

Zfp143 Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

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Project Overview

Project Name

Zfp143

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp143* gene. The schematic diagram is as follows:



- The *Zfp143* gene has 5 transcripts. According to the structure of *Zfp143* gene, exon3-exon8 of *Zfp143-204* (ENSMUST00000209505.1) transcript is recommended as the knockout region. The region contains 650bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp143* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous disruption of this locus results in fertility defects.
- The *Zfp143* gene is located on the Chr7. 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)

Zfp143 zinc finger protein 143 [Mus musculus (house mouse)]

Gene ID: 20841, updated on 31-Jan-2019

Summary



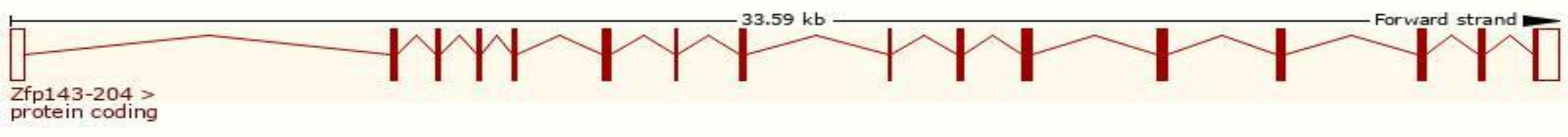
Official Symbol	Zfp143 provided by MGI
Official Full Name	zinc finger protein 143 provided by MGI
Primary source	MGI:MGI:1277969
See related	Ensembl:ENSMUSG00000061079
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA959806, AU015869, D7Ert805e, KRAB14, SBF, Staf, Zfp79, Zfp80-rs1, Znf143, pHZ-1
Expression	Ubiquitous expression in thymus adult (RPKM 6.7), CNS E11.5 (RPKM 6.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

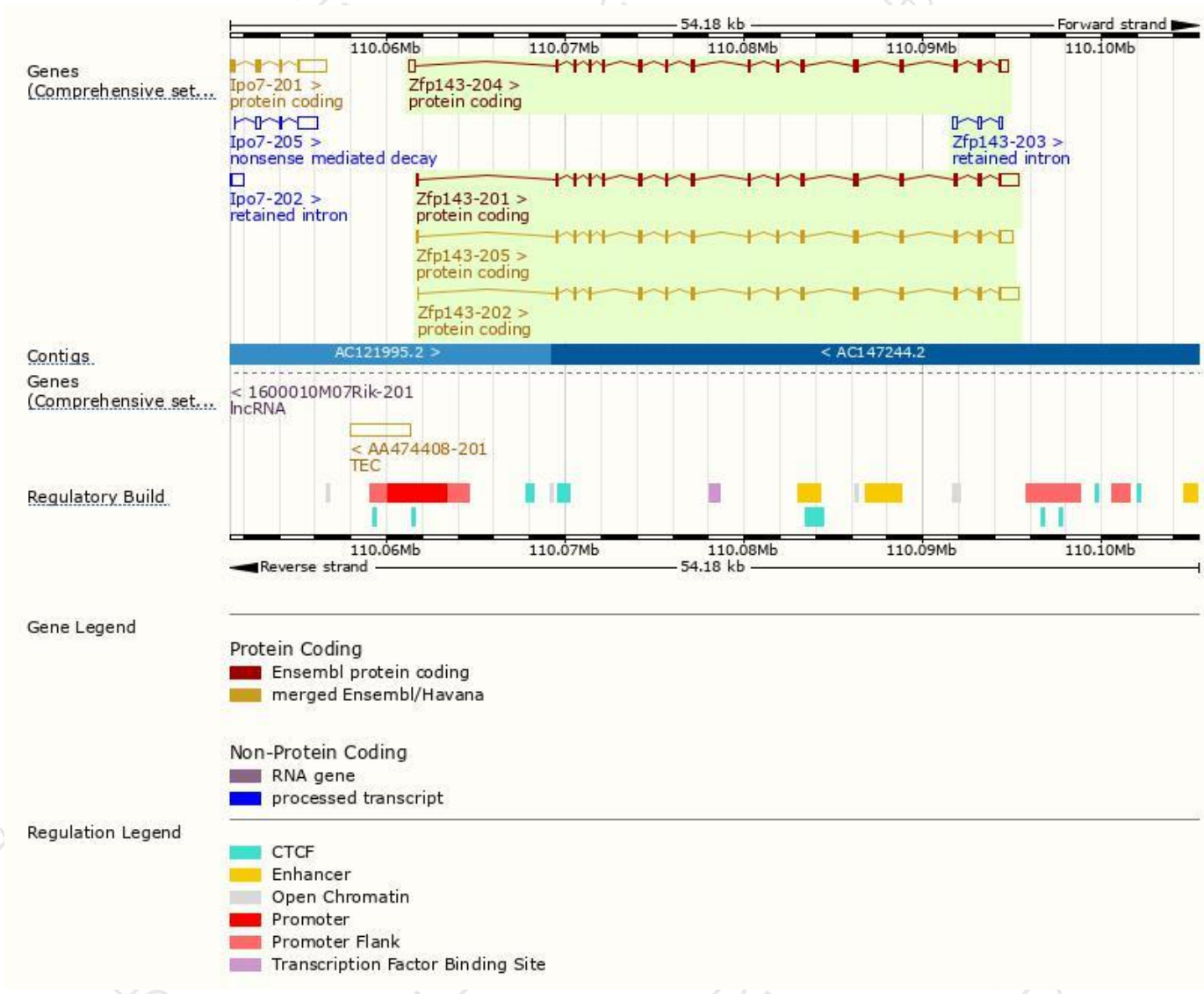
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp143-204	ENSMUST00000209505.1	2693	637aa	Protein coding	CCDS57580	O70230	TSL:1 GENCODE basic APPRIS P2
Zfp143-205	ENSMUST00000211798.1	2631	637aa	Protein coding	CCDS57580	O70230	TSL:1 GENCODE basic APPRIS P2
Zfp143-201	ENSMUST00000084727.10	3003	638aa	Protein coding	-	O70230	TSL:1 GENCODE basic APPRIS ALT1
Zfp143-202	ENSMUST00000169638.3	2914	610aa	Protein coding	-	O70230	TSL:1 GENCODE basic
Zfp143-203	ENSMUST00000209252.1	599	No protein	Retained intron	-	-	TSL:2

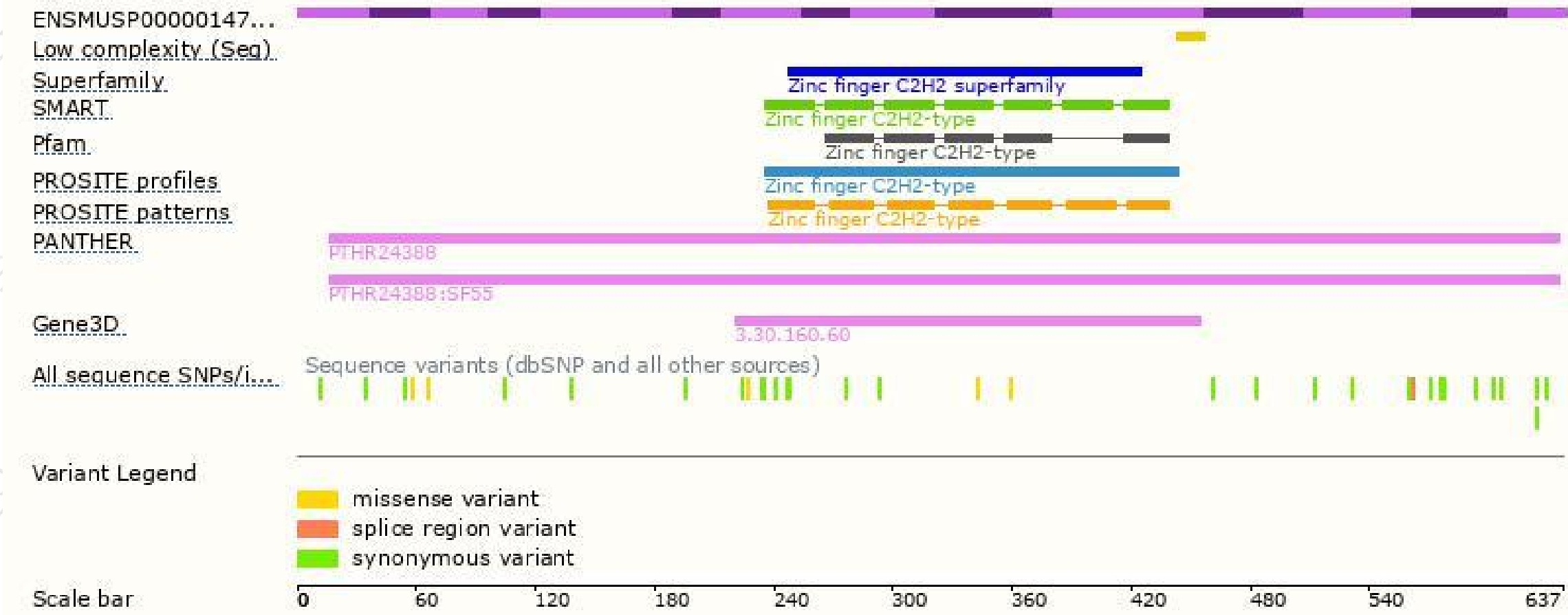
The strategy is based on the design of *Zfp143-204* transcript,The transcription is shown below



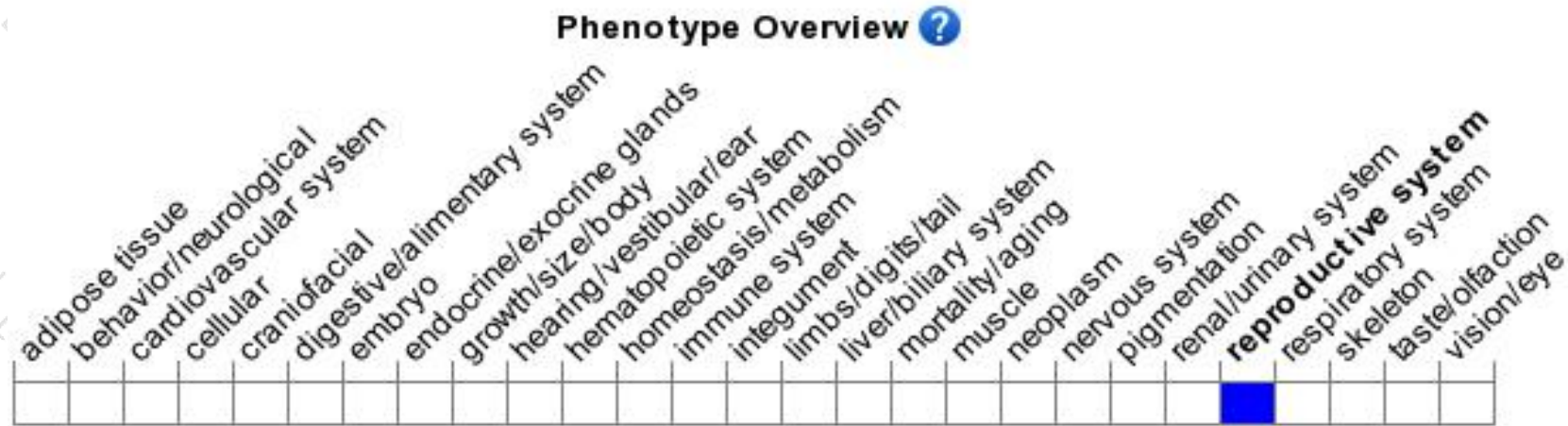
Genomic location distribution



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, Homozygous disruption of this locus results in fertility defects.

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

Tel: 400-9660890

