

Yes1 Cas9-KO Strategy

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Project Overview

Project Name

Yes1

Project type

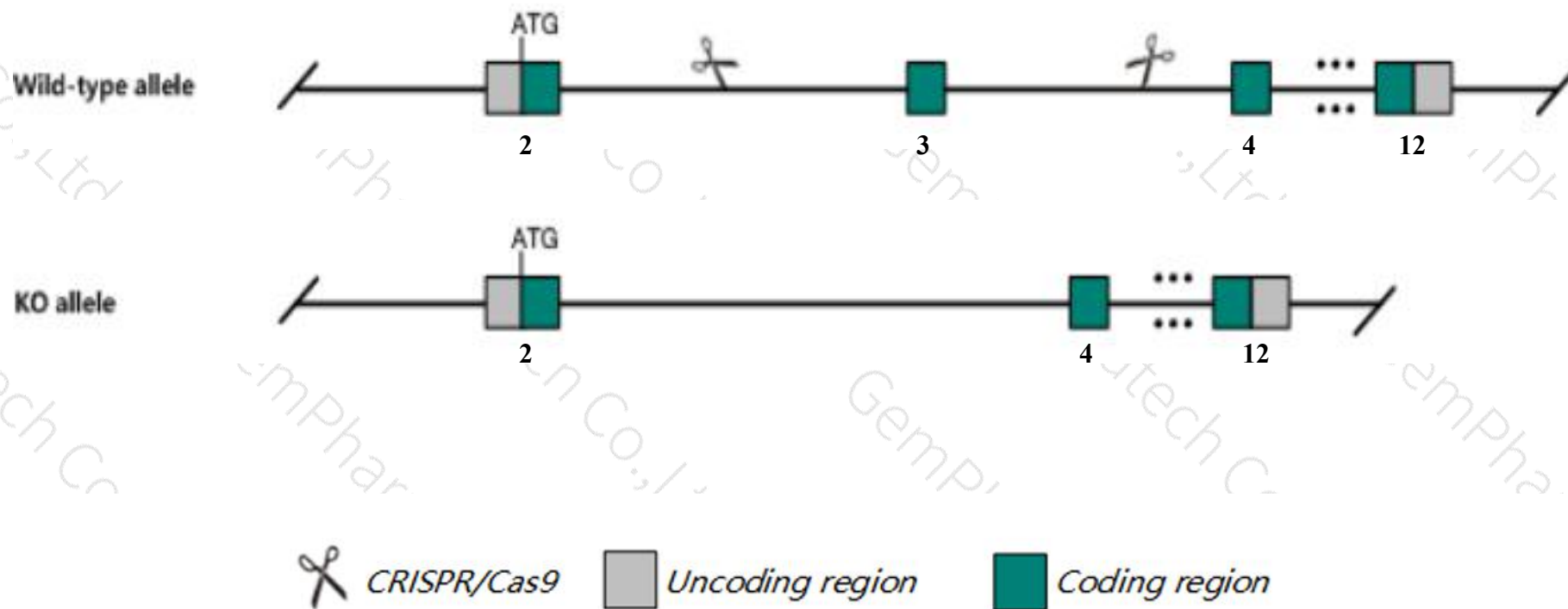
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Yes1* gene. The schematic diagram is as follows:



- The *Yes1* gene has 5 transcripts. According to the structure of *Yes1* gene, exon3 of *Yes1-201* (ENSMUST00000072311.12) transcript is recommended as the knockout region. The region contains 100bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Yes1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, homozygotes for targeted null alleles have no overt phenotype, but mice homozygous for both *yes* and *src* null mutations exhibit impaired movement and breathing, resulting in perinatal lethality.
- The KO region contains partial intron of the *Gm15614* gene. Knockout the region may affect the function of *Gm15614* gene.
- The *Yes1* gene is located on the Chr5. 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)

Yes1 YES proto-oncogene 1, Src family tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 22612, updated on 15-Mar-2020

Summary



Official Symbol	Yes1 provided by MGI
Official Full Name	YES proto-oncogene 1, Src family tyrosine kinase provided by MGI
Primary source	MGI:MGI:99147
See related	Ensembl:ENSMUSG00000014932
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	Yes, p61-Yes
Expression	Ubiquitous expression in placenta adult (RPKM 4.0), CNS E11.5 (RPKM 3.5) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）



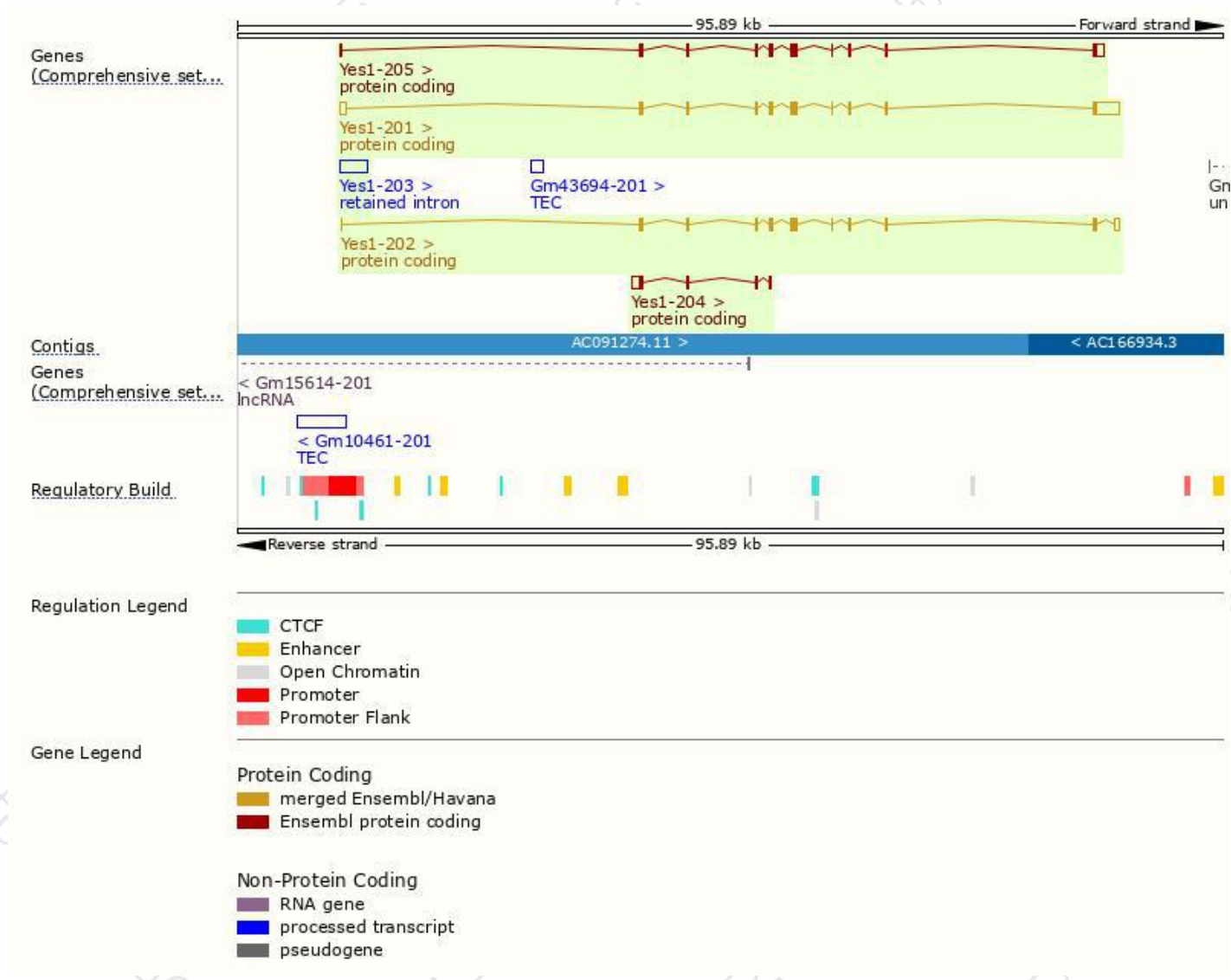
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Yes1-201	ENSMUST00000072311.12	4586	541aa	Protein coding	CCDS39061	Q04736_Q3TJ17	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
Yes1-205	ENSMUST00000202543.3	2657	541aa	Protein coding	CCDS39061	Q04736_Q3TJ17	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
Yes1-202	ENSMUST00000168707.5	2259	541aa	Protein coding	CCDS39061	Q04736_Q3TJ17	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
Yes1-204	ENSMUST00000200999.1	1403	198aa	Protein coding	-	A0A0J9YUV2	CDS 3' incomplete TSL:5
Yes1-203	ENSMUST00000200779.1	2749	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Yes1-201* transcript,the transcription is shown below:



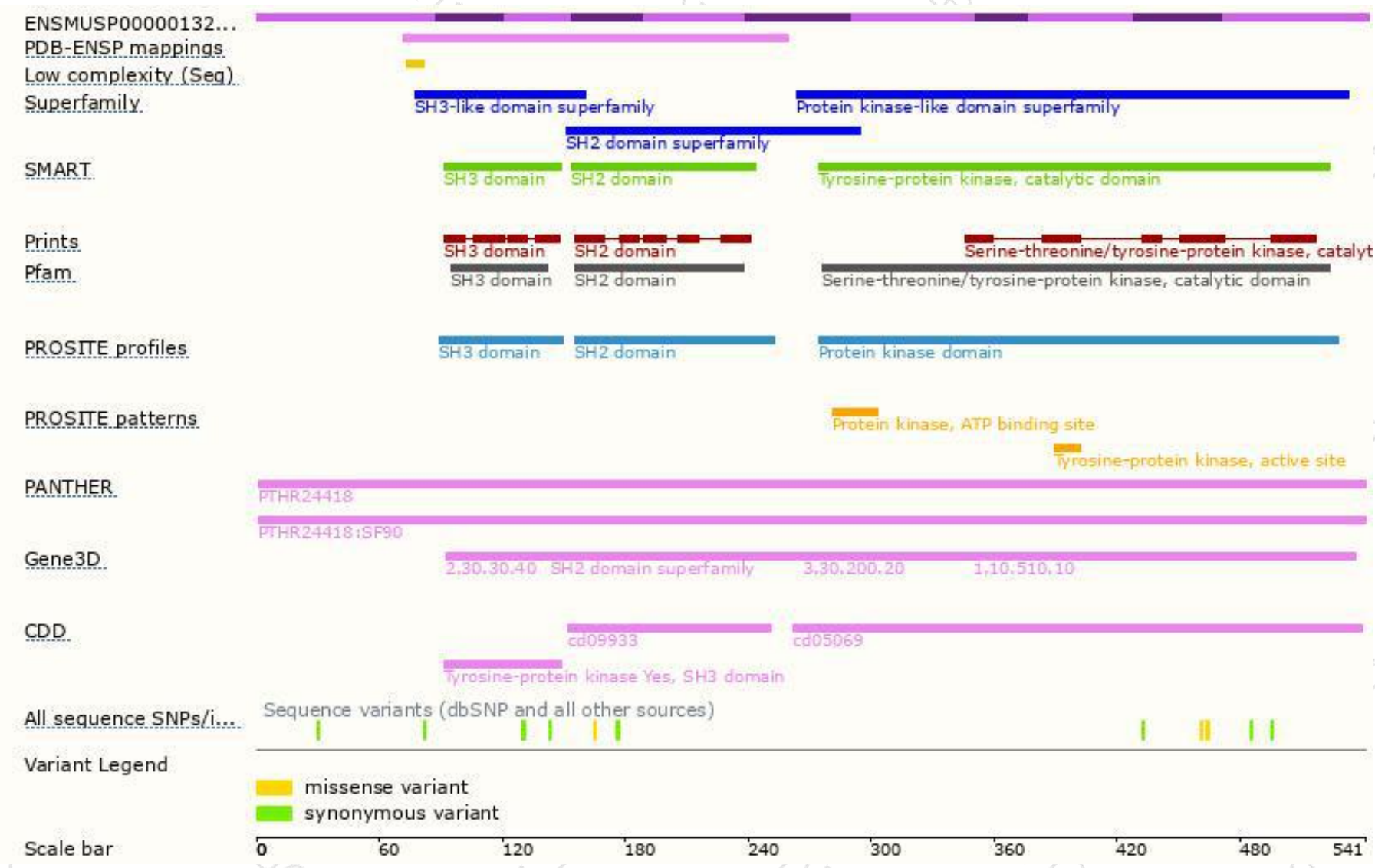
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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

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