

Zfp526 Cas9-CKO Strategy

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Overview

Target Gene Name

- *Zfp526*

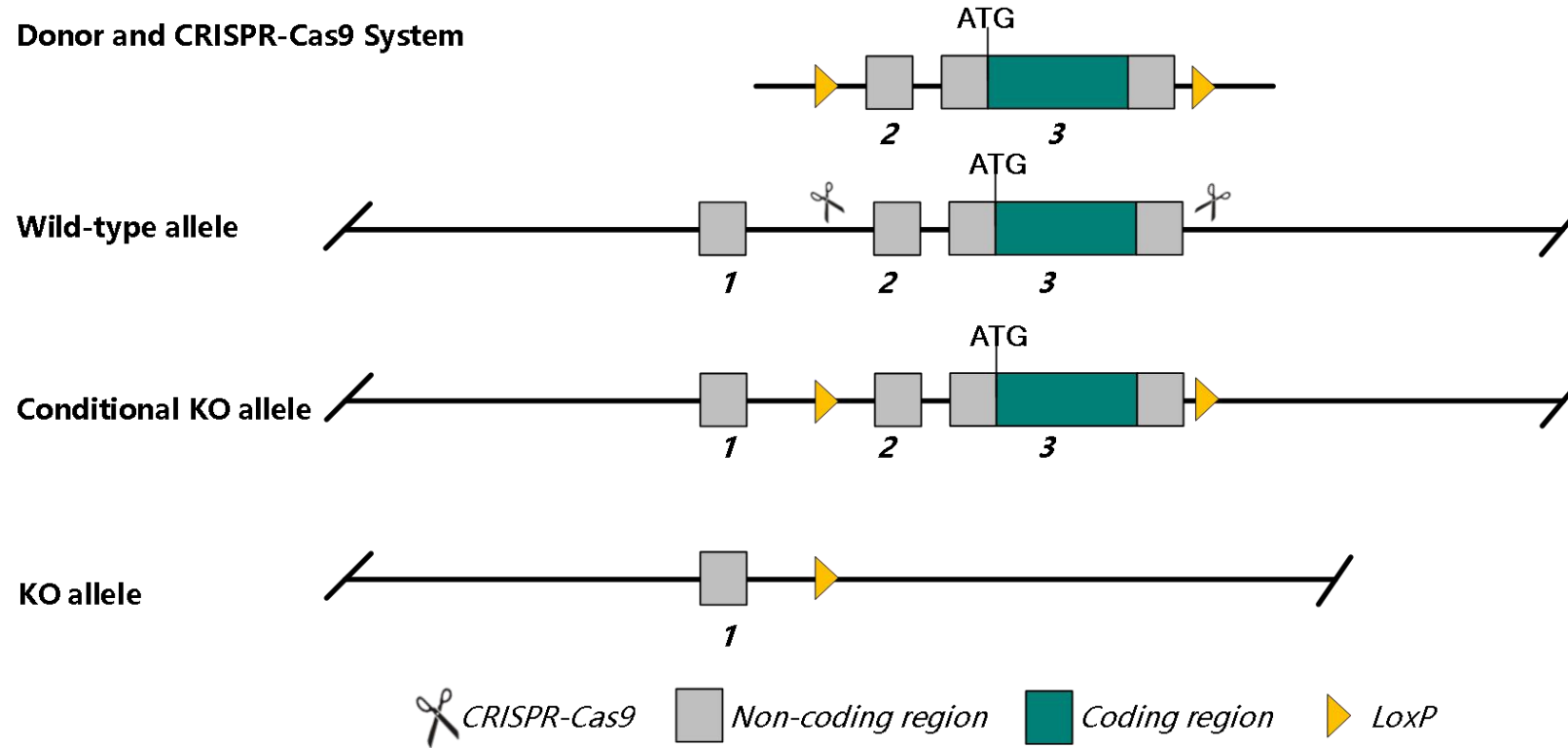
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Zfp526* gene.

Technical Information

- The *Zfp526* gene has 1 transcript. According to the structure of *Zfp526* gene, exon 2-3 of *Zfp526*-201 (ENSMUST00000055604.6) is recommended as the knockout region. The region contains all coding sequence and part of 5'UTR. Knocking out the region may result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Zfp526* gene. The brief process is as follows: CRISPR-Cas9 system 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be 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.

Gene Information

Zfp526 zinc finger protein 526 [*Mus musculus* (house mouse)]

Gene ID: 210172, updated on 5-Mar-2024

[Download Datasets](#)

Summary

| | |
|---------------------------|--|
| Official Symbol | Zfp526 provided by MGI |
| Official Full Name | zinc finger protein 526 provided by MGI |
| Primary source | MGI:MGI:2445181 |
| See related | Ensembl:ENSMUSG00000046541 AllianceGenome:MGI:2445181 |
| 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 | Znf526; D030024H03Rik |
| Summary | Predicted to enable DNA-binding transcription factor activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Predicted to be involved in regulation of transcription by RNA polymerase II. Predicted to be active in nucleus. Is expressed in genitourinary system. Orthologous to human ZNF526 (zinc finger protein 526). [provided by Alliance of Genome Resources, Apr 2022] |
| Expression | Ubiquitous expression in testis adult (RPKM 12.7), thymus adult (RPKM 11.5) and 28 other tissues See more |
| Orthologs | human all |
| NEW | Try the new Gene table Try the new Transcript table |

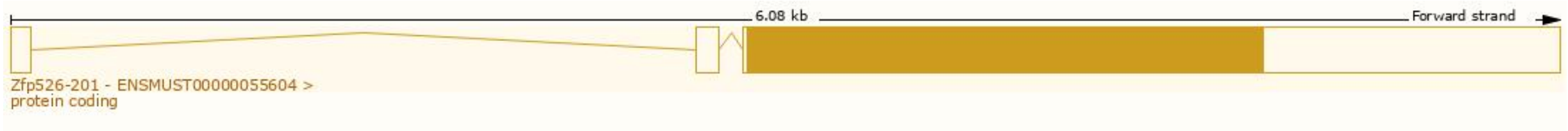
<https://www.ncbi.nlm.nih.gov/gene/210172>

Transcript Information

The gene has 1 transcript, the transcript are shown below:

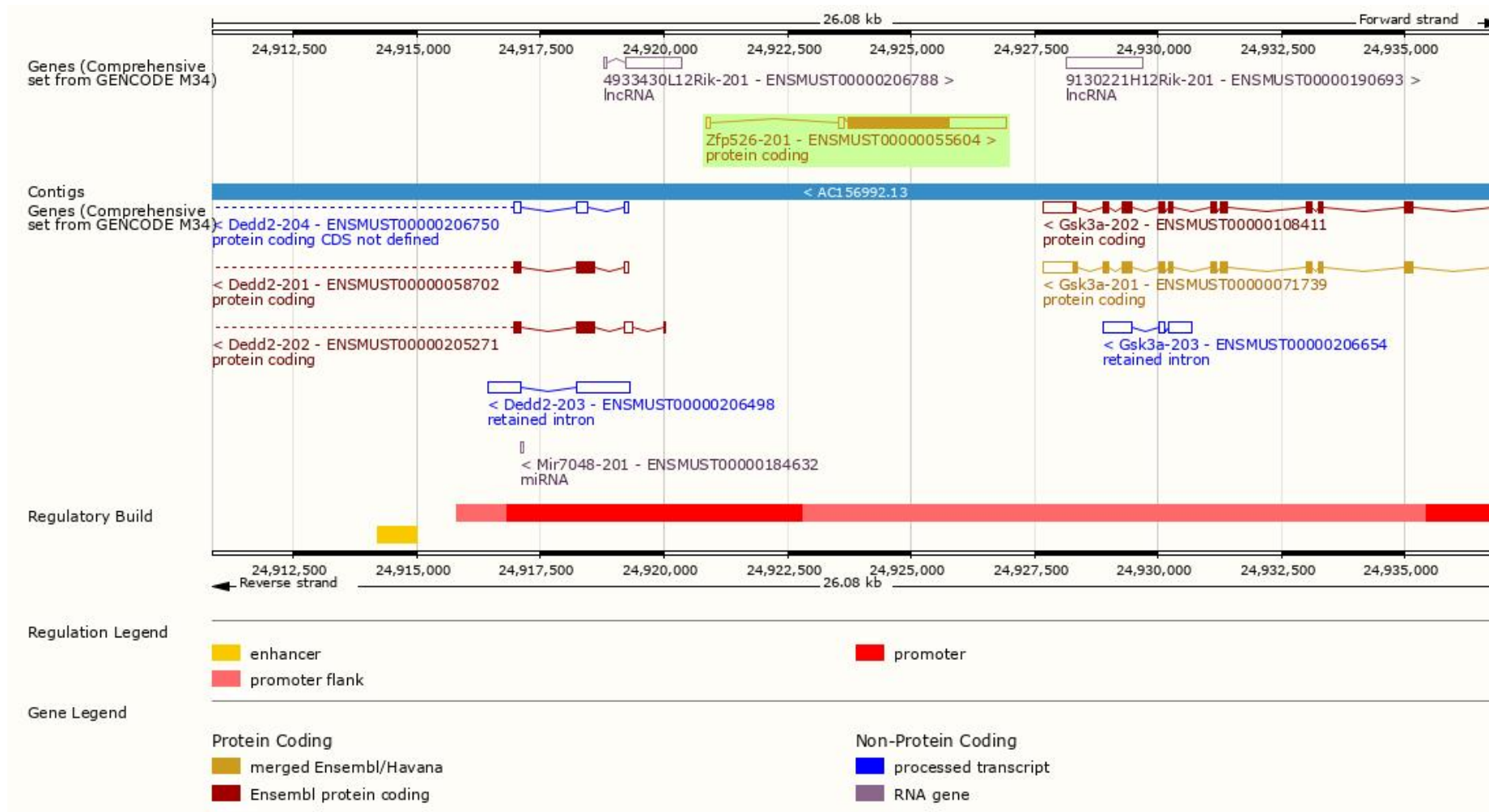
| Show/hide columns (1 hidden) | | | | | | | Filter | |
|--------------------------------------|------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------|-------------------------------|
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags | |
| ENSMUST00000055604.6 | Zfp526-201 | 3380 | 675aa | Protein coding | CCDS20975 | Q8BI66 | Ensembl Canonical | GENCODE basic APPRIS P1 TSL:1 |

The strategy is based on the design of *Zfp526-201* transcript, the transcription is shown below:

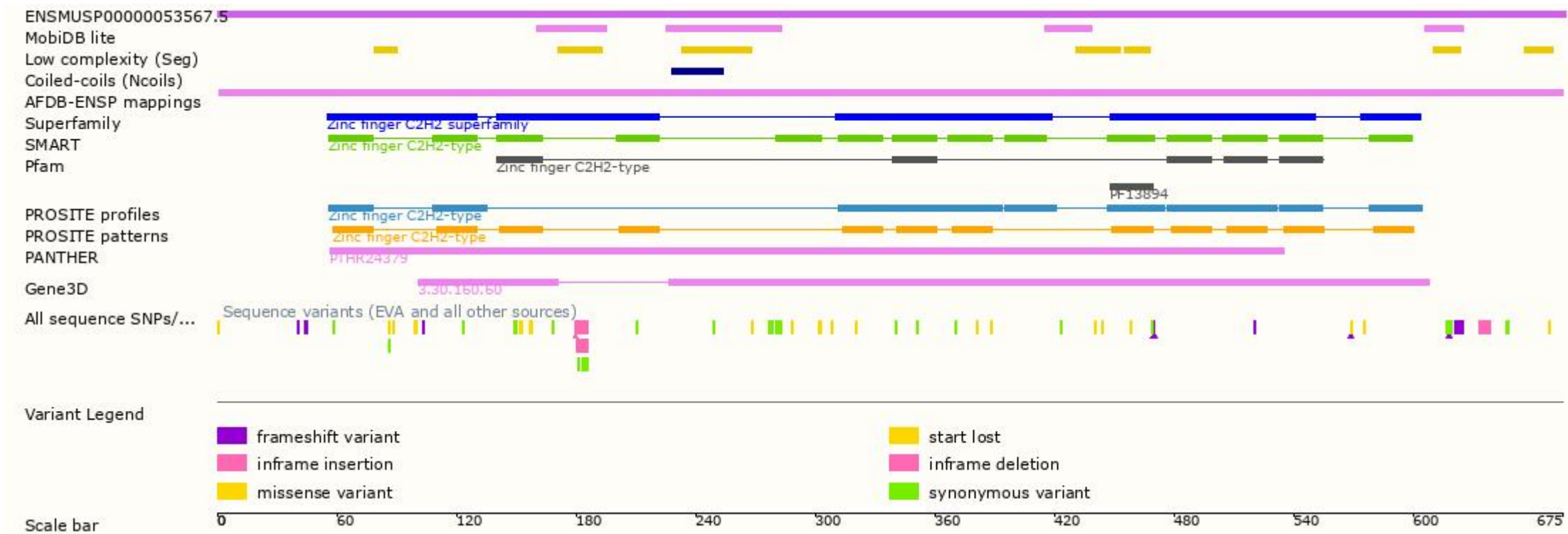


Source: <http://asia.ensembl.org/>

Genomic Information



Protein Information



Important Information

- The loxp site is inserted in intron1-2, which may disrupt the 5' regulation of *Zfp526*.
- The knockout region is about 3 kb away from the 5' of *Dedd2*, the risk is unknown.
- The knockout region is about 0.5 kb away from the 3' of *Gsk3a*, the risk is unknown.
- The knockout region is about 1 kb away from the 5' of *9130221H12Rik* and 2.5kb away from the 3' of *4933430L12Rik*, the risk is unknown.
- *Zfp526* is located on Chr 7. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.