

***Zscan10* Cas9-KO Strategy**

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Reviewer:

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Design Date:

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Project Overview

Project Name

Zscan10

Project type

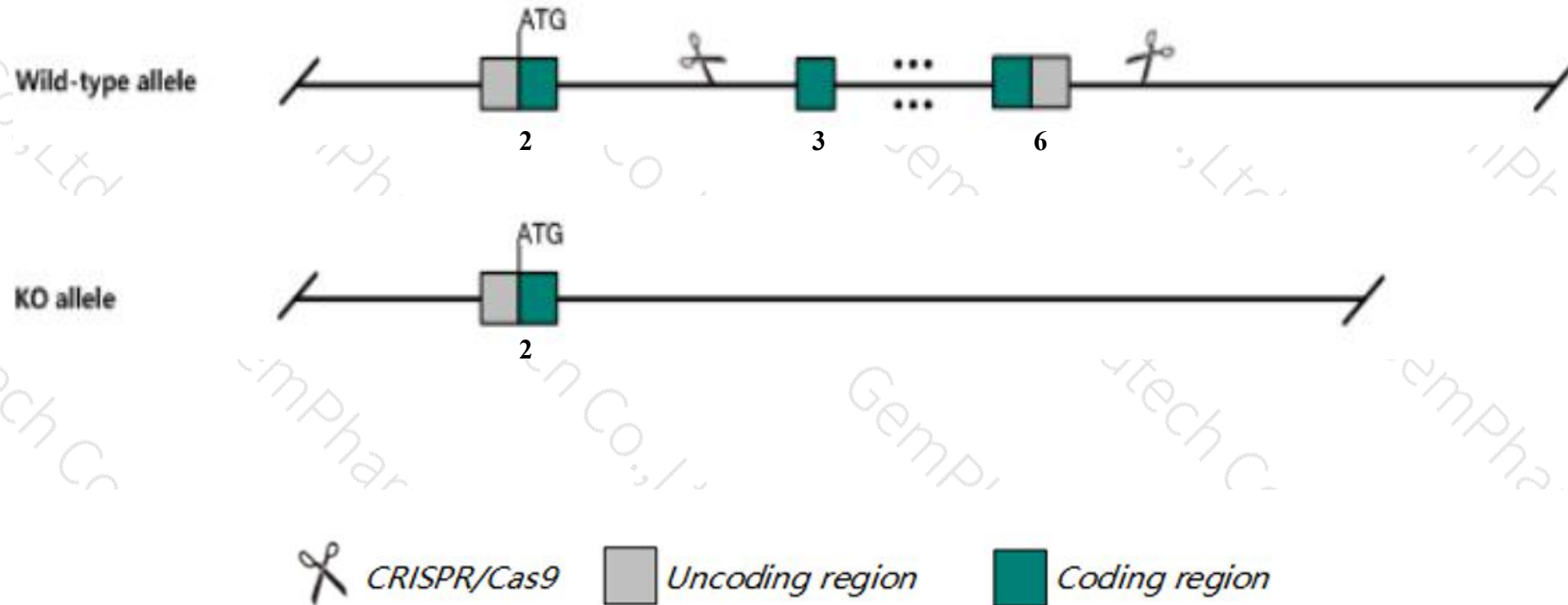
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zscan10* gene. The schematic diagram is as follows:



- The *Zscan10* gene has 12 transcripts. According to the structure of *Zscan10* gene, exon3-exon6 of *Zscan10-201* (ENSMUST00000095595.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zscan10* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit a pleiotropic phenotype including reduced weight, mild hypoplasia in the spleen, heart and long bones, eye malformations including microphthalmia, altered platelet counts, an activated immune status, and behavioral alterations.
- The *Zscan10* gene is located on the Chr17. 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)

Zscan10 zinc finger and SCAN domain containing 10 [*Mus musculus* (house mouse)]

Gene ID: 332221, updated on 10-Oct-2019

Summary

- Official Symbol** Zscan10 provided by [MGI](#)
- Official Full Name** zinc finger and SCAN domain containing 10 provided by [MGI](#)
- Primary source** [MGI:MG1:3040700](#)
- See related** [Ensembl:ENSMUSG00000023902](#)
- 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** Zfp206; Znf206; BC068284; Zkscan10
- Expression** Biased expression in testis adult (RPKM 1.9), cerebellum adult (RPKM 0.3) and 4 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

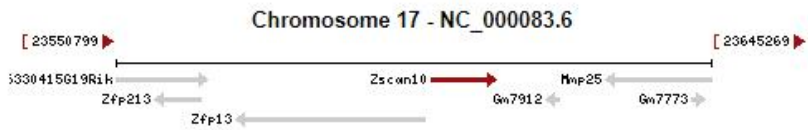
Genomic context

Location: 17; 17 A3.3

See Zscan10 in [Genome Data Viewer](#)

Exon count: 7

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (23600826..23611019)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (23737823..23747986)

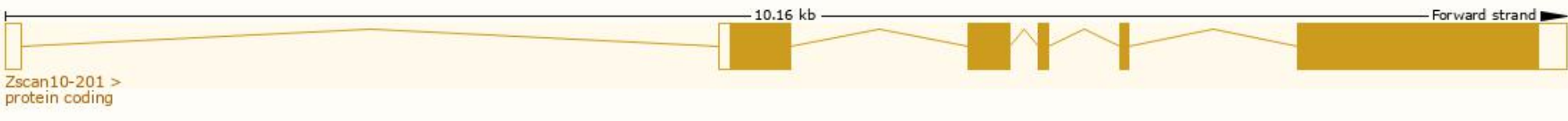


Transcript information (Ensembl)

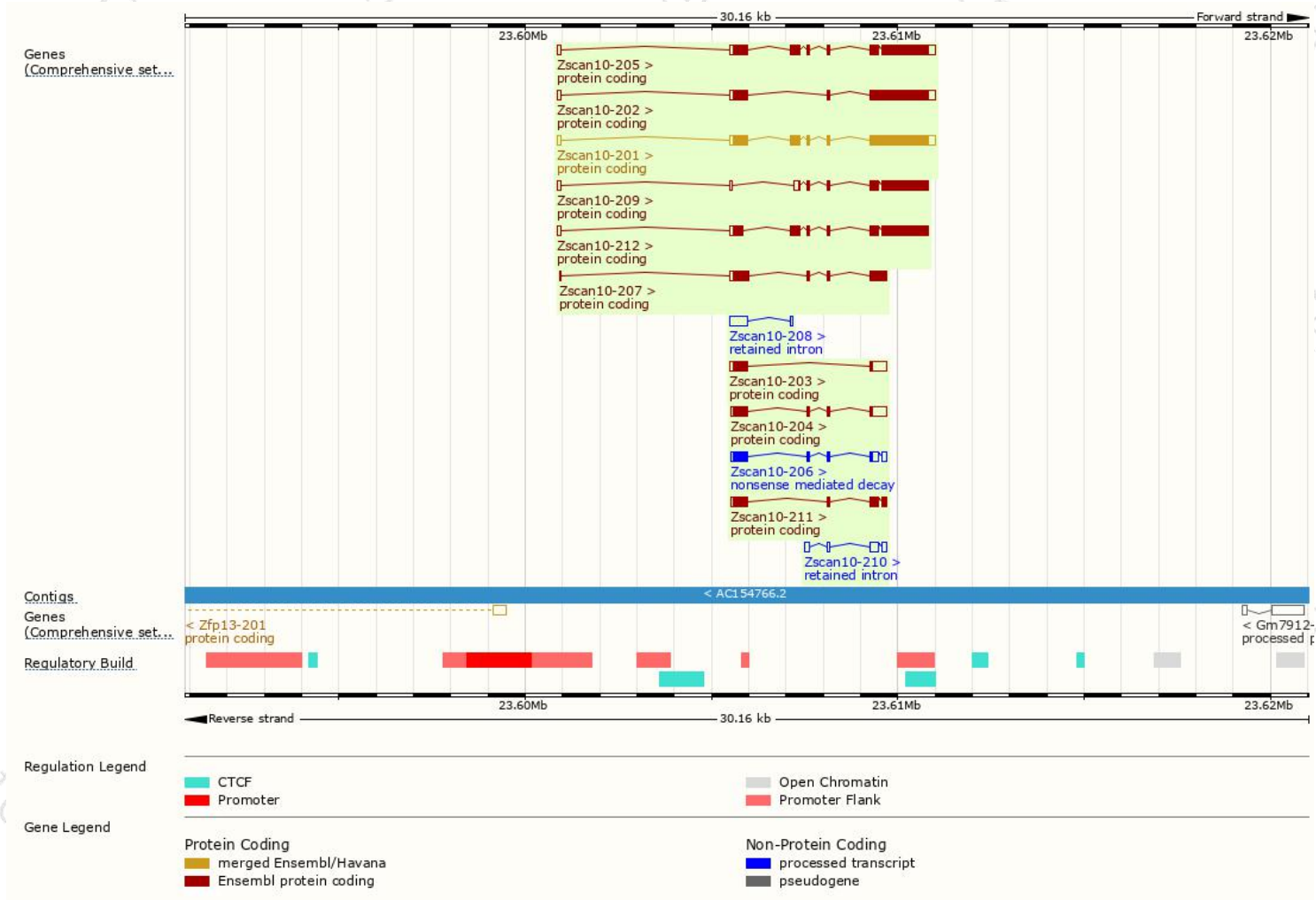
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zscan10-201	ENSMUST00000095595.8	2698	782aa	Protein coding	CCDS28451	Q3URR7	TSL:1 GENCODE basic APPRIS P3
Zscan10-205	ENSMUST00000120967.7	2609	750aa	Protein coding	CCDS70766	Q3URR7	TSL:1 GENCODE basic
Zscan10-202	ENSMUST00000115509.7	2368	672aa	Protein coding	CCDS79510	Q3URR7	TSL:1 GENCODE basic APPRIS ALT2
Zscan10-212	ENSMUST00000148062.7	2271	702aa	Protein coding	-	E9PXB1	CDS 3' incomplete TSL:1
Zscan10-209	ENSMUST00000129227.7	1902	543aa	Protein coding	-	E9PV84	CDS 3' incomplete TSL:1
Zscan10-207	ENSMUST00000123866.7	1074	329aa	Protein coding	-	D3Z3Z6	CDS 3' incomplete TSL:1
Zscan10-204	ENSMUST00000118369.1	1006	190aa	Protein coding	-	E9PX93	TSL:1 GENCODE basic
Zscan10-203	ENSMUST00000117606.1	891	149aa	Protein coding	-	D3YWR9	TSL:1 GENCODE basic
Zscan10-211	ENSMUST00000138487.1	844	262aa	Protein coding	-	D3YVM1	CDS 3' incomplete TSL:1
Zscan10-206	ENSMUST00000122285.7	909	190aa	Nonsense mediated decay	-	E9PX93	TSL:1
Zscan10-210	ENSMUST00000133749.1	548	No protein	Retained intron	-	-	TSL:2
Zscan10-208	ENSMUST00000125912.1	531	No protein	Retained intron	-	-	TSL:3

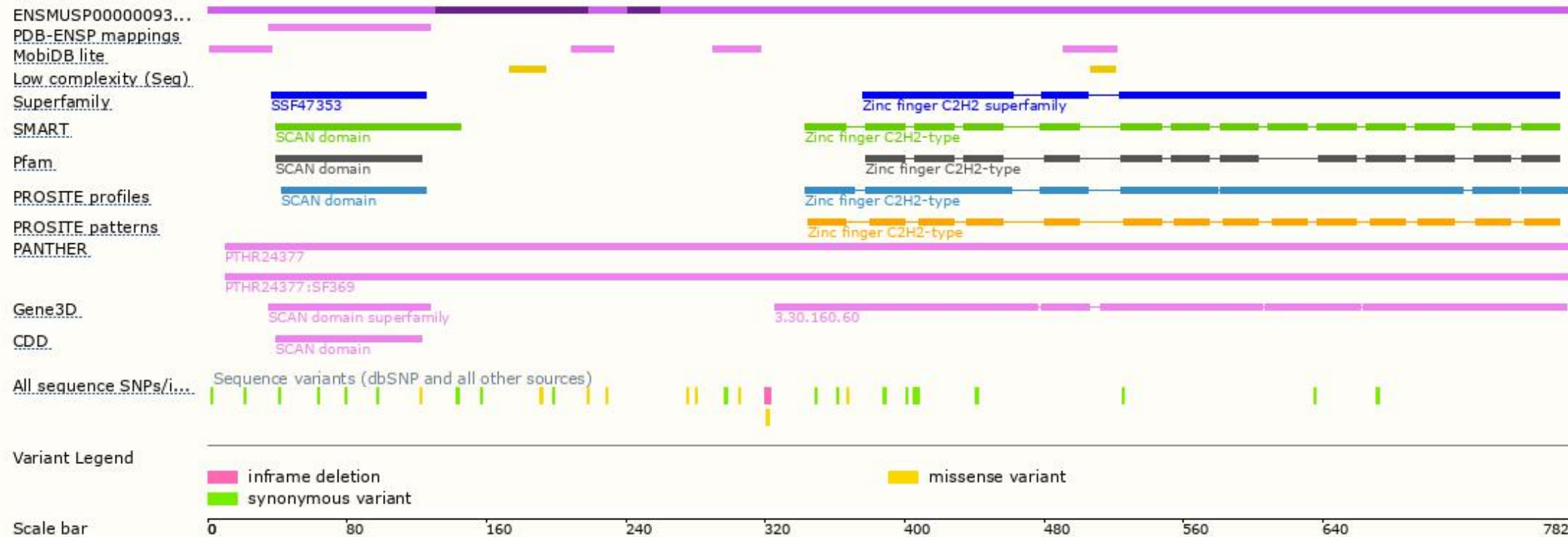
The strategy is based on the design of *Zscan10-201* transcript, the transcription is shown below



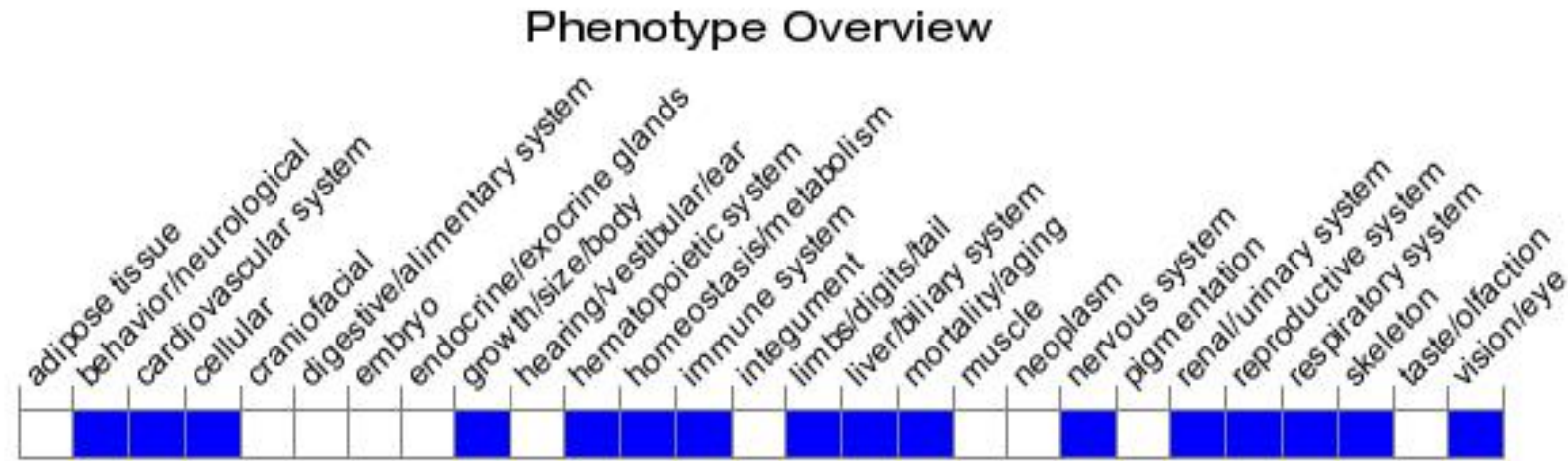
Genomic location distribution



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, mice homozygous for a gene trap allele exhibit a pleiotropic phenotype including reduced weight, mild hypoplasia in the spleen, heart and long bones, eye malformations including microphthalmia, altered platelet counts, an activated immune status, and behavioral alterations.

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

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