

***Task2* Cas9-KO Strategy**

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Project Overview

Project Name

Task2

Project type

Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tesk2* gene. The schematic diagram is as follows:



- The *Tesk2* gene has 4 transcripts. According to the structure of *Tesk2* gene, exon4 of *Tesk2-201* (ENSMUST00000045542.12) transcript is recommended as the knockout region. The region contains 49bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tesk2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Tesk2* gene is located on the Chr4. 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)

Task2 testis-specific kinase 2 [Mus musculus (house mouse)]

Gene ID: 230661, updated on 13-Mar-2020

Summary



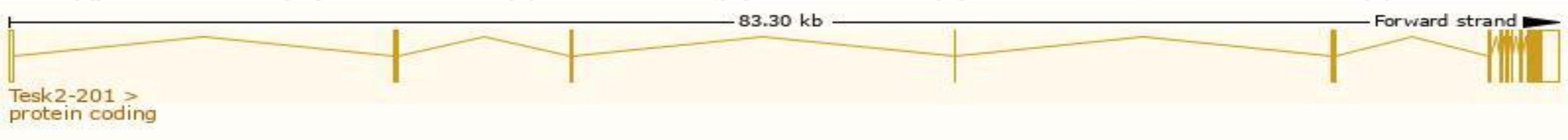
Official Symbol	Task2 provided by MGI
Official Full Name	testis-specific kinase 2 provided by MGI
Primary source	MGI:MGI:2385204
See related	Ensembl:ENSMUSG000000033985
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in testis adult (RPKM 12.8), large intestine adult (RPKM 7.1) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

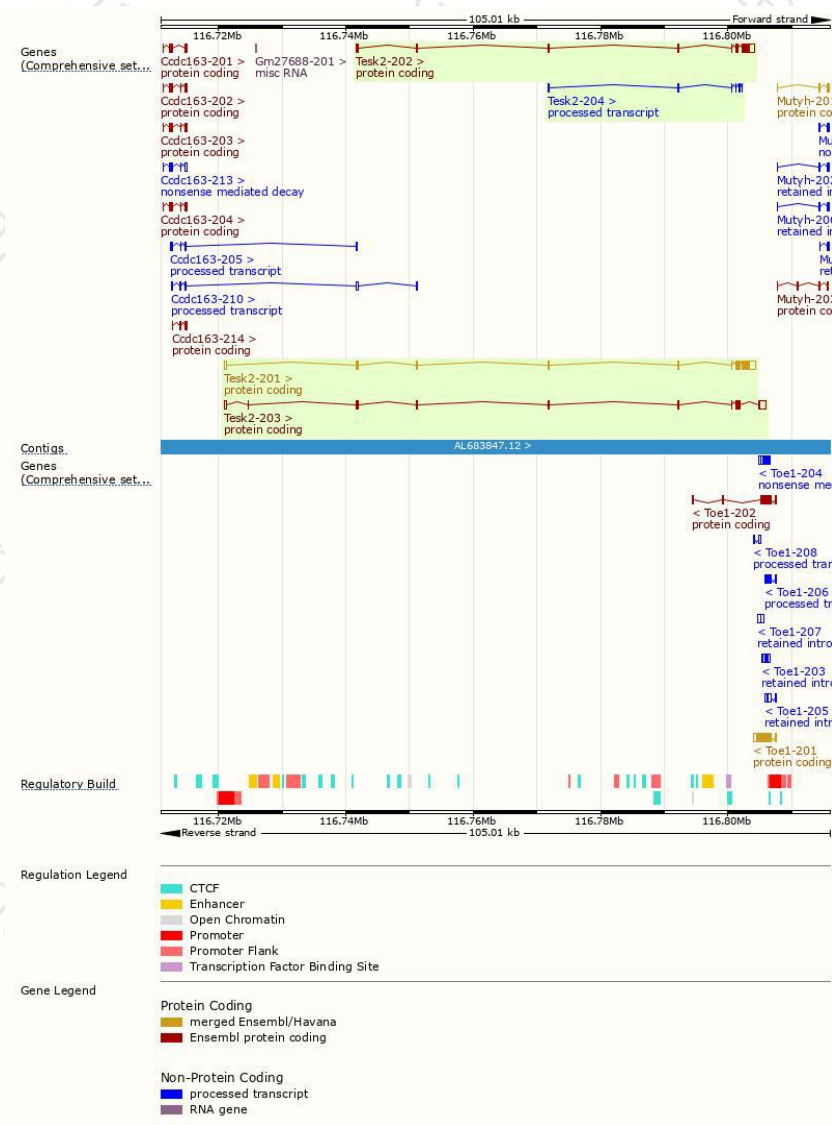
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Test2-201	ENSMUST00000045542.12	3033	570aa	Protein coding	CCDS18516	Q8VCT9	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 P1
Test2-203	ENSMUST00000106459.7	2444	319aa	Protein coding	-	A2AGE0	TSL:1 GENCODE basic
Test2-202	ENSMUST00000106456.1	2430	541aa	Protein coding	-	A2AGD9	TSL:5 GENCODE basic
Test2-204	ENSMUST00000142529.1	530	No protein	Processed transcript	-	-	TSL:3

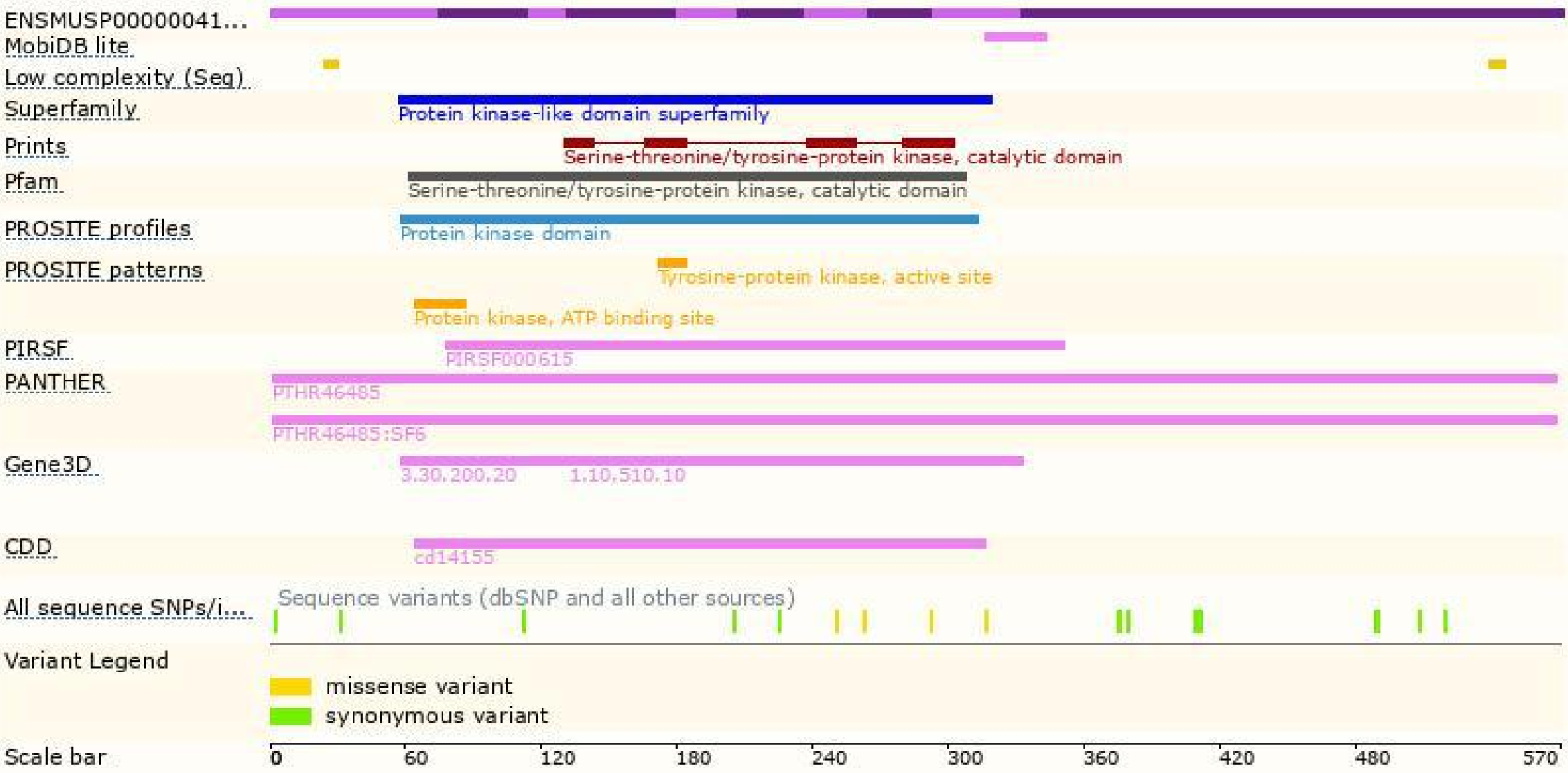
The strategy is based on the design of *Test2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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