

Task2 Cas9-CKO Strategy

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Project Overview

Project Name

Task2

Project type

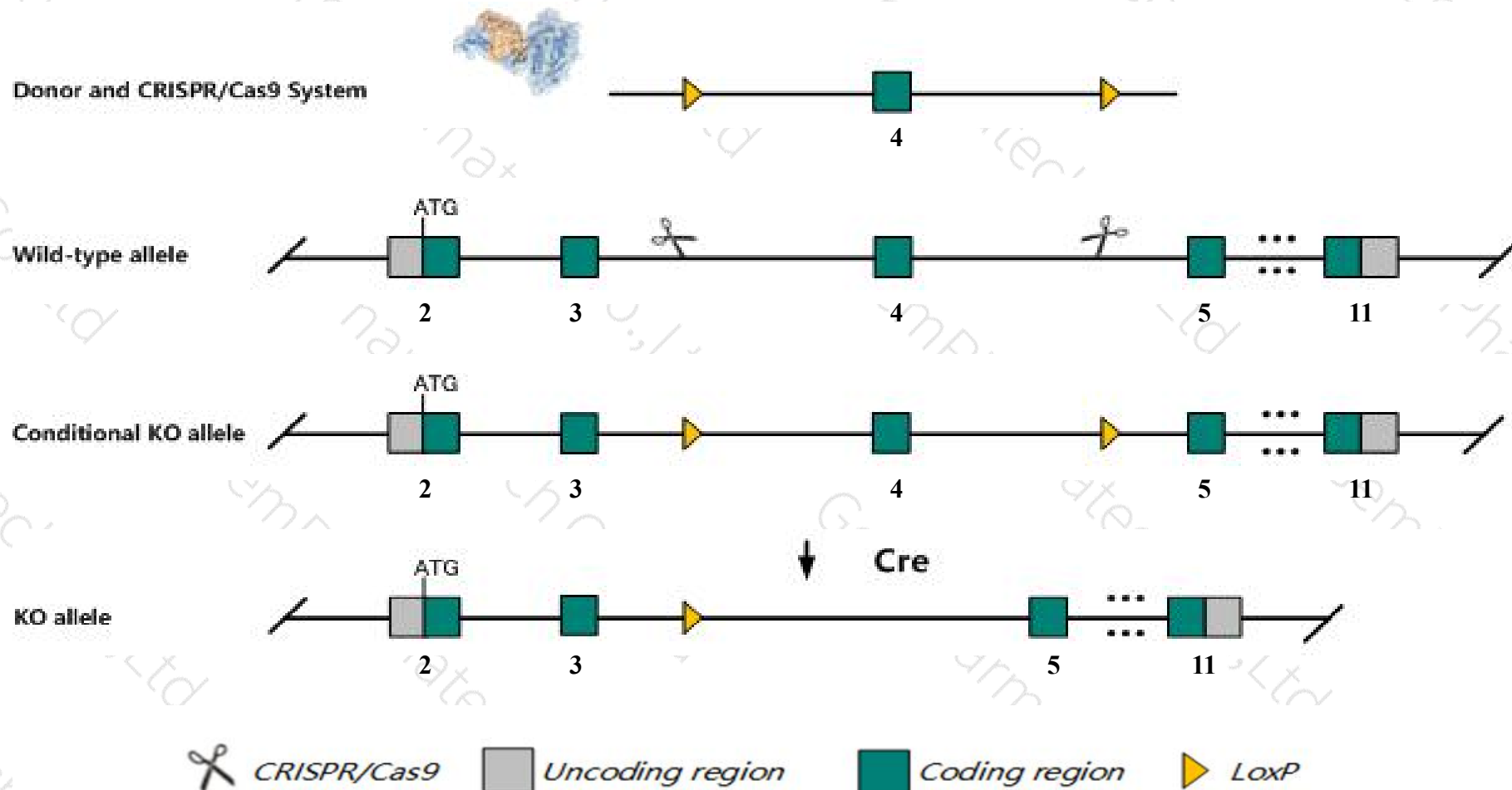
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

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



Technical routes

- 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 and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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:ENSMUSG00000033985
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

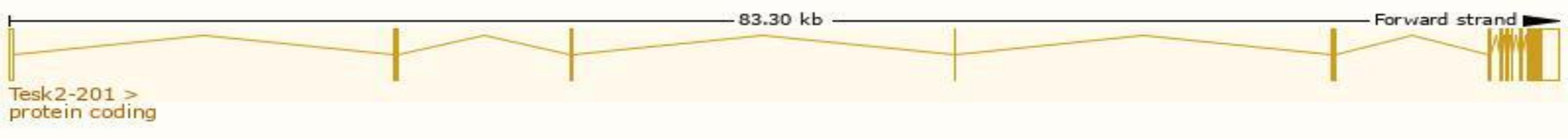
Transcript information (Ensembl)



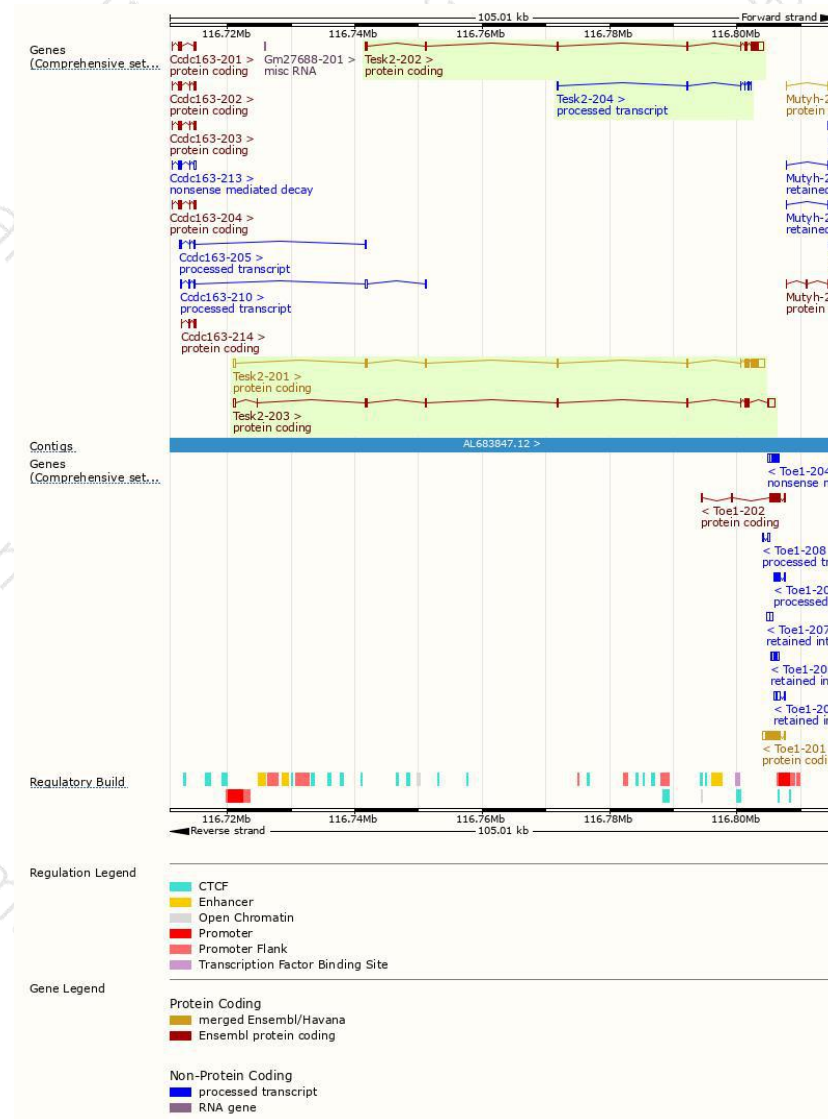
The gene has 4 transcripts,all transcripts are shown below:

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

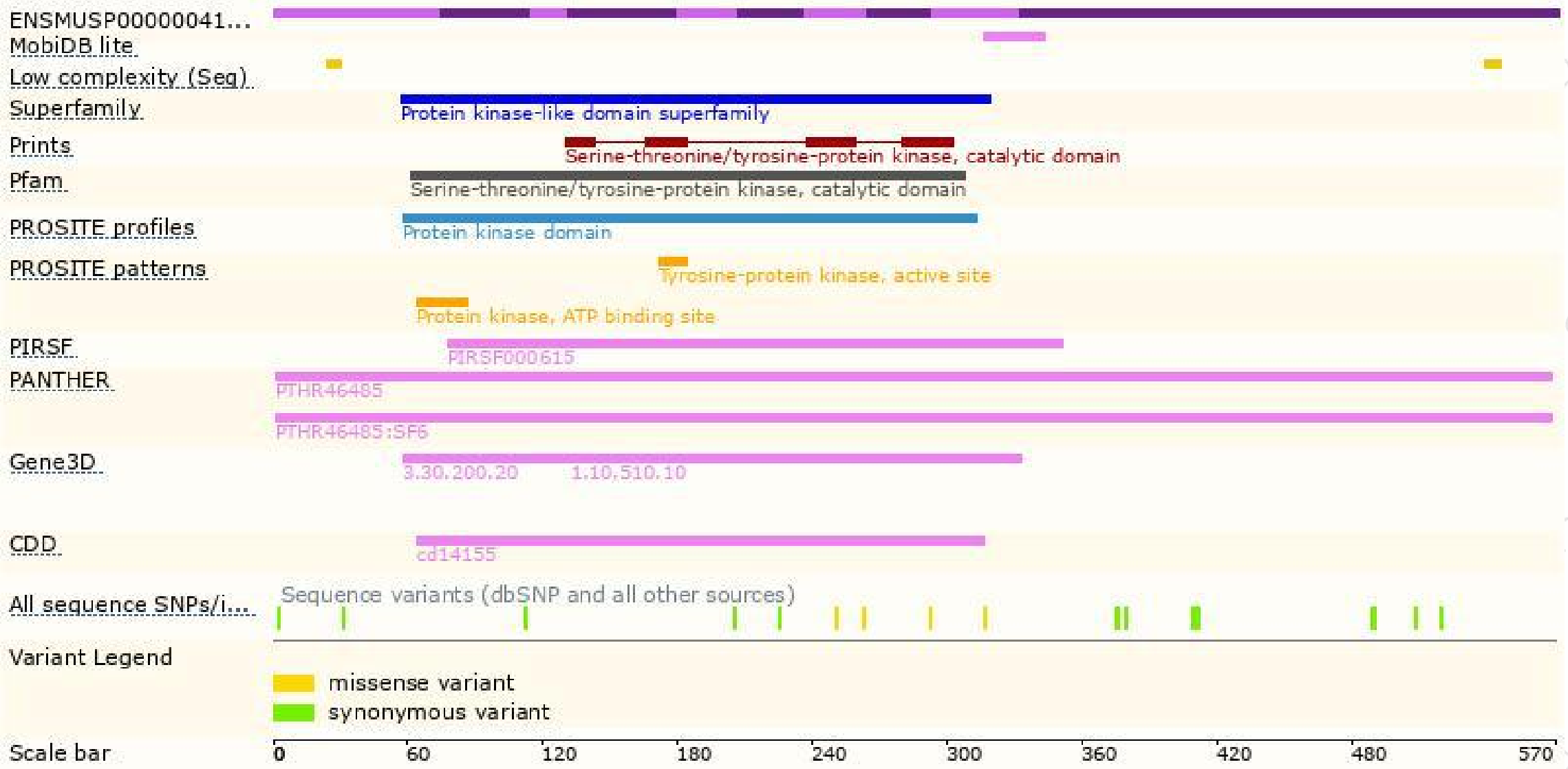
The strategy is based on the design of *Test2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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