

Zkscan17 Cas9-CKO Strategy

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Project Overview

Project Name

Zkscan17

Project type

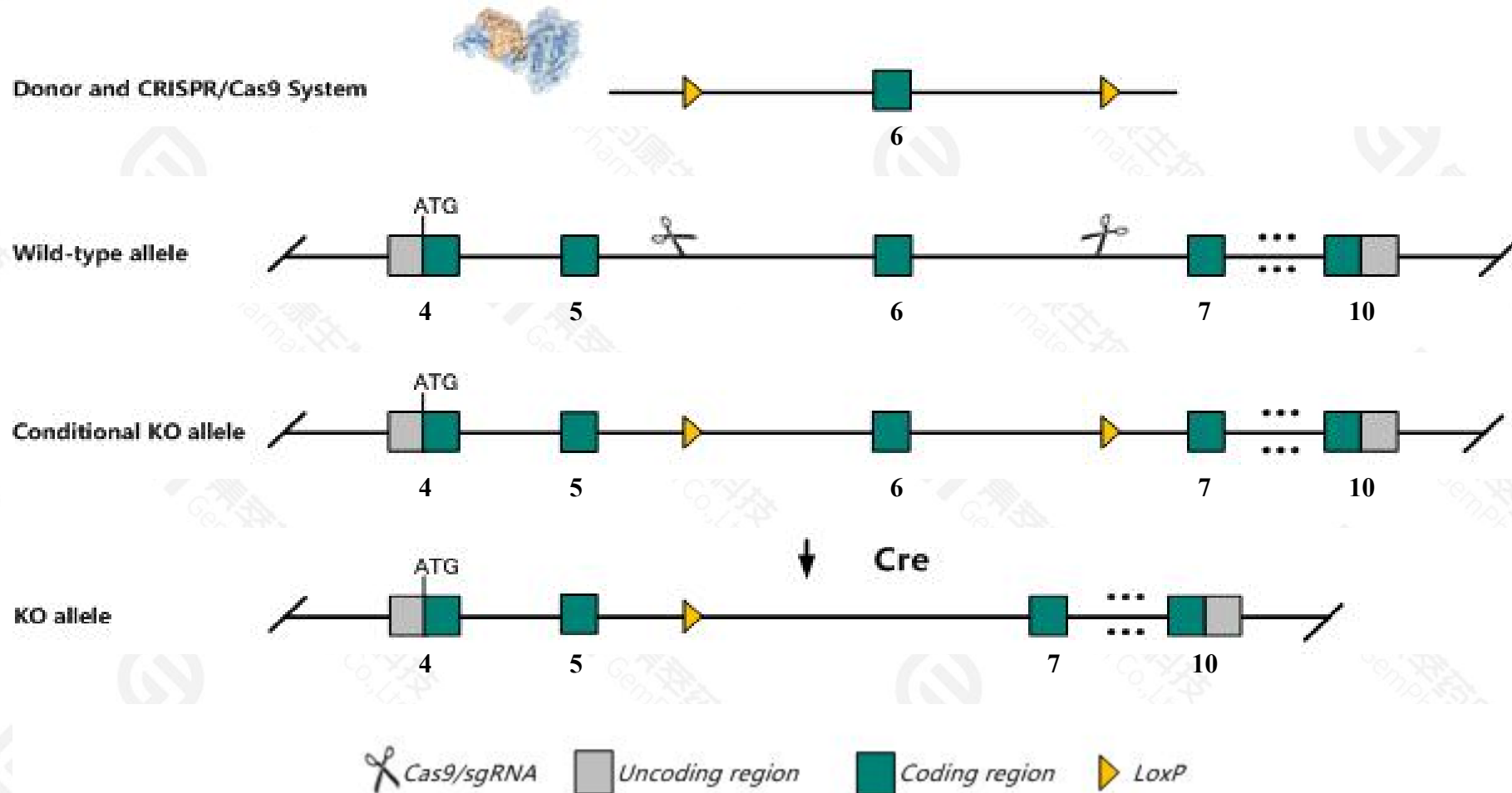
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zkscan17* gene. The schematic diagram is as follows:



- The *Zkscan17* gene has 6 transcripts. According to the structure of *Zkscan17* gene, exon6 of *Zkscan17-201*(ENSMUST00000013262.15) transcript is recommended as the knockout region. The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zkscan17* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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 *Zkscan17* gene is located on the Chr11. 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.
- Some amino acids remain at the N terminal, and part of the protein's function may be preserved.
- 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)

Zkscan17 zinc finger with KRAB and SCAN domains 17 [Mus musculus (house mouse)]

Gene ID: 268417, updated on 17-Dec-2020

Summary



Official Symbol Zkscan17 provided by [MGI](#)

Official Full Name zinc finger with KRAB and SCAN domains 17 provided by [MGI](#)

Primary source [MGI:MGI:2679270](#)

See related [Ensembl:ENSMUSG00000020472](#)

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 Ni, Nizp1, Zfp49, Zfp496, Znf496

Expression Ubiquitous expression in testis adult (RPKM 32.5), ovary adult (RPKM 10.5) and 28 other tissues [See more](#)

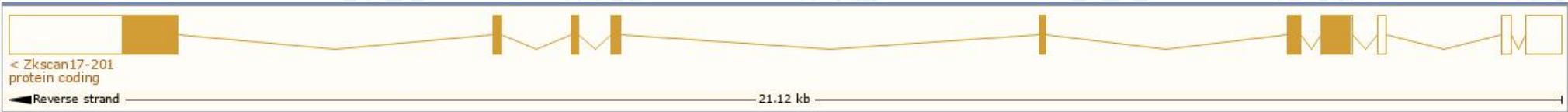
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

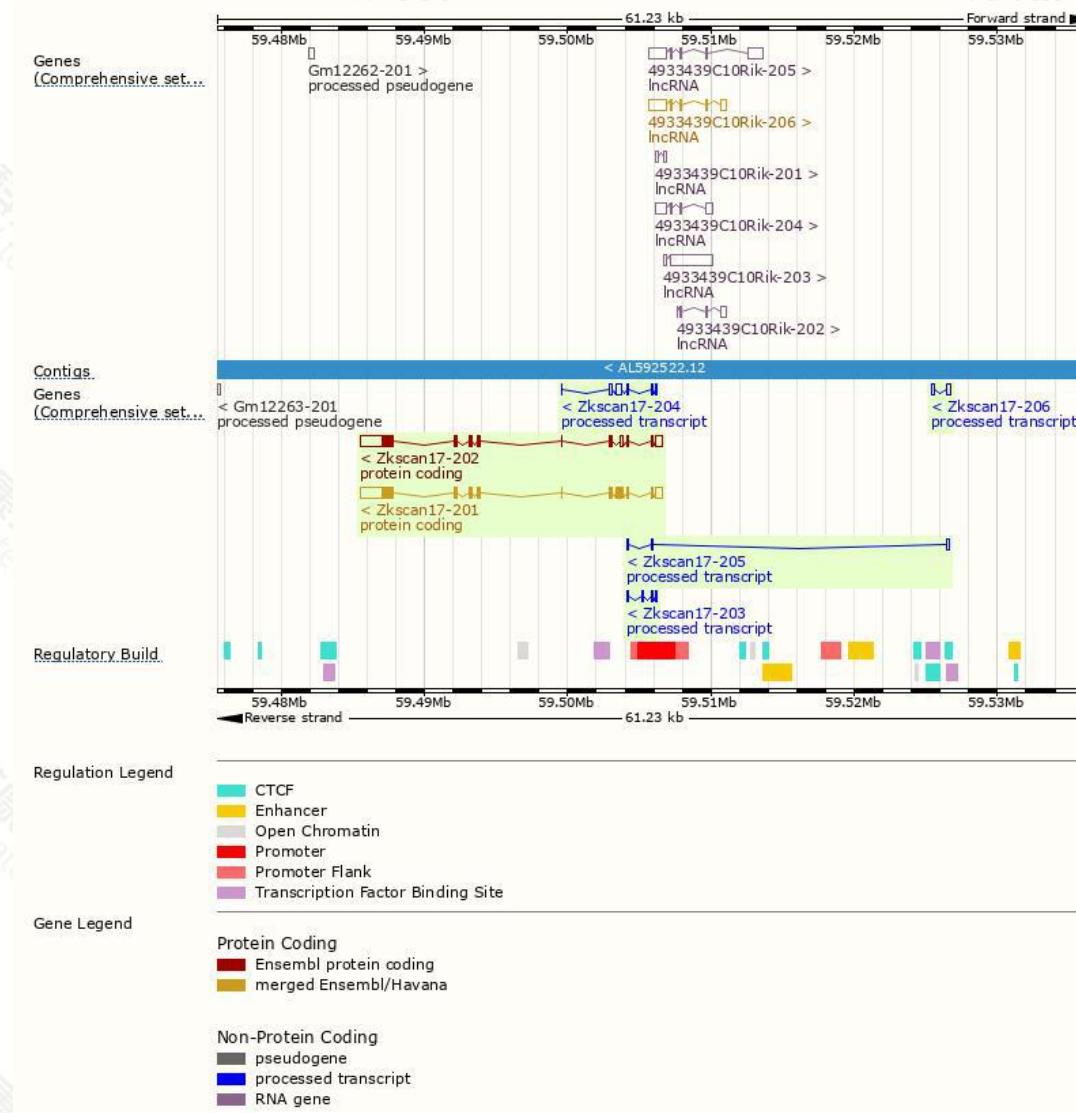
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zkscan17-201	ENSMUST00000013262.15	4064	585aa	Protein coding	CCDS24770		TSL:1 , GENCODE basic , APPRIS P1 ,
Zkscan17-202	ENSMUST000000101150.9	3771	429aa	Protein coding	CCDS70197		TSL:1 , GENCODE basic ,
Zkscan17-204	ENSMUST000000134522.8	937	No protein	Processed transcript	-		TSL:5 ,
Zkscan17-203	ENSMUST000000129941.2	423	No protein	Processed transcript	-		TSL:3 ,
Zkscan17-205	ENSMUST000000139093.8	361	No protein	Processed transcript	-		TSL:2 ,
Zkscan17-206	ENSMUST000000139707.2	360	No protein	Processed transcript	-		TSL:3 ,

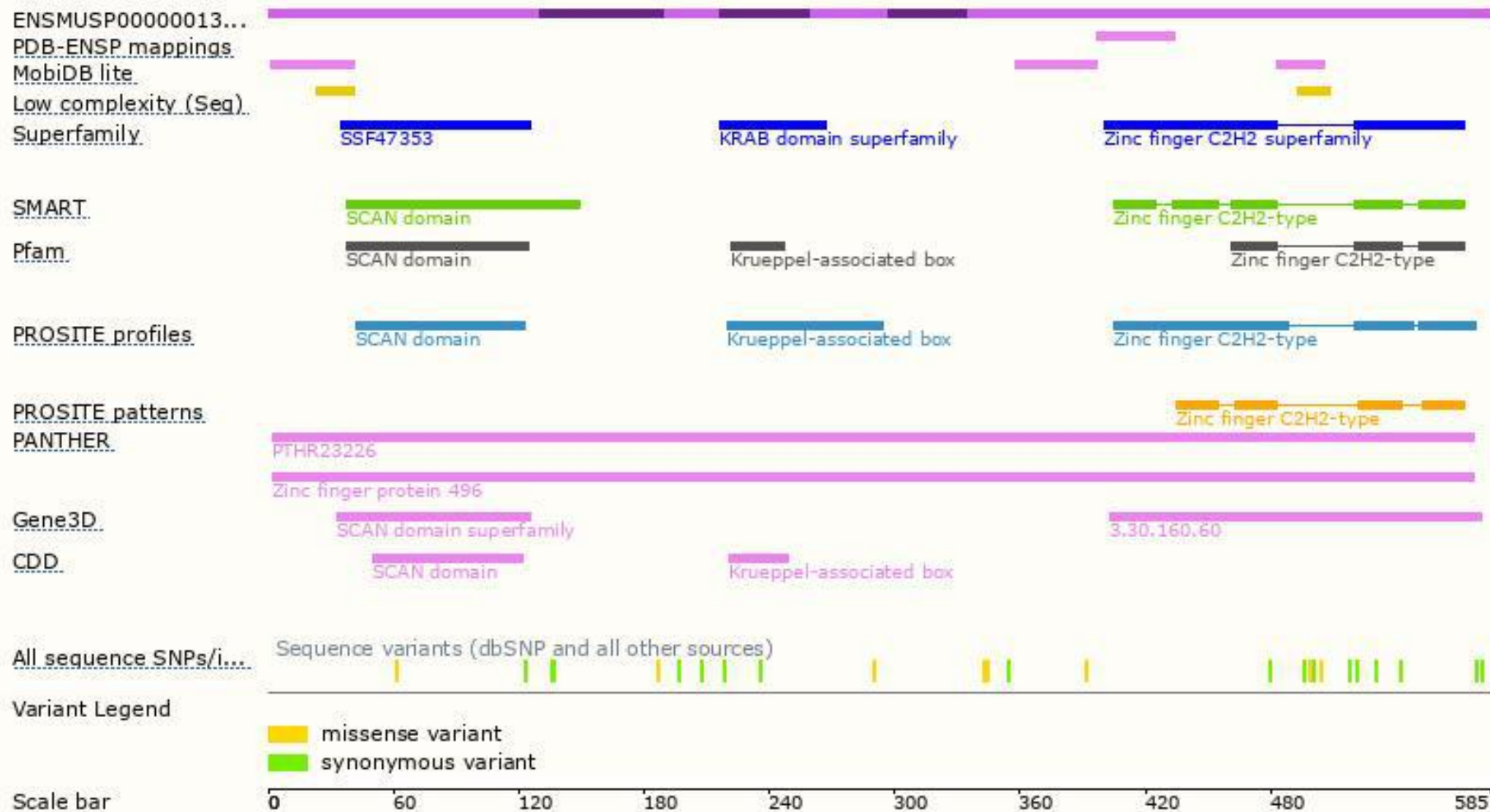
The strategy is based on the design of *Zkscan17-201* transcript,the transcription is shown below:



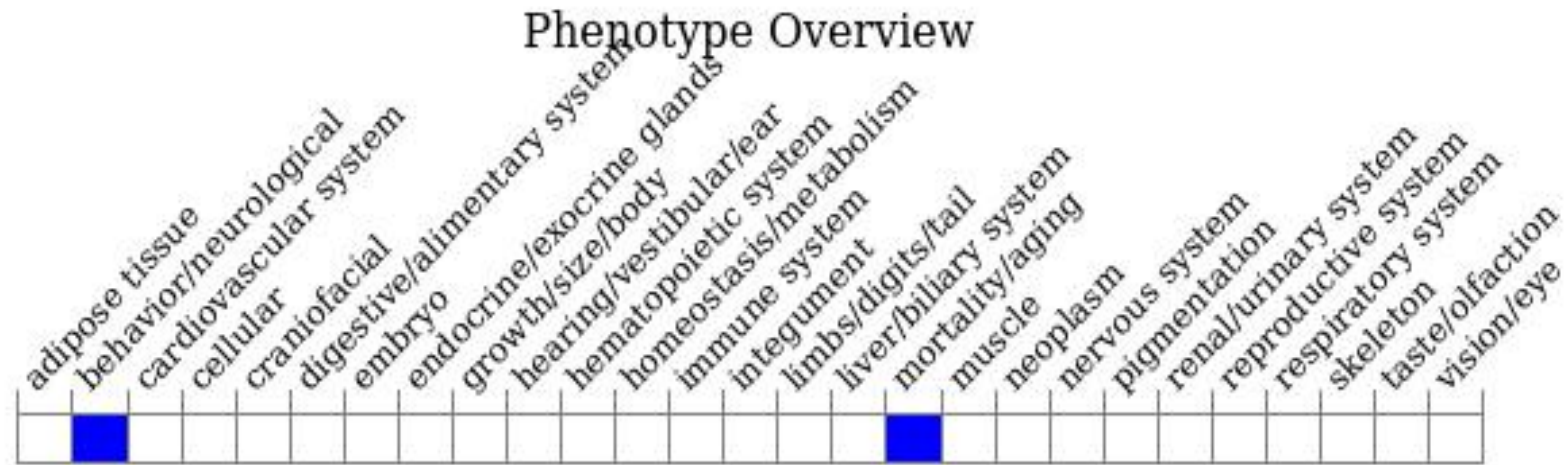
Genomic location distribution



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/>).

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

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