

Ybx3 Cas9-CKO Strategy

Designer:

Huan Wang

Reviewer:

Huan Fan

Design Date:

2020-4-16

Project Overview

Project Name

Ybx3

Project type

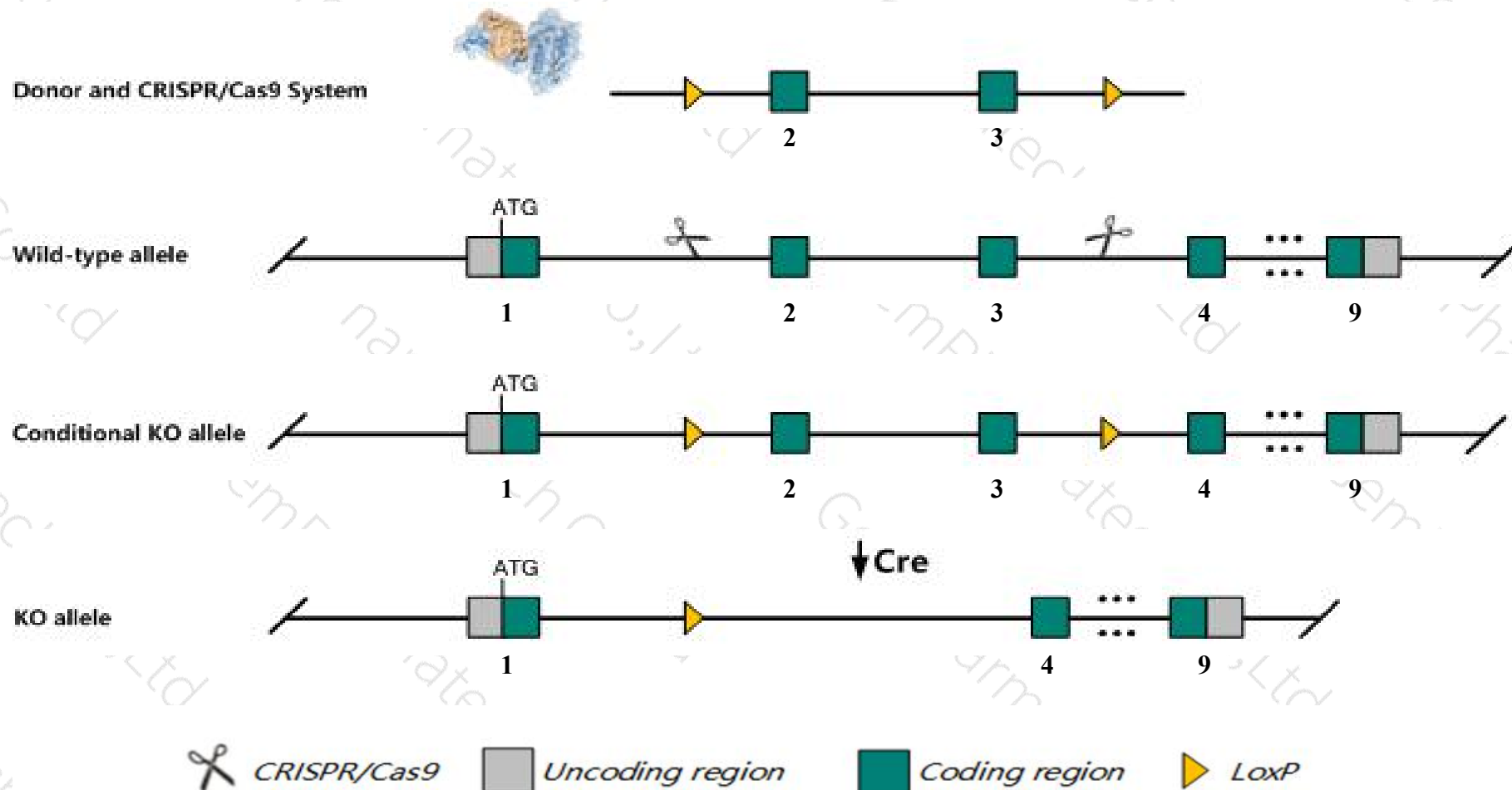
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ybx3* gene. The schematic diagram is as follows:



- The *Ybx3* gene has 5 transcripts. According to the structure of *Ybx3* gene, exon2-exon3 of *Ybx3-201* (ENSMUST00000032309.12) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ybx3* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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 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.

- According to the existing MGI data, half of mice homozygous for a knock-out allele exhibit male infertility associated with smaller testes and reduced sperm production, partly due to increased spermatocyte apoptosis during mid to late spermatogenesis and progressive seminiferous tubule degeneration.
- The *Ybx3* gene is located on the Chr6. 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)

Ybx3 Y box protein 3 [Mus musculus (house mouse)]

Gene ID: 56449, updated on 13-Mar-2020

Summary



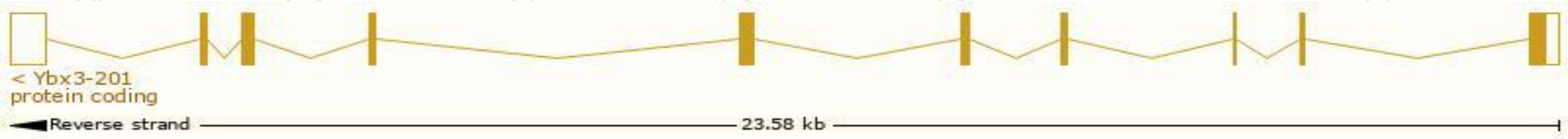
Official Symbol	Ybx3 provided by MGI
Official Full Name	Y box protein 3 provided by MGI
Primary source	MGI:MGI:2137670
See related	Ensembl:ENSMUSG000000030189
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Csda, Dpba, MSY3, MSY4, Yb2, dbpA, oxyR
Expression	Broad expression in testis adult (RPKM 404.0), liver E14 (RPKM 96.6) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

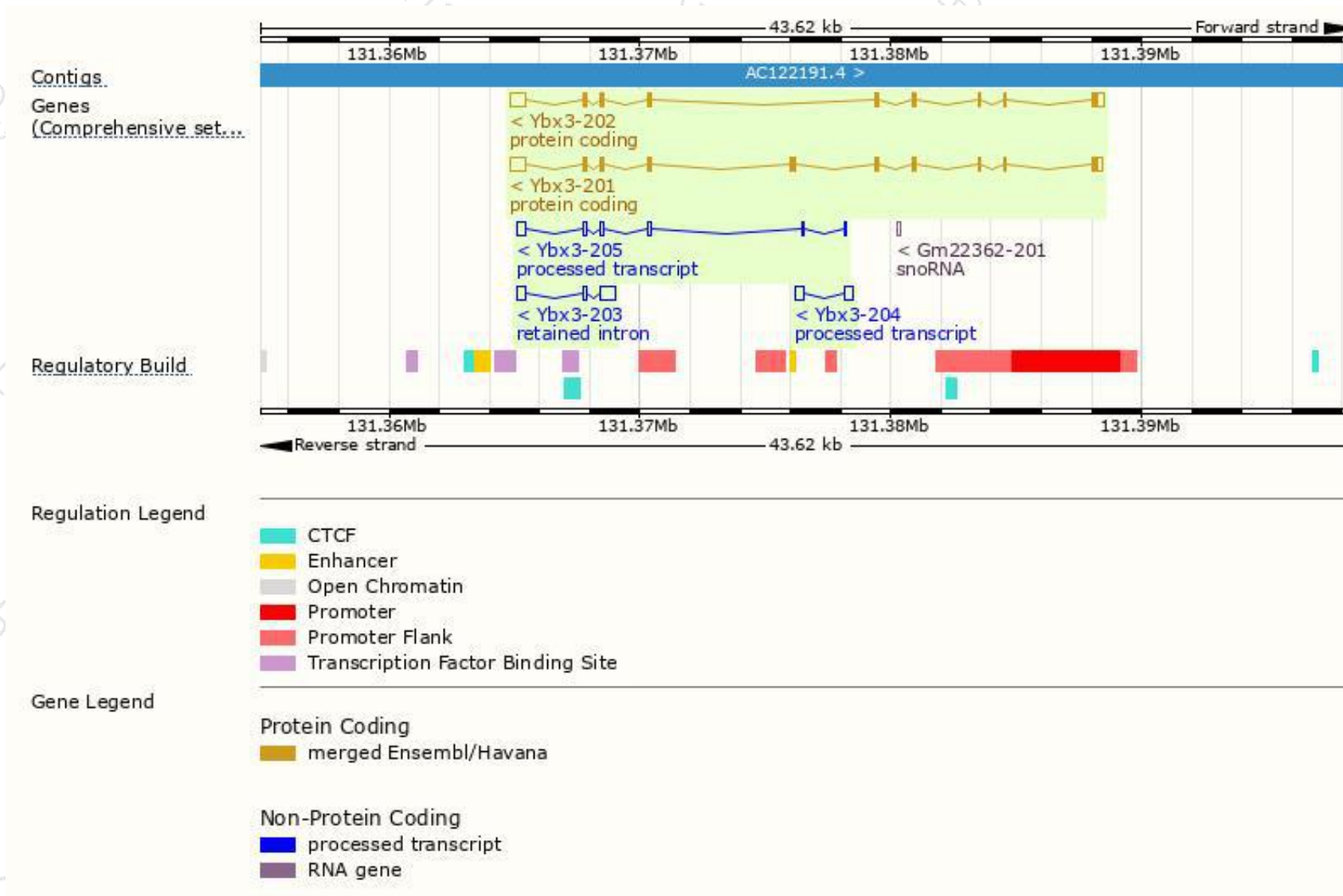
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ybx3-201	ENSMUST00000032309.12	1853	361aa	Protein coding	CCDS20606	Q9JKB3	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 P4
Ybx3-202	ENSMUST00000087865.3	1684	292aa	Protein coding	CCDS20605	Q9JKB3	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
Ybx3-205	ENSMUST00000205035.2	838	No protein	Processed transcript	-	-	TSL:3
Ybx3-204	ENSMUST00000204481.1	745	No protein	Processed transcript	-	-	TSL:3
Ybx3-203	ENSMUST00000203157.1	1035	No protein	Retained intron	-	-	TSL:2

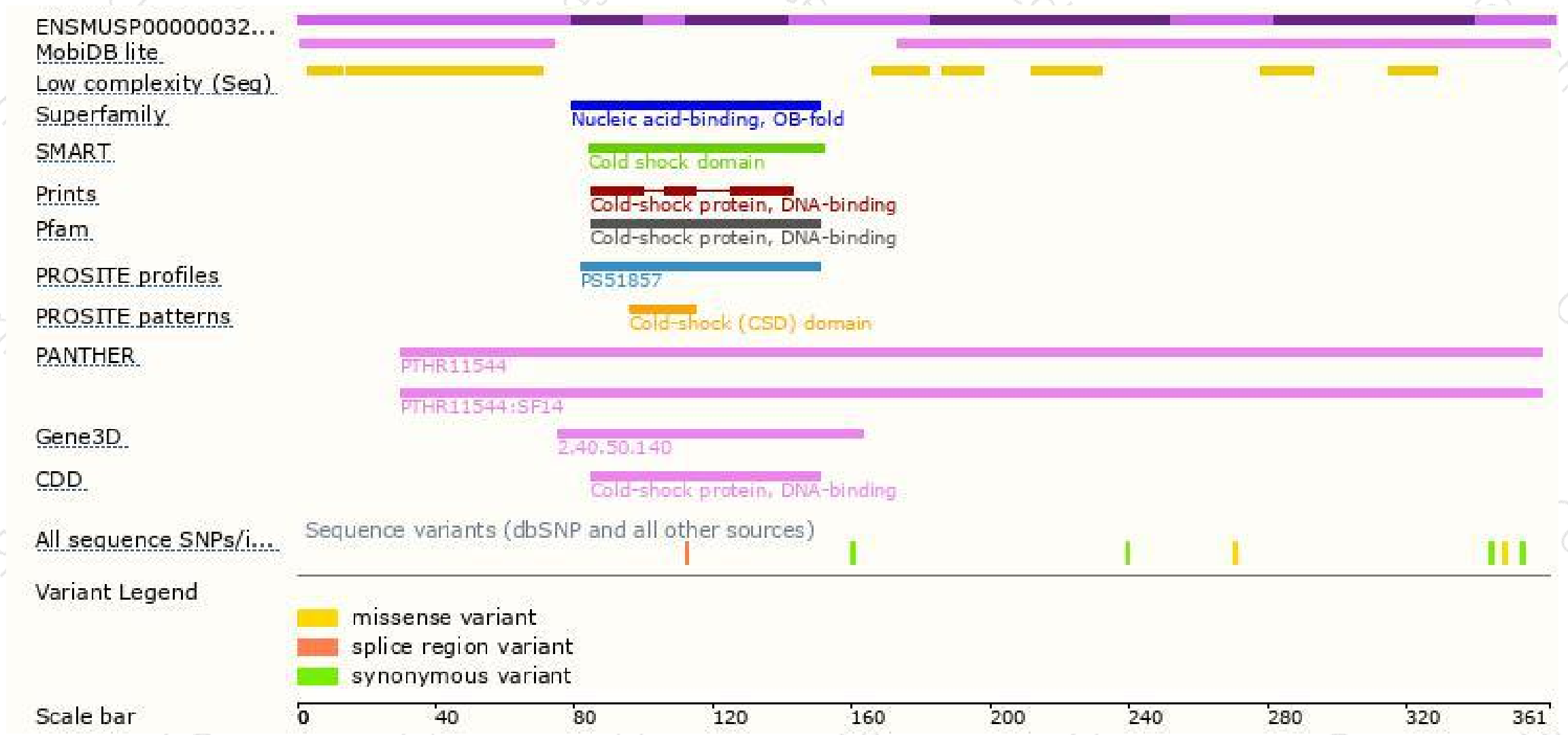
The strategy is based on the design of *Ybx3-201* transcript,the transcription is shown below



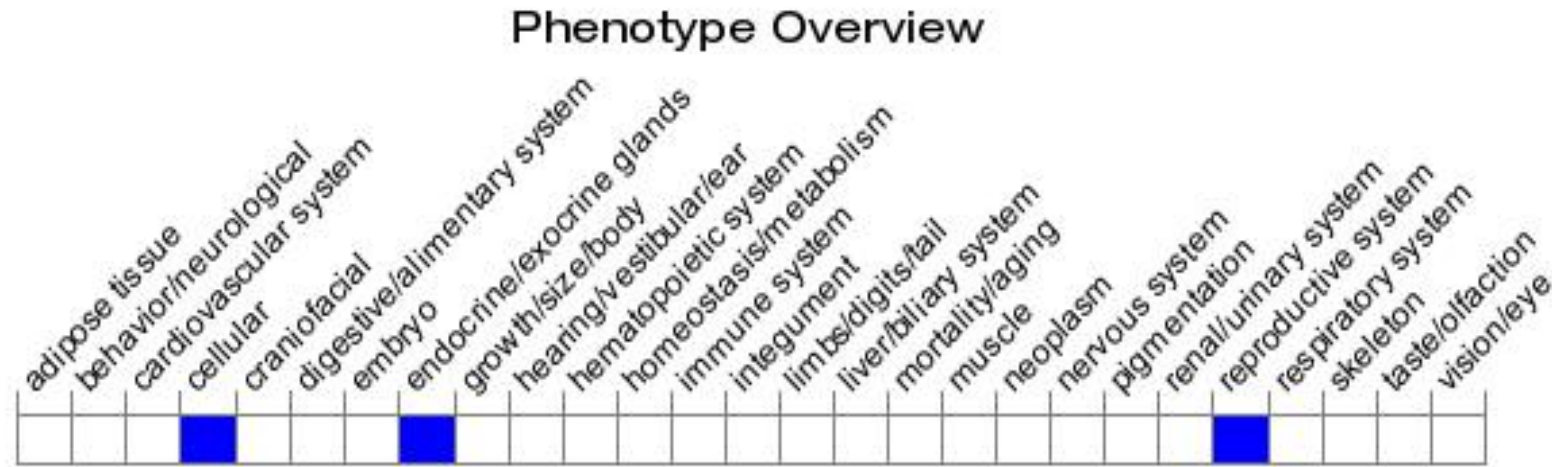
Genomic location distribution



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/>).

According to the existing MGI data, half of mice homozygous for a knock-out allele exhibit male infertility associated with smaller testes and reduced sperm production, partly due to increased spermatocyte apoptosis during mid to late spermatogenesis and progressive seminiferous tubule degeneration.

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

Tel: 400-9660890

