

***Zfp105* Cas9-KO Strategy**

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Project Overview

Project Name

Zfp105

Project type

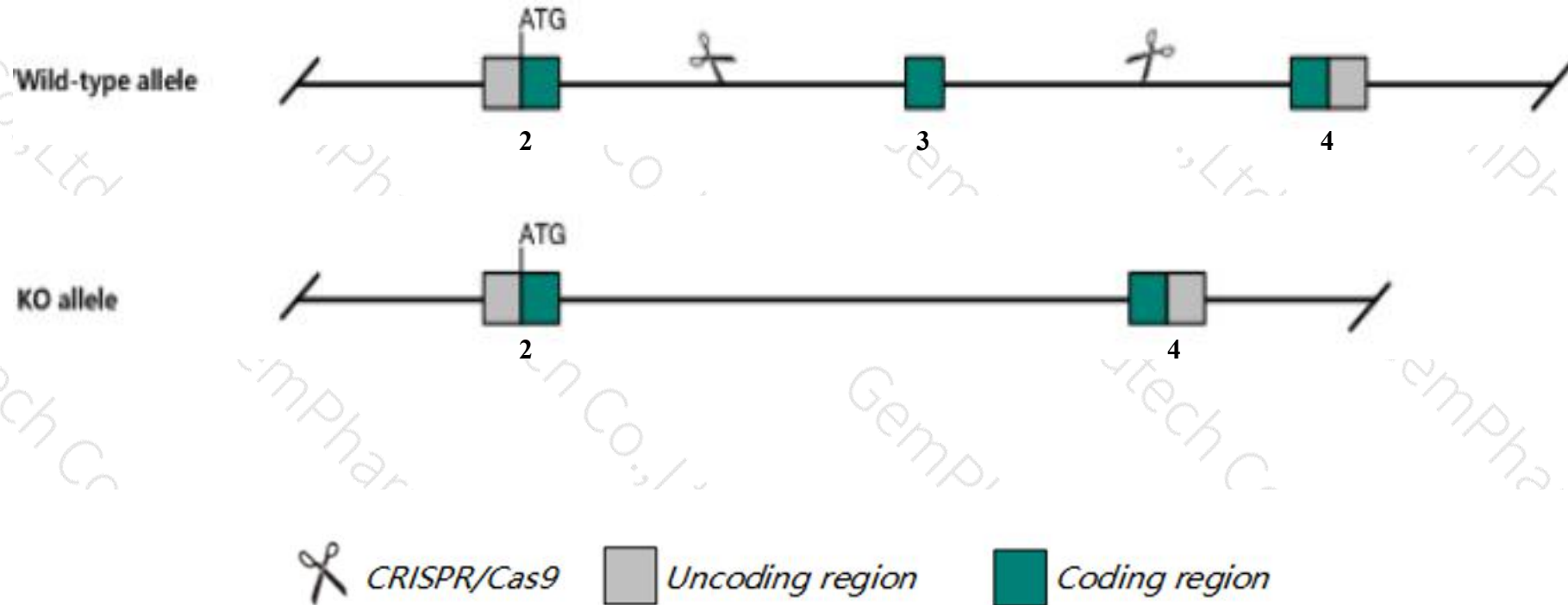
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp105* gene. The schematic diagram is as follows:



- The *Zfp105* gene has 2 transcripts. According to the structure of *Zfp105* gene, exon3 of *Zfp105*-201(ENSMUST00000051667.13) transcript is recommended as the knockout region. The region contains 145bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp105* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a gene trapped allele display abnormal spermatogenesis and reduced male fertility.
- The *Zfp105* gene is located on the Chr9. 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)

Zfp105 zinc finger protein 105 [Mus musculus (house mouse)]

Gene ID: 22646, updated on 13-Mar-2020

Summary



Official Symbol Zfp105 provided by [MGI](#)

Official Full Name zinc finger protein 105 provided by [MGI](#)

Primary source [MGI:MGI:1277119](#)

See related [Ensembl:ENSMUSG00000057895](#)

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 AW557864

Expression Broad expression in testis adult (RPKM 7.2), CNS E11.5 (RPKM 6.8) and 16 other tissues [See more](#)

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

Transcript information (Ensembl)

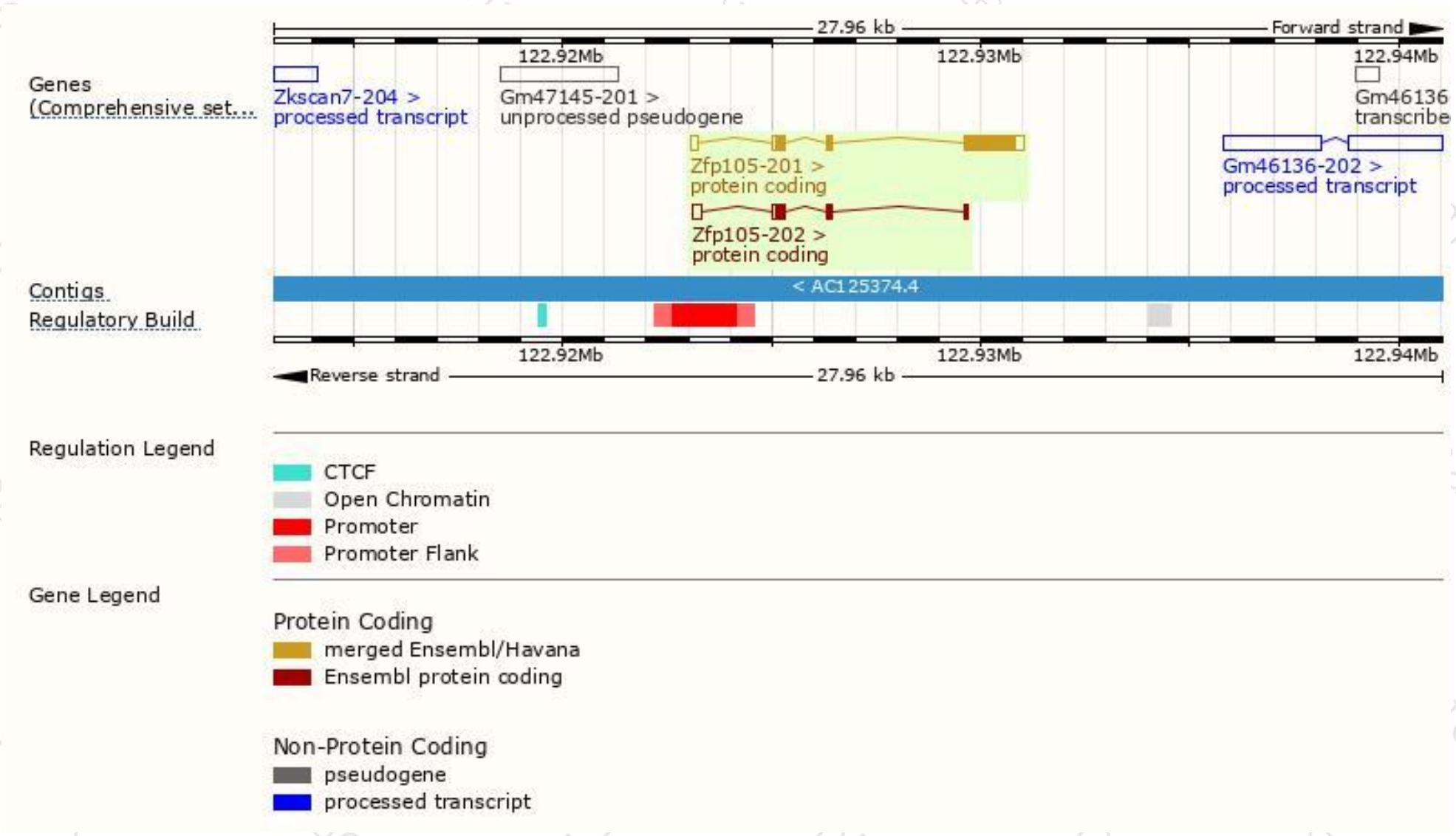
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp105-201	ENSMUST00000051667.13	2010	524aa	Protein coding	CCDS23649	G3X9I0	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 P1
Zfp105-202	ENSMUST00000148851.1	753	137aa	Protein coding	-	D3Z140	CDS 3' incomplete TSL:3

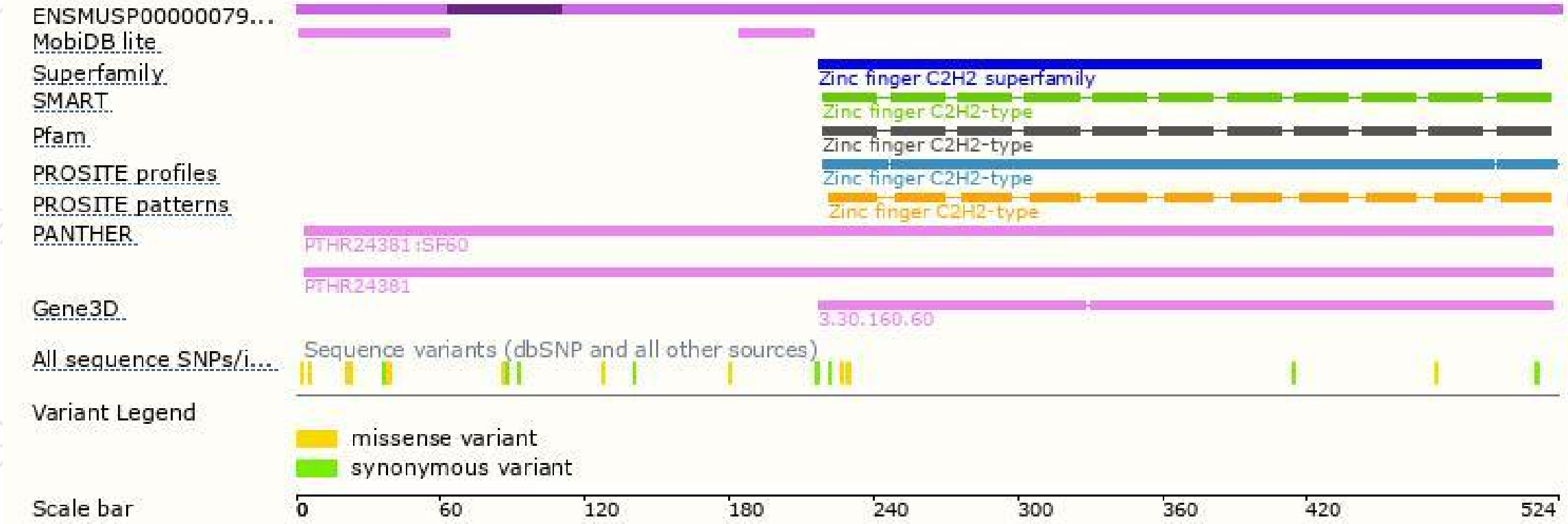
The strategy is based on the design of *Zfp105-201* transcript,the transcription is shown below:



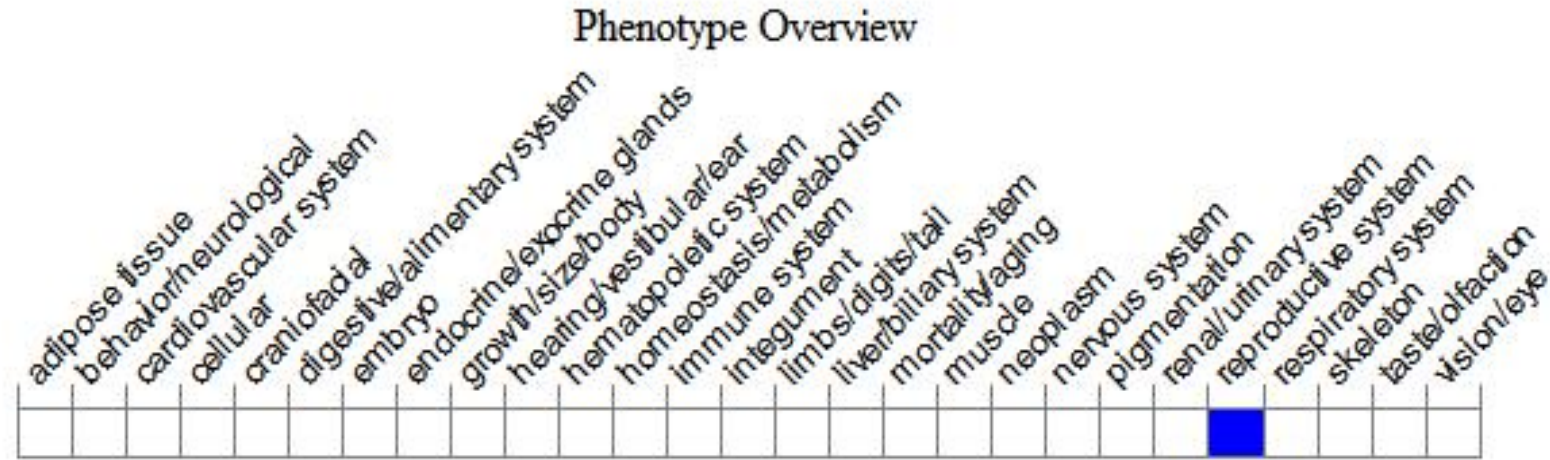
Genomic location distribution



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 trapped allele display abnormal spermatogenesis and reduced male fertility.

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

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