A140LJ33</a>	CDS 3' incomplete TSL:5

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

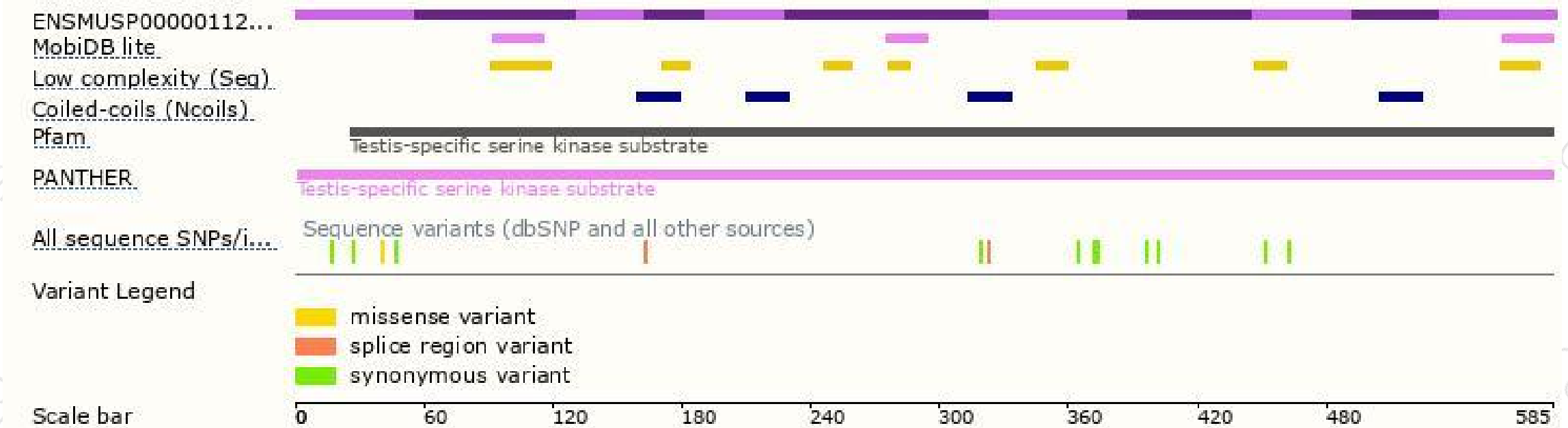


# Genomic location distribution

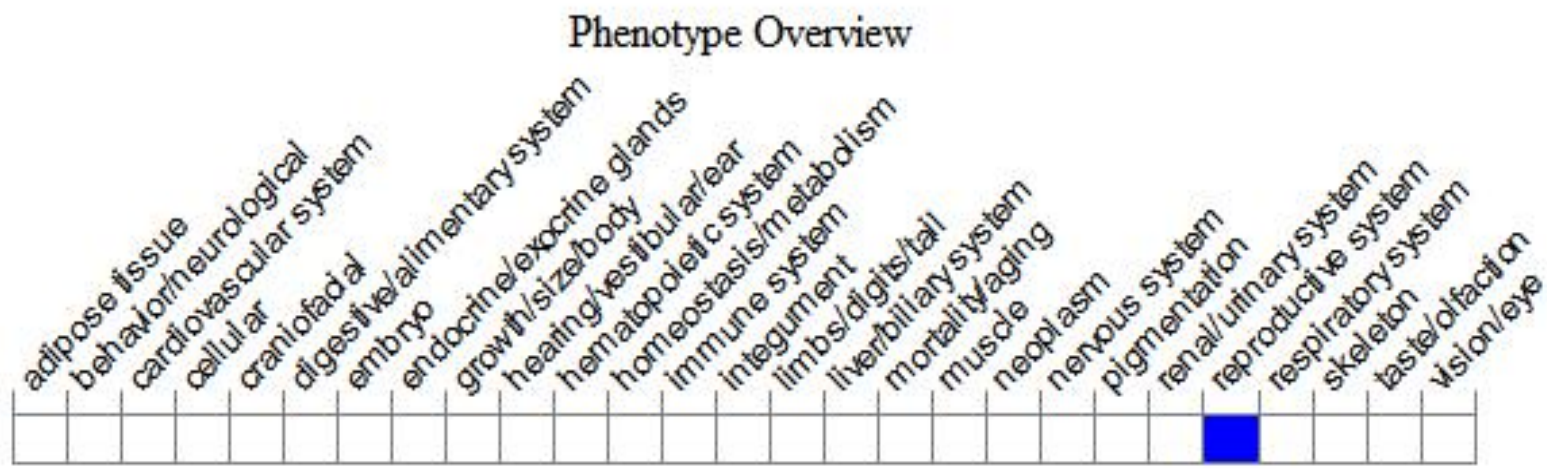




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

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

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