

***Zscan21* Cas9-KO Strategy**

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Date: 2020-02-07

Project Overview

Project Name

Zscan21

Project type

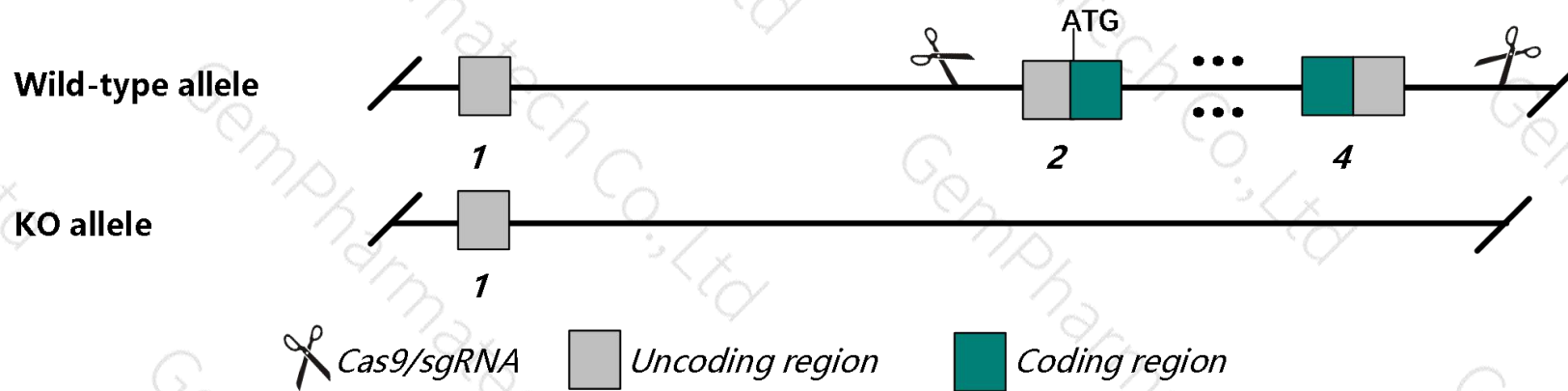
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zscan21* gene. The schematic diagram is as follows:



- The *Zscan21* gene has 7 transcripts. According to the structure of *Zscan21* gene, exon2-exon4 of *Zscan21*-203 (ENSMUST00000110959.1) transcript is recommended as the knockout region. The region contains all 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 *Zscan21* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a targeted null mutation appear to be phenotypically normal.
- The *Zscan21* 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)

Zscan21 zinc finger and SCAN domain containing 21 [*Mus musculus* (house mouse)]

Gene ID: 22697, updated on 12-Aug-2019

Summary

Official Symbol Zscan21 provided by [MGI](#)
Official Full Name zinc finger and SCAN domain containing 21 provided by [MGI](#)
Primary source [MGI:MGI:99182](#)
See related [Ensembl:ENSMUSG00000037017](#)
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 RU49; Zfp38; Zfp-38; Zipro1; CTfin51; AI326272
Expression Broad expression in CNS E11.5 (RPKM 21.4), CNS E14 (RPKM 21.2) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 5 G2; 5 76.96 cM

See Zscan21 in [Genome Data Viewer](#)

Exon count: 6

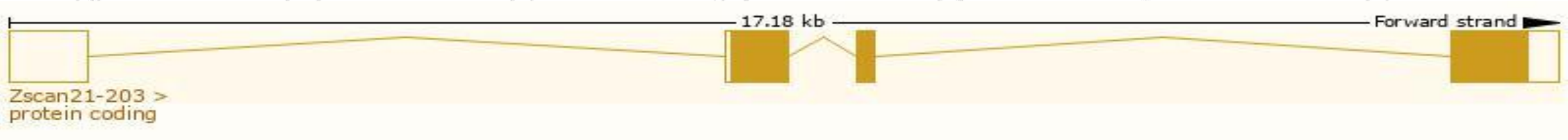
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (138116899..138134265)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (138558133..138575489)

Transcript information (Ensembl)

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zscan21-203	ENSMUST00000110959.1	2964	555aa	Protein coding	CCDS19790	Q07231	TSL:1 GENCODE basic APPRIS P1
Zscan21-205	ENSMUST00000110961.8	2310	555aa	Protein coding	CCDS19790	Q07231	TSL:1 GENCODE basic APPRIS P1
Zscan21-201	ENSMUST00000062350.14	2252	555aa	Protein coding	CCDS19790	Q07231	TSL:1 GENCODE basic APPRIS P1
Zscan21-204	ENSMUST00000110960.8	2204	555aa	Protein coding	CCDS19790	Q07231	TSL:1 GENCODE basic APPRIS P1
Zscan21-202	ENSMUST00000080732.9	2134	555aa	Protein coding	CCDS19790	Q07231	TSL:1 GENCODE basic APPRIS P1
Zscan21-206	ENSMUST00000136425.1	754	160aa	Protein coding	-	D3Z1X7	CDS 3' incomplete TSL:5
Zscan21-207	ENSMUST00000142185.7	496	166aa	Protein coding	-	F6QX94	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5

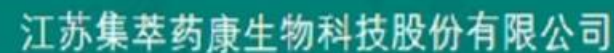
The strategy is based on the design of *Zscan21-203* transcript,The transcription is shown below



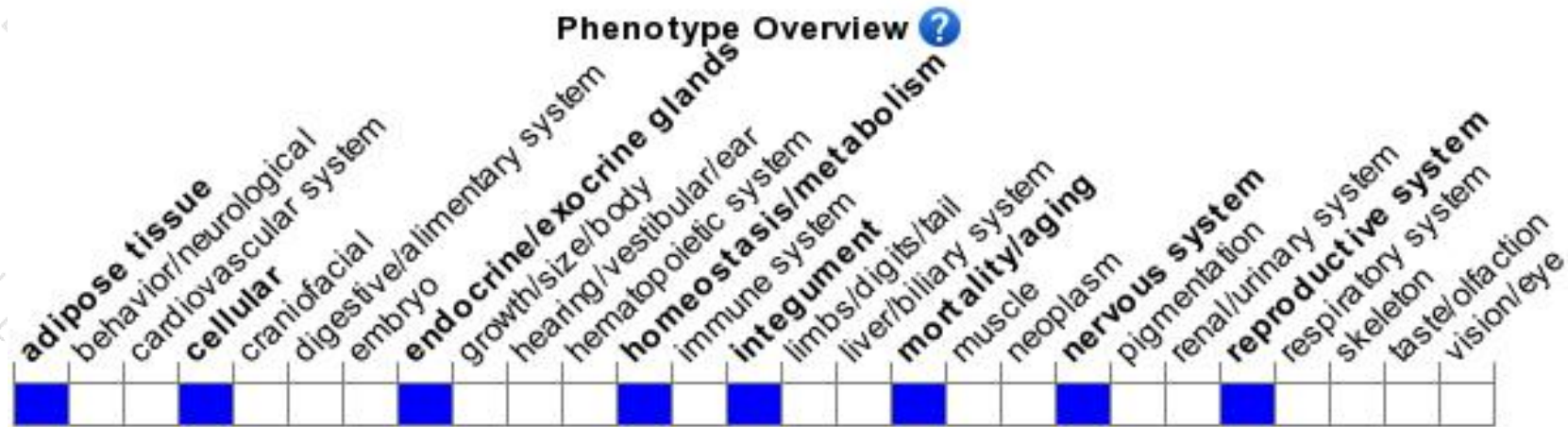
Genomic location distribution



集萃药康
GemPharmatech



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, Homozygotes for a targeted null mutation appear to be phenotypically normal.

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

Tel: 400-9660890

