

***Zkscan5* Cas9-CKO Strategy**

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Project Overview

Project Name

Zkscan5

Project type

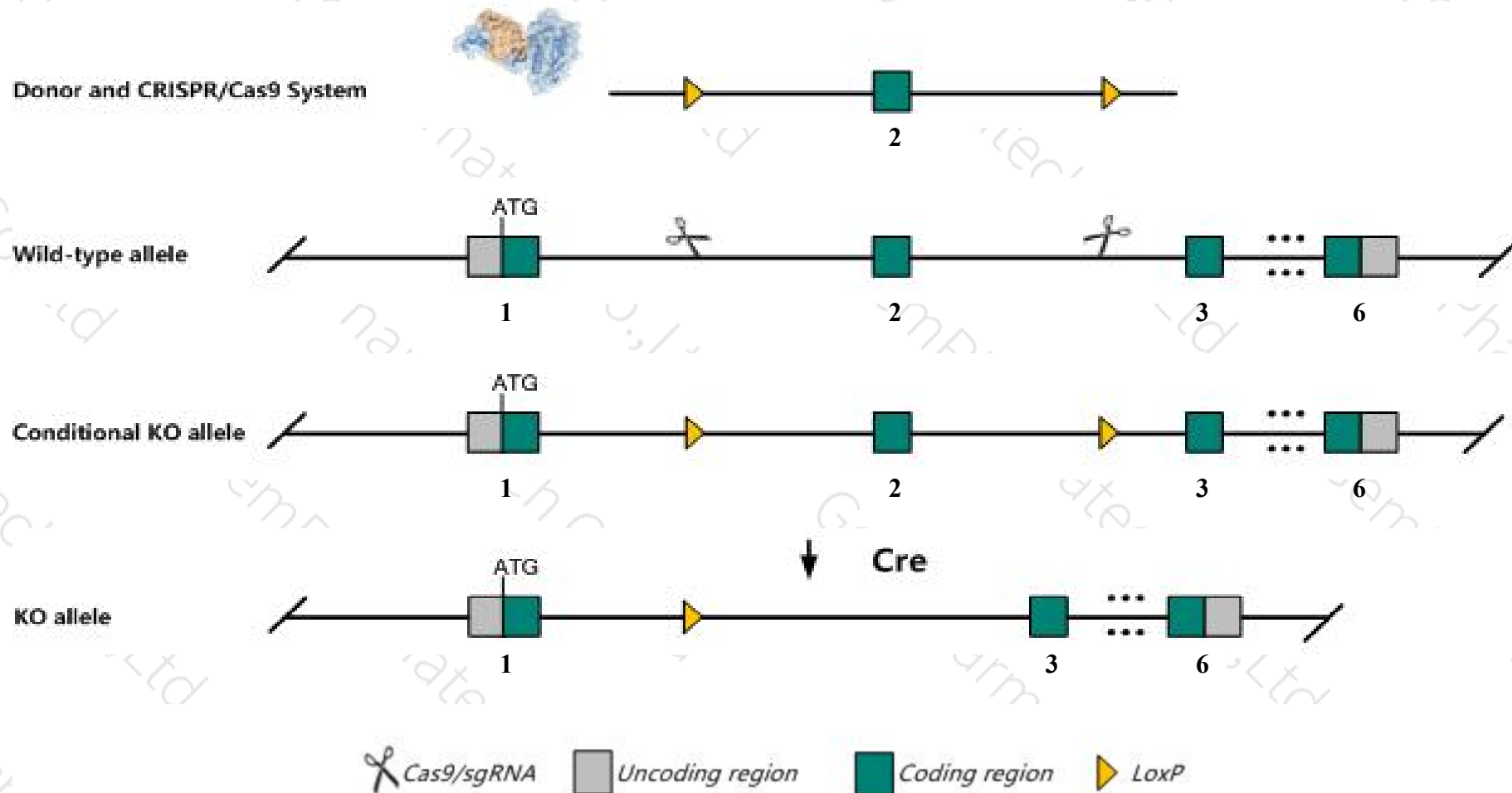
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zkscan5* gene. The schematic diagram is as follows:



- The *Zkscan5* gene has 6 transcripts. According to the structure of *Zkscan5* gene, exon2 of *Zkscan5*-202(ENSMUST00000085671.9) transcript is recommended as the knockout region. The region contains 133bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zkscan5* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector 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 *Zkscan5* 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.
- Transcript *Zkscan5*-203 may not be affected.
- The effect on transcript *Zkscan5*-204 is unknown.
- The floxed region is near to the N-terminal of *Zkscan14* gene, this strategy may influence the regulatory function of the N-terminal of *Zkscan14* gene.
- 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)

Zkscan5 zinc finger with KRAB and SCAN domains 5 [Mus musculus (house mouse)]

Gene ID: 22757, updated on 13-Mar-2020

Summary

Official Symbol Zkscan5 provided by [MGI](#)

Official Full Name zinc finger with KRAB and SCAN domains 5 provided by [MGI](#)

Primary source [MGI:MGI:107533](#)

See related [Ensembl:ENSMUSG00000055991](#)

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 AI132486, AI326970, Zfp95, hKraba1

Expression Ubiquitous expression in CNS E11.5 (RPKM 3.5), testis adult (RPKM 3.4) and 28 other tissues [See more](#)

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

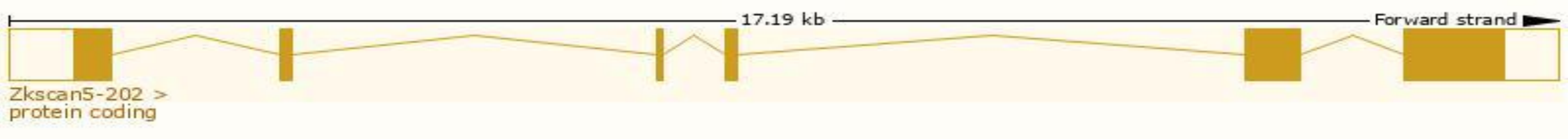
Transcript information (Ensembl)



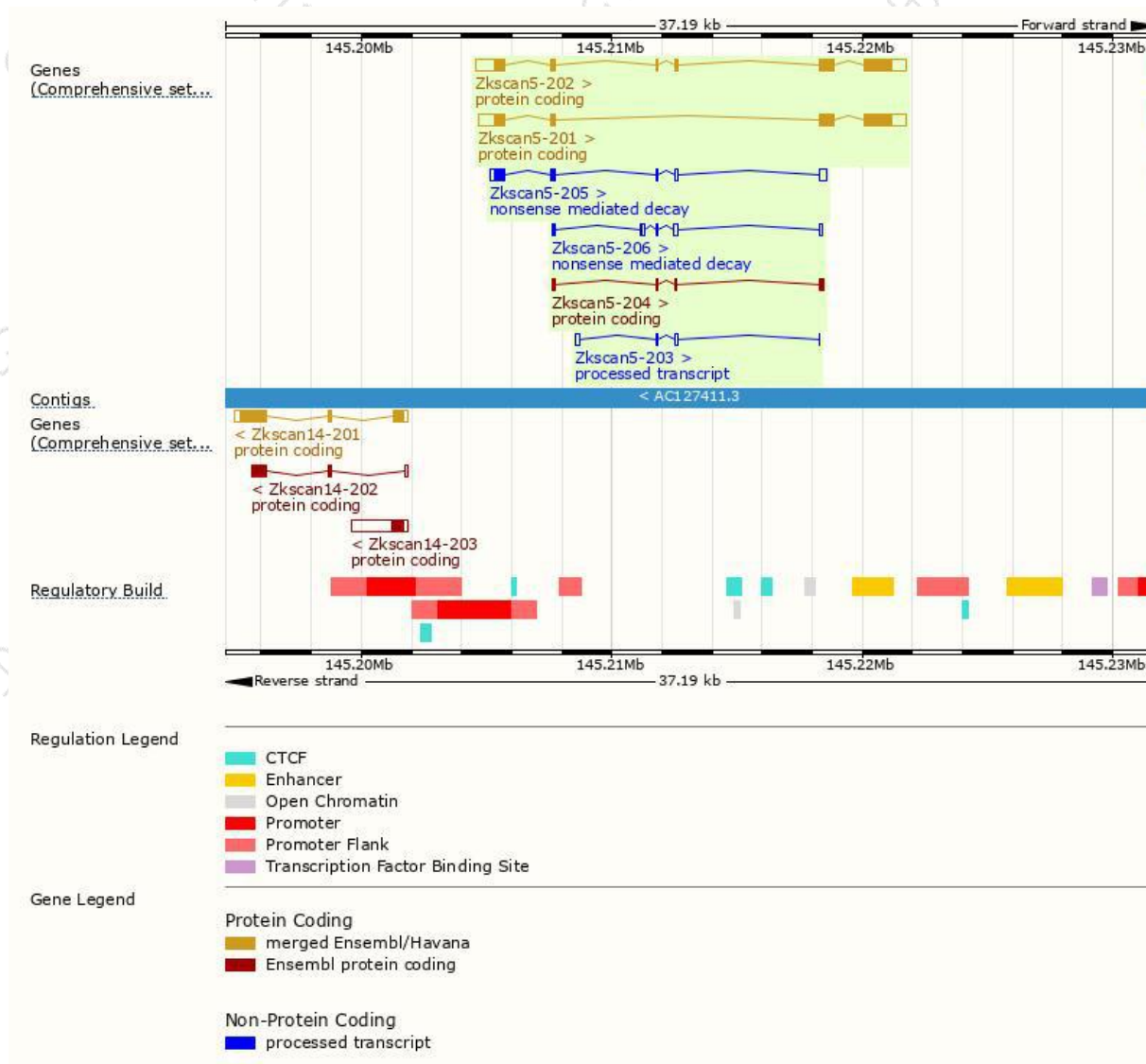
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zkscan5-202	ENSMUST00000085671.9	3794	819aa	Protein coding	CCDS39386	Q9Z1D8	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 P3
Zkscan5-201	ENSMUST00000031601.7	3469	746aa	Protein coding	CCDS51697	Q6PAK4	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
Zkscan5-204	ENSMUST00000161881.1	443	148aa	Protein coding	-	F6SSC9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Zkscan5-205	ENSMUST00000161896.1	1227	219aa	Nonsense mediated decay	-	E0CX87	TSL:3
Zkscan5-206	ENSMUST00000162168.7	622	52aa	Nonsense mediated decay	-	F6TRS7	CDS 5' incomplete TSL:3
Zkscan5-203	ENSMUST00000160162.1	378	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Zkscan5-202* 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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