Zfp105 Cas9-CKO Strategy

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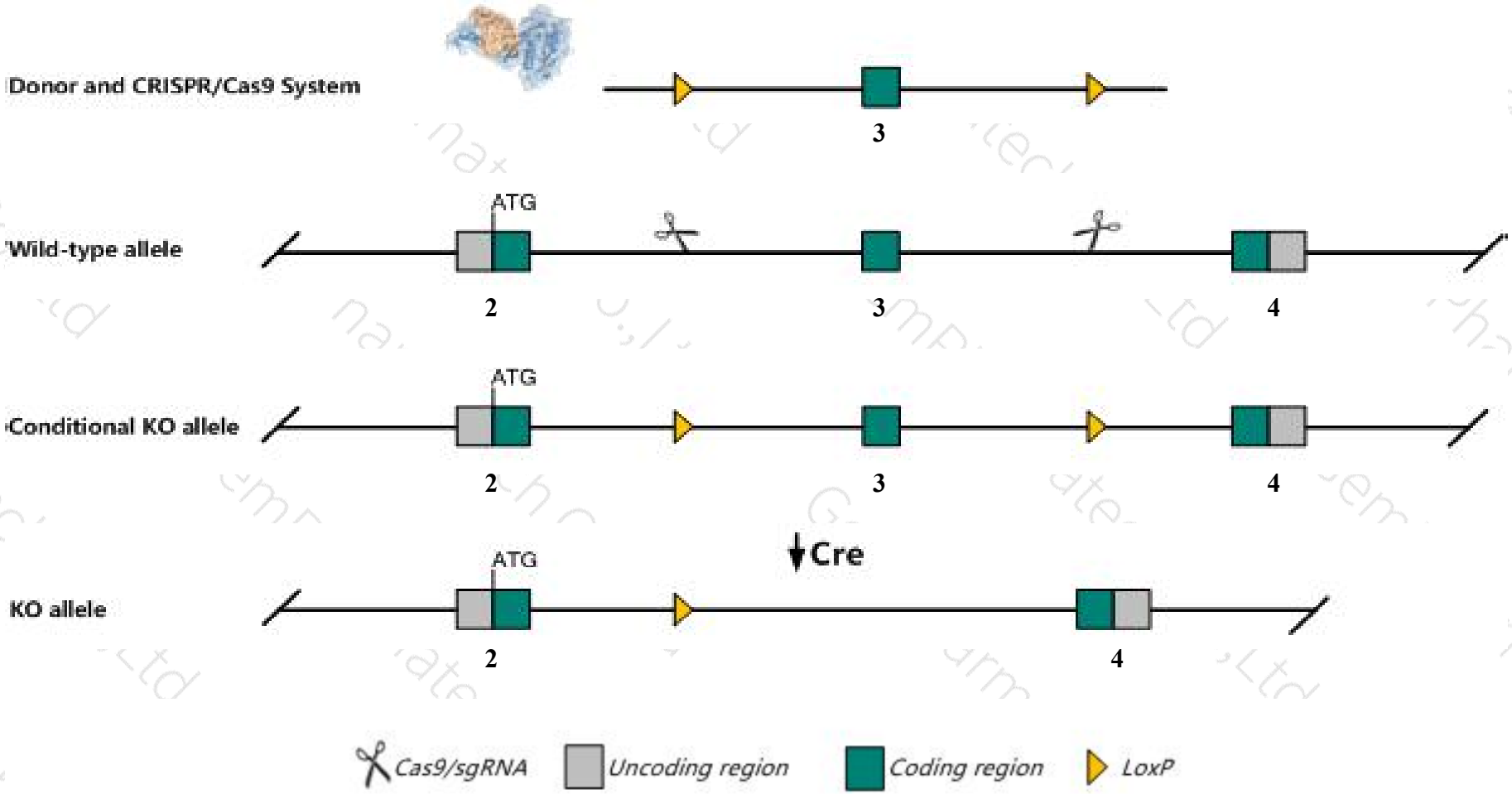
Project Overview

Project Name	***Zfp105***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

➢ 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: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.

Notice

➢ 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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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 byMGI
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 tissuesSee more
Orthologs	human all

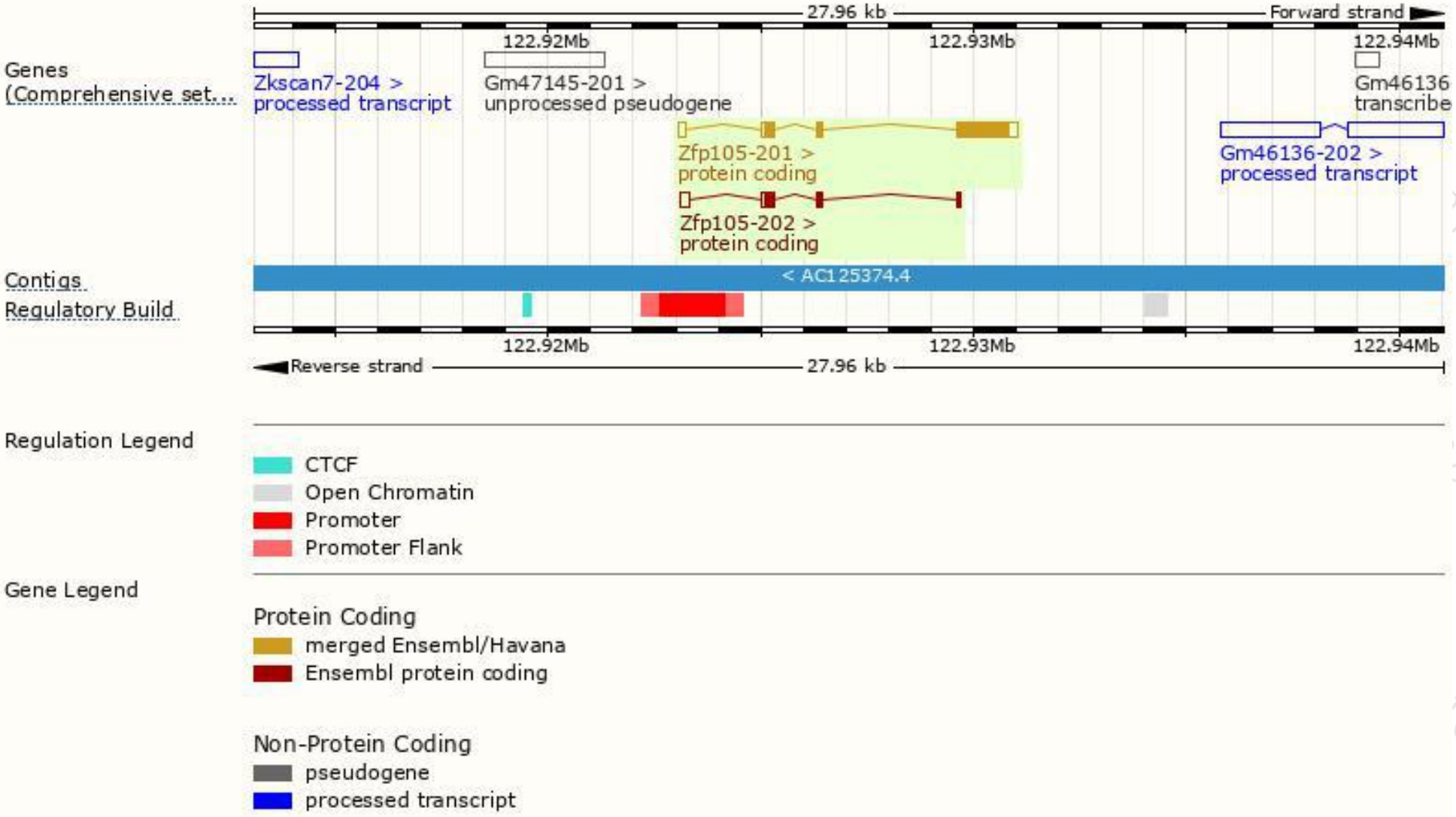
Transcript information（Ensembl）

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

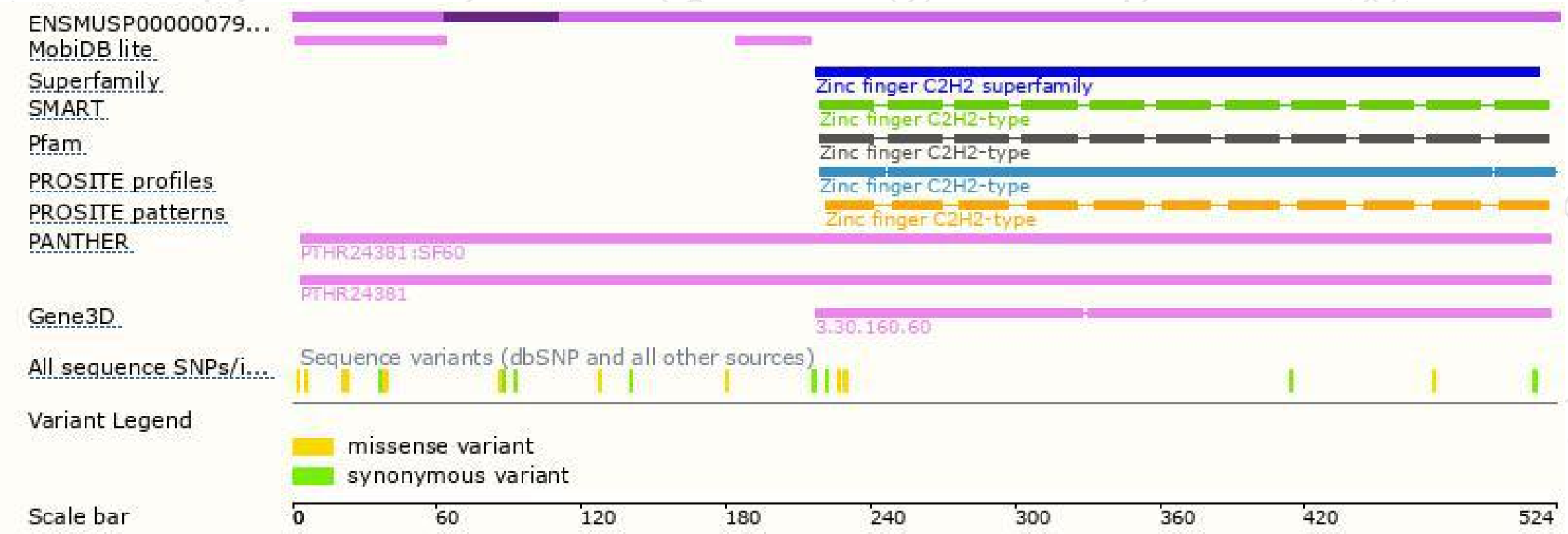
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp105-201	ENSMUST00000051667.13	2010	524aa	Protein coding	CCDS23649	G3X9I0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important 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:

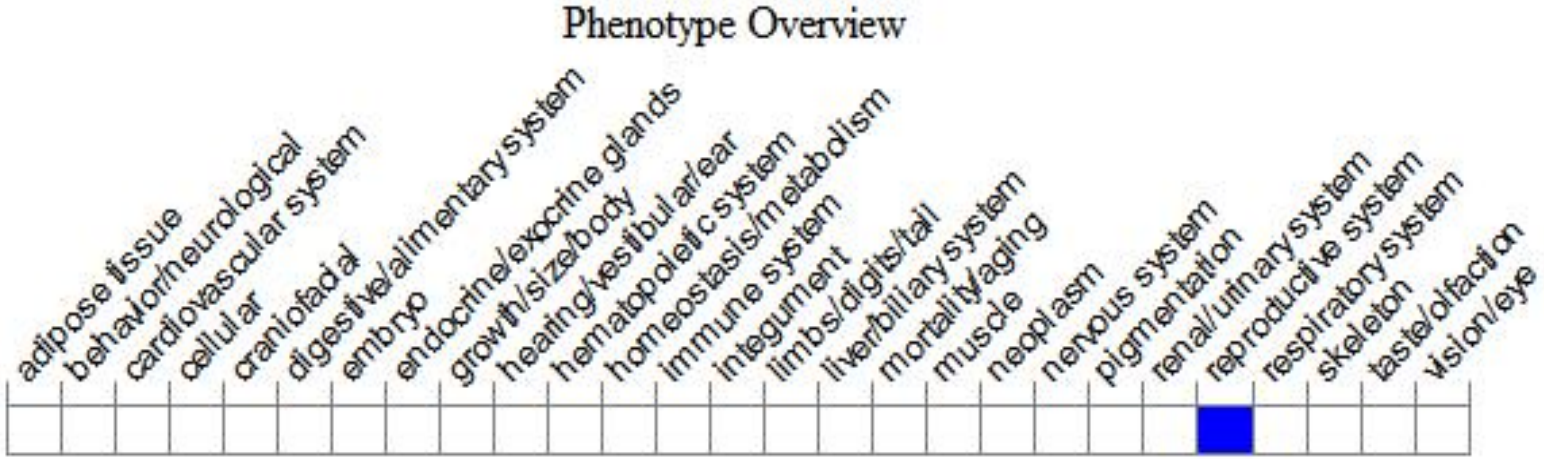
Genomic location distribution



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/).

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

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